Final Report **Project WFD72C**

River Invertebrate Classification Tool

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EXECUTIVE SUMMARY

WFD72C: River Invertebrate Classification Tool (June, 2008)

Project funders/partners: SNIFFER

Background to research

The Regulatory Agencies in the UK (the Environment Agency; Scottish Environment Protection Agency; and the Environment & Heritage Service) currently use RIVPACS III+ software to classify the ecological quality of rivers. However, because RIVPACS III+ pre-dates the WFD, there has been a requirement to ensure that the RIVPACS reference sites are fully WFD compliant, to add new biotic indices to the RIVPACS models, and to improve the robustness of the RIVPACS software to fully meet the needs of the Agencies in their delivery of WFD monitoring. These issues have been addressed in this project and have led to the development of new RIVPACS IV predictive models that will be programmed into a new River Invertebrate Classification Tool being built by SEPA. This new system will be based on a modern software programming language, be compatible with the agencies' computer systems and include the ability to predict new biological indices, produce biological status assessments based on these new indices and be able to estimate the errors involved in using these new indices. Because access to the new system will be essential for the UK Agencies to be able to implementation the WFD, the new tool will be readily and freely available to anyone who might seek to use it.

Objectives of research

- The overall objective of the project was to produce a new set of RIVPACS predictive models for use within a new River Invertebrate Classification Tool that will be used to classify the ecological status of rivers for Water Framework Directive compliance monitoring

- The new RIVPACS models constructed with this project required considerably enhanced functionality compared to RIVPACS III+ to properly address the monitoring requirements of the UK Agencies in their implementation of the Water Framework Directive.

Key findings and recommendations

This project has produced new RIVPACS IV models with considerably enhanced functionality compared to RIVPACS III+. These models incorporate:

- A full revision of the taxonomic framework of RIVPACS to bring the taxonomy up-to-date and enable compatibility across the revised Maitland, Furse code and National Biodiversity Network taxon coding systems used across the UK Agencies and beyond

- Predictions that fully satisfy the WFD definition of 'reference condition' by adjusting predictions for certain stream types and by removal of sites that were not in reference condition when sampled

- Allocation of actual abundance values to family level records in the RIVPACS reference data set. Lack of actual abundance data, especially at family level, has affected all versions of RIVPACS and has constrained the types of biotic indices that RIVPACS can predict

- Extension to the suite of biotic indices so that the new system can predict a wider range of reference state “expected” index values. This enables full WFD quality reporting capabilities as well as providing the system with the general functionality to predict a much wider range of indices e.g. intercalibration indices, stress-specific indices, and ecological and functional trait indices

- Extension of the uncertainty/errors module to estimate and assess uncertainty in (i) assignment to status class and (ii) comparison of samples for temporal change in quality and status. This needs to be done for a wider range of biotic indices (including those incorporating abundance data)

These new RIVPACS IV models can be used by the UK Agencies across Great Britain and Northern Ireland in their WFD compliance monitoring. All of the algorithms, variables and data necessary to build these models have been provided to SEPA for programming into a new River Invertebrate Classification Tool that will be disseminated free of charge to all interested users

Key words: RIVPACS IV, River Invertebrate Classification Tool, Water Framework Directive

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1. INTRODUCTION

The Regulatory Agencies in the UK (the Environment Agency; Scottish Environment Protection Agency; and the Environment & Heritage Service) currently use RIVPACS III+ software to classify the ecological quality of rivers. RIVPACS is a multi-variate model that predicts the invertebrate community that would be found at an unpolluted test site and is based upon a database of reference samples considered to be the best available of their type. RIVPACS predictions are site-specific; using the environmental variables recorded at a test site to predict the fauna expected at that site. RIVPACS also predicts 'expected' biotic index values for test sites. The ratio of an observed over an expected biotic index provides an environmental quality index (EQI) that allows different types of streams to be compared on a common scale. RIVPACS III+ also calculates the statistical confidence (confidence of grade, change of grade etc.), associated with each assessment. RIVPACS III+ is therefore a critical component of the biological classification schemes used by the UK agencies.

RIVPACS has been influential in the drafting of the European Union Water Framework Directive (WFD), (Council of the European Communities, 2000) and many of the key concepts that were developed in RIVPACS have been adopted in the WFD. The concept of reference sites, O/E ratios and the importance of quantifying the uncertainty associated with assessments have all been drawn from RIVPACS. However, because RIVPACS III+ pre-dates the WFD, there has been a requirement to ensure that the RIVPACS reference sites are fully WFD compliant, to add some additional functionality to the RIVPACS models, and to improve the robustness of the RIVPACS software to fully meet the needs of the Agencies in their delivery of WFD monitoring. These issues have been addressed in this project and have led to the development of new RIVPACS IV predictive models that will be programmed into a new River Invertebrate Classification Tool.

This new system will be based on a modern software programming language, be compatible with the agencies' computer systems and must include the ability to predict new biological indices, produce biological status assessments based on these new indices and be able to estimate the uncertainty involved in using these new indices. Because access to the new system will be essential for the UK Agencies to be able to implementation the WFD, the new tool will be readily and freely available to anyone who might seek to use it. The overall objective of the project has therefore been to produce a new river invertebrate status classification tool with the features necessary for WFD use.

There are four main components to the overall RIVPACS re-development work:

Stage 1: Business and technical analysis to ensure that the system will match the business needs of end users and be compatible with the information systems of the environment agencies and other users (performed by SNIFFER)

Stage 2: The underpinning science required to develop the algorithms necessary to produce the system (this project)

Stage 3: Programming of the algorithms into the final product (presently ongoing in SEPA)

Stage 4: Product roll out and training (UK Agencies)

This project represents stage 2 of the RIVPACS re-development work and provides all of the underpinning science required to develop the new tool. Stage 2 of the RIVPACS re-development work therefore necessitated the production of completely new RIVPACS models with functionality above and beyond that available in RIVPACS III+.

In addition to the underlying RIVPACS prediction and status classification engine, the new system incorporates:

- A revised taxonomic framework
- Resolution of the dual coverage of upland Scottish sites in the RIVPACS III+ GB and Highlands models. This has led to confusion about which model should be used for sites within this ill-defined bio-geographical area.
- A reviewed and re-developed prediction mechanism to improve predictive abilities so that a wider range of biotic indices of environmental quality can be calculated. These will be the indices which the Agencies are likely to use for classification and intercalibration
- Mechanisms for adjusting the expected values of indices to reflect WFD reference conditions
- A system for calculating WFD compatible ecological quality classifications based on ratios of observed/expected values of biotic indices
- A mechanism for adjusting expected biotic indices to better reflect WFD definitions of reference conditions
- Updating the software to a modern state-of-the-art computing language whilst also increasing user friendliness (e.g. windows interface, modern file formats for data input and export, reducing user effort involved in running software, better integration with Agency IT systems, and reduction in specialist knowledge required to run the software)

The project was sub-divided into a group of work elements that are listed below:

WORK ELEMENT 1: Review of detailed system specification, support to programmers and identification of algorithms in generic form

WORK ELEMENT 2: Compilation of data from other projects and data gathered by the Agencies and others to develop the predictive system and errors module

WORK ELEMENT 3: Development of rationale, testing and allocation of nominal numerical abundance values to family level records in the RIVPACS reference data set

WORK ELEMENT 4: Review and testing of options for optimising predictive ability. This then led to the definition of geographical modules and to end groups. Sites identified as unacceptably impacted were removed at this point. Development of a metric prediction module, enabling the prediction of multiple biological indices and metrics. This also incorporated work to investigate methods of adjusting predicted index values to allow for WFD reference condition

WORK ELEMENT 5: Development of error module to estimate classification errors for biological indices (including those incorporating abundance data)

WORK ELEMENT 6: Development of a comparison module to enable comparison of samples to determine differences in quality based on a range of indices

WORK ELEMENT 7: Production of final report

Each of these Work Elements (WE) were reported separately to the Project Board during the course of the project and this final report brings all of the WE reports together with summaries of their main outputs and findings.

This project draws on a number of other river invertebrate projects including:

- Previous RIVPACS developments
- The phase 1 project (SNIFFER project WFD46), which has compiled all the RIVPACS reference *site* data, resolved data ownership issues and assessed the condition of the RIVPACS reference sites in terms of the WFD concept of reference conditions (Davy-Bowker *et al*., 2007a, Davy-Bowker *et al*., 2007b)
- Development of AWIC scores (Davy-Bowker et al, 2005)
- Development of LIFE scores (Extence et al., 1999)
- Revision of BMWP scores being undertaken by Staffordshire University's Centre for Intelligent Environmental Studies (SNIFFER project WFD72a)
- The use of Artificial Intelligence projects being undertaken by Staffordshire University's Centre for Intelligent Environmental Studies
- EU 5th framework project STAR, in particular the ASTERICS (Furse et al., 2006) and STARBUGS (Clarke, & Hering, 2006) software and work enabling intercalibration of ecological status boundaries

There are three main target audiences for this work.

- Operational staff in environmental protection agencies of the United Kingdom. The products are of particular relevance for biologists, water quality and water resources staff responsible for implementing WFD. It is also aimed at those interpreting the results of biological surveys and planning programmes of measures to maintain or restore good ecological quality. Some of these people may not have specialist computing or other skills, so the system will require a simple, clear and intuitively simple user interface and supporting documents. The products will also be used by third parties wanting to undertake the same tasks, including other water users, none governmental organisations, conservation organisations and universities
- Computer and data systems staff of environmental protection agencies responsible for maintaining computer network systems and staff developing integrated software systems for WFD and other environmental management purposes
- Those developing other ecological prediction, classification and modelling tools for the sponsoring organisations, in particular those developing other WFD classification and modelling tools for algae, macrophytes and fish

References

Clarke, R.T. & Hering, D. 2006. Errors and uncertainty in bioassessment methods – major results and conclusions from the STAR project and their application using STARBUGS. *Hydrobiologia*, 566, 433-440.

Council of the European Communities, 2000. Directive 2000/60/EC, *Establishing a framework for community action in the field of water policy*. European Commission PE-CONS 3639/1/100 Rev 1, Luxembourg.

Davy-Bowker, J., Murphy, J.F., Rutt, G.P., Steel, J.E.C. & Furse, M.T. (2005) The development and testing of a macroinvertebrate biotic index for detecting the impact of acidity on streams. *Archiv für Hydrobiologie* 163: 383-403.

Davy-Bowker J., Clarke R., Furse M., Davies C., Corbin T., Murphy J. and Kneebone N. (2007a) *RIVPACS Database Documentation*. A report to the Scotland and Northern Ireland Forum for Environmental Research. 22pp & 3 appendices.

Davy-Bowker J., Clarke R., Furse M., Davies C., Corbin T., Murphy J. and Kneebone N. (2007b) *RIVPACS Pressure Data Analysis*. A report to the Scotland and Northern Ireland Forum for Environmental Research. 22pp & 5 appendices.

Extence, C.A., Balbi, D.M. & Chadd, R.P. (1999) River flow indexing using British benthic macroinvertebrates: a framework for setting hydroecological objectives. *Regulated Rivers: Research & Management* 15: 543-574

Furse, M., D. Hering, O. Moog, P. Verdonschot, L. Sandin, K. Brabec, K. Gritzalis, A. Buffagni, P. Pinto, N. Friberg, J. Murray-Bligh, J. Kokes, R. Alber, P. Usseglio-Polatera, P. Haase, R. Sweeting, B. Bis, K. Szoszkiewicz, H. Soszka, G. Springe, F. Šporka & I. Krno. 2006. The STAR project: context, objectives and approaches. *Hydrobiologia*, 566, 3-29.

2. WORK ELEMENT SUMMARIES

The following work element summaries draw together the main results, findings and conclusions from each of the Work Elements of the project. For most of the Work Elements, detailed Work Element reports are provided in the sections that follow.

WE 1.2 Review of IT analyst's system specification

In this work element, John Davy-Bowker (CEH) and Ralph Clarke (Bournemouth University) have provided comments on the detailed software specification that was developed in WFD72C Stage 1 by the SEPA appointed Business/IT Analyst. The aim of these comments was to ensure that the specification correctly identifies the system structure and required algorithms. As noted in the original project specification, the System Specification was an evolving document and as such several drafts were passed for comment. Early drafts also contained several gaps both due to lack of detail on algorithms at the time of writing and because internal business requirement within the Agencies have not been fully finalised at the time of writing.

In general we considered that the System Specification was well written and well organised and either already contained, or identified the need for information on, all of the necessary aspects of the system that needed to be covered. In our detailed comments (not included in this report), we clarified some areas and suggested changes to some sections where we thought that a misconception might have possibly existed. We also asked for clarification/suggested discussion in some areas where the functionality of the new tool was beyond that of the existing RIVPACS III+ models and a greater degree of specification was required.

WE 1.3-1.7 Generic algorithms for discriminant functions

One crucial aim of project WFD72C has been to provide the project manager and SEPA-employed IT software designer and programmer with precise, unambiguous and clear algorithms explaining and defining each of the logical and quantitative steps involved in the implementation of RIVPACS predictive models and the simulation assessment of uncertainty in O/E values and confidence of class for test sites within the RIVPACS models.

This has been achieved by developing and revising a working comprehensive 'Algorithms document'. This contained precise algorithms and formulae or software code for:

- discriminant functions and their use to determine probabilities of end-group membership (WE1.3)

- internal conversion of predictive variables (WE1.4):
  - Latitude/Longitude from national grid reference
  - Estimation of mean and range of air temperature from interpolation of internal spatial grid of long-term average temperature data – extended to cover the Scottish islands
  - transformations of environmental predictor variables

- prediction of expected values of biotic indices based on weighted average of end-group probabilities and end-group means of observed index values for reference sites. Also includes site- and season- specific expected probability of occurrence and expected (family-level) abundances of individual families and species (WE1.5).

- Rules and checks for user-supplied values of environmental variables and overall environmental suitability of any test site for valid prediction based on multiple discriminant analysis (MDA) end-group probabilities (WE1.6)

- Algorithms for simulating the effects of sampling variability/error and other “errors” on the uncertainty of O/E values and the confidence of assignment to WFD ecological status classes (WE1.7). This involved detailed equations and algorithms explaining the simulation approach used in RIVPACS III+, but also included new formulae and procedures (developed within WE5 and WE6) to assess uncertainty of status class for any 3-year monitoring period based on estimates of the average O/E values for a site over the whole period.

WE 1.8 Ad hoc Support to Programmers

In this work element, John Davy-Bowker (CEH) and Ralph Clarke (Bournemouth University) have provided *ad hoc* support to the SEPA appointed Business/IT Analyst. The aim of this support was to provide feedback in response to queries raised, clarification and comment on any issues of difficulty that arose during the programming of the RIVPACS IV models into the River Invertebrate Classification Tool.

WE 2.1 Refinement of Reference Sites

RIVPACS III+ currently utilises 835 reference sites across its four models. At the project start up meeting at CEH (21st June 2007) it was agreed that the goal of this work element was to remove sites where there was demonstrable reason for removal and that the adjustment algorithms within WE 4.5 would be used to correct for the effect of less significant stress on biotic index values at other sites. Information on sites that have been identified as unduly impacted in various predecessor projects and through more recent examination of the reference site data both by the Agencies and CEH is integrated into a single list of sites to be removed prior to the development of new predictive models.

- 42 sites (40 from GB and 2 from Northern Ireland) were removed and we provide supporting information and reasoning for these decisions
- In Great Britain, the new RIVPACS model constructed within this project will excludes these sites
- In Northern Ireland it is not necessary (nor were there any plans or resources within this project) to redevelop a new TWINSPAN classification and predictive model. Our recommended solution is that we retain the current TWINSPAN classification and end groups but that these 2 sites are ignored when calculating the end group mean values of indices, probabilities of occurrence and abundances of taxa.

WE 2.2 Report on Data for Errors and Compare

RIVPACS predictive models produce predictions of the fauna and biotic index values to be expected at test sites in reference state. Comparison of RIVPACS predicted biotic index values with those observed at a test site provide an assessment of the biological quality of the site. As with any bio-assessment methodology it is vital to be able to quantify the uncertainty associated with these assessments.

The current RIVPACS III+ software produces assessments of biological quality within a single year and bases its estimates of uncertainty in the biotic indices NTAXA, BMWP and ASPT on the Biological Assessment Methods Study (BAMS) dataset (Clarke et al, 2002). This dataset comprises three replicate samples in each of the 3 RIVPACS seasons within the same year at sites on rivers of a variety of types and under a variety of organic pollution stress levels. However, the RIVPACS IV models under development as part of the current project will incorporate new functionality to enable assessments to be made across a 3-year period, with observed values being provided in any of 1, 2 or all 3 years. The new RIVPACS IV models will also incorporate a more extensive list of biotic indices. This has therefore created a need for new replicate sample datasets to calculate new error terms to account for replicate sampling variability between years and for a wider range of biotic indices.

Four datasets have been assembled:

- A new 28-site dataset from the former Tay River Purification Board
- A new 416-site dataset from East and North-East Scotland
- A new 12-site Community Change dataset from Northern Ireland
- The existing 16-site Biological Assessment Methods (BAMS) dataset

The following biotic indices (see Appendix II) were calculated for various different combinations of sample replicates as appropriate for each of the datasets above:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

WE 2.3 Compilation of Biological Data for Estimating Nominal Abundances to be applied to the RIVPACS samples

All current and previous RIVPACS models have been based upon samples with taxa recorded at both species and family levels. Species records were recorded as simply presence/absence while family level records have been enumerated using the $\log_{10}$ abundance categories shown below:

Log_{10} category	Numerical abundance
1	1-9
2	10-99
3	100-999
4	1,000-9,999
5	10,000+

However, it has been recognised for some time that the lack of numerical abundance data for the RIVPACS samples, both at species and family level, presents a potential difficulty for the integration of abundance weighted biotic indices into RIVPACS models. Lack of numerical abundances also leads to problems where samples from more than one season need to be pooled for combined season estimates. It has therefore been necessary to develop and test a rationale for ascribing estimated numerical abundances to the taxa in the RIVPACS dataset. At the pre-project interview (28th May 2007) it was agreed by the Project Board that no attempt would be made to allocate estimates of abundances to the species level records in the RIVPACS reference site dataset because of the lack of adequate supporting data, the potential costs and the lower practical priority compared to allocating numerical abundances to the RIVPACS families.

In recent years the UK Agencies have been recording the numerical abundances of families in their routine monitoring data. In this WE new family level datasets from the Environment Agency, Scottish Environment Protection Agency, and Environment and Heritage Service (listed below) were collated to derive estimates of the numerical abundances of families within $\log_{10}$ abundance categories that could then be applied to the RIVPACS family level data (in WE 3.2).

- SEPA 2004 GQA dataset from the Scottish mainland, Highlands and Islands
- EA 2006 GQA dataset from England & Wales
- EHS 2007 GQA dataset from Northern Ireland

These datasets were combined into a UK-wide dataset of family level records with numerical abundances providing excellent geographical coverage across the whole of Great Britain (including most of the Scottish Islands) and Northern Ireland.

WE3.1 Revision of Taxonomic Framework in RIVPACS Database

There has been a requirement to review the taxonomic framework of the RIVPACS IV models being developed for inclusion within the new WFD72C Tool. This was necessary in order to update the taxonomy of the species and family level predicted taxon lists and to ensure that the taxonomy used in the calculation of biotic index values is both correct and up-to-date. Furthermore, unlike previous versions of RIVPACS that exclusively used revised Maitland codes for taxon coding purposes, the new Tool needs to be fully compatible with the Agencies NBN (National Biodiversity Network) taxon coding system. In this Work Element, the following issues have been addressed:

- The taxonomic groupings (BMWP composite families) have been revised to accurately reflect modern taxonomy (e.g. by renaming the BMWP family *Ancylidae* as *Ancylus* group and renaming *Planorbidae* as *Planorbidae* excluding *Ancylus group*). This ensures that taxonomic predictions based on existing BMWP taxa are taxonomically correct, even if they constitute artificial groups
- The names for other taxonomic levels have been brought up-to-date to reflect current practice (e.g. *Siphonoperla/Chloroperla*)
- BMWP composite families have been split and renamed where possible to be compatible with the revised BMWP scoring system (also known as the WHPT index) and general modern taxonomic conventions. Determination of estimated $\log_{10}$ abundances for the separate families derived from BMWP composites was dependent upon WE 3.2 (allocation of numerical abundances to families).
- RIVPACS III+ taxonomy (Revised Maitland Code) has been retained. In addition, updated CEH Furse Codes and names, as well as National Biodiversity Network (NBN) codes and names have also been added to the RIVPACS dataset (and subsequently the new RIVPACS IV models) ensuring that RIVPACS IV can provide predicted taxon lists in all 3 of the major taxonomic coding systems currently in use in the UK.

WE 3.2 Generation of Family Level Abundance Data

Families within the RIVPACS dataset are currently enumerated with $\log_{10}$ abundance categories (see WE 3.1 summary). To be able to assign numerical abundances to these family level records, a substantial dataset of numerical abundance data for macroinvertebrate families across the UK was required. The datasets collated in WE 3.1 were pooled and mean numerical abundances, within each of the five $\log_{10}$ abundance categories, were calculated for each family across the UK. A clear trend was readily apparent within the abundance data. Those families that generally had low numerical abundances within $\log_{10}$ category 1 tended not to found at high $\log_{10}$ abundances. Conversely, families that tended to be recorded with high numerical abundance in $\log_{10}$ abundance category 1 were more likely to be found at higher $\log_{10}$ abundance categories. It is therefore clear that the average numerical abundances of families within the $\log_{10}$ abundance categories differs between different families and that where possible it was sensible to allocate numerical abundances to the RIVPACS family level records that mirrored this trend. These family-specific estimates of numerical abundances were appended to each family within each $\log_{10}$ abundance category within the RIVPACS dataset.

While there was a clear pattern that average numerical and $\log_{10}$ abundances were linked and varied between the families, analysis of geographical trends in the abundances did not show any tendency for the numerical abundances within the $\log_{10}$ categories to be higher within certain geographical regions compared to others.

The UK Agencies no longer take summer samples so it was not possible to include season specific numerical abundance estimates.

WE 4.1 Allocation of reference sites to geographical models and end groups

The former RIVPACS III+ bio-assessment software (also known as RPBATCH) geographic module structure consisted of the main GB module (GB, 614 reference sites, in 35 end groups), the Scottish Highlands module (SH, 110 sites of which 52 also in main GB module, in 10 end groups) and the Scottish Islands module (SI, 55 sites, in 5 end groups), together with a separate module for Northern Ireland (NI, 110 sites, in 11 end groups).

Prior to any new RIVPACS model development, the complete set of GB, SH, SI and NI RIVPACS III+ reference sites were reviewed in the light of the WFD to re-assess whether they were of adequate quality at the time of RIVPACS sampling to use as Reference sites in the new model(s) and predictions (This was done in WE2.1 ‘Refinement of Reference sites for model development’). Thirty five sites from the old GB model, five sites exclusive to the Scottish Highlands model and two sites from the Northern Ireland model were considered to be unduly impacted or subject to sampling problems in one of more the seasons in which they were sampled for use as RIVPACS reference sites.

New single GB-inclusive model

The GB and SH reference sites overlap in geographic coverage with no obvious clear bio-geographical boundary, while many of the Scottish Islands (SI) sites are near the mainland (e.g. Skye) and thus may not have distinct island macroinvertebrate communities and therefore predictions might be improved by integration with mainland GB reference sites.

A single new GB-inclusive predictive model based on the remaining 685 reference sites from the previous GB, SH and SI modules was developed using exactly the same statistical techniques as for the existing RIVPACS III+ models.

This involved a TWINSPAN (Two-Way Indicator Species Analysis) hierarchical biological classification of the reference sites into end groups (using three season combined sample data involving both the abundance categories of families and the presence-absence of species based on the existing RIVPACS taxonomic data), followed by MDA (Multiple Discriminant Analysis) of the end-groups based on the standard set of RIVPACS environmental predictor variables. (The previous background spatial database giving the mean and range of air-temperatures for any mainland GB site had already been extended in WE1.4 to cover all Scottish Islands).

The final selected classification of the 685 GB-inclusive reference sites was into 43 end groups (Figure 1). The number of reference sites in each end group varied from 6 to 32, with a median size of 15 sites. All 9 Shetland reference sites formed a distinct biological end-group and all 9 Orkney sites (excluding the two sites on Hoy) were assigned to a single end-group. For mapping and descriptive summary purposes the 43 end-groups can be combined into TWINSPAN higher level super-groups (Table 1 and Figure 1).

The new GB-inclusive 43 end-group prediction model explains 56% (for TAXA) and 72% (for ASPT) of total variation in observed index values for the 685 reference sites, which is similar to equivalent values for RIVPACS III+. The overall fit of the prediction model is often measured by the standard deviation (SD (O/E)) of the O/E values for the reference sites; these were 0.140 (for O/E_{TAXA}) and 0.053 (for O/E_{ASPT}) (slightly higher than the equivalent SD of 0.138 for O/E_{TAXA} and slightly lower than the SD of 0.057 for O/E_{ASPT} for the previous 614 GB model).

Slightly more than half (57%) of reference sites have higher expected TAXA value values in the new GB model compared to in RIVPACS III+; this is because the 40 RIVPACS III+ reference sites excluded from the new GB-inclusive predictive model tended to have relatively low O/E_{TAXA}. Where major changes in expected values of TAXA or ASPT for a site occurred the resulting O/E values were usually closer to unity.

The lower 5% and 10% percentiles of the frequency distributions of the O/E values for three-seasons combined samples the 685 GB-inclusive reference sites were 0.785 and 0.820 for O/E_{TAXA} and 0.910 and 0.930 for O/E_{ASPT}.

Overall, the new GB-inclusive model provides a single, integrated and consistent prediction model and assessment system to use for the whole of GB including all the Scottish islands. It eliminates problems of which module (GB or SH) to use for Scottish sites which might be considered to be “highlands” sites. It also enables predictions for non-remote Scottish islands sites to involve information from similar mainland sites.

Northern Ireland module

The set of Northern Ireland (NI) reference sites and their RIVPACS model was considered to represent a natural geographic split from GB and it was agreed that this would be retained as a separate model.

As only two of the original 110 RIVPACS III+ NI reference sites were rejected as being of inadequate quality, no new NI model was developed. The current RIVPACS III+ biological classification of the NI Reference sites into the 11 end groups was retained, along with the current MDA discriminant functions for this NI module. However, new end group mean values for each of the biotic indices (upon which predicted index values are based) were supplied based on the mean values for each end group excluding these two rejected sites.

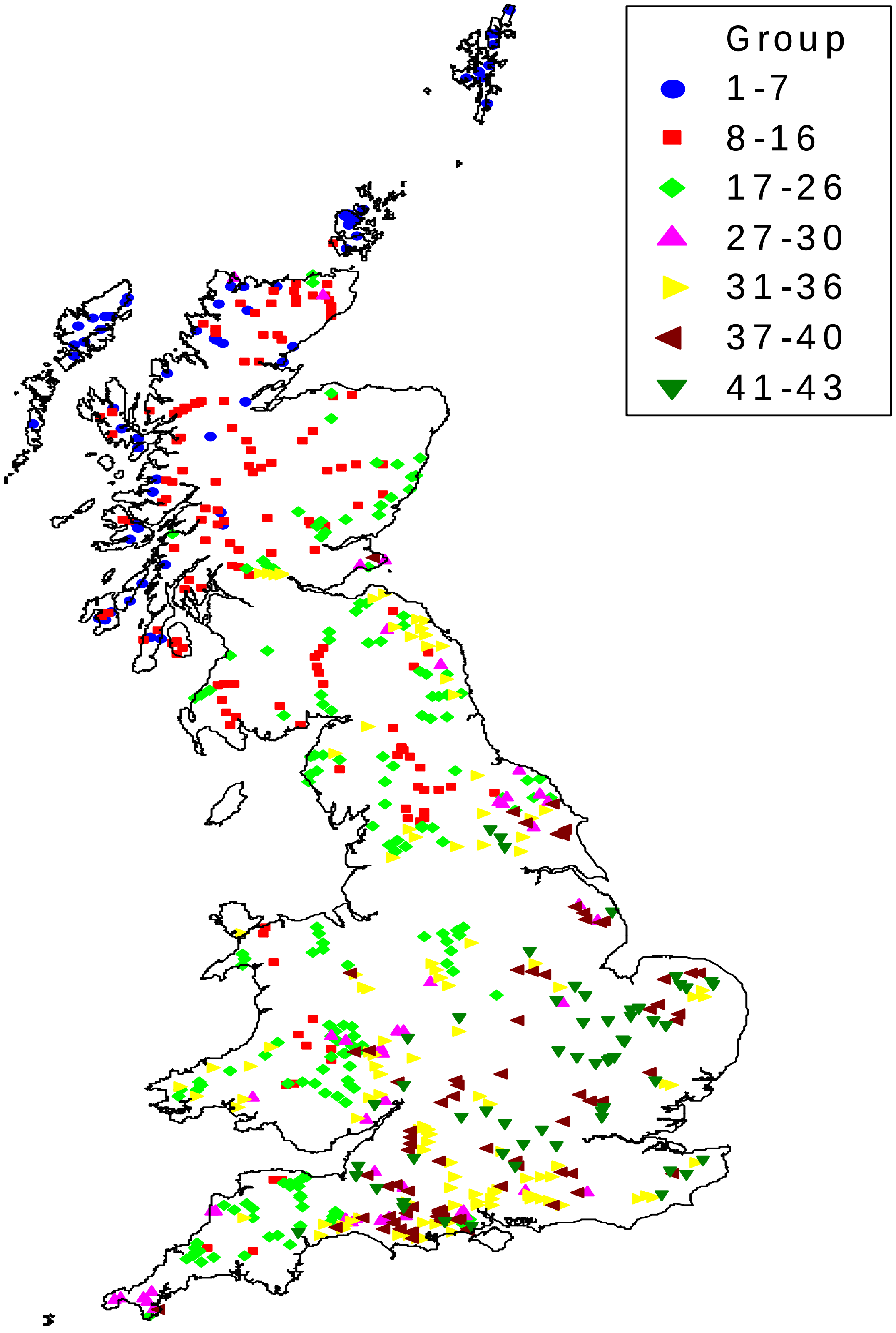


Figure 1. Geographic location of the reference sites in each of the seven major groupings of the 43 end groups for the 685 reference sites in the new all GB-inclusive RIVPACS model.

Super-group	N sites	Mean TAXA	Mean ASPT	Dominant characteristics
1-7	64	23.0	6.27	All in Scotland mostly islands
8-16	148	25.2	6.79	Upland streams, mainly in Scotland and N England
17-26	169	31.7	6.42	Intermediate rivers, SE Scotland, Wales, N & SW England
27-30	48	27.1	6.25	Small steeper streams, within 13km of source, discharge1/2
31-36	115	34.8	5.84	Intermediate size lowland streams, including chalk, SE
37-40	84	32.7	5.58	Small lowland streams, including chalk, SE Britain
41-43	57	32.7	5.14	Lowland streams, SE England, larger, fine sediments

Table 1 Seven super-group level of classification of the 43 end groups of the 685 GB reference sites.

WE 4.3 Confirmed variables for taxonomic prediction

It has always been considered a great strength of RIVPACS that it can predict the taxa that should occur at a test site together with probabilities of occurrence. The new models produced in this project retain that functionality and no generic change in the mechanism by which this achieved is envisaged. All the current RIVPACS combined season/individual season options will also be retained. However, the variables (datasets) upon which the probabilities of capture are based do need to be updated in light of the revised end groups and geographic modules (WE 4.1). Similarly, revised of the taxonomic framework in RIVPACS IV (WE 3.1) now supports three different taxon coding systems, and the predicted taxon lists that are produced by the new models also need to produce outputs in all of these taxon coding systems.

The levels of taxonomic prediction supported in the new software are as follows:

- TL1 - Current BMWP “families” for each of the RIVPACS season combinations
- TL2 - Revised BMWP “families” for each of the RIVPACS season combinations*
- TL3 - All families for each of the RIVPACS season combinations
- TL4 - All ‘RIVPACS’ species for each of the RIVPACS season combinations

*a new taxonomic level not previously available in RIVPACS models

For each taxonomic level, we have derived data tables to support the following types of taxonomic predictions:

- predictions of the probabilities of occurrence of taxa
- supports predictions of the average $\log_{10}$ abundance of taxa
- predictions of probability of a given taxon being found at a given $\log_{10}$ abundance category

Taxa in all three of the above files have been supplied with Revised Maitland codes and names, Furse codes and names, and NBN codes and names.

WE 4.4 Confirmed variables for predicting indices

At present RIVPACS III+ predicts the expected index values of BMWP, NTAXA and ASPT, however, this list of indices has now been expanded to include:

BMWP
NTAXA
ASPT

AWIC (family level)
LIFE (family level)*
Non-Abundance Weighted WHPT Score*
Non-Abundance Weighted WHPT NTAXA*
Non-Abundance Weighted WHPT ASPT*
Abundance Weighted WHPT Score*
Abundance Weighted WHPT NTAXA*
Abundance Weighted WHPT ASPT*

*2 versions calculated based on BMWP composite data and based on distinct families

Within this Work Element the reference values of the above indices were calculated together with end group means for the new RIVPACS IV GB and NI models. These indices and end group means were calculated for all seven valid RIVPACS season combinations. All of the above indices have also been checked against any that were previously calculated in SNIFFER project WFD46 and a random sample of all the calculated indices has also been manually checked.

Where possible scientific publications or reports are cited as sources for the indices, and in all cases, the exact details of each of the above indices are reproduced in full in this report. This will enable the UK Agencies to be fully informed about the methods used to calculate the reference values of the indices used in the new Tool so that expected values for test sites can be calculated in the same way, thereby ensuring that their observed/expected ratios used in bio-assessment are fully compatible and therefore correct.

Spring and autumn combined Inter-calibration Common Metric component metrics (ICMs) for the 614 RIVPACS III+ GB and 110 Northern Ireland sites have also been supplied by John Murray-Bligh (Environment Agency). These metrics were calculated in a manner consistent with the European WFD intercalibration process using the ASTERICS software and have also been included in the database accompanying this report (although end group means are not required and have not been calculated).

WE 4.5 Adjustment of RIVPACS Predicted Indices to a standard WFD reference state

Despite iterative attempts over the years to eliminate inadequate RIVPACS reference sites, the references only generally represent the best available sites and the perceived ecological status of the RIVPACS reference sites still varies, and most importantly varies between stream types and end groups. Derived predictions of expected index values for a site will therefore depend on the status of the environmentally-similar reference sites actively involved in predictions for the site.

In a previous part (WFD72B) of overall SNIFFER project WFD72, we developed a general statistical model (M4), procedure and algorithm to make these adjustments and applied the procedures to estimate adjustment factors for the existing BMWP indices.

Within WFD72C WE4.5, we concluded that it was not statistically logical to apply this adjustment algorithm directly to the observed values for the reference sites and then average the adjusted values by RIVPACS end-group to obtain adjusted end-group mean values of each index which would then be used to derive pre-adjusted predicted index values.

It had already been shown in WFD72B that it was best to use a single fit of model M4 to all UK reference sites. Therefore the estimates of the multiplicative adjustment factors ($A_1 - A_5$) to be used to adjust RIVPACS expected values for all UK sites were obtained from fitting model M4 to the new combined set of 685 GB and 108 NI reference sites involved in the new RICT software (Table 2).

	Index	Estimate of adjustment parameter				
		A_1	A_2	A_3	A_4	A_5
Original BMWP	Score	0.994	1.014	1.000	0.938	0.867
	NTAXA	0.993	1.004	1.000	0.959	0.912
	ASPT	1.000	1.010	1.000	0.979	0.952
Revised BMWP Non-weighted	Score	0.998	1.018	1.000	0.946	0.884
	NTAXA	0.996	1.009	1.000	0.967	0.926
	ASPT	1.003	1.008	1.000	0.979	0.954
Revised BMWP Abundance-weighted	Score	0.998	1.017	1.000	0.945	0.875
	NTAXA	0.996	1.009	1.000	0.967	0.926
	ASPT	1.002	1.008	1.000	0.977	0.945
AWIC	AWIC	1.000	1.002	1.000	1.012	1.039
LIFE	LIFE	0.995	1.002	1.000	0.996	0.986

Table 2. Estimates of adjustment parameters (A_1 – A_5) for the effects of assessment score (1 (top-high), 2 (mid-high), 3 (high/good), 4 (mid-good) 5 (good/moderate)) in model (M4) for each biotic index based on using every possible combination of single and multiple season samples for the 793 UK-wide reference sites (AWIC and LIFE based on all single season samples only)

These adjustment equations, algorithms and parameter estimates were then supplied to the project manager and IT programmer for coding and incorporation into the RICT software.

WE 5 & 6 Algorithms to estimate uncertainty for biological indices, confidence of class and assess confidence of change between samples and sites

The previous BAMS R&D project (Furse *et al* 1995, Clarke *et al* 2002) used a combination of replicated field sampling studies and statistical analyses of RIVPACS sample audit data to derive procedures and associated estimates for simulating and assessing the uncertainty in RIVPACS O/E index values arising from replicate sampling variation and macroinvertebrate sample processing errors. These uncertainty assessment procedures for the original BMWP number of TAXA and ASPT indices were incorporated into the RIVPACS III+ software to derive estimates of confidence of class and of change between samples and/or sites. The philosophy behind this approach is that it is not possible for practical and especially financial reasons to take replicate samples at all, or even most, sites and sampling occasions and therefore we must prior estimates of typical sampling variability obtained from existing datasets providing information on replicate and other sampling variability.

For surveillance monitoring and WFD classification purposes, the UK environment agencies intend to move from the use of single year's data towards using estimates of the average quality of a three-year period in order to reflect the longer term underlying condition of the biology. For each metric, the agencies will use the average of the EQR values for each of the individual years available over the three year period of interest. To assess uncertainty associated with such estimates of average quality, we needed estimates of temporal variance in index values, both short-term within-season temporal variance and inter-year (within period) variance. The new uncertainty algorithms and software need to cope with both the former type of assessment for one site at one point in time or in one year and with estimates of average quality over a three-year period.

In WE5 and WE6, we developed and supplied statistical formulae to represent the combined effect of replicate sample variance, within-season and inter-year temporal variance on the overall variance in index values over a three year period and on the resulting uncertainty associated with any estimate of average O/E.

Deriving estimates of each of these variance components for each biotic index has not been easy. For example, observed variation in index values between years is due to real systematic changes between years, but also, and perhaps largely due to the fact that they are merely different samples such to replicate sampling variability. Therefore, to estimate true inter-year variance we need to first “subtract” estimated variability due to the replicate sample variance. Ideally this would be done based on a comprehensive dataset with replicate samples taken on more than one day in each season, over a large number of years, at each of a wide range of types and qualities of river site and water body. However, no such single dataset exists.

Therefore estimates of the various variance components were obtained by hierarchical analysis of variance techniques using a blend of the following datasets (prepared as part of WE2.2):

- BAMS dataset : 16 sites throughout England (4 types by 4 quality classes), each with 3 replicates in each of 3 seasons in one year

- TAY dataset : 28 Tay River Purification Board sites, including 18 sites with 4 replicate samples in each of spring and autumn for each of five years (1990-1994)

- SEPA dataset: 416 sites covering a much wider area of Scotland and with c.200 instances of samples being taken on more than one day within the same RIVPACS season of a year.

- NI dataset: 12 sites in Northern Ireland sampled once each month in one year

These datasets were then used in appropriate combinations to derive estimates of the various variance components for a few key indices, likely to be used for classification and/or regulatory purposes by the agencies; these were the original BMWP indices, revised BMWP indices, abundance weighted revised BMWP indices, AWIC (family level) and LIFE (family level).

The BAMS and TAY datasets were analysed separately, together and as weighted averages to derive estimates of the replicate sampling standard deviations (SDRep) for each index for single season samples, two-season and three-season (BAMS only) samples.

Temporal variance components (within-season and inter-year) were estimated by integrated analysis of the combined BAMS, TAY and SEPA datasets. The NI dataset was used as a check on the within-season temporal variance estimates.

The relative size of temporal to replicate sample variance for two-season, and especially three-season, combined samples had to been inferred from the corresponding estimates and proportions obtained for single season samples.

The recommended estimates of the variance components for each index for single, two- and three- season combined samples, based on the best information currently available, are given in Table 11 of the WE5-6 Interim Report. These will be incorporated into the new RICT tool.

The current functionality of bias correction need to be incorporated in the new system for any new biotic indices that are to be used in the overall site assessments. At present only the explicit algorithms and parameter estimates developed for RIVPACS III+ for the original BMWP indices are supplied and incorporated into the new RICT tool. Algorithms and procedures for other indices would require future analyses of audit data to establish the typical pattern of consequences of sample processing errors on biases in these indices.

Assessments of uncertainty of change between two estimates of O/E (formerly derived in RIVPACS procedure COMPARE) are to be based on similar simulation logic in the new RICT software. The two case O/E values being compared could, in theory, be from the same site in different years/periods, or different sites in the same or different years/periods. In any one simulation, the appropriate variance of the observed and O/E values for each of the two cases (which could involve different seasons or number of seasons) is used to derive independent stochastic simulations of the potential O/E values and their difference that could have been obtained. The frequency distribution of these simulated differences in O/E and status class is then used to assess likelihood of change in O/E and change in class.

The uncertainty algorithms currently supplied are based on the (project-agreed) assumption that estimates of site quality assessed in the current version of the new RICT tool would be based on a single O/E value for any one year (although this could be either from just a single season sample or a two- or three-season combined sample). Moreover, it is assumed with the supplied formulae that the same sampling procedure (i.e. spring only, or spring-autumn combined samples) is used in each of the sampled years within any three-year monitoring period over which an assessment of average quality is required. Assessments of change (procedure Compare) can be based on different sampling regimes.

Recommendations for further research

It would be useful to develop more general algorithms to measure uncertainty of site assessments involving replicate sampling on some days/seasons/years and/or sampling on more than one month in some (but not all) seasons/years, but this is more complex and would require recommended further research work.

In retrospect, it might be useful to base estimates of uncertainty on direct estimates of the observed variability in O/E values arising from different replicate samples, dates, seasons and years. This would make it easier to allow for, and statistically condition on, any temporal changes in the expected E values of indices within a site into the assessment. However, this requires us to have appropriate/valid values of the RIVPACS environmental predictor variables and thus RIVPACS E values for every sample at each site to be used in the statistical hierarchical analysis of variance components for index O/E values. This is a recommendation for future research.

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 1.3-1.7 Deliverable – Generic Algorithms
25th March 2008

Identification and details of generic algorithms for use by the programmers in their development of the new River Invertebrate Classification Tool (RICT) software

Document sections changed from previous version

30th Oct 2007	Base version
15th Nov 2007	Section WE1.7 Algorithms for simulating uncertainty (i) new sub-section on 'Single and multi-year runs and site assessments' (ii) Algorithms : Simulating potential observed index values (iii) Simulating uncertainty in expected values (iv) FORTRAN code at end of section WE1.7 to generate random deviates from either a Normal distribution or a Poisson distribution
7th Dec 2007	Section WE1.3 Algorithms for using discriminant functions – only details (p19) of 'Supplied internally-derived data files' giving the discriminant function (DF) coefficients and the DF End-group means have been changed to reflect the data files actually supplied on 7/12/07
25th Mar 2008	Section WE1.7: brief sub-section on page 43-44 on 'Confidence (and statistical test) of change/difference in EQI' – added explanation of how to create 2-sided statistical test

1. INTRODUCTION (extracted from final revised Tender (29th June 2007)

WORK ELEMENT 1. Review of detailed system specification, support to programmers and identification of established algorithms in generic form.

This work element consists of those objectives and tasks required for support to the system programming before, during and after the science element of the project. We will:-

WE1.1 Project management (as detailed in Section 8).

WE1.2 Provide *feedback* on the detailed software system specification (developed in Stage 1 by the business/IS analyst) to ensure that it correctly identifies system structure and required algorithms.

On 27th June 2007 AC sent JDB the latest version of the Functional Specification for CEH to provide feedback.

Identify and deliver algorithms in generic format to enable the programmers to develop the code for the methodological and statistical aspects of the system. This involves a range of elements, of varying complexity. From our detailed understanding as developers of the existing system, we anticipate these will specifically include:-

WE1.3 Algorithms for using discriminant functions to calculate probabilities of belonging to each RIVPACS site end group

WE1.4 Algorithms for internal conversion of predictive variables, namely:

(i) derivation of Latitude and Longitude from National Grid References

(ii) estimation of long term average mean and range of air temperatures from Latitude and Longitude. Algorithms will be provided in WE1 (Note: currently interpolated air temperatures are only encoded within RIVPACS for mainland GB – we have obtained the equivalent hardcopy maps for the Scottish islands and further work will be done to ensure that the necessary data are available to plug into these algorithms ready for the software testing and release)

(iii) calculating mean substratum composition (in phi units)
(iv) estimating alkalinity (if unavailable) from conductivity, hardness or calcium
(v) transformation (logarithm) of predictor variables

WE1.5 Algorithms for prediction of expected values of any index based on probability of end group membership and average values of the index amongst reference sites in each end group. Algorithms for taxonomic prediction (including prediction of occurrence and expected abundances)

WE1.6 Rules and checks that user-supplied values of environmental variables are within ranges covered by the RIVPACS reference sites in the relevant model. Rules for checking the environmental suitability (coded 1-7 in RIVPACS output) of the test site for prediction by RIVPACS based on its multivariate discriminant analysis (MDA) distance from each end group

WE1.7 Algorithms for simulating effects of sampling error/variability and other “errors” on bioassessment uncertainty.

(i) This will initially be based on the mathematical methods used in RIVPACS III+, and as such will incorporate estimates of the effects of sampling variation and sample processing errors (biases) for the existing BMWP indices (NTAXA, BMWP Score and ASPT).

(ii) Generic algorithms for simulating effects of sampling variability (replicate and/or temporal) for any index will be provided (estimates for some other key indices to be derived in WE5).

(iii) The effects of sample processing errors are complex, will depend on the type of metric, and are not yet understood or assessed for other metrics *also suitable audit information is not readily available on taxonomic abundances. It was agreed at the pre-project interview meeting of 28/05/07 that the algorithms to represent the effect of sampling processing errors will have to be limited to the simple generic methods adopted for the STARBUGS system (STAR Bioassessment Uncertainty Guidance Software; Clarke 2005, Clarke & Herring 2006). Note that, within this stage 2 of the project, estimates of the parameters of these algorithms for effects of sample processing errors will only be supplied for the three original BMWP indices (as developed and used in RIVPACS III+).*

(iv) Algorithms for comparing the O/E values and status class assignments for two samples. Initially these will be identical to the methods using the RIVPACS III+ procedure COMPARE, as this is our currently recommended general approach, and is the approach we at CEH adapted in our development of STARBUGS.

The detailed system specification developed in stage 1 of this project will have identified where algorithms are required for the system to achieve the necessary functionality.

The format for supplying the algorithms was clarified in CEH’s replies of 11/05/07 to SNIFFER’s request for clarifications of 03/05/07, and agreed at the pre-project interview of 28/05/07. Algorithms will be supplied by CEH in the form of equations in Microsoft Word documents.

The suite of algorithms would use unambiguous (i.e. non-repeated) letters and symbols for variables and parameters and would be written to show the logical order in which the algorithms should be applied in the software. This is most easily done using a logical flow of equations (each carefully explained) within a simple Word document (as would be done in any journal paper). Obviously we may need to give some initial explanation to help the programmers get started but then the format and style should be consistent, clear and unambiguous. We hope our proposed approach is now clear and acceptable.

2. OVERVIEW OF ALGORITHMS.

The various algorithms needed by the programmers to support them in their development of the RICT software are provided below. The algorithms are ordered in sections which correspond to sub-elements (or parts thereof) of the WE1 agreed tender details given in the Introduction above.

The algorithms are, of necessity, a mixture of ordered statements, mathematical equations, and/or where most appropriate, actual sections of FORTRAN subroutine code (as agreed with Alan Croal the Project Manager).

The algorithms should be executed in the order in which they are presented below.

In providing these algorithms, it is assumed that the raw user-supplied biological and environmental input data for test sites have already been imported using a database storage and extraction method to be determined by the Agencies and programmers.

3. ALGORITHMS

The algorithms follow, in order of required use, on subsequent pages.

> Any associated internal data files (e.g. file TEMPGRID.DAT needed to calculate air temperature mean and range) will be supplied with the completed version of this WE1 algorithms specification deliverable

WE1.4 (i) Derivation of Latitude and Longitude from National Grid references

(a) Deriving Latitude and Longitude for GB model sites

User-Input variables giving National Grid reference of the test site:

NGRLET = 2 letters indicating the National Grid 100km x 100km grid square
NGREAST = 3 digit Easting within the 100km grid square (to nearest 100m)
NGRNORTH = 3 digit Northing within the 100km grid square (to nearest 100m)

Internal data file: NGRLETTERS_GB.XLS (supplied in EXCEL format -convert as required)

This file contains three columns defining the numeric 100km Easting square and numeric 100km Northing square associated with each two-letter prefix of a National Grid Reference.

LETTER100 = two-letter prefix of a National Grid Reference.
EAST100 = numeric 100km Easting square (range of values is 0-6)
NORTH100 = numeric 100km Northing square (range of values is 0-12)

Algorithm:

Find row (k) in file NGRLETTERS_GB.XLS for which column ‘LETTER100’ = NGRLET

E100 = EAST100 value for row k
N100 = NORTH100 value for row k

IGEAST = 1000 * E100 + NGREAST
IGNORTH = 1000 * N100 + NGRNORTH

Then the following part of the algorithm (given as FORTRAN subroutine GRIDCON) is used to derive Latitude (LAT) and Longitude (LONG), in decimal degrees, from the Easting (IGEAST) and Northing (IGNORTH), both to the nearest 100m.

The supplied FORTRAN program LATLONG_GB.FOR (below) and the example file LATLONG_GB.DAT (supplied separately) can be used to read values of IGEAST and IGNORTH, pass them through your version of this subroutine code and output the values of LAT and LONG to file LATLONG_GB.OUT for checking for agreement with the last two columns of LATLONG_GB.DAT.

```
    PROGRAM LATLONG_GB
    INTEGER*4 IGEAST,IGNORTH
    REAL*4 LAT,LONG
    open(7,file='LatLong_GB.dat')
    open(8,file='LatLong_GB.out')
400 read(7,'(20x,i5,i6)',end=500) IGEAST,IGNORTH
    CALL GRIDCON(IGEAST,IGNORTH,LAT,LONG)
    write(6,'(i5,i6,2f8.3)') IGEAST,IGNORTH,LAT,LONG
    write(8,'(i5,i6,2f8.3)') IGEAST,IGNORTH,LAT,LONG
    goto 400
500 continue
    end
```

```
      SUBROUTINE GRIDCON(IGEAST,IGNORTH,LAT,LONG)
C IGEAST  is the NGR Easting  to the nearest 100m (input to
subroutine)
C IGNORTH is the NGR Northing to the nearest 100m (input to
subroutine)
C LAT and LONG are the Latitude and Longitude (in decimal degrees)
C              derived within the routine and output
C
      REAL*4 LAT,LONG
      INTEGER*4 IGEAST,IGNORTH
      DOUBLE PRECISION A,ESQRD,GCONJ,GSCON,ADASH,BDASH
      DOUBLE PRECISION CDASH,DDASH,LOCMRA,LACMRA,FE,FN,CFACT
      DOUBLE PRECISION Y,YTRY,PHP,DIF,CPHP,SPHP,TPHP,SN,SQSN
      DOUBLE PRECISION FACT,SQTP,X,SQX,ESSF,PN,PE
      EQUIVALENCE (Y,CPHP),(YTRY,SPHP,SN),(DIF,TPHP)

      A=0.637754218D+7
      ESQRD=0.667054D-2
      GCONJ=0.100671533D+1
      GSCON=0.999601272D+0
      ADASH=0.636689343D+7
      BDASH=0.1597981D+5
      CDASH=0.1671D+2
      DDASH=0.216D-1
      LOCMRA=-0.3490658504D-1
      LACMRA=0.8552113335D+0
      FE=0.4D+6
      FN=-1.D+5
      CFACT=0.100000372D+1

C    READ GRIDS AND CONVERT TO GEOGRAPHICALS IN RADIANS
      PE=IGEAST*1.D+2
      PN=IGNORTH*1.D+2

C    DOES SPHEROID CALCULATION
      ESSF=ADASH*LACMRA-BDASH*DSIN(LACMRA+LACMRA)
     &    +CDASH*DSIN(4.D+0*LACMRA)-DDASH*DSIN(6.D+0*LACMRA)
      Y=(PN-FN)/CFACT+ESSF*GSCON
      YTRY=Y
    2 PHP=YTRY/ADASH
      ESSF=ADASH*PHP-BDASH*DSIN(PHP+PHP)+CDASH*DSIN(4.D+0*PHP)
     &     -DDASH*DSIN(6.D+0*PHP)
      DIF=Y-ESSF*GSCON
      YTRY=YTRY+DIF
      IF(DABS(DIF).GE.1.D-2) GOTO 2
    3 CPHP=DCOS(PHP)
      SPHP=DSIN(PHP)
      TPHP=SPHP/CPHP
      SN=A/DSQRT(1.D+0-ESQRD*SPHP*SPHP)*GSCON
      SQSN=SN*SN
      FACT=1.D+0+(GCONJ-1.D+0)*CPHP*CPHP
      SQTP=TPHP*TPHP
      X=(PE-FE)/CFACT
      SQX=X*X
      PE=PHP-(1.D+0-(5.D+0+3.D+0*SQTP)*SQX*8.333333333D-2/SQSN)
     &   *SQX*TPHP/((SN+SN)*SN/FACT)
      PN=LOCMRA+(1.D+0-(FACT+SQTP+SQTP-(5.D+0+(2.8D+1+2.4D+1*SQTP)
     &   *SQTP)*SQX*5.D-2/SQSN)*SQX/(6.D+0*SQSN))/(CPHP*SN)*X
      LAT=SNGL(PE*.572958D+2)
      LONG=SNGL(PN*.572958D+2)
      RETURN
      END
```

(b) Deriving Latitude and Longitude for Northern Ireland (NI) model sites

User-Input variables giving National Grid reference of the test site:

NGRLET = 2 letters indicating the National Grid 100km x 100km grid square
(for NI sites, first letter must be 'I' – needs error checking code)
NGREAST = 3 digit Easting within the 100km grid square (to nearest 100m)
NGRNORTH = 3 digit Northing within the 100km grid square (to nearest 100m)

Then the following algorithm (given as FORTRAN subroutine IRISHG) derives Latitude (LAT) and Longitude (LONG), in decimal degrees, from NGRLET,NGREAST and NGRNORTH.

Supplied FORTRAN program LATLONG_NI.FOR (below) and example file LATLONG_NI.DAT (supplied separately) can be used to read values of NGRLET, NGREAST and NGRNORTH, pass them through your subroutine code and output the values of LAT and LONG to file LATLONG_NI.OUT for checking for agreement with the last two columns of LATLONG_NI.DAT.

```
      PROGRAM LATLONG_NI
      CHARACTER*2 NGRLET
      INTEGER*4 NGREAST,NGRNORTH
      REAL*4 LAT,LONG
      open(7,file='LatLong_NI.dat')
      open(8,file='LatLong_NI.out')
  400 read(7,'(9x,a2,2i4)',end=500) NGRLET,NGREAST,NGRNORTH
      CALL IRISHG(NGRLET,NGREAST,NGRNORTH,LAT,LONG)
      write(6,'(1x,a2,2i4,2f10.6)') NGRLET,NGREAST,NGRNORTH,LAT,LONG
      write(8,'(1x,a2,2i4,2f10.6)') NGRLET,NGREAST,NGRNORTH,LAT,LONG
      goto 400
  500 continue
      end

      SUBROUTINE IRISHG(NGRLET,NGREAST,NGRNORTH,LAT,LONG)
      CHARACTER*2  NGRLET
      INTEGER*4    NGREAST, NGRNORTH, gi, hi, i
      REAL*4  s(2), t(3), c, d, LAT, LONG
      REAL*8  k(7), l(6), m(9), pi, x(16), xx, yy, nn, kk, zz, f, g,
h
      REAL*8  q, r

      pi=3.1415926536D0
      kk = pi/180.

      x(1)=1.005034396D0
      x(2)=5.044926593D-3
      x(3)=1.055158829D-5
      x(4)=2.059762235D-8
      x(5)=0.9983172081D0
      x(6)=2.525251575D-3
      x(7)=2.661454803D-6
      x(8)=3.461562818D-9
      x(9)=6.670534610748291D-3
      x(10)=6.768170197224D-3
      x(11)=1.000035D0
      x(12)=6377563.396D0
      x(13)=6.722670023D-3
      x(14)=6378388.0D0
      x(15)=500000.0D0
      x(16)=0.9996D0

      IF (NGRLET(1:1).NE.'I') then
```

```
       write(6,*) 'ERROR: first letter of NGR is not I'
       stop
  ENDIF

  gi = INDEX('VQLFAWRMGBXSNHCYTOJDZUPKE', NGRLET(2:2))
  hi = INDEX('VWXYZQRSTULMNOPFGHJKABCDE', NGRLET(2:2))
  IF ((gi .EQ. 0) .OR. (hi .EQ. 0)) then
       write(6,*) 'ERROR: NGR second letter not valid for NI'
       stop
  ENDIF

  gi = (gi-1)/5
  hi = (hi-1)/5
  c = NGREAST/10.
  d = NGRNORTH/10.
  xx = 1000.*(100.*gi+c)
  yy = 1000.*(100.*hi+d)
  nn = yy+5680030.5D0
  DO 1 i=1,6
1    k(i+1) = x(11)**i
  m(1) = nn/(x(12)*(1-x(9))*x(11))
  zz = m(1)/x(1)
  gi = 0
  DO WHILE((m(3) .GE. 0.001) .OR. (gi .LT. 5))
   m(2) = x(1)*zz-x(2)/2*DSIN(2*zz)+x(3)/4*DSIN(4*zz)
 &       -x(4)/6*DSIN(6*zz)
   m(3) = m(1)-m(2)
   m(4) = m(3)/x(1)
   m(3) = ABS(m(3)*x(12)*(1-x(9))*x(11))
   zz = zz+m(4)
   gi = gi + 1
  END DO
  s(1) = DSIN(zz)
  s(2) = s(1)**2
  f = DCOS(zz)
  g = f**2
  h = f**4
  t(1) = DTAN(zz)
  t(2) = t(1)**2
  t(3) = t(1)**4
  m(5) = x(12)/SQRT(1-x(9)*s(2))
  m(6) = t(1)/(2*m(5)**2*k(3))*(1+x(9)*g)*1000000000000D0
  m(7) = 5+3*t(2)+6*x(10)*g-6*x(10)*s(2)-3*x(10)**2*hi
 &       - 9*x(10)**2*g*s(2)
  m(7) = t(2)/(24*m(5)**4*k(5))*1D+24*m(7)
  m(8) = 1000000./(m(5)*x(11)*f)
  m(9)=1/(f*6*(m(5)**3)*k(4))*(1+2*t(2)+x(10)*g)*1D+18
  IF (xx .GT. 200000.) THEN
     k(1) = xx - 200000.
  ELSE
     k(1) = 200000. - xx
  END IF
  q = k(1)*0.000001
  l(1) = 45*x(10)*t(2)*s(2)
  r = (m(5)/10000.)**6
  l(1)=61+90*t(2)+45*t(2)+45*t(3)+107*x(10)*g-162*x(10)*s(2)-l(1)
  l(1) = q**6/(720*r*k(7))*t(1)*l(1)*1000000000000D0
  l(2) = 1/(f*120*m(5)**5*k(6))*(5+28*t(2)+24*t(3)+6*x(10)*g
 &       + 8*x(10)*s(2))
  l(2) = q**5*l(2)*1D+30
  l(6) = zz - m(6)*q**2+m(7)*q**4-l(1)
```

```
l(4) = m(8)*q - m(9)*q**3+l(2)
d = 352
IF (xx .GT. 200000.) THEN
   l(5)=d+l(4)/kk
ELSE
   l(5) = d-l(4)/kk
END IF
LAT = l(6)/kk
LONG = l(5)
IF (LONG .GT. 180.) LONG = LONG - 360.
RETURN
END
```

WE1.4 (ii) Estimation of long-term average mean and range of air temperature from geographic location (Easting and Northing) - for GB model sites only (N/A for Northern Ireland)

Definitions:

IGEAST = 4-digit Easting of test site to nearest 100m
IGNORTH = 4-digit Northing of test site to nearest 100m
(both previously derived from NGR – algorithm in section WE1.4 (i) (a))

TEMPM = Mean air temperature (degrees C)
TEMPR = Air temperature range (degrees C)

Algorithm:

The following algorithm (given below as FORTRAN subroutine TEMPCAL) derives TEMPM and TEMPR, from IGEAST and IGNORTH.

Subroutine TEMPCAL calls subroutine AVCALL
Subroutine TEMPCAL reads an internal data file TEMPGRID.DAT which contains previously-derived values for TEMPM and TEMPR for points in the centres of 5km interval grid squares covering the whole of Great Britain landmass (including the Scottish islands).

Data File TEMPGRID.DAT is in the following format:

EASTING (to nearest 100m)	NORTHING (to nearest 100m)	TEMPM	TEMPR
1075	9125	8.58	8.40
4315	11775	10.23	12.90
...			

Estimates of TEMPM and TEMPR for a test site are derived by averaging a sufficient number of surrounding points on the gird weighed inversely by the grid points distance from the test site.

Supplied FORTRAN program TEMPGRID.FOR (below) and example file LATLONG_GB.DAT (supplied separately) can be used to read values of IGEAST and IGNORTH, pass them through your subroutine code, and output values of TEMPM and TEMPR to file TEMPGRID.OUT which can be checked for agreement with the 4th and 5th columns of file LATLONG_GB.DAT.

```
      PROGRAM TEMPGRID
C       PROGRAM TO CALCULATE MEAN TEMPERATURE AND ANNUAL TEMPERATURE
C       RANGE FROM ARRAY STORED AT 5 KM INTERVALS
      REAL*4 VMEAN(140,260),VRANGE(140,260)
      COMMON VMEAN,VRANGE
C Read in all available values of Temp mean and Temp range
C extracted as non-zero values from a 5km grid:
C Grid Ref read as usual RIVPACS 4 digit easting and Northing
C (to nearest 100km)

      open(1,file='TempVars_GB.dat')
  100 read(1,*,end=200) IVEAST,IVNORTH,VM,VR
      I=(IVEAST-25)/50
      J=(IVNORTH-25)/50
      VMEAN(I,J)=VM
      VRANGE(I,J)=VR
      goto 100
  200 CONTINUE
      CLOSE(1)
```

```
      open(7,file='LatLong_GB.dat')
      open(8,file='TempGrid.out')

  400 read(7,'(20x,i5,i6)',end=500) IGEAST,IGNORTH
      CALL TEMPCAL(IGEAST,IGNORTH,TEMPM,TEMPR)
      write(6,'(i5,i6,2f7.2)') IGEAST,IGNORTH,TEMPM,TEMPR
      write(8,'(i5,i6,2f7.2)') IGEAST,IGNORTH,TEMPM,TEMPR
      goto 400
  500 continue
      end


      SUBROUTINE TEMPCAL(IGEAST,IGNORTH,TMEAN,TRANGE)
C       SUBROUTINE TO OPEN FILES OF TEMPERATURE VALUES AND
INTERPOLATE
C       GIVEN GRID CO-ORDINATES IN TENTHS OF KILOMETRES
      INTEGER*2  ME1,ME2,MN1,MN2,KE,KN,NP,KSQE,KSQN,IREME,IREMN,da
      REAL*4     SMEAN,SRANGE
      COMMON / tc / ME1,ME2,MN1,MN2,KE,KN,NP,SMEAN,SRANGE

C       ROWS ARE VALUES FROM 2.5 KM E TO  702.5 KM E, IN INTERVALS OF
5 KM
C       COLUMNS FROM 2.5 KM N TO 1302.5 KM N, IN INTERVALS OF 5 KM
C       MUST REDUCE TEST SITE CO-ORDINATES BY 2.5 KM IN EACH
DIRECTION
C       AS GRID TEMP VALUES ARE AT CENTRES OF 5KM SQUARES, NOT
VERTICES

      KE=IGEAST-25
      KN=IGNORTH-25
C       FIND NEAREST 5KM-POINT TO SW AND DISTANCES E AND N FROM THAT
      KSQE=INT(KE/50)
      KSQN=INT(KN/50)
      IREME=KE-50*KSQE
      IREMN=KN-50*KSQN
C       TEST IF AT A 5-KM POINT OR A VERTICAL OR HORIZONTAL BETWEEN
THEM
      IF (IREME.EQ.0.AND.IREMN.EQ.0) GOTO 120
      IF (IREME.EQ.0) GOTO 130
      IF (IREMN.EQ.0) GOTO 140
C       MUST INTERPOLATE BETWEEN 4 VALUES
      ME1=KSQE
      ME2=ME1+1
      MN1=KSQN
      MN2=MN1+1
      CALL AVCALL
      IF (NP.GT.2) GOTO 150
C       LESS THAN 3 OF POSSIBLE 4 POINTS KNOWN, SO TAKE MEAN FROM 16
      ME1=ME1-1
      ME2=ME2+1
      MN1=MN1-1
      MN2=MN2+1
      CALL AVCALL
      IF (NP.LT.4) GOTO 160
C       IF LESS THAN 4 OF 16 POINTS KNOWN, NO VALUES POSSIBLE
      GOTO 150

120   ME1=KSQE
      ME2=ME1
      MN1=KSQN
      MN2=MN1
```

```
      CALL AVCALL
      IF (NP.EQ.1) GOTO 150
C       EXACT POINT IS NOT KNOWN, SO TAKE MEAN FROM 8
      ME1=ME1-1
      ME2=ME2+1
      MN1=MN1-1
      MN2=MN2+1
      CALL AVCALL
      IF (NP.GT.3) GOTO 150
C       LESS THAN 4 OF POSSIBLE 8 POINTS KNOWN, SO TAKE MEAN FROM 24
      ME1=ME1-1
      ME2=ME2+1
      MN1=MN1-1
      MN2=MN2+1
      CALL AVCALL
      IF (NP.LT.4) GOTO 160
C       IF LESS THAN 4 OF 24 POINTS KNOWN, NO VALUES POSSIBLE
      GOTO 150

C       INTERPOLATE BETWEEN TWO VALUES ON N-S LINE
130   ME1=KSQE
      ME2=ME1
      MN1=KSQN
      MN2=MN1+1
      CALL AVCALL
      IF (NP.EQ.2) GOTO 150
C       LESS THAN 2 OF POSSIBLE 2 POINTS KNOWN, SO TAKE MEAN FROM 6
      ME1=ME1-1
      ME2=ME2+1
      CALL AVCALL
      IF (NP.GT.3) GOTO 150
C       LESS THAN 4 OF POSSIBLE 6 POINTS KNOWN, SO TAKE MEAN FROM 12
      MN1=MN1-1
      MN2=MN2+1
      CALL AVCALL
      IF (NP.LT.4) GOTO 160
C       IF LESS THAN 4 OF 12 POINTS KNOWN, NO VALUES POSSIBLE
      GOTO 150

C       INTERPOLATE BETWEEN TWO VALUES ON E-W LINE
140   ME1=KSQE
      ME2=ME1+1
      MN1=KSQN
      MN2=MN1
      CALL AVCALL
      IF (NP.EQ.2) GOTO 150
C       LESS THAN 2 OF POSSIBLE 2 POINTS KNOWN, SO TAKE MEAN FROM 6
      MN1=MN1-1
      MN2=MN2+1
      CALL AVCALL
      IF (NP.GT.3) GOTO 150
C       LESS THAN 4 OF POSSIBLE 6 POINTS KNOWN, SO TAKE MEAN FROM 12
      ME1=ME1-1
      ME2=ME2+1
      CALL AVCALL
      IF (NP.LT.4) GOTO 160
C       IF LESS THAN 4 OF 12 POINTS KNOWN, NO VALUES POSSIBLE
      GOTO 150

150   TMEAN=SMEAN
      TRANGE=SRANGE
```

```
      RETURN

C       IF VALUES CANNOT BE FOUND, ZERO VALUES ARE RETURNED
160   TMEAN=0.0
      TRANGE=0.0
      RETURN
      END

      SUBROUTINE AVCALL
C       CALCULATE AVERAGE VALUE WEIGHTED INVERSELY BY DISTANCE AND
C       NUMBER OF AVAILABLE VALUES, OVER A PRE-DEFINED GRID OF POINTS
      INTEGER*2 rn,ME1,ME2,MN1,MN2,KE,KN,NP,I,J
      REAL*4    SMEAN,SRANGE,DSUM
      REAL*4 VMEAN(140,260),VRANGE(140,260)
      COMMON VMEAN,VRANGE
      COMMON / tc / ME1,ME2,MN1,MN2,KE,KN,NP,SMEAN,SRANGE
      NP=0
      DSUM=0
      SMEAN=0
      SRANGE=0
      DO 300 I=ME1,ME2
      DO 300 J=MN1,MN2
      IF (I.LT.1.OR.I.GT.140.OR.J.LT.1.OR.J.GT.260) GOTO 300
      IF (VMEAN(I,J).EQ.0) GOTO 300
      NP=NP+1
      D=(I*50-KE)**2+(J*50-KN)**2
      IF (D.EQ.0) D=0.01
      DSUM=DSUM+1/D
      SMEAN=SMEAN+VMEAN(I,J)/D
      SRANGE=SRANGE+VRANGE(I,J)/D
300   CONTINUE
      IF (NP.EQ.0) GOTO 310
      SMEAN=SMEAN/DSUM
      SRANGE=SRANGE/DSUM
310   RETURN
      END
```

WE1.4 (iii) Calculate mean substratum composition (MSUBST) (in phi units)

MSUBST is derived from the following user-supplied environmental data for the river bed substratum composition at the test site:

BOLDCOBB = percentage cover of Boulders/Cobbles
PEBBGRAV = percentage cover of Pebbles/Gravel
SAND = percentage cover of sand
SILTCLAY = percentage cover of silt/clay

Algorithm:

TOTSUB = BOLDCOBB + PEBBGRAV + SAND + SILTCLAY

MSUBST = (-7.75*BOLDCOBB - 3.25*PEBBGRAV + 2*SAND + 8*SILTCLAY) / TOTSUB

Error Check: TOTSUB is between 97 and 103

WE1.4 (iv) Estimating discharge category (if unavailable) from stream velocity

If a value for discharge category (DCH) is not supplied by the user for the test site, then the program assumes that discharge category is to be estimated from a measurement of water velocity obtained for the site.

A supplied value means a value which is not equal to the missing indicator value of -9.

Algorithm:

```
DATA cdch / 0.31, 0.62, 1.25, 2.5, 5.0, 10.0, 20.0, 40.0, 80.0 /
CDCH(1) = 0.31
CDCH(2) = 0.62
CDCH(3) = 1.25
CDCH(4) = 2.50
CDCH(5) = 5.0
CDCH(6) = 10.0
CDCH(7) = 20.0
CDCH(8) = 40.0
CDCH(9) = 80.0
VELC(1) = 5.0
VELC(2) = 17.5
VELC(3) = 37.5
VELC(1) = 75.0
VELC(1) = 150.0

IF (DCH=-9) THEN
  IF (VEL=-9) THEN
          “Problem : No value for discharge category or stream velocity”
  ELSE
       RDCH = DEPTH/100. * WIDTH * VELC(VEL)/100
       K=10
       REPEAT
          DCH=K
          K=K-1
       UNTIL RDCH>CDCH(K)
  ENDIF
ENDIF
```

Error check:

If used to determine a value for discharge, the value of VEL must be between 1 and 5.

User-supplied values of zero for velocity (i.e. no perceived flow) should be reset to 1.

WE1.4 (iv) Estimating alkalinity (if unavailable) from conductivity, hardness or calcium

If a value for alkalinity (ALK) is not supplied by the user for the test site, then the program assumes that alkalinity is to be estimated from, in order of preference, the user-supplied values for either water hardness (HARD), calcium concentration (CALCIUM) or the conductivity (CONDUCT), as follows:

A supplied value means a value which is not equal to the missing indicator value of -9.

Algorithm:

```
IF (ALK=-9) THEN
    IF (HARD>-9) THEN
        ALK = 4.677 + 0.6393*HARD
    ELSE
        IF (CALCIUM>-9) THEN
            ALK = 14.552 + 1.7606*CALCIUM
        ELSE
            IF (CONDUCT>-9) THEN
                ALK = 0.3201*CONDUCT -8.0593
            ELSE
              "Problem : No value for alkalinity"
            END IF
        ENDIF
    ENDIF
ENDIF

IF ALK < 0.1 ALK = 0.1
```

Error check: If used to determine a value for alkalinity, the value of ALK, HARD, CALCIUM or CONDUCT must be > 0.0

WE1.6 (i) Rules and checks that user-supplied values of environmental variables are within ranges covered by the RIVPACS reference sites in the relevant model.

The following checks should be made (in this order):

(a) Check that the user-supplied values of the environmental variables for a test site are not missing (i.e. blank) or set to the missing value indicator (currently -9 or -9.) for the variables in the table below marked '(M)'

(b) Check that the user-supplied values of the environmental variables for a test site lie within the overall valid range (VMIN to VMAX) for UK sites, as given in the table below:

If a value is less than the valid minimum (VMIN) or greater than the valid maximum (VMAX) for that environmental variable, then:

- it should be flagged as INVALID DATA for that variable,
- calculations should stop for that site, and proceed to the next site
- the relevant output files for that run should be supplied with an output "row/record" for that site with missing value indicators (-9 or -9,) for all of the normal output values (e.g. probabilities of group membership, Expected values, O/E, status class assignments and their probabilities).

Having an output file row/record for any sites with invalid values will ensure that the output files still match up with the input files (site-for-site).

Environmental predictor variable	Units	User-input	Check if missing value (M)	VMIN	VMAX
Latitude	^{o} North	LAT		49.0	71.0
Longitude	^{o} West	LONG		-11.0	2.0
Altitude	m	ALT	(M)	0.0	1345
Distance from source	km	DIST	(M)	0.0	
Stream width	m	WIDTH	(M)	0.0	
Stream depth	cm	DEPTH	(M)	0.0	
Discharge category		DCH	(M)	0	10
Alkalinity	mg l^{-1} $CaCo_3$	ALK	(M)		
Slope at site	m km^{-1}	SLOPE	(M)		
% Boulders & cobbles		BOLDCOBB	(M)	0	100
% Pebbles & gravel		PEBBGRAV	(M)	0	100
% sand		SAND	(M)	0	100
% silt & clay		SILTCLAY	(M)	0	100

(c) Check that the user-supplied values of the environmental variables for a test site lie within the range (GMIN to GMAX) covered by the RIVPACS Reference sites for the appropriate geographic model (GB or NI), as given in the table below:

			GB		Northern Ireland	
Environmental predictor variable	Units	User-input	GMIN	GMAX	GMIN	GMAX
Latitude *	° North	LAT	50.8	62.0	54.0	55.2
Longitude *	° West	LONG	-8.0	1.4	-8.1	-5.7
Altitude	m	ALT	1	590	3	180
Distance from source	km	DIST	0.1	202.8	2.2	75.0
Stream width	m	WIDTH	0.4	117	2.0	37
Stream depth	cm	DEPTH	1.7	300	15.0	183
Mean substratum	phi	MSUBST	-7.71	8.00	-7.75	6.61
Discharge cat		DCH	1	9	1	8
(Velocity category)		VEL	1	5	1	5
Alkalinity	mg l^{-1} $CaCo_3$	ALK	1.2	366	2.5	194
Slope at site	m km^{-1}	SLOPE	0.1	150.0	0.1	50.0
Mean air temperature	°C	TEMPM	7.5	11.5	---	---
air temperature range	°C	TEMPR	8.3	13.9	---	---

* internally-derived from NGR by algorithm in WE1.4(i)

If a value is less than the minimum (GMIN) or greater than the maximum (GMAX) for that environmental variable, then:

- it should be flagged as
  ‘WARNING : OUT OF REFERENCE SITE RANGE for that variable,
  giving the observed value (and perhaps also the covered range GMIN – GMAX)
- run calculations should continue (as at present) for this test site
  (the multiple discriminant functions will provide a later multivariate check of whether the environmental conditions at the test site are encompassed by the reference sites)

Note: Previous RIVPACS III+ models required all values of SLOPE to be no more than 99.9, slopes greater were entered as 99.9. As MDA models are based on the actual slope (including the one GB site with slope>100 (i.e. 150), it would be better to read in site slope allowing for values >100.

(d) Values of variables for which VMIN is zero, but which are used in the predictions in their logarithmic form, are reset to the following values:

IF ALT = 0 THEN ALT = 1
IF DIST <0.1 THEN DIST = 0.1
IF WIDTH < 0.1 WIDTH = 0.1
IF DEPTH < 1 DEPTH = 1
IF DCH = 0 DCH = 0.1
IF ALK < 0.1 ALK = 0.1

WE1.3 Algorithms for using discriminant functions to calculate probabilities of belonging to each RIVPACS site end group

Definitions:

v = id of current environmental predictor variable
vN = number of environmental predictor variables

g = id of current end group
gN = number of end groups in current Reference end group set (set: 1 = GB, 2 =NI)

$NRef_g$ = number of reference sites in end group g

d = id of current discriminant function axis
dN = number of discriminant function axes in current Reference end group set

$DFCoef_{v,d}$ = discriminant function coefficient for predictor variable v on discriminant function d

Env_v = value of environmental predictor variable v for the current test site

$DFScore_d$ = discriminant function score on axis d for the current test site

$DFMean_{g,d}$ = mean discriminant function score of end group g on axis d

$MahDist_g$ = Mahalanobis distance of test site from end group g

$Prob_g$ = Probability test site belongs to end group g

$x_1 + ... + x_n$ = sum of the list of *n* variables x_1, $x_{2,}$, x_3 ... up to x_n

$b_1 * x_1 + ... b_n * x_n$ = sum of the list of *n* items ($b_1 * x_1$), ($b_2 * x_2$), up to ($b_{1n} * x_{1n}$) where ($b_1 * x_1$) denotes b_1 multiplied by x_1

Algorithm:

$DFScore_d$ = $DFCoef_{1,d} * Env_1 + ... + DFCoef_{vN,d} * Env_{vN}$; for d = 1,...,dN

$MahDist_g$ = $(DFScore_1 - DFMean_{g,1})^2 + ... + (DFScore_{dN} - DFMean_{g,dN})^2$; for g = 1,...,gN

$MahDist_{min}$ = minimum of ($MahDist_1$,...,$MahDist_{gN}$)

$PDist_g$ = $NRef_g * EXP(-MahDist_g / 2)$; where EXP is the natural exponential function

$PDistTot$ = $PDist_1 + ... + PDist_{gN}$

$Prob_g$ = $PDist_g / PDistTot$

Internally-supplied Data files for Discriminant Functions (DF) and DF End-group Means:

File DFCOEFF_GB685.DAT
- holds the discriminant function coefficients ($DFCoef_{v,d}$) for 685 site New GB model
- number of rows = vN =13 ;
- number of numeric columns (excluding first text column) = dN = 13
- supplied 7/12/07

File DFCOEFF_NI.DAT
- hold the discriminant functions coefficients ($DFCoef_{v,d}$) for NI model
- number of rows = vN =11
- number of numeric columns (excluding first text column) = dN = 10
- supplied end July 2007 (and re-supplied unaltered 7/12/07)

File DFCOEFF_GB614.DAT
- holds the discriminant function coefficients ($DFCoef_{v,d}$) for 614 site Old GB model
- number of rows = vN =13 ;
- number of numeric columns (excluding first text column) = dN = 13
- supplied 7/12/07

where $DFCoef_{v,d}$ is stored as the numeric element/column *d* in row *v* of the files
(Note first item in each row is the environmental variable text name for variable *v* which is given merely to improve readability and could be removed by the programmers)

File DFMEAN_GB685.DAT
- holds discriminant functions end group mean values ($DFMean_{g,d}$) for New GB model
- number of rows = gN = 43
- number of numeric columns (excluding first text column) = dN = 13
- supplied 7/12/07

File DFMEAN_NI.DAT
- holds discriminant functions end group mean values ($DFMean_{g,d}$) for NI model
- number of rows = gN =11
- number of numeric columns (excluding first text column) = dN = 10
- supplied end July 2007 (and re-supplied unaltered 7/12/07)

File DFMEAN_GB614.DAT
- holds discriminant functions end group mean values ($DFMean_{g,d}$) for Old GB model
- number of rows = gN = 35
- number of numeric columns (excluding first text column) = dN = 13
- supplied 7/12/07

where $DFMean_{g,d}$ is stored as the item in column *d* in row *g* of the files

WE1.4 (v) Environmental predictor variables, their transformations and use in the discriminant functions

The discriminant functions for the 'GB' model (reference end group set 1) use 13 environmental predictor variables (i.e. vN = 13), as detailed below.

The Northern Ireland (NI) model (Reference end group set 2) uses the same set of variables apart from air temperature mean (TEMPM) and air temperature range (TEMPR), which were not available for Northern Ireland and probably would not add discriminatory power within this relatively small geographic region.

However, for the purposes of specifying the discriminant functions and inputting their coefficients ($DFCoeff_{v,d}$), it is simpler (and mathematically equivalent) to treat both discriminant functions models as having the same set of vN=13 variables, but with the discriminant function coefficients for TEMPM and TEMPR set to zero. The values for TEMPM and TEMPR will then have no effect but need to be set to some arbitrary value (say 0.0) for use in calculating the discriminant function scores for any test site in Northern Ireland.

Some of the environmental predictor variables are used in the discriminant functions in a logarithm to base 10 transformed form (denoted Log_{10}), as detailed below.

The precise order and form of the environmental variables to be used as Env_1 – Env_{vN} in the discrimination functions equations used to calculate the discriminant function axes scores ($DFScore_d$) is as follows:

Env_v	Environmental predictor variable	User-input	Internally-derived	Form used in discriminant functions
Env_1	Latitude	LAT		LAT
Env_2	Longitude	LONG		LONG
Env_3	Altitude	ALT		LGALT = Log_{10}(ALT)
Env_4	Distance from source	DIST		LGDIST = Log_{10}(DIST)
Env_5	Stream width	WIDTH		LGWIDTH = Log_{10}(WIDTH)
Env_6	Stream depth	DEPTH		LGDEPTH = Log_{10}(DEPTH)
Env_7	Mean substratum		MSUBST	MSUBST
Env_8	Discharge category	DCH		DCH
Env_9	Alkalinity*	ALK		ALK
Env_{10}	Alkalinity*	ALK		LGALK = Log_{10}(ALK)
Env_{11}	Slope at site	SLOPE		LGSLOPE = Log_{10}(SLOPE)
Env_{12}	Mean air temperature		TEMPM	TEMPM
Env_{13}	Air temperature range		TEMPR	TEMPR

* Alkalinity is involved in the discriminant functions in both untransformed form (as Env_9) and in log_{10} transformed form (as Env_{10}) to represent its non-linear impact on the biota

WE1.6 (ii) Rules for determining the environmental suitability (coded 1-5) in RIVPACS output) of the test site for prediction by RIVPACS based on its multivariate discriminant analysis (MDA) distance from each end group

Definitions:

$MahDist_g$ = Mahalanobis distance of test site from end group g

$MahDist_{min}$ = minimum of ($MahDist_1$,...,$MahDist_{gN}$)

SuitCode = suitability code for the test site

SuitText = Upper limit of class of probability that test site belongs to any end group

Data Table: Chi-square values (CQ_1, CQ_2, CQ_3, CQ_4) used in determining the suitability code for a test site

End group set	CQ_1	CQ_2	CQ_3	CQ_4
1 = GB	21.02606	24.05393	26.21696	32.90923
2 = NI	18.30700	21.16080	23.20930	29.58830

Algorithm:

Use the following order of rules to determine SuitCode and SuitProb:

Range of values for $MahDist_{min}$	SuitCode	SuitText
$MahDist_{min} < CQ_1$	1	'>5%'
$CQ_1 \leq MahDist_{min} < CQ_2$	2	'< 5%'
$CQ_2 \leq MahDist_{min} < CQ_3$	3	'<2%'
$CQ_3 \leq MahDist_{min} < CQ_4$	4	'<1%'
$MahDist_{min} \geq CQ_4$	5	'<0.1%'

(SuitCode values >5 are no longer used in RIVPACS)

The value of SuitCode is output in the RIVPACS output O-E type 1 and 2 files containing the O,E, O/E, status classes and confidence of class for individual sites (.OE1 type files) and comparison of sites (.OE2 type files).

In RIVPACS, a warning about the suitability of a test site for RIVPACS predictions was output in the RIVPACS/RPBATCH output text 'listing file', and on screen when previous versions of RIVPACS were run in RIVPACS interactive mode. Any such text output warning should say:

'The probability that this site belongs to any group in the classification is ' [SuitText]

For example, if SuitCode = 2, the warning should say:
'The probability that this site belongs to any group in the classification is <5%'

WE1.5 Algorithms for prediction of expected values of any index based on probability of end group membership and average values of the index amongst reference sites in each end group. Algorithms for taxonomic prediction (including prediction of occurrence and expected abundances)

Definitions:

g = id of current end group
gN = number of end groups in current Reference end group set (set: 1 = GB, 2 =NI)

Prob_g = Probability test site belongs to end group g

i = id of current biological index
iN = total number of biological indices

t = id of current taxon
tN = number of taxon at the selected taxonomic level
(possible taxonomic levels: BMWP families, revised BMWP families all families, or species)

s = id of selected season(s) combination (referred to as 'season *s*');
(1 = spring, 2 = summer, 3 = autumn, 4 = spring+summer,
5 = spring+autumn, 6 = summer+autumn, 7 = all three seasons)

$\text{IDXMean}_{i,s,g}$ = Mean value of index *i* for season *s* for reference sites in end group *g*

$\text{TAXAPR}_{t,s,g}$ = Proportion of reference sites in end group *g* with taxon *t* for season *s*

$\text{TAXAAB}_{t,s,g}$ = Average of log abundance categories for taxon *t* for season *s* amongst reference sites in end group *g*

$\text{TAXAPRAB}_{t,s,g,a}$ = Proportion of reference sites in end group *g* with taxon *t* at abundance category *a* for season *s* (optional)

ExpIDX_i = Expected value of index *i* for selected season *s* for current test site

$\text{ExpTAXAPR}_{t,s}$ = Expected probability of occurrence of taxon *t* for season *s* for the current test site

$\text{ExpTAXAAB}_{t,s}$ = Expected log abundance category values of taxon *t* for season *s* for the current test site

$\text{ExpTAXAPRAB}_{t,s,a}$ = Expected probability of occurrence of taxon *t* at abundance category *a* for season *s* for the current test site (optional)

Algorithm:

$\text{ExpIDX}_i = \text{Prob}_1 * \text{IDXmean}_{i,s,1,} + \ldots + \text{Prob}_{gN} * \text{IDXmean}_{i,s,gN}$

$\text{ExpTAXAPR}_{t,s} = \text{Prob}_1 * \text{TAXAPR}_{t,s,1,} + \ldots + \text{Prob}_{gN} * \text{TAXAPR}_{t,s,gN}$

$\text{ExpTAXAAB}_{t,s} = \text{Prob}_1 * \text{TAXAAB}_{t,s,1} + \ldots + \text{Prob}_{gN} * \text{TAXAAB}_{t,s,gN}$

$\text{ExpTAXAPRAB}_{t,s,a} = \text{Prob}_1 * \text{TAXAPRAB}_{t,s,1,a} + \ldots + \text{Prob}_{gN} * \text{TAXAPR}_{t,s,gN,a}$ (optional)

Internally-supplied Data files :

A separate EXCEL file will be provided with the values of each of :

$\text{IDXMean}_{i,s,g}$ = Mean value of index *i* for season *s* for reference sites in end group *g*

$\text{TAXAPR}_{t,s,g}$ = Proportion of reference sites in end group *g* with taxon *t* for season *s*

$\text{TAXAAB}_{t,s,g}$ = Average of log abundance categories for taxon *t* for season *s* amongst reference sites in end group *g*

$\text{TAXAPRAB}_{t,s,g,a}$ = Proportion of reference sites in end group *g* with taxon *t* at abundance category *a* for season *s* (optional)

There file layouts are expected to be as follows (subject to agreement with the project manager and IS software programmers):

File IDXMEAN.XLS with illustrative example cell values

Model (1=GB, 2=NI)	Index *i* (i = 1,...,iN)	season *s* (s = 1,...,7)	end group *g* (g = 1,...,gN)	$\text{IDXMean}_{i,s,g}$
1	1	1	1	15.2
1	1	1	2	19.3
...				
2	iN	7	11	6.45

Note: number of end groups gN is different for model 1 (GB) and model 2 (NI); for NI it is already known that gN = 11

File TAXAPR.XLS - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (t = 1,...,tN)	season *s* (s = 1,...,7)	end group *g* (g = 1,...,gN)	$\text{TAXAPR}_{t,s,g}$
1	1	1	1	0.843
1	1	1	2	0.750
...				
2	tN	7	11	0.333

File TAXAAB.XLS - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (*t* = 1,...,tN)	season *s* (*s* = 1,...,7)	end group *g* (*g* = 1,...,gN)	$\mathrm{TAXAAB}_{t,s,g}$
1	1	1	1	1.582
1	1	1	2	0.923
...				
2	tN	7	11	1.800

File TAXAPRAB.XLS - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (*t* = 1,...,tN)	season *s* (*s* = 1,...,7)	end group *g* (*g* = 1,...,gN)	abundance category *a*	$\mathrm{TAXAPRAB}_{t,s,g,a}$
1	1	1	1	1	0.85
1	1	1	1	2	0.00
...					
2	tN	7	11	4	0.35

The above internal data files to be supplied by CEH in EXCEL format by end 2007.

It may be better to have separate files for the two geographic models (GB and NI) because their number of end groups is different.

Optional: It is up to the WFD72C Project Board whether they would like to include the new extra functionality provided by the output derived by File TAXAPRAB.XLS and the accompanying output of values of $\mathrm{TAXAPRAB}_{t,s,g,a}$, as defined above. This is a new idea from CEH which could provide useful output, but the software is no longer working with any input observed taxonomic info with which to compare the predicted taxonomic abundances with directly, so perhaps this is not of high priority.

WE1.7 Algorithms for simulating effects of sampling error/variability and other "errors" on bioassessment uncertainty and confidence of class.

Last updated: 25/09/07

Background to agreed approach

The final project revised tender and draft project plan (28th June 2007) states that for WE1.7:

(v) This will initially be based on the mathematical methods used in RIVPACS III+, and as such will incorporate the same estimates of the effects of sampling variation and sample processing errors (biases) for the existing BMWP indices (NTAXA, BMWP Score and ASPT).

(vi) Generic algorithms for simulating effects of sampling variability (replicate and/or temporal) for any index will be provided (estimates for some other key indices to be derived in WE5).

(vii) The effects of sample processing errors are complex, will depend on the type of metric, and are not yet understood or assessed for other metrics *Also suitable audit information is not readily available on taxonomic abundances. It was agreed at the pre-project interview meeting of 28/05/07 that the algorithms to represent the effect of sampling processing errors will have to be limited to the simple generic methods adopted for the STARBUGS system (STAR Bioassessment Uncertainty Guidance Software; Clarke 2005, Clarke & Herring 2006). Note that, within this stage 2 of the project, estimates of the parameters of these algorithms for effects of sample processing errors will only be supplied for the three original BMWP indices (as developed and used in RIVPACS III+).*

(viii) Algorithms for comparing the O/E values and status class assignments for two samples. Initially these will be identical to the methods using the RIVPACS III+ procedure COMPARE, as this is our currently recommended general approach, and is the approach we at CEH adapted in our development of STARBUGS.

Uncertainties in observed (O) and expected (E) values of biological indices and thus in their Ecological Quality Index (EQI = O/E) values and the resulting confidence of assigning test sites to ecological status classes are all assessed using statistical Monte Carlo simulation procedures. Based on previously-derived estimates of variance parameters for the effects of typical replicate sampling variation, within-season temporal variation and between-year variation (for multi-year assessments) in index values, Monte Carlo simulations are used to generate a large number of simulated potential values of the observed (O) and the expected (E) values of each index and hence of the O/E ratios. The lower and upper 2.5% values of the frequency distribution of the simulated O/E values are used to estimate 95% confidence limits for the true average O/E ratio for the site during that time period. Each simulated O/E value can also be classified to ecological status class based on O/E class limits for each index. The proportions of simulated values falling in each class can be used to estimate the probabilities of each class being the true (average) quality of the test site during that time period.

At least 9999 simulations should be used, and that the same arbitrary but fixed random number seed is used each run so that exactly the same uncertainty results and probabilities of class are obtained in repeated runs on the same data.

The general statistical procedures used in RIVPACS III+ and to be used in the new RICT software were developed by Furse *et al.* (1995) and summarised in Clarke (2000) and Clarke et al (2002).

In this WE1.7 deliverable, we provide the recommended analogous and enhanced algorithms to be used to simulate and assess uncertainty of bioassessments within the new RICT software.

Furse *et al.* (1995) used an intensive replicated sampling programme to estimate the typical replicate sampling variation that occurs in observed values of the three BMWP indices (BMWP Score, Number of BMWP taxa (NTAXA) and ASPT (Average Score Per Taxon) for a wide range of sites of differing ecological quality and environmental type. They found that:

(i) Sampling variation in observed values of the square root ($\surd$) of the number of BMWP taxa approximately follows a Normal statistical distribution for all types and quality and site, with the standard deviation, $SD_{\surd T}$, only varying according to the number of seasons involved in the overall (combined season) sample ($SD_{\surd T}$: 0.228 (1-season), 0.164 (2-seasons), 0.145 (3-seasons).

(ii) Sampling variation in observed values of ASPT approximately follows a Normal statistical distribution for all types and quality and site, with the standard deviation, SD_A, only varying according to the number of seasons involved in the overall (combined season) sample (SD_A : 0.249 (1-season), 0.161 (2-seasons), 0.139 (3-seasons).

Furse *et al.* (1995) also compared the taxonomic lists for samples collected, sorted and identified by the then NRA (primary analysis) with the equivalent lists when the same samples were audited for sorting efficiency and accuracy of identification by the then Institute of Freshwater Ecology (now CEH). Furse *et al*. (1995) estimated that, on average, 51% of taxa missed in any single season sample are not subsequently found in a second sample from that site in another season of the same year. Furthermore, 37% of taxa missed in a single sample are not found in either of the samples taken from the two other RIVPACS sampling seasons.

Furse *et al.* (1995) also quantified the effects of recorder variation in estimating the values of the RIVPACS predictor environmental variables from these sites and derived estimates of their effects on uncertainty in estimates of expected values of the BMWP indices.

Uncertainty assessments in RIVPACS III+ were based on the results, conclusions and uncertainty parameter estimates derived from that study. The same approach and simulation algorithms are provided for use in the new RICT software for assessing uncertainty in these three indices. A similar general approach and use of simulation algorithms is suggested and provided for other indices.

Single- and multi-year runs and site assessments

The new RICT software is to include single- and multi-year site assessments.

Single year assessments are assumed to be based on one observed sample (obtained in either a single season or combined from two or three seasons (spring, summer autumn)) and thus one observed value for each biological index. This is divided by the single expected value for that site and 'season' to give a single O/E value for any particular index.

Multi-year assessments are to be based on an estimate of the average quality over a three year period. Observed (O) index values will be available for one, two or all three years in the period. The same field-based environmental predictor variables may or may not have been measured in each year. If a single expected (E) index value is used in each of the up to three sampled years, then:

average of the (O/E) = average of the (O) / E.

If different E values are available for each year then:

average of the (O/E) ≠ average of the (O) / average of the (E).

However, for any single site, the expected (E) is relatively constant and insensitive/robust to the typical degree of within-site changes in the environmental variables that occur (Armitage, P.D. 2000. The potential of RIVPACS for predicting the effects of environmental change. In: Wright, J.F., D.W. Sutcliffe and Furse, M..T. (eds). *pp 93-112. Freshwater Biological Association*, Ambleside.).

To assess uncertainty in site assessments, we have available and have used a mixture of replicated samples and time series of observed RIVPACS sample data to estimate components of uncertainty in the average O index value for a period (single- or multi-year).

For a combination of the above reasons, the estimate of the average quality for a three year period that is to be used in RICT multi-year assessments is defined as:

Estimate of average quality = average of the (O) / average of the (E).

The uncertainty variance associated with this estimator or average quality can then be estimated from the uncertainty associated with estimate average O value and the uncertainty associated with estimating the average E value for the three year period at that site.

Notes on assumptions:

(i) The RICT simulations of the stochastic variability assume that the observed index values are based on a single sample from that 'season' in any one year (where 'single sample' for a spring and autumn combined season sample analysis means one sample in spring and one sample in autumn in the same year have been combined). Multi-year assessments are based on the assumption that the observed index value (ObsIDX_i) is the average of 'single samples' from 'season' s in the N_{year} sampled years. If some future assessments were based on more than one sample in each 'season' of each year then the observed sample values would have smaller random uncertainty terms (SDObs_{ir}), but these are not expected to occur and thus are not catered for here.

(ii) The RICT (and RIVPACS III+) uncertainty assessments are based on the assumption that the same single sampling site with a WFD water body has been sampled on each occasion, and that furthermore, this site is representative of the ecological status of the WFD water body as a whole. Therefore the uncertainty estimates are actually for ecological quality at that river site; there is potentially additional uncertainty due to un-quantified spatial variability between possible sampling sites with the water body.

Definitions:

i = id of current biological index
iN = total number of biological indices

rN = number of simulations used to assess uncertainty

At present iN = 12, with indices referred to in the following order of id:

Index id i	Index Name	Transformation of index prior to adding simulated "error" terms
1	BMWP Score	derived from indices 2 & 3 [+]
2	NTAXA	square root
3	ASPT	none
4	Revised BMWP Score (non abundance weighted)	derived from indices 5 & 6 [+]
5	Revised NTAXA (non abundance weighted)	square root
6	Revised ASPT (non abundance weighted)	none
7	Revised BMWP Score (abundance weighted)	derived from indices 8 & 9 [+]
8	Revised NTAXA (abundance weighted)	square root (probably)
9	Revised ASPT (abundance weighted)	none (probably)
10	AWIC (family level)	not yet known
11	LIFE (family level)	not yet known
12	ICMi (from its individual components)	not yet known

[+] Because $ObsIDX_{1s}$ = $ObsIDX_{2s}$ * $ObsIDX_{3s}$ (apart from rounding errors), we derive simulated values for $ObsIDX_{1s}$ from simulated values for $ObsIDX_{2s}$ and $ObsIDX_{3s}$; similarly for $ObsIDX_{4s}$ and $ObsIDX_{7s}$ (we anticipate).

s = id of selected season(s) combination (referred to as 'season');
(1 = spring, 2 = summer, 3 = autumn, 4 = spring + summer,
5 = spring + autumn, 6 = summer + autumn, 7 = all three seasons)

The term "sample" refers to the total sample for which the index values were calculated; this could be a single season sample, or a two or three season combined sample.

$ObsIDX_i$ = Observed sample value of index *i* (for selected season *s*) for current test site

$ExpIDX_i$ = Expected value of index *i* (for selected season *s*) for the current test site

Note: In multi-year runs
$ObsIDX_i$ = average of the observed (O) values of index *i*
and $ExpIDX_i$ = average of the expected (E) values of index *i*
for current test site over the three-year period.

Note: Because any single software run only involves one selected season combination *s* the subscript *s* is dropped for the observed and expected index values to make it easier to include a subscript for the r^{th} simulated value of the observed and expected values of each index.

Thus (for example):

$ObsIDX_1$ = Observed value of BMWP Score for the current test site
$ObsIDX_2$ = Observed value of NTAXA for the current test site
$ObsIDX_3$ = Observed value of ASPT for the current test site

$ExpIDX_1$ = Expected value of BMWP Score for the current test site
$ExpIDX_2$ = Expected value of NTAXA for season *s* for the current test site
$ExpIDX_3$ = Expected value of ASPT for season *s* for the current test site

SD denotes standard deviation (where appropriate on the transformed index scale)

$SDRep_{is}$ = Replicate sampling SD of transformed observed values of index *i* for ‘season’ *s*

$SDTSeas_{is}$ = Within-season temporal variability SD of transformed observed values of index *i* for ‘season’ *s*

$SDTYear_{is}$ = Between-year variability SD of transformed observed values of index *i* for ‘season’ *s* (based on inter-year variance within 3-year periods)

$SDObs_{is}$ = Overall uncertainty SD for observed value of index *i* for ‘season’ *s* (based on a combination of the individual component SD)

Estimates of $SDRep_{is}$ for the original BMWP indices (indices 1-3) were derived in the BAMS study and can be used in the RICT software. Estimates of $SDRep_{is}$ for other indices and estimates of $SDTSeas_{is}$ and $SDTYear_{is}$ for all indices will be estimated and supplied as part of WE5-WE6 of SNIFFER project WFD72C (due mid-December 2007).

Single-year or multi-year (3-year) assessment runs:

The RICT software will have two periods over which site quality can be estimated and assessed:

(a) single-year run - assessing site quality for a single year
- based on single O value ($ObsIDX_i$) / single E value ($ExpIDX_i$)

(b) multi-year run - assessing average site quality over a three year period
- based on average O value ($ObsIDX_i$) / average E value ($ExpIDX_i$)

$NObs_{year}$ = number of years (1, 2 or 3) for which a sample was involved in the estimate of the average O value

$NExp_{year}$ = 1 for single-year run
= number of years (1, 2 or 3) for which a separate estimate of the E value was involved in the estimate of average E value (for multi-year run)

If a single estimate of E is used for all three years, then $NExp_{year}$ = 1)

Algorithms

Simulating potential observed index values

The simulated potential observed values ($ObsIDX_{ir}$) are generated by transforming the observed sample value to the appropriate scale, then adding the appropriate random error term ($ZObs_{ir}$), then back-transforming to the original index scale. (For example, with index 2 (NTAXA), we square root (√) the observed sample value, add a random error term, and then square the result to get a simulation of the potential value of NTAXA we could have obtained by chance if a different single replicate sample had been taken at the site in the same season(s)).

For single-year runs:

$$SDObs_{is} = \sqrt{((SDRep_{is})^2 + (SDTSeas_{is})^2)}$$

For multi-year (3-year) runs:

$$SDObs_{is} = \sqrt{(((SDRep_{is})^2 + (SDTSeas_{is})^2 + (SDTYear_{is})^2 * (1 - NObs_{year} / 3)) / NObs_{year})}$$

For each simulation *r*, for both single- and multi-year runs, derive:

$ZNorm_{ir}$ = Random number deviate from a standard Normal distribution with a mean of 0.0 and SD of 1.0 for index *i* in simulation *r*

$ZObs_{ir}$ = Random deviate for potential observed sample value of index *i* in simulation *r*

$ZObs_{ir}$ = $ZNorm_{ir}$ * $SDObs_{is}$

Note: RICT software programmers can either use an existing function code to generate such random numbers from a standard normal distribution or use the FORTRAN code used in RIVPACS III+ supplied at the end of this document)

$ObsIDX_{ir}$ = Simulation *r* Observed sample value of index *i* for current test site

Calculate:

For original BMWP indices (NTAXA, ASPT and BMWP score):

$ObsIDX_{2r} = (\sqrt{(ObsIDX_2)} + ZObs_{2r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{3r} = ObsIDX_3 + ZObs_{3r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{1r} = ObsIDX_{2r} * ObsIDX_{3r}$ = r^{th} simulated value for observed BMWP Score

Similarly for the Revised non-abundance-weighted BMWP indices:

$ObsIDX_{5r} = (\sqrt{(ObsIDX_5)} + ZObs_{5r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{6r} = ObsIDX_6 + ZObs_{6r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{4r} = ObsIDX_{5r} * ObsIDX_{6r}$ = r^{th} simulated value for observed BMWP Score

And possible also for the Revised abundance-weighted BMWP indices (to be confirmed):

$ObsIDX_{8r} = (\sqrt{(ObsIDX_8)} + ZObs_{8r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{9r} = ObsIDX_9 + ZObs_{9r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{7r} = ObsIDX_{8r} * ObsIDX_{9r}$ = r^{th} simulated value for observed BMWP Score

Similar algorithms will be supplied for the new indices 10 (AWIC), 11 (LIFE) and 12 (ICMi), all at family level, when the replicate sample and temporal data has been analysed in WE5-6 in autumn 2007. The most appropriate transformation of index values to minimise variance dependence on index values will also be determined in WE5-6.

Simulating corrections for biases in observed index values due to sample processing errors

The quantitative effects of sample processing errors can only be assessed by a detailed analysis of the data provided by an external audit and re-examination of the sorting and taxonomic identification accuracy for macroinvertebrate samples. As explained in the background introduction above to WE1.7, this has currently only been done for the existing BMWP indices (BMWP Score, NTAXA and ASPT). Therefore below, we detail the precise algorithms used to simulate the biases for these three indices (1-3). It is likely that these bias-correction algorithms will also be appropriate for their revised unweighted counterparts (indices 4-6). Analogous bias-correction algorithms are assumed to apply for the Revised Abundance-weighted BMWP indices (7-9) and algorithms and equations are provided for software coding, but their parameter values are unknown.

For other indices, we merely give the simple generic procedures for bias-correction incorporated into STARBUGS.

Definitions:

ObsIDX_{ir} = Simulation *r* Observed sample value of index *i* for current test site (uncorrected for bias)

Ubias_2 = estimate of average net under-estimation of NTAXA for selected ‘season’ sample

Ubias_{ir} = Estimate of bias (net under-estimation) of index *i* for simulation *r*

ObsIDX_{irB} = Bias-corrected observed value of index *i* for simulation r

Simulating bias-corrections for indices 1-3 (BMWP Score, NTAXA and ASPT)

Bias_{2s} = User-supplied estimates of the average under-estimation of NTAXA (index 2) due to sample sorting and identification errors for single season samples taken in season *s* (1 = spring, 2 = summer, 3 = autumn)

Kseas_{s} = 1 if the overall sample of interest involves season *s*
= 0 otherwise

Ubias = $\text{Bias}_{21} * \text{Kseas}_{1} + \text{Bias}_{22} * \text{Kseas}_{2} + \text{Bias}_{23} * \text{Kseas}_{13}$

For single season samples : Ubias_{2} = Ubias
For two season combined samples : Ubias_{2} = 0.51 * Ubias
For three season combined samples : Ubias_{2} = 0.37 * Ubias

Special case: when no BMWP taxa were recorded in the sample (i.e. $\text{ObsIDX}_{2} = 0$), assume none were missed (i.e, set $\text{Ubia}_{2} = 0$)

Ubias_{2r} = bias (net under-estimate of number of BMWP taxa) for simulated sample r, estimated as a random deviate from a Poisson distribution with a mean of Ubias_{2} (program code for Poisson random deviates to be supplied, if required)

Note: RICT software programmers can either use an existing function code or detailed code to generate such random numbers from a Poisson distribution or we can provide the FORTRAN code used in RIVPACS III+)

Zbias_{3r} = Random number deviate from a standard Normal distribution with a mean of 0.0 and SD of 1.0

Ubias_{3r} = ASPT of the Ubias_{2r} missed taxa for simulated sample r
= $u_{3a} + u_{3b} * \text{ObsIDX}_{2} + \text{Zbias}_{3r} * u_{3c} / \sqrt{\text{Ubias}_{2r}}$)

where $u_{3a} = 4.29$, $u_{3b} = 0.077$, $u_{3c} = 2.0$

Note: It is unlikely, but mathematically feasible with this algorithm to derive values of Ubias_{3r} >10 (maximum real value), such values of Ubias_{3r} should be reset to 10;
similarly, any values of Ubias_{3r} <1 should be reset to 1).

$\text{Ubias}_{1r} = \text{Ubias}_{2r} * \text{Ubias}_{3r}$ = under-estimate of BMWP score for simulated sample r

$\text{ObsIDX}_{1rB} = \text{ObsIDX}_{1r} + \text{Ubias}_{1r}$ = bias-corrected observed BMWP Score for simulation r

$\text{ObsIDX}_{2rB} = \text{ObsIDX}_{2r} + \text{Ubias}_{2r}$ = bias-corrected observed NTAXA for simulation r

$\text{ObsIDX}_{3rB} = \text{ObsIDX}_{1rB} / \text{ObsIDX}_{2rB}$ = bias-corrected observed ASPT for simulation r

Simulating bias-corrections for indices 4-6 (Revised non--weighted BMWP Score, NTAXA and ASPT)

For simplicity, it is assumed that the bias for the number of Revised unweighted BMWP taxa (index 5) is the same as the bias for the number of BMWP taxa (index 2)

$Ubias_{6r}$ = Revised unweighted ASPT of the $Ubias_{2r}$ missed taxa for simulated sample r
= $u_{6a} + u_{6b} * ObsIDX_2 + Zbias_{3r} * u_{6c} / \sqrt{Ubias_{2r}})$

where estimates of u_{6a} , u_{6b} and u_{6c} are currently unavailable, but it may be adequate to use the equivalent values to those derived for the original ASPT, namely:

$u_{6a} = 4.29$, $u_{6b} = 0.077$, $u_{6c} = 2.0$

Then for simulation *r* :

$Ubias_{4r} = Ubias_{2r} * Ubias_{6r}$ = under-estimate of BMWP score for simulated sample r

$ObsIDX_{4rB} = ObsIDX_{4r} + Ubias_{4r}$ = bias-corrected observed revised BMWP Score (index 4)
$ObsIDX_{5rB} = ObsIDX_{5r} + Ubias_{2r}$ = bias-corrected observed revised NTAXA (index 5)
$ObsIDX_{6rB} = ObsIDX_{4rB} / ObsIDX_{5rB}$ = bias-corrected observed revised ASPT (index 6)

Note: these algorithms for indices 4-6 may change slightly after further assessment of the derivation and characteristics of the newly-derived revised BMWP indices in the WFD72a final revised index development project.

Note: It is unlikely, but mathematically feasible with this algorithm to derive values of $Ubias_{6r}$ (the unweighted revised ASPT of missed taxa) which are outside the mathematically possible bounds of this index (no longer 1-10). Values less than min possible should be reset to min and values >max possible should be reset to max.

Simulating bias-corrections for indices 7-9 (Revised Abundance-weighted BMWP Score, NTAXA and ASPT)

For simplicity, it is assumed that the bias for the number of Revised Abundance-weighted BMWP taxa (index 8) is the same as the bias for the number of BMWP taxa (index 2)

$Ubias_{9r}$ = Revised abundance-weighted ASPT of the $Ubias_{2r}$ missed taxa for simulated sample r
= $u_{9a} + u_{9b} * ObsIDX_2 + Zbias_{3r} * u_{9c} / \sqrt{}Ubias_{2r})$

where estimates of u_{9a}, u_{9b} and u_{9c} are not available.

Note: Using the equivalent values for u_{9a}, u_{9b} and u_{9c} to those derived for the original ASPT, namely could give misleading bias-corrections for the Revised abundance-weighted BMWP indices and should not be used.

However, the bias-correction algorithms for these Revised Abundance-weighted indices can still be encode in the software as:

$Ubias_{7r} = Ubias_{2r} * Ubias_{9r}$ = under-estimate of Revised Abundance-weighted BMWP score for simulated sample r

$ObsIDX_{7rB} = ObsIDX_{7r} + Ubias_{7r}$ = bias-corrected observed Revised Abundance-weighted BMWP Score for simulation r

$ObsIDX_{8rB} = ObsIDX_{2r} + Ubias_{2r}$ = bias-corrected observed Revised Abundance-weighted NTAXA for simulation r

$ObsIDX_{9rB} = ObsIDX_{7rB} / ObsIDX_{8rB}$ = bias-corrected observed Revised Abundance-weighted ASPT for simulation r

Simulating bias-corrections for any other System or User indices

For any other indices, allowance for the effects of sample processing errors on biasing observed values of indices is only incorporated in the standard generic manner developed for use in the STARBUGS software. Specifically:

Definitions:

$AvBias_i$ = User-supplied estimate of the average bias (net under-estimation) of the values of index *i* appropriate for the current test sample and its ‘season’ (e.g. derived from an audit of samples taken during the season combination (or at least same number of seasons) and ideally processed by the same staff/laboratory during a time period covering the processing of this sample).

$SDBias_i$ = User-supplied estimate of the SD of the bias (net under-estimation) of the values of index *i* appropriate for the current test sample and its ‘season’ (i.e. standard deviation of the estimates of the net under-estimation of the index value for index values obtained from the audit of samples taken during the season combination (or at least same number of seasons) and ideally processed by the same staff/laboratory during a time period covering the processing of this sample).

Algorithms:

$Zbias_{ir}$ = Random number deviate from a standard Normal distribution with a mean of 0.0 and SD of 1.0, for use in simulation *r* for index *i*

$Ubias_{ir} = AvBias_i + Zbias_{ir} * SDBias_i$

$ObsIDX_{irB} = ObsIDX_{ir} + Ubias_{ir}$

Note: Although this functionality for bias-correction needs to be incorporated into the new RICT software, estimates of $AvBias_i$ and $SDBias_i$ for any of these indices do not currently exist and will not be derived and made available within this current project (as agreed at the project Start-up meeting of 21st June 2007).

Simulating uncertainty in expected values

The estimates of the site- and season-specific expected values of the indices are also assumed to have uncertainty associated with them. It is very difficult, or almost impossible, to measure the unknown (or unknowable) true errors in estimating the macroinvertebrate fauna expected at a site in the absence of any environmental stress because the expected depends on which, and how, environmental variables are measured and used to set the "target" expected fauna.

In RIVPACS III+, only the uncertainty in the original BMWP indices due to variation and errors in different people measuring and deriving the values of the environmental predictor variables for a site were assessed and incorporated into the uncertainty assessments. This was done within the same BAMS replicated sampling study. At each BAMS site, four people measured each of the following variables completely independently:

From maps	National Grid Ref., distance from source, altitude, slope, discharge category
In the field	Stream width, stream depth, mean substratum composition (each measured in spring, summer and autumn and then averaged for use as RIVPACS predictor variables)

Then each person's values for the environmental variables were run through RIVPACS III to derive four independent RIVPACS estimates of the expected fauna and expected index values for each site. The typical SD in these estimates of expected index values for a site were then included in the RIVPACS III+ uncertainty assessments.

The same approach and estimates will be included in the new RICT software for indices 1-3.

For other indices an equivalent SD parameter and simulation of errors in expected values should be included in the software (but no estimates of the error SD will be provided within this initial software development – as agreed at the Start-up meeting of 21st June 2007).

Definitions:

$ExpIDX_i$ = Expected value of index *i* (for selected season *s*) for the current test site
(this is the average site-specific E value in multi-year assessments)

$ExpIDX_{ir}$ = Expected value of index *i* in simulation *r* for the current test site

$SDExp_i$ = Error SD for expected value of index *i*

$NExp_{year}$ = 1 for single-year run
= number of years (1, 2 or 3) for which a separate estimate of the E value was involved in the estimate of average E value (for multi-year run)

Algorithms for expected (E) values:

$ZExp_{ir}$ = Random number deviate from a standard Normal distribution with a mean of 0.0 and SD of 1.0, for use in simulation *r* for index *i*

$ExpIDX_{ir} = ExpIDX_i + ZExp_{ir} * SDExp_i / \sqrt{(NExp_{year})}$

Note: RICT software programmers can either use an existing function code to generate such random numbers from a standard normal distribution or we can provide the FORTRAN code used in RIVPACS III+)

Parameter Estimates:

$SDExp_1 = 4.3$ = Measurement error SD of Expected values of BMWP Score (index 1)

$SDExp_2 = 0.53$ = Measurement error SD of Expected values of NTAXA (index 2)

$SDExp_3 = 0.081$ = Measurement error SD of Expected values of ASPT (index 3)

Simulating O/E ratios (EQI)

For each simulated sample r, the simulated observed ($ObsIDX_{ir}$) and expected ($ExpIDX_{ir}$) values of each index are used to derive the O/E ratio (EQI_{ir}) for any index *i*, ignoring or uncorrected for any biases due to sample sorting and identification errors. These are known as the “face value” O/E ratios, in the sense that these would be the quoted values in the absence of any knowledge of sample processing errors.

Similarly, the O/E ratio (EQI_{irB}) for simulation *r* of index *i*, corrected for bias, is based on the simulation *r* of the observed value of index *i*, corrected for bias, namely $ObsIDX_{irB}$, and $ExpIDX_{ir}$.

Definitions:

EQI_{ir} = EQI value for index *i* in simulation *r* (uncorrected for bias) = ‘face value’ EQI

EQI_{irB} = EQI value for index *i* in simulation *r* (corrected for bias)

Algorithms:

$EQI_{ir} = ObsIDX_{ir} / ExpIDX_{ir}$

$EQI_{irB} = ObsIDX_{irB} / ExpIDX_{ir}$

Uncertainty SD and Confidence limits for an EQI

The frequency distribution of all the *rN* simulated EQI_{ir} values for a particular BMWP index *i* represents the degree of uncertainty in the true EQI value for that index for the site at that time period (either uncorrected or corrected for bias). This uncertainty can be summarised by the standard deviation (SD) of the simulated values. Additionally, 95% confidence limits for the true value are estimated as the lower and upper 2.5 percentiles of this frequency distribution (ie 2.5% of simulated O/E values were less than the lower limit and 2.5% were higher than the upper limit).

When corrected for bias, the confidence limits for EQI will tend to wider because of the extra degree of uncertainty introduced by estimating the bias for the sample. However, bias-corrected EQI values should, by definition, be correct, on average, and no longer have a tendency to under- (or over-) estimate the true quality at the site during that time period.

Definitions:

SDEQI_i = SD of the *rN* simulated values of EQI_i (uncorrected for bias) for index i for the current test site
SDEQI_{iB} = SD of the *rN* simulated values of EQI_i (corrected for bias) for index i for the current test site

$\mathrm{L95EQI}_i$ = Lower 2.5 percentile of the *rN* simulated values (EQI_{ir}) of EQI (uncorrected for bias) for index *i* for the current test site
$\mathrm{U95EQI}_i$ = Upper 2.5 percentile of the *rN* simulated values (EQI_{ir}) of EQI (uncorrected for bias) for index *i* for the current test site
$\mathrm{L95EQI}_{iB}$ = Lower 2.5 percentile of the *rN* simulated values (EQI_{irB}) of EQI (corrected for bias) for index *i* for the current test site
$\mathrm{U95EQI}_{iB}$ = Upper 2.5 percentile of the *rN* simulated values (EQI_{irB}) of EQI (corrected for bias) for index *i* for the current test site

Algorithms:

Separately for simulated values (a) uncorrected for bias and (b) corrected for bias:

Calculate the SD, (SDEQI_i and SDEQI_{iB}) of the *rN* values of EQI_{ir} and EQI_{irB} respectively, in the usual way for calculating any SD.

Determine the lower and upper 2.5 percentiles and thus 95% confidence limits by sorting all of the *rN* simulated EQI values into order from smallest to largest. Then the lower and upper percentiles are given by the mL and mU smallest values, where:

mL = nearest integer to 0.025 * (*rN* + 1)
mU = nearest integer to 0.975 * (*rN* + 1)

For the recommended *rN* = 9999, mL = 250 and mU = 9750.

The average (AvEQI_{iB}) of the bias-corrected EQR_{irB} values can be used in the output as the best bias-corrected estimate of EQI_i for the sample/site.

Assignment to ecological status class and confidence of class

The WFD requires that all water bodies, including rivers sites, are classified into one of five ecological status class. For the purposes of software coding, it is recommended that they are coded as classes 1-5 with 1= 'high', 2='good', 3='moderate', 4='poor' and 5='bad'.

Individual index class limits and classifications

The ecological status class of a test site is based on the EQI values (or corresponding WFD EQR (Ecological Quality Ratio) in the case of the ICMi index). The potential range of EQI values for any particular index is divided into classes corresponding to each status class. The user-supplied class limits are specified by providing the lower inclusive EQI value for each class. For example, lower class limits of 1.00 for 'high', 0.90 for 'good', 0.77 for 'moderate' and 0.65 for 'poor', means that all samples with EQI values for this index between 0.90 and up to, but not including, 1.00 would be classified as 'good'; while all samples with EQI values less than 0.65 would be classified as 'bad'.

Classifications based on multiple metrics (Multi-metrics)

The overall status class for sample/site is usually based on combining information from more than one index.
There are two main ways of combining information from two or indices:

(i) combine the individual indices EQI/EQR values into a single multi-metric EQI/EQR. This can done as some form of averaging (perhaps weighted) of the individuals indices' EQI/EQR. (e.g. ICMi is a weighted average of the EQR values of six indices/metrics)

(ii) determine the status class of the test site based on the EQI value of each index independently and then apply a pre-set rule for deriving the overall status class based on the classes for the individual metrics. (e.g. the current UK GQA biological classification system rule (MINTA) is to use the worst of the two classes determined by EQI for NTAXA and EQI for ASPT for a test site – this is a simple example of what is known as the "worst case" rule.

The status class limits for the EQI/EQR values of individual indices and rules for multi-index classifications all need to be decided by the UK Environment Agencies. It is beyond the remit of this Phase II of the WFD72C to set those limits and rules.

'Status classification method': For the purpose of defining the algorithms to assess uncertainty in such status class assignments (i.e. confidence of class), we merely refer to the chosen methods of determining the status class of test sites, whether based on individual indices or a suite of indices combined in a simple or hierarchical manner, as the 'status classification method'.

Applying the 'status classification method' to the 'face value' EQI values derived from the observed sample gives the 'face value' class of the site based on each index and overall.

Applying the 'status classification method' to the average($AvEQI_{iB}$) of the simulated bias-corrected EQI values for the test site give the 'bias-corrected face value' class of the site based on each index and overall.

Confidence of class

The likelihood of the true status class (i.e. averaged across all possible samples) of a test site being each of the five possible WFD classes is estimated simply by applying the 'status classification method' to each simulation sample *r* in turn. Thus the class for simulation *r* is based on the EQI/EQR values for simulation *r*, namely the set of EQI_{ir}.

This can be done for EQI values uncorrected for bias and, if available, corrected for bias.

For each index and overall, the proportion of simulations assigned to a status class estimates the probability that the true (average) quality of the test site for that time period was of that ecological status class (based on its macroinvertebrates).

Procedure COMPARE: Assessing changes in EQI, status class and confidence of change

Procedure Compare allows the user to assess whether there is a real difference in EQI values and/or status class between a pair of samples and/or sites and/or time periods. This is done using an extension of the simulation techniques and algorithms described above that are used to assess the EQIs and ecological status class and the associated uncertainty for individual samples/sites and time periods.

The first sample in a pair is known as sample A and the second as sample B.

In each simulation r, independent simulated EQI values are calculated for each index *i* for each of the two samples using the methods described above for single samples. In this context, independent simulations means that the various random uncertainty terms are different and completely independent for the two simulated samples A and B for any simulation *r*.

For each simulation *r*, the difference in the two simulated EQI values (sample B value minus sample A value) is calculated for each index *i* to give:

DiffEQI_{ir} when uncorrected for bias,

and DiffEQI_{irB} when corrected for bias.

Confidence (and statistical test) of change/difference in EQI:

Confidence limits for the difference in EQI values are obtained from the frequency distribution of the differences (DiffEQI_{ir} or DiffEQI_{irB}) using the same approach as for single sample EQI values described above, namely, order the differences from smallest to largest and find the 2.5 and 97.5 percentile values of the order distribution.

Strictly speaking we can't do a normal type of statistical test for the statistical significance of the difference (DiffEQI_{ir} or DiffEQI_{irB}) in EQI becuase we only actually have one sample on each occasion with no actually replication. However, we can generate a type of statistical test using the simulated EQI values, or more specifically, the frequency distribution of the simulated differences (DiffEQI_{ir} or DiffEQI_{irB}).

Calculate:

PDiff0 = proportion of simulated differences less than or equal to zero.

PDiff1 = proportion of simulated differences greater than or equal to zero.

PDiff = 2 * minimum of (PDiff0, PDiff1)

Then PDiff is the two-sided test probability of the null hypothesis of no difference in true EQI values between the sites and/or times from which the two samples were taken. [True EQI for a site, in this sense, means average EQI amongst all possible samples from the sites as estmated from the simulated values of EQI].

Confidence of change in status class:

Each of the two simulated samples is assigned to a status class by applying the 'status classification method' independently to the simulated EQI values for each sample for that simulation. This is done repeatedly in *rN* simulations to build up a two-way frequency (and hence probability) distribution that the site (in its time period) from which sample A was taken was of status class 'x' (say) and the sites (in its time period) from which sample B was taken was of class 'y'.

From this two-way probability distribution, the probability that samples A and B are from the same quality band can be estimated, together with the probabilities that sample B is one band better than A, one band worse, two or more bands better, or two or more bands worse.

In terms of RICT software outputs, there is potentially one of these 5 x 5 probability tables of changes in class based on each index for which class limits are to be used and also for each multi-index classification and the overall status classification method.

In each case, a wide range of outputs could be derived from this table; the example below gives some examples output from RIVPACS III+ and some suggestions for extra outputs.

If for coding purposes classes ‘high’ to ‘bad’ are referred to as classes 1-5 respectively, then

$PrCh_{ij}$ = Proportion of simulations for which simulated sample A was classified as class *i* and simulated sample B was classified as class *j*.
= Estimated probability of change in status from class *i* to class *j*

		Status class of sample B				
		high (1)	good (2)	mod (3)	poor (4)	bad (5)
Status class of sample A	high (1)	$PrCh_{11}$	$PrCh_{12}$	$PrCh_{13}$	$PrCh_{14}$	$PrCh_{15}$
	good (2)	$PrCh_{21}$	$PrCh_{22}$	$PrCh_{23}$	$PrCh_{24}$	$PrCh_{25}$
	mod (3)	$PrCh_{31}$	$PrCh_{32}$	$PrCh_{33}$	$PrCh_{34}$	$PrCh_{35}$
	poor (4)	$PrCh_{41}$	$PrCh_{42}$	$PrCh_{43}$	$PrCh_{44}$	$PrCh_{45}$
	bad (5)	$PrCh_{51}$	$PrCh_{52}$	$PrCh_{53}$	$PrCh_{54}$	$PrCh_{55}$

Probability status class of site(s) from which samples A and B were taken is:

Both status class *i* = $PrCh_{ii}$

Both the same class = $PrCh_{11} + PrCh_{22} + PrCh_{33} + PrCh_{44} + PrCh_{55}$

Both B worse than A = sum of all { $PrCh_{ij}$ } for which $j > i$

Both B better than A = sum of all { $PrCh_{ij}$ } for which $j < i$

Both B one class worse than A = sum of all { $PrCh_{ij}$ } for which $j = i + 1$

Both B one class better than A = sum of all { $PrCh_{ij}$ } for which $j = i - 1$

The output listing file (.LST) and O-E Type 1 (.OE1) and O-E Type 2 (.OE2) output files from existing RIVPACS RPBATCH software runs gives examples of potential formats and types of output of uncertainty estimates for both single sample runs (old Procedure Prediction) and for comparing change between two samples/sites (old Procedure Compare).

FORTRAN code to generate random a random deviates from a Normal distribution

```
      FUNCTION ZNORM(ZSET)
C Returns a standard normal deviate (N(0,1) with zero mean, unit
variance)
C Uses the Polar method of Box, Muller and Marsaglia (1958)
C
C On odd-numbered calls to the function (indicated by parameter
ZSET=999,
C the function internally-derives two new random normal deviates,
C one set to the function result (ZNORM),
C the other stored as the function argument (ZSET)
C
C On even-numbered calls to the function, it simply sets ZNORM = ZSET
C and sets ZSET = 999
C
C Parameter ZSET must have been set externally to 999 before the
first
C call to this function
C
      REAL R1,R2,V1,V2,R,FAC,ZSET

      IF (ZSET.GT.998) THEN
    8   continue
C Generate two random uniform deviates in the range 0-1(stored as R1,
R2)
C using your chosen programming languages random uniform number
function
        CALL RANDOM(R1) # Fortran built-in random uniform deviate
function
        CALL RANDOM(R2)
        V1=2*R1-1
        V2=2*R2-1
        R=V1*V1+V2*V2
        IF (R.GE.1) GOTO 8
        FAC=SQRT(-2.*LOG(R)/R)
        ZSET=V1*FAC
        ZNORM=V2*FAC
      ELSE
        ZNORM=ZSET
        ZSET=999
      ENDIF
      RETURN
      END
```

Example calling program:

```
      xset=999
      open(7,file='ZNormtest.out')
      do 100 i=1,10000
      x=znorm(xset)
      if (i.lt.20) write(6,*) i,x
      write(7,*) x
  100 continue
      end
```

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 2.1 Deliverable – Refinement of Reference Sites
31st July 2007

Background

RIVPACS III+ currently utilises 835 reference sites across its four models. In this work element, John Davy-Bowker (CEH) and Ralph Clarke (Bournemouth University) provide the definitive list of sites to be used in the predictive models underpinning the new Classification Tool. At the project start up meeting at CEH (21st June 2007) it was agreed that the goal of this work element was to remove sites where there was demonstrable reason for removal and that the adjustment algorithms (WE 4.5) would be used to correct for the effect of less significant stress on biotic index values at other sites. Information on sites that have been identified as unduly impacted in various predecessor projects and through more recent examination of the reference site data both by the Agencies and CEH is integrated into a single list of sites to be removed prior to the development of new predictive models.

Sources of information on sites to be removed

Information on a total of 60 RIVPACS reference sites that were considered to have been potentially stressed at the time of sampling, and/or sites that seem to have unrealistic or abnormal biological communities, has been collated from several sources:

1) 3 sites were identified for removal from the RIVPACS dataset due to low flow:
   Clarke R.T., Armitage P.D., Hornby D.D., Scarlett P. & Davy-Bowker J. (2003) Investigation of the relationship between the LIFE index and RIVPACS. Putting LIFE into RIVPACS. Environment Agency, R&D Technical Report W6-044/TR1.

2) 40 sites were identified as ‘potentially stressed’ in the SNIFFER WFD46 project:
   Davy-Bowker J., Clarke R.T., Furse M.T., Davies C.E., Corbin T.A., Murphy J.F. & Kneebone N.T. (2007). RIVPACS pressure data analysis. Scotland & Northern Ireland Forum for Environmental Research report.

3) 4 sites were identified as ‘potentially stressed’ in the SNIFFER WFD72B project:
   Clarke R.T. & Davy-Bowker J. (2006). Development of the scientific rationale and formulae for altering RIVPACS predicted indices for WFD reference condition. Scotland & Northern Ireland Forum for Environmental Research report.

4) 10 sites were rated ‘6’ in the Environment Agency, Scottish Environment Protection Agency and Environment & Heritage Service Biologist’s assessment scores. Details of the Biologist’s assessment scores are given in:
   Clarke R.T. & Davy-Bowker J. (2006). Development of the scientific rationale and formulae for altering RIVPACS predicted indices for WFD reference condition. Scotland & Northern Ireland Forum for Environmental Research report.

5) 14 sites were identified by Robin Guthrie (Scottish Environment Protection Agency) and John Murray-Bligh (Environment Agency) on the 28th June 2007. These sites typically had inexplicably poor faunas in one or more seasons (usually autumn) and in many cases were thought to have been sampled in spate conditions. Doubt was also expressed about the correct sampling location and site name for one site.

6) At the WFD72C project start up meeting on 15th June 2007 Peter Hale (Environment & Heritage Service) was consulted to see if any sites in Northern Ireland should be removed. None of the 110 sites in Northern Ireland were considered to require removal.

Some sites were identified from more than one of the sources described above.

Further assessment using lower 5% O/E_{TAXA} and O/E_{ASPT} ratios

Information on the 60 sites suggested for removal from the RIVPACS dataset has been collated into a single table (Table 3). We examined each site on a case-by-case basis. To assist in this process, for all 60 sites identified in any of the information sources detailed above, an additional assessment has been carried out using observed/expected (O/E) ratios for number of taxa (O/E_{TAXA}) and Average Score Per Taxon (O/E_{ASPT}) in each separate season. The lower 5% value of the distribution of O/E_{TAXA} and O/E_{ASPT} ratios for all single seasons (i.e. spring, summer and autumn samples) across the GB reference sites was used to identify threshold O/E_{TAXA} and O/E_{ASPT} ratios in each single season as given below:

Lower 5% value of $O/E_{TAXA} = 0.67$
i.e. remove potentially stressed sites where any separate season $O/E_{TAXA} < 0.67$

Lower 5% value of $O/E_{ASPT} = 0.87$
i.e. remove potentially stressed sites where any separate season $O/E_{ASPT} < 0.87$

These rules enable assessments to be made of the biological condition of the sites in relation to the other reference sites (by virtue of using O/E ratios), and in separate seasons thereby revealing problems in individual seasons that might not show up in combined season data and combined season sample O/Es.

Final decisions on sites to be removed

In the tables that follow we provide a final decision on whether each site identified in the information sources above should be retained or removed, together with the supporting information and reasoning for these decisions. In the three tables that follow we provide:

- Decisions on which of the 60 potentially stressed RIVPACS reference sites should be retained (n=18) and which sites should be removed (n=42) (Table 3).
- A list of the 40 GB and 2 NI RIVPACS reference sites to be removed from the dataset (Table 4).
- A full list of the 685 GB and 108 NI RIVPACS reference sites to be retained in the reference site dataset for subsequent model construction in this project (Appendix I).

In Northern Ireland four of the 110 sites were previously identified as potentially stressed in the SNIFFER project WFD46. Subsequent analysis in this WE of their biological condition using O/E ratios identified that 2 of these were probably not good enough at the time of sampling to be reference sites. However, it is not necessary (nor were there any plans or resources within this project) to remove these sites and redevelop a whole new TWINSPAN classification and predictive model for Northern Ireland.

Our recommended solution is that we retain the current TWINSPAN classification and end groups but that these 2 sites are ignored when calculating the end group mean values of indices, probabilities of occurrence and abundances of taxa. If the project Board agrees with this then CEH will provide end group mean values of indices, probabilities of occurrence and abundances of taxa on this basis.

Table 3 – The 60 reference sites identified for potential removal from the RIVPACS reference site dataset together with the final decision on which sites should actually be removed. Those to be retained (n=18) and those to be removed (n=42) are identified in the column ‘Final list’.

Country	Site ID	River	Site	Reason(s) for Removal	Agency Biologist's assessment score	OTaxa1	OTaxa2	OTaxa3	O/ETaxa1	O/ETaxa2	O/ETaxa3	O/EASPT1	O/EASPT2	O/EASPT3	Any separate season O/ETAXA <0.67	Any separate season O/EASPT <0.87	Final list 0 = retain 1 = remove
England	1105	Brede/Line	Sedlescombe Street	Agency Biologist's Assessment Scores of '6'.	6	24	17	19	1.00	0.73	0.79	0.96	0.83	0.91	0	1	1
England	1407	Lee	Ware Weir	WFD46 - Organic/Nutrients	3	19	23	26	0.80	0.91	1.06	0.81	0.89	0.95	0	1	1
England	1907	Perry	Milford	WFD46 – Metals	4	21	19	23	0.86	0.78	0.93	0.87	0.85	0.87	0	1	1
England	1909	Perry	Mytton	WFD46 - Metals	4	20	17	24	0.86	0.74	1.03	1.00	0.91	0.98	0	0	0
England	2001	Blithe	Cookshill	WFD46 – Organic	5	13	14	16	0.59	0.67	0.72	0.78	0.81	0.79	1	3	1
England	2103	Smite	Colston Bassett	WFD46 - Nutrients	4	22	25	24	1.06	1.11	1.12	1.00	1.04	0.94	0	0	0
England	2211	Dove	Monk's Bridge	WFD46 - Metals	3	10	12	24	0.43	0.54	0.98	0.88	0.82	1.00	2	1	1
England	2305	Colne	Earl's Colne	WFD46 - Organic/Nutrients	3	23	25	21	0.98	1.00	0.87	0.96	0.94	0.95	0	0	0
England	2307	Colne	Fordstreet Bridge	WFD46 - Nutrients	3	22	20	25	0.93	0.80	1.03	0.96	0.98	1.00	0	0	0
England	2507	Glen	Banthorpe Lodge	WFD46 - Nutrients	3	15	18	21	0.65	0.73	0.89	0.84	0.88	0.82	1	2	1
England	2509	Glen	South of Twenty	WFD46 - Organic	3	19	23	22	0.78	0.90	0.91	0.95	0.95	0.99	0	0	0
England	2719	Ribble/Gayle Beck	Mitton Bridge	WFD46 - Organic/Nutrients	4	21	13	17	0.94	0.60	0.75	0.82	1.07	0.82	1	2	1
England	2815	Weaver	Beam Bridge	WFD46 - Organic/Nutrients Agency Biologist's Assessment Scores of '6'	6	18	22	17	0.65	0.78	0.59	0.84	0.81	0.70	2	3	1
England	3309	Swale	Morton-on-Swale	WFD46 – Metals WFD72B	2	21	15	16	0.88	0.66	0.64	1.01	1.15	0.95	2	0	1
England	3405	Tees	Dent Bank	"RG/JMB" - Inexplicable but uncharacteristically poor autumn scores	2	15	13	9	0.81	0.72	0.53	1.03	0.95	1.03	1	0	1
England	3407	Tees	Barnard Castle	"RG/JMB" - Inexplicable but uncharacteristically poor autumn scores	2	16	14	10	0.81	0.73	0.54	0.99	0.99	0.93	1	0	1
England	3503	South Tyne	Alston	"RG/JMB" - Inexplicable but uncharacteristically poor autumn scores	2	17	15	9	0.99	0.92	0.55	1.09	1.11	1.18	1	0	1
England	3507	South Tyne	Featherstone	"RG/JMB" - Inexplicable but uncharacteristically poor autumn scores	2	13	15	10	0.75	0.90	0.60	0.97	0.97	0.92	1	0	1
England	3509	South Tyne	Bardon Mill	'WFD46 – Organic	3	11	21	12	0.56	1.12	0.64	0.94	1.00	0.94	2	0	1
England	5001	Otter	Fairhouse Farm	WFD46 - Organic/Nutrients [high BOD,SRP,nitrite,ammonia,SS but all O/E fine -retain]	2	24	22	28	1.05	1.06	1.27	1.05	0.98	1.04	0	0	0

Country	Site ID	River	Site	Reason(s) for Removal	Agency Biologist's assessment score	OTaxa1	OTaxa2	OTaxa3	O/ETaxa1	O/ETaxa2	O/ETaxa3	O/EASPT1	O/EASPT2	O/EASPT3	Any separate season O/ETAXA <0.67	Any separate season O/EASPT <0.87	Final list 0 = retain 1 = remove
England	5009	Otter	Newton Poppleford	WFD46 - Nutrients [high SRP but O/E fine -retain]	3	32	26	29	1.23	1.03	1.10	0.94	0.96	0.98	0	0	0
England	5401	Beult	Hadman's Place	Agency Biologist's Assessment Scores of '6' (8km dfs) (all 4 Beult sites sampled in 1982)	6	24	21	21	1.08	0.89	0.91	0.96	0.86	0.92	0	1	1
England	5403	Beult	Slaney Place	Agency Biologist's Assessment Scores of '6' (18km dfs)	6	26	20	19	1.15	0.83	0.81	0.89	0.88	0.83	0	1	1
England	5405	Beult	Stile Bridge	Agency Biologist's Assessment Scores of '6' (23km dfs) [O/E just ok but whole Beult classed as D/E chemically 1988 onwards, so remove]	6	23	21	23	1.03	0.88	0.99	0.94	0.87	0.91	0	0	1
England	5407	Beult	Hunton	Agency Biologist's Assessment Scores of '6' (23km dfs) [O/E just ok but whole Beult classed as D/E chemically 1988 onwards, so remove]	6	23	25	25	1.03	1.05	1.07	0.99	0.91	1.00	0	0	1
England	5845	Unnamed	Dinmore Manor	'WFD46 - Organic AND WFD72B	2	18	10	14	1.04	0.81	0.99	0.94	0.79	0.95	0	1	1
England	6001	Blythe	Cheswick Green	WFD46 - Metals	5	18	22	15	0.86	1.05	0.72	0.89	0.90	0.83	0	1	1
England	6259	Babraham/Grant	Hildersham	LIFE Report W6-044/TR1 Clarke et al 2003	3	18	19	21	0.83	0.81	0.94	0.93	0.87	0.90	0	0	1
England	6811	Stour	Longham	LIFE Report W6-044/TR1 Clarke et al 2003	3	31	27	28	1.19	1.00	1.06	1.00	0.93	0.95	0	0	1
England	6845	Unnamed	Alton Common	WFD46 - Organic/Nutrients AND WFD72B	2	20	9	8	1.13	0.70	0.55	0.95	0.85	0.83	1	2	1
England	7127	Moors/Crane	East Moors Farm	Agency Biologist's Assessment Scores of '6' (sampled 1985-86) (chemically class A 1988-900 [all O/E fine -retain], Wright et al, 1988 (Dorset proceedings, vol 110 indicates that these sites are OK)	6	24	26	31	1.04	1.07	1.28	0.94	0.89	1.04	0	0	0
England	7143	Ed	Upper Farm	Agency Biologist's Assessment Scores of '6' (sampled 1985-86) (chemically class A 1988-90 in stretch starting 2-3km downstream) all O/E fine -retain], Wright et al, 1988 (Dorset proceedings, vol 110 indicates that these sites are OK)	6	29	27	24	1.25	1.15	1.15	0.99	1.06	1.10	0	0	0
England	7145	Ed	Pains Moor	Agency Biologist's Assessment Scores of '6' (sampled 1985-86) (chemically class A 1988-90 in stretch starting 2-3km downstream) all O/E fine -retain], Wright et al, 1988 (Dorset proceedings, vol 110 indicates that these sites are OK)	6	28	23	26	1.19	0.98	1.18	1.01	1.04	1.12	0	0	0
England	8289	Clun	Jay	WFD46 - Metals	3	20	18	16	0.79	0.76	0.64	1.00	1.03	1.00	1	0	1
England	9113	Hull/West Beck	Corpslanding	LIFE Report W6-044/TR1 Clarke et al 2003	5	22	27	18	0.99	1.15	0.77	0.91	0.97	0.81	0	1	1
England	9585	Lathkill	Congreave	"RG/JMB" - Inexplicable but uncharacteristically poor autumn scores	3	26	17	6	1.07	0.75	0.25	1.16	1.09	0.79	1	1	1
England	AN06	Rase	Bully Hills	'WFD46 - Organic [high ammonia only - O/E ok - retain]	2	20	19	19	0.89	0.88	0.90	1.05	0.97	1.05	0	0	
England	NW07	Waver	Waver Bridge	'WFD46 - Organic	5	24	25	24	1.05	1.09	1.02	0.95	0.86	0.83	0	2	1
England	SN01	Ditton Stream	Ditton	WFD46 - Metals	5	16	21	20	0.71	0.94	0.91	0.77	0.91	0.85	0	2	1

Country	Site ID	River	Site	Reason(s) for Removal	Agency Biologist's assessment score	OTaxa1	OTaxa2	OTaxa3	O/ETaxa1	O/ETaxa2	O/ETaxa3	O/EASPT1	O/EASPT2	O/EASPT3	Any separate season O/ETAXA <0.67	Any separate season O/EASPT <0.87	Final list 0 = retain 1 = remove
England	TH06	Clayhill Brook	u/s Burghfield STW	'WFD46 - Organic AND Agency Biologist's Assessment Scores of '6'	6	17	12	20	0.83	0.69	1.05	0.95	0.78	0.90	0	1	1
Scotland	4107	Stinchar	Pinmore Bridge	'WFD46 - Organic [high SS only -O/E not extreme - retain]	1	17	16	19	0.78	0.76	0.88	0.93	1.00	1.00	0	0	0
Scotland	4409	Inver	Lochinver	"RG/JMB" - Uncharacteristically poor summer and autumn scores	1	17	8	8	0.86	0.47	0.43	0.99	0.79	0.78	2	2	1
Scotland	4885	Unnamed	Westerdale	'WFD46 - Organic [low %oxygen only - retain]	1	26	19	13	1.49	1.20	0.75	0.90	0.97	0.90	0	0	0
Scotland	4909	Tweed	Peebles Gauge	WFD46 - Nutrients [high SRP & nitrate for site type + v.high O/E TAXA -remove]	2	25	22	33	1.32	1.20	1.87	0.97	0.99	0.99	0	0	1
Scotland	7605	Kyle of Sutherland/Oykel	Caplich	"RG/JMB" - Sampled in autumn in large spate	2	19	19	5	0.94	1.08	0.26	1.05	1.05	0.90	1	0	1
Scotland	7611	Kyle of Sutherland/Oykel	Strath Oykel	"RG/JMB" - Sampled in autumn in large spate	2	20	14	3	0.93	0.77	0.14	1.14	0.96	0.74	1	1	1
Scotland	8921	Black Water	Creag Dhubh	"RG/JMB" - Inexplicable but extremely poor autumn fauna	1	20	14	6	1.21	0.91	0.37	1.01	1.01	0.87	1	0	1
Scotland	SEPA_E08	Tay/Dochart/Fillan/Cononish	Taymount Mains	WFD46 - Organic/Nutrients [highest TON & SS of 'Highlands' but O/E ok -retain	2	29	27	28	1.12	1.38	1.12	0.98	1.03	0.89	0	0	0
Scotland	SEPA_N09	Yell: Easter Burn of Bouster	Bouster	'WFD46 - Organic [low %oxygen saturation, but O/E taxa high and O/E ASPT fine -retain]	2	14	11	16	1.39	1.13	1.29	1.01	0.97	0.97	0	0	0
Scotland	SEPA_N65	Scaddle	Aryhoulan	"RG/JMB" - Inexplicable but extremely poor autumn fauna	1	17	10	4	1.10	0.70	0.30	1.05	1.03	1.15	1	0	1
Scotland	SEPA_W24	Etive	Alltchaorunn	"RG/JMB" - Inexplicable but extremely poor autumn fauna	1	14	12	4	0.96	0.87	0.34	1.09	0.94	1.09	1	0	1
Scotland	SEPA_W27	Orchy/Water of Tulla	Catnish Footbridge	"RG/JMB" - uncharacteristically poor summer and autumn scores	1	13	9	7	0.90	0.67	0.60	0.98	1.00	1.05	1	0	1
Scotland	SEPA_W29	Orchy/Water of Tulla	Gorton	"RG/JMB" - Inexplicable but extremely poor autumn fauna	1	17	16	6	1.17	1.12	0.48	0.94	1.02	1.13	1	0	1
Scotland	SEPA_W32	Allt na Feithe	Altnafeadh	"RG/JMB" - Doubts about location and correct naming of site	1	13	10	7	0.88	0.67	0.53	0.99	0.98	0.86	1	1	1
Scotland	SEPA_W38	Carradale Water	B842 Bridge	'WFD46 - Organic [marginally highest SS for type, but all O/E fine - retain]	1	19	21	20	1.11	1.29	1.15	0.96	0.98	0.93	0	0	0
Scotland	TA07	Elliot Water	Elliot	WFD46 - Organic/Nutrients	4	17	17	20	0.80	0.81	0.90	0.91	0.86	1.08	0	1	1
N. Ireland	20201101	Owenrigh River	Carnanbane	WFD46 - Metals WFD72B	2	13	14	14	0.67	0.77	0.76	1.03	1.05	1.00	0	0	0
N. Ireland	20303403	Blackwater	Moy	"WFD46 - Organic– Exclude from calculation of end group means for determining expected values]	3	13	15	19	0.61	0.57	0.74	0.81	0.87	0.92	2	1	1
N. Ireland	NI_24	Crew Burn	Carrols Bridge	WFD46 - Organic/Nutrients [high BOD, SRP, ammonia, only autumn O/E ASPT low – Exclude from calculation of end group means for determining expected values]	5	23	18	15	1.04	0.89	0.72	0.94	1.01	0.76	0	1	1
N. Ireland	NI_32	Mullagh River	Mullagh Bridge	WFD46 - Nutrients [high nitrate, nitrite, TON - but all O/E fine - retain]	5	27	19	25	1.23	0.93	1.05	1.02	0.96	0.98	0	0	0

Table 4 – The 42 reference sites removed (out of the original 835 reference sites) and now no longer available for model construction in this project

Country	Site ID	River	Site
England	1105	Brede/Line	Sedlescombe Street
England	1407	Lee	Ware Weir
England	1907	Perry	Milford
England	2001	Blithe	Cookshill
England	2211	Dove	Monk's Bridge
England	2507	Glen	Banthorpe Lodge
England	2719	Ribble/Gayle Beck	Mitton Bridge
England	2815	Weaver	Beam Bridge
England	3309	Swale	Morton-on-Swale
England	3405	Tees	Dent Bank
England	3407	Tees	Barnard Castle
England	3503	South Tyne	Alston
England	3507	South Tyne	Featherstone
England	3509	South Tyne	Bardon Mill
England	5401	Beult	Hadman's Place
England	5403	Beult	Slaney Place
England	5405	Beult	Stile Bridge
England	5407	Beult	Hunton
England	5845	Unnamed	Dinmore Manor
England	6001	Blythe	Cheswick Green
England	6259	Babraham/Granta	Hildersham
England	6811	Stour	Longham
England	6845	Unnamed	Alton Common
England	8289	Clun	Jay
England	9113	Hull/West Beck	Corpslanding
England	9585	Lathkill	Congreave
England	NW07	Waver	Waver Bridge
England	SN01	Ditton Stream	Ditton
England	TH06	Clayhill Brook	u/s Burghfield STW
Scotland	4409	Inver	Lochinver
Scotland	4909	Tweed	Peebles Gauge
Scotland	7605	Kyle of Sutherland/Oykel	Caplich
Scotland	7611	Kyle of Sutherland/Oykel	Strath Oykel
Scotland	8921	Black Water	Creag Dhubh
Scotland	SEPA_N65	Scaddle	Aryhoulan
Scotland	SEPA_W24	Etive	Alltchaorunn
Scotland	SEPA_W27	Orchy/Water of Tulla	Catnish Footbridge
Scotland	SEPA_W29	Orchy/Water of Tulla	Gorton
Scotland	SEPA_W32	Allt na Feithe	Altnafeadh
Scotland	TA07	Elliot Water	Elliot
N. Ireland	NI_24	Crew Burn	Carrols Bridge
N. Ireland	20303403	Blackwater	Moy

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 2.2 – Report on Data for Errors and Compare
Report describing datasets to be used and identifying gaps – revised 29 Jan 2008

Background

RIVPACS predictive models produce predictions of the fauna and biotic index values to be expected at test sites in reference state. Comparison of RIVPACS predicted biotic index values with those observed at a test site provide an assessment of the biological quality of the site. As with any bio-assessment methodology it is vital to be able to quantify the uncertainty associated with these assessments.

The current RIVPACS III+ software produces assessments of biological quality within a single year and bases its estimates of uncertainty in the biotic indices NTAXA, BMWP and ASPT on the Biological Assessment Methods Study (BAMS) dataset (Clarke et al, 2002). This dataset comprises three replicate samples in each of the 3 RIVPACS seasons within the same year at sites on rivers of a variety of types and qualities. However, the RIVPACS IV models under development as part of the current project will incorporate new functionality to enable assessments to be made across a 3-year period, with observed values being provided in any of 1, 2 or all 3 years and any of 1, 2 or all 3 RIVPACS seasons). The new RIVPACS IV models will also incorporate a more extensive list of biotic indices. This has therefore created a need for new replicate sample datasets to calculate new error terms to account for replicate sampling variability between years and for a wider range of biotic indices.

This report describes the work done to collate new datasets to calculate biotic index values and also identifies any gaps that might exist in the provision of data needed to calculate uncertainty terms.

Datasets

Two datasets have been provided by the Robin Guthrie (RG) of SEPA:

28-site dataset from the Tay River Purification Board
416-site dataset from East and North-East Scotland

In addition, the Environment Agency 16-site Biological Assessment Methods (BAMS) dataset that is already used to quantify uncertainty within RIVPACS III+ was further enhanced by calculating a wider range of biotic indices.

A further additional dataset from Northern Ireland has also recently been added to the errors database. This dataset comprises monthly samples from 12 sites throughout a full year and is unique in its replication of sampling within the same RIVPACS season but on a different sampling day.

28-site Tay RPB Dataset

This dataset was generated by biologists from the Tay River Purification Board (RPB) that is now part of SEPA. The then Tay RPB had a network of “primary sites”, mainly on larger rivers in the Tay catchment (including the River Earn) and various other rivers between the Tay and the North Esk catchment in Angus.
The biological quality of the sites was generally high or good, but 4 of the 28 stand out as having impacted invertebrate faunas. These are:

8538 DEAN W. AT BRIDGEND
7989 DIGHTY W. AT BALMOSSIE MILL
7844 LUNAN W. AT KIRKTON MILL
7672 LUTHER W. AT LUTHER BRIDGE

Of the remainder, site 8688 (RIVER TUMMEL AT ALDOUR RD BDG PITLOCHRY), occasionally had poor biotic index scores due to the difficulty of sampling this river which has quite marked variation in water levels due to hydro-electric influences. The size of site 8322 (RIVER TAY AT RAIL BR. PERTH) has also made sampling difficult on occasion. The remaining sites were generally of high or good quality although sporadic sheep dip problems in the mid 1990s affected many of the rivers.

The sites were sampled between 1988 and 1997 and four replicate samples were taken at each site on each sampling occasion in spring and autumn. Although not all sites were sampled in all years, many sites have concurrent runs of data, especially in the 5-year period 1990 to 1994.

Of the 4 replicate samples taken on each sampling occasion, three were analysed to BMWP family level and one was analysed to a mixed taxonomic level.

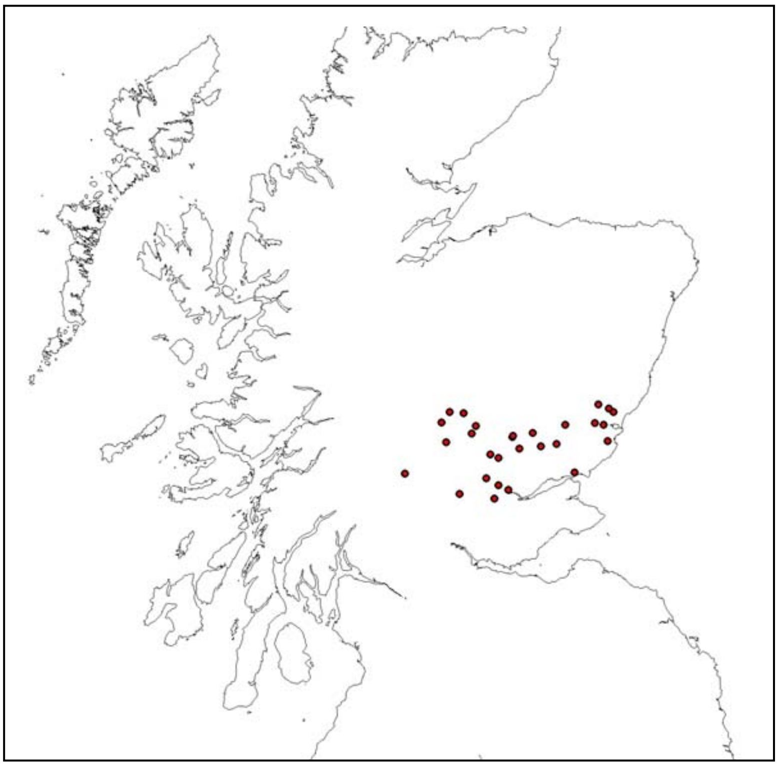


Figure 2. Map of the 28 sites in the Tay River Purification Board

From 1990 onwards the samples were sampled and processed following the now standard SEPA methodology with the same AQC/audit scheme as used in the 1990 GQA survey. Pre 1990 the exact methods are uncertain.

The taxonomic data was stored on paper until approximately 2004, when the data was compiled into electronic format. The data has been checked extensively by Robin Guthrie (RG) and was considered free of any systematic errors. Should bias correction be needed, RG has estimated that a value of 1.7 net gains per sample would be appropriate as this was the average of the AQC results for the Tay RPB in 1990 and 1995. 1.7 net gains is also consistent with the current overall SEPA performance.

The mixed taxonomic level samples varied in the extent to which taxa were resolved, particularly for earlier samples. Generally, most taxa were taken to species or genus where possible with the exception of Oligochaeta (which were often but not consistently taken to family level and sometimes to species level), Chironomidae (sometimes sub-family), Sphaeriidae (Genus usually), Simuliidae often were only recorded as Simuliidae. Non-scoring Diptera were frequently left at family, as were other non-scoring taxa.

In the family level replicates the 8 artificial BMWP composite families were not distinguished. The families more recently regarded as composites were not split:

Siphlonuridae (including Ameletidae)
Heptageniidae (including Arthropleidae)
Limnephilidae (including Apataniidae)

Table Structure

After initial evaluation of the 28-site dataset, CEH converted the database into a simpler flat file structure with fewer tables. The new SITE, SAMPLE and TAXA tables now also have table relationships invoking referential integrity to simplify subsequent querying.

Taxonomic Resolution

The taxonomic resolution of the samples was then addressed. The original database contained 5 replicates from each site, in each year, in both spring and autumn:

Rep 1 - a Species level sample
Rep 2 - a Family level sample (including some non-BMWP families)
Rep 3 - a Family level sample (including some non-BMWP families)
Rep 4 - a Family level sample (including some non-BMWP families)
Rep 5 - a BMWP Family level sample generated by RG from Replicate 1

The original Replicate 1 (Species level sample) was retained (now called 1S) and a new Family level Replicate 1 was generated (now called 1F) based on the species sample giving the following replicates:

Rep 1S - Species level sample (processed at Species level in the first instance)
Rep 1F - Family level sample including some non-BMWP families (derived from replicate 1S)
Rep 2F - Family level sample including some non-BMWP families (processed at Family level)
Rep 3F - Family level sample including some non-BMWP families (processed at Family level)
Rep 4F - Family level sample including some non-BMWP families (processed at Family level)

Replicates 1F, 2F, 3F and 4F can be regarded as fully equivalent family level replicates. Replicate 1S provides further information on the prevalence of species within the dataset.

The next step was to convert the raw data TAXA table (containing the replicates above) into 5 different datasets, each adjusted to the exact taxonomic resolution for the calculation of the required biotic indices:

1) BMWP Family Level Taxa
2) AWIC Family Level Taxa
3) LIFE Family Level Taxa*
4) WHPT Family Level Taxa*
5) All Separated Family Level Taxa^

^Although the 5th dataset was not used for any specific indices it is created for future use with other types of indices that may include families not used in the above indices.

*For the LIFE and WHPT data, the BMWP artificial taxon groups from the raw data were split as follows:

Hydrobiidae (including Bithyniidae) are all taken to be Hydrobiidae
(as there were no species level records for Bithynia)

Planariidae (including Dugesiidae) are all taken to be Planariidae
(as there were only two species level records for Dugesia)

Ancylidae (including Acroloxidae) are all taken to be Ancylidae
(as there was only one species level record for Acroloxus)

Psychomyiidae (including Ecnomidae) are all taken to be Psychomyiidae
(as there were no species level records for Ecnomidae)

Dytiscidae (including Noteridae) are all taken to be Dytiscidae
(as there were no species level records for Noteridae)

Hydrophilidae (including Hydraenidae) are all taken to be Hydraenidae
(as there were only two species level non-Hydraenidae records)

Gammaridae (including Crangonyctidae & Niphargidae) are all taken to be Gammaridae
(as there were only 6 species level Crangonyx records and no Niphargidae)

Splitting the BMWP composite family Rhyacophilidae (including Glossosomatidae) proved to be more problematic as both of the families Rhyacophilidae and Glossosomatidae occurred frequently in the species level replicates. To derive separate Rhyacophilidae and Glossosomatidae records from the composite families, the species level replicate 1S was used to find out if either or both families were present in that replicate. The Rhyacophilidae (including Glossosomatidae) records at the other replicates at the same site on the same day were then split into separate Rhyacophilidae and Glossosomatidae records based on the species level sample. The abundances of the species in the species level sample were also used to calculate the proportion of Rhyacophilidae and Glossosomatidae across the overall $\log_{10}$ abundance of the combined Rhyacophilidae (including Glossosomatidae) records. This was then used to distribute the recorded $\log_{10}$ abundance of Rhyacophilidae (including Glossosomatidae) across the $\log_{10}$ abundance categories in the separate families Rhyacophilidae and Glossosomatidae in the same proportions.

Other families also regarded as composites were treated as follows:

Siphlonuridae (including Ameletidae) – were all regarded as Siphlonuridae
Heptageniidae (including Arthropleidae) – were all regarded as Heptageniidae
Limnephilidae (including Apataniidae) – were all regarded as Limnephilidae

Combined Replicate Data

In addition to preparing the datasets above for the calculation of biotic indices for single replicate samples in both spring and autumn across a series of years, the error terms needed for the new Tool require an estimate of the variability of biotic index values between different samples taken on the same day, in the same season within a given year. To achieve this the spring Replicate 1F, 2F, 3F and 4F samples were combined with the autumn Replicate 1F, 2F, 3F and 4F samples (taking the maximum of the log10 abundance categories in the 2 season samples) as follows:

	Spring 1F	**Spring 2F**	**Spring 3F**	**Spring 4F**
Autumn 1F	Sp 1F & Aut 1F	Sp 2F & Aut 1F	Sp 3F & Aut 1F	Sp 4F & Aut 1F
Autumn 2F	Sp 1F & Aut 2F	Sp 2F & Aut 2F	Sp 3F & Aut 2F	Sp 4F & Aut 2F
Autumn 3F	Sp 1F & Aut 3F	Sp 2F & Aut 3F	Sp 3F & Aut 3F	Sp 4F & Aut 3F
Autumn 4F	Sp 1F & Aut 4F	Sp 2F & Aut 4F	Sp 3F & Aut 4F	Sp 4F & Aut 4F

This therefore gave 16 additional spring summer combined samples. This was done for each the 4 taxonomic resolutions needed for the various biotic indices.

In total we therefore created 4 spring and 4 autumn replicates at each site in each year and 16 spring-autumn combined replicates at each site in each year (at 4 taxonomic resolutions to cater for the family level biotic indices included in the project).

Biotic Index Calculation

The following biotic indices were calculated using the 4 taxonomic levels of data above:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

Full details of the above indices, including references where possible, are included in the Appendix II at the end of this report. For LIFE and both the non-abundance weighted WHPT and abundance weighted WHPT indices, distinct families were used for scoring rather than BMWP composites.

416-site East and North-East Scotland Dataset

This dataset generated by SEPA comprises sites predominantly from the East and North-East of Scotland and covers a wide range of Scottish river types from very large, oligotrophic rivers such as the Spey through to small, lowland streams in arable areas and rivers in predominantly urban settings.

The sites range in quality between nearly pristine to very severely degraded. The range of impacts includes organic pressures, hydro-morphological pressures, various toxic pressures, nutrient pressures and acidification.

The dataset has been compiled by RG from a range of databases held by the former River Purification Boards and from SEPA's current corporate systems. RG has checked the data extensively and was satisfied with the quality. The scores for all samples were consistent with RG's expectations for these sites (many of which RG is very familiar with). Additionally, the scores for samples from any given site are generally consistent with each other (low scoring sites tended to have consistently low scores while and high scoring sites tend to be consistently high). RG has checked the unexpectedly low scores with local biologists and found them to be correct (i.e. not due to a data problem).

The sites were sampled between 1990 and 2004 and include samples from spring, summer and autumn in each year (although summer samples are fewer in number as monitoring over the later part of this period tended to be based primarily on spring and autumn samples alone). From 1990 onwards the samples were sampled and processed following the now standard SEPA methodology with the same AQC/audit scheme as used in the 1990 GQA survey. Should bias correction be required, RG has estimated that a figure of 1.7 net gains per sample would be appropriate as this was consistent with the current overall SEPA performance.

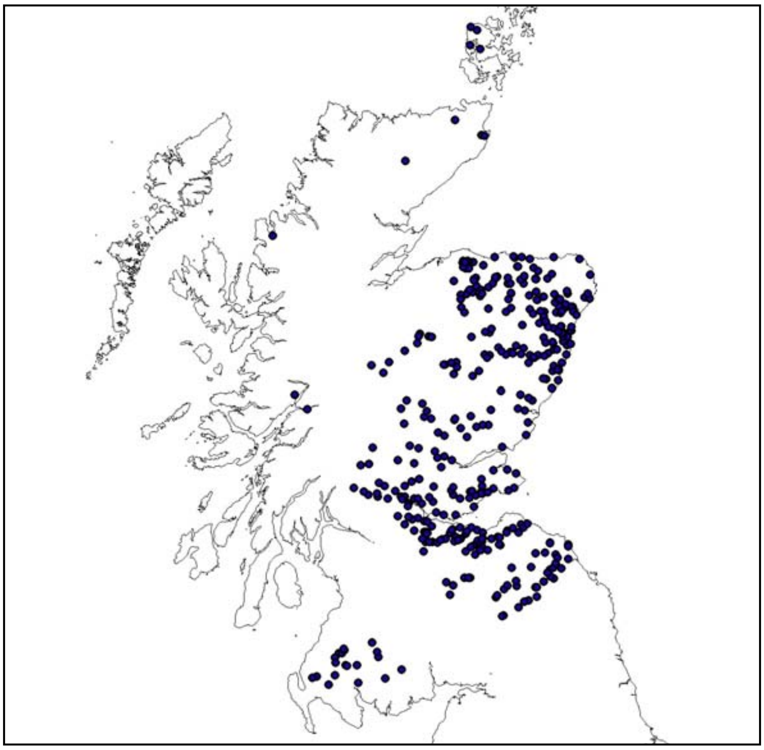


Figure 3. Map of the 416 sites in the East and North-East of Scotland

The samples were originally processed to a mixture of species and family levels with most sites typically having several family level samples and one species sample in a given year. RG has converted the taxonomic resolution of all of the samples to BMWP family level.

Where there were no abundances (numerical values) recorded, RG has generated synthetic abundances by allocating the average numerical abundance of that taxon at the recorded log abundance category, derived from that portion of the dataset where numerical abundances were recorded. Thus, to obtain an overall abundance for a family when deriving this from a species sample where the abundances were only recorded as log abundance RG allocated the mean numerical abundance value for that species at that log abundance category derived from those species samples where there were abundance counts. The synthetic abundance for each species within a family was then summed to give the overall family abundance.

RG also allocated synthetic abundances to all other family level records where there were no numerical abundances by deriving the mean numerical abundance of each family at each abundance category from data where the actual counts existed. In some instances (particularly for log abundance category E or for rare taxa) there weren't values available for each abundance category for that taxon so the mean numerical abundance of all taxa in that abundance category was used (e.g. the numerical abundance value 11000 was allocated to log abundance category E).

Table Structure

After initial evaluation of the 416-site dataset, CEH converted the database into a simpler flat file structure with fewer tables. The new SITE, SAMPLE and TAXA tables now also have table relationships invoking referential integrity to simplify subsequent querying.

Taxonomic Resolution

The taxonomic resolution of the samples was then addressed. The taxonomic records as supplied by RG had been converted to BMWP family level. The next step was to convert TAXA table into 5 different datasets, each adjusted to the exact taxonomic resolution for the calculation of the required biotic indices:

1) BMWP Family Level Taxa
2) AWIC Family Level Taxa
3) LIFE Family Level Taxa*
4) WHPT Family Level Taxa*
5) All Separated Family Level Taxa^

^Although the 5th dataset was not used for any specific indices it is created for future use with other types of indices that may include families not used in the above indices.

*For the LIFE and WHPT data, the BMWP artificial taxon groups from the raw data were split as follows:

Hydrobiidae (including Bithyniidae) are all taken to be Hydrobiidae
(as there was only one species level record for Bithynia)

Planariidae (including Dugesiidae) are all taken to be Planariidae
(as only 1.5% of the original species level records were for Dugesia)

Ancylidae (including Acroloxidae) are all taken to be Ancylidae
(as only 1.2% of the original species level records were for Acroloxus)

Psychomyiidae (including Ecnomidae) are all taken to be Psychomyiidae
(as there were no species level records for Ecnomidae)

Dytiscidae (including Noteridae) are all taken to be Dytiscidae
(as there were no species level records for Noteridae)

Hydrophilidae (including Hydraenidae) are all taken to be Hydraenidae
(as only 5% of the original species level records were non-Hydraenidae)

Gammaridae (including Crangonyctidae & Niphargidae) are all taken to be Gammaridae
(as only 3.5% of the original species level records were for Crangonyx and there were no records for Niphargidae)

Rhyacophilidae (including Glossosomatidae) - both families occur commonly in Scotland so each record of Rhyacophilidae (including Glossosomatidae) was split into a record of Rhyacophilidae and a record of Glossosomatidae. Both were allocated the $\log_{10}$ abundance category of the composite family.

Other families also regarded as composites were treated as follows:
Siphlonuridae (including Ameletidae) – were all regarded as Siphlonuridae
Heptageniidae (including Arthropleidae) – were all regarded as Heptageniidae
Limnephilidae (including Apataniidae) – were all regarded as Limnephilidae

Combined Seasons Data

In addition to preparing the datasets above for the calculation of biotic indices for single season samples at a give site in a given year, the error terms needed for the new Tool require an estimate of the variability of combined season biotic index values. To achieve this spring, summer and autumn samples within the same year were combined (where appropriate samples existed within that year) as below:

Season combination	RIVPACS season code
Spring	1
Summer	2
Autumn	3
Spring & Summer	4
Spring & Autumn	5
Summer & Autumn	6
Spring, Summer & Autumn	7

Log10 abundance categories were combined across the 2-season sample combinations by taking the maximum of the log10 abundance categories. For the 3-season combinations, the maximum log10 abundance category was taken (unless all 3 abundances were the same in which case the abundance was increased by 1, i.e. the Max+1 rule was used). This therefore gave up to 7 separate and combined season samples at each site in each year. This was done for each the 4 taxonomic resolutions needed for the various biotic indices.

Within Seasons Replicates

A further element of variability that needs to be quantified is the extent to which samples taken on a different day vary (within the same season in the same year at the same site). Examination of the 416-site dataset has shown that there are 180 occasions where the same site was sampled in the same year and in the same season but on a different day. Typically there were either 2 spring samples taken or 2 autumn samples taken (replicate summer samples are much rarer). At a subset of 4 of these, 2 samples were taken in spring and 2 samples were taken in autumn, on different days, in the same year.

Biotic Index Calculation

As with the 28-site dataset, the following biotic indices were calculated using the 4 taxonomic levels of data above:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

The details of the above indices are the same as those used for the 28-site dataset and are included in the Appendix II. For LIFE and both the non-abundance weighted WHPT and abundance weighted WHPT indices, distinct families were used for scoring rather than BMWP composites.

16-site Biological Assessment Methods (BAMS) dataset

The Environment Agency 16-site Biological Assessment Methods (BAMS) dataset is already used to quantify uncertainty within RIVPACS III+ (Furse et al., 1995). Within project WFD72C this dataset has been further enhanced by the calculation new biotic indices that are required for the new Tool.

The BAMS dataset comprises 16 sites covering a range of physical stream types within England and Wales and a range of biological qualities. Each site was sampled in the three RIVPACS sampling seasons spring, summer and autumn in 1994. In each season, 3 replicate samples were taken (two samples were taken by one operator and one sample was taken by a different operator).

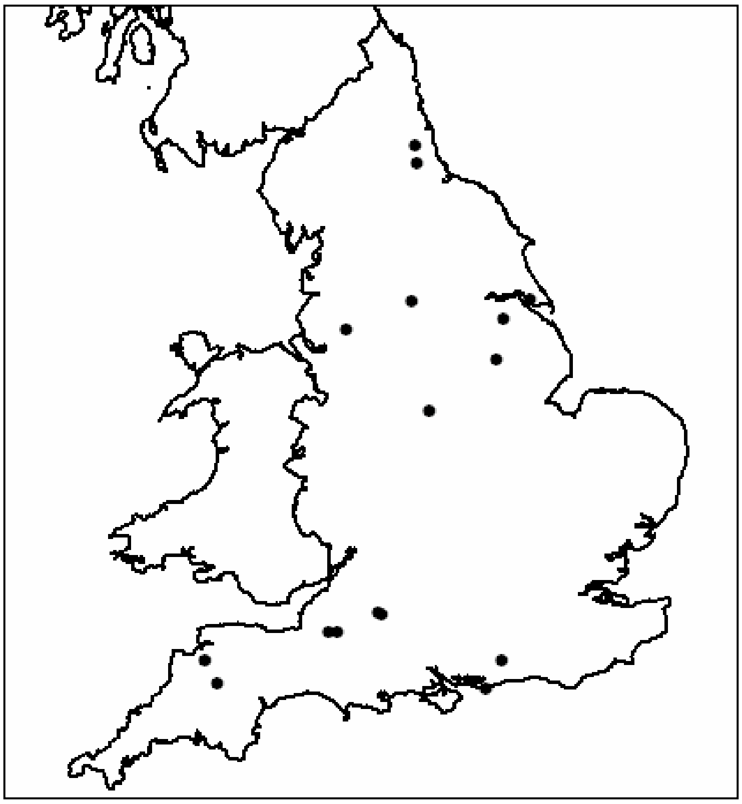


Figure 4. Map of the 16 BAMS sites in England and Wales

The samples were identified to BWMP family level and abundances were recorded as log10 categories.

Taxonomic Resolution

Although the BAMS dataset had only been identified to BMWP family level, the wide geographical coverage of the 16 sites made it difficult to develop rules to split the artificial BMWP composite groups into their constituent families and this was not attempted. All of the indices were therefore calculated using BMWP family level data.

Replicate Data

Replicate samples from the BAMS dataset comprised 16 sites, with 3 spring, 3 summer and 3 autumn samples at each site. These samples were also combined to give two and three season combined samples as below:

Season combinations (For each of the 16 sites)	RIVPACS season code
3 Spring samples	1
3 Summer samples	2
3 Autumn samples	3
9 Spring and Summer combined samples	4
9 Spring and Autumn combined samples	5
9 Summer and Autumn combined samples	6
27 Spring, Summer and Autumn combined samples	7

These totalled 63 samples per site (1008 samples across the whole dataset).

Log10 abundance categories were combined across the 2-season sample combinations by taking the maximum of the log10 abundance categories. For the 3-season combinations, the maximum log10 abundance category was taken (unless all 3 abundances were the same in which case the abundance was increased by 1, i.e. the Max+1 rule was used).

Biotic Index Calculation

As with the Scottish datasets, the following biotic indices were calculated, although this time, all using BMWP family level data:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

The details of the above indices are the same as those used for the Scottish datasets and are included in the Appendix II. For LIFE and both the non-abundance weighted WHPT and abundance weighted WHPT indices, BMWP composite families were used for scoring as opposed to distinct families.

12-site Northern Ireland Community Change Study dataset

This Community Change Study dataset comprising samples from 12 sites in Northern Ireland (see map below) and was supplied by Tommy McDermott of the Environment and Heritage Service, Lisburn. Each site was sampled in February, March, April, May, June, July, August, September, October and November/December 2006 and in January 2007. There were therefore 132 samples in all.

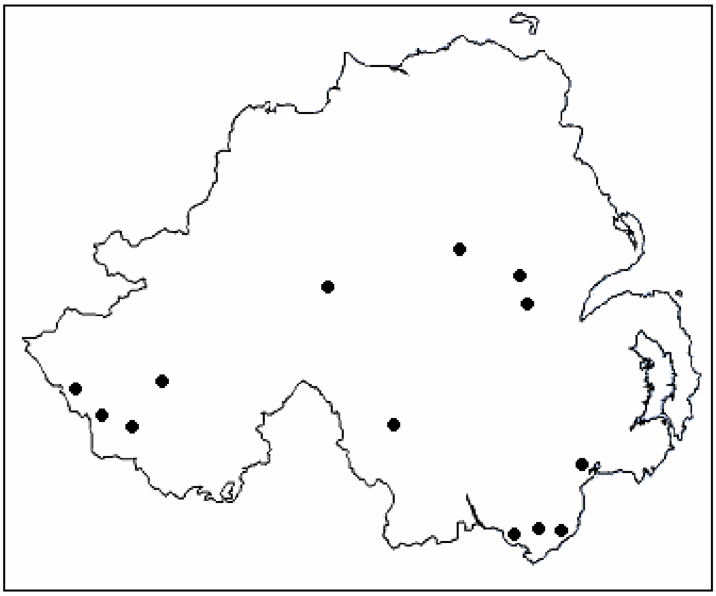


Figure 5. Map of the 12 Northern Ireland Community Change Study sites

The Community Change Study dataset is of particular interest because unlike the other datasets it contains replicate samples within each of the spring, summer and autumn RIVPACS sampling seasons with samples collected on different days. This dataset potentially enables estimates to be made of within-season sampling variability.

Taxonomic Resolution

All of the samples are identified to BMWP family level and most taxa were enumerated with log10 abundance categories. Taxa in some samples were only enumerated as presence/absence records and in these cases all taxa were simply regarded as having occurred at log10 abundance category 1. Information on the nature of the abundance data (true log10 abundance categories versus presence/absence based log10 category 1 assigned abundance) has been preserved in the collated dataset.

Replicate Data

The dataset was collated to obtain all valid combinations of single and combined season samples from each of the 12 sites. To achieve this, the original 11 samples from each site were filtered down to include only those 9 months in the RIVPACS sampling seasons Spring (March, April and May), Summer (June, July and August) and Autumn (September, October and November/December). December samples were regarded as being suitable for inclusion as Autumn samples.

This dataset of 108 samples (12 sites x 9 samples per site) was then used to form 63 single season , two-season combined and three-season combined samples from each site, making 756 (12 x 63) samples in all. The sample combinations are shown in the table below.

Single Season	Two-Season	Three-Season
March	March + June	March + June + September
April	March + July	March + June + October
May	March + August	March + June + November
June	April + June	March + July + September
July	April + July	March + July + October
August	April + August	March + July + November
September	May + June	March + August + September

October	May + July	March + August + October
November	May + August	March + August + November
	March + September	April + June + September
	March + October	April + June + October
	March + November	April + June + November
	April + September	April + July + September
	April + October	April + July + October
	April + November	April + July + November
	May + September	April + August + September
	May + October	April + August + October
	May + November	April + August + November
	June + September	May + June + September
	June + October	May + June + October
	June + November	May + June + November
	July + September	May + July + September
	July + October	May + July + October
	July + November	May + July + November
	August + September	May + August + September
	August + October	May + August + October
	August + November	May + August + November

Biotic Index Calculation

As with the Scottish datasets and the BAMS dataset, the following biotic indices were calculated using the BMWP family level data:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

The details of the above indices are the same as those used for the Scottish and BAMS datasets and are included in Appendix II. For LIFE and both the non-abundance weighted WHPT and abundance weighted WHPT indices, BMWP composite families were used for scoring as opposed to distinct families.

Particular attention is drawn to the fact that log10 abundance category data for some of the Community Change Study dataset was not available and that this will affect the abundance weighted WHPT and LIFE scores.

Gaps in the supplied datasets

The combined datasets have supplied provide good coverage of all the major sources of variability. While the uncertainty work for the new Tool is a new and therefore a developing area, at this point in time we think that the data that has been provided should be fully sufficient. These data should enable us to obtain an assessment of uncertainty for the core metrics in the new Tool arising from inter-operator variability (as in RIVPACS III+), natural within-season variability and natural inter-annual variability.

References

Furse M.T., Clarke R.T., Winder J.M., Symes K.L., Blackburn J.H., Grieve N.J. & Gunn R.J.M (1995) Biological assessment methods: controlling the quality of biological data. Package 1 – The variability of data used for assessing the biological condition of rivers. R&D Note 412, Environment Agency, Bristol. 139 pp.

WFD72C River Invertebrate Classification Tool (Stage 2)

Work Element 2.3 – Compilation of Biological Data for Estimating Nominal Abundances to be applied to the RIVPACS samples

Report describing datasets to be used and identifying gaps – 18th Jan 2008

Background

All current and previous RIVPACS models have been based upon samples with taxa recorded at both species and family levels. Species records were recorded as simply presence/absence while family level records have been enumerated using the log$_{10}$ abundance categories as shown below:

Log$_{10}$ category	Numerical abundance
5	1-9
6	10-99
7	100-999
8	1,000-9,999
5	10,000+

However, it has been recognised for some time that the lack of numerical abundance data for the RIVPACS samples, both at species and family level, presents a potential difficulty for the integration of abundance weighted biotic indices into RIVPACS models. Lack of numerical abundances also leads to problems where samples from more than one season need to be pooled for combined season estimates. It is therefore necessary to develop and test a rationale for ascribing estimated numerical abundances to the taxa in the RIVPACS dataset.

At the pre-project interview (28th May 2007) it was agreed by the Project Board that no attempt would be made to allocate estimates of abundances to the species level records in the RIVPACS reference site dataset because of the lack of adequate supporting data, the potential costs and the lower practical priority compared to allocating numerical abundances to the RIVPACS families.

At the second project meeting (26th September 2007) the appropriateness of assigning numerical abundances across the whole of the UK using data from only England and Wales (as was originally planned) was discussed. It was agreed that ideally data should be obtained from across the UK so that geographical changes in abundance patterns could be investigated and if necessary factored into the estimates of numerical abundances to be applied to the RIVPACS samples. It was also agreed that in addition to numerical abundance data for the families these datasets should contain information on quality classes and most probable RIVPACS end group membership. These additional pieces of information should enable the sites to be screened to exclude any sites not in the ‘high’ or ‘good’ quality categories and interpret geographical changes in abundances in terms of RIVPACS end groups.

In recent years the UK Agencies have been recording the numerical abundances of families in their routine monitoring data. This WE report therefore describes work done to collate new family level datasets from the Environment Agency, Scottish Environment Protection Agency, and Environment and Heritage Service. These datasets will be used in WE 3.2 to derive and then apply estimates of numerical abundances to the RIVPACS family level data.

Datasets

John Murray-Bligh (EA), Robin Guthrie (SEPA) and Tommy McDermott (EHS) have provided the following three datasets:

EA 2006 GQA dataset from England & Wales
SEPA 2004 GQA dataset from the Scottish mainland, Highlands and Islands
EHS 2007 GQA dataset from Northern Ireland

EA 2006 GQA dataset from England & Wales

Five spreadsheets and one database were received from John Murray-Bligh. These gave numerical abundances of families from the EA 2006 GQA survey across England and Wales, GQA quality classes and RIVPACS predictor variables.

Numerical Family Abundance Data

> These data were supplied in two Excel spreadsheets, covering spring 2006 and autumn 2006 samples respectively (no summer 2006 data was collected). These spreadsheets each contained eleven work sheets where each worksheet was a matrix of samples from a given EA region by those families found in the samples. These 22 worksheets were collated by passing them through a reformatting spreadsheet to convert the matrix format data into a list format. The 22 lists were then combined to produce a single table of all of the EA 2006 family abundance data in an Access database.

Quality Class Data

The database supplied by John Murray-Bligh gave the 2006 spring and autumn combined GQA quality classes. This was stripped down to the required fields in a second Access database

RIVPACS End Groups

The remaining EA spreadsheets were used to collate a set of RIVPACS environmental predictor variables for the EA 2006 monitoring sites. These data were then used to produce a RIVPACS format environmental data file and then run through RIVPACS RPBATCH 3.3 (GB model) to obtain the most probable RIVPACS end group (and probability of end group membership) for each EA GQA monitoring site.

Combined data

The numerical family abundance data, quality class data and RIVPACS end group data were then further combined into a single Access database table giving all the required fields as a flat file.

SEPA 2004 GQA dataset from the Scottish mainland, Highlands and Islands

A single Access database was received from Robin Guthrie. This gave numerical abundances of families from the SEPA 2000, 2001, 2002, 2003 and 2004 GQA surveys across the Scottish mainland, Scottish Highlands and the Scottish Islands, as well as RIVPACS predictor variables and GQA quality classes (although not for all sites).

Numerical Family Abundance Data

Numerical abundance data was available for several years within the SEPA database but this was filtered to the most current year (2004) for the purposes of this WE. Data from the whole of Scotland including the Highlands and Islands was available.

Quality Class Data

> To obtain quality class data for all of the Scottish sites, the SEPA dataset site and sample data was queried to extract RIVPACS environmental predictor variables. These data were then used to produce a RIVPACS format environmental data file and this was then run through RIVPACS RPBATCH 3.3 (GB model) to obtain the expected spring and autumn combined BMWP indices for the Scottish mainland. Robin Guthrie also supplied separate RIVPACS environmental data files for the Scottish Highlands and the Scottish

Islands. These were also run through RIVPACS RPBATCH 3.3 (Scottish Highlands and Scottish Islands models) to obtain the expected spring and autumn combined BMWP indices for sites in the Scottish Highlands and Islands.

Observed values for the spring and autumn combined samples from all of the Scottish sites were calculated within the SEPA database. Spring and autumn combined observed/expected NTAXA and ASPT were then manually calculated and categorised into GQA quality classes.

RIVPACS End Groups

The RIVPACS RPBATCH runs using SEPA data in the GB, Scottish Highlands and Scottish Islands models (see section above) also generated most probable RIVPACS end groups and probability of end group membership for each SEPA GQA monitoring site in the Scottish mainland, Highlands and islands.

Combined data

The numerical family abundance data, quality class data and RIVPACS end group data were then further combined into a single Access database table giving all the required fields as a flat file.

EHS 2007 GQA dataset from Northern Ireland

Nine spreadsheets were received from Tommy McDermott. These gave numerical abundances of families from the EHS 2007 GQA survey across Northern Ireland; GQA quality classes based on spring samples and RIVPACS predictor variables. The Northern Ireland samples were separated into three types – primary sites, secondary sites and minor sites. Primary and secondary sites had both spring and autumn 2007 samples while minor sites had only a single season (usually spring 2007). Primary and secondary sites were equivalent and were pooled for the purposed of this WE. Minor sites were not used.

Numerical Family Abundance Data

These data were supplied in four Excel spreadsheets, covering primary and secondary sites in spring 2007 and autumn 2007. The spreadsheets each contained a matrix of samples by those families found in the samples. The spreadsheets were collated by passing them through a reformatting spreadsheet to convert the matrix format data into a list format. The four lists were then combined to produce a single table of all EHS primary and secondary site 2007 family abundance data in an Access database.

Quality Class Data

Quality class data based on spring samples was available within the EHS spreadsheets for all EHS primary and secondary sites. These data were pooled into a single EHS quality class table within an Access database.

RIVPACS End Groups

The most probable RIVPACS end groups and probability of end group membership for all EHS sites was also available within the EHS and this was queried down to the required fields in an Access database table.

Combined data

The numerical family abundance data, quality class data and RIVPACS end group data were then further combined into a single Access database table giving all the required fields as a flat file.

UK-wide Combined Dataset

The final step in data collation was to combine the numerical family abundance data, quality class data and RIVPACS end group data from the EA 2006, SEPA 2004 and EHS 2007 GQA surveys into a single Access database table giving all the required fields as a flat file (Table 5). This data set comprises 126,221 family level numerical abundances and provides excellent geographical coverage across the whole of Great Britain and Ireland including the Scottish Islands. This dataset is regarded as fully adequate to support the allocation of numerical abundances to the RIVPACS dataset (WE 3.2) and there is no requirement for any further data.

Table 5. Example of the compiled data for the estimation of nominal abundances to be applied to the RIVPACS samples (126,221 rows in full GB-wide dataset).

Agency	Year	Site code	Sample Code	Season	Family Code	Family Name	Numerical Abundance	Log10 Category	Model	Most Probable End Group	Probability of Most Probable End Group	O_E NTAXA	O_E ASPT	Quality Grade
SEPA	2004	320	7385	Spring	161Z0000	Hydrobiidae (incl. Bithyniidae)	9	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	16220000	Lymnaeidae	6	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	162Z0000	Ancylidae (incl. Acroloxidae)	8	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	17130000	Sphaeriidae	4	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	20000000	Oligochaeta	4	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	22310000	Erpobdellidae	1	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	24000000	Hydracarina	1	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	36110000	Asellidae	15	2	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	371Z0000	Gammaridae (incl. Crangonyctidae & Niphargidae)	2	1	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	40120000	Baetidae	50	2	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	40130000	Heptageniidae	30	2	GB	6	0.579	1.011	0.921	b
SEPA	2004	320	7385	Spring	41110000	Taeniopterygidae	1	1	GB	6	0.579	1.011	0.921	b

WFD72C River Invertebrate Classification Tool (Stage 2)
WE3.1 - Revision of Taxonomic Framework in RIVPACS Database
1st June 2008

Background

There is a requirement to review the taxonomic framework of the RIVPACS IV models being developed for inclusion within the new WFD72C Tool. This is necessary to update the taxonomy of the species and family level predicted taxon lists and to ensure that the taxonomy used in the calculation of biotic index values is both correct and up-to-date. Furthermore, unlike previous versions of RIVPACS that exclusively used Maitland codes for taxon coding purposes, the new Tool will need to be fully compatible with the Agencies NBN (National Biodiversity Network) taxon coding system.

The previous work element report (WE3.1 - Review of the Taxonomic Framework, 23rd September 2007) provided a review of the following generic issues:

1. To ensure that the taxonomic groupings for the existing BMWP taxa accurately reflect modern taxonomy as used by the Environment Agencies (e.g. renaming BMWP family *Ancylidae* as *Ancylus/Acroloxidae* group and renaming *Planorbidae* as *Planorbidae* not including *Ancylus*). This will ensure that, for example, taxonomic predictions based on existing BMWP taxa are correct, even if they represent artificial taxonomic groups.

2. To update names for other taxonomic levels to reflect current practice (e.g. *Siphonoperla/Chloroperla*)

3. To split and rename taxa where possible to be compatible with the revised BMWP scores and modern taxonomic conventions. This will be relatively easy for presence/absence data for “families” as the species records in the RIVPACS dataset will indicate where the composite BMWP family records actually contain records of different species that belong to the different groups. Determining the actual abundance for each record will depend on the allocation of nominal abundances detailed below.

4. All taxa in the reference database will be recoded using the NBN taxon list used by the Environment Agency. (The original Maitland codes will be retained in the database as well).

The September 2007 review compared the taxonomy of the three nomenclatures (coding systems) of freshwater macroinvertebrates that are in use in the UK:

1) RIVPACS III+ Taxonomy (Revised Maitland Code)
2) The Updated CEH Coded Checklist of Freshwater Macroinvertebrates (Furse Code)
3) National Biodiversity Network Taxonomy (NBN Code)

The RIVPACS III+ dataset includes 1061 unique taxonomic units (across both family and species levels). For these 1061 unique taxa, the three coding systems were examined to see the extent to which one or other taxonomy is more up-to-date than the other and to examine the extent of matches between the coding systems (showing which coding systems may lack codes to cope with taxa required by RIVPACS).

The September 2007 analysis drew the following conclusions:

1) The recently updated CEH coded checklist of freshwater macroinvertebrates was by far the most up-to-date of the three. The RIVPACS III+ taxonomy was the most out of date. The National Biodiversity Network taxonomy was only more up-to-date than the RIVPACS III+ taxonomy in a few selected areas.

2) The National Biodiversity Network taxonomy lacked some 81 taxa that are required by RIVPACS. These were typically artificial taxon groups that represent reliable end points in

macroinvertebrate identification (e.g. Polycelis nigra group which includes the difficult to separate Polycelis nigra & Polycelis tenuis). The absence of these artificial taxon groups in the National Biodiversity Network taxonomy was identified as a significant problem because the new RIVPACS IV models will need to be able to code these taxa in their taxonomic outputs. It was decided that new ‘manifestly synthetic’ NBN codes would be generated by CEH to cope with these omissions (prefixed <NEW-CODE> to distinguish them from native NBN codes).

These new codes are given in Appendix III.

3) The updated CEH coded checklist of freshwater macroinvertebrates lacked nine codes (all of which have now been added).

Composite BMWP Families

The BMWP scoring system uses several artificial families that are composites of two or more real families. The September 2007 analysis examined the particularly troublesome taxonomic issues around the composite family Ancylidae (including Acroloxidae). Recent taxonomic revisions have meant that the genera Ancylus and Ferrissia have moved into the family Planorbidae and the family Ancylidae is no longer valid in modern taxonomy. The artificial taxon groups proposed to deal with the Ancylidae problem have been revised slightly since the previous version of this Work Element and are presented below.

The following families are proposed to address the Ancylus problem:

16230000	Planorbidae[1]
162X0000	Planorbidae (excluding Ancylus group)[2]
162Y0000	Ancylus group[3]
162Z0000	Ancylus group (including Acroloxidae)[4]
16250000	Acroloxidae[5]

[1] The modern family Planorbidae including the genera Ancylus, Anisus, Bathyomphalus, Ferrissia, Gyraulus, Hippeutis, Menetus, Planorbarius, Planorbis and Segmentina

[2] The family Planorbidae but excluding Ancylus fluviatilis & Ferrissia clessiniana.
NB - Ferrissia clessiniana was formerly known as Ferrissia wautieri

[3] The now non-existent family Ancylidae comprising the taxa Ancylus fluviatilis and Ferrissia clessiniana.

[4] The now non-existent family Ancylidae together with the family Acroloxidae. Comprises the taxa Ancylus fluviatilis, Ferrissia clessiniana and Acroloxus lacustris

[5] Acroloxidae remains unchanged and contains just one species (Acroloxus lacustris)

The treatment of Ancylidae and Planorbidae together with the other composite families used in the “BMWP families” taxonomic level are summarised in Appendix IV.

Revision of Taxonomic Framework

Since the initial September 2007 review was written, considerable work has been done on producing the files for taxonomic prediction for RIVPACS IV (work element 4.3). This work has driven the requirements for all three of the taxonomic coding systems.

To produce the files for taxonomic predictions, data in the RIVPACS database was 'standardised' to 4 taxonomic levels that will be available as outputs:

1) TL1 BMWP families
2) TL2 Revised (WHPT) BMWP families
3) TL3 All families
4) TL4 RIVPACS species

The raw data (either at family or species level) in the RIVPACS database has now been standardised to the above four taxonomic levels. In many cases the data remained unchanged (e.g. the family Lepidostomatidae exists in the raw data and was used directly in taxonomic levels 1, 2 and 3). However, in some cases the RIVPACS database contained data at a finer level of taxonomic resolution that then needed to be downgraded (e.g. the distinct families of Oligochaeta were downgraded to the order Oligochaeta). In other cases, the RIVPACS database contained data that was at a coarser level of taxonomic resolution e.g. the artificial taxon Planariidae including Dugesiidae (in this case the taxon was split). Recent changes in taxonomy have also led to further requirements for new codes and meant that some existing codes in RIVPACS are no longer required.

Within each taxonomic level, data for taxonomic predictions have been provided under each of the three taxonomic coding systems. For example, data to support BMWP family level predictions are stored under Revised Maitland, National Biodiversity Network and Furse code coding systems (see table below).

Taxonomic Level	Coding System	Coding System	Coding System
TL1 BMWP families	Revised Maitland	National Biodiversity Network	Furse code
TL2 Revised BMWP	Revised Maitland	National Biodiversity Network	Furse code
TL3 All families	Revised Maitland	National Biodiversity Network	Furse code
TL4 RIVPACS species	Revised Maitland	National Biodiversity Network	Furse code

This process of producing taxonomic data at four different taxonomic levels under 3 different coding systems and has created requirements to code some groups that were not foreseen in the September 2007 review, and has also removed the requirement to be able to code others. The files for taxonomic prediction described above have now been produced (only requiring adjustments to abundances for some taxa that have been split – see WE 3.2 – Generation of Family Level Abundance Data) and the taxonomy is now fixed and known.

It is now possible to describe the taxonomy that is used in RIVPACS IV in its final form under each of these taxonomic levels and this is given in Appendices V, VI, VII and VIII

WFD72C River Invertebrate Classification Tool (Stage 2)
WE 3.2 Deliverable - Generation of Family Level Abundance Data for the RIVPACS database

1) Introduction

Families within the RIVPACS dataset are currently enumerated with $\log_{10}$ abundance categories while species are simply listed if present. However, it has long been recognised that the absence of numerical abundances for the taxa in the RIVPACS reference dataset has prevented the calculation of predicted values of family and species level indices which require numerical abundances. While there are numerical abundance data available for many of the taxon records on the original hard copy RIVPACS reference site lab sheets, entering these data into the RIVPACS database would have required an estimated 12 months full-time work, which would not have been feasible within this project. Whilst it is anticipated that future additions to the RIVPACS database will ensure that all families and species are recorded with numerical abundances, it is has been necessary to derive and test a rationale for ascribing estimates of the numerical abundances of families to the RIVPACS dataset. Assigning numerical abundances to the species level records in the RIVPACS database was considered to be beyond the scope of the current project due to lack of adequate species level data upon which to base the estimates, costs and its lower practical priority (agreed by the Project Board on 28/05/07).

2) Families in RIVPACS requiring numerical abundances

Family records within the RIVPACS dataset were identified to a standard level of taxonomic resolution. This included the separation of the families within the Oligochaeta and sub-families within the Chironomidae. Families that are not part of the BMWP scoring system were also recorded in full (including all families of Diptera). Families that were originally recorded as BMWP composite families e.g. Planariidae (including Dugesiidae) have now been separated into their constituent families (see WE3.1.2 - Revision of the Taxonomic Framework in the RIVPACS Database).

3) Numerical Abundance Data from the UK Agencies

To be able to make estimates of the numerical abundances of the family level records within the RIVPACS database a substantial external dataset was required that would have enough data to make reasonably robust estimates of average numerical abundances for each family. This dataset would also need to have a good coverage of as many of the required families as possible. The UK Agencies have recently begun enumerating families in their routine biological samples with numerical abundances (this had previously been done using $\log_{10}$ abundance categories). Recent family level datasets from across the whole of England, Wales, Scotland and Northern Ireland were therefore requested for this task.

The datasets received from the UK Agencies were first filtered to remove sites not in the current GQA high and good quality bands. Some of the datasets received already had GQA quality bands while others needed to be run through RIVPACS III+ to obtain these quality bands. This step was considered as essential to ensure that the Agency data was comparable to the RIVPACS dataset in terms of site quality (so that the abundances of families were not distorted away from ‘reference’ abundances by reductions or increases in the abundances of families due to any form of pollution). The RIVPACS end groups of each of the sites had also been requested so that any potential geographical or stream-type specific patterns in numerical abundances could be investigated.

The datasets from across the UK were then pooled and processed to provide a $\log_{10}$ abundance category to go alongside each of the recorded numerical abundances. The numerical abundances of each family within each $\log_{10}$ category are shown in Figure 6 (and Appendix IX). A clear trend exists within the abundance data, namely, that families that generally have low numerical abundances within $\log_{10}$ category 1 tend not to found at high $\log_{10}$ abundances. Conversely, families that tend to be recorded with higher $\log_{10}$ categories in $\log_{10}$ abundance category 1 are more likely to be found at higher log10 categories. It is therefore clear that the average numerical abundances of families within the $\log_{10}$ abundance categories differs between different families and that where possible it would be sensible to allocate numerical abundances to the RIVPACS family level records that mirror this trend.

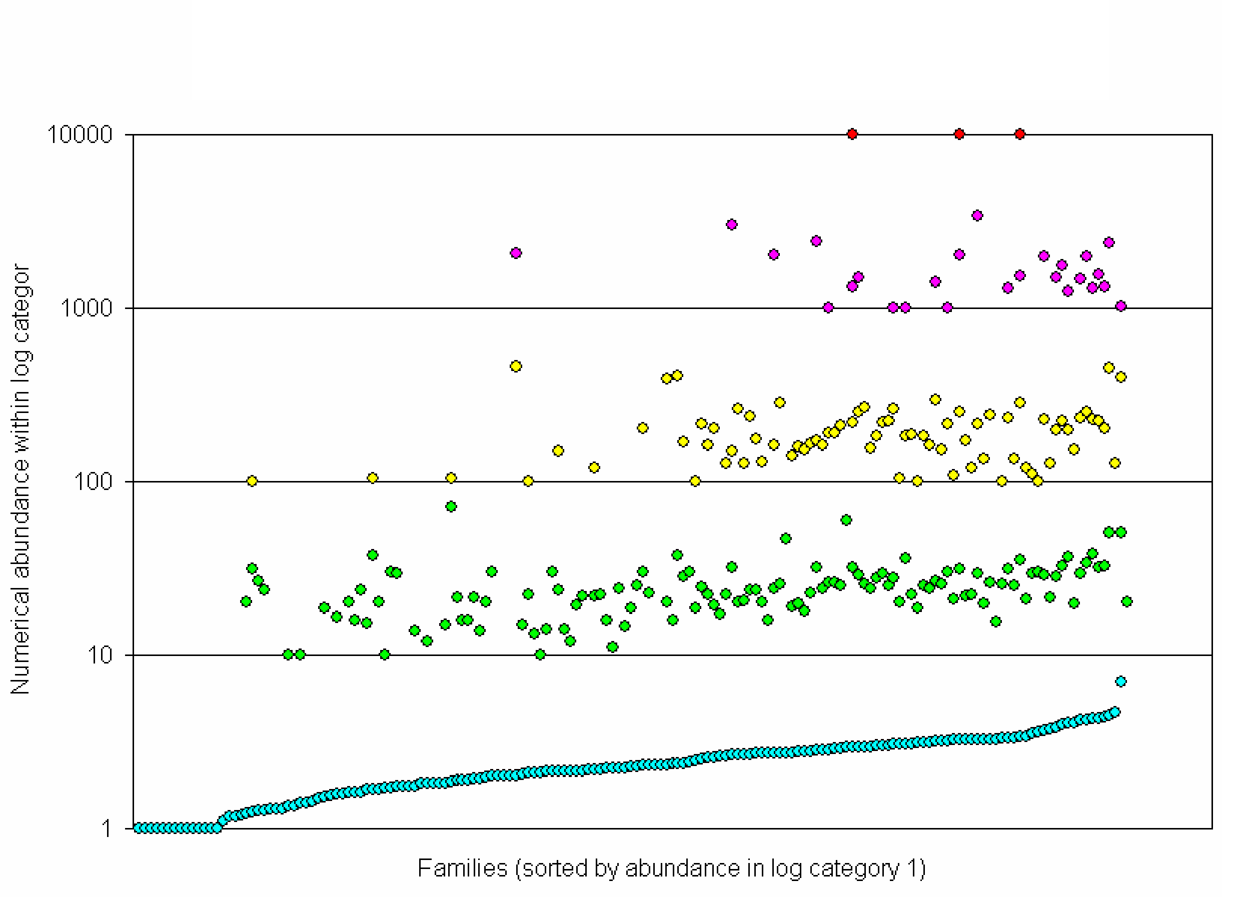


Figure 6. Numerical abundances of families within $\log_{10}$ abundance categories (based on data from the EA, SEPA and EHS).

While there was a clear pattern that average numerical and $\log_{10}$ abundances were linked and varied between the families, analysis of geographical trends in the abundances did not show any tendency for the numerical abundances within the $\log_{10}$ categories to be higher within certain geographical regions compared to others. Put another way, while the $\log_{10}$ abundances of families clearly differed between different types of streams, the numerical abundances within each $\log_{10}$ category did not show any obvious enough trends to permit any further refinement of the rules for assigning abundances to the RIVPACS families above and beyond allocating family specific values. It was therefore decided that stream type patterns would not be investigated further and that a single UK-wide family specific estimate of the abundance would be applied to all records in that $\log_{10}$ abundance category in the RIVPACS dataset.

NB - the UK Agencies no longer take summer samples so it was not possible to include season specific numerical abundance estimates so the numerical abundances within each log10 abundance category have been derived from all available seasons in the Agencies data and will be applied to all 3 seasons in the RIVPACS dataset.

4) Estimates of numerical abundances where no data available

Close examination of the datasets supplied by the Agencies revealed that some families that had been found in the RIVPACS samples had not subsequently been encountered in the Agency samples. Together with the problem that no numerical abundances were available for the families of Oligochaeta or the sub-families of Chironomidae (as discussed in section 2 above), there were therefore a group of families where the numerical abundances had to be estimated by other methods. For the separate families of Oligochaeta, numerical estimates were obtained from the Environmental Change Network datasets (supplied by CEH). For the other families were no (or very little) numerical data were available, broad global estimates of the average numerical abundances of all families within each numerical abundance category had to be applied.

5) Applying numerical abundances to the RIVPACS dataset

The estimates of numerical abundances were then applied to each family within each log10 abundance category within the RIVPACS dataset.

One further adjustment was then required to address a problem from earlier in the project when the BMWP composite taxa had been split to obtain records for the individual families in the RIVPACS dataset (WE3.1 Review and Development of the Taxonomic Framework). Although the separate families had been correctly created on the basis of the species known to have been present in the sample, at the time the $\log_{10}$ abundance categories of the separated families had to be obtained by simply duplicating the $\log_{10}$ abundances of the original composite families. However, $\log_{10}$ abundances for families were available from the data supplied by the Agencies, so it was possible to return to the problem of the abundances of the separated BMWP composites to devise a better solution. The $\log_{10}$ abundances of the component families that make up the BMWP composite taxa were analysed to derive some general rules about the commonest distribution of $\log_{10}$ abundances across these pairs of families. For example, in the case of the BMWP composite family Planariidae (including Dugesiidae) recorded at $\log_{10}$ abundance category 2, it can be show that the $\log_{10}$ abundance categories of the component families are typically $\log_{10}$ category 2 for Planariidae and $\log_{10}$ category 1 for Dugesiidae. While these data were not extensive and (and some estimates also to be made where there were no data available), it was possible to devise some a rules for how the $\log_{10}$ abundances should be distributed across the separate families of the BMWP composite taxa (Appendix X). These changes were therefore applied to the family level records that had been obtained by splitting BMWP composite family records. As a final step, given that the $\log_{10}$ abundances of some of these families had therefore been adjusted (downwards) it was necessary to re-assign the numerical abundance values to these families (using the same method described in section 4).

6) Biotic indices

The newly calculated estimates of $\log_{10}$ abundance categories for family level records in RIVPACS have been used to calculate versions of the revised BMWP and LIFE biotic index scores using distinct BMWP composite families and have also been used in the files underpinning the taxonomic predictions that will be produced by RIVPACS IV. However, it is important to note that the numerical abundance data available for many of the taxon records on the original hard copy RIVPACS reference site lab sheets should ideally be entered into the RIVPACS dataset. CEH has already has made some initial progress with this task (outside this project) and from the samples entered so far it appears that numerical abundances estimates can be obtained for some 85% of the RIVPACS families and species. This approach also benefits from the fact that the numerical abundances obtained from the original laboratory sheets are at exactly the right taxonomic level and the data can provide season and stream-type specific abundances. It is hoped that this research need will be included in any future RIVPACS project funded by SNIFFER or the Agencies

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 4.1 Deliverable
Revision of Geographic modules and site end groups

1. Background

The current RIVPACS III+ Release 3.3 bio-assessment software (also known as RPBATCH) geographic module structure consists of the main GB module (GB, 614 reference sites, in 35 end groups), the Scottish Highlands module (SH, 110 sites of which 52 also in main GB module, in 10 end groups) and the Scottish Islands module (SI, 55 sites, in 5 end groups), together with a separate module for Northern Ireland (NI, 110 sites, in 11 end groups).

The GB and SH reference sites overlap in geographic coverage with no obvious clear bio-geographical boundary, while many of the Scottish Islands (SI) sites are near the mainland (e.g. Skye) and thus may not have distinct island macroinvertebrate communities and therefore predictions might be improved by integration with mainland GB reference sites.

In this WE4.1, the aim was to try to build a new single GB-inclusive model for all UK sites except Northern Ireland to be based on the reference sites in the current RIVPACS models for mainland GB, the Scottish Highlands and the Scottish Islands. It was acknowledged that if it was not possible to ensure that predictions for biologically-distinct taxonomically poorer islands such the Shetlands are appropriately based on similar island sites, it may be necessary to develop a separate remote island model.

The Northern Ireland reference sites and RIVPACS model was considered to represent a natural geographic split and it was agreed that this would be retained as a separate model.

For pragmatic reasons, it was agreed at the pre-project interview (28/05/07) that the revision of predictive models and end groups and model assessments will be based on the current RIVPACS taxonomic data and the current BMWP indices; this will also aid comparison with existing models. Moreover, the updating of the taxonomy used in RIVPACS sample data and bioassessments (being undertaken in WE3.1) was not considered to be sufficient to have any major effect on the reference sites biological classifications and subsequent predictions of expected values of biotic indices.

2. Refinement of Reference sites for model development

Prior to model development, the complete set of GB, SH, SI and NI RIVPACS III+ reference sites were reviewed in the light of the WFD to re-assess whether they were of adequate quality at the time of RIVPACS sampling to use as Reference sites in the new model(s) and predictions. Thirty five sites from the old GB model, five sites exclusive to the Scottish Highlands model and two sites from the Northern Ireland model were considered to be unduly impacted or subject to sampling problems in one of more the seasons in which they were sampled for use as RIVPACS Reference sites. This work was carried out under WE2.1 of this project, and further details, including the list of 42 sites to be removed from future model development and predictions, are given in project interim report:
“01 WE2.1 Refinement of Reference sites.doc” dated 01/08/07.

3. Northern Ireland model predictions

The RIVPACS III+ module for Northern Ireland is based on 110 Reference sites from Northern Ireland, classified into 11 end groups (1-11). One of the two reference sites re-assessed in WE2.1 and judged to be of insufficient quality was the 'Moy' site on the river Blackwater (site id 20303403) from end group 11 (comprising 7 sites) and the other was the 'Carrols Bridge' site on Crew Burn (site id NI_24) from end group 6 (comprising 13 sites).

As only two of the current 110 reference sites are to be rejected, the changes should not cause major alterations to NI model predictions. Therefore it was agreed at the second project meeting (27/09/07) that the current RIVPACS III+ biological classification of Reference sites into the 11 end groups would be retained, along with the current MDA discriminant functions for this NI module. However, the end group mean values for each of the biotic indices (upon which predicted index values are based) would be based on the mean values for each end group excluding these two rejected sites. These will be supplied by CEH as part of WE4.4 deliverable, expected at the end of November 2007.

4. New GB-inclusive model and predictions

The aim was to develop a new GB-inclusive model based on the 579 retained sites from the old GB model, together with the 51 retained sites specific to the Scottish Highlands model and the 55 Scottish Islands reference sites, making a total of 685 reference sites.

Model development

The new model was developed using the same statistical procedures as used for the existing RIVPACS III+ modules. First the 685 reference sites were classified into end groups on the basic of their macroinvertebrate composition using the TWINSPAN hierarchical divisive classification method. As in previous models, the site classification was based on the best available data for each reference site, namely the three season combined sample data, using both the abundance categories of families and the presence-absence of species. The three season combined sample abundance category for a family was taken as the maximum of the three individual seasons' categories for that family, or one category higher if all three were the same.

Then the statistical technique of multiple discriminant analysis (MDA) was used to derive predictive equations for the probability of any site belonging to each of the site groups based on its values for the RIVPACS environmental variables (see Clarke, Furse and Wright 2003 for statistical details of methods). All of the environmental predictor variables involved in the RIVPACS preferred predictor variable set for previous GB model (RIVPACS III+ software environmental option 1) were used in the MDA. These therefore included two variables based on internal-determined estimates of the mean and annual range of air temperature at a site (The previous background air-temperature database for GB has already been extended to cover all Scottish Islands, as part of this project's WE1 detailing the algorithms and associated data involved in making RIVPACS predictions. All of the environment variables individually exhibited statistically significant discrimination (i.e. differences) between at least some of the end groups.

The final choice of end groups for the biological classification of the 685 references sites was based on an iterative approach. In TWINSPAN, the sites are progressively sub-divided into finer-scale groups based on their biological community ordinations and taxonomic differences. We used the rule that a group would not be split further if either sub-group had less than 6 sites (a subjective number (used in previous models) intended to prevent any site's predictions being concentrated on too few reference sites). This initially led to 57 end groups. MDA was then used to derive the discriminant functions which were used to estimate the probability of a site belonging to each end group, and assess whether the most probable group(s) included the actual biological end group. The probabilities of end group membership were then used to calculate the expected values of the two primary biotic indices, number of BMWP taxa (TAXA) and ASPT. The statistical distribution of the ratio (O/E) of the observed to expected values of these indices for the reference sites was then determined and assessed, both overall and by end group. The overall fit of the model can be measured by the standard deviation (SD(O/E)) of the O/E values, but ideally the model predictions should be equally good and unbiased for all types of site, as measured by the average and variability in O/E values for each end group. (However, remember that the end groups are only a semi-arbitrary dissection of a biological continuum of variability that is a convenient intermediary step in the prediction of the site-specific expected fauna (Clarke, Furse and Wright 2003)).

Using all these assessment procedures at each iteration, appropriate pairs of hierarchically similar end groups were re-combined into larger groups, and the whole process repeated until a parsimonious balance was reached between increasing end group size (and group mean precision) and reduced distinguishing of biological site types.

Final classification into 43 end groups

The final selected classification of the 685 reference sites was into 43 end groups as shown in Figure 7. The number of reference sites in each end group varies from 6 (End group 7) to 32 (End group 41), with a median size of 15 sites.

All 9 Shetland reference sites form a distinct biological group as End group 1. All 9 Orkney sites (i.e. excluding the two site on Hoy) were also classified together as End group 2 which also contained two north Scottish mainland sites.

It is useful for mapping and descriptive summary purposes to combine the 43 groups into higher level groupings based on the hierarchical TWINSPAN classification in Figure 7. This has been done to form 7 super-groups (Table 6).

Table 6 Seven super-group level of classification of the 43 end groups of the 685 reference sites

Super-group	N sites	Mean TAXA	Mean ASPT	Dominant characteristics
1-7	64	23.0	6.27	All in Scotland mostly islands
8-16	148	25.2	6.79	Upland streams, mainly in Scotland and N England
17-26	169	31.7	6.42	Intermediate rivers, SE Scotland, Wales, N & SW England
27-30	48	27.1	6.25	Small steeper streams, with 13km of source, discharge1/2
31-36	115	34.8	5.84	Intermediate size lowland streams, including chalk, SE
37-40	84	32.7	5.58	Small lowland streams, including chalk, SE Britain
41-43	57	32.7	5.14	Lowland streams, SE England, larger, fine sediments

MDA effectiveness

In the MDA on the final 43 end-groups, 51.8% of reference sites were allocated to their “correct” TWINSPAN end-group (as the most probable group) using the MDA re-substitution method and 38.8% by the cross-validation method. This is similar to the equivalent values for the old GB model of 614 sites in 35 groups, which were 51.6% and 40.9% respectively, especially considering the higher number of end groups and slightly reduced average end group size.

End group differences in biotic index values

A principal aim of using a RIVPACS-type predictive model to set site-specific target expected biota and index values is to account for, and adjust for, natural variation in biotic indices between river sites of different physical types. Differences between the 43 end-groups account for 64% of the total variation in observed TAXA and 78% of the total variation in observed ASPT values amongst the 685 reference sites (based on analyses of variance). The equivalent percentages for the 614 RIVPACS III+ GB reference sites in 35 end-groups were 58% and 80% respectively. Figure 9 shows the variation of observed TAXA and ASPT for individual sites in relation to their end-group, indicating the pattern of differences between end-groups.

Comparison of observed, expected and O/E values

Not all of the biotic differences between end-groups, including in index values, will be predictable from the MDA discriminant functions estimated site-specific expected values. However, the percentage of total variation in observed index values for the 685 reference sites which is accounted for by the new GB-inclusive 43 end-group prediction model is reasonably high, namely 56% for TAXA and 72% for ASPT, which are both high proportions (0.87 and 0.90) of the above total between end-group index variability. This indicates that the environmental variables, MDA and prediction method are highly effective at explaining the major biological differences between the end-groups.

The overall fit of the prediction model is often measured by the standard deviation (SD(O/E)) of the O/E values for the 685 reference sites; these were:

SD (O/E_{TAXA}) = 0.140 SD(O/E_{ASPT}) = 0.053

These are slightly higher than the equivalent SD of 0.138 for O/E_{TAXA} and slightly lower than the SD of 0.057 for O/E_{ASPT} for the previous 614 GB model.

The null model SD (Van Sickle *et al.* 2005) are much higher at 0.209 and 0.097 for O/E_{TAXA} and O/E_{ASPT} respectively, re-enforcing our conclusion that the RIVPACS prediction model is effective in eliminating the effects of major physical differences between GB river sites on the biota.

Thus the overall fit and precision of the new GB-inclusive model is at good as the previous GB model. However, it is important that the prediction does not tend to grossly over- or under-predict particular types of site. . Ideally the O/E values should be centred around unity for all site types and end-groups. Figure 10 shows the distribution of O/E values for the reference sites in each of the 43 end-groups.

Many of the chalk streams occur in end-groups 34 and 37. As with RIVPACS III+, there is still some tendency to under-predict the expected number of taxa and thus over-estimate O/E_{TAXA} for such sites (Figure 10).

Inspection shows that the largest systematic discrepancies in O/E_{TAXA} (defined as end-group mean O/E_{TAXA} outside the range 0.92-1.08) are a tendency for O/E_{TAXA} to be less than unity for reference sites in end-groups 14 and 16 and above unity for reference sites in end-groups 6, 31, 37 and 40. The largest systematic discrepancies from unity for $O/_{EASPT}$ (defined as end-group mean O/E_{ASPT} outside the range 0.96-1.04) occur in end-groups 38 and 41 both of which tend to have values less than unity. The extent of apparent systematic deviations of O/E values from unit within each end-group is certainly not greater occurred in the RIVPACS III+ GB module.

Comparison of expected values between RIVPACS III+ and new GB-inclusive model

In a comparison of the expected values of TAXA across all reference sites in the new GB-inclusive model and the RIVPACS III+ models (GB+SH+SI), 57% of sites had higher values for the new model, slightly more than half. This might be anticipated because the 40 RIVPACS III+ Reference sites excluded prior to developing the new model tended to have relatively low O/E_{TAXA} and thus relatively low taxa richness for their type which would lead to an overall tendency to slightly increased average observed taxa richness and consequently expected taxa richness for relevant site types.

For expected ASPT, 49% of sites had higher values for the new model compared to the RIVPACS II+ values, and 51% had lower values, almost exactly 50:50.

Consequently, 57% of values of O/E_{TAXA} and 49% of values of O/E_{ASPT} were lower in the New GB model.

Although the majority of changes in expected TAXA were small (94.7% of changes were within +/- 4 taxa), the expected value of one site (code 3505) increased by 5.8 (24.3 → 30.1). Moreover the expected TAXA at two sites (codes 1081 and 7149) decreased by just over 10 taxa (from 32-33 to approximately 22 taxa), although in both cases the resulting O/E_{TAXA} was closer to unity than in RIVPACS III+.

The vast majority of changes in expected ASPT were small (95.0% were within +/- 0.3), but one site (code 6242) had expected ASPT 0.97 higher (5.05 → 6.02), while two sites had expected ASPT values reduced by just over one (site 3157:- 6.67 → 5.60; site 3163:- 6.63 → 5.46), in both latter cases the new O/E_{TAXA} values were closer to unity in the new model.

Overall summary

Figure 11 shows the overall frequency distribution of the O/E_{TAXA} and O/E_{ASPT} for the 685 reference sites. The lower percentile values of these distributions are as follows:

685 reference sites	Lower percentile	
	5%	10%
O/E for TAXA	0.785	0.820
O/E for ASPT	0.910	0.930

Overall, the new GB-inclusive model appears to provide an adequate single integrated consistent prediction model and assessment system to use for the whole of GB including all the Scottish islands. It eliminates problems of which module (GB or SH) to use for Scottish sites which might be considered to be “highlands” sites. It also enables predictions for non-remote Scottish islands sites to involve information from similar mainland sites.

Appendix XI gives the end-group for each of the 685 reference sites in the new GB-inclusive model, sorted by end-group (1-43).

A separate deliverable EXCEL file:

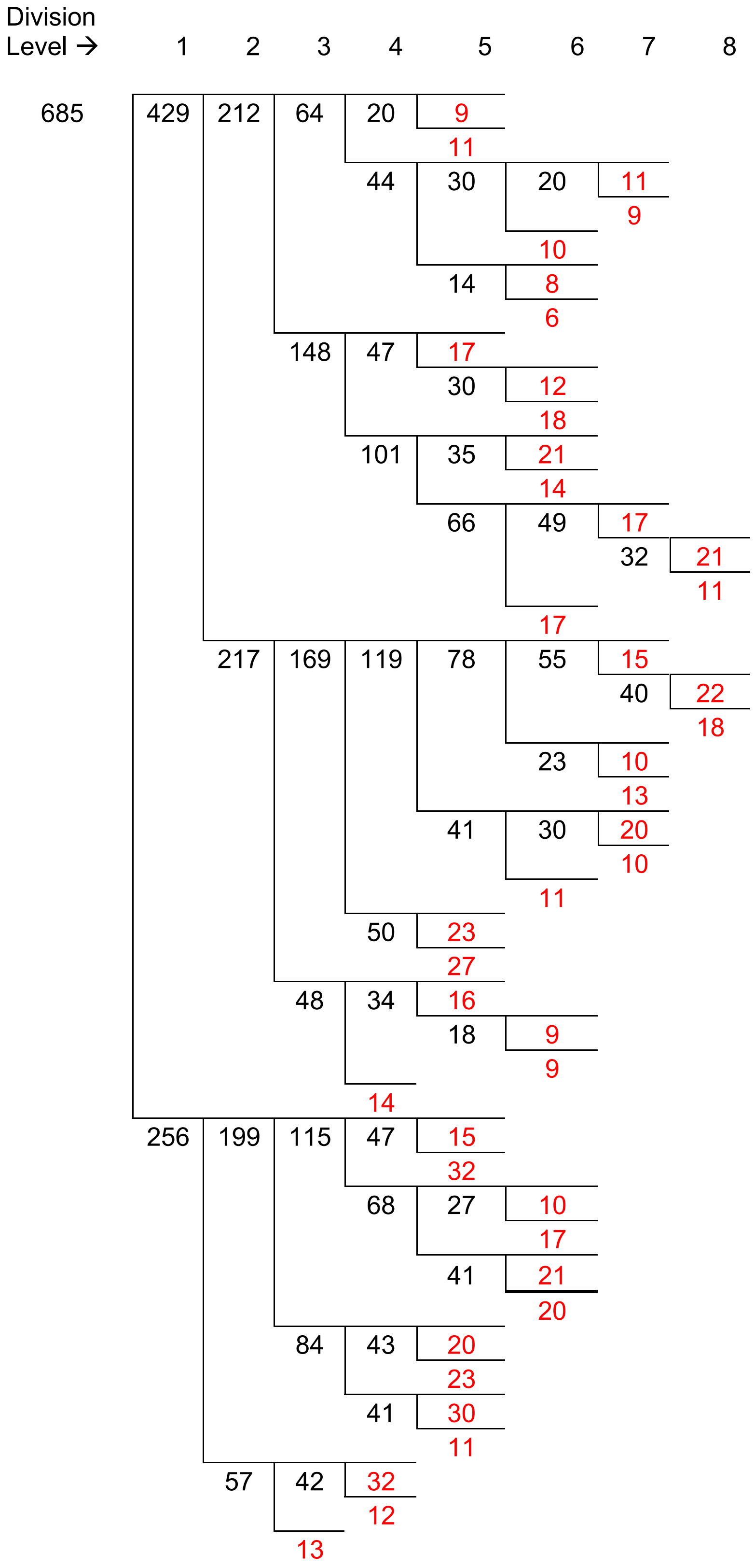
’02 WE4_1 End group(1-43) of 685 sites in New GB-inclusive model 101207.xls’

gives the same information plus extra details of observed, expected and O/E values for TAXA and ASPT.

References

Clarke R.T., Wright J.F. & Furse M.T. (2003) RIVPACS models for predicting the expected macroinvertebrate fauna and assessing the ecological quality of rivers. *Ecological Modelling* 160, 219-233.

Figure 7. Dendrogram showing the hierarchical classification of the 685 New GB model Reference sites into 43 End-groups (1-43). End-group code indicates the TWINSPAN binary code for the hierarchical splitting for groups.



End Group Id	End group Code	N sites
1	00000	9
2	00001	11
3	0001000	11
4	0001001	9
5	000101	10
6	000110	8
7	000111	6
8	00100	17
9	001010	12
10	001011	18
11	001100	21
12	001101	14
13	0011100	17
14	00111010	21
15	00111011	11
16	001111	17
17	0100000	15
18	01000010	22
19	01000011	18
20	0100010	10
21	0100011	13
22	0100100	20
23	0100101	10
24	010011	11
25	01010	23
26	01011	27
27	01100	16
28	011010	9
29	011011	9
30	0111	14
31	10000	15
32	10001	32
33	100100	10
34	100101	17
35	100110	21
36	100111	20
37	10100	20
38	10101	23
39	10110	30
40	10111	11
41	1100	32
42	1101	12
43	1111	13

Figure 8. Geographic location of the reference sites in each of the seven major groupings of the 43 end groups for the 685 reference sites in the new all GB-inclusive RIVPACS model.

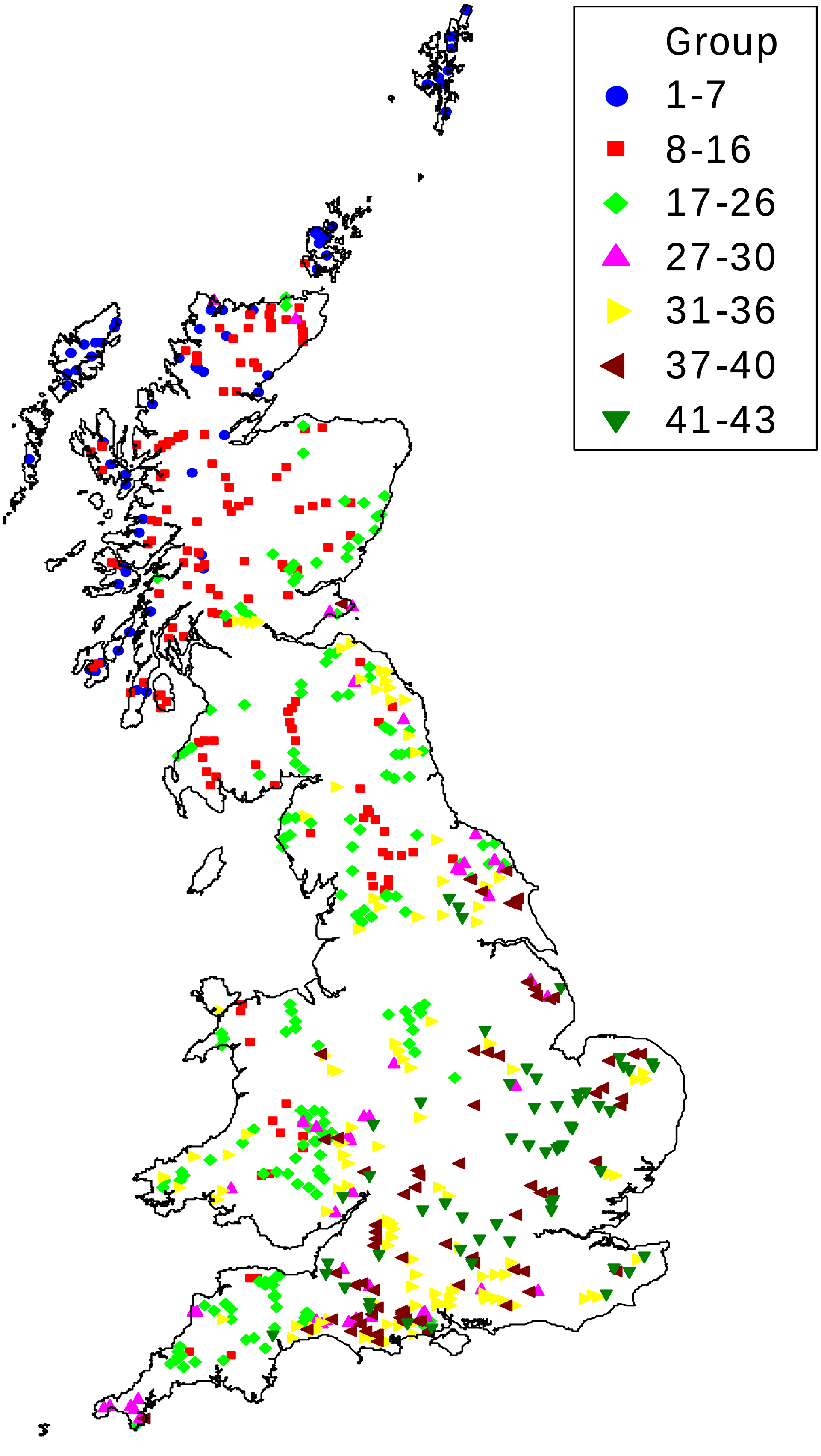


Figure 9. Plot of the (a) observed number of BMWP taxa (TAXA) and (b) observed ASPT per reference site, grouped by their new GB-inclusive end group (1-43). Vertical dashed lines separate the seven super-groups described in Table 6.

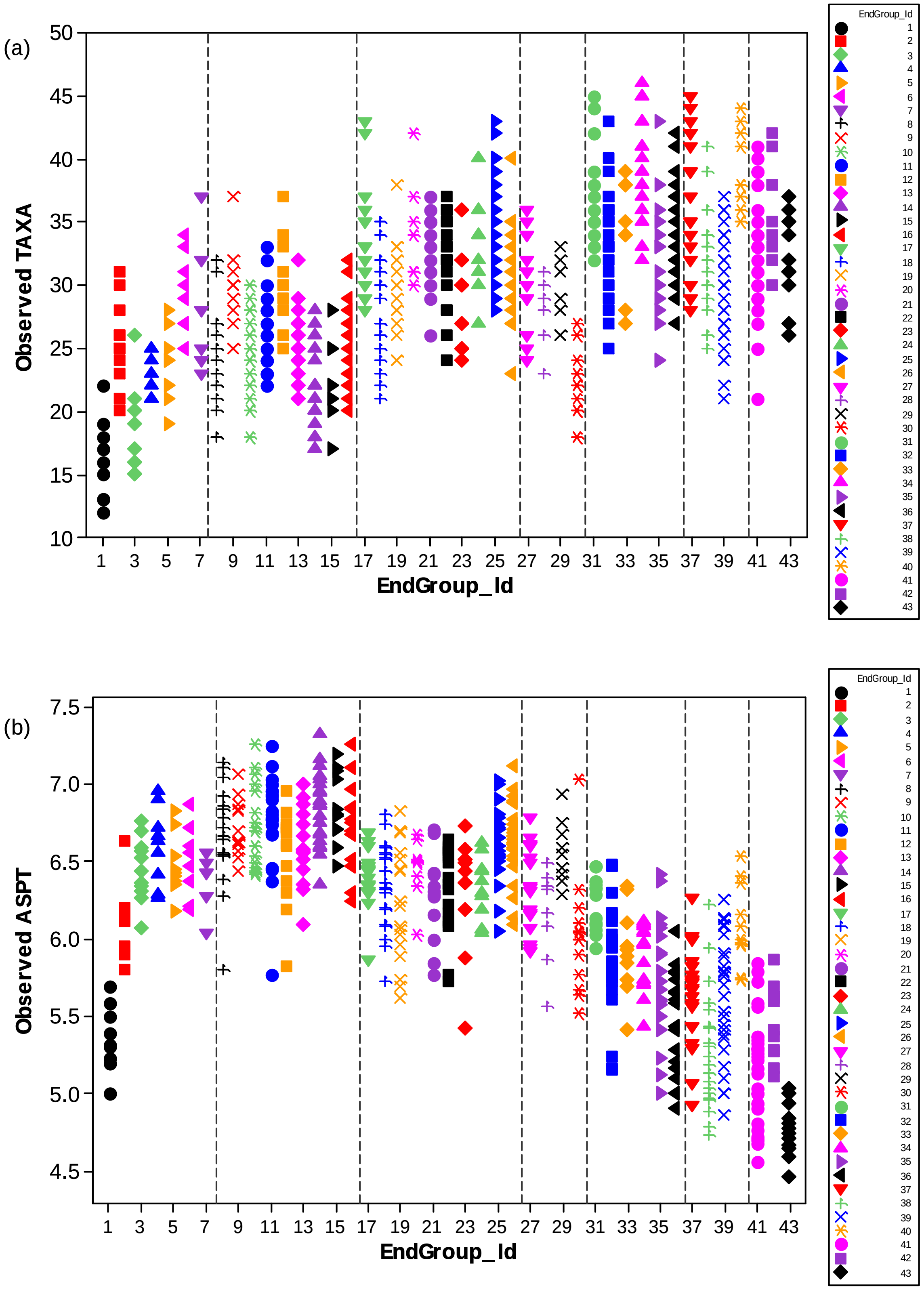


Figure 10. Plot of (a) O/E number of BMWP taxa (TAXA) and (b) O/E ASPT for reference sites grouped by their new GB-inclusive end group (1-43). Dashed lines indicate O/E values of unity.

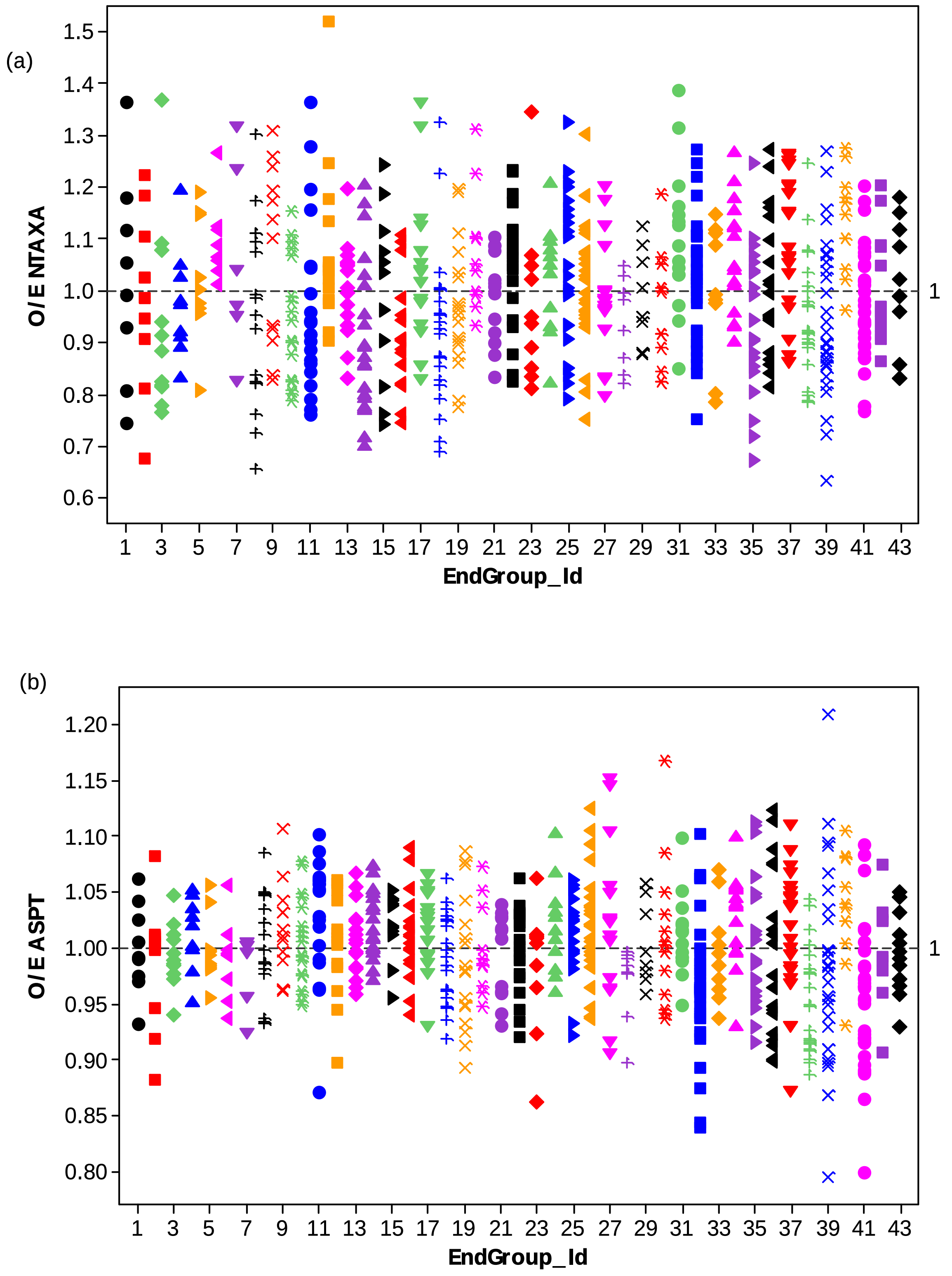
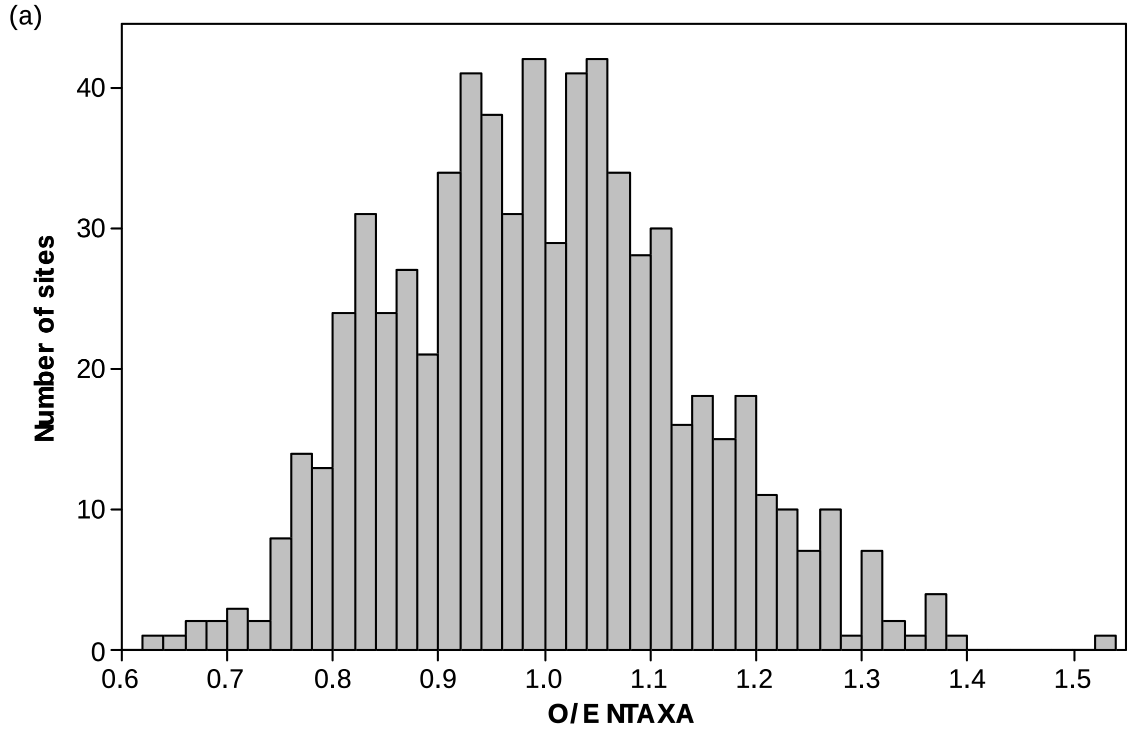
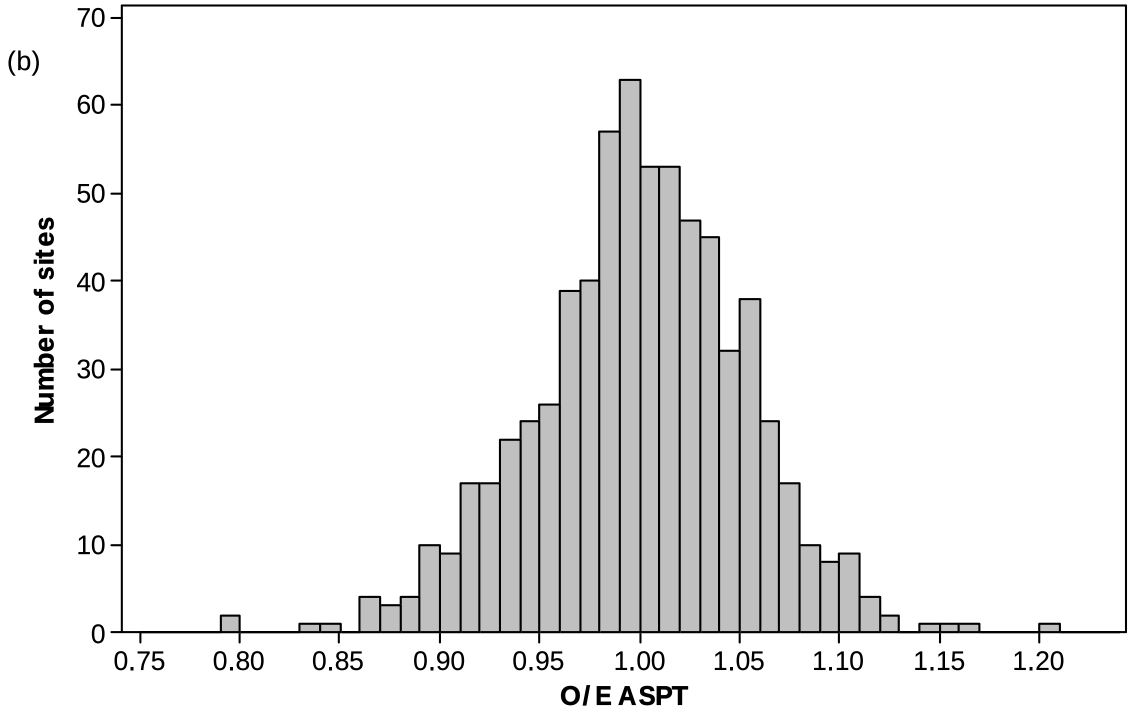


Figure 11. Frequency histogram showing the statistical distribution of the values of (a) O/E_{TAXA} and (b) O/E_{ASPT} for the 685 reference sites in the new GB-inclusive RIVPACS model with 43 end-groups.





WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 4.3 Deliverable
Confirmed variables for taxonomic prediction

1. Background

It has always been considered a great strength of RIVPACS that it can predict the taxa that should occur at a test site together with probabilities of occurrence. The new models produced in this project retain that functionality and no generic change in the mechanism by which this achieved is envisaged. All the current RIVPACS combined season/individual season options will also be retained. However, the variables (datasets) upon which the probabilities of capture are based do need to be updated in light of the revised end groups and geographic modules (WE 4.1). Similarly, revised of the taxonomic framework in RIVPACS IV (WE 3.1) now supports three different taxon coding systems, and the predicted taxon lists that are produced by the new models also need to produce outputs in all of these taxon coding systems.

The levels of taxonomic prediction to be included in the software system are as follows:

- TL1 - Current BMWP “families” for each of the RIVPACS season combinations
- TL2 - Revised BMWP “families” for each of the RIVPACS season combinations*
- TL3 - All families for each of the RIVPACS season combinations
- TL4 - All ‘RIVPACS’ species for each of the RIVPACS season combinations

*a new taxonomic level not previously available in RIVPAVCS models

For each taxonomic level, we have derived the following supporting data tables using the RIVPACS reference site dataset (also see WE 1.5 generic algorithms):

File TAXAPR - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (*t* = 1,...,tN)	season *s* (*s* = 1,...,7)	end group *g* (*g* = 1,...,gN)	$TAXAPR_{t,s,g}$
1	1	1	1	0.843
1	1	1	2	0.750
...				
2	tN	7	11	0.333

TAXAPR supports predictions of the probabilities of occurrence of taxa. Within a given model, for a given taxon, in a given single or season combination, within a given end group, this file gives the probability of capture of taxa. This file is relevant for all 4 taxonomic levels (see above).

File TAXAAB - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (*t* = 1,...,tN)	season *s* (*s* = 1,...,7)	end group *g* (*g* = 1,...,gN)	$TAXAAB_{t,s,g}$
1	1	1	1	1.582
1	1	1	2	0.923
...				
2	tN	7	11	1.800

File TAXAAB supports predictions of the average $\log_{10}$ abundance of taxa. Within a given model, for a given taxon, in a given single or season combination, within a given end group, this file gives the average $\log_{10}$ abundance category of taxa. This file is relevant for the 3 family taxomonic levels (TL1, TL2 and TL3), but not TL4 – RIVPACS species level.

File TAXAPRAB - with illustrative example cell values:

Model (1=GB, 2=NI)	Taxa *t* (*t* = 1,...,tN)	season *s* (*s* = 1,...,7)	end group *g* (*g* = 1,...,gN)	abundance category *a*	$TAXAPRAB_{t,s,g,a}$
1	1	1	1	1	0.85
1	1	1	1	2	0.00
...					
2	tN	7	11	4	0.35

File TAXAPRAB supports predictions of probability of a given taxon being found at a given $\log_{10}$ abundance category. Within a given model, for a given taxon, in a given single or season combination, within a given end group, for a given $\log_{10}$ abundance category, this file gives the probability of a taxon being found at that $\log_{10}$ abundance category. This file is relevant for the 3 family taxonomic levels (TL1, TL2 and TL3), but not TL4 – RIVPACS species level.

Taxa in all three of the above files have been supplied with Revised Maitland codes and names, Furse codes and names, and NBN codes and names.

WFD72C River Invertebrate Classification Tool (Stage 2)
WE 4.4 – Report on the Calculation of Biotic Indices for the RIVPACS Reference Sites & the Calculation of End Group Means
19th Dec 2007

Background

At present RIVPACS III+ predicts the expected index values of BMWP, NTAXA and ASPT, however, the WFD72C project specification requires than the RIVPACS IV models within the new Tool must be capable of predicting reference values for a wider range of biotic indices:

BMWP
NTAXA
ASPT
AWIC (family level)
LIFE (family level)
Non-Abundance Weighted WHPT Score
Non-Abundance Weighted WHPT NTAXA
Non-Abundance Weighted WHPT ASPT
Abundance Weighted WHPT Score
Abundance Weighted WHPT NTAXA
Abundance Weighted WHPT ASPT

The reference values of the above indices are calculated within this Work Element and provided in an accompanying Access database. All of the above indices have been recalculated within this project and checked against any that were previously calculated in SNIFFER project WFD46.

A sample of all the indices has also been manually checked within this Work Element (both as separate season and combined season scores – see below).

Appendix II of this report details the versions of the indices used (which are the same as those used in WE2.2 – Compilation Data for Errors & Compare).

Spring and autumn combined Inter-calibration Common Metric component metrics (ICMs) for the 614 RIVPACS III+ GB and 110 Northern Ireland sites have been supplied by John Murray-Bligh (Environment Agency). These metrics were calculated in a manner consistent with the European WFD intercalibration process using the ASTERICS software and have also been included in the database accompanying this report (although end group means are not required and have not been calculated). John Murray-Bligh has also supplied supporting step-by-step instructions detailing how these indices were calculated (delivered alongside this report – Instruction_text_ASTERICS.doc).

Where possible scientific publications or reports are cited as sources for the indices, and in all cases, the exact details of each of the above indices are reproduced in full in this report. This will enable the UK Agencies to be fully informed about the methods used to calculate the reference values of the indices used in the new Tool so that expected values for test sites can be calculated in the same way, thereby ensuring that their observed/expected ratios used in bio-assessment are fully compatible and therefore correct.

Site and Season Specific Biotic Indices

As in RIVPACS III+, for each of the indices above reference site-specific separate and combined season reference values have been calculated as below:

Season combination	RIVPACS season code
Spring	1
Summer	2
Autumn	3

Spring & Summer	4
Spring & Autumn	5
Summer & Autumn	6
Spring, Summer & Autumn	7

End Group Means

Although the new RIVPACS Reference Site Database that will arise from project WFD72C will store the site and season specific reference biotic index scores described above, the new Tool will actually only store mean values of the biotic indices for each of the biological (TWINSPAN) end groups in the new RIVPACS IV models (see Work Element 4.1 – Allocation of Reference Sites to End Groups). These mean values are also calculated within this Work Element.

For Great Britain, the reference sites in the RIVPACS III+ GB, Scottish Highlands and Scottish Islands models have been combined to produce a new GB-wide model with 43 TWINSPAN biological end groups (based on 685 GB sites). All of the sites in each end group have been used in the calculation of end group mean biotic index values. Although a larger pool of 725 RIVPACS reference sites were available, 40 of these were deemed to be too stressed (see Work Element 2.1 - Refinement of Reference Sites) and played no part in either the TWINSPAN classification or in the calculation of mean biotic index values for the GB TWINSPAN groups.

For Northern Ireland, the original RIVPACS III+ TWINSPAN classification based on 110 sites with 11 end groups has been retained although 2 sites that were considered to have been too stressed at the time they were sampled (see Work Element 2.1 - Refinement of Reference Sites). These sites still contribute to the TWINSPAN classification but have been excluded from the calculation of end group mean biotic index values:

Crew Burn at Carrols Bridge (site NI_24)
Blackwater at Moy (site 20303403)

Taxonomic Resolution of the RIVPACS Dataset

The RIVPACS reference site data set is identified to both family and species level with $\log_{10}$ abundances at family level and simple presence information for species. At family level, BMWP composite families are not distinguished, although the distinct families can be derived from the species records. At the time of writing, abundances of the distinct families within the BMWP composite families cannot be determined although this is being addressed later in the project (WE3.2 – Generation of Family Level Abundance Data).

For each of the indices described above, taxonomic conversions (usually downgrades) were required to enable the indices to be calculated. These are described below.

BMWP, NTAXA, ASPT and AWIC (family level)

To calculate the BMWP indices and AWIC (fam) several RIVPACS families were amalgamated to create taxa required by the indices:

> Lumbriculidae, Haplotaxidae, Enchytraeidae, Naididae, Tubificidae & Lumbricidae records were amalgamated to match the BMWP and AWIC family 'Oligochaeta'
>
> Tanypodinae, Diamesinae, Prodiamesinae, Orthocladiinae, Chironomini & Tanytarsini records were amalgamated to match the BMWP and AWIC family 'Chironomidae'

Non-Abundance Weighted WHPT, NTAXA and ASPT (using BMWP composites)

To calculate the Non-Abundance Weighted WHPT Score, NTAXA and ASPT several RIVPACS families were amalgamated to create taxa required by the indices:

> Lumbriculidae, Haplotaxidae, Enchytraeidae, Naididae, Tubificidae & Lumbricidae records were amalgamated to match the BMWP and AWIC family 'Oligochaeta'
>
> Tanypodinae, Diamesinae, Prodiamesinae, Orthocladiinae, Chironomini & Tanytarsini records were amalgamated to match the BMWP and AWIC family 'Chironomidae'
>
> All Rhagionidae were converted to Athericidae.

At the time of calculation of Non-Abundance Weighted WHPT scores, distinct abundances for the individual families in the 8 artificial BMWP taxa recorded in RIVPACS were not available. WHPT scores were therefore calculated using the WHPT scores allocated to the BMWP composite families rather than the WHPT scores for the separate families.

Abundance Weighted WHPT, NTAXA and ASPT (using BMWP composites)

To calculate the Abundance Weighted WHPT Score, NTAXA and ASPT several RIVPACS families were amalgamated to create taxa required by the indices:

> Lumbriculidae, Haplotaxidae, Enchytraeidae, Naididae, Tubificidae & Lumbricidae records were amalgamated to match the BMWP and AWIC family 'Oligochaeta'
>
> Tanypodinae, Diamesinae, Prodiamesinae, Orthocladiinae, Chironomini & Tanytarsini records were amalgamated to match the BMWP and AWIC family 'Chironomidae'
>
> All Rhagionidae were converted to Athericidae.

At the time of calculation of Abundance Weighted WHPT scores, distinct abundances for the individual families in the 8 artificial BMWP taxa recorded in RIVPACS were not available. WHPT scores were therefore calculated using the WHPT scores allocated to the BMWP composite families rather than the WHPT scores for the separate families.

Abundances for combined season samples (where samples from any 2 seasons were combined) were calculated by taking the maximum $\log_{10}$ abundance of a give family in any of the seasons involved. For 3-season combined samples, the maximum $\log_{10}$ abundance category was taken (unless all 3 abundances were the same in which case the abundance was increased by 1, i.e. the Max+1 rule was used).

LIFE - family level (using BMWP composites)

At the time of calculation of LIFE (family level), distinct abundances for the individual families in the 8 artificial BMWP taxa recorded in RIVPACS were not available. LIFE (family level) was therefore calculated using the scores allocated to the first family in the composites rather than the LIFE scores for the separate families.

Abundances for combined season samples (where samples from any 2 seasons were combined) were calculated by taking the maximum $\log_{10}$ abundance of a give family in any of the seasons involved. For 3-season combined samples, the maximum $\log_{10}$ abundance category was taken (unless all 3 abundances were the same in which case the abundance was increased by 1, i.e. the Max+1 rule was used).

In the case of the WHPT and LIFE indices, while the indices provided here are based on BMWP composite taxa, once Work Element 3.2 (Generation of Family Level Abundance Data) is completed, these indices will also be supplied using distinct (i.e. separated BMWP) families and abundances.

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Element 4.5 Deliverable
Adjustment of RIVPACS Predicted Indices to a standard WFD reference state
Interim Report: 24th January 2008

1. Background

Part of the following background information is adapted from the section on WE4.5 in CEH's final WFD72C Detailed Project Plan document (dated 28/06/07):

The perceived ecological status of the RIVPACS reference sites varies, and most importantly varies between stream types and end groups. Derived predictions of expected index values for a site will therefore depend on the status of the environmentally-similar reference sites actively involved in predictions for the site. The modifications required to allow for alterations in the predicted index values to reflect a standard WFD reference state need to be integrated within the software tool to be built by the IS programmers (Stage 3).

In a previous part (WFD72b) of overall SNIFFER project WFD72, we at CEH developed a general statistical model (M4), procedure and algorithm to make these adjustments and applied the procedures to estimate adjustment factors for the existing BMWP indices.

An initial aim in WE4.5 was investigate the validity of applying the adjustment mechanisms developed in project WFD72b to actual values of the BMWP indices for the individual RIVPACS reference sites and thus the potential to adjust the observed values of the BMWP indices of the RIVPACS reference sites prior to summarising the mean index values by end group. This would avoid the need for an additional programming step in the new RICT software tool to encode the adjustment procedures developed by CEH within WFD72b directly within the software. Thus, the software system would be able to predict unadjusted or adjusted expected values of the metrics by reference to previously determined unadjusted or adjusted summary values by end group.

However, subsequent consideration by Ralph Clarke led to the realisation that it was not statistically logical to apply the adjustment algorithm developed in WFD72C to the observed values for the reference sites and then average the adjusted values by RIVPACS end-group to obtain adjusted end-group mean values of each index which would then be used to derive pre-adjusted predicted index values.

Therefore, it was concluded and agreed with the WFD72C project board that, in WE4.5, the adjustment factors (a_1, a_2, a_3, a_4, a_5) in model (M4) (see section 2 below) need to be estimated for each of the standard set of biotic indices to be involved in the initial RICT software.

Agreed Deliverable:
Confirmation of algorithms required to adjust for RIVPACS reference condition, together with estimates of the adjustment factors for each biotic index

In WE2.1 of project WFD72C, 40 GB sites and two Northern Ireland references sites from RIVPACS III+ were re-judged to be inappropriate as reference sites and excluded from future model developments and predictions, leaving 108 sites in Northern Ireland and 685 sites in GB (including the Scottish Highlands and islands), giving of UK total of 793 reference sites.
In WE4.1 of project WFD72C, a new all-GB RIVPACS IV predictive model was developed which involved a TWINSPAN classification of the 685 all-GB reference sites into 43 end-groups. These end-groups are used here as the end-group representation of site type in fitting the adjustment model (M4).

The 108 remaining Northern Ireland reference sites were assigned to the same end-groups as originally developed for RIVPACS III+ (Release 2.1) and used in RIVPACS III+ Release 3.3 (RPBATCH).

2. Statistical model, data and estimates of adjustment factors

It was concluded in project WFD72B that the best statistical model to fit to estimate the adjustment factors associated with each level (1-5) of the biologist assessment scores for the reference sites was model (M4):

$$\log_{10} O_{ijk} = \log_{10} M_i + a_j + e_{ijk}$$
(M4)

where

O_{ijk} = Observed index value for the k^{th} site with assessment score j in site group i
M_i = term for average index value for TWINSPAN site group i
a_j = effect of assessment score j on $\log_{10}$ index values (re-scaled to give $a_3 = 0$).
e_{ijk} = residual value for the k^{th} site with assessment score j in group i

Model (M4) is a multiplicative model, in that by analysing the observed index values on their logarithmic scale, the effect of a particular assessment score *j* on the observed index value for a site is assumed to be a constant multiple (i.e. proportion) of the value expected for that type of site (i.e. end group) if it was of high/good boundary quality (i.e. assessment score of 3). Model (M4) is also non-linear in that it does not assume that the (proportional) difference in index values between sites of similar types with scores of, say 1 and 3, is the same as the difference between sites with score of say 3 and 5. The non-linearity of effects of score was shown to be statistically significant in WFD72B for both BMWP TAXA and ASPT. This general non-linear model was therefore used here to estimate adjustment factors for all of the indices involved in the new RICT software.

In project WFD72B, model (M4) was initially fitted separately for the reference sites in each of the four RIVPACS III+ (RPBATCH) modules (GB, Northern Ireland (NI), Scottish Highlands (SH) and Scottish Islands (SI). However, in WFD72B analyses, there were no statistically significant interactions between the effect of score and module for either TAXA or ASPT. Therefore, it was concluded that a single set of adjustment factors is applicable for all UK sites based on fitting model (M4) to all UK reference sites (see WFD72B Final Report for further details).

Furthermore, detailed analyses in project WFD72B involving fitting model (M4) separately to the reference sites sample data for each season or season combination, found similar patterns in the estimates of model parameters ($a_i - a_5$) across seasons and it was concluded that it was best to estimate a single set of adjustment parameters to be applied to test site samples from any RIVPACS season option. This is to be based on analysing all possible season options samples together.

However, the AWIC and LIFE indices were designed and evaluated using single season samples; their values for combined season samples have not yet been assessed. Therefore the estimates of adjustment parameters in model (M4) were fitted using all the single season samples values of AWIC and LIFE only. These are however expected to be similar adjustment factors are obtained using all season combinations samples.

In project WFD72B, it was concluded that there were insufficient sites with an assessment score of 6 (10 in total) for the estimates of parameter a_6 to be statistically significant or reliable. It was recommended that, in deriving adjustments to expected index values for test sites, those few reference sites given assessment scores of 6 by Agency biologist's should be treated as having assessment scores of 5. Note however, that the scores of 6 are retained in the actual fitting of model (M4*); the estimate of parameter a_6 is just not used in the subsequent algorithms to derived adjustments to expected index values for test sites.

In WE4.5, we have therefore fitted model (M4) to all 793 UK reference sites involved in the new RIVPACS IV models incorporated into the RICT software. The final choice of estimates was based on fitting a form of model (M4) to all the 793 UK-wide reference sites using every possible combination of single and multiple season samples (i.e. a total of 793 sites by 7 season options = 5551 samples). This is done by fitting the modified model (M4*):

$log_{10}\ O_{isjk} = log_{10}\ M_{is} + a_j + e_{isjk}$
(M4*)

where

O_{isjk} = Observed index value for the k^{th} site with assessment score j in site group i in season s
M_{is} = term for average index value for TWINSPAN site group i in season s
a_j = effect of assessment score j on $\log_{10}$ index values (re-scaled to give $a_3 = 0$).
e_{isjk} = residual value for the k^{th} site with assessment score j in group i in season s

The estimates the adjustment parameters ($a_1 - a_5$) obtained by fitting model (M4*) to the observed sample values of each biotic index are given in Table 7.

The fitted regression model (M4*) can be re-expressed as:

$$O_{isj} = M_{is} A_j \qquad \text{where} \quad A_j = 10^{a_j} \qquad \text{(M4**)}$$

In this model, the effect of a unit change in assessment score is not assumed to be constant across the range of assessment scores; however, a given assessment score is assumed to a constant multiplicative effect on the observed index values for the reference sites. Specifically an assessment score of j is assumed on average to increase the observed index values of reference sites by a factor of A_j (i.e. increase index values by $100(A_j - 1)$ percent). Therefore the expected index values of any sites based on reference sites with a score of j are on average over-estimated by a factor A_j. In such cases, the correction should therefore be to divide the RIVPACS expected values by the same factor A_j. As the RIVPACS predictions for real test sites are always based on site groups and sites with reference sites with more than one assessment score, the multiplicative adjustment factor for the expected values are based on the reciprocal of a weighted average of the factors A_j, as follows:

Adjusted expected value E for a test site = E / $(\sum_{j=1}^{6} R_j A_j)$
(M4a)

where $R_j = \sum_{i=1}^{g} P_i Q_{ij}$ = weighted proportion of the reference sites involved in the prediction with an assessment score of j.

and

P_i = RIVPACS probability test site belongs to TWINSPAN site group i
Q_{ij} = Proportion of reference sites in group i with assessment score j
g = number of TWINSPAN site groups

The estimates of the multiplicative adjustment factors ($A_1 - A_5$) for RIVPACS expected values derived from UK-wide versions of model (M4*) (and thus M4**) are given for each index in Table 8.

Table 7. Estimates of adjustment parameters (a_1 – a_5) for the effects of assessment score (1-5) in model (M4) for each biotic index based on using every possible combination of single and multiple season samples for the 793 UK-wide reference sites (AWIC and LIFE based on all single season samples only); p = model test probability value for effect of score.

	Original BMWP		
	Score	NTAXA	ASPT
p	<0.001	<0.001	<0.001
a_1	-0.00275 ± 0.00415	-0.00291 ± 0.00356	0.00016 ± 0.00132
a_2	0.00595 ± 0.00303	0.00164 ± 0.00261	0.00431 ± 0.00097
a_3	0	0	0
a_4	-0.02761 ± 0.00414	-0.01831 ± 0.00356	-0.00930 ± 0.00132
a_5	-0.06182 ± 0.00659	-0.04024 ± 0.00566	-0.02159 ± 0.00210
	Revised BMWP Non-weighted		
	Score	NTAXA	ASPT
p	<0.001	<0.001	<0.001
a_1	-0.00077 ± 0.00399	-0.00192 ± 0.00361	0.00116 ± 0.00125
a_2	0.00765 ± 0.00292	0.00408 ± 0.00264	0.00356 ± 0.00091
a_3	0	0	0
a_4	-0.02404 ± 0.00398	-0.01474 ± 0.00361	-0.00931 ± 0.00125
a_5	-0.05364 ± 0.00634	-0.03340 ± 0.00574	-0.02025 ± 0.00198
	Revised BMWP Abundance-weighted		
	Score	NTAXA	ASPT
p	<0.001	<0.001	<0.001
a_1	-0.00104 ± 0.00410	-0.00192 ± 0.00361	0.00087 ± 0.00143
a_2	0.00753 ± 0.00300	0.00408 ± 0.00264	0.00345 ± 0.00104
a_3	0	0	0
a_4	-0.02474 ± 0.00409	-0.01474 ± 0.00361	-0.01001 ± 0.00142
a_5	-0.05809 ± 0.00651	-0.03340 ± 0.00574	-0.02471 ± 0.00226
	AWIC	LIFE	
p	<0.001	0.004	
a_1	-0.00017 ± 0.00192	-0.00218 ± 0.00148	
a_2	0.00107 ± 0.00144	0.00072 ± 0.00108	
a_3	0	0	
a_4	0.00517 ± 0.00197	-0.00157 ± 0.00148	
a_5	0.01648 ± 0.00891	-0.00607 ± 0.00235	

The estimates of the multiplicative adjustment factors (A_1 – A_5) used to adjust expected index values are similar for the original BMWP and revised WHPT forms of BMWP score, TAXA and ASPT (Table 8). We have given the adjustments for the three forms of BMWP/WHPT score in case these are needed to adjusted expected values of these indices directly.

The estimated effect of being of assessment score 5, compared to reference sites of a similar type (i.e. end-group) with assessment scores of 3, is on average to reduce the number of taxa (TAXA index) by 8.8% using the original BMWP taxa and by 7.4% when based on the revised WHPT taxa (Table 8).

Few of the reference sites were identified as specifically having any signs of either flow or acidity related stress. Therefore, reference sites with high assessment scores (i.e. poorer perceived quality) may not tend to have systematically different values of either AWIC or LIFE than other sites. However, the "innocent" statistical fitting of model (M4*) for these index values did show statistically significant effects of assessment score. The estimates suggest that AWIC index values were, on average, 1.2% higher (i.e. A_4 = 1.012) and 3.9% higher for reference sites with assessment scores of 4 and 5 respectively compared to reference sites of the same type (i.e. RIVPACS end-group) with assessment scores of 3 (i.e. on the high/good boundary of quality) (Table 8). We believe this pattern may be at least partly statistical and correlative rather than causal and should be interpreted and used with caution.

These model (M4*) fit for the LIFE index suggests the weakest association with assessment score and reference sites with assessment scores of 5 were, on average, only 1.4% lower than those with assessment scores of 3.

Table 8. Estimates of adjustment parameters (A_1 – A_5) for the effects of assessment score (1-5) in model (M4) for each biotic index based on using every possible combination of single and multiple season samples for the 793 UK-wide reference sites (AWIC and LIFE based on all single season samples only); p = model test probability value for effect of score. (Note: A_i = 10 to the power a_i , where a_i is as in Table 1)

	Index	Estimate of adjustment parameter				
		A_1	A_2	A_3	A_4	A_5
Original BMWP	Score	0.994	1.014	1.000	0.938	0.867
	NTAXA	0.993	1.004	1.000	0.959	0.912
	ASPT	1.000	1.010	1.000	0.979	0.952
Revised BMWP Non-weighted	Score	0.998	1.018	1.000	0.946	0.884
	NTAXA	0.996	1.009	1.000	0.967	0.926
	ASPT	1.003	1.008	1.000	0.979	0.954
Revised BMWP Abundance-weighted	Score	0.998	1.017	1.000	0.945	0.875
	NTAXA	0.996	1.009	1.000	0.967	0.926
	ASPT	1.002	1.008	1.000	0.977	0.945
	AWIC	1.000	1.002	1.000	1.012	1.039
	LIFE	0.995	1.002	1.000	0.996	0.986

3. Procedures and algorithms for adjusting RIVPACS Expected values of indices

The recommended procedure for adjusting the RIVPACS or RICT model predictions of expected values of each biotic index are exactly as previously specified in detail in Section 5 of the Final Report for SNIFFER project WFD72B (Clarke and Davy-Bowker, Sept 2006).

These equations and algorithms need to be coded into the RICT software.

Section 5.2 of that report gives a detailed worked example of the calculations.

Section 6 of that report explains how the algorithms were encoded into an EXCEL adjustment calculator. This may also aid the RICT software programmers in determining what is needed.

The values for the adjustment parameters (A_1 – A_5) for each index should be taken from Table 8 above.

Finally, Section 6.1 of that WFD72B Final Report explains why and how, John Murray-Bligh's original method of making adjustments to RIVPACS expected values, as used by him for WFD Inter-calibration purposes, could also be performed using the same algorithms as proposed in WFD72B and here.

This report is necessarily brief, but provides the programmers with the required parameter estimates for adjusting index expected values.

Table 9. Number of Reference sites with each Assessment Score (1-5) in each End-Group

Module		Assessment Score					
	End-group	1	2	3	4	5	Total sites
New All GB 685 Reference sites	1	0	8	1	0	0	9
	2	4	5	1	1	0	11
	3	6	4	1	0	0	11
	4	5	4	0	0	0	9
	5	8	2	0	0	0	10
	6	3	5	0	0	0	8
	7	2	4	0	0	0	6
	8	10	3	3	1	0	17
	9	7	4	0	1	0	12
	10	8	9	1	0	0	18
	11	3	12	6	0	0	21
	12	3	7	4	0	0	14
	13	8	7	2	0	0	17
	14	13	7	1	0	0	21
	15	6	4	1	0	0	11
	16	7	5	5	0	0	17
	17	0	7	8	0	0	15
	18	2	5	11	4	0	22
	19	0	6	11	1	0	18
	20	1	6	3	0	0	10
	21	1	4	4	4	0	13
	22	1	9	9	1	0	20
	23	2	1	4	3	0	10
	24	0	7	4	0	0	11
	25	1	12	10	0	0	23
	26	8	10	8	1	0	27
	27	2	6	4	4	0	16
	28	0	4	2	3	0	9
	29	1	2	5	1	0	9
	30	5	7	0	1	1	14
	31	0	9	6	0	0	15
	32	0	8	22	2	0	32
	33	0	3	5	2	0	10
	34	0	9	7	1	0	17
	35	0	1	7	10	3	21
	36	0	2	13	4	1	20
	37	2	10	6	1	1	20
	38	0	3	15	3	2	23
	39	0	13	13	3	1	30
	40	0	4	6	0	1	11
	41	0	3	22	3	4	32
	42	1	0	4	6	1	12
	43	0	1	8	3	1	13
	Total						685

Northern Ireland
108 Reference sites

	Assessment Score					
End-group	1	2	3	4	5	Total sites
1	2	2	4	0	0	8
2	1	0	3	1	2	7
3	2	3	4	1	2	12
4	2	0	1	4	0	7
5	2	1	5	4	1	13
6	0	0	3	6	3	12
7	2	2	2	9	2	17
8	0	1	2	2	5	10
9	0	2	5	1	1	9
10	1	2	3	1	0	7
11	0	0	1	3	2	6
Total						108

WFD72C River Invertebrate Classification Tool (Stage 2)
Work Elements 5 and 6 Deliverable
Uncertainty algorithms and parameter estimates
Revised Report: 31st March 2008

1. Background

The following background information is extracted from CEH's final Detailed Project Plan document (dated 28/06/07):

WORK ELEMENT 5. Development of algorithms to estimate classification errors for biological indices (including those incorporating abundance data).

This will focus on developing the algorithms for a generic error estimation procedure and then establishing the estimate of error variance values for a few key indices, likely to be used for classification and/or regulatory purposes by the agencies. This will include the original BMWP indices, revised BMWP indices, abundance weighted revised BMWP indices, AWIC (family level) and LIFE (family level).

The environment agencies intend to move from the use of single year's data towards the use of multiple years' invertebrate data for status assessment and confidence of class will be based on this. Specifically, the agencies wish to base their site status classifications on up to three years' worth of sample data in order to reflect the longer term underlying condition of the biology. For each metric, the agencies will use the average of the EQR values for each of the individual years available over the three year period of interest. Thus, class is defined for a three year period but does not necessarily require three separate years' data. If only one year's spring and autumn combined sample data were used it would still give an estimate of the three year mean condition. Three years' data would, however, give a more precise estimate.

Incorporation of error terms which account for temporal variability is a vital part of WE5 and WE6.

The current functionality of bias correction will also need to be incorporated in the new system, but only the explicit algorithms and parameter estimates developed for RIVPACS III+ for the BMWP indices will be delivered in detail.

From our unique experience in CEH via the BAMS project (Furse *et al* 1995) and the EU STAR project Haase *et al*. 2006), we know that it is very difficult to assess and quantify the effect of sample processing errors on potential biases in metrics. Each metric should be assessed in its own right. This can only be done by reference to sample audit data (i.e. CEH's audit of agency samples) and subsequent re-construction of corresponding audit-corrected "true" samples from which comparison of the paired original and audit-corrected sample index values for a wide range of samples can used to assess the effect of sample processing errors on biases in observed index values. However, biases will vary with the extent of sample processing errors, which may vary over time, and therefore applicable bias-correction procedures for all situations are index specific and difficult to generalise.

Estimate of sampling variance and temporal (inter-annual) variance for the original BMWP indices, revised BMWP indices, abundance weighted revised BMWP indices, AWIC (family level) and LIFE (family level) will be derived from statistical analysis of the data compiled in WE2.2 (on which the estimates are therefore dependent).

We will develop procedures and algorithms to combine the components of variance (sampling and temporal) to determine the uncertainty/"error" associated with an assessment of status class for a three-year period based on 1, 2 or 3 years (combined season) sample data.

The work element will provide algorithms and estimates of “error” parameters, wherever possible, to help the programmers in the development of the error estimation/confidence of class module in the new software tool to do the following:-

1. Apply bias correction to the observed scores of the current BMWP indices, (and by equivalence to the revised presence/absence BMWP indices) for all valid season combinations based on the way bias error terms are currently handled in RIVPACS
2. Give bias uncorrected O/E ratios, their standard deviations and lower and upper 95% confidence limits for all valid season combinations for the original BMWP indices, revised BMWP indices, abundance weighted revised BMWP indices, AWIC (family level) and LIFE (family level) based on the way error terms are currently handled in RIVPACS or STARBUGS.
3. Give bias corrected O/E ratios, their standard deviations and lower and upper 95% confidence limits for all valid season combinations for the indices with estimable bias terms, with procedures based on the way error terms and biases are currently handled in RIVPACS or STARBUGS.
4. Give “confidence of class” based on the above *and using status class boundaries and rules for combining metrics and their classes using methods determined by the UK agencies outside of Phase 2 of this project.* In this instance “confidence of class” effectively means confidence that the “average” O/E value of these indices (over a three year period) falls in certain quality bands as the way actual WFD class will be defined will invoke multiple years’ data and the above can more accurately be considered as a means of defining whether any particular sample, or the average of a combination of samples, considered as a “spot estimate”, has achieved certain standards.

The functionality above basically matches that available in the current RIVPACS III+. The methods and procedures we will recommend is used to estimate the uncertainties of EQRs and status class assignments in the new software tool will be based on the Monte Carlo simulation methods developed for the RIVPACS III+ system. These simulation approaches were also adapted by us at CEH in our development of the STARBUGS (STAR Bioassessment Uncertainty Guidance Software, Clarke 2005, Clarke & Herring 2006) within the European Union project STAR (Furse *et al*. 2006).

The additional functionality which will be incorporated into the new system and which will, therefore, require additional error/uncertainty algorithm development is for the development of classifications based on multiple years’ data. The key difference to what is currently done for classification is that there will be incorporation of error terms to account for temporal variability between years. Each year (combined spring and autumn or combined spring, summer and autumn) effectively represents one data point within this three year classification period, there being a minimum of one and a maximum of three potential data points from which to calculate the mean O/E, the number of samples involved will affect its precision.

WORK ELEMENT 6. Development of procedures to be used in the “COMPARE” module of the software tool to enable comparison of samples to determine differences in quality based on a range of indices

This software module is required to allow comparisons of two or more samples (which may each be composite samples collected in more than one season) to determine whether differences in quality/class are statistically significant. It will focus on the key potential classification metrics detailed above in WE5.

The key requirements of the software will be:

- to be able to compare one “sample” against another (sample being one, two or three season combined) based on the way error terms are currently handled in RIVPACS. This would typically be used, for example, for upstream and downstream assessments of discharges where the requirement is to assess whether the “point estimate” of the condition of the biology upstream of a discharged is significantly different to that downstream.

- to be able to compare one year's worth of data against another year's data. This would typically be used to determine whether the condition of the biology at a given site has "genuinely" declined or improved at a given site from one year to the next or whether the change is within the level of variability typically expected due to sampling error and the typical temporal variability experienced by sites of the given mean quality.
- to be able to compare one three year period's classification against another three year period's classification and determine whether the change in class is significant.

In WE6, we will deliver general procedures to provide this functionality of assessing the significance of changes and differences in observed index values and EQRs based on using estimates of the typical sampling variation and other uncertainty associated with those indices. Estimates of uncertainty/error components for the key indices specified in WE5 above will be determined jointly with the work of WE5.

It was agreed that the results from the work of WE5 and WE6 will delivered together.

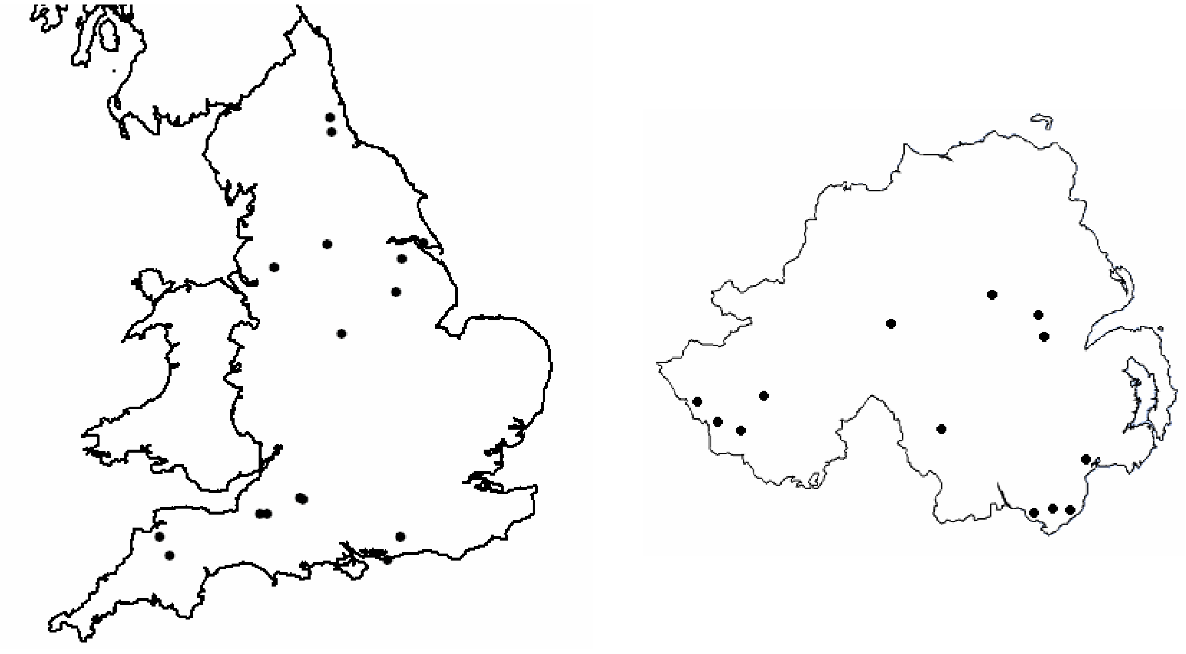
Key deliverables of WE5 and WE6:

1. *Briefing* report commenting on approach and indicating any considerations
2. Suite of confirmed algorithms and variance parameter estimates for selected indices for error estimation module (including those required for bias correction for the BMWP indices)
3. Suite of confirmed algorithms/parameters for COMPARE module

3. Datasets analysed

Four datasets have been used in the estimation of the various error variance parameters for each of the biotic indices (Figure 12). The first two datasets were supplied by Robin Guthrie (SEPA), the third is the BAMS dataset (Furse *et al*. 1995, Clarke *et al*. 2002) and the fourth was supplied by Tommy McDermott of the Northern Ireland EHS. Further details of each dataset were provided as WE2.2 Deliverable interim report:
'10 WE 2.2 Deliverable v3 - Report on Data for Errors and Compare.doc', latest version dated 29/01/08 - to which you are referred for further details.

(a) 28 Tay River Purification Board sites (b) 416 sites in the East and NE of Scotland



(c) 16 BAMS sites in England and Wales (d) 12 Northern Ireland sites

Figure 12. Geographic distribution of the sites used to estimate one or more biotic index variance parameters: (a) 28 Tay River Purification Board sites, (b) 416 SEPA sites in the East and NE of Scotland, (c) 16 BAMS sites in England and Wales, (d) 12 Northern Ireland sites.

3. Recommended procedures and algorithms to be used for assessing uncertainty in observed index values, EQRs, confidence of class and change in class

The recommended procedures and mathematical algorithms to be used to simulate uncertainty in observed index values, EQRs and ecological status class have been developed within and refined within WFD72C WE1, WE5 and WE6, as our ideas have evolved.

The latest version of the recommended uncertainty algorithms was supplied as section WE1.7 within the document 'WE1 Algorithms 071207.doc'.

The relevant section WE1.7 is repeated here to provide the context and mathematics definitions of parameters which we have estimated as part of WE5/WE6 and report in Section 4 of this report.

3.1 Background to agreed approach

The final project revised tender and draft project plan (28th June 2007) states that for WE1.7:

(ix) This will initially be based on the mathematical methods used in RIVPACS III+, and as such will incorporate the same estimates of the effects of sampling variation and sample processing errors (biases) for the existing BMWP indices (NTAXA, BMWP Score and ASPT).

(x) Generic algorithms for simulating effects of sampling variability (replicate and/or temporal) for any index will be provided (estimates for some other key indices to be derived in WE5).

(xi) The effects of sample processing errors are complex, will depend on the type of metric, and are not yet understood or assessed for other metrics *Also suitable audit information is not readily available on taxonomic abundances. It was agreed at the pre-project interview meeting of 28/05/07 that the algorithms to represent the effect of sampling processing errors will have to be limited to the simple generic methods adopted for the STARBUGS system (STAR Bioassessment Uncertainty Guidance Software; Clarke 2005, Clarke & Herring 2006). Note that, within this stage 2 of the project, estimates of the parameters of these algorithms for effects of sample processing errors will only be supplied for the three original BMWP indices (as developed and used in RIVPACS III+).*

(xii) Algorithms for comparing the O/E values and status class assignments for two samples. Initially these will be identical to the methods using the RIVPACS III+ procedure COMPARE, as this is our currently recommended general approach, and is the approach we at CEH adapted in our development of STARBUGS.

Uncertainties in observed (O) and expected (E) values of biological indices and thus in their Ecological Quality Index (EQI = O/E) values and the resulting confidence of assigning test sites to ecological status classes are all assessed using statistical Monte Carlo simulation procedures. Based on previously-derived estimates of variance parameters for the effects of typical replicate sampling variation, within-season temporal variation and between-year variation (for multi-year assessments) in index values, Monte Carlo simulations are used to generate a large number of simulated potential values of the observed (O) and the expected (E) values of each index and hence of the O/E ratios. The lower and upper 2.5% values of the frequency distribution of the simulated O/E values are used to estimate 95% confidence limits for the true average O/E ratio for the site during that time period. Each simulated O/E value can also be classified to ecological status class based on O/E class limits for each index. The proportions of simulated values falling in each class can be used to estimate the probabilities of each class being the true (average) quality of the test site during that time period.

At least 9999 simulations should be used, and that the same arbitrary but fixed random number seed is used each run so that exactly the same uncertainty results and probabilities of class are obtained in repeated runs on the same data.

The general statistical procedures used in RIVPACS III+ and to be used in the new RICT software were developed by Furse *et al.* (1995) and summarised in Clarke (2000) and Clarke et al (2002).

In this WE1.7 deliverable, we provide the recommended analogous and enhanced algorithms to be used to simulate and assess uncertainty of bioassessments within the new RICT software.

Furse *et al.* (1995) used an intensive replicated sampling programme to estimate the typical replicate sampling variation that occurs in observed values of the three BMWP indices (BMWP Score, Number of BMWP taxa (NTAXA) and ASPT (Average Score Per Taxon) for a wide range of sites of differing ecological quality and environmental type. They found that:

(i) Sampling variation in observed values of the square root (√) of the number of BMWP taxa approximately follows a Normal statistical distribution for all types and quality and site, with the standard deviation, $SD_{\sqrt{T}}$, only varying according to the number of seasons involved in the overall (combined season) sample ($SD_{\sqrt{T}}$: 0.228 (1-season), 0.164 (2-seasons), 0.145 (3-seasons).

(ii) Sampling variation in observed values of ASPT approximately follows a Normal statistical distribution for all types and quality and site, with the standard deviation, SD_A, only varying according to the number of seasons involved in the overall (combined season) sample (SD_A : 0.249 (1-season), 0.161 (2-seasons), 0.139 (3-seasons).

Furse *et al.* (1995) also compared the taxonomic lists for samples collected, sorted and identified by the then NRA (primary analysis) with the equivalent lists when the same samples were audited for sorting efficiency and accuracy of identification by the then Institute of Freshwater Ecology (now CEH). Furse *et al*. (1995) estimated that, on average, 51% of taxa missed in any single season sample are not subsequently found in a second sample from that site in another season of the same year. Furthermore, 37% of taxa missed in a single sample are not found in either of the samples taken from the two other RIVPACS sampling seasons.

Furse *et al.* (1995) also quantified the effects of recorder variation in estimating the values of the RIVPACS predictor environmental variables from these sites and derived estimates of their effects on uncertainty in estimates of expected values of the BMWP indices.

Uncertainty assessments in RIVPACS III+ were based on the results, conclusions and uncertainty parameter estimates derived from that study. The same approach and simulation algorithms are provided for use in the new RICT software for assessing uncertainty in these three indices. A similar general approach and use of simulation algorithms is suggested and provided for other indices.

Single- and multi-year runs and site assessments

The new RICT software is to include single- and multi-year site assessments.

Single year assessments are assumed to be based on one observed sample (obtained in either a single season or combined from two or three seasons (spring, summer autumn)) and thus one observed value for each biological index. This is divided by the single expected value for that site and 'season' to give a single O/E value for any particular index.

Multi-year assessments are to be based on an estimate of the average quality over a three year period. Observed (O) index values will be available for one, two or all three years in the period. The same field-based environmental predictor variables may or may not have been measured in each year. If a single expected (E) index value is used in each of the up to three sampled years, then:

average of the (O/E) = average of the (O) / E.

If different E values are available for each year then:

average of the (O/E) ≠ average of the (O) / average of the (E).

However, for any single site, the expected (E) is relatively constant and insensitive/robust to the typical degree of within-site changes in the environmental variables that occur (Armitage, P.D. 2000. The potential of RIVPACS for predicting the effects of environmental change. In: Wright, J.F., D.W. Sutcliffe and Furse, M.T. (eds). *pp 93-112. Freshwater Biological Association*, Ambleside.).

To assess uncertainty in site assessments, we have available and have used a mixture of replicated samples and time series of observed RIVPACS sample data to estimate components of uncertainty in the average O index value for a period (single- or multi-year).

For a combination of the above reasons, the estimate of the average quality for a three year period that is to be used in RICT multi-year assessments is defined as:

Estimate of average quality = average of the (O) / average of the (E).

The uncertainty variance associated with this estimator or average quality can then be estimated from the uncertainty associated with estimate average O value and the uncertainty associated with estimating the average E value for the three year period at that site.

Notes on assumptions:

(i) The RICT simulations of the stochastic variability assume that the observed index values are based on a single sample from that 'season' in any one year (where 'single sample' for a spring and autumn combined season sample analysis means one sample in spring and one sample in autumn in the same year have been combined). Multi-year assessments are based on the assumption that the observed index value ($ObsIDX_i$) is the average of 'single samples' from 'season' s in the N_{year} sampled years. If some future assessments were based on more than one sample in each 'season' of each year then the observed sample values would have smaller random uncertainty terms ($SDObs_{ir}$), but these are not expected to occur and thus are not catered for here.

(ii) The RICT (and RIVPACS III+) uncertainty assessments are based on the assumption that the same single sampling site with a WFD water body has been sampled on each occasion, and that furthermore, this site is representative of the ecological status of the WFD water body as a whole. Therefore the uncertainty estimates are actually for ecological quality at that river site; there is potentially additional uncertainty due to un-quantified spatial variability between possible sampling sites with the water body.

Definitions:

i = id of current biological index
iN = total number of biological indices on which to assess uncertainty
rN = number of simulations used to assess uncertainty

At present iN = 11, with indices referred to in the following order of id:

Index id i	Index Name	Transformation of index prior to adding simulated "error" terms
1	BMWP Score	derived from indices 2 & 3 +
2	NTAXA	square root
3	ASPT	none
4	Revised BMWP Score (non abundance weighted)	derived from indices 5 & 6 +
5	Revised NTAXA (non abundance weighted)	square root
6	Revised ASPT (non abundance weighted)	none
7	Revised BMWP Score (abundance weighted)	derived from indices 8 & 9 +
8	Revised NTAXA (abundance weighted)	square root
9	Revised ASPT (abundance weighted)	none
10	AWIC (family level)	not yet known
11	LIFE (family level)	not yet known

+ Because $ObsIDX_{1s} = ObsIDX_{2s} * ObsIDX_{3s}$ (apart from rounding errors), we can derive simulated values for $ObsIDX_{1s}$ from simulated values for $ObsIDX_{2s}$ and $ObsIDX_{3s}$; similarly for $ObsIDX_{4s}$ and $ObsIDX_{7s}$ (we anticipate).

s = id of selected season(s) combination (referred to as 'season');
(1 = spring, 2 = summer, 3 = autumn, 4 = spring + summer,
5 = spring + autumn, 6 = summer + autumn, 7 = all three seasons)

The term "sample" refers to the total sample for which the index values were calculated; this could be a single season sample, or a two or three season combined sample.

$ObsIDX_i$ = Observed sample value of index *i* (for selected season *s*) for current test site

$ExpIDX_i$ = Expected value of index *i* (for selected season *s*) for the current test site

Note: In multi-year runs
$ObsIDX_i$ = average of the observed (O) values of index *i*
and $ExpIDX_i$ = average of the expected (E) values of index *i*
for current test site over the three-year period.

Note: Because any single software run only involves one selected season combination *s* the subscript *s* is dropped for the observed and expected index values to make it easier to include a subscript for the r^{th} simulated value of the observed and expected values of each index.

Thus (for example):

$ObsIDX_1$ = Observed value of BMWP Score for the current test site
$ObsIDX_2$ = Observed value of NTAXA for the current test site
$ObsIDX_3$ = Observed value of ASPT for the current test site

$ExpIDX_1$ = Expected value of BMWP Score for the current test site
$ExpIDX_2$ = Expected value of NTAXA for season *s* for the current test site
$ExpIDX_3$ = Expected value of ASPT for season *s* for the current test site

SD denotes standard deviation (where appropriate on the transformed index scale)

$SDRep_{is}$ = Replicate sampling SD of transformed observed values of index *i* for ‘season’ *s*

$SDTSeas_{is}$ = Within-season temporal variability SD of transformed observed values of index *i* for ‘season’ *s*

$SDTYear_{is}$ = Between-year variability SD of transformed observed values of index *i* for ‘season’ *s* (based on inter-year variance within 3-year periods)

$SDObs_{is}$ = Overall uncertainty SD for observed value of index *i* for ‘season’ *s* (based on a combination of the individual component SD)

Single-year or multi-year (3-year) assessment runs:

The RICT software will have two periods over which site quality can be estimated and assessed:

(c) single-year run - assessing site quality for a single year
- based on single O value ($ObsIDX_i$) / single E value ($ExpIDX_i$)

(d) multi-year run - assessing average site quality over a three year period
- based on average O value ($ObsIDX_i$) / average E value ($ExpIDX_i$)

$NObs_{year}$ = number of years (1, 2 or 3) for which a sample was involved in the estimate of the average O value

$NExp_{year}$ = 1 for single-year run
= number of years (1, 2 or 3) for which a separate estimate of the E value was involved in the estimate of average E value (for multi-year run)

If a single estimate of E is used for all three years, then $NExp_{year} = 1$)

3.2 Recommended Algorithms

Simulating potential observed index values

The simulated potential observed values ($ObsIDX_{ir}$) are generated by transforming the observed sample value to the appropriate scale, then adding the appropriate random error term ($ZObs_{ir}$), then back-transforming to the original index scale. (For example, with index 2 (NTAXA), we square root (√) the observed sample value, add a random error term, and then square the result to get a simulation of the potential value of NTAXA we could have obtained by chance if a different single replicate sample had been taken at the site in the same season(s)).

For single-year runs:

$$SDObs_{is} = \sqrt{((SDRep_{is})^2 + (SDTSeas_{is})^2)} \qquad (Eq3.1)$$

For multi-year (3-year) runs:

$$SDObs_{is} = \sqrt{(((SDRep_{is})^2 + (SDTSeas_{is})^2 + (SDTYear_{is})^2 * (1 - NObs_{year} / 3)) / NObs_{year})}$$

(Eq3.2)

For each simulation *r*, for both single- and multi-year runs, derive:

$ZNorm_{ir}$ = Random number deviate from a standard Normal distribution with a mean of 0.0 and SD of 1.0 for index *i* in simulation *r*

$ZObs_{ir}$ = Random deviate for potential observed sample value of index *i* in simulation *r*

$ZObs_{ir} = ZNorm_{ir} * SDObs_{is}$

Note: RICT software programmers can either use an existing function code to generate such random numbers from a standard normal distribution or use the FORTRAN code used in RIVPACS III+ supplied at the end of this document)

$ObsIDX_{ir}$ = Simulation *r* Observed sample value of index *i* for current test site

Calculate:

For original BMWP indices (NTAXA, ASPT and BMWP score):

$ObsIDX_{2r} = (\sqrt{(ObsIDX_2)} + ZObs_{2r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{3r} = ObsIDX_3 + ZObs_{3r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{1r} = ObsIDX_{2r} * ObsIDX_{3r}$ = r^{th} simulated value for observed BMWP Score

Similarly for the Revised non-abundance-weighted BMWP indices:

$ObsIDX_{5r} = (\sqrt{(ObsIDX_5)} + ZObs_{5r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{6r} = ObsIDX_6 + ZObs_{6r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{4r} = ObsIDX_{5r} * ObsIDX_{6r}$ = r^{th} simulated value for observed BMWP Score

Similarly for the Revised abundance-weighted BMWP indices:

$ObsIDX_{8r} = (\sqrt{(ObsIDX_8)} + ZObs_{8r})^2$ = r^{th} simulated value for observed NTAXA
$ObsIDX_{9r} = ObsIDX_9 + ZObs_{9r}$ = r^{th} simulated value for observed ASPT
$ObsIDX_{7r} = ObsIDX_{8r} * ObsIDX_{9r}$ = r^{th} simulated value for observed BMWP Score

Similar algorithms have be developed and supplied for the new indices 10 (AWIC) and 11 (LIFE), both at family level, based on analysis of the replicate sample and temporal data for these indices (see Sections 4-6 below).

The AWIC index does appear to have lower levels of sampling variability for site with AWIC values close to the maximum possible value of 6.0, such that its variance for single season samples is best described by a quadratic relationship with its observed value for a site (see equation (Eq4.1) and Section 4 below). However, to fit in with the above transformation framework for the BMWP indices, it is temporarily recommended that the variance of AWIC is assumed to behave in the same way as BMWP ASPT and estimated by a constant derived from the supplied uncertainty datasets (see Section 4-6 below).

Variance in the family-level LIFE index does not seem to vary consistently with its observed value, but it does appear to be subject to higher levels of sampling variability when fewer LIFE-scoring taxa are present in samples from a particular site (see equation (Eq4.3) and Section 4 below). It could be possible to include the number of life-scoring taxa for an observed test sample as an extra input variable to user data within the RICT software tool, and then use an adaptation of equation (Eq4.3) which included temporal as well as replicate sampling variances to simulate overall sampling uncertainty in the LIFE index. However, to fit in with the simple convenient transformation options for the BMWP indices, it is temporarily recommended that the variance of LIFE is assumed to independent of its observed value and estimated by a constant derived from the supplied uncertainty datasets (see Sections 4-6 below).

Thus to simulate uncertainty in observed values of family-level AWIC and LIFE, use:

$\mathrm{ObsIDX}_{10r} = \mathrm{ObsIDX}_{10} + \mathrm{ZObs}_{10r}$ = r^{th} simulated value for observed AWIC

$\mathrm{ObsIDX}_{11r} = \mathrm{ObsIDX}_{11} + \mathrm{ZObs}_{11r}$ = r^{th} simulated value for observed LIFE

3.3 Estimation of Sampling variability/uncertainty parameters

Appropriate estimates of SDRep_{is}, $\mathrm{SDTSeas}_{is}$ and $\mathrm{SDTYear}_{is}$ have been derived for all 11 indices from statistical analysis of the three main supplied datasets (namely the 28 Tay sites, 416 SEPA sites and 16 BAMS sites detailed in Section 2); details of the analyses are given in Sections 4 and 5 and recommended parameter estimates are summarised in Section 6, as a Deliverable within WE5/WE6. Dataset 4 (namely the 12 NI sites) was used to provide a check on the estimates of the total within-season SD (SDWSeas) based on the combined effect of SDRep and SDTSeas (see section 5.1.2).

The overall uncertainty in the observed (O) values of metrics and in the EQR values is then assessed by simulation procedures as detailed in Sections 3.1 and 3.2 above, and in the WE1 Algorithms deliverable (latest version dated 07/12/07). The above SD component parameters which can be estimated directly, or partially, using information from each dataset are indicated in Table 10.

Variability component	SD	No. of Seasons involved	28 TAY sites	416 SEPA sites	16 BAMS sites	12 NI sites
Replicate sampling	SDRep	1	√		√	
		2	√		√	
		3			√	
Within-season Temporal	SDTSeas	1		√		√
		2				
		3				
Inter-year Temporal	SDTYear	1	√	√		
		2	√	√		
		3				

Table 10. Components of variability which can be estimated, or for which there is information, within each dataset (indicated by ticks).

Strictly speaking the temporal SD parameters, SDTSeas and SDTYear, can only be estimated from analyses of variance based on the 416 SEPA sites dataset when that data set is combined with the other two datasets in order to enable us to ‘subtract’ the variance due to replicate sampling effects from the overall observed temporal variation in index values.

Strictly speaking, the 12 site NI dataset, which has a single replicate in each RIVPACS sampling month (Mar-Nov) in 2006, can only be used to estimate the combined effect of replicate variability (SDRep) and within-season temporal variability (SDTSeas).

The indirect methods which had to be used to derive estimates of SDTSeas and SDTYear for two- and three-season combined samples are described in Section 5, along with the estimates themselves.

4. Estimates of replicate sampling variability, transformation scale and SDRep

The first step in assessing the variability in biotic index values due to replicate sampling effects was to plot the sampling standard deviation of replicate samples from the same site, year and season against the mean value of those replicate samples to help assess whether, and how, the variability between replicate samples varies with the general level of each index. This was done for the two datasets with replicate samples, namely the 16 BAMS and 28 Tay sites. This is shown for single season samples for each index in Figures 13-17.

4.1 BMWP indices (original and revised) replicate sampling SD

Figures 2-4 highlight the differences between the two replicated sample datasets in the typical BMWP index values. The BAMS sites were carefully selected to cover a wide range of biological qualities and thus encompass a wide range of values of BMWP score, NTAXA and ASPT in both original and revised forms. In contrast, the vast majority of samples from the Tay dataset are from high or reasonable good quality relatively taxon-rich sites with generally high values of BMWP score and ASPT, although the high values may be partly due to the natural physical characteristics of these sites. However, the plots of replicate SD against replicate mean for the two datasets overlap with no major systematic differences in the SD to mean relationship (Figure 13-15), which is encouraging; but this is assessed in more detail below. Together the two datasets complement each other by covering most of the practical range of values recorded for these indices in any field samples, which means that variance parameter estimates based on their combined analysis should provide reasonable estimates for general use in uncertainty simulation software.

The approach in RIVPACS to simulating index uncertainty was to find the best transformation of observed values of an index to make the replicate sampling variability as homogeneous as possible, or at least not varying systematically with the replicate mean value. An established method of determining an appropriate transformation with these types of metric is to regress the logarithm of variance of replicate samples against the logarithm of mean of the replicate samples, as: Log (Replicate variance) = $a + b$ Log (Replicate mean) (Clarke *et al*. 2002). The regression slope b indicates the power with which the variance amongst replicate increases with their mean value. Moreover, values of b of around 1.0 and 2.0 indicate, respectively, that a square root transformation and a logarithmic transformation of index values will make the replicate variance (of transformed values) more independent of the replicate mean value. Values of b around zero indicate that no simple power transformation will either be needed or be effective in making the replicate variance for the index more homogeneous across all sites. Negative values of b would suggest that variation in the index values between replicates tends to decrease as their value increases.

Table 11 summarises these log variance to log mean regression relationships for each single season sample values of each index, first based on just the BAMS dataset (as used by Clarke *et al* 2002) and then using the BAMS and Tay catchment sites datasets combined to get the single best overall relationship.

		(a) BAMS sites			(b) BAMS + Tay sites		
		b	SE(b)	r^2	b	SE(b)	r^2
Original BMWP	BMWP Score	1.23	0.22	42%	1.07	0.12	21%
	NTAXA	0.92	0.26	22%	0.81	0.18	7%
	ASPT	0.26	0.88	0%	0.03	0.30	0%
Revised BMWP Non-weighted	BMWP Score	1.20	0.23	39%	1.07	0.13	20%
	NTAXA	0.77	0.29	14%	0.81	0.18	7%
	ASPT	0.61	0.84	1%	0.47	0.29	1%
Revised BMWP Abundance-weighted	BMWP Score	1.21	0.21	42%	1.14	0.10	29%
	NTAXA	0.77	0.29	14%	0.81	0.18	7%
	ASPT	-1.40	0.54	13%	-0.36	0.20	1%
AWIC (family level)		-8.50	5.12	6%	-2.89	0.64	7%
LIFE (family level)		-6.20	1.57	22%	-1.41	0.66	2%

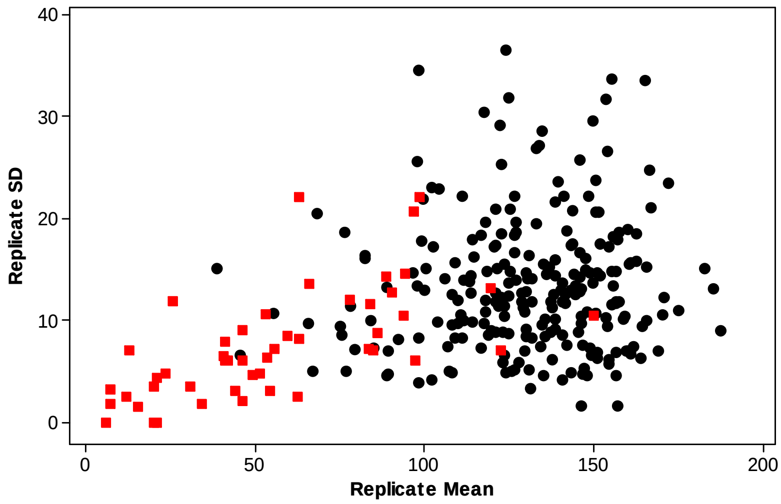
Table 11 Taylor's power law regressions of log replicate variance again log replicate mean for the single season samples for the (a) 16 BAMS sites and (b) BAMS + Tay datasets combined; b = regression slope, SE(b) = standard error of b, r^2 = % variation explained).

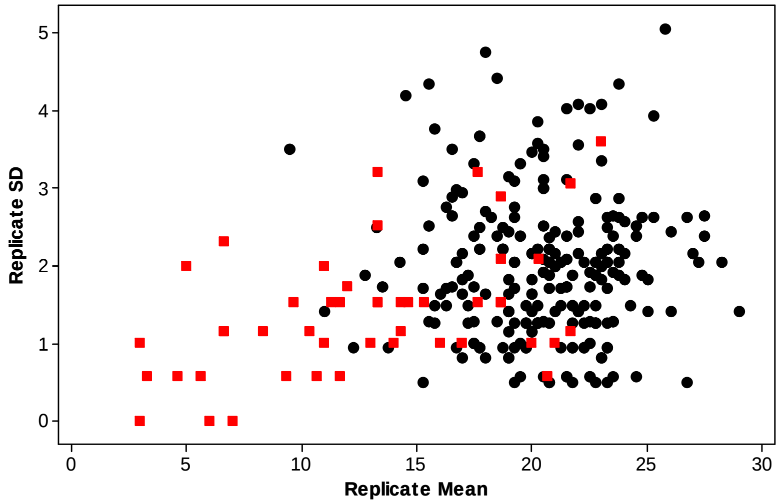
The log variance –log mean regression slopes for all three forms of the BMWP score index are all greater than but not statistically significantly different from 1.0, indicating that the square root transformation is optimal. For the original and revised forms of NTAXA, the regression slopes range from 0.77 – 0.92, but they are not statistically significantly different from 1.0, indicating that analysing variation in the three NTAXA type indices on the square root scale is also an appropriate way of reducing systematic between-site heterogeneity in the replicate sampling standard deviation (SDRep) and, by implication, in the temporal variability terms, SDTSeas and SDTYear.

By working with the square root of the sample values of BMWP score and NTAXA (in either original or revised form), the replicate sampling SD no longer varies in any systematic way with the average size of the replicate values (Figure 16). This indicates that the square root transformation helps us to make the inter-sample variability of such indices more consistent across sites, increasing the justification for the use of single overall SD parameter estimates for variability in BMWP score and NTAXA (on this transformed scale).

There appears to be no major systematic variation between the SD of replicate sample values of ASPT and the replicate mean value of ASPT, whether in original or revised ASPT form (Figures 13(c), 14(c), 15(c)). However, there is some suggestion that replicate variation in the revised abundance-weighted form of ASPT may be greater for some very poor quality sites with ASPT values less than three or so (Figure 15(c)).

The original BMWP scoring system scored BMWP families on the scale 1-10, so that ASPT must lie between 1 and 10. However, in practice values greater 8 are very rare (only 7 of 17011 samples amongst the three study datasets) because 10-scoring sensitive taxa always with as many lower-scoring less sensitive BMWP families. Thus, in practice, replicate and, by implication, other sampling variation in ASPT does not become less at the upper end of observed replicate mean values (Figures 13(c), 14(c), 15(c)).


(a) Original BMWP Score


(b) Original BMWP NTAXA

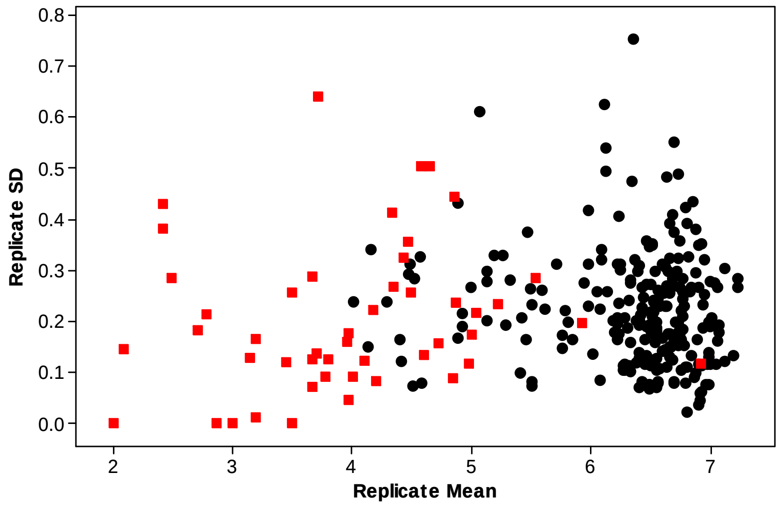
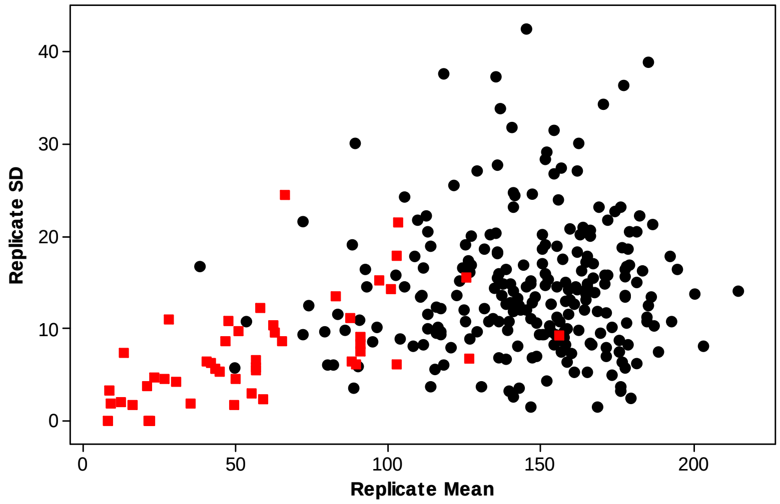
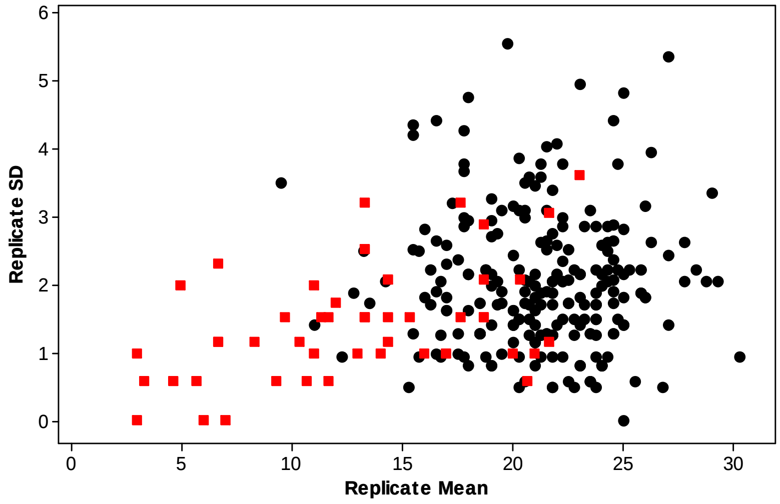

(c) Original ASPT

Figure 13. Plot of the relationship between replicate sampling SD and mean of the replicate single season sample values for all available combinations of sites and seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●) for the original BMWP (a) BMWP Score, (b) NTAXA and (c) ASPT.

(a) Revised non-weighted BMWP Score



(b) Revised non-weighted BMWP NTAXA



(c) Revised non-weighted ASPT

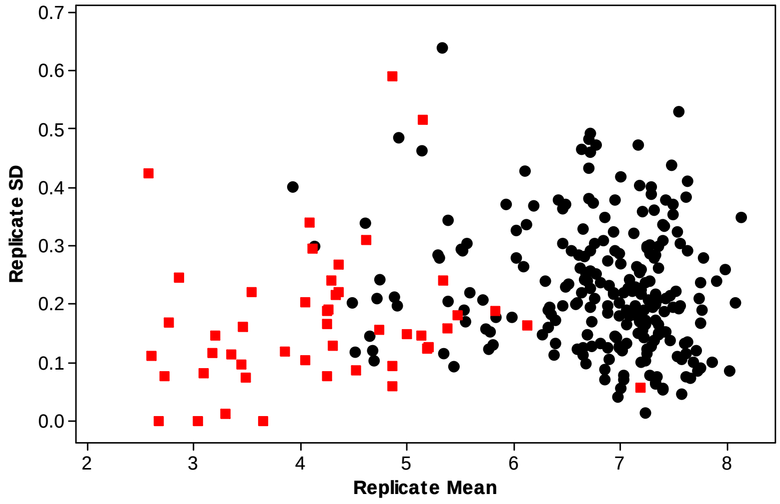
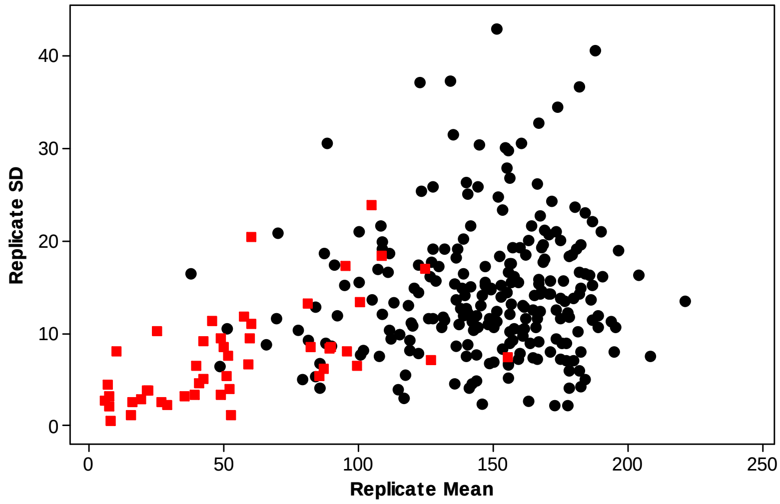
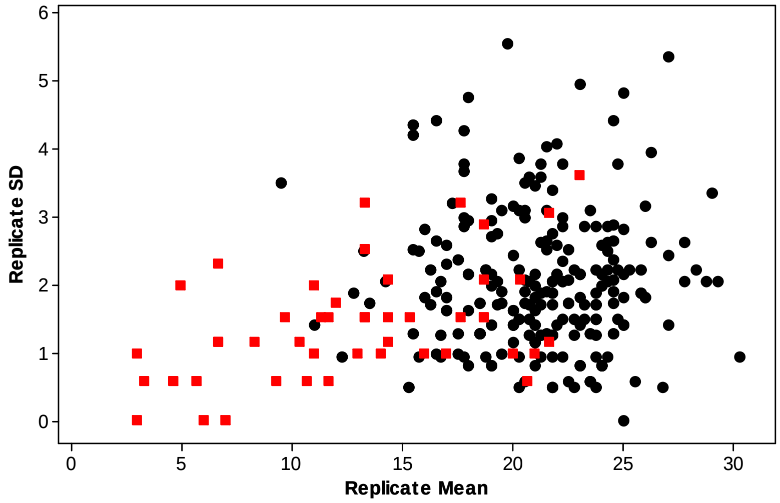


Figure 14. Plot of the relationship between replicate sampling SD and mean of the replicate single season sample values for all available combinations of sites and seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●) for the Revised non-weighted BMWP (a) BMWP Score, (b) NTAXA and (c) ASPT.

(a) Revised abundance-weighted BMWP Score



(b) Revised abundance-weighted BMWP NTAXA



(c) Revised abundance-weighted ASPT

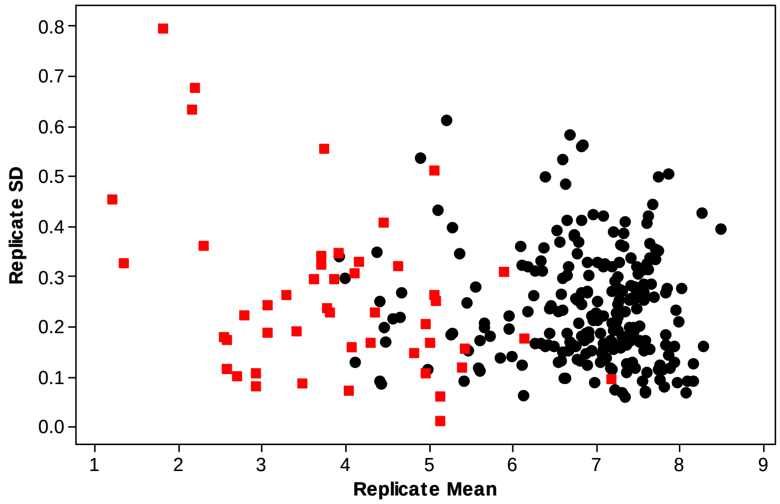
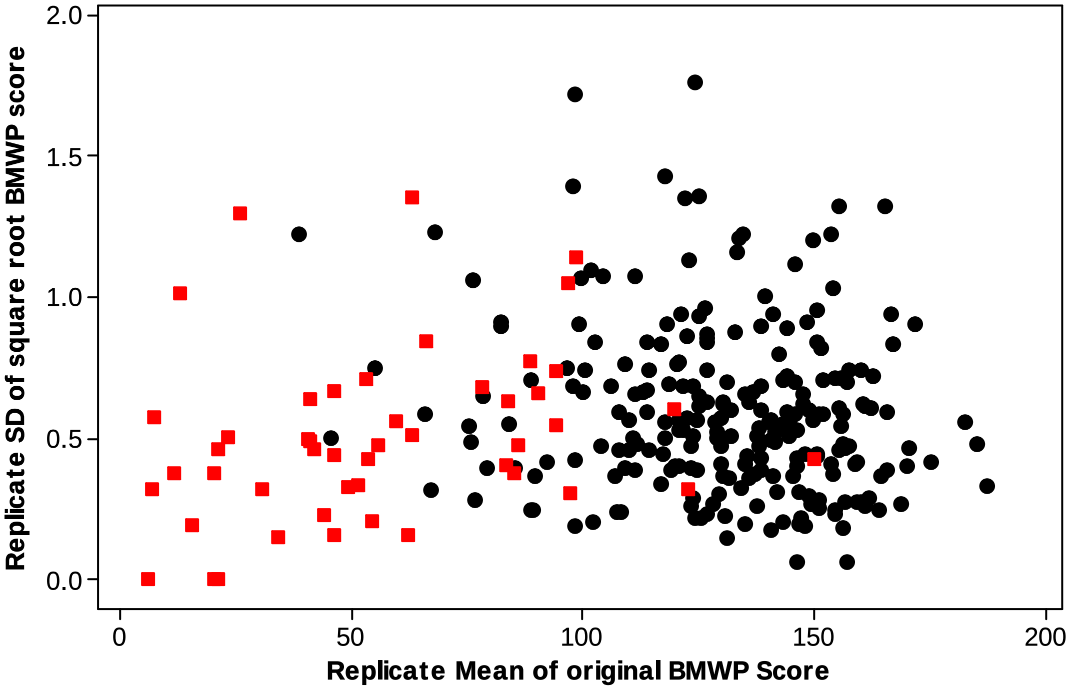


Figure 15. Plot of the relationship between replicate sampling SD and mean of the replicate single season sample values for all available combinations of sites and seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●) for the Revised abundance-weighted BMWP (a) BMWP Score, (b) NTAXA and (c) ASPT.

(a) Original BMWP Score



(b) Original NTAXA

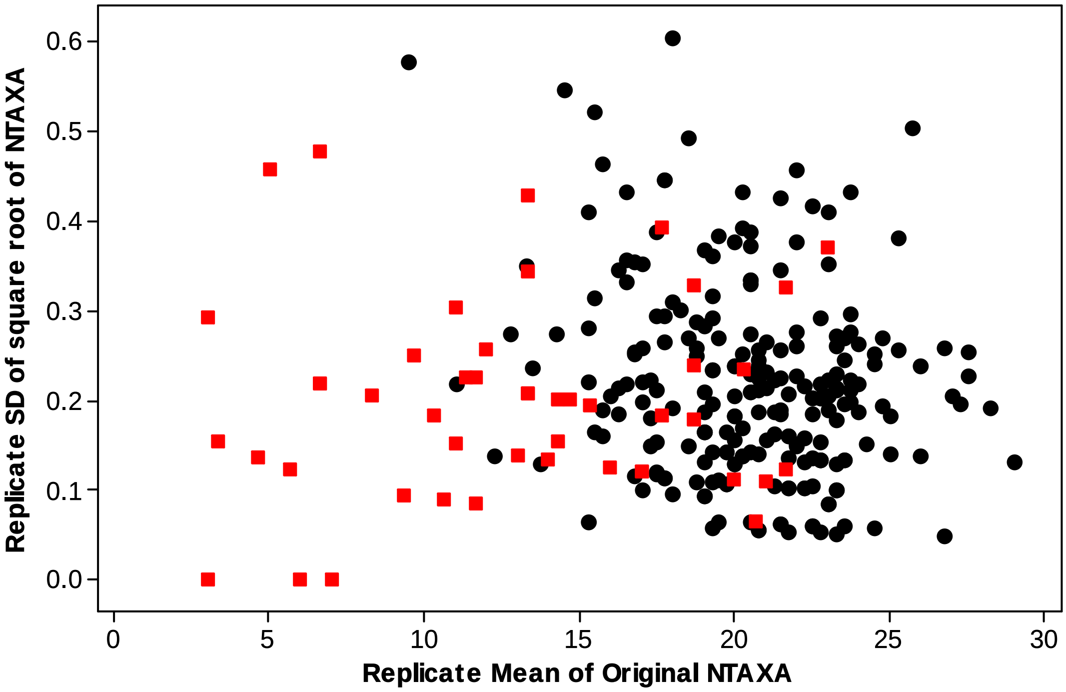


Figure 16. Plot of the relationship between (a) replicate sampling SD of square root of original BMWP score and replicate mean value of BMWP score and (b) replicate sampling SD of square root of original NTAXA and replicate mean value of NTAXA, based on all single season sample values for all available combinations of sites and seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●).

4.2 AWIC (family) replicate sampling SD

Although, the AWIC index is also a form of 'average-score-per-taxon' type index, but based on taxa scored 1-6 according to their preference/tolerance of acid conditions (6=least tolerant), two-thirds (34 of 51) of AWIC-scoring families have an AWIC score of the maximum value of 6 (see Appendix in WFD72C Deliverable '08 WE 2.2 Deliverable v2 - Report on Data for Errors and Compare.doc'). Partly because of this, some actual samples have AWIC values close to 6 (and 10% of all study values were over 5.3), such that some high-pH sites tended to always have high sample values for AWIC. In such cases, the replicate sampling SD of AWIC tends to be less than for the vast majority of sites (Figure 17(a)).

The relationship between replicate SD and replicate mean of AWIC (family level) was represented by the following fitted quadratic regression (regression coefficient standard errors given in brackets):

$$\text{AWIC Replicate SD} = \underset{(0.340)}{-0.934} + \underset{(0.142)}{0.484}\,(\text{Mean AWIC}) - \underset{(0.0148)}{0.0536}\,(\text{Mean AWIC})^2 \qquad (\text{Eq4.1})$$

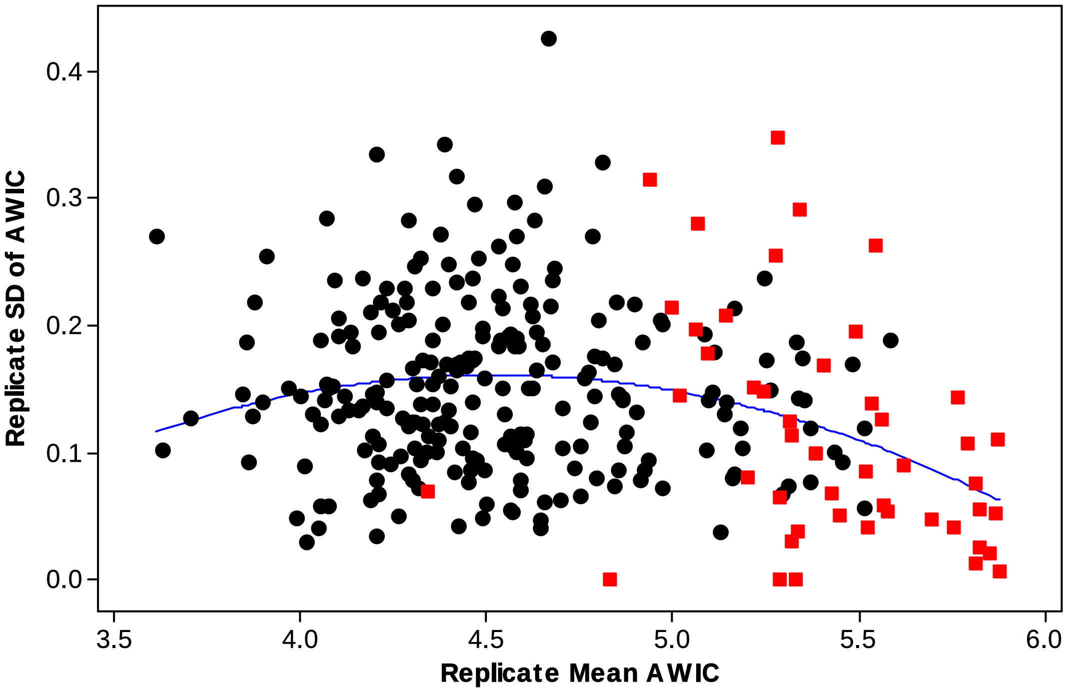
Although the overall relationship is not strong (R^2 = 9%), partly due to inherent sampling variability in the individual estimates of replicate SD, it is statistically-significant and the equation (Eq4.1) could be used to provide improved estimates of the potential uncertainty associated with single season sample AWIC values due to replicate sampling (Table 12). It makes sense not to constrain the SD to be zero at the maximum observable AWIC value of 6.0 because it is quite possible in real application for the single observed sample to have an AWIC value of 6 when other replicate samples from the same site would have had lower values (any simulated values greater than 6 could be treated as 6).

It is difficult to extend this regression logic to the more complex situation involving the combined effect of both replicate and temporal variance components, as these are partially estimated from different datasets and varying time periods. Therefore, estimates are also given in later analyses of the overall best single estimate of SDRep, SDTSeas and SDTYear for AWIC, which should be adequate for use with most samples, except those from sites with either very high or very low pH.

AWIC value	3.5	4.0	4.5	5.0	5.5	6.0
Estimated Replicate SD	0.105	0.146	0.161	0.148	0.109	0.044

Table 12 Quadratic regression estimates of Replicate SD of single season sample AWIC values for replicate mean or observed single sample values of AWIC.

(a) AWIC



(b) LIFE

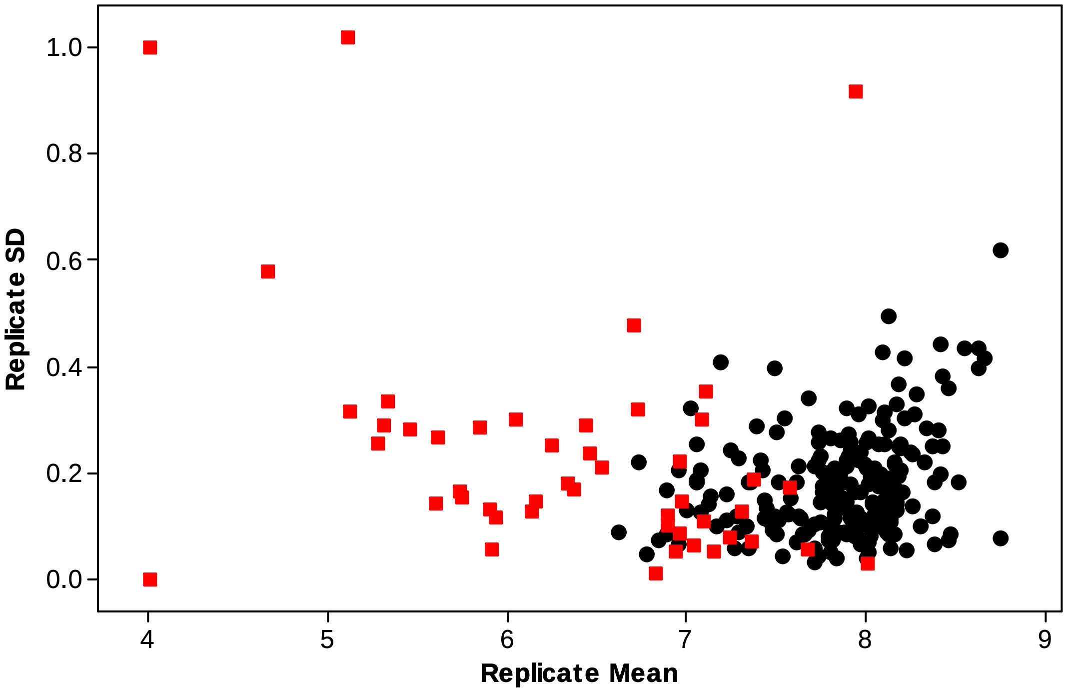


Figure 17. Plot of the relationship between replicate sampling SD and mean of the replicate single season sample values for all available combinations of sites and seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●) for (a) AWIC (family level) and (b) LIFE. Solid line denotes fitted quadratic regression for AWIC SD-Mean relationship.

4.3 LIFE (family) replicate sampling SD

The LIFE index (Extence *et al*. 1999) is an abundance-weighted ‘average-score-per-taxon’ index, with taxa scores varying from 1 to 12; however, in practice most sites’ family-level LIFE values vary between 5 and 9. There is no apparent general relationship between the replicate SD of single season sample LIFE values and the mean of the replicate sample LIFE values (Figure 17(b)). This was also the conclusion of Clarke *et al.* (2003) in their corresponding analyses based on just the BAMS dataset. Clarke *et al*. (2003) also concluded that the sampling SD of LIFE does not vary systematically between different types of site or between seasons.

However, Clarke *et al*. (2003) found that although the sampling SD does not appear to vary with the mean of the replicate values of LIFE, some pattern emerges when the SD of replicate samples from a BAMS site was plotted against the mean number of LIFE-scoring families involved in calculating the replicate values of LIFE for that site (Figure 18). The highest values of SD (i.e. >0.5) all occurred when the replicate values of LIFE were based on an average of less than 5 families. At the other extreme, when the average number of LIFE-scoring families found in replicate samples is at least 15, the sampling SD is always relatively small (i.e. <0.2) (Figure 18(b)). The Spearman rank correlation between sampling SD and average number of families is –0.54; the correlation is still –0.54 when the observations based on an average of less than five families are ignored (Figure 18(b)).

This potential for increased sampling variability at sites with few families present is illustrated by BAMS site 4 in spring, which has a very high average LIFE score, but it is still very variable between replicate samples. The second and third replicate samples had similar values of LIFE (7.33 and 7.50) both based on six families, but sample 1 only had two LIFE-scoring families present, Baetidae at log abundance category 3 and Simuliidae at log abundance category 1, both in LIFE flow group II, giving a value of LIFE of 9.00. This gave a SD between the three replicates of 0.92 (pointed marked Y in Figure 18(b)).

When few LIFE-scoring families are present at site, the sampling variance of LIFE is more volatile and potentially more difficult to predict. As an example of one extreme, all three replicate samples at Site 16 in summer contained only Hydrobiidae at log abundance category 3 (plus the ubiquitous Oligochaeta and Chironomidae, which are ignored in the LIFE system). All three samples therefore had values of LIFE of 4.00 and hence an estimated sampling SD of zero (outlier marked Z in Figure 17). Finding just one more family in one sample could have given a quite different value for LIFE and hence estimated SD.

Based on the BAMS dataset, we conclude that the sampling SD of LIFE does tend to decline systematically with the number (N_{LIFE}) of LIFE-scoring families present. The relationship is best estimated by a linear regression relationship between log SD and N_{LIFE}, which is statistically significant (r = -0.48; p = 0.001) and given by (standard errors of regression coefficients given underneath in brackets):

$$\log_e \mathrm{SD} = -0.910 \quad - \quad 0.0843\, N_{LIFE}$$

(Eq4.2a)

$$\qquad (0.277) \qquad (0.0226)$$

The back-transformed predicted relationship is:

$$\text{sampling SD} = 0.403(0.9192)^{N_{LIFE}}$$

(Eq4.2b)

which is superimposed as the solid line in Figure 18(b). The outlier observation Z is highly influential on the estimated regression relationship; without Z the correlation is much stronger (r = -0.68, p < 0.001) and the following equivalent relationships are obtained:

$$\text{loge SD} = -0.528 \quad - \quad 0.1154\, N_{LIFE}$$

(Eq4.3a)

$$\qquad (0.224) \qquad (0.0180)$$

sampling SD = $0.590(0.8945)^{N_{LIFE}}$
(Eq4.3b)

As the estimate of sampling SD for the outlier Z could have been quite different if just one more family had been found in any one of the three replicate samples, we conclude that it is best to ignore this point and use equation (Eq4.3) shown as the dashed lines in Figure 18).

This equation can be used to provide an estimate for the unknown replicate sampling SD of single season samples for any site using just the observed number of LIFE-scoring families present in a single sample; examples are given in Table 13.

Number of LIFE-scoring families present (N_{LIFE})	Sampling SD
1	0.528
2	0.472
3	0.422
4	0.378
5	0.338
6	0.302
7	0.270
8	0.241
9	0.216
10	0.193
12	0.155
15	0.111
20	0.063
25	0.036

Table 13. Estimate of sampling standard deviation (SD) of observed LIFE for sites where N_{LIFE} LIFE-scoring families are present in a sample (estimates based on equation (6.2))

The implication is that when very few taxa are present, the sampling SD is greater, so a larger change in value of LIFE would be needed to have any confidence that it is not just due to chance sampling variation.

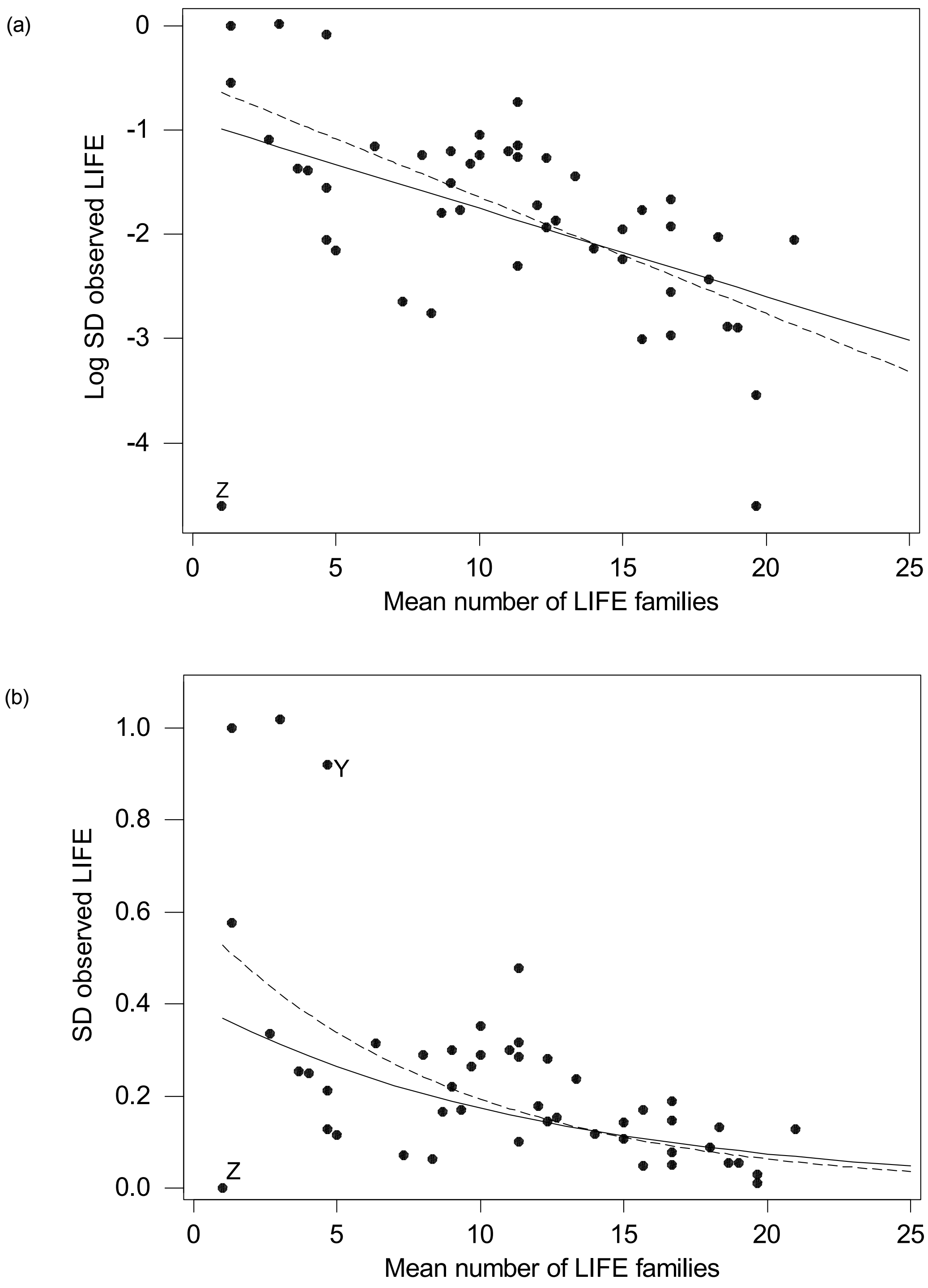


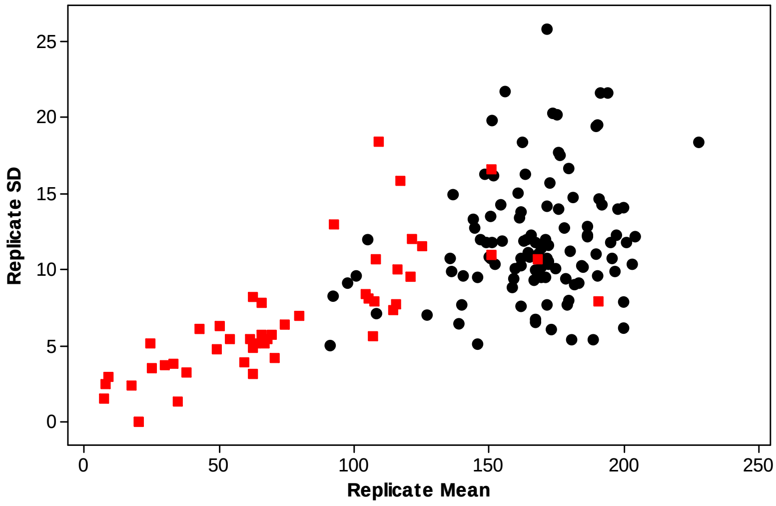
Figure 18. Relationship between standard deviation (SD) of the three replicate values of LIFE for each season at each BAMS site and the mean number of LIFE-scoring families present in each replicate (*n* = 48 = 16 sites x 3 seasons). (a) and (b) show SD on logarithmic and untransformed scales respectively. Y and Z denotes cases discussed in text. Solid and dashed lines denote fitted regression relationship of equations (EQ2) and (EQ3) with and without outlier Z respectively

4.4 Combined season sample replicated sampling SD

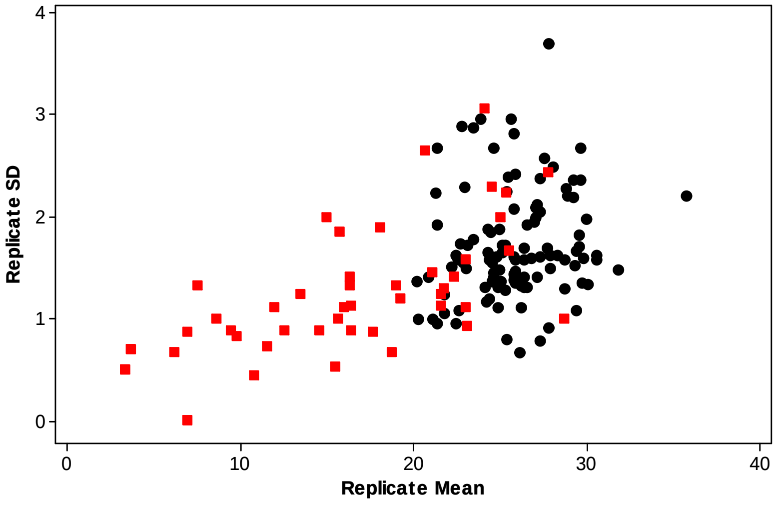
As present, the AWIC and LIFE indices have only been developed and designed and tested for use on single season samples. The original BMWP indices are already used nationally in bio-assessments based on both single season sample values and two- or three-season combined sample values (all appropriately adjusted by the RIVPACS prediction/expected values for that type of site and for that season or combination of seasons. Presumably, equivalent combined-season bio-assessments could be made using the revised BMWP indices in either presence-absence or abundance-weighted form.

The relationship between replicate sampling SD and replicate sampling mean observed for single season sample values of BMWP score and NTAXA (in both original and revised form) also apply for both two and three- seasons combined samples, as illustrated in Figure 19 for the two-season combined replicate sampling variation in the original BMWP indices. In fact, the relationships between replicate SD and replicate mean for both BMWP score and NTAXA are both even stronger than for their single season equivalents (Figures 19 and 13); this is mostly because of the reduced stochastic variation in combined season sample taxonomic composition and thus index values. Thus the same square root transformation can be applied to the two- and three- season combined sample values of BMWP score and NTAXA, whether in original or revised form, to help make variability more consistent across sites and increase the validity of using a single set of estimates of the parameters SDRep, SDTSeas and SDTYear for all sites and samples, with parameter estimates only depending on the number of seasons involved (1, 2 or 3). These estimates were derived and are summarised in section 4.2.

(a) Original BMWP Score



(b) Original BMWP NTAXA



(c) Original ASPT

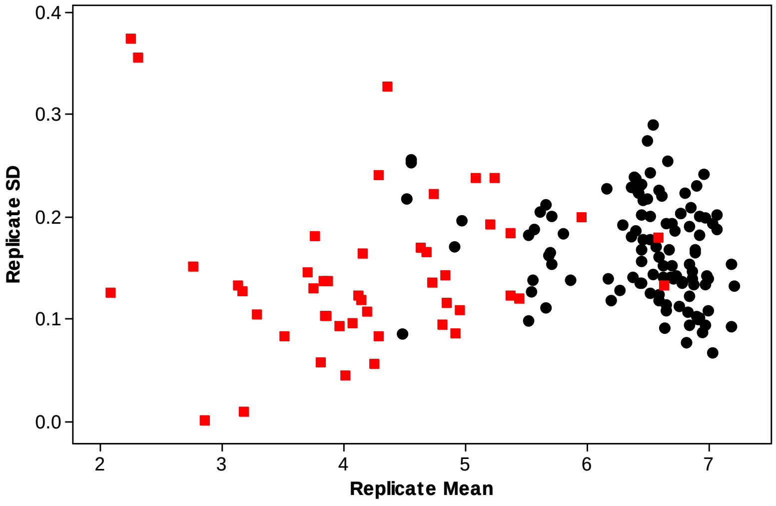


Figure 19 Plot of the relationship between replicate sampling SD and mean of the replicate two-season combined sample values for all available combinations of sites and pairs of seasons with replicate sampling for the 16 BAMS sites (■) and the 28 Tay sites (●) for the original BMWP (a) BMWP Score, (b) NTAXA and (c) ASPT.

4.5 Correlation among indices: overall and amongst replicate samples

The revised versions of the BMWP score index are highly correlated with the original BMWP score index, whether in revised non-weighted form (correlation *r* = 0.984) or abundance-weighted form (*r* = 0.981) (Table 14(a)).

Although the revised BMWP values for NTAXA were up to six taxa higher than the original BMWP NTAXA index, the two forms of NTAXA are highly correlated (*r* = 0.985). Note, that the values of NTAXA for the non-weighted and abundance-weighted form of the revised BMWP indices are, by definition, always the same (Table 14).

		Original			Revised Non-Weighted			Revised Abundance-weighted			
(a) raw values		Score	TAXA	ASPT	Score	TAXA	ASPT	Score	TAXA	ASPT	AWIC
Original	TAXA	**0.939**									
	ASPT	0.775	0.522								
Revised non-weighted	Score	**0.984**	**0.917**	0.779							
	TAXA	**0.926**	**0.985**	0.521	**0.930**						
	ASPT	0.703	0.440	**0.970**	0.737	0.448					
Revised Abundance-weighted	Score	**0.981**	**0.910**	0.783	**0.997**	**0.923**	0.743				
	TAXA	**0.926**	**0.985**	0.521	**0.930**	**1.000**	0.448	**0.923**			
	ASPT	**0.986**	0.776	0.477	**0.959**	0.759	0.485	**0.986**	0.776	0.485	
AWIC		-0.384	-0.119	-0.744	-0.420	-0.121	-0.806	-0.425	-0.121	-0.775	
LIFE		0.505	0.278	0.769	0.537	0.298	0.780	0.558	0.298	0.801	-0.522
(a) replicate residuals		Score	TAXA	ASPT	Score	TAXA	ASPT	Score	TAXA	ASPT	AWIC
Original	TAXA	**0.947**									
	ASPT	0.738	0.502								
Revised non-weighted	Score	**0.974**	**0.958**	0.639							
	TAXA	**0.939**	**0.999**	0.494	**0.958**						
	ASPT	0.673	0.504	0.800	0.708	0.503					
Revised Abundance-weighted	Score	**0.931**	**0.920**	0.625	**0.951**	**0.920**	0.670				
	TAXA	**0.939**	**0.999**	0.494	**0.958**	**1.000**	0.503	**0.929**			
	ASPT	0.504	0.415	0.602	0.514	0.414	0.672	0.708	0.414		
AWIC		-0.141	-0.035	-0.210	-0.197	-0.037	-0.439	-0.196	-0.037	-0.257	
LIFE		-0.017	-0.050	0.165	-0.020	-0.051	0.196	0.123	-0.051	0.481	-0.138

Table 14. Pearson correlations between the biotic indices (transformed where appropriate) based on single season samples for (a) raw values for all three datasets combined and (b) residual variation in index values among replicate samples after allowing for all site and season combination differences for the BAMS dataset. Correlation >0.9 highlighted in bold.

Indices which respond in the same way to physical, environmental and/or anthropogenic variation will tend have high correlations across a wide range of sites, for example, as found in this study for BMWP score and NTAXA. The independence, or lack or it, amongst indices, as indicates of general and specific stresses, is obviously of great importance in general bio-assessment.

However, within this project and especially WE5 and WE6 on assessing uncertainty, we restricted our interest to assessing the extent to which the sampling variability amongst these indices is correlated. Specifically, Table 14(b) gives the correlations between the residual values of each pair of indices after removing all differences in values due to site, year and season combination differences. To avoid involving the many sites/year/season combinations with no replication which would all have had zero residuals and inappropriately increased the apparent correlation amongst residuals, the correlations were based on the replicate residuals for the 16 BAMS sites.

The correlations among replicate residuals was very high between original BMWP score and TAXA (r = 0.947), but relatively low between TAXA and ASPT (*r* = 0.502). These residual correlations, first obtained by Furse *et al*. (1995 - their Table 5.2), were used to justify simulating independent random error terms for sampling variation in NTAXA and ASPT in the development of the uncertainty simulation algorithms used in RIVPACS III+, RPBATCH and to be used in the new RICT software (see project WFD72C WE1 Algorithms document deliverable for further details).

The residual (and raw) values of BMWP score and TAXA in their revised forms are all highly correlated; they are also highly correlated with the residual values for the original BMWP score and NTAXA (all *r* > 0.92) (Table 14). These high correlations between indices suggest that the revised forms of BMWP score and NTAXA are likely to give broadly similar EQI values to those obtained using the original BMWP scoring system for the vast majority of sites; however the changes in values may lead to some small improvements in estimates of river status.

4.6 Estimates of replicate sampling SD for single and combined season samples for all indices

The estimates of replicate sampling SD for each index (transformed as appropriate) were obtained using one-way analysis of variance (ANOVA) where each combination of site, year and season was treated as a separate factor level. The residual mean square then equates to overall estimate of the average replicate sampling variance across the whole dataset; the estimate of 'average' replicate SD is then the square root of this residual mean square. Separate estimates of replicate SD were derived for the 16 BAMS sites dataset and the 28 TAY sites dataset (Table 15).

This was done separately for all single season samples (regardless of season), for two-season combined samples (regardless of season combination) and for three-seasons combined samples (Table 15). It has already been shown for the BMWP indices (Clarke et al 2002) and for the LIFE index (Clarke et al 2003) that there were not consistent differences in replicate variability between seasons. Three-seasons combined replicate samples and thus estimates of their SD were only available for the BAMS dataset.

When based on either the BAMS or the Tay datasets, the estimates of replicate sampling SD are all smaller for two-season combined samples than for single season samples, and smaller for three-seasons combined samples compared to two-seasons combined samples (Table 15). This is as might be expected because combining information from two or more samples is, in a way, a form of averaging, and hence likely to reduce the effects of stochastic sampling (i.e. local spatial) variability on the taxonomic composition and thus any derived indices.

If the ANOVA are repeated on the combined datasets, the estimates of Replicate SD are very similar to those for the Tay dataset. This is because the majority (18) of the 28 Tay sites have four replicate samples in each of spring and autumn for each of five years (1990-1994), which means they provide the vast majority of the degrees of freedom and weight in the combined dataset estimates of replicate SD. Because the overall estimates of replicate SD are intended to be sued in the new RICT software to assess uncertainty across all river sites throughout the UK, we think it is best not to weight the estimates unduly towards just the sites in the relatively small Tay region. Therefore, the overall estimates of replicate SD for each index were obtained as weighted averages of the estimates for the two datasets given in Table 15 (a) and (b), where the two estimates were weighted by the number of sites sampled, namely 16 for BAMS and 28 for Tay; the weighted average estimates are given in Table 15(c).

		Transform scale	Number of seasons involved		
(a) 16 BAMS sites			1	2	3
Original BMWP	BMWP Score	√	0.588	0.418	0.361
	NTAXA	√	0.228	0.164	0.145
	ASPT		0.249	0.161	0.139
Revised BMWP Non-weighted	BMWP Score	√	0.576	0.411	0.357
	NTAXA	√	0.230	0.165	0.146
	ASPT		0.207	0.137	0.115
Revised BMWP Abundance-weighted	BMWP Score	√	0.600	0.448	0.418
	NTAXA	√	0.230	0.165	0.146
	ASPT		**0.305**	**0.239**	0.225
AWIC (family level)			0.144	0.108	0.095
LIFE (family level)			**0.326**	**0.239**	0.238
(b) 28 SEPA Tay sites			1	2	3
Original BMWP	BMWP Score	√	**0.668**	**0.487**	---
	NTAXA	√	**0.244**	**0.178**	---
	ASPT		**0.250**	**0.175**	---
Revised BMWP Non-weighted	BMWP Score	√	**0.685**	**0.510**	---
	NTAXA	√	**0.250**	**0.187**	---
	ASPT		**0.251**	**0.175**	---
Revised BMWP Abundance-weighted	BMWP Score	√	**0.682**	**0.505**	---
	NTAXA	√	**0.250**	**0.187**	---
	ASPT		0.262	0.179	---
AWIC (family level)			**0.167**	**0.115**	---
LIFE (family level)			0.202	0.135	---
(c) BAMS + SEPA Tay			1	2	3
Original BMWP	BMWP Score	√	0.639	0.462	0.361
	NTAXA	√	0.238	0.173	0.145
	ASPT		0.250	0.170	0.139
Revised BMWP Non-weighted	BMWP Score	√	0.645	0.474	0.357
	NTAXA	√	0.243	0.179	0.146
	ASPT		0.235	0.161	0.115
Revised BMWP Abundance-weighted	BMWP Score	√	0.652	0.484	0.418
	NTAXA	√	0.243	0.179	0.146
	ASPT		0.278	0.201	0.225
AWIC (family level)			0.159	0.112	0.095
LIFE (family level)			0.247	0.173	0.238

Table 15. Estimates of the Replicated sampling standard deviation (SDRep) of indices for either (1) single season samples or, 2- or 3- season combined samples based on (a) 28 SEPA Tay sites dataset, (b) 16 sites BAMS dataset and (c) weighted average (i.e. weighted by number of sites in dataset); highest of individual dataset estimates highlighted in bold; only BAMS dataset has 3-season combined replicate samples.

5. Estimates of temporal and other variability parameters for indices

5.1 Single season sample estimates of temporal variance parameters

5.1.1 Estimates based on SEPA, Tay and BAMS datasets combined

Estimation of within-season temporal variability in each index requires cases where RIVPACS samples have been taken on different dates within the same RIVPACS season (spring, summer or autumn). Such cases are only available for the 416 site SEPA dataset, where there are 181 situations where two (and in three cases three) sample were taken on different days (and usually months) within the same season of the same year.

Ideally, at these same sites and seasons, there would also be replicate samples taken on the same day, so that we could easily ‘subtract’ away the variability between samples on different days which was due to the fact that any two replicate samples vary. However, the 416 site SEPA dataset does not have any same-day sample replication. Therefore, to estimate the variance due to real within-season temporal variability, we needed to analyse the 416 sites SEPA dataset combined with the other datasets. We could have just combined the SEPA dataset with the Tay dataset, as both datasets are sites in Scotland which might be expected to make the sampling variability more similar. However, the 416 SEPA sites cover a much wider geographical and environmental range than the 28 Tay sites (Figure 12). For this reason, it was considered best to also include the 16 BAMS sites dataset, even though, as mentioned before, the 28 Tay sites were sampled in more years and thus carrying far greater weight in determining the overall estimate and replicate sampling SD.

In the future, the aim is make assessments of site ecological status based on average quality over a three-year period. The uncertainty in these estimates when all three years are not sampled will depend on inter-year variance in index values due to difference between years in the (unknown) average index values for each year. Therefore, we need to derive an estimate of inter-year variance parameter for three-year periods rather than over all years sampled at each site within the datasets. This was done by coding the years into three-year periods as follows: (1987-89, 1990-92, 1993-1995, 1996-98, 1999-2001, 2002-04).

The statistical estimation of parameters was carried out using a hierarchical model with the following variance components:

$SDRep^2$ Replicate sampling variance (Model: M5.1)
$SDTSeas^2$ Within-season temporal variance
$SDTYear^2$ Inter-year within 3-year period temporal variance
\+
$SDTPeriod^2$ Inter-period variance
$SDSite.Seas^2$ Variance due to differences between sites and season combinations

The last two parameters are of less interest and the Site by Season component could perhaps have been considered as a fixed effect factor, but their effect needed to allowed for to estimate the important three lower-level parameters.

This hierarchical variance model was fitted using the REML directive (Residual or Restricted maximum Likelihood) in the GENSTAT statistical software package (Genstat Release 8.1, 2005) treated all of the hierarchical sources of variation as random effects factors.

This analysis can only be done properly for all single season samples, as sampling on more than one day within a season was only available for more than season within the same year on four occasions – this is not enough to derive meaningful estimates of SDTSeas for two-season combined samples.

The estimates of each variance parameter obtained from the REML fits to each index model are provided in Table 16(a). The variance parameters are equal to the square of the equivalent SD parameter.

To assess the relative size of the three variance components which determine the total variance of index values in a typical three-year period, the components for replicate variance, within-seasonal temporal and inter-year variance are expressed as a percentage of their sum in table 16(b). Replicate sampling variance generally contributes just under half of the total variance within a 3-year period, ranging from 38% for (square root of) revised abundance-weighted BMWP score, to 55% for the family-level LIFE index.

It is useful to calculate the following parameter:

%TempSeas = estimate of percentage of total within-period temporal variance which is due to within-season temporal variability, as estimated from single season samples and given in Tables 16 and 17 for each index.

Estimates of this parameter, given in Table 16, highlight that the variance estimates for short term within-season temporal variability are, rather surprisingly, about the same or higher than the longer-tern inter-year temporal variance estimates for all indices except LIFE. This raises the concern held by us prior to any data analysis that any additional samples taken on a later date within the same season may be more likely to have been taken from a site if it was suspected, or known, that there was either some recent problem at the site, or the previous sample in that season was suspect. Thus the available data to estimate within-season temporal variance may not completely typical, but moreover may tend to over-estimate the typical/average within-season variance, which in tern would lead to some under-estimation of the true inter-year variance components. However, with that caveat, these estimates are the best available.

Table 16(c) gives the estimates of the SD parameters (obtained as the square roots of the equivalent variance terms). Estimates of SDRep, SDTSeas and SDTYear can be used in (Eq3.1) and (Eq3.2) to estimate the overall uncertainty SD (SDObs) associated with the estimate of the three-year average observed index value used to estimate the average EQR and ecological status class of the site for that 3-year period (see Section 3 for further details).

Equations (Eq3.1) and (Eq3.2) are the same as specified in the uncertainty section of the WFD72C algorithms deliverable provided to project manager Alan Croal and the RICT software programmers (latest version dated 07/12/07).

(a) Variance	Index	Var Rep	Var TSeas	Var TYear	Var TPeriod	Var Site.Seas
Original BMWP	√ Score	0.4320	0.2957	0.2746	0.2615	2.5196
	√ NTAXA	0.0578	0.0350	0.0365	0.0291	0.2154
	ASPT	0.0654	0.0596	0.0209	0.0359	0.7859
Revised BMWP Non-weighted	√ Score	0.4510	0.3682	0.3074	0.3516	2.8809
	√ NTAXA	0.0608	0.0446	0.0390	0.0391	0.2295
	ASPT	0.0617	0.0658	0.0171	0.0396	0.9748
Revised BMWP Abundance-weighted	√ Score	0.4490	0.4273	0.3091	0.3916	3.2213
	√ NTAXA	0.0608	0.0446	0.0390	0.0391	0.2295
	ASPT	0.0722	0.0780	0.0304	0.0589	1.2042
AWIC		0.0269	0.0262	0.0027	0.0078	0.2035
LIFE		0.0446	0.0139	0.0222	0.0132	0.2462
(b) % Variance		%Var Rep	%Var TSeas	%Var TYear	%Temp Seas	
Original BMWP	√ Score	43	30	27	52	
	√ NTAXA	45	27	28	49	
	ASPT	45	41	14	74	
Revised BMWP Non-weighted	√ Score	40	33	27	54	
	√ NTAXA	42	31	27	53	
	ASPT	43	45	12	79	
Revised BMWP Abundance-weighted	√ Score	38	36	26	58	
	√ NTAXA	42	31	27	53	
	ASPT	40	43	17	72	
AWIC		48	47	5	91	
LIFE		55	17	28	39	
(c) SD		SD Rep	SD TSeas	SD TYear	SD TPeriod	SD Site.Seas
Original BMWP	√ Score	0.657	0.544	0.524	0.511	1.587
	√ NTAXA	0.240	0.187	0.191	0.171	0.464
	ASPT	0.256	0.244	0.144	0.189	0.886
Revised BMWP Non-weighted	√ Score	0.672	0.607	0.554	0.593	1.697
	√ NTAXA	0.247	0.211	0.198	0.198	0.479
	ASPT	0.248	0.257	0.131	0.199	0.987
Revised BMWP Abundance-weighted	√ Score	0.670	0.654	0.556	0.626	1.795
	√ NTAXA	0.247	0.211	0.198	0.198	0.479
	ASPT	0.269	0.279	0.174	0.243	1.097
AWIC		0.164	0.162	0.052	0.088	0.451
LIFE		0.211	0.118	0.149	0.115	0.496

Table 16. Estimates of single season sample values for (a) variance and (c) SD (√Variance) parameters for within-season temporal variability (SDTSeas), inter-year variability (SDTYear), replicate sampling (SDRep) and other variance components based on all data from the BAMS, Tay and SEPA datasets combined; (b) gives variance components as a percentage of the average total variance (VarRep + VarTSeas + VarTYear) within three-year periods; %TempSeas = 100VarTSeas/(VarTSeas+VarTYear).

5.1.2 Estimates involving Northern Ireland monthly-sampled 12 sites dataset

In the previous sub-section 5.1.1, we highlighted our concern about potential over-estimation of the within-season temporal SD (SDTSeas) derived from the SEPA dataset (when combined with the Tay and BAMS replicated sample datasets). Our concern was that the occasions when samples were taken on more than one day in the same season at a site may often have been because of some perceived recent problem at the site and hence tend to over-estimate typical within-season variability.

Later in the WFD72C project, we received a new Community Change study dataset from Tommy McDermott containing monthly samples over a period of one year (Feb-Jan) at each of 12 sites in Northern Ireland. From this NI dataset, we extracted a sample in each of the three months in each of the three RIVPACS seasons, spring (Feb-May), summer (June-Aug), and autumn (Sep-Nov) at each of the 12 sites.

We then analysed this dataset using variance components analysis removing all site x season effects to provide an independent estimate of the average overall within-season variance (VarWSeas) or its SD equivalent (SDWSeas).

The overall variance within a season (VarWSeas) is the sum of the replicate sampling variance (VarRep) and the within-season temporal variance (VarTSeas), and therefore:

$\text{SDWSeas} = \sqrt{(\text{SDRep}^2 + \text{SDTSeas}^2)}$.

However, for the NI dataset, only a single sample was taken at each site in each month, so there is no information to separate replicate variance from within-season temporal variance; we can only estimate their combined effect (SDWSeas).

Table 17 compares the estimates of SDWSeas for each index based on the NI dataset with those given in Table 16(c) based on the combined Tay+SEPA+BAMS datasets.

		(a) SEPA+Tay+BAMS			(b) NI
Variance	Index	SD Rep	SD TSeas	SD WSeas	SD WSeas
Original BMWP	√ Score	0.657	0.544	0.853	1.127
	√ NTAXA	0.240	0.187	0.304	0.392
	ASPT	0.256	0.244	0.354	0.467
Revised BMWP Non-weighted	√ Score	0.672	0.607	0.906	1.125
	√ NTAXA	0.247	0.211	0.325	0.392
	ASPT	0.248	0.257	0.357	0.480
Revised BMWP Abundance-weighted	√ Score	0.670	0.654	0.936	1.172
	√ NTAXA	0.247	0.211	0.325	0.392
	ASPT	0.269	0.279	0.388	0.510
AWIC		0.164	0.162	0.231	0.280
LIFE		0.211	0.118	0.242	0.267

Table 17. Estimates of single season sample values for overall SD within a season (SDWSeas), based on the combined effect of replicate and within-season temporal variability, for (a) SEPA, Tay and BAMS datasets combined, and (b) NI monthly-sampled dataset.

The estimates of SDWSeas were actually higher for the NI dataset for each of the indices.

Assuming that replicate sampling SD is about the same for these 12 NI stream sites as for the average BAMS and Tay site, then we conclude that our previous estimates of within-season temporal SD based on the SEPA+ Tay+BAMS combined datasets may be reasonable and appropriate for use in assessing uncertainty.

5.2 Two-season combined sample estimates of temporal variance parameters

The 416 sites SEPA dataset contained 181 occasions when a sample was taken on more than one date within the same season of any one year at a site; this was used to estimate within-season-temporal variance and distinguish it from inter-year variance for estimates of uncertainty for single season sample. Neither the BAMS nor the Tay datasets had any cases where samples were taken on more than one day in the same season at a site.

Unfortunately, the were only four occasions in the 416 sites SEPA dataset when samples were taken at site on more than day within each of two seasons within any one year. This is not enough cases to derive a reliable estimate of within-season temporal variance for two-season combined samples.

Therefore, the estimates of the two temporal variance components, VarTSeas and VarTYear, must be derived indirectly. This was done by analysing all of the two-season combined samples from all three datasets combined, and using the REML directive in the Genstat statistical package to fit a hierarchical model with the following variance components:

$SDRep^2$ = VarRep = Replicate sampling variance
$SDTemp^2$ = VarTemp = Total temporal variance within a three year period (equal to $SDTSeas^2$ + $SDTYear^2$)
+
$SDTPeriod^2$ = VarTPeriod = Inter-period variance
$SDSite.Seas^2$ = VarVariance = Differences between sites and season combinations

In this case, the available data does not permit direct estimation of the two variance components, $SDTSeas^2$ and $SDTYear^2$, but only their sum, $SDTemp^2$.

Therefore, we decided that it was best to derive values for the two separate components by assuming that, for any particular index, the relative size of these two variances was the same for two-season combined samples as had been estimated for single season samples. Specifically, we estimate:

$$\text{VarTSeas} = \%\text{TempSeas} \times (\text{VarTemp})/100 \qquad \text{(Eq5.1)}$$

$$\text{VarTYear} = \text{Vartemp} - \text{VarTSeas} \qquad \text{(Eq5.2)}$$

where

VarTemp = estimate of total temporal variance for two season combined samples

and %TempSeas = estimate of percentage of total within-period temporal variance which is due to within-season temporal variability, as estimated from single season samples and given in Table 16 for each index.

Values of %TempSeas vary from 39% for LIFE to 91% for AWIC, but for the three forms of BMWP score and NTAXA, just over half of the total temporal variability within three periods is, on average, within-season variability, while for original and revised form ASPT indices, the equivalents percentages are 72-79%.

The estimates of VarTSeas and VarTYear, and thus SDTSeas and SDTYear, derived from equations (Eq5.1) and (Eq5.2), are given in Table 18.

(a) Variance	Index	Var Rep	VarTemp		Var TPeriod	Var Site.Seas
Original BMWP	√ Score	0.2260	0.3742		0.2275	3.0147
	√ NTAXA	0.0306	0.0421		0.0262	0.2538
	ASPT	0.0299	0.0487		0.0209	0.7281
Revised BMWP Non-weighted	√ Score	0.2430	0.3964		0.3096	3.4454
	√ NTAXA	0.0334	0.0476		0.0368	0.2693
	ASPT	0.0286	0.0435		0.0247	0.9288
Revised BMWP Abundance-weighted	√ Score	0.2450	0.4172		0.3552	4.0317
	√ NTAXA	0.0334	0.0476		0.0368	0.2693
	ASPT	0.0369	0.0542		0.0437	1.2701
AWIC		0.0130	0.0168		0.0053	0.1810
LIFE		0.0247	0.0196		0.0079	0.2629
(b) % Variance		%Var Rep	Var TSeas	Var TYear	%Temp Seas - from Table 16	
Original BMWP	√ Score	38	0.1946	0.1796	52	
	√ NTAXA	42	0.0206	0.0215	49	
	ASPT	38	0.0360	0.0127	74	
Revised BMWP Non-weighted	√ Score	38	0.2141	0.1823	54	
	√ NTAXA	41	0.0252	0.0224	53	
	ASPT	40	0.0344	0.0091	79	
Revised BMWP Abundance-weighted	√ Score	37	0.2420	0.1752	58	
	√ NTAXA	41	0.0252	0.0224	53	
	ASPT	41	0.0390	0.0152	72	
AWIC		44	0.0153	0.0015	91	
LIFE		56	0.0076	0.0120	39	
(c) SD		SD Rep	SD TSeas	SD TYear	SD TPeriod	SD Site.Seas
Original BMWP	√ Score	0.475	0.441	0.424	0.477	1.736
	√ NTAXA	0.175	0.144	0.147	0.162	0.504
	ASPT	0.173	0.190	0.112	0.144	0.853
Revised BMWP Non-weighted	√ Score	0.493	0.463	0.427	0.556	1.856
	√ NTAXA	0.183	0.159	0.150	0.192	0.519
	ASPT	0.169	0.185	0.096	0.157	0.964
Revised BMWP Abundance-weighted	√ Score	0.495	0.492	0.419	0.596	2.008
	√ NTAXA	0.183	0.159	0.150	0.192	0.519
	ASPT	0.192	0.197	0.123	0.209	1.127
AWIC		0.114	0.124	0.039	0.073	0.425
LIFE		0.157	0.087	0.109	0.089	0.513

Table 18. Estimates of two-season combined sample values for (a) variance and (c) SD (√Variance) parameters for within-season temporal variability (SDTSeas), inter-year variability (SDTYear), replicate sampling (SDRep) and other variance components based on all data from the BAMS, Tay and SEPA datasets combined; (b) %VarRep = Replicate variance as percentage of total variance (VarRep + VarTemp) within three-year periods.

5.3 Three-season combined sample estimates of temporal variance parameters

The logic, assumptions and procedures used to develop estimates of the two temporal variance components, VarTSeas and VarTYear, involved in the uncertainty of index values for two-season combined samples was extended to derive equivalent estimates of VarTSeas and VarTYear, and thus SDTSeas and SDTYear, for three-seasons combined samples (Table 19).

The REML fit of the hierarchical model (M5.1) to all available three season combined sample data gave estimates of parameters which were lower than their equivalent parameter values based on two-season combined samples (compare Tables 18 and 19), which as one might expect. Nonetheless, it is encouraging that the uncertainty parameter estimates are sufficiently precise not to mask any expected trends as the number of samples (1, 2 or 3) involved in determining an index value involved is increased

Surprisingly, the three-season combined sample estimates of temporal variability with a three-year period, after allowing for replicate sampling variability, is zero. This may be reasonable, but might be partly due to the complex dependence of the sampling variability in LIFE being partly dependent on the number of LIFE-scoring families present in the sample. Three-season combined samples covering a range of site qualities will have a very wide range in number of LIFE-scoring families present, which has not been allowed for in our overall hierarchical model which has only one assumed variance parameter for each hierarchical level, regardless of the site and number of taxa present.

(a) Variance	Index	Var Rep	VarTSeas + VarTYear		Var TPeriod	Var Site.Seas
Original BMWP	√ Score	0.1300	0.3437		0.1629	3.7391
	√ NTAXA	0.0209	0.0332		0.0194	0.3169
	ASPT	0.0194	0.0436		0.0092	0.7578
Revised BMWP Non-weighted	√ Score	0.1270	0.3898		0.2211	4.2867
	√ NTAXA	0.0210	0.0406		0.0296	0.3370
	ASPT	0.0133	0.0456		0.0086	0.9695
Revised BMWP Abundance-weighted	√ Score	0.1740	0.3562		0.2568	5.3482
	√ NTAXA	0.0210	0.0406		0.0296	0.3370
	ASPT	0.0504	0.0214		0.0261	1.5496
AWIC		0.0091	0.0126		0.0011	0.1725
LIFE		0.0456	0.0000		0.0036	0.3834
(b) % Variance		%Var Rep	Var TSeas	Var TYear	%Temp Seas - from Table 16	
Original BMWP	√ Score	38	0.1787	0.1650	52	
	√ NTAXA	42	0.0163	0.0169	49	
	ASPT	38	0.0322	0.0113	74	
Revised BMWP Non-weighted	√ Score	38	0.2105	0.1793	54	
	√ NTAXA	41	0.0215	0.0191	53	
	ASPT	40	0.0360	0.0096	79	
Revised BMWP Abundance-weighted	√ Score	37	0.2066	0.1496	58	
	√ NTAXA	41	0.0215	0.0191	53	
	ASPT	41	0.0154	0.0060	72	
AWIC		44	0.0115	0.0011	91	
LIFE		56	0	0	39	
(c) SD		SD Rep	SD TSeas	SD TYear	SD TPeriod	SD Site.Seas
Original BMWP	√ Score	0.361	0.423	0.406	0.404	1.934
	√ NTAXA	0.145	0.128	0.130	0.139	0.563
	ASPT	0.139	0.180	0.106	0.096	0.871
Revised BMWP Non-weighted	√ Score	0.356	0.459	0.423	0.470	2.070
	√ NTAXA	0.145	0.147	0.138	0.172	0.581
	ASPT	0.115	0.190	0.098	0.093	0.985
Revised BMWP Abundance-weighted	√ Score	0.417	0.455	0.387	0.507	2.313
	√ NTAXA	0.145	0.147	0.138	0.172	0.581
	ASPT	0.224	0.124	0.077	0.161	1.245
AWIC		0.095	0.107	0.034	0.032	0.415
LIFE		0.214	0.000	0.000	0.060	0.619

Table 19. Estimates of three-season combined sample values for (a) variance and (c) SD (√Variance) parameters for within-season temporal variability (SDTSeas), inter-year variability (SDTYear), replicate sampling (SDRep) and other variance components based on all data from the BAMS, Tay and SEPA datasets combined; (b) %VarRep = Replicate variance as percentage of total variance (VarRep + VarTemp) within three-year periods.

6. Deliverable: Table of recommended estimates of all replicate sampling and temporal variability parameters for use in the RICT software

The recommended set of uncertainty parameters estimates for each index for use in the RICT software are the estimates of replicate sampling SD parameter (SDRep) derived as a weighted average of the separate estimates for the 16 BAMS sites and 28 Tay sites datasets given in Table 15(c), together with the estimates of the temporal variability parameters, SDTSeas and SDTYear, given for single season samples in Table 16, two-season combined samples in Table 18 and three-seasons combined samples in Table 19.

All these parameter estimates are collected together in Table 20.

		Index	SD Rep	SD TSeas	SD TYear
(a) Single Season samples	Original BMWP	√ Score	0.657	0.544	0.524
		√ NTAXA	0.240	0.187	0.191
		ASPT	0.256	0.244	0.144
	Revised BMWP Non-weighted	√ Score	0.672	0.607	0.554
		√ NTAXA	0.247	0.211	0.198
		ASPT	0.248	0.257	0.131
	Revised BMWP Abundance-weighted	√ Score	0.670	0.654	0.556
		√ NTAXA	0.247	0.211	0.198
		ASPT	0.269	0.279	0.174
		AWIC	0.164	0.162	0.052
		LIFE	0.211	0.118	0.149
(b) Two-season Combined Samples	Original BMWP	√ Score	0.475	0.441	0.424
		√ NTAXA	0.175	0.144	0.147
		ASPT	0.173	0.190	0.112
	Revised BMWP Non-weighted	√ Score	0.493	0.463	0.427
		√ NTAXA	0.183	0.159	0.150
		ASPT	0.169	0.185	0.096
	Revised BMWP Abundance-weighted	√ Score	0.495	0.492	0.419
		√ NTAXA	0.183	0.159	0.150
		ASPT	0.192	0.197	0.123
		AWIC	0.114	0.124	0.039
		LIFE	0.157	0.087	0.109
(c) Three-season Combined Samples	Original BMWP	√ Score	0.361	0.423	0.406
		√ NTAXA	0.145	0.128	0.130
		ASPT	0.139	0.180	0.106
	Revised BMWP Non-weighted	√ Score	0.356	0.459	0.423
		√ NTAXA	0.145	0.147	0.138
		ASPT	0.115	0.190	0.098
	Revised BMWP Abundance-weighted	√ Score	0.417	0.455	0.387
		√ NTAXA	0.145	0.147	0.138
		ASPT	0.224	0.124	0.077
		AWIC	0.095	0.107	0.034
		LIFE	0.214	0.000	0.000

Table 20. Recommended estimates of SD parameters of each index for replicate sampling (SDRep), within-season temporal variability (SDTSeas) and inter-year variability (SDTYear) for (a) single season samples, (b) two-season combined samples and (c) three-season combined samples.

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6. APPENDICES

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Appendix I The 793 reference sites retained (out of the original 835 reference sites) and now available for model construction in this project

Appendix I The 793 reference sites retained (out of the original 835 reference sites) and now available for model construction in this project

Country	Site ID	River	Site
England	0101	Camel	Pencarrow Bridge
England	0103	Camel	Tuckingmill
England	0105	Camel	Helland Bridge
England	0107	Camel	Brocton
England	0181	DeLank River	Bradford
England	0185	DeLank River	Keybridge
England	0201	Axe	Mosterton
England	0203	Axe	Oathill Farm
England	0205	Axe	Broom
England	0207	Axe	Whitford Bridge
England	0221	Synderford	Venn Hill
England	0223	Blackwater	Beerhall
England	0225	Kit Brook	Kit Bridge
England	0227	Yarty	Crawley Bridge
England	0229	Yarty	Gammons Hill
England	0231	Corry Brook	Coryton
England	0233	Umbourne Brook	Easy Bridge
England	0301	Exe	Warren Farm
England	0303	Exe	Exford
England	0305	Exe	Edbrooke
England	0307	Exe	Exebridge
England	0309	Exe	Lythecourt
England	0311	Exe	Bramford Speke
England	0313	Exe	Flowerpot
England	0381	Barle	Goat Hill
England	0385	Barle	Cow Castle
England	0389	Barle	South Hill
England	0393	Barle	Pixton Hill
England	0401	Torridge	Fordmill Farm
England	0403	Torridge	Woodford Bridge
England	0405	Torridge	Kingsley Mill
England	0407	Torridge	Hele Bridge
England	0409	Torridge	Beaford Bridge
England	0411	Torridge	Great Torrington Town Mills
England	0501	Avill	Wheddon Cross
England	0503	Avill	Timberscombe
England	0505	Avill	Dunster
England	0601	Avon	Patney
England	0603	Avon	Rushall
England	0605	Avon	Bulford
England	0607	Avon	Stratford-sub-Castle
England	0609	Avon	Breamore
England	0610	Avon	Moortown
England	0613	Avon	Christchurch

Country	Site ID	River	Site
England	0701	Avon	Easton Grey
England	0703	Tetbury Avon	Brockenborough
England	0705	Avon	Cow Bridge
England	0707	Avon	Great Somerford
England	0709	Avon	Kellaway'S Weir
England	0711	Avon	Lacock
England	0713	Avon	Staverton Weir
England	0771	By Brook	Gatcombe Hill
England	0773	By Brook	Slaughterford
England	0775	By Brook	Ashley
England	0781	Avon	Washpool Bridge
England	0801	Avon Water	Wootton Bridge
England	0803	Avon Water	Gordleton Mill
England	0805	Avon Water	Efford Bridge
England	0901	Candover Brook	Abbotstone
England	0903	Itchen	Chilland
England	0905	Itchen	Itchen St.Cross
England	0907	Itchen	Otterbourne Water Works
England	0909	Itchen	d/s Chickenhall SDW
England	1001	Rother	u/s Liss STW
England	1003	Rother	Stodham Park
England	1005	Rother	Durford Bridge
England	1007	Rother	Stedham
England	1009	Rother	Selham
England	1011	Rother	Hardham
England	1013	Arun	Magpie Bridge
England	1081	Hammer's Pond Tributary	Carter's Lodge
England	1083	Rother	Hawkley Mill
England	1101	Dudwell	Burwash Weald
England	1109	Rother	Etchingham
England	1111	Rother	Udiam
England	1113	Rother	d/s Newenden
England	1201	Evenlode	Moreton-in-the-Marsh
England	1203	Evenlode	Evenlode
England	1207	Evenlode	Fawler
England	1209	Evenlode	Cassington
England	1301	Tilling Bourne	Wotton
England	1303	Tilling Bourne	u/s Albury Village
England	1305	Wey	Wyck
England	1307	Wey	Tilford
England	1309	Wey	Eashing
England	1311	Wey	Burpham
England	1403	Mimram	Codicote Bottom
England	1405	Mimram	Panshanger
England	1409	Lee	Meadgate
England	1411	Lee	Fisher's Green
England	1413	Lee	Enfield Weir
England	1807	Leadon	Ketford

Country	Site ID	River	Site
England	1809	Leadon	Upleadon
England	1901	Perry	Perry Farm
England	1903	Perry	Rednal Mill
England	1909	Perry	Mytton
England	2003	Blithe	Cresswell
England	2005	Blithe	Field
England	2007	Blithe	Newton
England	2009	Blithe	Hamstall Ridware
England	2103	Smite	Colston Bassett
England	2107	Devon	Knipton
England	2109	Devon	Bottesford
England	2111	Devon	Hawton
England	2201	Dove	Glutton Bridge
England	2203	Dove	Hartington
England	2205	Dove	Dove Dale
England	2207	Dove	u/s Rocester
England	2209	Dove	Sudbury
England	2301	Stambourne Brook	Great Yeldham
England	2303	Colne	d/s Hedingham STW
England	2305	Colne	Earl's Colne
England	2307	Colne	Fordstreet Bridge
England	2401	Great Eau	Ruckland
England	2403	Great Eau	Swaby
England	2405	Great Eau	Belleau
England	2409	Great Eau	Theddlethorpe-all-Saints
England	2505	Glen	Little Bytham
England	2509	Glen	South of Twenty
England	2513	Welland	Marston Trussel
England	2521	Welland	Tinwell
England	2523	Welland	Crowland
England	2601	Wensum	South Raynham
England	2605	Wensum	Great Ryburgh
England	2607	Wensum	Worthing
England	2609	Wensum	North of Elsing
England	2611	Wensum	Taverham
England	2619	Yare/Blackwater	North of Barford
England	2621	Yare/Blackwater	Earlham
England	2703	Hodder	Slaidburn
England	2705	Hodder	d/s Langden Brook
England	2707	Hodder	Higher Hodder Bridge
England	2709	Ribble/Gayle Beck	Cam End
England	2711	Ribble/Gayle Beck	Horton in Ribblesdale
England	2713	Ribble/Gayle Beck	Cleatop Barns
England	2715	Ribble/Gayle Beck	Halton Bridge
England	2717	Ribble/Gayle Beck	Sawley Bridge
England	2721	Ribble/Gayle Beck	Ribchester Bridge
England	2801	Dane	Hug Bridge
England	2901	Derwent	Grange-in-Borrowdale

Country	Site ID	River	Site
England	2903	Derwent	High Stock Bridge
England	2905	Derwent	Ouse Bridge
England	2907	Derwent	Cockermouth
England	2909	Derwent	Ribton Hall
England	2911	Derwent	Workington
England	3001	Ehen/Liza	Ennerdale Bridge
England	3003	Ehen/Liza	u/s Keekle
England	3005	Ehen/Liza	d/s Keekle
England	3007	Ehen/Liza	Braystones
England	3101	Derwent	Langdale End
England	3103	Derwent	West Ayton
England	3105	Derwent	Yedingham
England	3107	Derwent	Norton
England	3109	Derwent	Stamford Bridge
England	3111	Derwent	Thorganby
England	3141	Mill Beck	Bathingwell Wood
England	3144	Long Gill	Newgate Foot
England	3145	Halleykeld Spring Stream	Halleykeld Rigg
England	3150	Cowhouse Beck	Snaper House
England	3151	Mire Falls Gill	Reins Wood
England	3152	Sledhill Gill	Yowlass Wood
England	3153	Wheat Beck	Dale Head
England	3157	Holbeck	Hovingham Carrs
England	3160	Pickering Beck	Levisham
England	3162	Seph	Laskill
England	3163	Menethorpe Beck	Menethorpe
England	3166	Rye	Nunnington
England	3205	Esk	Lealholm
England	3207	Esk	Briggswath
England	3301	Swale	Keld
England	3303	Swale	Oxnop
England	3305	Swale	Grinton
England	3307	Swale	u/s Richmond
England	3311	Swale	Topcliffe
England	3313	Ouse/Ure	Aldwark Toll Bridge
England	3315	Ouse/Ure	Nether Poppleton
England	3317	Ouse/Ure	Acaster Malbis
England	3372	Cowside Beck	Nab End
England	3376	Cowside Beck	Arncliffe
England	3381	Wharfe	Hubberholme
England	3385	Wharfe	Grassington
England	3389	Wharfe	Addingham
England	3391	Gordale Beck	Seaty Hill
England	3393	Wharfe	Otley
England	3395	Gordale Beck	Gordale Bridge
England	3397	Wharfe	Wetherby
England	3401	Tees	Moorhouse
England	3403	Tees	Cauldron Snout

Country	Site ID	River	Site
England	3409	Tees	Gainford
England	3413	Tees	Over Dinsdale
England	3501	South Tyne	Dipper Bridge
England	3505	South Tyne	d/s Knarsdale
England	3511	South Tyne	Warden Bridge
England	3513	Tyne/North Tyne	Corbridge
England	3515	Tyne/North Tyne	Wylam
England	3581	South Tyne	South Tyne Head
England	3601	Wansbeck	Kirkwhelpington
England	3603	Wansbeck	Middleton
England	3605	Wansbeck	Meldon
England	3607	Wansbeck	Mitford Gauging Station
England	3609	Wansbeck	Bothal
England	5001	Otter	Fairhouse Farm
England	5003	Otter	Bidwell Farm
England	5005	Otter	Monkton
England	5007	Otter	Colhayes Farm
England	5009	Otter	Newton Poppleford
England	5101	Frome	Chantmarle
England	5103	Frome	Frampton
England	5105	Frome	Lower Bockhampton
England	5107	Frome	Moreton
England	5109	Frome	East Stoke
England	5183	Wool Stream	Wool
England	5201	Axe	Wookey Hole
England	5203	Axe	Bleadney
England	5207	Axe	Lower Weare
England	5301	Ober Water	Mill Lawn
England	5303	Ober Water	Puttles Bridge
England	5305	Highland Water	Millyford Bridge
England	5307	Lymington	Balmer Lawn
England	5309	Lymington	Boldre Bridge
England	5381	Ober Water	Vereley
England	5383	Bratley Water	Bratley
England	5385	Highland Water	Ocknell
England	5501	Stour/Great Stour	Stonebridge Green
England	5503	Stour/Great Stour	Little Chart Forstal
England	5505	Stour/Great Stour	Wye
England	5507	Stour/Great Stour	Milton Bridge
England	5509	Stour/Great Stour	Fordwich
England	5603	Lugg	Combe
England	5605	Lugg	Mortimer's Cross
England	5607	Lugg	Marlbrook
England	5609	Lugg	Wergin'S Bridge
England	5619	Wye	Bredwardine
England	5621	Wye	Huntsham Bridge
England	5623	Wye	Redbrook
England	5671	Monnow	Llanveynoe

Country	Site ID	River	Site
England	5673	Monnow	Clodock
England	5693	Arrow	Kington Urban
England	5695	Arrow	Folly Farm
England	5697	Arrow	Ivington
England	5841	Unnamed	Bredenbury
England	5844	Unnamed	Dunhampton Farm
England	5854	Back Brook	Kington
England	5855	Curl Brook	Pembridge
England	5856	Main Ditch	Leominster
England	5861	Hindwell Brook/Summergil Brook	Combe
England	5864	Lugg	Mordiford
England	6005	Blythe	Temple Balsall
England	6009	Blythe	Blythe Bridge
England	6101	Thet	Red Bridge, Shropham
England	6103	Thet	East Harling
England	6105	Thet	Nuns Bridge, Thetford
England	6107	Little Ouse	Brandon
England	6109	Little Ouse	Brandon Creek
England	6111	Ouse/Cam	Hilgay Bridge
England	6201	Unnamed	u/s Brackley
England	6213	Great Ouse	Sharnbrook
England	6215	Great Ouse	Roxton Lock
England	6242	Nine Wells Spring	Nine Wells
England	6258	Mill	Wendy
England	6261	Reach Lode	Upware Lock
England	6264	Rhee	Harston
England	6265	Ouse/Cam	Hauxton Mill
England	6285	Wissey	Linghills Farm
England	6289	Wissey	Didlington Lodge
England	6293	Wissey	Five Mile House
England	6381	Unnamed	Bonemills Hollow
England	6405	Brue	South Brewham
England	6409	Brue	Wyke
England	6413	Brue	Tootle Bridge
England	6417	Brue	Liberty Farm
England	6615	Severn	Stourport
England	6691	Dowles Brook	d/s Lem Brook
England	6693	Dowles Brook	u/s Dowles Manor
England	6701	Cannop Brook	Speculation
England	6801	Middlemarsh Stream	Grange Wood
England	6840	Unnamed	Gasper
England	6841	Unnamed	Woodlands Manor
England	6844	Unnamed	Lyon's Gate
England	6847	Unnamed	Farrington
England	6848	Unnamed	Woolland
England	6849	Unnamed	Okeford Fitzpaine
England	6856	Allen	Walford Mill
England	6857	Cale	Syles Farm

Country	Site ID	River	Site
England	6858	Stour	Trill Bridge
England	6862	Lydden	Bagber Bridge
England	6863	Stour	Spetisbury
England	6911	Thames/Isis	Malthouse
England	6913	Thames/Isis	Bablock Hythe
England	6915	Thames/Isis	Shillingford
England	6917	Thames/Isis	Reading
England	6919	Thames/Isis	Spade Oak
England	6921	Thames/Isis	Runnymede
England	6981	Loddon	Oliver's Battery
England	6985	Loddon	Sherfield on Loddon
England	6993	Enborne	Brimpton
England	7104	Moors/Crane	d/s Cranborne
England	7107	Moors/Crane	Great Rhymes Copse
England	7110	Moors/Crane	Pinnocks Moor
England	7113	Moors/Crane	Romford Bridge
England	7116	Moors/Crane	Redmans Hill
England	7119	Moors/Crane	Verwood
England	7122	Moors/Crane	King's Farm
England	7127	Moors/Crane	East Moors Farm
England	7143	Ed	Upper Farm
England	7145	Ed	Pains Moor
England	7149	Unnamed	In wood, u/s tributary
England	7153	Unnamed	d/s Wood
England	7189	Mannington Brook	Horton Heath
England	7192	Mannington Brook	Newman's Lane
England	7195	Mannington Brook	Penningston's Copse
England	8213	Teme	Brampton Bryan
England	8217	Teme	Tenbury
England	8221	Teme	Powick Bridge
England	8281	Clun	Whitcott Keysett
England	8285	Clun	Purslow
England	8305	Bure	Corpusty
England	8309	Bure	Whitehouse Farm Ford
England	8313	Bure	Buxton Mill
England	8317	Bure	Coltishall Bridge
England	8421	Test	Lower Brook
England	8425	Test	Romsey
England	8429	Test	Skidmore
England	8505	Piddle	Piddletrenthide
England	8509	Piddle	Druce
England	8513	Piddle	Brockhill Bridge
England	8517	Piddle	Wareham
England	8521	Bere Stream	Middle Bere
England	8605	Teign	Leigh Bridge
England	8609	Teign	Fingle Bridge
England	8613	Teign	Whetcombe Barton
England	8705	Fowey	Codda Ford

Country	Site ID	River	Site
England	8709	Fowey	Draynes Bridge
England	8713	Fowey	Leball Bridge
England	8805	Coombevalley Stream	Kilkhampton
England	8809	Coombevalley Stream	Coombe
England	9105	Hull/West Beck	Little Driffield
England	9109	Hull/West Beck	Wansford
England	9121	Kelk Beck/Frodingham Beck	Harpham
England	9205	Millburn Beck/Knock Ore Gill	Green Castle
England	9481	Walkham	Merrivale
England	9485	Walkham	Grenofen
England	9581	Lathkill	Alport
England	9603	Coquet	Carshope
England	9607	Coquet	Linshiels
England	9611	Coquet	Sharperton
England	9615	Coquet	Pauperhaugh
England	AN02	Cringle Brook	Thunderbridge
England	AN03	Reach Lode	Hallards Fen Road
England	AN04	Monk's Lode	Eternity Hall Bridge
England	AN05	Sixteen Foot Drain	Horseways Corner
England	AN06	Rase	Bully Hills
England	AN07	Waithe Beck	Kirmond Le Mire
England	AN08	Bain	Biscathorpe
England	AN09	Goulceby Beck	Goulceby
England	NH01	Till/Beamish	Etal
England	NH02	Till/Beamish	Chatton
England	NH03	Glen	Ewart
England	NH04	Glanton Burn	Rothill
England	NH05	Gate Burn	Framlington Gate
England	NH06	Kilton Beck	Lodge Wood
England	NH07	Balder	u/s Balderhead Reservoir
England	NH09	Wooler Water/Harthope Burn	Coronation Wood
England	NW01	Lune	Old Tebay
England	NW02	Lune	Rigmaden
England	NW03	Lune	Forge Wear
England	NW04	Eden	Temple Sowerby
England	NW05	Eden	Appleby
England	NW06	Eden	Warwick Bridge
England	SN02	Sutton Stream	Road Bridge
England	ST02	Severn	Isle Of Bicton
England	ST03	Sher Brook	Shugborough
England	ST04	Sence	Newton Linford
England	ST05	Derwent	Baslow
England	ST06	Derwent	Cromford Meadows
England	ST07	Wye	Ashford
England	SW01	Bodilly Stream	Bodilly Bridge
England	SW02	Drift/Newlyn River	Skimmel Bridge
England	SW04	Poltesco River	Poltesco Bridge
England	SW05	Stithians Stream	Searaugh Moor

Country	Site ID	River	Site
England	SW06	Trevaylor Stream	Trythogga
England	SW07	Gweek River	Mether-uny-Mill Bridge
England	SW08	Manaccan River	Polkanoggo
England	SW09	St.Keverne Stream	Porthoustock Bridge
England	TH01	Kennet	u/s Aldershot Water
England	TH02	Lambourn	Bagnor
England	TH03	Lyde River	Deanlands Farm
England	TH04	Coln	Fosse Bridge
England	TH05	Windrush	d/s Dickler
England	TH07	Ash	Easneye
England	TH08	Chess	u/s R. Colne
England	WE05	Morlas Brook	d/s Glyn Morlas
Wales	0007	Aber/Rhaeadr-fawr	Abergwyngregyn
Wales	1501	Gwendraeth Fach	Garn-Lwyd
Wales	1503	Gwendraeth Fach	Llangendeirne
Wales	1505	Gwendraeth Fach	u/s Kidwelly
Wales	1601	Teifi	Strata Florida
Wales	1603	Teifi	Tregaron Bog
Wales	1605	Teifi	Pont Gogoyan
Wales	1607	Teifi	Alltyblacca
Wales	1609	Teifi	Bangor Tyfi
Wales	1611	Teifi	Llechryd
Wales	1701	Clwyd	Melin-y-Wig
Wales	1703	Clwyd	Nantclwyd Hall
Wales	1705	Clwyd	Above Ruthin
Wales	1707	Clwyd	Glan-y-Wern
Wales	1709	Clwyd	Pont Llanerch
Wales	5601	Lugg	Monaughty
Wales	5613	Wye	Dolhelfa
Wales	5615	Wye	Llanwrthwl
Wales	5617	Wye	Hafodygarreg
Wales	5675	Monnow	Great Goytre
Wales	5677	Monnow	Rockfield
Wales	5681	Lugg	Crug
Wales	5691	Arrow	Kesty
Wales	5701	Usk	u/s Usk Reservoir
Wales	5703	Usk	d/s Usk Reservoir
Wales	5705	Usk	Trecastle
Wales	5707	Usk	Trallong
Wales	5709	Usk	Brecon Town Bridge
Wales	5711	Usk	Llandetty
Wales	5713	Usk	Crickhowell
Wales	5715	Usk	Llanellen Bridge
Wales	5717	Usk	Llantrissant
Wales	5801	Eastern Cleddau	Plasymeibion
Wales	5803	Eastern Cleddau	West of Llandissilio
Wales	5805	Eastern Cleddau	Llawhaden
Wales	5848	Unnamed	Glasnant

Country	Site ID	River	Site
Wales	5850	Unnamed	Crinfynydd
Wales	5851	Unnamed	Hill House Dingle
Wales	5852	Unnamed	Pen-Twyn
Wales	5881	Wern	Mynachlog-Ddu
Wales	5887	Western Cleddau	Wolf's Castle
Wales	5891	Western Cleddau	Treffgarne
Wales	5895	Western Cleddau	Crow Hill
Wales	5901	Dwyfach	Pant Glas
Wales	5903	Dwyfach	Pont y Felin
Wales	5905	Dwyfach	Bont Fechan
Wales	6501	Mounton Brook	Bully Hole Bottom
Wales	8205	Teme	Felindre
Wales	8209	Teme	Pennant Pound
Wales	ST01	Severn	Llandinam
Wales	WE01	Cynfal	Pont Newydd
Wales	WE03	Afon Caseg	Braichmelyn
Wales	WE04	Braint	Pont Mynach
Scotland	3701	Teith	Teith Bridge, Callander
Scotland	3703	Teith	Laighlands
Scotland	3704	Teith	Blackdub
Scotland	3705	Teith	Bridge of Teith, Doune
Scotland	3709	Forth	Aberfoyle Bridge
Scotland	3711	Forth	Parks of Garden
Scotland	3713	Forth	Kippen Bridge
Scotland	3715	Forth	Gargunnock Bridge
Scotland	3717	Forth	Drip Bridge
Scotland	3781	Caorainn Achaidh Burn	Comer
Scotland	3783	Allt Tairbh	Teapot
Scotland	3785	Green Burn	Dalmary
Scotland	3791	Balvag/Larig	Blaircreich
Scotland	3801	Tyne	Crichton
Scotland	3803	Tyne	Ormiston
Scotland	3805	Tyne	Easter Pencaitland
Scotland	3807	Tyne	Haddington Weir
Scotland	3809	Tyne	East Linton
Scotland	3903	Dee	Braemar
Scotland	3905	Dee	Balmoral
Scotland	3907	Dee	d/s Ballater
Scotland	3909	Dee	d/s Aboyne
Scotland	3911	Dee	Potarch Bridge
Scotland	3913	Dee	d/s Banchory
Scotland	3915	Dee	Cults
Scotland	4001	Spey	Garva Bridge
Scotland	4003	Spey	Laggan Bridge
Scotland	4005	Spey	Newtonmore
Scotland	4009	Spey	Boat of Garten
Scotland	4011	Spey	Grantown
Scotland	4013	Spey	Marypark

Country	Site ID	River	Site
Scotland	4017	Spey	Garmouth
Scotland	4101	Stinchar	Highbridge
Scotland	4103	Stinchar	d/s Dalquhairn
Scotland	4105	Stinchar	d/s Barr
Scotland	4107	Stinchar	Pinmore Bridge
Scotland	4109	Stinchar	d/s Colmonell
Scotland	4111	Stinchar	Ballantrae
Scotland	4201	Annan	Above Ericstane
Scotland	4203	Annan	Moffat
Scotland	4205	Annan	Newton Bridge
Scotland	4207	Annan	Millhouse Bridge
Scotland	4209	Annan	Williamwath Bridge
Scotland	4211	Annan	Brydekirk
Scotland	4301	Allt Coire Crubaidh	Allt Coire Crubaidh
Scotland	4303	Lair	Achnashellach Lodge
Scotland	4305	Fionn Abhainn	Fionn-Abhainn
Scotland	4307	Carron	d/s Loch Damhain
Scotland	4309	Carron	Craig
Scotland	4311	Carron	Balnacra
Scotland	4313	Carron	New Kelso
Scotland	4381	Carron	u/s Loch Sgamhain
Scotland	4401	Traligill	Glenbain
Scotland	4403	Loanan	d/s Loch Awe
Scotland	4405	Loanan	Inchnadamph
Scotland	4407	Inver	Little Assynt
Scotland	4601	Durness Stream	u/s Durness
Scotland	4701	Halladale	Forsinard Lodge
Scotland	4703	Halladale	Forsinain
Scotland	4705	Halladale	Millburn
Scotland	4707	Halladale	Golval
Scotland	4801	Burn of Aultachleven	u/s Loch Rangag
Scotland	4803	Little River	Tacher
Scotland	4805	Thurso	Westerdale
Scotland	4807	Thurso	Sordale
Scotland	4881	Unnamed	Achavanich
Scotland	4885	Unnamed	Westerdale
Scotland	4901	Tweed	Fingland
Scotland	4903	Tweed	Nether Rigs
Scotland	4905	Tweed	Kingledores
Scotland	4907	Tweed	Crownhead Bridge
Scotland	4911	Tweed	Old Tweed Bridge
Scotland	4913	Tweed	Dry Grange Bridge
Scotland	4915	Tweed	d/s Birgham
Scotland	4917	Tweed	Canny Island
Scotland	4971	Whiteadder Water	Cranshaws
Scotland	4975	Whiteadder Water	Preston Haugh
Scotland	4979	Whiteadder Water	u/s Allanton
Scotland	4983	Whiteadder Water	Chesterfield Ford

Country	Site ID	River	Site
Scotland	4987	Blackadder Water	Halliburton Bridge
Scotland	4991	Blackadder Water	Fogo
Scotland	4995	Blackadder Water	Blackadder Water Foot
Scotland	7001	Conon/Bran	Ledgowan
Scotland	7205	Cree	Wheeb Bridge
Scotland	7217	Cree	Newton Stewart
Scotland	7305	Strontian	Ariundle Oakwood NNR
Scotland	7311	Strontian	Anaheilt
Scotland	7405	Cnocloisgte Water	u/s Loch Caluim
Scotland	7413	Forss Water	Achalone
Scotland	7417	Forss Water	Crosskirk
Scotland	7505	Burn of Latheronwheel	Den Moss
Scotland	7511	Burn of Latheronwheel	Landhallow
Scotland	7705	Lunan Burn	Forneth
Scotland	8905	Brora	Dalnessie
Scotland	8909	Brora	u/s Balnacoil
Scotland	8913	Brora	d/s Loch Brora
Scotland	8925	Black Water	Pollie
Scotland	9009	Laxford	d/s Loch Stack
Scotland	9703	Bladnoch	Glassoch Bridge
Scotland	9711	Bladnoch	Spittal
Scotland	9903	Lusragan Burn	Cluny Villa
Scotland	CL02	Ayr	Nether Wellwood
Scotland	CL04	Ayr	Mainholm Ford
Scotland	CL05	Leven/Loch Lomond/Falloch	Keilator
Scotland	FO01	Cocklemill Burn	Kill Conquhar Mill
Scotland	FO02	Crail Burn	A917 Road Bridge
Scotland	FO03	Boghall Burn/Keil Burn	Pitcruvie Castle
Scotland	HI01	Finnan	Glen Finnan
Scotland	HI02	Foyers	Dalcrag
Scotland	HI03	Fechlin/Killin	Killin Lodge
Scotland	HI04	Spean	Corrie Coille
Scotland	HI05	Unnamed	Mon
Scotland	HI06	Unnamed	Craig Ghobhair
Scotland	HI07	Shiel	Shiel Bridge
Scotland	HI08	Arkaig/Dessarry	Strathan
Scotland	HI09	Meig	Bridgend
Scotland	HI10	Conon/Bran	Moy Bridge
Scotland	NE01	Lossie	Cloddach
Scotland	NE02	Lossie	u/s Blackburn
Scotland	NE03	Bervie Water	Inverbervie G.S.
Scotland	NE05	Carron Water	Tewel Ford
Scotland	NE06	Carron Water	Stonehaven
Scotland	SEPA_E01	Water of Ruchill	u/s Auchinner Bridge
Scotland	SEPA_E02	Invervar Burn	Invervar
Scotland	SEPA_E03	Tay/Dochart/Fillan/Cononish	Tayview House
Scotland	SEPA_E04	Tay/Dochart/Fillan/Cononish	1.5km u/s A9 Road Bridge
Scotland	SEPA_E05	Tay/Dochart/Fillan/Cononish	Pitnacree

Country	Site ID	River	Site
Scotland	SEPA_E06	Tay/Dochart/Fillan/Cononish	Boat of Murthly
Scotland	SEPA_E07	Tay/Dochart/Fillan/Cononish	Haugh of Kercock
Scotland	SEPA_E08	Tay/Dochart/Fillan/Cononish	Taymount Mains
Scotland	SEPA_E09	North Esk	Edzell
Scotland	SEPA_E10	North Esk	Galley Farm
Scotland	SEPA_N01	Shetland: Upper Loch of Brouster	Brouster
Scotland	SEPA_N03	Shetland:South Burn of Burrafirth	East Burrafirth
Scotland	SEPA_N04	Shetland: Burn of Sandwater	Stromfirth
Scotland	SEPA_N05	Shetland:Laxo/Gossawater	Laxo
Scotland	SEPA_N06	Shetland: Burn of Laxdale	North Voxter
Scotland	SEPA_N07	Unst: Burn of Mailand/Caldback	Stackhoull
Scotland	SEPA_N08	Yell: Laxa Burn	u/s B9081
Scotland	SEPA_N09	Yell: Easter Burn of Bouster	Bouster
Scotland	SEPA_N10	Yell:Burn of Arisdale	Hamnavoe
Scotland	SEPA_N11	Orkney: Hillside/Rusht	Deasbreck
Scotland	SEPA_N12	Orkney: Hillside/Rusht	Millgeo
Scotland	SEPA_N13	Orkney:Burn of Woodwick	Neigarth
Scotland	SEPA_N14	Orkney: Unnamed	Garth
Scotland	SEPA_N15	Orkney: Etheriegeo	Whitemire
Scotland	SEPA_N16	Orkney: Burn of Swartabeck	Harabreck
Scotland	SEPA_N17	Orkney: Hillside/Rusht	Kirbuster
Scotland	SEPA_N18	Orkney: Burn of Corrigal	Corrigal
Scotland	SEPA_N19	Hoy: South Burn	Glen
Scotland	SEPA_N20	Hoy: Withigill/Bailiefea	Burnhouse
Scotland	SEPA_N21	Rousay:Suso Burn	Sourin
Scotland	SEPA_N22	Skye:Sligachan	Sligachan
Scotland	SEPA_N23	Skye:Ose	Ose
Scotland	SEPA_N24	Skye:Snizort	Skeabost
Scotland	SEPA_N25	Skye:Snizort	B885
Scotland	SEPA_N26	Skye:Broadford River	Suardal
Scotland	SEPA_N27	Skye:Brittle	Leachd Thuilm
Scotland	SEPA_N28	Skye:Ord River	Minor Road
Scotland	SEPA_N29	Lewis:Airigh Sgridhe/Greeta/Abhainn Ghrioda	A859
Scotland	SEPA_N30	Lewis:Airigh Sgridhe/Greeta/Abhainn Ghrioda	A858
Scotland	SEPA_N31	Lewis: Tolsta Burn	B895
Scotland	SEPA_N32	Lewis: Abhainn a Loin	B8011
Scotland	SEPA_N33	Lewis: nan Torcan/Laxay	u/s Loch Valtos
Scotland	SEPA_N34	Lewis: Abhainn Geiraha	Port Geiraha
Scotland	SEPA_N35	Lewis: Abhainn Dhubh	d/s Loch Beag
Scotland	SEPA_N36	North Harris: Meavaig River	Meavaig
Scotland	SEPA_N37	North Harris: Scaladale River	A859
Scotland	SEPA_N39	South Harris: Laxdale	A859
Scotland	SEPA_N40	South Uist: Abhainn Roag	Snishival
Scotland	SEPA_N41	Dionard	Drochaidmhor
Scotland	SEPA_N42	Hope	Hope
Scotland	SEPA_N43	Hope	Strathmore
Scotland	SEPA_N44	Naver/Mudale/Meadie	Skelpick
Scotland	SEPA_N45	Naver/Mudale/Meadie	Syre

Country	Site ID	River	Site
Scotland	SEPA_N46	Naver/Mudale/Meadie	Altnaharra
Scotland	SEPA_N47	Meadie Burn	d/s Loch Meadie
Scotland	SEPA_N48	Clachan/nan Laogh	Unamed
Scotland	SEPA_N49	Kirkaig/Ledbeg	Inverkirkaig
Scotland	SEPA_N50	Allt nam Uamh	u/s River Loanan
Scotland	SEPA_N52	Carron/Abhainn a Ghlinne Mhoir	Amat
Scotland	SEPA_N53	Carron/Abhainn a Ghlinne Mhoir	Gledfield
Scotland	SEPA_N54	Kirkaig/Ledbeg	Rhisalach
Scotland	SEPA_N55	Ledmore/Loin Duibh	d/s Loch Borralan
Scotland	SEPA_N56	Ledmore/Loin Duibh	A837
Scotland	SEPA_N57	Dornoch Burn	u/s Camore
Scotland	SEPA_N58	Applecross/Allt Coire Attadale	Applecross
Scotland	SEPA_N59	Abhainn Bhuachaig	Tullich House
Scotland	SEPA_N60	Ewe/Kinlochewe River/Abhainn Bruach	Poolewe
Scotland	SEPA_N61	Beauly/Glass/Affric/Cam-ban	Forest Walk
Scotland	SEPA_N62	Enrick	Corrimony
Scotland	SEPA_N64	Moidart	u/s Brunery
Scotland	SEPA_N66	Croe	Innis a Chrotha
Scotland	SEPA_N67	Spean/Pattack/Chaoil-reidhe	Kinloch Laggan
Scotland	SEPA_N68	Coe	Pass of Glencoe
Scotland	SEPA_W01	Islay:Laggan/Barr	Storakaig
Scotland	SEPA_W02	Islay:Laggan/Barr	d/s Cattadale
Scotland	SEPA_W03	Islay:Laggan/Barr	Laggan Bridge
Scotland	SEPA_W04	Islay:Laggan/Barr	u/s Duich confluence
Scotland	SEPA_W05	Islay: Duich/Torra	Torra Bridge
Scotland	SEPA_W06	Islay: Duich/Torra	Drochaid Bheag
Scotland	SEPA_W07	Arran: Machrie Water	Monyquil
Scotland	SEPA_W08	Arran: Machrie Water	Machriewater Foot
Scotland	SEPA_W09	Arran:Sliddery Water	u/s Glenscorrodale
Scotland	SEPA_W10	Arran:Sliddery Water	Slidderywater Foot
Scotland	SEPA_W11	Mull:Aros River	u/s A848 Bridge
Scotland	SEPA_W12	Mull:Forsa	u/s Gaodhail
Scotland	SEPA_W13	Mull:Forsa	u/s A849 Bridge
Scotland	SEPA_W15	Mull:Coladoir River	A849 Bridge
Scotland	SEPA_W16	Mull: Allt an Lon Biolaireich	Allt an Lon Biolaireich
Scotland	SEPA_W17	Jura:Corran River	A846 Br
Scotland	SEPA_W18	Jura:Lussa River	Ardlussa Br
Scotland	SEPA_W19	Barbreck	A816 Bridge
Scotland	SEPA_W20	Allt Bragleenmore	Bragleenmore Farm Bridge
Scotland	SEPA_W21	Eachaig	Eckford
Scotland	SEPA_W22	Allt Maol Ruainidh	u/s A82 Bridge (Allt Maol)
Scotland	SEPA_W23	Etive	Kingshouse Hotel
Scotland	SEPA_W25	Etive	u/s Allt Mheuran
Scotland	SEPA_W26	Orchy/Water of Tulla	d/s Loch Tulla
Scotland	SEPA_W28	Orchy/Water of Tulla	Dalmally
Scotland	SEPA_W30	Orchy/Water of Tulla	A82 Bridge
Scotland	SEPA_W31	Abhainn Shira	Victoria Bridge
Scotland	SEPA_W33	Ruel	A886 Bridge

Country	Site ID	River	Site
Scotland	SEPA_W34	Ruel	A8003 Bridge
Scotland	SEPA_W35	Barr Water	Arnicle
Scotland	SEPA_W36	Barr Water	Glenbarr
Scotland	SEPA_W37	Carradale Water	u/s Auchenbreck
Scotland	SEPA_W38	Carradale Water	B842 Bridge
Scotland	SO01	Urr Water	Corsock
Scotland	SO02	Urr Water	Haugh of Urr
Scotland	SO03	Southwick Burn/Boreland Burn	Nr. Southwick House
Scotland	TA01	Earn	Forteviot
Scotland	TA02	Isla	Wester Cardean
Scotland	TA03	South Esk	Stannochy Bridge
Scotland	TA04	Braan	u/s Tay Confluence
Scotland	TA05	Prosen Water	Prosen Bridge
Scotland	TA06	Vinny Water	Pitmuies
Scotland	TA08	Kenly Water	Stravithie
Scotland	TW02	Tarth Water	Tarth Water Foot
Scotland	TW03	Eden Water	A6089 Bridge
N. Ireland	20100001	Foyle/Mourne/Strule/Camowen	Donnelly's Bridge
N. Ireland	20100003	Foyle/Mourne/Strule/Camowen	Moyle Bridge
N. Ireland	20100601	Derg	Aghyaran Bridge
N. Ireland	20100603	Derg	Crewe Bridge
N. Ireland	20100701	Owenkillew River/Broughderg Water	Killymore Bridge
N. Ireland	20100703	Owenkillew River/Broughderg Water	Monanameal Bridge
N. Ireland	20100801	Glenelly River	Clougherny Bridge
N. Ireland	20100901	Owenreagh River	Cashel Bridge
N. Ireland	20101001	Fairy Water	Mullanatoomog
N. Ireland	20101101	Drumragh River/Ballynahatty Water/O	Ballynahatty
N. Ireland	20101201	Quiggery Water/Routing Burn	Seskinore Mill Bridge
N. Ireland	20101203	Quiggery Water/Routing Burn	Edergoole Bridge
N. Ireland	20101301	Cloughfin River	Black Hill
N. Ireland	20200001	Faughan	Ardmore
N. Ireland	20200501	Roe	Corick Bridge
N. Ireland	20201001	Owenbeg River	Dungiven
N. Ireland	20201101	Owenrigh River	Carnanbane
N. Ireland	20300001	Bann/Lough Beg/Lough Neagh/Upper Ba	Ballydown
N. Ireland	20300003	Bann/Lough Beg/Lough Neagh/Upper Ba	Hilltown
N. Ireland	20300601	Aghadowey River	White Bridge
N. Ireland	20301101	Clady River	Glenone Bridge
N. Ireland	20301401	Moyola River	New Bridge
N. Ireland	20301601	Main/Clogh River	Glarryford Bridge
N. Ireland	20301603	Main/Clogh River	Dunmore Bridge
N. Ireland	20301801	Kells Water	Rock Bridge
N. Ireland	20301901	Braid River	Harryville Bridge
N. Ireland	20302101	Killagan Water	Dundermot Bridge
N. Ireland	20302201	Six Mile Water	Below Ballyclare
N. Ireland	20302301	Clady Water	Dunadry
N. Ireland	20302701	Doagh River	Dunamoy
N. Ireland	20302901	Ballinderry River	Ballinderry Bridge

Country	Site ID	River	Site
N. Ireland	20302903	Ballinderry River	Corkhill Bridge
N. Ireland	20302905	Ballinderry River	Doorless
N. Ireland	20303001	Lissan Water	Drumgrass Bridge
N. Ireland	20303101	Crumlin River	Airport Bridge
N. Ireland	20303401	Blackwater	Caledon Bridge
N. Ireland	20303405	Blackwater	Derrymeen Bridge
N. Ireland	20303801	Callan	Paper Mill Bridge
N. Ireland	20304101	Ballygawley Water	Lismore Bridge
N. Ireland	20304201	Fury River	Belalastera Bridge
N. Ireland	20304501	Cusher River	Knock Bridge
N. Ireland	20400001	Bush River	Seneirl Bridge
N. Ireland	20400003	Bush River	Ballyhoe
N. Ireland	20400201	Dervock River/Stracam River/Dougher	Iderown Bridge
N. Ireland	20400301	Glenshesk River	B15 Road Bridge
N. Ireland	20400701	Glenariff River	Callisnagh Bridge
N. Ireland	20400901	Glenarm River	Glenarm
N. Ireland	20500001	Larne River	Owens Bridge
N. Ireland	20500101	Glynn River/Glenoe Water	Glynn
N. Ireland	20500501	Lagan	Bulls Brook
N. Ireland	20501301	Quoile River/Annacloy River	Annacloy Bridge
N. Ireland	20600001	Shimna/Tollymore River	Tollymore Forest
N. Ireland	20600501	Annalong River	Annalong Bridge
N. Ireland	20600901	Cassy Water	Cassy Water Bridge
N. Ireland	20601301	Newry River	Carnmeen
N. Ireland	20601701	Kilcurry River/Forkhill River	Forkhill Lower Bridge
N. Ireland	23501101	Glen River	Garrison
N. Ireland	23600201	Garvary River	Larkhill
N. Ireland	23600301	Termon River	Killynoogan
N. Ireland	23600401	Bannagh River	Bannagh Bridge
N. Ireland	23600501	Kesh River/Glendurragh River	Ederny
N. Ireland	23600601	Ballycassidy/Ballinamallard River	Magheracross
N. Ireland	23600701	Sillees River	Drumkeen New Bridge
N. Ireland	23600703	Sillees River	Derrygonnelly
N. Ireland	23600801	Boho	Boho
N. Ireland	23600901	Arney River/Lough Macnean/Cornavann	Brockagh
N. Ireland	23601201	Black River	Drumkeenagh
N. Ireland	23601401	Colebrooke River	Tullyreagh Cross
N. Ireland	23601501	Finn River	Wattle Bridge
N. Ireland	NI_1	Douglas Burn	Lynnas Bridge
N. Ireland	NI_10	Granagh Burn	Carrickmore
N. Ireland	NI_11	Dunnyboe Burn	Dunnyboe Bridge
N. Ireland	NI_12	Owenalena	B84 Road Bridge
N. Ireland	NI_13	Inver River	Inver Bridge
N. Ireland	NI_14	Agivey River	Glen Ullin
N. Ireland	NI_15	Six Mile Water	Ballyboley Bridge
N. Ireland	NI_16	Legnagooly Burn	Legnagooly Bridge
N. Ireland	NI_17	Dunnstown Burn	Dunnstown
N. Ireland	NI_18	Cashel Burn	Downstream Bridge

Country	Site ID	River	Site
N. Ireland	NI_19	Ross Burn	Rossburn
N. Ireland	NI_2	Owenkillew River/Broughderg Water	Broughderg Bridge
N. Ireland	NI_20	Doagh R tributary	Dixons Corner
N. Ireland	NI_21	Kinnahalla River	U/S New Bridge
N. Ireland	NI_22	Shankys River	Tornamrock Park
N. Ireland	NI_23	Miltown Burn/Fallagoon Burn	A29 Road Bridge
N. Ireland	NI_25	Cam Burn	Ballynacally Beg
N. Ireland	NI_26	Coopers Water	Boomers Bridge
N. Ireland	NI_27	Begny Hill Feeder	Woodford Bridge
N. Ireland	NI_28	Gortin Water	Gortin Bridge
N. Ireland	NI_29	Douglas River	Boheradaile
N. Ireland	NI_3	Owenreagh River	B84 Road Bridge
N. Ireland	NI_30	Mayoghill River	Caheny Bridge
N. Ireland	NI_31	Spences River	Glassdrumman Bridge
N. Ireland	NI_32	Mullagh River	Mullagh Bridge
N. Ireland	NI_33	Kilnasaggart	Kilnasaggart Bridge
N. Ireland	NI_34	Coolaghty R	Coolaghty
N. Ireland	NI_35	Foxhill Burn	Drumcreen
N. Ireland	NI_36	Lisnabane Burn	Lisnabane Bridge
N. Ireland	NI_37	Lisblake Burn	Brockagh
N. Ireland	NI_38	Lack River	Croneen
N. Ireland	NI_39	Cooneen Water	Legatillida
N. Ireland	NI_4	Cloughfin River	Ballykeel Bridge
N. Ireland	NI_40	Cleen River	Kiltermon Bridge
N. Ireland	NI_5	Dreenan Burn	Dreenan Bridge
N. Ireland	NI_6	Tullynadall Burn	Tullynadall
N. Ireland	NI_7	Oughtmame Burn	Oughtmame
N. Ireland	NI_8	Glashagh Burn	Cashel Wood
N. Ireland	NI_9	Black Water	Carrickaness Bridge

Appendix II Biotic Indices

This appendix gives full details of the biotic indices used in the calculation of biotic indices at the RIVPACS reference sites and in the compilation of data for the errors and compares modules of the new Tool. Where possible a cited reference is also given.

ICMi indices for spring and autumn combined RIVPACS samples were supplied by John Murray-Bligh (Environment Agency). ICMi is complex and is not described here but details are available in the file: Instruction_text_ASTERICS.doc that can be obtained from John Murray-Bligh

Biological Monitoring Working Party (BMWP)

Reference: No definitive reference exists that gives the current scoring taxa, the artificial taxon composites, and the taxon scores for the 82 BMWP taxa

Indices:
BMWP (sum of scores)
NTAXA (count of scores)
ASPT (BMWP/NTAXA)

Family	Score
Planariidae (incl. Dugesiidae)	5
Dendrocoelidae	5
Neritidae	6
Viviparidae	6
Valvatidae	3
Hydrobiidae (incl. Bithyniidae)	3
Physidae	3
Lymnaeidae	3
Planorbidae (excl. Ancylidae)	3
Ancylus group	6
Unionidae	6
Sphaeriidae	3
Oligochaeta	1
Piscicolidae	4
Glossiphoniidae	3
Hirudinidae	3
Erpobdellidae	3
Astacidae	8
Asellidae	3
Corophiidae	6
Gammaridae (incl. Crangonyctidae & Niphargidae)	6
Siphlonuridae	10
Baetidae	4
Heptageniidae	10
Leptophlebiidae	10
Potamanthidae	10
Ephemeridae	10
Ephemerellidae	10
Caenidae	7
Taeniopterygidae	10
Nemouridae	7
Leuctridae	10
Capniidae	10
Perlodidae	10
Perlidae	10
Chloroperlidae	10
Platycnemididae	6
Coenagrionidae	6
Lestidae	8

Family	**Score**
Calopterygidae	8
Gomphidae	8
Cordulegastridae	8
Aeshnidae	8
Corduliidae	8
Libellulidae	8
Mesoveliidae	5
Hydrometridae	5
Gerridae	5
Nepidae	5
Naucoridae	5
Aphelocheiridae	10
Notonectidae	5
Pleidae	5
Corixidae	5
Haliplidae	5
Hygrobiidae	5
Dytiscidae (incl. Noteridae)	5
Gyrinidae	5
Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)	5
Scirtidae	5
Dryopidae	5
Elmidae	5
Sialidae	4
Rhyacophilidae (incl. Glossosomatidae)	7
Hydroptilidae	6
Philopotamidae	8
Psychomyiidae (incl. Ecnomidae)	8
Polycentropodidae	7
Hydropsychidae	5
Phryganeidae	10
Brachycentridae	10
Lepidostomatidae	10
Limnephilidae	7
Goeridae	10
Beraeidae	10
Sericostomatidae	10
Odontoceridae	10
Molannidae	10
Leptoceridae	10
Tipulidae	5
Simuliidae	5
Chironomidae	2

Acid Water Indicator Community (AWIC)

Reference: Davy-Bowker, J., Murphy J.F., Rutt G.P., Steel J.E.C. & Furse M.T. (2005) The development and testing of a macroinvertebrate biotic index for detecting the impact of acidity on streams. Archiv für Hydrobiologie 163: 383-403

Indices: AWIC (sum of scores/count of scores)

Family	**Score**
Planariidae (incl. Dugesiidae)	4
Valvatidae	6
Hydrobiidae (incl. Bithyniidae)	6
Physidae	6
Lymnaeidae	6
Planorbidae (excl. Ancylidae)	6
Ancylus group	6
Sphaeriidae	6
Oligochaeta	6
Piscicolidae	6
Glossiphoniidae	6
Erpobdellidae	6
Asellidae	6
Gammaridae (incl. Crangonyctidae & Niphargidae)	6
Baetidae	6
Heptageniidae	6
Leptophlebiidae	6
Ephemeridae	6
Ephemerellidae	6
Caenidae	6
Taeniopterygidae	2
Nemouridae	1
Leuctridae	1
Perlodidae	2
Perlidae	6
Chloroperlidae	1
Coenagrionidae	6
Calopterygidae	6
Corixidae	6
Haliplidae	6
Dytiscidae (incl. Noteridae)	6
Gyrinidae	3
Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)	6
Scirtidae	6
Elmidae	6
Sialidae	6
Rhyacophilidae (incl. Glossosomatidae)	6
Hydroptilidae	6
Philopotamidae	3

Family	Score
Psychomyiidae (incl. Ecnomidae)	6
Polycentropodidae	1
Hydropsychidae	4
Lepidostomatidae	2
Limnephilidae	4
Goeridae	4
Sericostomatidae	4
Odontoceridae	6
Leptoceridae	6
Tipulidae	4
Simuliidae	3
Chironomidae	4

Lotic Invertebrate Flow Evaluation (LIFE)

Reference: Extence C.A., Balbi D.M. & Chadd R.P. (1999) River flow indexing using British benthic macroinvertebrates: a framework for setting hydroecological objectives. Regulated Rivers: Research & Management, 15: 543-574.

Indices: LIFE (mean of fs scores weighted by Flow Group and $\log_{10}$ abundance)

Family	Flow Group
Planariidae	***4***
Dugesiidae	*4*
Dendrocoelidae	4
Neritidae	2
Viviparidae	3
Valvatidae	4
Hydrobiidae	***4***
Bithyniidae	*4*
Physidae	4
Lymnaeidae	4
Planorbidae	4
Ancylidae	***2***
Acroloxidae	*4*
Margaritiferidae	2
Unionidae	4
Sphaeriidae	4
Dreissenidae	4
Piscicolidae	2
Glossiphoniidae	4
Hirudinidae	4
Erpobdellidae	4
Agelinidae	5
Chirocephalidae	6
Triopsidae	6
Astacidae	2
Mysidae	5
Asellidae	4
Corophiidae	3
Talitridae	6
Gammaridae	***2***
Crangonyctidae	*4*
Siphlonuridae	4
Baetidae	2
Heptageniidae	1

Family	Flow Group
Leptophlebiidae	2
Potamanthidae	3
Ephemeridae	2
Ephemerellidae	2
Caenidae	4
Taeniopterygidae	2
Nemouridae	4
Leuctridae	2
Capniidae	1
Perlodidae	1
Perlidae	1
Chloroperlidae	1
Platycnemididae	4
Coenagrionidae	4
Lestidae	4
Calopterygidae	3
Gomphidae	2
Cordulegastridae	2
Aeshnidae	4
Corduliidae	4
Libellulidae	4
Mesoveliidae	5
Hebridae	4
Hydrometridae	4
Veliidae	4
Gerridae	4
Nepidae	5
Naucoridae	4
Aphelocheiridae	2
Notonectidae	4
Pleidae	4
Corixidae	4
Haliplidae	4
Hygrobiidae	5

Family	Flow Group
Dytiscidae	***4***
Noteridae	*4*
Gyrinidae	4
Hydrophilidae	***4***
Hydraenidae	*4*
Scirtidae	4
Elmidae	2
Sialidae	4
Osmylidae	2
Sisyridae	4
Rhyacophilidae	***1***
Glossosomatidae	*2*
Hydroptilidae	4
Philopotamidae	1
Psychomyiidae	***2***
Ecnomidae	*3*
Polycentropodidae	4
Hydropsychidae	2
Phryganeidae	4
Brachycentridae	2
Lepidostomatidae	2
Limnephilidae	4
Goeridae	1
Beraeidae	2
Sericostomatidae	2
Odontoceridae	1
Molannidae	4
Leptoceridae	4
Tipulidae	4
Ptychopteridae	2
Chaoboridae	5
Culicidae	5
Simuliidae	2
Syrphidae	5

* BMWP composites italicised. Where BMWP composite families were used, the first family was used (emboldened) and the other member of the composite was ignored – as recommended by Extence et al., (1999).

Flow Group	Flow Group Description	Log_{10} Abundance Category	Score (fs)
1	Rapid	A	9
2	Moderate/fast	A	8
3	Slow/sluggish	A	7
4	Flowing/standing	A	6
5	Standing	A	5
6	Drought resistant	A	4
1	Rapid	B	10
2	Moderate/fast	B	9
3	Slow/sluggish	B	7
4	Flowing/standing	B	5
5	Standing	B	4
6	Drought resistant	B	3
1	Rapid	C	11
2	Moderate/fast	C	10
3	Slow/sluggish	C	7
4	Flowing/standing	C	4
5	Standing	C	3
6	Drought resistant	C	2
1	Rapid	D	12
2	Moderate/fast	D	11
3	Slow/sluggish	D	7
4	Flowing/standing	D	3
5	Standing	D	2
6	Drought resistant	D	1
1	Rapid	E	12
2	Moderate/fast	E	11
3	Slow/sluggish	E	7
4	Flowing/standing	E	3
5	Standing	E	2
6	Drought resistant	E	1

Walley, Hawkes, Paisley, Trigg (WHPT)
(Non-Abundance Weighted & Abundance Weighted)

Reference: No definitive reference exists. This index supplied by email to John Davy-Bowker from John Murray-Bligh, 4th July 2007.

Indices:
Non-abundance weighted WHPT (sum of PO scores)
Non-abundance weighted NTAXA (count PO of scores)
Non-abundance weighted ASPT (WHPT /NTAXA)

Abundance weighted WHPT (sum of $AB_{1\text{-}4+}$ scores)
Abundance weighted NTAXA (count $AB_{1\text{-}4+}$ of scores)
Abundance weighted ASPT (WHPT /NTAXA)

		Log$_{10}$ Abundance weighted			
Family	**PO**	**AB1**	**AB2**	**AB3**	**AB4+**
Planariidae	4.90	4.70	5.40	5.40	5.4
Dugesiidae	2.90	2.80	3.10	3.10	3.1
Dendrocoelidae	3.00	3.00	2.60	2.60	2.6
Neritidae	6.40	6.40	6.50	6.90	6.9
Viviparidae	5.70	5.20	6.70	6.70	6.7
Valvatidae	3.20	3.30	3.10	2.70	2.7
Hydrobiidae	4.20	4.10	4.20	4.60	3.7
Bithyniidae	3.70	3.60	3.80	3.30	3.3
Physidae	2.40	2.70	2.00	0.40	0.4
Lymnaeidae	3.30	3.60	2.50	1.20	1.2
Planorbidae	3.10	3.20	3.00	2.40	2.4
Ancylidae	5.70	5.80	5.50	5.50	5.5
Acroloxidae	3.60	3.60	3.80	3.80	3.8
Unionidae	5.30	5.20	6.80	6.80	6.8
Sphaeriidae (Pea mussels)	3.90	4.40	3.50	3.40	2.3
Dreissenidae	3.70	3.70	3.70	3.70	3.7
Oligochaeta	2.70	3.60	2.30	1.40	-0.6
Piscicolidae	5.20	5.20	4.90	4.90	4.9
Glossiphoniidae	3.20	3.40	2.50	0.80	0.8
Hirudinidae	-0.80	-0.80	-0.80	-0.80	-0.8
Erpobdellidae	3.10	3.60	2.00	-0.80	-0.8
Astacidae	7.90	7.90	7.90	7.90	7.9
Asellidae	2.80	4.00	2.30	0.80	-1.6
Corophiidae	5.80	5.70	5.80	5.80	5.8
Crangonyctidae	3.90	3.80	4.00	3.60	3.6
Gammaridae	4.40	4.20	4.50	4.60	3.9
Niphargidae	6.30	6.30	6.30	6.30	6.3
Siphlonuridae	11.50	11.30	12.20	12.20	12.2
Baetidae	5.50	3.60	5.90	7.20	7.5
Heptageniidae	9.70	8.50	10.30	11.10	11.1
Leptophlebiidae	8.80	8.80	9.10	9.20	9.2
Potamanthidae	10.00	9.80	10.40	10.40	10.4
Ephemeridae	8.40	8.30	8.80	9.40	9.4
Ephemerellidae	8.20	7.90	8.50	9.00	9

		Log$_{10}$ Abundance weighted			
Family	**PO**	**AB1**	**AB2**	**AB3**	**AB4+**
Caenidae	6.50	6.50	6.50	6.50	6.5
Taeniopterygidae	11.30	11.00	11.90	12.10	12.1
Nemouridae	9.30	8.70	10.70	10.70	10.7
Leuctridae	10.00	9.30	10.60	10.60	10.6
Capniidae	9.60	9.70	9.40	9.40	9.4
Perlodidae	10.80	10.50	11.50	11.50	11.5
Perlidae	12.70	12.60	13.00	13.00	13
Chloroperlidae	11.60	11.40	12.20	12.20	12.2
Platycnemididae	6.00	6.00	6.00	6.00	6
Coenagriidae	3.50	3.40	3.80	3.80	3.8
Calopterygidae	6.00	5.90	6.20	6.20	6.2
Cordulegasteridae	9.80	9.80	9.80	9.80	9.8
Aeshnidae	4.70	4.70	4.70	4.70	4.7
Libellulidae	4.10	4.10	4.10	4.10	4.1
Mesoveliidae	4.70	4.70	4.70	4.70	4.7
Hydrometridae	4.30	4.30	4.30	4.30	4.3
Veliidae	4.50	4.50	3.90	3.90	3.9
Gerridae	5.20	5.20	5.50	5.50	5.5
Nepidae	2.90	2.90	2.90	2.90	2.9
Naucoridae	3.70	3.70	3.70	3.70	3.7
Aphelocheiridae	8.50	8.60	8.50	8.00	8
Notonectidae	3.40	3.40	3.90	3.90	3.9
Pleidae	3.30	3.30	3.30	3.30	3.3
Corixidae	3.80	3.70	3.90	3.70	3.7
Haliplidae	3.60	3.60	3.40	3.40	3.4
Hygrobiidae	3.80	3.80	3.80	3.80	3.8
Noteridae	3.20	3.20	3.20	3.20	3.2
Dytiscidae	4.50	4.50	4.80	4.80	4.8
Gyrinidae	8.20	8.10	9.00	9.00	9
Hydrophilidae	6.20	5.80	8.80	8.80	8.8
Hydraenidae	8.90	8.50	10.50	10.50	10.5
Scirtidae	6.90	6.90	6.80	6.80	6.8
Dryopidae	6.00	6.00	6.00	6.00	6
Elmidae	6.60	5.30	7.40	8.30	8.3
Sialidae	4.30	4.20	4.40	4.40	4.4
Sisyridae	5.70	5.70	5.70	5.70	5.7
Rhyacophilidae	8.40	8.10	9.20	8.30	8.3
Glossosomatidae	7.70	7.80	7.60	7.20	7.2
Hydroptilidae	6.20	6.10	6.50	6.80	6.8
Philopotamidae	11.20	11.20	11.10	11.10	11.1
Psychomyiidae	5.80	5.80	5.70	5.70	5.7
Polycentropodidae	8.10	8.20	8.10	8.10	8.1
Hydropsychidae	6.60	5.80	7.20	7.40	7.4
Phryganeidae	5.50	5.50	5.50	5.50	5.5
Brachycentridae	9.50	9.60	9.50	8.90	8.9
Lepidostomatidae	10.10	9.90	10.30	10.20	10.2

		Log$_{10}$ Abundance weighted			
Family	**PO**	**AB1**	**AB2**	**AB3**	**AB4+**
Limnephilidae	6.20	5.90	6.90	6.90	6.9
Goeridae	8.80	8.80	8.80	9.40	9.4
Beraeidae	8.70	8.80	7.30	7.30	7.3
Sericostomatidae	9.10	8.90	9.40	9.50	9.5
Odontoceridae	11.00	11.10	10.30	10.30	10.3
Molannidae	6.60	6.50	7.60	7.60	7.6
Leptoceridae	6.70	6.70	6.90	7.10	7.1
Tipulidae	5.90	5.40	6.90	6.90	7.1
Psychodidae	4.40	4.50	3.00	3.00	3
Ptychopteridae	6.40	6.40	6.40	6.40	6.4
Dixidae	7.00	7.00	7.00	7.00	7
Chaoboridae	3.00	3.00	3.00	3.00	3
Culicidae	2.00	2.00	1.90	1.90	1.9
Ceratopogonidae	5.50	5.40	5.50	5.50	5.5
Simuliidae	5.80	5.50	6.10	5.80	3.9
Chironomidae	1.10	1.20	1.30	-0.90	-0.9
Stratiomyidae	3.60	3.60	3.60	3.60	3.6
Rhagionidae	9.60	9.60	9.60	9.60	9.6
Tabanidae	7.10	7.10	7.30	7.30	7.3
Athericidae	9.30	9.30	9.50	9.50	9.5
Empididae	7.10	7.00	7.60	7.60	7.6
Dolichopodidae	4.90	4.90	4.90	4.90	4.9
Syrphidae	1.90	1.90	1.90	1.90	1.9
Sciomyzidae	3.40	3.40	3.40	3.40	3.4
Ephydridae	4.40	4.40	4.40	4.40	4.4
Muscidae	3.90	4.00	2.60	2.60	2.6
BMWP Composite taxa*					
Planariidae (incl. Dugesiidae)	5.0	4.8	5.4	5.3	5.3
Hydrobiidae (Incl. Bithyniidae)	4.2	4.1	4.2	4.5	3.7
Ancylidae (incl. Acroloxidae)	5.8	5.9	5.6	5.4	5.4
Gammaridae (incl. Crangonyctidae & Niphargidae)	4.5	4.3	4.7	4.7	3.9
Dytiscidae (incl. Noteridae)	4.7	4.7	5.0	5.0	5.0
Hydrophilidae (incl. Hydraenidae)	7.4	7.0	9.5	9.5	9.5
Rhyacophilidae (incl. Glossosomatidae)	8.2	7.9	8.8	7.5	7.5
Psychomyiidae (incl. Ecnomidae)	5.9	5.9	5.8	5.8	5.8

* BMWP composites italicised. Where BMWP composite families were used, the distinct families are ignored, as recommended by John Murray-Bligh, 4th July 2007, NB – Ecnomidae, as a distinct family do not score.

Appendix III The 63 NBN codes newly created by CEH

Appendix III The 63 NBN codes newly created by CEH

NBN Code	NBN Name
<NEW-CODE>100001	Polycelis nigra group
<NEW-CODE>100002	Dugesia polychroa group
<NEW-CODE>100004	Anodonta group
<NEW-CODE>100005	Lumbriculus group
<NEW-CODE>100006	Nais communis group
<NEW-CODE>100007	Nais simplex group
<NEW-CODE>100008	Thalassodrilus prostatus
<NEW-CODE>100011	Baetis scambus group
<NEW-CODE>100012	Heptagenia lateralis
<NEW-CODE>100013	Caenis pseudorivulorum group
<NEW-CODE>100014	Caenis luctuosa group
<NEW-CODE>100015	Nemoura cambrica group
<NEW-CODE>100016	Coenagrion puella group
<NEW-CODE>100019	Gyrinus natator group
<NEW-CODE>100020	Anacaena lutescens
<NEW-CODE>100022	Agrypnia obsoleta group
<NEW-CODE>100025	Micropterna group
<NEW-CODE>100026	Potamophylax group
<NEW-CODE>100029	Tipula (Savtshenkia) signata group
<NEW-CODE>100030	Tipula (Yamatotipula) montium group
<NEW-CODE>100033	Pedicia (Pedicia) group
<NEW-CODE>100034	Pericoma trivialis group
<NEW-CODE>100036	Dixa maculata complex
<NEW-CODE>100038	Simulium angustitarse group
<NEW-CODE>100039	Simulium cryophilum group
<NEW-CODE>100040	Simulium vernum group
<NEW-CODE>100041	Simulium aureum group
<NEW-CODE>100042	Simulium argyreatum group
<NEW-CODE>100043	Simulium ornatum group
<NEW-CODE>100046	Thienemannimyia group
<NEW-CODE>100047	Zavrelimyia group
<NEW-CODE>100048	Potthastia gaedii group
<NEW-CODE>100049	Potthastia longimana group
<NEW-CODE>100050	Eukiefferiella group
<NEW-CODE>100051	Cricotopus group
<NEW-CODE>100052	Hydrobaenus group
<NEW-CODE>100055	Micropsectra group
<NEW-CODE>100057	Stempellinella group
<NEW-CODE>100059	Tabanus group
<NEW-CODE>100060	Chelifera group
<NEW-CODE>100061	Hemerodromia group
<NEW-CODE>100064	Clinocerinae
<NEW-CODE>100067	Planariidae (incl. Dugesiidae)
<NEW-CODE>100068	Hydrobiidae (incl. Bithyniidae)
<NEW-CODE>100069	Ancylidae (incl. Acroloxidae)
<NEW-CODE>100070	Gammaridae (incl. Crangonyctidae & Niphargidae)
<NEW-CODE>100071	Dytiscidae (incl. Noteridae)
<NEW-CODE>100072	Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)
<NEW-CODE>100073	Rhyacophilidae (incl. Glossosomatidae)
<NEW-CODE>100074	Psychomyiidae (incl. Ecnomidae)
<NEW-CODE>100075	Enchytraeidae (incl. Propappidae)
<NEW-CODE>100076	Pristina (Pristinella) sp.
<NEW-CODE>100081	Lumbricidae (incl. Glossoscolecidae)
<NEW-CODE>100082	Einfeldia group
<NEW-CODE>100083	Endochironomus group
<NEW-CODE>100101	Ameletidae
<NEW-CODE>100103	Helophoridae
<NEW-CODE>100105	Hydrochidae
<NEW-CODE>100106	Apataniidae
<NEW-CODE>100110	Siphlonuridae (incl. Ameletidae)
<NEW-CODE>100111	Limnephilidae (incl. Apataniidae)
<NEW-CODE>100112	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)
<NEW-CODE>100114	Hydrophilidae (incl. Helophoridae, Georissidae & Hydrochidae)

Appendix IV Treatment of artificial ‘families’ within RIVPACS IV (in Furse taxonomy)

Appendix IV Treatment of artificial ‘families’ within RIVPACS IV (in Furse taxonomy)

TL1 - “BMWP family” level	**TL2 “Revised BMWP” (WHPT) Families**	**TL3 – “All Families”**
Planariidae (including Dugesiidae)	Planariidae	Planariidae
	Dugesiidae	Dugesiidae
Hydrobiidae (including Bithyniidae)	Hydrobiidae	Hydrobiidae
	Bithyniidae	Bithyniidae
Planorbidae (excluding Ancylus group)	Planorbidae (excluding Ancylus group)	*Planorbidae (excluding Ancylus group)*
Ancylus group (including Acroloxidae)	*Ancylus group*	Ancylus group
	Acroloxidae	Acroloxidae
Gammaridae (including Crangonyctidae and Niphargidae)	Gammaridae	Gammaridae
	Crangonyctidae	Crangonyctidae
	Niphargidae	Niphargidae
Heptageniidae[1]	Heptageniidae[1]	Heptageniidae[1]
Siphlonuridae (including Ameletidae)	Siphlonuridae (including Ameletidae)	Siphlonuridae
		Ameletidae
Dytiscidae (including Noteridae)	Dytiscidae	Dytiscidae
	Noteridae	Noteridae
Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)	Hydrophilidae (incl. Helophoridae, Georissidae & Hydrochidae)	Hydrophilidae
		Hydrochidae
		Georissidae
		Hydraenidae
	Hydraenidae	Helophoridae
Rhyacophilidae (including Glossosomatidae)	Rhyacophilidae	Rhyacophilidae
	Glossosomatidae	Glossosomatidae
Psychomyiidae (including Ecnomidae)	Psychomyiidae	Psychomyiidae
	n/a	Ecnomidae
Limnephilidae (including Apataniidae)	Limnephilidae (including Apataniidae)	Limnephilidae
		Apataniidae
Tipulidae (including Limoniidae, Cylindrotomidae and Pediciidae)	Tipulidae (including Limoniidae, Cylindrotomidae and Pediciidae)	Tipulidae
		Limoniidae
		Cylindrotomidae
		Pediciidae

[1] Heptageniidae (including Arthropleidae) - Arthropleidae regarded as extinct and all modern records are assumed to be the Heptageniidae

Appendix V Taxonomic Level 1 – The 78 “BMWP family” level taxa in RIVPACS IV

Appendix V Taxonomic Level 1 – The 78 "BMWP family" level taxa in RIVPACS IV

Rev. Maitland Code	Rev. Maitland Name	Furse Code	Furse Name	NBN Code	NBN Name
05130000	Dendrocoelidae	05130000	Dendrocoelidae	NBNSYS0000042255	Dendrocoelidae
051Z0000	Planariidae (incl. Dugesiidae)	051Z0000	Planariidae (including Dugesiidae)	<NEW-CODE>100067	Planariidae (incl. Dugesiidae)
16110000	Neritidae	16110000	Neritidae	NBNSYS0000160519	Neritidae
16120000	Viviparidae	16120000	Viviparidae	NBNSYS0000161255	Viviparidae
16130000	Valvatidae	16130000	Valvatidae	NBNSYS0000042348	Valvatidae
161Z0000	Hydrobiidae (incl. Bithyniidae)	161Z0000	Hydrobiidae (including Bithyniidae)	<NEW-CODE>100068	Hydrobiidae (incl. Bithyniidae)
16210000	Physidae	16210000	Physidae	NBNSYS0000160706	Physidae
16220000	Lymnaeidae	16220000	Lymnaeidae	NBNSYS0100003744	Lymnaeidae
16230000	Planorbidae	162X0000	Planorbidae (excluding Ancylus group)	NBNSYS0000050415	Planorbidae
162Z0000	Ancylidae (incl. Acroloxidae)	162Z0000	Ancylus group (incl. Acroloxidae)	<NEW-CODE>100069	Ancylidae (incl. Acroloxidae)
17120000	Unionidae	17120000	Unionidae	NBNSYS0000161229	Unionidae
17130000	Sphaeriidae	17130000	Sphaeriidae	NBNSYS0100015301	Sphaeriidae (Pea mussels)
20000000	Oligochaeta	20000000	Oligochaeta	NBNSYS0000022328	Oligochaeta
22110000	Piscicolidae	22110000	Piscicolidae	NBNSYS0000160725	Piscicolidae
22120000	Glossiphoniidae	22120000	Glossiphoniidae	NHMSYS0000068846	Glossiphoniidae
22210000	Hirudinidae	22210000	Hirudinidae	NBNSYS0000160169	Hirudinidae
22310000	Erpobdellidae	22310000	Erpobdellidae	NBNSYS0000042263	Erpobdellidae
34310000	Astacidae	34310000	Astacidae	NBNSYS0000159453	Astacidae
36110000	Asellidae	36110000	Asellidae	NBNSYS0000040168	Asellidae
37110000	Corophiidae	37110000	Corophiidae	NBNSYS0000159759	Corophiidae
371Z0000	Gammaridae (incl. Crangonyctidae & Niphargidae)	371Z0000	Gammaridae (including Crangonyctidae and Niphargidae)	<NEW-CODE>100070	Gammaridae (incl. Crangonyctidae & Niphargidae)
40120000	Baetidae	40120000	Baetidae	NHMSYS0000066929	Baetidae
40130000	Heptageniidae	40130000	Heptageniidae	NHMSYS0000066933	Heptageniidae
401Z0000	Siphlonuridae (incl. Ameletidae)	401Z0000	Siphlonuridae (including Ameletidae)	<NEW-CODE>100110	Siphlonuridae (incl. Ameletidae)
40210000	Leptophlebiidae	40210000	Leptophlebiidae	NHMSYS0000066934	Leptophlebiidae
40310000	Potamanthidae	40310000	Potamanthidae	NHMSYS0000066935	Potamanthidae
40320000	Ephemeridae	40320000	Ephemeridae	NHMSYS0000066932	Ephemeridae
40410000	Ephemerellidae	40410000	Ephemerellidae	NHMSYS0000066931	Ephemerellidae
40510000	Caenidae	40510000	Caenidae	NHMSYS0000066930	Caenidae
41110000	Taeniopterygidae	41110000	Taeniopterygidae	NBNSYS0000161088	Taeniopterygidae
41120000	Nemouridae	41120000	Nemouridae	NBNSYS0000042302	Nemouridae
41130000	Leuctridae	41130000	Leuctridae	NBNSYS0000160305	Leuctridae
41140000	Capniidae	41140000	Capniidae	NBNSYS0000159582	Capniidae
41210000	Perlodidae	41210000	Perlodidae	NBNSYS0000042311	Perlodidae
41220000	Perlidae	41220000	Perlidae	NBNSYS0000160662	Perlidae
41230000	Chloroperlidae	41230000	Chloroperlidae	NBNSYS0000159672	Chloroperlidae
42110000	Platycnemididae	42110000	Platycnemididae	NBNSYS0000160735	Platycnemididae
42120000	Coenagriidae	42120000	Coenagrionidae	NBNSYS0000159733	Coenagriidae
42140000	Calopterygidae	42140000	Calopterygidae	NBNSYS0100009819	Calopterygidae
42210000	Gomphidae	42210000	Gomphidae	NBNSYS0000189701	Gomphidae
42220000	Cordulegasteridae	42220000	Cordulegastridae	NBNSYS0000159754	Cordulegasteridae
42230000	Aeshnidae	42230000	Aeshnidae	NBNSYS0000159316	Aeshnidae
42250000	Libellulidae	42250000	Libellulidae	NBNSYS0000160307	Libellulidae
43110000	Mesovelidae	43110000	Mesoveliidae	NBNSYS0100013065	Mesoveliidae
43210000	Hydrometridae	43210000	Hydrometridae	NBNSYS0000160190	Hydrometridae

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
43230000	Gerridae	43230000	Gerridae	NBNSYS0000040170	Gerridae
43310000	Nepidae	43310000	Nepidae	NBNSYS0000160516	Nepidae
43410000	Naucoridae	43410000	Naucoridae	NBNSYS0000160500	Naucoridae
43420000	Aphelocheiridae	43420000	Aphelocheiridae	NBNSYS0000159394	Aphelocheiridae
43510000	Notonectidae	43510000	Notonectidae	NBNSYS0000039904	Notonectidae
43610000	Corixidae	43610000	Corixidae	NBNSYS0000040176	Corixidae
45110000	Haliplidae	45110000	Haliplidae	NBNSYS0000007492	Haliplidae
45150000	Gyrinidae	45150000	Gyrinidae	NBNSYS0000040169	Gyrinidae
451Z0000	Dytiscidae (incl. Noteridae)	451Z0000	Dytiscidae (including Noteridae)	<NEW-CODE>100071	Dytiscidae (incl. Noteridae)
453Z0000	Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)	453Z0000	Hydrophilidae (including Hydraenidae, Helophoridae, Georissidae and Hydrochidae)	<NEW-CODE>100072	Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)
45510000	Scirtidae	45510000	Scirtidae	NBNSYS0000160955	Scirtidae
45620000	Dryopidae	45620000	Dryopidae	NBNSYS0000159891	Dryopidae
45630000	Elmidae	45630000	Elmidae	NBNSYS0000007782	Elmidae
46110000	Sialidae	46110000	Sialidae	NBNSYS0000160993	Sialidae
48130000	Hydroptilidae	48130000	Hydroptilidae	NBNSYS0000042282	Hydroptilidae
481Z0000	Rhyacophilidae (incl. Glossosomatidae)	481Z0000	Rhyacophilidae (including Glossosomatidae)	<NEW-CODE>100073	Rhyacophilidae (incl. Glossosomatidae)
48210000	Philopotamidae	48210000	Philopotamidae	NBNSYS0000160680	Philopotamidae
48240000	Polycentropodidae	48240000	Polycentropodidae	NBNSYS0100014707	Polycentropodidae
48250000	Hydropsychidae	48250000	Hydropsychidae	NBNSYS0000042280	Hydropsychidae
482Z0000	Psychomyiidae (incl. Ecnomidae)	482Z0000	Psychomyiidae (including Ecnomidae)	<NEW-CODE>100074	Psychomyiidae (incl. Ecnomidae)
48310000	Phryganeidae	48310000	Phryganeidae	NBNSYS0000160695	Phryganeidae
48320000	Brachycentridae	48320000	Brachycentridae	NBNSYS0000159525	Brachycentridae
48330000	Lepidostomatidae	48330000	Lepidostomatidae	NBNSYS0000042287	Lepidostomatidae
48350000	Goeridae	48350000	Goeridae	NBNSYS0000042269	Goeridae
48360000	Beraeidae	48360000	Beraeidae	NBNSYS0000159496	Beraeidae
48370000	Sericostomatidae	48370000	Sericostomatidae	NBNSYS0000042336	Sericostomatidae
48380000	Odontoceridae	48380000	Odontoceridae	NBNSYS0000160553	Odontoceridae
48390000	Molannidae	48390000	Molannidae	NBNSYS0000160441	Molannidae
483Z0000	Limnephilidae (incl. Apataniidae)	483Z0000	Limnephilidae (including Apataniidae)	<NEW-CODE>100111	Limnephilidae (incl. Apataniidae)
48410000	Leptoceridae	483A0000	Leptoceridae	NBNSYS0000042288	Leptoceridae
501Z0000	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)	501Z0000	Tipulidae (including Limoniidae, Cylindrotomidae and Pediciidae)	<NEW-CODE>100112	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)
50360000	Simuliidae	50360000	Simuliidae	NBNSYS0000040183	Simuliidae
50400000	Chironomidae	50400000	Chironomidae	NBNSYS0000027300	Chironomidae

Appendix VI Taxonomic Level 2 – The 103 “Revised BMWP” (WHPT) taxa in RIVPACS IV

Appendix VI Taxonomic Level 2 – The 103 "Revised BMWP" (WHPT) taxa in RIVPACS IV

Rev. Maitland Code	Rev. Maitland Name	Furse Code	Furse Name	NBN Code	NBN Name
05110000	Planariidae	05110000	Planariidae	NBNSYS0000042315	Planariidae
05120000	Dugesiidae	05120000	Dugesiidae	NBNSYS0000159893	Dugesiidae
05130000	Dendrocoelidae	05130000	Dendrocoelidae	NBNSYS0000042255	Dendrocoelidae
16110000	Neritidae	16110000	Neritidae	NBNSYS0000160519	Neritidae
16120000	Viviparidae	16120000	Viviparidae	NBNSYS0000161255	Viviparidae
16130000	Valvatidae	16130000	Valvatidae	NBNSYS0000042348	Valvatidae
16140000	Hydrobiidae	16140000	Hydrobiidae	NBNSYS0000042277	Hydrobiidae
16160000	Bithyniidae	16160000	Bithyniidae	NBNSYS0100001902	Bithyniidae
16210000	Physidae	16210000	Physidae	NBNSYS0000160706	Physidae
16220000	Lymnaeidae	16220000	Lymnaeidae	NBNSYS0100003744	Lymnaeidae
16230000	Planorbidae	162X0000	Planorbidae (excluding Ancylus group)	NBNSYS0000050415	Planorbidae
16240000	Ancylidae	162Y0000	Ancylus group	NBNSYS0000040187	Ancylidae
16250000	Acroloxidae	16250000	Acroloxidae	NBNSYS0100009207	Acroloxidae
17120000	Unionidae	17120000	Unionidae	NBNSYS0000161229	Unionidae
17130000	Sphaeriidae	17130000	Sphaeriidae	NBNSYS0100015301	Sphaeriidae (Pea mussels)
17140000	Dreissenidae	17140000	Dreissenidae	NBNSYS0100002783	Dreissenidae
20000000	Oligochaeta	20000000	Oligochaeta	NBNSYS0000022328	Oligochaeta
22110000	Piscicolidae	22110000	Piscicolidae	NBNSYS0000160725	Piscicolidae
22120000	Glossiphoniidae	22120000	Glossiphoniidae	NHMSYS0000068846	Glossiphoniidae
22210000	Hirudinidae	22210000	Hirudinidae	NBNSYS0000160169	Hirudinidae
22310000	Erpobdellidae	22310000	Erpobdellidae	NBNSYS0000042263	Erpobdellidae
34310000	Astacidae	34310000	Astacidae	NBNSYS0000159453	Astacidae
36110000	Asellidae	36110000	Asellidae	NBNSYS0000040168	Asellidae
37110000	Corophiidae	37110000	Corophiidae	NBNSYS0000159759	Corophiidae
37130000	Crangonyctidae	37130000	Crangonyctidae	NBNSYS0000159766	Crangonyctidae
37140000	Gammaridae	37140000	Gammaridae	NBNSYS0000160038	Gammaridae
37150000	Niphargidae	37150000	Niphargidae	NBNSYS0000160523	Niphargidae
40120000	Baetidae	40120000	Baetidae	NHMSYS0000066929	Baetidae
40130000	Heptageniidae	40130000	Heptageniidae	NHMSYS0000066933	Heptageniidae
401Z0000	Siphlonuridae (incl. Ameletidae)	401Z0000	Siphlonuridae (including Ameletidae)	<NEW-CODE>100110	Siphlonuridae (incl. Ameletidae)
40210000	Leptophlebiidae	40210000	Leptophlebiidae	NHMSYS0000066934	Leptophlebiidae
40310000	Potamanthidae	40310000	Potamanthidae	NHMSYS0000066935	Potamanthidae
40320000	Ephemeridae	40320000	Ephemeridae	NHMSYS0000066932	Ephemeridae
40410000	Ephemerellidae	40410000	Ephemerellidae	NHMSYS0000066931	Ephemerellidae
40510000	Caenidae	40510000	Caenidae	NHMSYS0000066930	Caenidae
41110000	Taeniopterygidae	41110000	Taeniopterygidae	NBNSYS0000161088	Taeniopterygidae
41120000	Nemouridae	41120000	Nemouridae	NBNSYS0000042302	Nemouridae
41130000	Leuctridae	41130000	Leuctridae	NBNSYS0000160305	Leuctridae
41140000	Capniidae	41140000	Capniidae	NBNSYS0000159582	Capniidae
41210000	Perlodidae	41210000	Perlodidae	NBNSYS0000042311	Perlodidae
41220000	Perlidae	41220000	Perlidae	NBNSYS0000160662	Perlidae
41230000	Chloroperlidae	41230000	Chloroperlidae	NBNSYS0000159672	Chloroperlidae
42110000	Platycnemididae	42110000	Platycnemididae	NBNSYS0000160735	Platycnemididae
42120000	Coenagriidae	42120000	Coenagrionidae	NBNSYS0000159733	Coenagriidae
42140000	Calopterygidae	42140000	Calopterygidae	NBNSYS0100009819	Calopterygidae

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
42220000	Cordulegasteridae	42220000	Cordulegastridae	NBNSYS0000159754	Cordulegasteridae
42230000	Aeshnidae	42230000	Aeshnidae	NBNSYS0000159316	Aeshnidae
42250000	Libellulidae	42250000	Libellulidae	NBNSYS0000160307	Libellulidae
43110000	Mesovelidae	43110000	Mesoveliidae	NBNSYS0100013065	Mesoveliidae
43210000	Hydrometridae	43210000	Hydrometridae	NBNSYS0000160190	Hydrometridae
43220000	Veliidae	43220000	Veliidae	NBNSYS0000040171	Veliidae
43230000	Gerridae	43230000	Gerridae	NBNSYS0000040170	Gerridae
43310000	Nepidae	43310000	Nepidae	NBNSYS0000160516	Nepidae
43410000	Naucoridae	43410000	Naucoridae	NBNSYS0000160500	Naucoridae
43420000	Aphelocheiridae	43420000	Aphelocheiridae	NBNSYS0000159394	Aphelocheiridae
43510000	Notonectidae	43510000	Notonectidae	NBNSYS0000039904	Notonectidae
43610000	Corixidae	43610000	Corixidae	NBNSYS0000040176	Corixidae
45110000	Haliplidae	45110000	Haliplidae	NBNSYS0000007492	Haliplidae
45130000	Noteridae	45130000	Noteridae	NBNSYS0000160531	Noteridae
45140000	Dytiscidae	45140000	Dytiscidae	NBNSYS0000007515	Dytiscidae
45150000	Gyrinidae	45150000	Gyrinidae	NBNSYS0000040169	Gyrinidae
453Y0000	Hydrophilidae (incl. Helophoridae, Georissidae & Hydrochidae)	453Y0000	Hydrophilidae (including Helophoridae, Georissidae and Hydrochidae)	<NEW-CODE>100114	Hydrophilidae (incl. Helophoridae, Georissidae & Hydrochidae)
45410000	Hydraenidae	45410000	Hydraenidae	NBNSYS0000160184	Hydraenidae
45510000	Scirtidae	45510000	Scirtidae	NBNSYS0000160955	Scirtidae
45620000	Dryopidae	45620000	Dryopidae	NBNSYS0000159891	Dryopidae
45630000	Elmidae	45630000	Elmidae	NBNSYS0000007782	Elmidae
46110000	Sialidae	46110000	Sialidae	NBNSYS0000160993	Sialidae
47120000	Sisyridae	47120000	Sisyridae	NBNSYS0000161008	Sisyridae
48110000	Rhyacophilidae	48110000	Rhyacophilidae	NBNSYS0000042331	Rhyacophilidae
48120000	Glossosomatidae	48120000	Glossosomatidae	NBNSYS0000160068	Glossosomatidae
48130000	Hydroptilidae	48130000	Hydroptilidae	NBNSYS0000042282	Hydroptilidae
48210000	Philopotamidae	48210000	Philopotamidae	NBNSYS0000160680	Philopotamidae
48220000	Psychomyiidae	48220000	Psychomyiidae	NBNSYS0000042326	Psychomyiidae
48240000	Polycentropodidae	48240000	Polycentropodidae	NBNSYS0100014707	Polycentropodidae
48250000	Hydropsychidae	48250000	Hydropsychidae	NBNSYS0000042280	Hydropsychidae
48310000	Phryganeidae	48310000	Phryganeidae	NBNSYS0000160695	Phryganeidae
48320000	Brachycentridae	48320000	Brachycentridae	NBNSYS0000159525	Brachycentridae
48330000	Lepidostomatidae	48330000	Lepidostomatidae	NBNSYS0000042287	Lepidostomatidae
48350000	Goeridae	48350000	Goeridae	NBNSYS0000042269	Goeridae
48360000	Beraeidae	48360000	Beraeidae	NBNSYS0000159496	Beraeidae
48370000	Sericostomatidae	48370000	Sericostomatidae	NBNSYS0000042336	Sericostomatidae
48380000	Odontoceridae	48380000	Odontoceridae	NBNSYS0000160553	Odontoceridae
48390000	Molannidae	48390000	Molannidae	NBNSYS0000160441	Molannidae
483Z0000	Limnephilidae (incl. Apataniidae)	483Z0000	Limnephilidae (including Apataniidae)	<NEW-CODE>100111	Limnephilidae (incl. Apataniidae)
48410000	Leptoceridae	483A0000	Leptoceridae	NBNSYS0000042288	Leptoceridae
501Z0000	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)	501Z0000	Tipulidae (including Limoniidae, Cylindrotomidae and Pediciidae)	<NEW-CODE>100112	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)
50210000	Psychodidae	50210000	Psychodidae	NBNSYS0000042324	Psychodidae
50220000	Ptychopteridae	50220000	Ptychopteridae	NBNSYS0000160848	Ptychopteridae
50310000	Dixidae	50310000	Dixidae	NBNSYS0000037200	Dixidae
50320000	Chaoboridae	50320000	Chaoboridae	NBNSYS0000040186	Chaoboridae
50330000	Culicidae	50330000	Culicidae	NBNSYS0000040182	Culicidae
50350000	Ceratopogonidae	50350000	Ceratopogonidae	NBNSYS0000037064	Ceratopogonidae
50360000	Simuliidae	50360000	Simuliidae	NBNSYS0000040183	Simuliidae
50400000	Chironomidae	50400000	Chironomidae	NBNSYS0000027300	Chironomidae
50610000	Stratiomyidae	50610000	Stratiomyidae	NBNSYS0000161064	Stratiomyidae

Rev. Maitland Code	Rev. Maitland Name	Furse Code	Furse Name	NBN Code	NBN Name
50630000	Tabanidae	50630000	Tabanidae	NBNSYS0000050594	Tabanidae
50640000	Athericidae	50640000	Athericidae	NBNSYS0100001562	Athericidae
50710000	Empididae	50710000	Empididae	NBNSYS0000042259	Empididae
50720000	Dolichopodidae	50720000	Dolichopodidae	NBNSYS0000159881	Dolichopodidae
50810000	Syrphidae	50810000	Syrphidae	NBNSYS0000040188	Syrphidae
50820000	Sciomyzidae	50820000	Sciomyzidae	NBNSYS0000160954	Sciomyzidae
50830000	Ephydridae	50830000	Ephydridae	NBNSYS0000159951	Ephydridae
50850000	Muscidae	50850000	Muscidae	NBNSYS0000160470	Muscidae

Appendix VII Taxonomic Level 3 – The 132 “All Families” taxa in RIVPACS IV

Appendix VII Taxonomic Level 3 – The 132 "All Families" taxa in RIVPACS IV

Rev. Maitland Code	Rev. Maitland Name	Furse Code	Furse Name	NBN Code	NBN Name
02110000	Spongillidae	02110000	Spongillidae	NBNSYS0000161044	Spongillidae
03110000	Hydridae	03110000	Hydridae	NBNSYS0000160186	Hydridae
05110000	Planariidae	05110000	Planariidae	NBNSYS0000042315	Planariidae
05120000	Dugesiidae	05120000	Dugesiidae	NBNSYS0000159893	Dugesiidae
05130000	Dendrocoelidae	05130000	Dendrocoelidae	NBNSYS0000042255	Dendrocoelidae
09120000	Chordodidae	09120000	Chordodidae	NBNSYS0000159680	Chordodidae
10000000	Nematoda	10000000	Nematoda	NBNSYS0000160506	Nematoda
14000000	Ectoprocta	14000000	Ectoprocta	NBNSYS0100011478	Ectoprocta
16110000	Neritidae	16110000	Neritidae	NBNSYS0000160519	Neritidae
16120000	Viviparidae	16120000	Viviparidae	NBNSYS0000161255	Viviparidae
16130000	Valvatidae	16130000	Valvatidae	NBNSYS0000042348	Valvatidae
16140000	Hydrobiidae	16140000	Hydrobiidae	NBNSYS0000042277	Hydrobiidae
16160000	Bithyniidae	16160000	Bithyniidae	NBNSYS0100001902	Bithyniidae
16210000	Physidae	16210000	Physidae	NBNSYS0000160706	Physidae
16220000	Lymnaeidae	16220000	Lymnaeidae	NBNSYS0100003744	Lymnaeidae
16230000	Planorbidae	162X0000	Planorbidae (excluding Ancylus group)	NBNSYS0000050415	Planorbidae
16240000	Ancylidae	162Y0000	Ancylus group	NBNSYS0000040187	Ancylidae
16250000	Acroloxidae	16250000	Acroloxidae	NBNSYS0100009207	Acroloxidae
17110000	Margaritiferidae	17110000	Margaritiferidae	NBNSYS0000160380	Margaritiferidae
17120000	Unionidae	17120000	Unionidae	NBNSYS0000161229	Unionidae
17130000	Sphaeriidae	17130000	Sphaeriidae	NBNSYS0100015301	Sphaeriidae (Pea mussels)
17140000	Dreissenidae	17140000	Dreissenidae	NBNSYS0100002783	Dreissenidae
19110000	Aeolosomatidae	19110000	Aeolosomatidae	NBNSYS0100009282	Aeolosomatidae
20110000	Lumbriculidae	20110000	Lumbriculidae	NBNSYS0000037208	Lumbriculidae
20210000	Haplotaxidae	20210000	Haplotaxidae	NBNSYS0100012393	Haplotaxidae
20330000	Naididae	20330000	Naididae	NBNSYS0000042298	Naididae
20340000	Tubificidae	20340000	Tubificidae	NBNSYS0000042565	Tubificidae
203Z0000	Enchytraeidae (incl. Propappidae)	203Z0000	Enchytraeidae (including Propappidae)	<NEW-CODE>100075	Enchytraeidae (incl. Propappidae)
20420000	Lumbricidae	20420000	Lumbricidae	NBNSYS0000042293	Lumbricidae
22110000	Piscicolidae	22110000	Piscicolidae	NBNSYS0000160725	Piscicolidae
22120000	Glossiphoniidae	22120000	Glossiphoniidae	NHMSYS0000068846	Glossiphoniidae
22210000	Hirudinidae	22210000	Hirudinidae	NBNSYS0000160169	Hirudinidae
22310000	Erpobdellidae	22310000	Erpobdellidae	NBNSYS0000042263	Erpobdellidae
24000000	Hydracarina	24000000	Hydracarina	NBNSYS0100012468	Hydracarina
34310000	Astacidae	34310000	Astacidae	NBNSYS0000159453	Astacidae
36110000	Asellidae	36110000	Asellidae	NBNSYS0000040168	Asellidae
37110000	Corophiidae	37110000	Corophiidae	NBNSYS0000159759	Corophiidae
37130000	Crangonyctidae	37130000	Crangonyctidae	NBNSYS0000159766	Crangonyctidae
37140000	Gammaridae	37140000	Gammaridae	NBNSYS0000160038	Gammaridae
37150000	Niphargidae	37150000	Niphargidae	NBNSYS0000160523	Niphargidae
40110000	Siphlonuridae	40110000	Siphlonuridae	NHMSYS0000066936	Siphlonuridae
40120000	Baetidae	40120000	Baetidae	NHMSYS0000066929	Baetidae
40130000	Heptageniidae	40130000	Heptageniidae	NHMSYS0000066933	Heptageniidae
40140000	Ameletidae	40140000	Ameletidae	<NEW-CODE>100101	Ameletidae
40210000	Leptophlebiidae	40210000	Leptophlebiidae	NHMSYS0000066934	Leptophlebiidae
40310000	Potamanthidae	40310000	Potamanthidae	NHMSYS0000066935	Potamanthidae
40320000	Ephemeridae	40320000	Ephemeridae	NHMSYS0000066932	Ephemeridae

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
40410000	Ephemerellidae	40410000	Ephemerellidae	NHMSYS0000066931	Ephemerellidae
40510000	Caenidae	40510000	Caenidae	NHMSYS0000066930	Caenidae
41110000	Taeniopterygidae	41110000	Taeniopterygidae	NBNSYS0000161088	Taeniopterygidae
41120000	Nemouridae	41120000	Nemouridae	NBNSYS0000042302	Nemouridae
41130000	Leuctridae	41130000	Leuctridae	NBNSYS0000160305	Leuctridae
41140000	Capniidae	41140000	Capniidae	NBNSYS0000159582	Capniidae
41210000	Perlodidae	41210000	Perlodidae	NBNSYS0000042311	Perlodidae
41220000	Perlidae	41220000	Perlidae	NBNSYS0000160662	Perlidae
41230000	Chloroperlidae	41230000	Chloroperlidae	NBNSYS0000159672	Chloroperlidae
42110000	Platycnemididae	42110000	Platycnemididae	NBNSYS0000160735	Platycnemididae
42120000	Coenagriidae	42120000	Coenagrionidae	NBNSYS0000159733	Coenagriidae
42140000	Calopterygidae	42140000	Calopterygidae	NBNSYS0100009819	Calopterygidae
42210000	Gomphidae	42210000	Gomphidae	NBNSYS0000189701	Gomphidae
42220000	Cordulegasteridae	42220000	Cordulegastridae	NBNSYS0000159754	Cordulegasteridae
42230000	Aeshnidae	42230000	Aeshnidae	NBNSYS0000159316	Aeshnidae
42250000	Libellulidae	42250000	Libellulidae	NBNSYS0000160307	Libellulidae
43110000	Mesovelidae	43110000	Mesoveliidae	NBNSYS0100013065	Mesoveliidae
43210000	Hydrometridae	43210000	Hydrometridae	NBNSYS0000160190	Hydrometridae
43220000	Veliidae	43220000	Veliidae	NBNSYS0000040171	Veliidae
43230000	Gerridae	43230000	Gerridae	NBNSYS0000040170	Gerridae
43310000	Nepidae	43310000	Nepidae	NBNSYS0000160516	Nepidae
43410000	Naucoridae	43410000	Naucoridae	NBNSYS0000160500	Naucoridae
43420000	Aphelocheiridae	43420000	Aphelocheiridae	NBNSYS0000159394	Aphelocheiridae
43510000	Notonectidae	43510000	Notonectidae	NBNSYS0000039904	Notonectidae
43610000	Corixidae	43610000	Corixidae	NBNSYS0000040176	Corixidae
45110000	Haliplidae	45110000	Haliplidae	NBNSYS0000007492	Haliplidae
45130000	Noteridae	45130000	Noteridae	NBNSYS0000160531	Noteridae
45140000	Dytiscidae	45140000	Dytiscidae	NBNSYS0000007515	Dytiscidae
45150000	Gyrinidae	45150000	Gyrinidae	NBNSYS0000040169	Gyrinidae
45330000	Helophoridae	45330000	Helophoridae	<NEW-CODE>100103	Helophoridae
45350000	Hydrophilidae	45350000	Hydrophilidae	NBNSYS0000037258	Hydrophilidae
45360000	Hydrochidae	45360000	Hydrochidae	<NEW-CODE>100105	Hydrochidae
45410000	Hydraenidae	45410000	Hydraenidae	NBNSYS0000160184	Hydraenidae
45510000	Scirtidae	45510000	Scirtidae	NBNSYS0000160955	Scirtidae
45620000	Dryopidae	45620000	Dryopidae	NBNSYS0000159891	Dryopidae
45630000	Elmidae	45630000	Elmidae	NBNSYS0000007782	Elmidae
46110000	Sialidae	46110000	Sialidae	NBNSYS0000160993	Sialidae
47110000	Osmylidae	47110000	Osmylidae	NBNSYS0000160595	Osmylidae
47120000	Sisyridae	47120000	Sisyridae	NBNSYS0000161008	Sisyridae
48110000	Rhyacophilidae	48110000	Rhyacophilidae	NBNSYS0000042331	Rhyacophilidae
48120000	Glossosomatidae	48120000	Glossosomatidae	NBNSYS0000160068	Glossosomatidae
48130000	Hydroptilidae	48130000	Hydroptilidae	NBNSYS0000042282	Hydroptilidae
48210000	Philopotamidae	48210000	Philopotamidae	NBNSYS0000160680	Philopotamidae
48220000	Psychomyiidae	48220000	Psychomyiidae	NBNSYS0000042326	Psychomyiidae
48230000	Ecnomidae	48230000	Ecnomidae	NBNSYS0000159907	Ecnomidae
48240000	Polycentropodidae	48240000	Polycentropodidae	NBNSYS0100014707	Polycentropodidae
48250000	Hydropsychidae	48250000	Hydropsychidae	NBNSYS0000042280	Hydropsychidae
48310000	Phryganeidae	48310000	Phryganeidae	NBNSYS0000160695	Phryganeidae
48320000	Brachycentridae	48320000	Brachycentridae	NBNSYS0000159525	Brachycentridae
48330000	Lepidostomatidae	48330000	Lepidostomatidae	NBNSYS0000042287	Lepidostomatidae

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
48340000	Limnephilidae	48340000	Limnephilidae	NBNSYS0000042292	Limnephilidae
48350000	Goeridae	48350000	Goeridae	NBNSYS0000042269	Goeridae
48360000	Beraeidae	48360000	Beraeidae	NBNSYS0000159496	Beraeidae
48370000	Sericostomatidae	48370000	Sericostomatidae	NBNSYS0000042336	Sericostomatidae
48380000	Odontoceridae	48380000	Odontoceridae	NBNSYS0000160553	Odontoceridae
48390000	Molannidae	48390000	Molannidae	NBNSYS0000160441	Molannidae
483B0000	Apataniidae	483B0000	Apataniidae	<NEW-CODE>100106	Apataniidae
48410000	Leptoceridae	483A0000	Leptoceridae	NBNSYS0000042288	Leptoceridae
49110000	Pyralidae	49110000	Pyralidae	NBNSYS0000160856	Pyralidae
50110000	Tipulidae	50110000	Tipulidae	NBNSYS0000037145	Tipulidae
50130000	Limoniidae	50130000	Limoniidae	NBNSYS0100003656	Limoniidae
50140000	Pediciidae	50140000	Pediciidae	NHMSYS0000524741	Pediciidae
50210000	Psychodidae	50210000	Psychodidae	NBNSYS0000042324	Psychodidae
50220000	Ptychopteridae	50220000	Ptychopteridae	NBNSYS0000160848	Ptychopteridae
50310000	Dixidae	50310000	Dixidae	NBNSYS0000037200	Dixidae
50320000	Chaoboridae	50320000	Chaoboridae	NBNSYS0000040186	Chaoboridae
50330000	Culicidae	50330000	Culicidae	NBNSYS0000040182	Culicidae
50340000	Thaumaleidae	50340000	Thaumaleidae	NBNSYS0000161135	Thaumaleidae
50350000	Ceratopogonidae	50350000	Ceratopogonidae	NBNSYS0000037064	Ceratopogonidae
50360000	Simuliidae	50360000	Simuliidae	NBNSYS0000040183	Simuliidae
50420000	Tanypodinae	50420000	Tanypodinae	NBNSYS0100016092	Tanypodinae
50440000	Diamesinae	50440000	Diamesinae	NBNSYS0100011289	Diamesinae
50450000	Prodiamesinae	50450000	Prodiamesinae	NBNSYS0100014790	Prodiamesinae
50460000	Orthocladiinae	50460000	Orthocladiinae	NBNSYS0100014066	Orthocladiinae
50470000	Chironomini	50470000	Chironomini	NBNSYS0100010010	Chironomini
50490000	Tanytarsini	50490000	Tanytarsini	NBNSYS0100016093	Tanytarsini
50610000	Stratiomyidae	50610000	Stratiomyidae	NBNSYS0000161064	Stratiomyidae
50630000	Tabanidae	50630000	Tabanidae	NBNSYS0000050594	Tabanidae
50640000	Athericidae	50640000	Athericidae	NBNSYS0100001562	Athericidae
50710000	Empididae	50710000	Empididae	NBNSYS0000042259	Empididae
50720000	Dolichopodidae	50720000	Dolichopodidae	NBNSYS0000159881	Dolichopodidae
50810000	Syrphidae	50810000	Syrphidae	NBNSYS0000040188	Syrphidae
50820000	Sciomyzidae	50820000	Sciomyzidae	NBNSYS0000160954	Sciomyzidae
50830000	Ephydridae	50830000	Ephydridae	NBNSYS0000159951	Ephydridae
50850000	Muscidae	50850000	Muscidae	NBNSYS0000160470	Muscidae

Appendix VIII Taxonomic Level 4 – The 652 “Species” level taxa in RIVPACS IV (including component members of species groups)

Appendix VIII Taxonomic Level 4 – The 652 "Species" level taxa in RIVPACS IV (including component members of species groups)

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
02110000	Spongillidae	02110000	Spongillidae	NBNSYS0000161044	Spongillidae
03110000	Hydridae	03110000	Hydridae	NBNSYS0000160186	Hydridae
05110101	Planaria torva (Muller)	05110101	Planaria torva (Müller, 1774)	NBNSYS0000013180	Planaria torva
05110201	Polycelis felina (Dalyell)	05110201	Polycelis felina (Dalyell, 1814)	NBNSYS0000013183	Polycelis felina
0511020Z	Polycelis nigra group	0511020Z	Polycelis nigra group	<NEW-CODE>100001	Polycelis nigra group
05110301	Phagocata vitta (Duges)	05110301	Phagocata vitta (Duges, 1830)	NBNSYS0000013186	Phagocata vitta
05110401	Crenobia alpina (Dana)	05110401	Crenobia alpina (Dana, 1766)	NBNSYS0000013188	Crenobia alpina
05120103	Dugesia tigrina (Girard)	05120103	Dugesia tigrina (Girard, 1850)	NBNSYS0000188431	Dugesia tigrina
0512010Z	Dugesia polychroa group	0512010Z	Dugesia polychroa group	<NEW-CODE>100002	Dugesia polychroa group
05130101	Bdellocephala punctata (Pallas)	05130101	Bdellocephala punctata (Pallas, 1774)	NBNSYS0000013191	Bdellocephala punctata
05130201	Dendrocoelum lacteum (Muller)	05130201	Dendrocoelum lacteum (O.F.Müller, 1774)	NBNSYS0000013190	Dendrocoelum lacteum
09120000	Chordodidae	09120000	Chordodidae	NBNSYS0000159680	Chordodidae
10000000	Nematoda	10000000	Nematoda	NBNSYS0000160506	Nematoda
14000000	Ectoprocta	14000000	Ectoprocta	NBNSYS0100011478	Ectoprocta
16110101	Theodoxus fluviatilis (L.)	16110101	Theodoxus fluviatilis (Linnaeus, 1758)	NBNSYS0000006601	Theodoxus fluviatilis
16120102	Viviparus viviparus (L.)	16120102	Viviparus viviparus (Linnaeus, 1758)	NBNSYS0000006602	Viviparus viviparus
16130101	Valvata cristata Muller	16130111	Valvata (Valvata) cristata O.F. Müller, 1774	NBNSYS0000006604	Valvata cristata
16130102	Valvata macrostoma Morch	16130121	Valvata (Tropidina) macrostoma Morch, 1864	NBNSYS0000006605	Valvata macrostoma
16130103	Valvata piscinalis (Muller)	16130131	Valvata (Cincinna) piscinalis (O.F. Müller, 1774)	NBNSYS0000006606	Valvata piscinalis
16140301	Potamopyrgus jenkinsi (Smith)	16140301	Potamopyrgus antipodarum (J.E.Gray, 1843)	NBNSYS0000006613	Potamopyrgus jenkinsi
16160101	Bithynia leachii (Sheppard)	16160121	Bithynia (Codiella) leachii (Sheppard, 1823)	NBNSYS0000006616	Bithynia leachii
16160102	Bithynia tentaculata (L.)	16160111	Bithynia (Bithynia) tentaculata (Linnaeus, 1758)	NBNSYS0000006615	Bithynia tentaculata
16210101	Aplexa hypnorum (L.)	16210101	Aplexa hypnorum (Linnaeus, 1758)	NBNSYS0000006624	Aplexa hypnorum
16210202	Physa fontinalis (L.)	16210202	Physa fontinalis (Linnaeus, 1758)	NBNSYS0000006625	Physa fontinalis
1621020Z	Physa acuta group	16210321	Physella (Costatella) acuta (Draparnaud, 1805)	NBNSYS0000006626	Physa acuta
16220101	Lymnaea auricularia (L.)	16220601	Radix auricularia (Linnaeus, 1758)	NBNSYS0000006634	Lymnaea auricularia
16220103	Lymnaea palustris (Muller)	16220401	Stagnicola palustris (O.F. Müller, 1774)	NBNSYS0000006632	Lymnaea palustris
16220104	Lymnaea peregra (Muller)	16220602	Radix balthica (Linnaeus, 1758)	NBNSYS0000006635	Lymnaea peregra
16220105	Lymnaea stagnalis (L.)	16220105	Lymnaea stagnalis (Linnaeus, 1758)	NBNSYS0000006633	Lymnaea stagnalis
16220106	Lymnaea truncatula (Muller)	16220301	Galba truncatula (O.F. Müller, 1774)	NBNSYS0000006630	Lymnaea truncatula
16230101	Planorbis carinatus Muller	16230111	Planorbis (Planorbis) carinatus (O.F. Müller, 1774)	NBNSYS0000006638	Planorbis carinatus
16230102	Planorbis planorbis (L.)	16230112	Planorbis (Planorbis) planorbis (Linnaeus, 1758)	NBNSYS0000006637	Planorbis planorbis
16230201	Anisus leucostoma (Millet)	16230211	Anisus (Anisus) leucostoma (Millet, 1813)	NBNSYS0000006639	Anisus leucostoma
16230202	Anisus vortex (L.)	16230221	Anisus (Disculifer) vortex (Linnaeus, 1758)	NBNSYS0000006640	Anisus vortex
16230301	Bathyomphalus contortus (L.)	16230301	Bathyomphalus contortus (Linnaeus, 1758)	NBNSYS0000006642	Bathyomphalus contortus
16230402	Gyraulus albus (Muller)	16230412	Gyraulus (Gyraulus) albus (O.F. Müller, 1774)	NBNSYS0000006645	Gyraulus albus
16230403	Gyraulus laevis (Alder)	16230421	Gyraulus (Torquis) laevis (Alder, 1838)	NBNSYS0000006643	Gyraulus laevis
16230501	Armiger crista (L.)	16230431	Gyraulus (Armiger) crista (Linnaeus, 1758)	NBNSYS0000006646	Armiger crista
16230601	Hippeutis complanatus (L.)	16230601	Hippeutis complanatus (Linnaeus, 1758)	NBNSYS0000006647	Hippeutis complanatus
16230701	Segmentina nitida Muller	16230701	Segmentina nitida (O.F. Müller, 1774)	NBNSYS0000006648	Segmentina nitida
16230801	Planorbarius corneus (L.)	16230801	Planorbarius corneus (Linnaeus, 1758)	NBNSYS0000006649	Planorbarius corneus
16240101	Ancylus fluviatilis Muller	16231101	Ancylus fluviatilis O.F. Müller, 1774	NBNSYS0000006651	Ancylus fluviatilis
16250101	Acroloxus lacustris (L.)	16250101	Acroloxus lacustris (Linnaeus, 1758)	NBNSYS0000006652	Acroloxus lacustris
17110101	Margaritifera margaritifera (L.)	17110101	Margaritifera margaritifera (Linnaeus, 1758)	NBNSYS0000006779	Margaritifera margaritifera
17120100	Unio sp.	17120100	Unio sp.	NBNSYS0000138782	Unio
17120Z00	Anodonta group	17120Z00	Anodonta group	<NEW-CODE>100004	Anodonta group
17130101	Sphaerium corneum (L.)	17130101	Sphaerium corneum (Linnaeus, 1758)	NBNSYS0000006786	Sphaerium corneum

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
17130102	Sphaerium lacustre (Muller)	17130301	Musculium lacustre (Müller, 1774)	NBNSYS0000006790	Sphaerium lacustre
17130103	Sphaerium rivicola (Lamarck)	17130103	Sphaerium rivicola (Lamarck, 1818)	NBNSYS0000006787	Sphaerium rivicola
17130105	Sphaerium transversum (Say)	17130302	Musculium transversum (Say, 1829)	NBNSYS0000006789	Sphaerium transversum
17130201	Pisidium amnicum (Muller)	17130201	Pisidium amnicum (Müller, 1774)	NBNSYS0000006793	Pisidium amnicum
17130202	Pisidium casertanum (Poli)	17130202	Pisidium casertanum (Poli, 1791)	NBNSYS0000006794	Pisidium casertanum
17130204	Pisidium henslowanum (Sheppard)	17130204	Pisidium henslowanum (Sheppard, 1823)	NBNSYS0000006802	Pisidium henslowanum
17130205	Pisidium hibernicum Westerlund	17130205	Pisidium hibernicum Westerlund, 1894	NBNSYS0000006804	Pisidium hibernicum
17130206	Pisidium lilljeborgii Clessin	17130206	Pisidium lilljeborgii Clessin, 1886	NBNSYS0000006803	Pisidium lilljeborgii
17130207	Pisidium milium Held	17130207	Pisidium milium Held, 1836	NBNSYS0000006799	Pisidium milium
17130208	Pisidium moitessierianum Paladilhe	17130208	Pisidium moitessierianum Paladilhe, 1866	NBNSYS0000006807	Pisidium moitessierianum
17130209	Pisidium nitidum Jenyns	17130209	Pisidium nitidum Jenyns, 1832	NBNSYS0000006805	Pisidium nitidum
17130211	Pisidium obtusale (Lamarck)	17130211	Pisidium obtusale (Lamarck, 1818)	NBNSYS0000006797	Pisidium obtusale
17130212	Pisidium personatum Malm	17130212	Pisidium personatum Malm, 1855	NBNSYS0000006796	Pisidium personatum
17130214	Pisidium pulchellum Jenyns	17130214	Pisidium pulchellum Jenyns, 1832	NBNSYS0000006806	Pisidium pulchellum
17130215	Pisidium subtruncatum Malm	17130215	Pisidium subtruncatum Malm, 1855	NBNSYS0000006800	Pisidium subtruncatum
17130216	Pisidium supinum Schmidt	17130216	Pisidium supinum Schmidt, 1851	NBNSYS0000006801	Pisidium supinum
17130217	Pisidium tenuilineatum Stelfox	17130217	Pisidium tenuilineatum Stelfox, 1918	NBNSYS0000006792	Pisidium tenuilineatum
17140101	Dreissena polymorpha (Pallas)	17140101	Dreissena polymorpha (Pallas, 1771)	NBNSYS0000006809	Dreissena polymorpha
19110100	Aeolosoma sp.	19110100	Aeolosoma sp.	NBNSYS0100009274	Aeolosoma
20110301	Stylodrilus brachstylus Hrabe	20110301	Stylodrilus brachystylus Hrabe, 1928	NBNSYS0100015937	Stylodrilus brachystylus
20110302	Stylodrilus heringianus Claparede	20110302	Stylodrilus heringianus Claparède, 1862	NBNSYS0000037072	Stylodrilus heringianus
20110303	Stylodrilus lemani (Grube)	20110601	Bythonomus lemani Grube, 1880	NBNSYS0100015938	Stylodrilus lemani
20110401	Eclipidrilus lacustris (Verrill)	20110401	Eclipidrilus lacustris (Verrill, 1871)	NBNSYS0100011475	Eclipidrilus lacustris
20110Z00	Lumbriculus group	20110Z00	Lumbriculus group	<NEW-CODE>100005	Lumbriculus group
20210101	Haplotaxis gordioides (Hartmann)	20210101	Haplotaxis gordioides (Hartmann, 1821)	NBNSYS0100012396	Haplotaxis gordioides
20330100	Chaetogaster sp.	20330100	Chaetogaster sp.	NBNSYS0000180312	Chaetogaster
20330401	Specaria josinae (Vejdovsky)	20330401	Specaria josinae (Vejdovsky,1883)	NBNSYS0100015273	Specaria josinae
20330501	Uncinais uncinata (Orsted)	20330501	Uncinais uncinata (Orsted, 1842)	NBNSYS0000188175	Uncinais uncinata
20330601	Ophidonais serpentina (Muller)	20330601	Ophidonais serpentina (Müller, 1774)	NBNSYS0000022329	Ophidonais serpentina
20330701	Nais alpina Sperber	20330701	Nais alpina Sperber, 1948	NBNSYS0100013282	Nais alpina
20330703	Nais bretscheri Michaelsen	20330703	Nais bretscheri Michaelsen, 1899	NBNSYS0100013284	Nais bretscheri
20330705	Nais elinguis Muller	20330705	Nais elinguis Müller, 1773	NBNSYS0000188457	Nais elinguis
20330706	Nais pardalis Piguet	20330706	Nais pardalis Piguet, 1906	NBNSYS0100013285	Nais pardalis
2033070Y	Nais communis group	2033070Y	Nais communis group	<NEW-CODE>100006	Nais communis group
2033070Z	Nais simplex group	2033070Z	Nais simplex group	<NEW-CODE>100007	Nais simplex group
20330801	Slavina appendiculata (d'Udekem)	20330801	Slavina appendiculata (d'Udekem, 1855)	NBNSYS0000022331	Slavina appendiculata
20330901	Vejdovskyella comata (Vejdovsky)	20330901	Vejdovskyella comata (Vejdovsky, 1883)	NBNSYS0100016460	Vejdovskyella comata
20330902	Vejdovskyella intermedia (Bretscher)	20330902	Vejdovskyella intermedia (Bretscher, 1896)	NBNSYS0100016461	Vejdovskyella intermedia
20331101	Ripistes parasita (Schmidt)	20331101	Ripistes parasita (Schmidt, 1847)	NBNSYS0100015033	Ripistes parasita
20331201	Stylaria lacustris (L.)	20331201	Stylaria lacustris (Linnaeus, 1767)	NBNSYS0000022333	Stylaria lacustris
20331301	Piguetiella blanci (Piguet)	20331301	Piguetiella blanci (Piguet, 1906)	NBNSYS0100014353	Piguetiella blanci
20331411	Dero digitata (Muller)	20331411	Dero (Dero) digitata (Müller, 1774)	NBNSYS0100011250	Dero digitata
20331501	Pristina aequiseta Bourne	20331511	Prisina (Pristina) aequiseta Bourne, 1891	NBNSYS0100014761	Pristina aequiseta
2033150Z	Pristina idrensis group	20331520	Pristina (Pristinella) sp.	<NEW-CODE>100076	Pristina (Pristinella) sp.
20340102	Tubifex ignotus (Stolc)	20340102	Tubifex ignotus (Štolc, 1886)	NBNSYS0000022334	Tubifex ignotus
20340106	Tubifex tubifex (Muller)	20340106	Tubifex tubifex (Müller, 1774)	NBNSYS0000037053	Tubifex tubifex
20340201	Limnodrilus cervix Brinkhurst	20340201	Limnodrilus cervix Brinkhurst, 1963	NBNSYS0100012809	Limnodrilus cervix
20340202	Limnodrilus claparedeianus Ratzel	20340202	Limnodrilus claparedianus Ratzel, 1869	NBNSYS0100012810	Limnodrilus claparedeianus
20340203	Limnodrilus hoffmeisteri Claparede	20340203	Limnodrilus hoffmeisteri Claparède, 1862	NBNSYS0000188460	Limnodrilus hoffmeisteri
20340204	Limnodrilus profundicola (Verrill)	20340204	Limnodrilus profundicola (Verrill, 1871)	NBNSYS0000037175	Limnodrilus profundicola
20340205	Limnodrilus udekemianus Claparede	20340205	Limnodrilus udekemianus Claparède, 1862	NBNSYS0000051118	Limnodrilus udekemianus

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
20340301	Psammoryctides albicola (Michaelsen)	20340301	Psammoryctides albicola (Michaelsen, 1901)	NBNSYS0100014824	Psammoryctides albicola
20340302	Psammoryctides barbatus (Grube)	20340302	Psammoryctides barbatus (Grube, 1891)	NBNSYS0000037079	Psammoryctides barbatus
20340401	Potamothrix bavaricus (Oschmann)	20340401	Potamothrix bavaricus (Oschmann, 1913)	NBNSYS0100014744	Potamothrix bavaricus
20340402	Potamothrix hammoniensis (Michaelsen)	20340402	Potamothrix hammoniensis (Michaelsen, 1901)	NBNSYS0100014745	Potamothrix hammoniensis
20340403	Potamothrix heuscheri Bretscher	20340403	Potamothrix heuscheri (Bretscher, 1900)	NBNSYS0100014746	Potamothrix heuscheri
20340404	Potamothrix moldaviensis (Vejdovsky & Mrazek)	20340404	Potamothrix moldaviensis Vejdovsky & Mrazek, 1903	NBNSYS0000037220	Potamothrix moldaviensis
20340405	Potamothrix vejdovskyi (Hrabe)	20340405	Potamothrix vejdovskyi (Hrabe, 1941)	NBNSYS0100014747	Potamothrix vejdovskyi
20340501	Ilyodrilus templetoni (Southern)	20340501	Ilyodrilus templetoni (Southern, 1909)	NBNSYS0100012579	Ilyodrilus templetoni
20340601	Spirosperma ferox (Eisen)	20340601	Spirosperma ferox Eisen, 1879	NBNSYS0100015372	Spirosperma ferox
20340602	Spirosperma velutinus (Grube)	20341701	Embolocephalus velutinus (Grube, 1879)	NBNSYS0100015373	Spirosperma velutinus
20340801	Haber simsi (Brinkhurst)	20340801	Haber speciosus (Hrabe, 1931)	NBNSYS0100012313	Haber simsi
20340901	Aulodrilus limnobius Bretscher	20340901	Aulodrilus limnobius Bretscher, 1899	NBNSYS0100009627	Aulodrilus limnobius
20340903	Aulodrilus pluriseta (Piguet)	20340903	Aulodrilus pluriseta (Piguet, 1906)	NBNSYS0000037336	Aulodrilus pluriseta
20341101	Rhyacodrilus coccineus (Vejdovsky)	20341101	Rhyacodrilus coccineus (Vejdovsky, 1876)	NBNSYS0000042329	Rhyacodrilus coccineus
20341102	Rhyacodrilus falciformis Bretscher	20341102	Rhyacodrilus falciformis Bretscher, 1901	NBNSYS0100015018	Rhyacodrilus falciformis
20341301	Branchiura sowerbyi Beddard	20341301	Branchiura sowerbyi Beddard, 1892	NBNSYS0100009733	Branchiura sowerbyi
20341601	Thalassodrilus prostatus (Knöllner)	20341601	Thalassodrilus prostatus (Knöllner, 1935)	<NEW-CODE>100008	Thalassodrilus prostatus
203Z0000	Enchytraeidae (incl. Propappidae)	203Z0000	Enchytraeidae (including Propappidae)	<NEW-CODE>100075	Enchytraeidae (incl. Propappidae)
204Z0000	Lumbricidae (incl. Glossoscolecidae)	204Z0000	Lumbricidae (including Glossoscolecidae)	<NEW-CODE>100081	Lumbricidae (incl. Glossoscolecidae)
22110101	Piscicola geometra (L.)	22110101	Piscicola geometra (Linnaeus, 1761)	NHMSYS0000068867	Piscicola geometra
22120201	Theromyzon tessulatum (Muller)	22120201	Theromyzon tessulatum (O.F.Müller, 1774)	NHMSYS0000068877	Theromyzon tessulatum
22120301	Hemiclepsis marginata (Muller)	22120301	Hemiclepsis marginata (O.F.Müller, 1774)	NHMSYS0000068875	Hemiclepsis marginata
22120401	Glossiphonia complanata (L.)	22120401	Glossiphonia complanata (Linnaeus, 1758)	NBNSYS0000013205	Glossiphonia complanata
22120402	Glossiphonia heteroclita (L.)	22120801	Alboglossiphonia heteroclita (Linnaeus, 1761)	NBNSYS0000013204	Glossiphonia heteroclita
22120501	Batracobdella paludosa (Carena)	22120404	Glossiphonia paludosa (Carena, 1824)	NBNSYS0000013206	Batracobdella paludosa
22120601	Boreobdella verrucata (Muller)	22120403	Glossiphonia verrucata (Fr. Müller, 1844)	NBNSYS0000013207	Boreobdella verrucata
22120701	Helobdella stagnalis (L.)	22120701	Helobdella stagnalis (Linnaeus, 1758)	NBNSYS0000013208	Helobdella stagnalis
22210101	Haemopis sanguisuga (L.)	22210101	Haemopis sanguisuga (Linnaeus, 1758)	NBNSYS0000022371	Haemopis sanguisuga
22310101	Erpobdella octoculata (L.)	22310101	Erpobdella octoculata (Linnaeus, 1758)	NBNSYS0000022374	Erpobdella octoculata
22310102	Erpobdella testacea (Savigny)	22310102	Erpobdella testacea (Savigny, 1812)	NHMSYS0000068879	Erpobdella testacea
22310201	Dina lineata (Muller)	22310201	Dina lineata (O.F.Müller, 1774)	NHMSYS0000068878	Dina lineata
22310301	Trocheta bykowskii Gedroyc	22310301	Trocheta bykowskii Gedroyc, 1913	NBNSYS0000022377	Trocheta bykowskii
22310302	Trocheta subviridis Dutrochet	22310302	Trocheta subviridis Dutrochet, 1817	NBNSYS0000022376	Trocheta subviridis
24000000	Hydracarina	24000000	Hydracarina	NBNSYS0100012468	Hydracarina
34310000	Astacidae	34310000	Astacidae	NBNSYS0000159453	Astacidae
36110101	Asellus aquaticus (L.)	36110101	Asellus aquaticus (Linnaeus, 1758)	NBNSYS0000008589	Asellus aquaticus
36110104	Asellus meridianus Racovitza	36110202	Proasellus meridianus (Racovitza, 1919)	NBNSYS0000008591	Asellus meridianus
37110100	Corophium sp.	37110100	Corophium sp.	NBNSYS0000188483	Corophium
37130101	Crangonyx pseudogracilis Bousfield	37130101	Crangonyx pseudogracilis Bousfield, 1958	NBNSYS0000013808	Crangonyx pseudogracilis
37140202	Gammarus duebeni Liljeborg	37140202	Gammarus duebeni Liljeborg, 1852	NBNSYS0000013798	Gammarus duebeni
37140203	Gammarus lacustris Sars	37140203	Gammarus lacustris Sars, 1863	NBNSYS0000013799	Gammarus lacustris
37140206	Gammarus pulex (L.)	37140206	Gammarus pulex (Linnaeus, 1758)	NBNSYS0000013800	Gammarus pulex
37140208	Gammarus tigrinus Sexton	37140208	Gammarus tigrinus Sexton, 1939	NBNSYS0000033149	Gammarus tigrinus
37140209	Gammarus zaddachi Sexton	37140209	Gammarus zaddachi Sexton, 1912	NBNSYS0000013801	Gammarus zaddachi
37150201	Niphargus aquilex Schiodte	37150201	Niphargus aquilex Schiodte, 1855	NBNSYS0000013811	Niphargus aquilex
40110103	Siphlonurus lacustris Eaton	40110103	Siphlonurus lacustris (Eaton, 1870)	NBNSYS0000010862	Siphlonurus lacustris
40110201	Ameletus inopinatus Eaton	40140101	Ameletus inopinatus Eaton, 1887	NBNSYS0000010859	Ameletus inopinatus
40120101	Baetis atrebatinus Eaton	40120601	Labiobaetis atrebatinus (Eaton, 1870)	NBNSYS0100003541	Labiobaetis atrebatinus
40120102	Baetis buceratus Eaton	40120102	Baetis buceratus Eaton, 1870	NBNSYS0000010864	Baetis buceratus
40120103	Baetis digitatus Bengtsson	40120701	Nigrobaetis digitatus (Bengtsson, 1912)	NBNSYS0100004152	Nigrobaetis digitatus
40120105	Baetis muticus (L.)	40120501	Alainites muticus (Linnaeus, 1758)	NBNSYS0100001341	Alainites muticus

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40120106	Baetis niger (L.)	40120702	Nigrobaetis niger (Linnaeus, 1761)	NBNSYS0100004153	Nigrobaetis niger
40120107	Baetis rhodani (Pictet)	40120107	Baetis rhodani (Pictet, 1843-1845)	NHMSYS0000066962	Baetis rhodani
40120111	Baetis vernus Curtis	40120111	Baetis vernus Curtis, 1834	NBNSYS0000010871	Baetis vernus
4012011Z	Baetis scambus group	4012011Z	Baetis scambus group	<NEW-CODE>100011	Baetis scambus group
40120201	Centroptilum luteolum (Muller)	40120201	Centroptilum luteolum (Müller, 1776)	NHMSYS0000066963	Centroptilum luteolum
40120202	Centroptilum pennulatum Eaton	40120402	Procloeon pennulatum (Eaton, 1870)	NHMSYS0000066965	Procloeon pennulatum
40120301	Cloeon dipterum (L.)	40120301	Cloeon dipterum (Linnaeus, 1761)	NHMSYS0000066964	Cloeon dipterum
40120302	Cloeon simile Eaton	40120302	Cloeon simile Eaton, 1870	NBNSYS0000010875	Cloeon simile
40120401	Procloeon bifidum Bengtsson	40120401	Procloeon bifidum (Bengtsson, 1912)	NBNSYS0000010876	Procloeon bifidum
40130100	Rhithrogena sp.	40130100	Rhithrogena sp.	NHMSYS0000066955	Rhithrogena
40130201	Heptagenia fuscogrisea (Retzius)	40130601	Kageronia fuscogrisea (Retzius, 1783)	NBNSYS0100003524	Kageronia fuscogrisea
40130202	Heptagenia lateralis (Curtis)	40130502	Electrogena lateralis (Curtis, 1834)	<NEW-CODE>100012	Heptagenia lateralis
40130204	Heptagenia sulphurea (Muller)	40130204	Heptagenia sulphurea (Müller, 1776)	NHMSYS0000066973	Heptagenia sulphurea
40130400	Ecdyonurus sp.	40130400	Ecdyonurus sp.	NHMSYS0000066951	Ecdyonurus
40210101	Leptophlebia marginata (L.)	40210101	Leptophlebia marginata (Linnaeus, 1767)	NHMSYS0000066974	Leptophlebia marginata
40210102	Leptophlebia vespertina (L.)	40210102	Leptophlebia vespertina (Linnaeus, 1758)	NBNSYS0000010890	Leptophlebia vespertina
40210201	Paraleptophlebia cincta (Retzius)	40210201	Paraleptophlebia cincta (Retzius, 1835)	NBNSYS0000010891	Paraleptophlebia cincta
40210202	Paraleptophlebia submarginata (Stephens)	40210202	Paraleptophlebia submarginata (Stephens, 1835)	NBNSYS0000010892	Paraleptophlebia submarginata
40210203	Paraleptophlebia werneri Ulmer	40210203	Paraleptophlebia werneri Ulmer, 1919	NBNSYS0000010893	Paraleptophlebia werneri
40210301	Habrophlebia fusca (Curtis)	40210301	Habrophlebia fusca (Curtis, 1834)	NBNSYS0000010888	Habrophlebia fusca
40310101	Potamanthus luteus (L.)	40310101	Potamanthus luteus (Linnaeus, 1767)	NHMSYS0000066975	Potamanthus luteus
40320101	Ephemera danica Muller	40320101	Ephemera danica Müller, 1764	NHMSYS0000066970	Ephemera danica
40320102	Ephemera lineata Eaton	40320102	Ephemera lineata Eaton, 1870	NBNSYS0000010898	Ephemera lineata
40320103	Ephemera vulgata L.	40320103	Ephemera vulgata Linnaeus, 1758	NBNSYS0000010899	Ephemera vulgata
40410101	Ephemerella ignita (Poda)	40410201	Serratella ignita (Poda, 1761)	NBNSYS0100005389	Serratella ignita
40410102	Ephemerella notata Eaton	40410102	Ephemerella notata Eaton, 1887	NBNSYS0000010895	Ephemerella notata
40510101	Brachycercus harrisella Curtis	40510101	Brachycercus harrisellus Curtis, 1834	NBNSYS0000010900	Brachycercus harrisella
40510201	Caenis horaria (L.)	40510201	Caenis horaria (Linnaeus, 1758)	NHMSYS0000066966	Caenis horaria
40510204	Caenis rivulorum Eaton	40510204	Caenis rivulorum Eaton, 1884	NBNSYS0000010904	Caenis rivulorum
40510205	Caenis robusta Eaton	40510205	Caenis robusta Eaton, 1884	NBNSYS0000010905	Caenis robusta
40510208	Caenis pusilla Navas	40510208	Caenis pusilla Navás, 1913	NHMSYS0000066969	Caenis pusilla
4051020X	Caenis pseudorivulorum group	4051020X	Caenis pseudorivulorum group	<NEW-CODE>100013	Caenis pseudorivulorum group
4051020Z	Caenis luctuosa group	4051020Z	Caenis luctuosa group	<NEW-CODE>100014	Caenis luctuosa group
41110101	Taeniopteryx nebulosa (L.)	41110101	Taeniopteryx nebulosa (Linnaeus, 1758)	NBNSYS0000022416	Taeniopteryx nebulosa
41110301	Brachyptera putata (Newman)	41110301	Brachyptera putata (Newman, 1838)	NBNSYS0000022413	Brachyptera putata
41110302	Brachyptera risi (Morton)	41110302	Brachyptera risi (Morton, 1896)	NBNSYS0000022414	Brachyptera risi
41120101	Protonemura meyeri (Pictet)	41120101	Protonemura meyeri (Pictet, 1841)	NBNSYS0000022425	Protonemura meyeri
41120102	Protonemura montana Kimmins	41120102	Protonemura montana Kimmins, 1941	NBNSYS0000022426	Protonemura montana
41120103	Protonemura praecox (Morton)	41120103	Protonemura praecox (Morton, 1894)	NBNSYS0000022427	Protonemura praecox
41120201	Amphinemura standfussi Ris	41120201	Amphinemura standfussi Ris, 1902	NBNSYS0000022417	Amphinemura standfussi
41120202	Amphinemura sulcicollis (Stephens)	41120202	Amphinemura sulcicollis (Stephens, 1836)	NBNSYS0000022418	Amphinemura sulcicollis
41120301	Nemurella picteti Klapalek	41120301	Nemurella picteti Klapálek, 1900	NBNSYS0100013706	Nemurella picteti
41120401	Nemoura avicularis Morton	41120401	Nemoura avicularis Morton, 1894	NBNSYS0000022419	Nemoura avicularis
41120403	Nemoura cinerea (Retzius)	41120403	Nemoura cinerea (Retzius, 1783)	NBNSYS0000022421	Nemoura cinerea
4112040Z	Nemoura cambrica group	4112040Z	Nemoura cambrica group	<NEW-CODE>100015	Nemoura cambrica group
41130101	Leuctra fusca (L.)	41130101	Leuctra fusca (Linnaeus, 1758)	NBNSYS0000022428	Leuctra fusca
41130102	Leuctra geniculata (Stephens)	41130102	Leuctra geniculata (Stephens, 1836)	NBNSYS0000022429	Leuctra geniculata
41130103	Leuctra hippopus (Kempny)	41130103	Leuctra hippopus Kempny, 1899	NBNSYS0000022430	Leuctra hippopus
41130104	Leuctra inermis Kempny	41130104	Leuctra inermis Kempny, 1899	NBNSYS0000022431	Leuctra inermis
41130105	Leuctra moselyi Morton	41130105	Leuctra moselyi Morton, 1929	NBNSYS0000022432	Leuctra moselyi
41130106	Leuctra nigra (Olivier)	41130106	Leuctra nigra (Olivier, 1811)	NBNSYS0000022433	Leuctra nigra

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41140101	Capnia atra Morton	41140101	Capnia atra Morton, 1896	NBNSYS0000022434	Capnia atra
41140102	Capnia bifrons (Newman)	41140102	Capnia bifrons (Newman, 1839)	NBNSYS0000022435	Capnia bifrons
41210201	Perlodes microcephala (Pictet)	41210201	Perlodes microcephalus (Pictet, 1833)	NBNSYS0000022441	Perlodes microcephala
41210301	Diura bicaudata (L.)	41210301	Diura bicaudata (Linnaeus, 1758)	NBNSYS0000022437	Diura bicaudata
41210401	Isoperla grammatica (Poda)	41210401	Isoperla grammatica (Poda, 1761)	NBNSYS0000022439	Isoperla grammatica
41220101	Dinocras cephalotes (Curtis)	41220101	Dinocras cephalotes (Curtis, 1827)	NBNSYS0000022442	Dinocras cephalotes
41220201	Perla bipunctata Pictet	41220201	Perla bipunctata Pictet, 1833	NBNSYS0000022443	Perla bipunctata
41230102	Chloroperla torrentium (Pictet)	41230301	Siphonoperla torrentium (Pictet, 1841)	NBNSYS0000022445	Chloroperla torrentium
41230103	Chloroperla tripunctata (Scopoli)	41230103	Chloroperla tripunctata (Scopoli, 1763)	NBNSYS0000022446	Chloroperla tripunctata
42110101	Platycnemis pennipes (Pallas)	42110101	Platycnemis pennipes (Pallas, 1771)	NBNSYS0000005598	Platycnemis pennipes
42120101	Pyrrhosoma nymphula (Sulzer)	42120101	Pyrrhosoma nymphula (Sulzer, 1776)	NBNSYS0000005599	Pyrrhosoma nymphula
42120201	Ischnura elegans (Van der Linden)	42120201	Ischnura elegans (Vander Linden, 1820)	NBNSYS0000005600	Ischnura elegans
42120301	Enallagma cyathigerum (Charpentier)	42120301	Enallagma cyathigerum (Charpentier, 1840)	NBNSYS0000005602	Enallagma cyathigerum
4212040Z	Coenagrion puella group	4212040Z	Coenagrion puella group	<NEW-CODE>100016	Coenagrion puella group
42120601	Erythromma najas (Hansemann)	42120601	Erythromma najas (Hansemann, 1823)	NBNSYS0000005610	Erythromma najas
42140101	Calopteryx splendens (Harris)	42140101	Calopteryx splendens (Harris, 1782)	NBNSYS0000005617	Calopteryx splendens
42140102	Calopteryx virgo (L.)	42140102	Calopteryx virgo (Linnaeus, 1758)	NBNSYS0000005616	Calopteryx virgo
42210101	Gomphus vulgatissimus (L.)	42210101	Gomphus vulgatissimus (Linnaeus, 1758)	NBNSYS0000005620	Gomphus vulgatissimus
42220101	Cordulegaster boltonii (Donovan)	42220101	Cordulegaster boltonii (Donovan, 1807)	NBNSYS0000005621	Cordulegaster boltonii
42230101	Brachytron pratense (Muller)	42230101	Brachytron pratense (Müller, 1764)	NBNSYS0000005622	Brachytron pratense
42230200	Aeshna sp.	42230200	Aeshna sp.	NBNSYS0000039880	Aeshna
42250100	Orthetrum sp.	42250100	Orthetrum sp.	NBNSYS0000135890	Orthetrum
42250300	Sympetrum sp.	42250300	Sympetrum sp.	NBNSYS0000039911	Sympetrum
43110101	Mesovelia furcata Mulsant & Rey	43110101	Mesovelia furcata Mulsant & Rey, 1852	NBNSYS0000010354	Mesovelia furcata
43210102	Hydrometra stagnorum (L.)	43210102	Hydrometra stagnorum (Linnaeus, 1758)	NBNSYS0000010358	Hydrometra stagnorum
43220100	Velia sp.	43220100	Velia sp.	NBNSYS0000138826	Velia
43230111	Gerris argentatus Schummel	43230111	Gerris argentatus Schummel, 1832	NBNSYS0000010368	Gerris argentatus
43230114	Gerris lacustris (L.)	43230114	Gerris lacustris (Linnaeus, 1758)	NBNSYS0000010369	Gerris lacustris
43230116	Gerris odontogaster (Zetterstedt)	43230116	Gerris odontogaster (Zetterstedt, 1828)	NBNSYS0000010370	Gerris odontogaster
43230117	Gerris thoracicus Schummel	43230117	Gerris thoracicus Schummel, 1832	NBNSYS0000010366	Gerris thoracicus
43230121	Gerris najas (Degeer)	43230301	Aquarius najas (DeGeer, 1773)	NBNSYS0100012076	Gerris najas
43310101	Nepa cinerea L.	43310101	Nepa cinerea Linnaeus, 1758	NBNSYS0000010374	Nepa cinerea
43410101	Ilyocoris cimicoides (L.)	43410101	Ilyocoris cimicoides (Linnaeus, 1758)	NBNSYS0000010376	Ilyocoris cimicoides
43420101	Aphelocheirus aestivalis (Fabricius)	43420101	Aphelocheirus aestivalis (Fabricius, 1794)	NBNSYS0000010377	Aphelocheirus aestivalis
43510101	Notonecta glauca L.	43510101	Notonecta glauca Linnaeus, 1758	NBNSYS0000010378	Notonecta glauca
43510102	Notonecta maculata Fabricius	43510102	Notonecta maculata Fabricius, 1794	NBNSYS0000010381	Notonecta maculata
43510103	Notonecta obliqua Gallen	43510103	Notonecta obliqua Gallén in Thunberg, 1787	NBNSYS0000010380	Notonecta obliqua
43610100	Micronecta sp.	43610100	Micronecta sp.	NBNSYS0000051126	Micronecta
43610302	Cymatia coleoptrata (Fabricius)	43610302	Cymatia coleoptrata (Fabricius, 1777)	NBNSYS0000010387	Cymatia coleoptrata
43610501	Callicorixa praeusta (Fieber)	43610501	Callicorixa praeusta (Fieber, 1848)	NBNSYS0000010389	Callicorixa praeusta
43610502	Callicorixa wollastoni (Douglas & Scott)	43610502	Callicorixa wollastoni (Douglas & Scott, 1865)	NBNSYS0000010390	Callicorixa wollastoni
43610601	Corixa affinis Leach	43610601	Corixa affinis Leach, 1817	NBNSYS0000010394	Corixa affinis
43610602	Corixa dentipes (Thomson)	43610602	Corixa dentipes (Thomson, 1869)	NBNSYS0000010391	Corixa dentipes
43610603	Corixa panzeri (Fieber)	43610603	Corixa panzeri (Fieber, 1848)	NBNSYS0000010395	Corixa panzeri
43610604	Corixa punctata (Illiger)	43610604	Corixa punctata (Illiger, 1807)	NBNSYS0000010393	Corixa punctata
43610702	Hesperocorixa linnei (Fieber)	43610702	Hesperocorixa linnaei (Fieber, 1848)	NBNSYS0000010396	Hesperocorixa linnei
43610704	Hesperocorixa sahlbergi (Fieber)	43610704	Hesperocorixa sahlbergi (Fieber, 1848)	NBNSYS0000010397	Hesperocorixa sahlbergi
43610910	Sigara (Sigara) sp.	43610910	Sigara (Sigara) sp.	NBNSYS0100015230	Sigara (Sigara)
43610921	Sigara distincta (Fieber)	43610921	Sigara (Subsigara) distincta (Fieber, 1848)	NBNSYS0000010404	Sigara distincta
43610922	Sigara falleni (Fieber)	43610922	Sigara (Subsigara) falleni (Fieber, 1848)	NBNSYS0000010405	Sigara falleni
43610924	Sigara fossarum (Leach)	43610924	Sigara (Subsigara) fossarum (Leach, 1817)	NBNSYS0000010407	Sigara fossarum

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43610925	Sigara scotti (Fieber)	43610925	Sigara (Subsigara) scotti (Douglas & Scott, 1868)	NBNSYS0000010408	Sigara scotti
43610941	Sigara lateralis (Leach)	43610941	Sigara (Vermicorixa) lateralis (Leach, 1817)	NBNSYS0000010409	Sigara lateralis
43610951	Sigara nigrolineata (Fieber)	43610951	Sigara (Pseudovermicorixa) nigrolineata (Fieber, 1848)	NBNSYS0000010410	Sigara nigrolineata
43610972	Sigara semistriata (Fieber)	43610972	Sigara (Retrocorixa) semistriata (Fieber, 1848)	NBNSYS0000010413	Sigara semistriata
43610973	Sigara venusta (Douglas & Scott)	43610973	Sigara (Retrocorixa) venusta (Douglas & Scott, 1869)	NBNSYS0000010414	Sigara venusta
45110101	Brychius elevatus (Panzer)	45110101	Brychius elevatus (Panzer, 1793)	NBNSYS0000007493	Brychius elevatus
45110302	Haliplus confinis Stephens	45110302	Haliplus confinis Stephens, 1828	NBNSYS0000007496	Haliplus confinis
45110303	Haliplus flavicollis Sturm	45110303	Haliplus flavicollis Sturm, 1834	NBNSYS0000007497	Haliplus flavicollis
45110304	Haliplus fluviatilis Aube	45110304	Haliplus fluviatilis Aubé, 1836	NBNSYS0000007498	Haliplus fluviatilis
45110307	Haliplus heydeni Wehncke	45110307	Haliplus heydeni Wehncke, 1875	NBNSYS0000007501	Haliplus heydeni
45110308	Haliplus immaculatus Gerhardt	45110308	Haliplus immaculatus Gerhardt, 1877	NBNSYS0000007502	Haliplus immaculatus
45110309	Haliplus laminatus Schaller	45110309	Haliplus laminatus (Schaller, 1783)	NBNSYS0000007503	Haliplus laminatus
45110311	Haliplus lineatocollis (Marsham)	45110311	Haliplus lineatocollis (Marsham, 1802)	NBNSYS0000007504	Haliplus lineatocollis
45110312	Haliplus lineolatus Mannerheim	45110312	Haliplus lineolatus Mannerheim, 1844	NBNSYS0000007505	Haliplus lineolatus
45110315	Haliplus ruficollis (Degeer)	45110315	Haliplus ruficollis (DeGeer, 1774)	NBNSYS0000007508	Haliplus ruficollis
45110318	Haliplus wehnckei (Gerhardt)	45110318	Haliplus sibericus Motschulsky, 1860	NBNSYS0000007511	Haliplus wehnckei
45130101	Noterus clavicornis (Degeer)	45130101	Noterus clavicornis (DeGeer, 1774)	NBNSYS0000007513	Noterus clavicornis
45140101	Laccophilus hyalinus (Degeer)	45140101	Laccophilus hyalinus (DeGeer, 1774)	NBNSYS0000007516	Laccophilus hyalinus
45140102	Laccophilus minutus (L.)	45140102	Laccophilus minutus (Linnaeus, 1758)	NBNSYS0000007517	Laccophilus minutus
45140301	Hyphydrus ovatus (L.)	45140301	Hyphydrus ovatus (Linnaeus, 1761)	NBNSYS0000007521	Hyphydrus ovatus
45140602	Hygrotus inaequalis (Fabricius)	45140612	Hygrotus (Hygrotus) inaequalis (Fabricius, 1777)	NBNSYS0000007526	Hygrotus inaequalis
45140604	Hygrotus versicolor (Schaller)	45140614	Hygrotus (Hygrotus) versicolor (Schaller, 1783)	NBNSYS0000007528	Hygrotus versicolor
45140801	Hydroporus angustatus Sturm	45140801	Hydroporus angustatus Sturm, 1835	NBNSYS0000007534	Hydroporus angustatus
45140807	Hydroporus ferrugineus Stephens	45140807	Hydroporus ferrugineus Stephens, 1829	NBNSYS0000007539	Hydroporus ferrugineus
45140817	Hydroporus memnonius Nicolai	45140817	Hydroporus memnonius Nicolai, 1822	NBNSYS0000007548	Hydroporus memnonius
45140821	Hydroporus nigrita (Fabricius)	45140821	Hydroporus nigrita (Fabricius, 1792)	NBNSYS0000007551	Hydroporus nigrita
45140822	Hydroporus obscurus Sturm	45140822	Hydroporus obscurus Sturm, 1835	NBNSYS0000007552	Hydroporus obscurus
45140824	Hydroporus palustris (L.)	45140824	Hydroporus palustris (Linnaeus, 1761)	NBNSYS0000007554	Hydroporus palustris
45140825	Hydroporus planus (Fabricius)	45140825	Hydroporus planus (Fabricius, 1782)	NBNSYS0000007555	Hydroporus planus
45140826	Hydroporus pubescens (Gyllenhal)	45140826	Hydroporus pubescens (Gyllenhal, 1808)	NBNSYS0000007556	Hydroporus pubescens
45140831	Hydroporus tessellatus Drapiez	45140831	Hydroporus tessellatus (Drapiez, 1819)	NBNSYS0000007560	Hydroporus tessellatus
45140901	Stictonectes lepidus (Olivier)	45140901	Stictonectes lepidus (Olivier, 1795)	NBNSYS0000007564	Stictonectes lepidus
45141004	Graptodytes pictus (Fabricius)	45141004	Graptodytes pictus (Fabricius, 1787)	NBNSYS0000007568	Graptodytes pictus
45141101	Porhydrus lineatus (Fabricius)	45141101	Porhydrus lineatus (Fabricius, 1775)	NBNSYS0000007569	Porhydrus lineatus
45141201	Deronectes latus (Stephens)	45141201	Deronectes latus (Stephens, 1829)	NBNSYS0000007570	Deronectes latus
45141301	Potamonectes assimilis (Paykull)	45141301	Nebrioporus assimilis (Paykull, 1798)	NBNSYS0100004083	Nebrioporus assimilis
45141303	Potamonectes depressus (Fabricius)	45141303	Nebrioporus depressus (Fabricius, 1775)	NBNSYS0000007572	Nebrioporus depressus
45141401	Stictotarsus duodecimpustulatus (Fabricius)	45141401	Stictotarsus duodecimpustulatus (Fabricius, 1792)	NBNSYS0000007576	Stictotarsus duodecimpustulatus
45141501	Oreodytes davisii (Curtis)	45141501	Oreodytes davisii (Curtis, 1831)	NBNSYS0000152835	Oreodytes davisii
45141502	Oreodytes sanmarkii (Sahlberg)	45141502	Oreodytes sanmarkii (C.R. Sahlberg, 1826)	NBNSYS0000152838	Oreodytes sanmarkii
45141503	Oreodytes septentrionalis (Sahlberg)	45141503	Oreodytes septentrionalis (Gyllenhal, 1826)	NBNSYS0000007580	Oreodytes septentrionalis
45141601	Scarodytes halensis (Fabricius)	45141601	Scarodytes halensis (Fabricius, 1787)	NBNSYS0000007581	Scarodytes halensis
45141901	Platambus maculatus (L.)	45141901	Platambus maculatus (Linnaeus, 1758)	NBNSYS0000007584	Platambus maculatus
45142004	Agabus bipustulatus (L.)	45142004	Agabus bipustulatus (Linnaeus, 1767)	NBNSYS0000007588	Agabus bipustulatus
45142006	Agabus chalconatus (Panzer)	45142108	Ilybius chalconatus (Panzer, 1796)	NBNSYS0000007590	Agabus chalconatus
45142009	Agabus didymus (Olivier)	45142009	Agabus didymus (Olivier, 1795)	NBNSYS0000007593	Agabus didymus
45142011	Agabus guttatus (Paykull)	45142011	Agabus guttatus (Paykull, 1798)	NBNSYS0000007594	Agabus guttatus
45142016	Agabus paludosus (Fabricius)	45142016	Agabus paludosus (Fabricius, 1801)	NBNSYS0000007599	Agabus paludosus
45142018	Agabus sturmii (Gyllenhal)	45142018	Agabus sturmii (Gyllenhal, 1808)	NBNSYS0000007601	Agabus sturmii
45142100	Ilybius sp.	45142100	Ilybius sp.	NBNSYS0000134103	Ilybius
45142301	Colymbetes fuscus (L.)	45142301	Colymbetes fuscus (Linnaeus, 1758)	NBNSYS0000007618	Colymbetes fuscus

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
45142705	Dytiscus marginalis L.	45142705	Dytiscus marginalis Linnaeus, 1758	NBNSYS0000007632	Dytiscus marginalis
45142706	Dytiscus semisulcatus Muller	45142706	Dytiscus semisulcatus O.F. Müller, 1776	NBNSYS0000007633	Dytiscus semisulcatus
45150201	Gyrinus aeratus Stephens	45150201	Gyrinus aeratus Stephens, 1835	NBNSYS0000007635	Gyrinus aeratus
45150204	Gyrinus distinctus Aube	45150204	Gyrinus distinctus Aubé, 1837	NBNSYS0000007638	Gyrinus distinctus
45150205	Gyrinus marinus Gyllenhal	45150205	Gyrinus marinus Gyllenhal, 1808	NBNSYS0000007639	Gyrinus marinus
4515020Z	Gyrinus natator group	4515020Z	Gyrinus natator group	<NEW-CODE>100019	Gyrinus natator group
45150212	Gyrinus urinator Illiger	45150212	Gyrinus urinator Illiger, 1807	NBNSYS0000007645	Gyrinus urinator
45150401	Orectochilus villosus (Muller)	45150401	Orectochilus villosus (O.F. Müller, 1776)	NBNSYS0000007646	Orectochilus villosus
45310201	Hydrochus angustatus Germar	45360101	Hydrochus angustatus Germar, 1824	NBNSYS0000007649	Hydrochus angustatus
45310341	Helophorus aequalis Thomson	45330141	Helophorus (Meghelophorus) aequalis Thomson, 1868	NBNSYS0000007655	Helophorus aequalis
45310342	Helophorus grandis Illiger	45330142	Helophorus (Meghelophorus) grandis Illiger, 1798	NBNSYS0000007662	Helophorus grandis
45310351	Helophorus arvernicus Mulsant	45330151	Helophorus (Rhopalohelophorus) arvernicus Mulsant, 1846	NBNSYS0000007657	Helophorus arvernicus
45310352	Helophorus brevipalpis Bedel	45330152	Helophorus (Rhopalohelophorus) brevipalpis Bedel, 1881	NBNSYS0000007658	Helophorus brevipalpis
45310362	Helophorus flavipes Fabricius	45330162	Helophorus (Helophorus) flavipes Fabricius, 1792	NBNSYS0000007660	Helophorus flavipes
45310368	Helophorus minutus Fabricius	45330168	Helophorus (Helophorus) minutus Fabricius, 1775	NBNSYS0000007667	Helophorus minutus
45310371	Helophorus obscurus Mulsant	4533016A	Helophorus (Helophorus) obscurus Mulsant, 1844	NBNSYS0000007670	Helophorus obscurus
45310372	Helophorus strigifrons Thomson	4533016B	Helophorus (Helophorus) strigifrons Thomson, 1868	NBNSYS0000007673	Helophorus strigifrons
45311002	Paracymus scutellaris (Rosenhauer)	45351002	Paracymus scutellaris (Rosenhauer, 1856)	NBNSYS0000007705	Paracymus scutellaris
45311101	Hydrobius fuscipes (L.)	45351101	Hydrobius fuscipes (Linnaeus, 1758)	NBNSYS0000010907	Hydrobius fuscipes
45311301	Anacaena bipustulata (Marsham)	45351301	Anacaena bipustulata (Marsham, 1802)	NBNSYS0000007707	Anacaena bipustulata
45311302	Anacaena globulus (Paykull)	45351302	Anacaena globulus (Paykull, 1829)	NBNSYS0000007708	Anacaena globulus
45311303	Anacaena limbata (Fabricius)	45351303	Anacaena limbata (Fabricius, 1792)	NBNSYS0000033265	Anacaena limbata
45311304	Anacaena lutescens (Stephens)	45351304	Anacaena lutescens (Stephens, 1829)	<NEW-CODE>100020	Anacaena lutescens
45311411	Laccobius biguttatus Gerhardt	45351411	Laccobius (Laccobius) colon (Stephens, 1829)	NBNSYS0000007713	Laccobius biguttatus
45311412	Laccobius minutus (L.)	45351412	Laccobius (Laccobius) minutus (Linnaeus, 1758)	NBNSYS0000007715	Laccobius minutus
45311421	Laccobius atratus Rottenburg	45351421	Laccobius (Macrolaccobius) atratus Rottenburg, 1874	NBNSYS0000007711	Laccobius atratus
45311422	Laccobius atrocephalus Reitter	45351422	Laccobius (Macrolaccobius) ytenensis Sharp, 1910	NBNSYS0000007712	Laccobius atrocephalus
45311426	Laccobius sinuatus Motschulsky	45351426	Laccobius (Macrolaccobius) sinuatus Motschulsky, 1849	NBNSYS0000007718	Laccobius sinuatus
45311427	Laccobius striatulus (Fabricius)	45351427	Laccobius (Macrolaccobius) striatulus (Fabricius, 1801)	NBNSYS0000007719	Laccobius striatulus
45311708	Enochrus testaceus (Fabricius)	45351708	Enochrus testaceus (Fabricius, 1801)	NBNSYS0000007733	Enochrus testaceus
45410103	Ochthebius bicolon Germar	45410103	Ochthebius bicolon Germar, 1824	NBNSYS0000007744	Ochthebius bicolon
45410104	Ochthebius dilatatus Stephens	45410104	Ochthebius dilatatus Stephens, 1829	NBNSYS0000007746	Ochthebius dilatatus
45410106	Ochthebius exsculptus Germar	45410106	Ochthebius exsculptus (Germar, 1824)	NBNSYS0000007748	Ochthebius exsculptus
45410109	Ochthebius minimus (Fabricius)	45410109	Ochthebius minimus (Fabricius, 1792)	NBNSYS0000007751	Ochthebius minimus
45410202	Hydraena gracilis Germar	45410202	Hydraena gracilis Germar, 1824	NBNSYS0000007759	Hydraena gracilis
45410204	Hydraena nigrita Germar	45410204	Hydraena nigrita Germar, 1824	NBNSYS0000007761	Hydraena nigrita
45410206	Hydraena pulchella Germar	45410206	Hydraena pulchella Germar, 1824	NBNSYS0000007763	Hydraena pulchella
45410208	Hydraena riparia Kugelann	45410208	Hydraena riparia Kugelann, 1794	NBNSYS0000007765	Hydraena riparia
45410209	Hydraena rufipes Curtis	45410209	Hydraena rufipes Curtis, 1830	NBNSYS0000007766	Hydraena rufipes
45410211	Hydraena testacea Curtis	45410211	Hydraena testacea Curtis, 1831	NBNSYS0000007767	Hydraena testacea
45410303	Limnebius nitidus (Marsham)	45410303	Limnebius nitidus (Marsham, 1802)	NBNSYS0000007770	Limnebius nitidus
45410305	Limnebius truncatellus (Thunberg)	45410305	Limnebius truncatellus (Thunberg, 1794)	NBNSYS0000007772	Limnebius truncatellus
45510100	Elodes sp.	45510100	Elodes sp.	NBNSYS0000132774	Elodes
45510300	Cyphon sp.	45510300	Cyphon sp.	NBNSYS0000132190	Cyphon
45510401	Prionocyphon serricornis (Muller)	45510401	Prionocyphon serricornis (Müller, 1821)	NBNSYS0000024184	Prionocyphon serricornis
45510501	Hydrocyphon deflexicollis (Muller)	45510501	Hydrocyphon deflexicollis (Müller, 1821)	NBNSYS0000024185	Hydrocyphon deflexicollis
45620101	Helichus substriatus (Muller)	45620101	Pomatinus substriatus (Müller, 1806)	NBNSYS0000148219	Helichus substriatus
45620200	Dryops sp.	45620200	Dryops sp.	NBNSYS0000132652	Dryops
45630101	Elmis aenea (Muller)	45630101	Elmis aenea (Müller, 1806)	NBNSYS0000007783	Elmis aenea
45630201	Esolus parallelepipedus (Muller)	45630201	Esolus parallelepipedus (Müller, 1806)	NBNSYS0000007784	Esolus parallelepipedus
45630301	Limnius volckmari (Panzer)	45630301	Limnius volckmari (Panzer, 1793)	NBNSYS0000007785	Limnius volckmari

Rev. Maitland Code	**Rev. Maitland Name**	**Furse Code**	**Furse Name**	**NBN Code**	**NBN Name**
45630401	Macronychus quadrituberculatus Muller	45630401	Macronychus quadrituberculatus Müller, 1806	NBNSYS0000007786	Macronychus quadrituberculatus
45630501	Normandia nitens (Muller)	45630501	Normandia nitens (Müller, 1817)	NBNSYS0000007787	Normandia nitens
45630601	Oulimnius major (Rey)	45630601	Oulimnius major (Rey, 1889)	NBNSYS0000007788	Oulimnius major
45630602	Oulimnius rivularis (Rosenhauer)	45630602	Oulimnius rivularis (Rosenhauer, 1856)	NBNSYS0000007789	Oulimnius rivularis
45630603	Oulimnius troglodytes (Gyllenhal)	45630603	Oulimnius troglodytes (Gyllenhal, 1827)	NBNSYS0000007790	Oulimnius troglodytes
45630604	Oulimnius tuberculatus (Muller)	45630604	Oulimnius tuberculatus (Müller, 1806)	NBNSYS0000007791	Oulimnius tuberculatus
45630701	Riolus cupreus (Muller)	45630701	Riolus cupreus (Müller, 1806)	NBNSYS0000007792	Riolus cupreus
45630702	Riolus subviolaceus (Muller)	45630702	Riolus subviolaceus (Müller, 1817)	NBNSYS0000007793	Riolus subviolaceus
46110101	Sialis fuliginosa Pictet	46110101	Sialis fuliginosa Pictet, 1836	NBNSYS0000010794	Sialis fuliginosa
46110102	Sialis lutaria (L.)	46110102	Sialis lutaria (Linnaeus, 1758)	NBNSYS0000010795	Sialis lutaria
46110103	Sialis nigripes Pictet	46110103	Sialis nigripes Pictet, 1865	NBNSYS0000010796	Sialis nigripes
47110101	Osmylus fulvicephalus (Scopoli)	47110101	Osmylus fulvicephalus (Scopoli, 1763)	NBNSYS0000010808	Osmylus fulvicephalus
47120100	Sisyra sp.	47120100	Sisyra sp.	NBNSYS0000137797	Sisyra
48110101	Rhyacophila dorsalis (Curtis)	48110101	Rhyacophila dorsalis (Curtis, 1834)	NBNSYS0000008339	Rhyacophila dorsalis
48110102	Rhyacophila munda Mclachlan	48110102	Rhyacophila munda McLachlan, 1862	NBNSYS0000008340	Rhyacophila munda
48110103	Rhyacophila obliterata Mclachlan	48110103	Rhyacophila obliterata McLachlan, 1863	NBNSYS0000008341	Rhyacophila obliterata
48110104	Rhyacophila septentrionis Mclachlan	48110104	Rhyacophila fasciata Hagen, 1859	NBNSYS0000008342	Rhyacophila septentrionis
48120100	Glossosoma sp.	48120100	Glossosoma sp.	NBNSYS0000042268	Glossosoma
48120200	Agapetus sp.	48120200	Agapetus sp.	NBNSYS0000037044	Agapetus
48130101	Agraylea multipunctata Curtis	48130101	Agraylea multipunctata Curtis, 1834	NBNSYS0000008349	Agraylea multipunctata
48130102	Agraylea sexmaculata Curtis	48130102	Agraylea sexmaculata Curtis, 1834	NBNSYS0000008350	Agraylea sexmaculata
48130201	Allotrichia pallicornis (Eaton)	48130201	Allotrichia pallicornis (Eaton, 1873)	NBNSYS0000008351	Allotrichia pallicornis
48130300	Hydroptila sp.	48130300	Hydroptila sp.	NBNSYS0000042281	Hydroptila
48130400	Oxyethira sp.	48130400	Oxyethira sp.	NBNSYS0000042308	Oxyethira
48130600	Ithytrichia sp.	48130600	Ithytrichia sp.	NBNSYS0000134173	Ithytrichia
48210101	Philopotamus montanus (Donovan)	48210101	Philopotamus montanus (Donovan, 1813)	NBNSYS0000008380	Philopotamus montanus
48210200	Wormaldia sp.	48210200	Wormaldia sp.	NBNSYS0000138908	Wormaldia
48210301	Chimarra marginata (L.)	48210301	Chimarra marginata (Linnaeus, 1761)	NBNSYS0000008384	Chimarra marginata
48220100	Lype sp.	48220100	Lype sp.	NBNSYS0000042295	Lype
48220201	Metalype fragilis (Pictet)	48220201	Metalype fragilis (Pictet, 1834)	NBNSYS0000008387	Metalype fragilis
48220301	Psychomyia pusilla (Fabricius)	48220301	Psychomyia pusilla (Fabricius, 1781)	NBNSYS0000008388	Psychomyia pusilla
48220402	Tinodes dives (Pictet)	48220402	Tinodes dives (Pictet, 1834)	NBNSYS0000008390	Tinodes dives
48220407	Tinodes unicolor (Pictet)	48220407	Tinodes unicolor (Pictet, 1834)	NBNSYS0000008395	Tinodes unicolor
48220408	Tinodes waeneri (L.)	48220408	Tinodes waeneri (Linnaeus, 1758)	NBNSYS0000008396	Tinodes waeneri
48230101	Ecnomus tenellus (Rambur)	48230101	Ecnomus tenellus (Rambur, 1842)	NBNSYS0000008397	Ecnomus tenellus
48240101	Cyrnus flavidus Mclachlan	48240101	Cyrnus flavidus McLachlan, 1864	NBNSYS0000008399	Cyrnus flavidus
48240103	Cyrnus trimaculatus (Curtis)	48240103	Cyrnus trimaculatus (Curtis, 1834)	NBNSYS0000008401	Cyrnus trimaculatus
48240202	Holocentropus picicornis (Stephens)	48240202	Holocentropus picicornis (Stephens, 1836)	NBNSYS0000008403	Holocentropus picicornis
48240301	Neureclipsis bimaculata (L.)	48240301	Neureclipsis bimaculata (Linnaeus, 1758)	NBNSYS0000008405	Neureclipsis bimaculata
48240402	Plectrocnemia conspersa (Curtis)	48240402	Plectrocnemia conspersa (Curtis, 1834)	NBNSYS0000008407	Plectrocnemia conspersa
48240403	Plectrocnemia geniculata Mclachlan	48240403	Plectrocnemia geniculata McLachlan, 1871	NBNSYS0000008408	Plectrocnemia geniculata
48240501	Polycentropus flavomaculatus (Pictet)	48240501	Polycentropus flavomaculatus (Pictet, 1834)	NBNSYS0000008409	Polycentropus flavomaculatus
48240502	Polycentropus irroratus (Curtis)	48240502	Polycentropus irroratus (Curtis, 1835)	NBNSYS0000008410	Polycentropus irroratus
48240503	Polycentropus kingi Mclachlan	48240503	Polycentropus kingi McLachlan, 1881	NBNSYS0000008411	Polycentropus kingi
48250101	Cheumatopsyche lepida (Pictet)	48250101	Cheumatopsyche lepida (Pictet, 1834)	NBNSYS0000008412	Cheumatopsyche lepida
48250201	Hydropsyche angustipennis (Curtis)	48250201	Hydropsyche angustipennis (Curtis, 1834)	NBNSYS0000008413	Hydropsyche angustipennis
48250203	Hydropsyche contubernalis Mclachlan	48250203	Hydropsyche contubernalis McLachlan, 1865	NBNSYS0000008415	Hydropsyche contubernalis
48250205	Hydropsyche fulvipes (Curtis)	48250205	Hydropsyche fulvipes (Curtis, 1834)	NBNSYS0000008417	Hydropsyche fulvipes
48250206	Hydropsyche instabilis (Curtis)	48250206	Hydropsyche instabilis (Curtis, 1834)	NBNSYS0000008418	Hydropsyche instabilis
48250207	Hydropsyche pellucidula (Curtis)	48250207	Hydropsyche pellucidula (Curtis, 1834)	NBNSYS0000008419	Hydropsyche pellucidula
48250208	Hydropsyche saxonica Mclachlan	48250208	Hydropsyche saxonica McLachlan, 1884	NBNSYS0000008420	Hydropsyche saxonica

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48250209	Hydropsyche siltalai Dohler	48250209	Hydropsyche siltalai Döhler, 1963	NBNSYS0000008421	Hydropsyche siltalai
48250301	Diplectrona felix Mclachlan	48250301	Diplectrona felix McLachlan, 1878	NBNSYS0000008422	Diplectrona felix
48310100	Agrypnia sp.	4831010Z	Agrypnia obsoleta group	<NEW-CODE>100022	Agrypnia obsoleta group
48310500	Phryganea sp.	48310500	Phryganea sp.	NBNSYS0000039909	Phryganea
48320101	Brachycentrus subnubilus Curtis	48320101	Brachycentrus subnubilus Curtis, 1834	NBNSYS0000008433	Brachycentrus subnubilus
48330101	Crunoecia irrorata (Curtis)	48330101	Crunoecia irrorata (Curtis, 1834)	NBNSYS0000008434	Crunoecia irrorata
48330201	Lasiocephala basalis (Kolenati)	48330201	Lasiocephala basalis (Kolenati, 1848)	NBNSYS0000008435	Lasiocephala basalis
48330301	Lepidostoma hirtum (Fabricius)	48330301	Lepidostoma hirtum (Fabricius, 1775)	NBNSYS0000008436	Lepidostoma hirtum
48340202	Apatania muliebris Mclachlan	483B0102	Apatania muliebris McLachlan, 1866	NBNSYS0000008439	Apatania muliebris
48340301	Drusus annulatus (Stephens)	48340301	Drusus annulatus (Stephens, 1837)	NBNSYS0000008442	Drusus annulatus
48340401	Ecclisopteryx guttulata (Pictet)	48340401	Ecclisopteryx guttulata (Pictet, 1834)	NBNSYS0000008443	Ecclisopteryx guttulata
48340600	Halesus sp.	48340600	Halesus sp.	NBNSYS0000042270	Halesus
48340701	Hydatophylax infumatus (Mclachlan)	48340701	Hydatophylax infumatus (McLachlan, 1865)	NBNSYS0000008448	Hydatophylax infumatus
48340801	Melampophylax mucoreus (Hagen)	48340801	Melampophylax mucoreus (Hagen, 1861)	NBNSYS0000008449	Melampophylax mucoreus
48341401	Anabolia nervosa (Curtis)	48341401	Anabolia nervosa (Curtis, 1834)	NBNSYS0000008462	Anabolia nervosa
48341501	Glyphotaelius pellucidus (Retzius)	48341501	Glyphotaelius pellucidus (Retzius, 1783)	NBNSYS0000008463	Glyphotaelius pellucidus
48341703	Limnephilus binotatus Curtis	48341703	Limnephilus binotatus Curtis, 1834	NBNSYS0000008468	Limnephilus binotatus
48341704	Limnephilus bipunctatus Curtis	48341704	Limnephilus bipunctatus Curtis, 1834	NBNSYS0000008469	Limnephilus bipunctatus
48341708	Limnephilus decipiens (Kolenati)	48341708	Limnephilus decipiens (Kolenati, 1848)	NBNSYS0000008473	Limnephilus decipiens
48341711	Limnephilus extricatus Mclachlan	48341711	Limnephilus extricatus McLachlan, 1865	NBNSYS0000008475	Limnephilus extricatus
48341712	Limnephilus flavicornis (Fabricius)	48341712	Limnephilus flavicornis (Fabricius, 1787)	NBNSYS0000008476	Limnephilus flavicornis
48341713	Limnephilus fuscicornis (Rambur)	48341713	Limnephilus fuscicornis (Rambur, 1842)	NBNSYS0000008477	Limnephilus fuscicornis
48341719	Limnephilus lunatus Curtis	48341719	Limnephilus lunatus Curtis, 1834	NBNSYS0000008483	Limnephilus lunatus
48341722	Limnephilus marmoratus Curtis	48341722	Limnephilus marmoratus Curtis, 1834	NBNSYS0000008485	Limnephilus marmoratus
48341725	Limnephilus politus Mclachlan	48341725	Limnephilus politus McLachlan, 1865	NBNSYS0000008488	Limnephilus politus
48341726	Limnephilus rhombicus (L.)	48341726	Limnephilus rhombicus (Linnaeus, 1758)	NBNSYS0000008489	Limnephilus rhombicus
48341732	Limnephilus vittatus (Fabricius)	48341732	Limnephilus vittatus (Fabricius, 1798)	NBNSYS0000008494	Limnephilus vittatus
48341W00	Micropterna group	48340W00	Micropterna group	<NEW-CODE>100025	Micropterna group
48341X00	Potamophylax group	48340X00	Potamophylax group	<NEW-CODE>100026	Potamophylax group
48350101	Goera pilosa (Fabricius)	48350101	Goera pilosa (Fabricius, 1775)	NBNSYS0000008498	Goera pilosa
48350201	Silo nigricornis (Pictet)	48350201	Silo nigricornis (Pictet, 1834)	NBNSYS0000008499	Silo nigricornis
48350202	Silo pallipes (Fabricius)	48350202	Silo pallipes (Fabricius, 1781)	NBNSYS0000008500	Silo pallipes
48360101	Beraea maurus (Curtis)	48360101	Beraea maurus (Curtis, 1834)	NBNSYS0000008501	Beraea maurus
48360102	Beraea pullata (Curtis)	48360102	Beraea pullata (Curtis, 1834)	NBNSYS0000008502	Beraea pullata
48360201	Beraeodes minutus (L.)	48360201	Beraeodes minutus (Linnaeus, 1761)	NBNSYS0000008503	Beraeodes minutus
48370101	Notidobia ciliaris (L.)	48370101	Notidobia ciliaris (Linnaeus, 1761)	NBNSYS0000008505	Notidobia ciliaris
48370201	Sericostoma personatum (Spence)	48370201	Sericostoma personatum (Spence in Kirby & Spence, 1826)	NBNSYS0000008506	Sericostoma personatum
48380101	Odontocerum albicorne (Scopoli)	48380101	Odontocerum albicorne (Scopoli, 1763)	NBNSYS0000008507	Odontocerum albicorne
48390101	Molanna angustata Curtis	48390101	Molanna angustata Curtis, 1834	NBNSYS0000008509	Molanna angustata
48410101	Athripsodes albifrons (L.)	483A0101	Athripsodes albifrons (Linnaeus, 1758)	NBNSYS0000008510	Athripsodes albifrons
48410102	Athripsodes aterrimus (Stephens)	483A0102	Athripsodes aterrimus (Stephens, 1836)	NBNSYS0000008512	Athripsodes aterrimus
48410103	Athripsodes bilineatus (L.)	483A0103	Athripsodes bilineatus (Linnaeus, 1758)	NBNSYS0000008513	Athripsodes bilineatus
48410104	Athripsodes cinereus (Curtis)	483A0104	Athripsodes cinereus (Curtis, 1834)	NBNSYS0000008514	Athripsodes cinereus
48410105	Athripsodes commutatus (Rostock)	483A0105	Athripsodes commutatus (Rostock, 1874)	NBNSYS0000008515	Athripsodes commutatus
48410201	Ceraclea albimacula (Rambur)	483A0201	Ceraclea albimacula (Rambur, 1842)	NBNSYS0000008516	Ceraclea albimacula
48410202	Ceraclea annulicornis (Stephens)	483A0202	Ceraclea annulicornis (Stephens, 1836)	NBNSYS0000008517	Ceraclea annulicornis
48410203	Ceraclea dissimilis (Stephens)	483A0203	Ceraclea dissimilis (Stephens, 1836)	NBNSYS0000008518	Ceraclea dissimilis
48410204	Ceraclea fulva (Rambur)	483A0204	Ceraclea fulva (Rambur, 1842)	NBNSYS0000008519	Ceraclea fulva
48410205	Ceraclea nigronervosa (Retzius)	483A0205	Ceraclea nigronervosa (Retzius, 1783)	NBNSYS0000008520	Ceraclea nigronervosa
48410206	Ceraclea senilis (Burmeister)	483A0206	Ceraclea senilis (Burmeister, 1839)	NBNSYS0000008521	Ceraclea senilis
48410302	Leptocerus lusitanicus (Mclachlan)	483A0302	Leptocerus lusitanicus (McLachlan, 1884)	NBNSYS0000008523	Leptocerus lusitanicus

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48410401	Mystacides azurea (L.)	483A0401	Mystacides azurea (Linnaeus, 1761)	NBNSYS0000008525	Mystacides azurea
48410402	Mystacides longicornis (L.)	483A0402	Mystacides longicornis (Linnaeus, 1758)	NBNSYS0000008526	Mystacides longicornis
48410403	Mystacides nigra (L.)	483A0403	Mystacides nigra (Linnaeus, 1758)	NBNSYS0000008527	Mystacides nigra
48410502	Adicella reducta (Mclachlan)	483A0502	Adicella reducta (McLachlan, 1865)	NBNSYS0000008529	Adicella reducta
48410701	Triaenodes bicolor (Curtis)	483A0701	Triaenodes bicolor (Curtis, 1834)	NBNSYS0000008531	Triaenodes bicolor
48410801	Ylodes conspersus (Rambur)	483A0801	Ylodes conspersus (Rambur, 1842)	NBNSYS0000008532	Ylodes conspersus
48410803	Ylodes simulans (Tjeder)	483A0803	Ylodes simulans (Tjeder, 1929)	NBNSYS0000008534	Ylodes simulans
48410902	Oecetis lacustris (Pictet)	483A0902	Oecetis lacustris (Pictet, 1834)	NBNSYS0000008536	Oecetis lacustris
48410903	Oecetis notata (Rambur)	483A0903	Oecetis notata (Rambur, 1842)	NBNSYS0000008537	Oecetis notata
48410904	Oecetis ochracea (Curtis)	483A0904	Oecetis ochracea (Curtis, 1825)	NBNSYS0000008538	Oecetis ochracea
48410905	Oecetis testacea (Curtis)	483A0905	Oecetis testacea (Curtis, 1834)	NBNSYS0000008539	Oecetis testacea
49110300	Parapoynx sp.	49110300	Parapoynx sp.	NBNSYS0000136119	Parapoynx
50110339	Tipula rufina Meigen	50110339	Tipula (Savtshenkia) rufina Meigen, 1818	NBNSYS0000007997	Tipula rufina
5011034Z	Tipula signata group	5011033Z	Tipula (Savtshenkia) signata group	<NEW-CODE>100029	Tipula (Savtshenkia) signata group
50110361	Tipula unca Wiedemann	50110361	Tipula (Beringotipula) unca Wiedemann, 1817	NBNSYS0000008010	Tipula unca
50110417	Tipula solstitialis Westhoff	501103A7	Tipula (Yamatotipula) pierrei Tonnoir, 1921	NBNSYS0000008038	Tipula solstitialis
5011041Z	Tipula montium group	501103AZ	Tipula (Yamatotipula) montium group	<NEW-CODE>100030	Tipula (Yamatotipula) montium group
50110422	Tipula oleracea L.	501103B2	Tipula (Tipula) oleracea Linnaeus, 1758	NBNSYS0000008040	Tipula oleracea
50110423	Tipula paludosa Meigen	501103B3	Tipula (Tipula) paludosa Meigen, 1830	NBNSYS0000008041	Tipula paludosa
50110433	Tipula maxima Poda	501103C3	Tipula (Acutipula) maxima Poda, 1761	NBNSYS0000008044	Tipula maxima
50110434	Tipula vittata Meigen	501103C4	Tipula (Acutipula) vittata Meigen, 1804	NBNSYS0000008045	Tipula vittata
50110500	Nephrotoma sp.	50110500	Nephrotoma sp.	NBNSYS0000135577	Nephrotoma
50130100	Limonia sp.	50130100	Limonia sp.	NBNSYS0000134615	Limonia
50130501	Antocha vitripennis (Meigen)	50130511	Antocha (Antocha) vitripennis (Meigen, 1830)	NBNSYS0000008106	Antocha vitripennis
50130601	Thaumastoptera calceata Mik	50130601	Thaumastoptera calceata Mik, 1866	NBNSYS0000008107	Thaumastoptera calceata
50130900	Helius sp.	50130900	Helius sp.	NBNSYS0000133707	Helius
50131040	Pedicia (Tricyphona) sp.	50140610	Tricyphona (Tricyphona) sp.	NBNSYS0000139107	Pedicia (Tricyphona)
501310Z0	Pedicia (Pedicia) group	501401Z0	Pedicia (Pedicia) group	<NEW-CODE>100033	Pedicia (Pedicia) group
50131500	Dicranota sp.	50140500	Dicranota sp.	NBNSYS0000008123	Dicranota
50131701	Austrolimnophila ochracea (Meigen)	50131711	Austrolimnophila (Austrolimnophila) ochracea (Meigen, 1804)	NBNSYS0000008140	Austrolimnophila ochracea
50131900	Pseudolimnophila sp.	50131900	Pseudolimnophila sp.	NBNSYS0000137020	Pseudolimnophila
50132010	Limnophila (Eloeophila) sp.	50132100	Eloeophila sp.	NBNSYS0000139082	Limnophila (Eloeophila)
50132030	Limnophila (Phylidorea) sp.	50132400	Phylidorea sp.	NBNSYS0000139085	Limnophila (Phylidorea)
50132040	Limnophila (Euphylidorea) sp.	50132200	Euphylidorea sp.	NBNSYS0000139083	Limnophila (Euphylidorea)
50132050	Limnophila (Limnophila) sp.	50132050	Limnophila (Limnophila) sp.	NBNSYS0100012813	Limnophila (Limnophila)
50132610	Pilaria (Neolimnomyia) sp.	50132520	Neolimnomyia (Neolimnomyia) sp.	NBNSYS0100014354	Pilaria (Neolimnomyia)
50132620	Pilaria (Pilaria) sp.	50132600	Pilaria sp.	NBNSYS0100014355	Pilaria (Pilaria)
50132800	Hexatoma sp.	50132800	Hexatoma sp.	NBNSYS0000133824	Hexatoma
50133700	Lipsothrix sp.	50133700	Lipsothrix sp.	NBNSYS0000134657	Lipsothrix
50134100	Erioptera sp.	50134100	Erioptera sp.	NBNSYS0000132967	Erioptera
50134800	Ormosia sp.	50134810	Ormosia (Ormosia) sp.	NBNSYS0100014065	Ormosia (Ormosia)
50135000	Scleroprocta sp.	50135000	Scleroprocta sp.	NBNSYS0000137625	Scleroprocta
50135300	Molophilus sp.	50135300	Molophilus sp.	NBNSYS0000135269	Molophilus
50135500	Rhypholophus sp.	50134900	Rhypholophus sp.	NBNSYS0000139103	Ormosia (Rhypholophus)
50210202	Pericoma blandula Eaton	50210231	Pericoma (Pericoma) blandula Eaton, 1893	NBNSYS0000027064	Pericoma blandula
50210203	Pericoma calcilega Feuerborn	50210232	Pericoma (Pericoma) calcilega Feuerborn, 1923	NBNSYS0000027065	Pericoma calcilega
50210204	Pericoma canescens (Meigen)	50210251	Pericoma (Pneumia) canescens (Meigen, 1804)	NBNSYS0000027066	Pericoma canescens
50210205	Pericoma cognata Eaton	50210271	Pericoma (Ulomyia) cognata Eaton, 1893	NBNSYS0000027067	Pericoma cognata
50210208	Pericoma diversa Tonnoir	50210233	Pericoma (Pericoma) diversa Tonnoir, 1920	NBNSYS0000027070	Pericoma diversa
50210209	Pericoma exquisita Eaton	50210234	Pericoma (Pericoma) exquisita Eaton, 1893	NBNSYS0000027071	Pericoma exquisita
50210212	Pericoma fallax Eaton	50210235	Pericoma (Pericoma) fallax Eaton, 1893	NBNSYS0000027073	Pericoma fallax

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50210213	Pericoma fuliginosa (Meigen)	50210272	Pericoma (Ulomyia) fuliginosa (Meigen, 1804)	NBNSYS0000027074	Pericoma fuliginosa
50210217	Pericoma neglecta Eaton	50211101	Bazarella neglecta (Eaton, 1893)	NBNSYS0000027078	Pericoma neglecta
50210223	Pericoma pseudoexquisita Tonnoir	50210237	Pericoma (Pericoma) pseudoexquisita Tonnoir, 1940	NBNSYS0000027083	Pericoma pseudoexquisita
50210224	Pericoma pulchra Eaton	50211303	Tonnoiriella pulchra (Eaton, 1893)	NBNSYS0000027084	Pericoma pulchra
50210225	Pericoma trifasciata (Meigen)	5021023A	Pericoma (Pericoma) trifasciata (Meigen, 1804)	NBNSYS0000027085	Pericoma trifasciata
5021022Z	Pericoma trivialis group	5021025Z	Pericoma trivialis group	<NEW-CODE>100034	Pericoma trivialis group
50210402	Peripsychoda fusca (Macquart)	50210402	Peripsychoda fusca (Macquart, 1826)	NBNSYS0000027105	Peripsychoda fusca
50210901	Psychoda alternata Say	50211800	Tinearia sp.	NBNSYS0000027122	Psychoda alternata
50210904	Psychoda gemina Eaton	50210904	Psychoda gemina (Eaton, 1904)	NBNSYS0000027127	Psychoda gemina
50210907	Psychoda phalaenoides (L.)	50210907	Psychoda phalaenoides (Linnaeus, 1758)	NBNSYS0000027133	Psychoda phalaenoides
50210908	Psychoda severini Tonnoir	50210908	Psychoda albipennis Zetterstedt, 1850	NBNSYS0000027136	Psychoda severini
50210909	Psychoda surcoufi Tonnoir	50210909	Psychoda surcoufi Tonnoir, 1922	NBNSYS0000027137	Psychoda surcoufi
50220100	Ptychoptera sp.	50220100	Ptychoptera sp.	NBNSYS0000137159	Ptychoptera
50310101	Dixa dilatata Strobl	50310101	Dixa dilatata Strobl, 1900	NBNSYS0000011553	Dixa dilatata
50310103	Dixa nebulosa Meigen	50310103	Dixa nebulosa Meigen, 1830	NBNSYS0000011555	Dixa nebulosa
50310105	Dixa puberula Loew	50310105	Dixa puberula Loew, 1849	NBNSYS0000011557	Dixa puberula
5031010Z	Dixa maculata complex	5031010Z	Dixa maculata complex	<NEW-CODE>100036	Dixa maculata complex
50310205	Dixella filicornis Edwards	50310205	Dixella filicornis (Edwards, 1926)	NBNSYS0000011563	Dixella filicornis
50320112	Chaoborus flavicans (Meigen)	50320112	Chaoborus (Chaoborus) flavicans (Meigen, 1830)	NBNSYS0000027140	Chaoborus flavicans
50330100	Anopheles sp.	50330100	Anopheles sp.	NBNSYS0000039883	Anopheles
50340100	Thaumalea sp.	50340100	Thaumalea sp.	NBNSYS0000138362	Thaumalea
50350000	Ceratopogonidae	50350000	Ceratopogonidae	NBNSYS0000037064	Ceratopogonidae
50360101	Prosimulium hirtipes (Fries)	50360101	Prosimulium hirtipes (Fries, 1824)	NBNSYS0000027744	Prosimulium hirtipes
50360102	Prosimulium latimucro (Enderlein)	50360102	Prosimulium latimucro (Enderlein, 1925)	NBNSYS0000027745	Prosimulium latimucro
50360103	Prosimulium tomosvaryi (Enderlein)	50360103	Prosimulium tomosvaryi (Enderlein, 1921)	NBNSYS0000027746	Prosimulium tomosvaryi
50360311	Simulium latipes (Meigen)	50360311	Simulium (Hellichiella) latipes (Meigen, 1804)	NBNSYS0000027756	Simulium latipes
50360323	Simulium costatum Friederichs	50360323	Simulium (Nevermannia) costatum Friederichs, 1920	NBNSYS0000005334	Simulium costatum
5036032Y	Simulium angustitarse group	5036032Y	Simulium (Nevermannia) angustitarse group	<NEW-CODE>100038	Simulium angustitarse group
5036032Z	Simulium cryophilum group	5036032Z	Simulium (Nevermannia) cryophilum group	<NEW-CODE>100039	Simulium cryophilum group
5036033Z	Simulium vernum group	5036032X	Simulium (Nevermannia) vernum group	<NEW-CODE>100040	Simulium vernum group
5036034Z	Simulium aureum group	5036034Z	Simulium (Eusimulium) aureum group	<NEW-CODE>100041	Simulium aureum group
50360350	Simulium (Wilhelmia) sp.	50360350	Simulium (Wilhelmia) sp.	NBNSYS0100015240	Simulium (Wilhelmia)
50360361	Simulium erythrocephalum (de Geer)	50360361	Simulium (Boophthora) erythrocephalum (DeGeer, 1776)	NBNSYS0000027766	Simulium erythrocephalum
50360382	Simulium rostratum Lundström	50360382	Simulium (Simulium) rostratum (Lundström, 1911)	NBNSYS0100005420	Simulium rostratum
50360384	Simulium morsitans Edwards	50360384	Simulium (Simulium) morsitans Edwards, 1915	NBNSYS0000027772	Simulium morsitans
50360385	Simulium noelleri Friederichs	50360385	Simulium (Simulium) noelleri Friederichs, 1920	NBNSYS0100005418	Simulium noelleri
50360387	Simulium posticatum Meigen	50360387	Simulium (Simulium) posticatum Meigen, 1838	NBNSYS0100005419	Simulium posticatum
50360388	Simulium reptans (L.)	50360388	Simulium (Simulium) reptans (Linnaeus, 1758)	NBNSYS0000027773	Simulium reptans
5036038Y	Simulium argyreatum group	5036038Y	Simulium (Simulium) argyreatum group	<NEW-CODE>100042	Simulium argyreatum group
5036038Z	Simulium ornatum group	5036038Z	Simulium (Simulium) ornatum group	<NEW-CODE>100043	Simulium ornatum group
50360391	Simulium tuberosum (Lundstrom)	5036038A	Simulium (Simulium) tuberosum (Lundström, 1911)	NBNSYS0000027776	Simulium tuberosum
50420101	Clinotanypus nervosus (Meigen)	50420101	Clinotanypus nervosus (Meigen, 1818)	NBNSYS0000027316	Clinotanypus nervosus
50420201	Apsectrotanypus trifascipennis (Zetterstedt)	50420201	Apsectrotanypus trifascipennis (Zetterstedt, [1838])	NBNSYS0000027303	Apsectrotanypus trifascipennis
50420400	Macropelopia sp.	50420400	Macropelopia sp.	NBNSYS0000134835	Macropelopia
50420500	Procladius sp.	50420500	Procladius sp.	NBNSYS0000037316	Procladius
50420601	Psectrotanypus varius (Fabricius)	50420601	Psectrotanypus varius (Fabricius, 1787)	NBNSYS0100004795	Psectrotanypus varius
50420800	Ablabesmyia sp.	50420800	Ablabesmyia sp.	NBNSYS0000139225	Ablabesmyia
50420Y00	Thienemannimyia group	50420Y00	Thienemannimyia group	<NEW-CODE>100046	Thienemannimyia group
50420Z00	Zavrelimyia group	50420Z00	Zavrelimyia group	<NEW-CODE>100047	Zavrelimyia group
50421200	Krenopelopia sp.	50421200	Krenopelopia sp.	NHMSYS0000079029	Krenopelopia
50421400	Larsia sp.	50421402	Larsia curticalcar (Kieffer, 1918)	NBNSYS0100003555	Larsia curticalcar

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50421501	Monopelopia tenuicalcar (Kieffer)	50421501	Monopelopia tenuicalcar (Kieffer, 1918)	NBNSYS0000027330	Monopelopia tenuicalcar
50421600	Natarsia sp.	50421600	Natarsia sp.	NBNSYS0000135473	Natarsia
50421701	Nilotanypus dubius (Meigen)	50421701	Nilotanypus dubius (Meigen, 1804)	NBNSYS0000027333	Nilotanypus dubius
50422201	Trissopelopia longimana (Staeger)	50422201	Trissopelopia longimana (Staeger, 1839)	NBNSYS0000027346	Trissopelopia longimana
50422300	Xenopelopia sp.	50422300	Xenopelopia sp.	NBNSYS0000138930	Xenopelopia
50422500	Tanypus sp.	50422500	Tanypus sp.	NBNSYS0000138230	Tanypus
50440200	Diamesa sp.	50440200	Diamesa sp.	NBNSYS0000132366	Diamesa
5044030Y	Potthastia gaedii group	5044030Y	Potthastia gaedii group	<NEW-CODE>100048	Potthastia gaedii group
5044030Z	Potthastia longimana group	5044030Z	Potthastia longimanus group	<NEW-CODE>100049	Potthastia longimana group
50440400	Pseudodiamesa sp.	50440400	Pseudodiamesa sp.	NBNSYS0000137006	Pseudodiamesa
50440600	Sympotthastia sp.	50440600	Sympotthastia sp.	NBNSYS0000138152	Sympotthastia
50450201	Odontomesa fulva (Kieffer)	50450201	Odontomesa fulva (Kieffer, 1919)	NBNSYS0000027429	Odontomesa fulva
50450301	Prodiamesa olivacea (Meigen)	50450301	Prodiamesa olivacea (Meigen, 1818)	NBNSYS0000027444	Prodiamesa olivacea
50460101	Acricotopus lucens (Zetterstedt)	50460101	Acricotopus lucens (Zetterstedt, 1850)	NBNSYS0000027374	Acricotopus lucens
50460301	Brillia longifurca Kieffer	50460301	Brillia flavifrons (Johannsen, 1905)	NBNSYS0100002008	Brillia flavifrons
50460302	Brillia modesta (Meigen)	50460302	Brillia bifida (Kieffer, 1909)	NBNSYS0000027376	Brillia modesta
50460400	Cardiocladius sp.	50460400	Cardiocladius sp.	NBNSYS0000131266	Cardiocladius
50460601	Diplocladius cultriger Kieffer	50460601	Diplocladius cultriger Kieffer, 1908	NBNSYS0000027406	Diplocladius cultriger
50460Y00	Eukiefferiella group	50460Y00	Eukiefferiella group	<NEW-CODE>100050	Eukiefferiella group
50460Z00	Cricotopus group	50460Z00	Cricotopus group	<NEW-CODE>100051	Cricotopus group
50461001	Eurycnemus crassipes (Panzer)	50461001	Eurycnemus crassipes (Meigen, 1810)	NBNSYS0000027418	Eurycnemus crassipes
50461201	Heterotanytarsus apicalis (Kieffer)	50461201	Heterotanytarsus apicalis (Kieffer, 1921)	NBNSYS0000027423	Heterotanytarsus apicalis
50461300	Heterotrissocladius sp.	50461300	Heterotrissocladius sp.	NBNSYS0000133821	Heterotrissocladius
50461400	Hydrobaenus sp.?	50461Z00	Hydrobaenus group	<NEW-CODE>100052	Hydrobaenus group
50461800	Nanocladius sp.	50461800	Nanocladius sp.	NHMSYS0000079156	Nanocladius
50462051	Orthocladius lignicola (Kieffer)	50462051	Orthocladius (Symposiocladius) lignicola Kieffer, 1915	NBNSYS0100004234	Orthocladius lignicola
50462101	Paracladius conversus (Walker)	50462101	Paracladius conversus (Walker, 1856)	NBNSYS0000027441	Paracladius conversus
50462700	Psectrocladius sp.	50462700	Psectrocladius sp.	NBNSYS0000136966	Psectrocladius
50462800	Rheocricotopus sp.	50462800	Rheocricotopus sp.	NBNSYS0000050291	Rheocricotopus
50462901	Synorthocladius semivirens (Kieffer)	50462901	Synorthocladius semivirens (Kieffer, 1909)	NBNSYS0000027461	Synorthocladius semivirens
50463500	Bryophaenocladius sp.	50463500	Bryophaenocladius sp.	NBNSYS0000131043	Bryophaenocladius
50463700	Chaetocladius sp.	50463700	Chaetocladius sp.	NBNSYS0000131468	Chaetocladius
50463800	Corynoneura sp.	50463800	Corynoneura sp.	NBNSYS0000131959	Corynoneura
50463901	Epoicocladius flavens (Malloch)	50463901	Epoicocladius ephemerae (Kieffer, 1924)	NBNSYS0000027493	Epoicocladius flavens
50464000	Gymnometriocnemus sp.	50464000	Gymnometriocnemus sp.	NBNSYS0000133538	Gymnometriocnemus
50464101	Heleniella ornaticollis (Edwards)	50464101	Heleniella ornaticollis (Edwards, 1929)	NBNSYS0000027497	Heleniella ornaticollis
50464200	Krenosmittia sp.	50464200	Krenosmittia sp.	NBNSYS0000134259	Krenosmittia
50464300	Limnophyes sp.	50464300	Limnophyes sp.	NBNSYS0000134609	Limnophyes
50464500	Metriocnemus sp.	50464500	Metriocnemus sp.	NBNSYS0000135110	Metriocnemus
50464700	Parakiefferiella sp.	50464700	Parakiefferiella sp.	NBNSYS0000136086	Parakiefferiella
50464901	Parametriocnemus boreoalpinus Gowin	50464901	Parametriocnemus boreoalpinus Gouin, 1942	NBNSYS0100004338	Parametriocnemus boreoalpinus
50464902	Parametriocnemus stylatus (Kieffer)	50464902	Parametriocnemus stylatus (Spärck, 1923)	NBNSYS0000027523	Parametriocnemus stylatus
50465000	Paraphaenocladius sp.	50465000	Paraphaenocladius sp.	NBNSYS0000136113	Paraphaenocladius
50465101	Parasmittia carinata Strenzke	50465101	Parasmittia carinata Strenzke, 1950	NBNSYS0100014173	Parasmittia carinata
50465201	Paratrissocladius excerptus (Walker)	50465201	Paratrissocladius excerptus (Walker, 1856)	NBNSYS0100004365	Paratrissocladius excerptus
50465300	Pseudorthocladius sp.	50465300	Pseudorthocladius sp.	NBNSYS0000137052	Pseudorthocladius
50465400	Pseudosmittia sp.	50465400	Pseudosmittia sp.	NBNSYS0000137059	Pseudosmittia
50465600	Smittia sp.	50465600	Smittia sp.	NBNSYS0000137817	Smittia
50465801	Thienemannia gracilis Kieffer	50465801	Thienemannia gracilis Kieffer, 1909	NBNSYS0000027549	Thienemannia gracilis
50465900	Thienemanniella sp.	50465900	Thienemanniella sp.	NBNSYS0000138410	Thienemanniella
50470300	Chironomus sp.	50470300	Chironomus sp.	NBNSYS0000037247	Chironomus

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50470400	Cladopelma sp.	50470400	Cladopelma sp.	NHMSYS0000078787	Cladopelma
50470500	Cryptochironomus sp.	50470500	Cryptochironomus sp.	NBNSYS0000132064	Cryptochironomus
50470600	Cryptotendipes sp.	50470600	Cryptotendipes sp.	NBNSYS0000132090	Cryptotendipes
50470801	Demicryptochironomus vulneratus (Zetterstedt)	50470811	Demicryptochironomus (Demicryptochironomus) vulneratus (Zetterstedt, [1838])	NBNSYS0000027591	Demicryptochironomus vulneratus
50470900	Dicrotendipes sp.	50470900	Dicrotendipes sp.	NHMSYS0000078853	Dicrotendipes
50471200	Glyptotendipes sp.	50471200	Glyptotendipes sp.	NBNSYS0000133427	Glyptotendipes
50471400	Harnischia sp.	50471400	Harnischia sp.	NBNSYS0000133649	Harnischia
50471501	Kiefferulus tendipediformis (Goetghebuer)	50471501	Kiefferulus tendipediformis (Goetghebuer, 1921)	NBNSYS0000027614	Kiefferulus tendipediformis
50471900	Microtendipes sp.	50471900	Microtendipes sp.	NBNSYS0000135188	Microtendipes
50471Y00	Endochironomus group	50471Y00	Endochironomus group	<NEW-CODE>100083	Endochironomus group
50471Z00	Einfeldia group	50471Z00	Einfeldia group	<NEW-CODE>100082	Einfeldia group
50472001	Nilothauma brayi (Goetghebuer)	50472001	Nilothauma brayi (Goetghebuer, 1921)	NBNSYS0000027632	Nilothauma brayi
50472300	Parachironomus sp.	50472300	Parachironomus sp.	NHMSYS0000079553	Parachironomus
50472400	Paracladopelma sp.	50472400	Paracladopelma sp.	NBNSYS0000136068	Paracladopelma
50472501	Paralauterborniella nigrohalteralis (Malloch)	50472501	Paralauterborniella nigrohalteralis (Malloch, 1915)	NBNSYS0000027646	Paralauterborniella nigrohalteralis
50472600	Paratendipes sp.	50472600	Paratendipes sp.	NBNSYS0000136135	Paratendipes
50472800	Phaenopsectra sp.	50472800	Phaenopsectra sp.	NBNSYS0000136335	Phaenopsectra
50472900	Polypedilum sp.	50472900	Polypedilum sp.	NBNSYS0000037187	Polypedilum
50473100	Stenochironomus sp.	50473100	Stenochironomus sp.	NBNSYS0000137999	Stenochironomus
50473200	Stictochironomus sp.	50473200	Stictochironomus sp.	NBNSYS0000138041	Stictochironomus
50473301	Xenochironomus xenolabis (Kieffer)	50473301	Xenochironomus xenolabis (Kieffer, 1916)	NBNSYS0100005907	Xenochironomus xenolabis
50490100	Cladotanytarsus sp.	50490100	Cladotanytarsus sp.	NBNSYS0000131693	Cladotanytarsus
50490300	Neozavrelia sp.	50490300	Neozavrelia sp.	NHMSYS0000079182	Neozavrelia
50490500	Paratanytarsus sp.	50490500	Paratanytarsus sp.	NBNSYS0000136134	Paratanytarsus
50490600	Rheotanytarsus sp.	50490600	Rheotanytarsus sp.	NBNSYS0000137314	Rheotanytarsus
50490701	Stempellina bausei (Kieffer)	50490701	Stempellina bausei (Kieffer, 1911)	NBNSYS0000027738	Stempellina bausei
50490W00	Micropsectra group	50490W00	Micropsectra group	<NEW-CODE>100055	Micropsectra group
50490Y00	Stempellinella group	50490Y00	Stempellinella group	<NEW-CODE>100057	Stempellinella group
50610200	Nemotelus sp.	50610200	Nemotelus sp.	NBNSYS0000135522	Nemotelus
50610300	Oxycera sp.	50610300	Oxycera sp.	NBNSYS0000135962	Oxycera
50610500	Odontomyia sp.	50610500	Odontomyia sp.	NBNSYS0000135728	Odontomyia
50620101	Atherix ibis (Fabricius)	50640101	Atherix ibis (Fabricius, 1798)	NBNSYS0000007858	Atherix ibis
50620102	Atherix marginata (Fabricius)	50640301	Ibisia marginata (Fabricius, 1781)	NBNSYS0000007859	Atherix marginata
50620201	Atrichops crassipes (Meigen)	50640201	Atrichops crassipes (Meigen, 1820)	NBNSYS0000007860	Atrichops crassipes
50630100	Chrysops sp.	50630100	Chrysops sp.	NBNSYS0000041854	Chrysops
50630Z00	Tabanus group	50630Z00	Tabanus group	<NEW-CODE>100059	Tabanus group
50710W00	Chelifera group	5071YW00	Chelifera group	<NEW-CODE>100060	Chelifera group
50710X00	Hemerodromia group	5071YX00	Hemerodromia group	<NEW-CODE>100061	Hemerodromia group
50720000	Dolichopodidae	50720000	Dolichopodidae	NBNSYS0000159881	Dolichopodidae
507X0000	Clinocerinae	5071X000	Clinocerinae	<NEW-CODE>100064	Clinocerinae
50810000	Syrphidae	50810000	Syrphidae	NBNSYS0000040188	Syrphidae
50820000	Sciomyzidae	50820000	Sciomyzidae	NBNSYS0000160954	Sciomyzidae
50830000	Ephydridae	50830000	Ephydridae	NBNSYS0000159951	Ephydridae
50850200	Limnophora sp.	50850200	Limnophora sp.	NBNSYS0000037023	Limnophora

Component members of species groups in Furse taxonomy– (aggregates of species that are difficult to separate as aquatic stages)

Furse Code	Furse Group Name	Constituent taxa
0511020Z	Polycelis nigra group	Polycelis nigra & Polycelis tenuis
0512010Z	Dugesia polychroa group	Dugesia polychroa & Dugesia lugubris
17120Z00	Anodonta group	Anodonta sp. & Pseudanodonta complanata
20110Z00	Lumbriculus group	Lumbriculus variegatus, Rhynchelmis limnosella (& other Lumbriculidae?)
2033070Y	Nais communis group	Nais communis & Nais variabilis
2033070Z	Nais simplex group	Nais simplex, Nais barbata & Nais pseudobtusa
4012011Z	Baetis scambus group	Baetis scambus & Baetis fuscatus
4051020X	Caenis pseudorivulorum group	Caenis pseudorivulorum, Caenis beskidensis & possibly other species
4051020Z	Caenis luctuosa group	Caenis luctuosa & Caenis macrura
4112040Z	Nemoura cambrica group	Nemoura cambrica & Nemoura erratica
4212040Z	Coenagrion puella group	Coenagrion puella & Coenagrion pulchellum
4515020Z	Gyrinus natator group	Gyrinus natator & Gyrinus substriatus
4831010Z	Agrypnia obsoleta group	Agrypnia obsoleta & Agrypnia varia
48340W00	Micropterna group	Micropterna sp. & Stenophylax sp.
48340X00	Potamophylax group	Potamophylax sp., Allogamus auricollis & Chaetopteryx villosa
5011033Z	Tipula (Savtshenkia) signata group	Tipula (Savtshenkia) signata & Tipula (Savtshenkia) staegeri
501103AZ	Tipula (Yamatotipula) montium group	Tipula (Yamatotipula) montium, Tipula (Yamatotipula) couckei & Tipula (Yamatotipula) lateralis
501401Z0	Pedicia (Pedicia) group	Pedicia (Pedicia) rivosa, Pedicia (Crunobia) sp. & Pedicia (Amalopsis) occulata
5021025Z	Pericoma trivialis group	Pericoma trivialis, Pericoma nubila (Meigen) + additional species ?
5036032Y	Simulium (Nevermannia) angustitarse group	Simulium (Nevermannia) angustitarse, Simulium (Nevermannia) lundstromi & Simulium (Nevermannia) latigonium
5036032Z	Simulium (Nevermannia) cryophilum group	Simulium (Nevermannia) cryophilum, Simulium (Nevermannia) armoricanum, Simulium (Nevermannia) dunfellense & Simulium (Nevermannia) urbanum
5036032X	Simulium (Nevermannia) vernum group	Simulium (Nevermannia) vernum, Simulium (Nevermannia) juxtacrenobium & Simulium (Nevermannia) naturale
5036034Z	Simulium (Eusimulium) aureum group	Simulium (Eusimulium) aureum, Simulium (Eusimulium) angustipes & Simulium (Eusimulium) velutinum
5036038Y	Simulium (Simulium) argyreatum group	Simulium (Simulium) argyreatum & Simulium (Simulium) variegatum
5036038Z	Simulium (Simulium) ornatum group	Simulium (Simulium) ornatum, Simulium (Simulium) trifasciatum & Simulium (Simulium) intermedium
50420Y00	Thienemannimyia group	Thienemannimyia sp., Arctopelopia sp., Rheopelopia sp. & Conchapelopia sp.
50420Z00	Zavrelimyia group	Zavrelimyia sp. & Paramerina sp.
5044030Y	Potthastia gaedii group	Potthastia gaedii + additional species ?
5044030Z	Potthastia longimanus group	Potthastia longimanus + additional species ?
50460Y00	Eukiefferiella group	Eukiefferiella sp. & Tvetenia sp.
50460Z00	Cricotopus group	Cricotopus sp., Paratrichocladius sp. & all species of Orthocladius except Orthocladius (Symposiocladius) lignicola
50461Z00	Hydrobaenus group	Indet Orthocladiinae resembling Hydrobaenus sp.
50471Y00	Endochironomus group	Endochironomus sp., Synendotendipes sp. & Tribelos sp.
50471Z00	Einfeldia group	Einfeldia sp. & Chironomus (Lobochironomus) dissidens
50490W00	Micropsectra group	Micropsectra sp., Tanytarsus sp., Virgatanytarsus sp., Tanytarsini gen. nov.? & Sublettia sp.?
50490Y00	Stempellinella group	Stempellinella sp. & Zavrelia sp.
50630Z00	Tabanus group	Tabanus sp. & Haematopota sp.
5071YW00	Chelifera group	Chelifera sp. + additional genera ?
5071YX00	Hemerodromia group	Hemerodromia sp. + additional genera ?

Notes

The Revised Maitland coded group 1621020Z Physa acuta group comprised *Physa acuta* Draparnaud & *Physa heterostropha* Say – both of which are now regarded as being synonymous with *Physella* (*Costatella*) *acuta* Draparnaud, 1805).

The Revised Maitland coded group 2033150Z *Pristina idrensis* group comprised *Pristina amphibiotica* Lastockin, *Pristina idrensis* Sperber & *Pristina menoni* (Aiyer) – all of which are downgraded to the genus Prinstina (Pristinella) sp. in RIVPACS IV.

Appendix IX Mean numerical abundances of UK freshwater macroinvertebrate families within $\log_{10}$ abundance categories.

Appendix IX – Mean numerical abundances of UK freshwater macroinvertebrate families within $\log_{10}$ abundance categories.

	1	2	3	4	5
Mean numerical abundances across all families:	2.4	24.4	193.3	1668	10000

Numerical abundances based on data from EA, SPEA and EHS	⬜
No data available - used mean across all taxa	🟨
Data available from ECN	🟧
Data available from Agencies for near identical taxon	🟩

	Family	1	2	3	4	5
02110000	Spongillidae	1.4	10.0			
03110000	Hydridae	1.8	29.5	193.3		
04000000	Microturbellaria	2.0	30.0			
05110000	Planariidae	2.9	26.3	187.9		
05120000	Dugesiidae	2.4	28.1	166.7		
05130000	Dendrocoelidae	2.3	18.5			
051Z0000	Planariidae (incl. Dugesiidae)	3.0	25.4	221.6		
08000000	Nemertea	1.0				
09000000	Nematomorpha	1.8				
09100000	Gordioidea	1.8				
09110000	Gordiidae	2.1	10.0			
09120000	Chordodidae	1.0				
10000000	Nematoda	2.3	15.7			
13000000	Acanthocephala	1.0				
14000000	Ectoprocta	2.4				
16000000	Gastropoda	7.0	51.0	394.3	1011.0	
16110000	Neritidae	3.5	29.2	111.5		
16120000	Viviparidae	2.8	19.7	157.0		
16130000	Valvatidae	3.1	27.7	262.2	1000.0	
16140000	Hydrobiidae	3.2	31.6	250.9	2029.4	10000.0
16160000	Bithyniidae	3.3	26.1	241.1	1668.0	10000.0
161Z0000	Hydrobiidae (incl. Bithyniidae)	3.2	26.8	293.7	1416.7	10000.0
16210000	Physidae	2.7	25.6	283.5	1668.0	
16220000	Lymnaeidae	2.7	24.1	161.9	2000.0	
16230000	Planorbidae	2.9	25.2	209.9	1668.0	
16240000	Ancylidae	3.2	25.8	153.0		
16250000	Acroloxidae	2.3	25.1	193.3		
162Z0000	Ancylidae (incl. Acroloxidae)	3.2	21.8	172.5		
16320000	Succineidae	2.1	15.0			
16350000	Zonitidae	1.8				
16380000	Helicidae	1.0				
17110000	Margaritiferidae	2.4				
17120000	Unionidae	1.7	37.3	104.0		
17130000	Sphaeriidae	2.9	31.6	216.6	1333.3	10000.0
17140000	Dreissenidae	2.7	46.7			
19110000	Aeolosomatidae	2.4				
20000000	Oligochaeta	4.3	31.7	222.7	1545.8	10000.0
20110000	Lumbriculidae	4.0	42.4	265.8	1668.0	
20210000	Haplotaxidae	1.0	24.4			
20330000	Naididae	3.9	35.3	295.9	2339.4	10000.0
20340000	Tubificidae	4.3	37.7	236.9	2062.5	
203Z0000	Enchytraeidae (incl. Propappidae)	3.0	27.1	283.0	1668.0	
20420000	Lumbricidae	3.3	25.9	119.0		

22110000	Piscicolidae	1.7	10.0			
22120000	Glossiphoniidae	2.6	20.1	262.6		
22210000	Hirudinidae	2.0				
22310000	Erpobdellidae	3.1	20.3	104.0		
24000000	Hydracarina	2.8	24.0	160.8		
25000000	Oribatei	1.3				
29000000	Cladocera	2.4	37.6	408.3		
29030000	Daphniidae	2.1	30.0			
29070000	Chydoridae	4.7		127.0		
30000000	Ostracoda	2.5	22.2	161.8		
31000000	Copepoda	2.3	30.0	200.0		
32010000	Argulidae	1.0				
34120000	Crangonidae	2.3				
34310000	Astacidae	1.8	12.0			
35110000	Mysidae	1.0				
36110000	Asellidae	3.3	29.3	216.0	3370.0	
37110000	Corophiidae	3.6	29.8	100.0	1668.0	
37120000	Talitridae		20.0			
37130000	Crangonyctidae	2.8	31.6	171.4	2401.0	
37140000	Gammaridae	3.4	35.6	282.4	1507.8	10000.0
37150000	Niphargidae	1.2	24.4			
371Z0000	Gammaridae (incl. Crangonyctidae & Niphargidae)	4.0	32.5	224.0	1766.7	10000.0
39000000	Collembola	1.3	26.7			
39130000	Isotomidae	1.3	31.0	100.0		
39210000	Sminthuridae	1.0				
40110000	Siphlonuridae	2.1	22.2	100.0		
40120000	Baetidae	4.3	38.0	226.9	1285.8	
40130000	Heptageniidae	4.0	36.7	199.2	1250.0	
40140000	Ameletidae	2.4	24.4			
401Z0000	Siphlonuridae (incl. Ameletidae)	2.4	24.4			
40210000	Leptophlebiidae	2.5	24.4	214.3		
40310000	Potamanthidae	1.0	24.4			
40320000	Ephemeridae	3.1	25.0	181.9		
40410000	Ephemerellidae	3.0	28.7	253.2	1500.0	
40510000	Caenidae	3.3	31.5	232.6	1310.0	
41110000	Taeniopterygidae	3.0	25.5	269.2		
41120000	Nemouridae	3.3	25.3	135.3	1668.0	
41130000	Leuctridae	3.8	28.4	199.0	1500.0	
41140000	Capniidae	1.9	15.9	193.3		
41210000	Perlodidae	3.3	19.7	135.8		
41220000	Perlidae	3.3	15.6	193.3		
41230000	Chloroperlidae	3.4	20.8	120.7		
42110000	Platycnemididae	1.6	20.0			
42120000	Coenagriidae	3.0	24.3	155.2		
42140000	Calopterygidae	2.7	19.0	140.0		
42200000	Anisoptera	1.0				
42210000	Gomphidae	1.0	24.4			
42220000	Cordulegasteridae	1.5	18.5			
42230000	Aeshnidae	1.4				
42250000	Libellulidae	1.4				
43110000	Mesoveliidae	1.2	20.0			
43210000	Hydrometridae	1.7	15.2			
43220000	Veliidae	1.3	24.4	193.3	1668.0	
43230000	Gerridae	2.2	15.9			
43310000	Nepidae	1.3				

43410000	Naucoridae	2.2	11.0			
43420000	Aphelocheiridae	3.1	36.3	182.7	1000.0	
43510000	Notonectidae	2.1	14.0			
43520000	Pleidae	2.4	30.0			
43610000	Corixidae	2.7	23.6	174.7	1668.0	
45110000	Haliplidae	2.1	23.6	150.3		
45120000	Hygrobiidae	1.9	71.0	105.0		
45130000	Noteridae	2.6	17.0	193.3		
45140000	Dytiscidae	2.7	20.7	127.8		
45150000	Gyrinidae	2.6	19.4	200.0		
451Z0000	Dytiscidae (incl. Noteridae)	2.5	18.5	100.0		
45330000	Helophoridae	2.4	24.4	193.3		
45350000	Hydrophilidae	1.7	30.2	193.3		
45360000	Hydrochidae	2.4				
453Y0000	Hydrophilidae (incl. Helophoridae, Georissidae & Hydrochidae)	2.4	24.4	193.3		
453Z0000	Hydrophilidae (incl. Hydraenidae)	2.7	15.7			
453Z0000	Hydrophilidae (incl. Hydraenidae, Helophoridae, Georissidae & Hydrochidae)			193.3		
45410000	Hydraenidae	3.2	21.0	107.5		
45510000	Scirtidae	2.2	21.8	120.0		
45620000	Dryopidae	1.3	23.5			
45630000	Elmidae	4.4	32.3	201.9	1320.8	
45710000	Chrysomelidae	1.6				
45800000	Curculionoidea	2.0				
45810000	Curculionidae	1.3	10.0			
46110000	Sialidae	2.2	22.1	193.3		
47110000	Osmylidae	2.0				
47120000	Sisyridae	1.9	21.3			
48000000	Trichoptera	2.0		460.7	2072.0	
48110000	Rhyacophilidae	3.8	21.5	127.5	1668.0	
48120000	Glossosomatidae	3.0	29.6	217.4	1668.0	
48130000	Hydroptilidae	3.0	27.8	180.8	1668.0	
481Z0000	Rhyacophilidae (incl. Glossosomatidae)	4.1	19.8	151.5	1668.0	
48210000	Philopotamidae	2.3	20.0	390.0		
48220000	Psychomyiidae	2.2	21.9	193.3		
48230000	Ecnomidae	1.0	24.4	193.3		
48240000	Polycentropodidae	2.8	22.8	165.1		
48250000	Hydropsychidae	4.2	29.4	231.2	1468.5	
482Z0000	Psychomyiidae (incl. Ecnomidae)	2.1	14.1	193.3		
48310000	Phryganeidae	1.8	15.0			
48320000	Brachycentridae	2.6	31.7	150.5	3000.0	
48330000	Lepidostomatidae	3.2	30.0	213.1	1000.0	
48340000	Limnephilidae	3.1	22.1	185.4		
48350000	Goeridae	2.7	20.0	129.3		
48360000	Beraeidae	1.6	16.0			
48370000	Sericostomatidae	3.1	24.2	162.6		
48380000	Odontoceridae	2.2	14.7	193.3		
48390000	Molannidae	2.2	24.1	193.3		
483B0000	Apataniidae		24.4			
483Z0000	Limnephilidae (incl. Apataniidae)	3.1	22.1	185.4		
48410000	Leptoceridae	2.8	26.0	188.2	1001.0	
49000000	Lepidoptera	2.9	60.0			
49110000	Pyralidae	2.2	19.3			
50000000	Diptera	4.5	50.7	445.0	2342.0	
50100000	Tipulidae	3.1	18.7	100.0		
50130000	Limoniidae	2.6	22.2	127.5		

50140000	Pediciidae	3.3	22.4	120.0		
501Z0000	Tipulidae (incl. Limoniidae, Cylindrotomidae & Pediciidae)	3.1	18.7	100.0		
50200000	Psychodoidea	1.5				
50210000	Psychodidae	1.8	13.7			
50220000	Ptychopteridae	1.9	21.5			
50310000	Dixidae	1.9	13.8			
50320000	Chaoboridae	2.2	24.4			
50330000	Culicidae	1.6	23.8			
50340000	Thaumaleidae	2.4				
50350000	Ceratopogonidae	2.7	23.7	238.3		
50360000	Simuliidae	3.7	28.9	225.0	1975.0	10000.0
50400000	Chironomidae	4.3	34.1	250.2	1960.0	
50420000	Tanypodinae	2.4	24.4	193.3	1668.0	
50440000	Diamesinae	2.4	24.4	193.3	1668.0	
50450000	Prodiamesinae	2.4	24.4	193.3		
50460000	Orthocladiinae	2.4	24.4	193.3	1668.0	
50470000	Chironomini	2.4	24.4	193.3	1668.0	
50490000	Tanytarsini	2.4	24.4	193.3	1668.0	
50610000	Stratiomyidae	1.6	16.3			
50620000	Rhagionidae	2.3	22.5			
50630000	Tabanidae	1.7	20.0			
50640000	Athericidae	3.3	25.4	100.0		
50710000	Empididae	2.8	17.9	152.0		
50720000	Dolichopodidae	1.6	24.4			
50810000	Syrphidae	1.1				
50820000	Sciomyzidae	2.3				
50830000	Ephydridae	1.8		193.3		
50850000	Muscidae	2.1	12.0	193.3		
51010000	Petromyzonidae	1.0				
51010000	Petromyzontidae	1.0				
52030000	Salmonidae	1.2				
52080000	Cyprinidae	1.9	16.0			
52090000	Cobitidae	1.4				
52120000	Anguillidae	1.2				
52130000	Gasterosteidae	2.1	13.3			
52210000	Cottidae	2.0	20.0			
52230000	Balitoridae	1.8				

Appendix X Rules for the distribution of $\log_{10}$ abundances across the separate families arising from previously combined BMWP composite records in the RIVPACS dataset (based on Agency samples where both families occur in the same sample)

Appendix X Rules for the distribution of $\log_{10}$ abundances across the separate families arising from previously combined BMWP composite records in the RIVPACS dataset (based on Agency samples where both families occur in the same sample)

🟨 = Estimated where little or no data

Log10 abundance categories		Number of instances in Agency data
Planariidae	Dugesiidae	
1	1	**57**
1	2	10
2	2	11
2	1	**27**
1	3	1
2	3	1
3	2	3
3	1	**7**

Composite $\log_{10}$ abundance		Most probable log10 abundances	
		Planariidae	Dugesiidae
	1	1	1
	2	2	1
	3	3	1
	4	(4)	(1)
	5	(5)	(1)

Log10 abundance categories		Number of instances in Agency data
Hydrobiidae	Bithyniidae	
1	1	**50**
1	2	39
2	2	42
2	1	**71**
1	3	2
2	3	2
3	3	3
3	2	**25**
3	1	23
4	3	1
4	2	**2**
4	1	2

Composite $\log_{10}$ abundance		Most probable log10 abundances	
		Hydrobiidae	Bithyniidae
	1	1	1
	2	2	1
	3	3	2
	4	4	2
	5	(5)	(2)

Log10 abundance categories		Number of instances in Agency data
Ancylidae	Acroloxidae	
1	1	**25**
1	2	1
2	2	2
2	1	**12**
3	2	1
3	1	**2**

Composite $\log_{10}$ abundance		Most probable log10 abundances	
		Ancylidae	Acroloxidae
	1	1	1
	2	2	1
	3	3	1
	4	(4)	(1)
	5	(5)	(1)

Log10 abundance categories		Number of instances in Agency data
Gammaridae	Crangonyctidae	
1	1	**64**
1	2	29
2	2	27
2	1	**66**
1	3	5
3	2	5
3	1	**19**

Composite $\log_{10}$ abundance		Most probable log10 abundances	
		Gammaridae	Crangonyctidae
	1	1	1
	2	2	1
	3	3	1
	4	(4)	(1)
	5	(5)	(1)

Log10 abundance categories		Number of instances in Agency data
Gammaridae	Niphargidae	
2	1	**2**
3	1	**1**

		Most probable log10 abundances	
		Gammaridae	Niphargidae
Composite log$_{10}$ abundance	1	1	1
	2	2	1
	3	3	1
	4	(4)	(1)
	5	(5)	(1)

Log10 abundance categories		Number of instances in Agency data
Dytiscidae	Noteridae	
1	1	**13**
2	1	**4**
2	2	1
1	2	1

		Most probable log10 abundances	
		Dytiscidae	Noteridae
Composite log$_{10}$ abundance	1	1	1
	2	2	1
	3	(3)	(1)
	4	(4)	(1)
	5	(5)	(1)

Log10 abundance categories		Number of instances in Agency data
Hydrophilidae	Hydraenidae	
1	1	**26**
2	1	1
1	2	**3**

		Most probable log10 abundances	
		Hydrophilidae	Hydraenidae
Composite log$_{10}$ abundance	1	1	1
	2	1	2
	3	(1)	(3)
	4	(1)	(4)
	5	(1)	(5)

Log10 abundance categories		Number of instances in Agency data
Rhyacophilidae	Glossosomatidae	
1	1	**190**
2	1	101
2	2	61
1	2	**122**
3	1	2
1	3	**31**
2	3	15

		Most probable log10 abundances	
		Rhyacophilidae	Glossosomatidae
Composite log$_{10}$ abundance	1	1	1
	2	1	2
	3	1	3
	4	(1)	(4)
	5	(1)	(5)

Log10 abundance categories		Number of instances in Agency data
Psychomyiidae	Ecnomidae	
1	1	**1**

		Most probable log10 abundances	
		Psychomyiidae	Ecnomidae
Composite log$_{10}$ abundance	1	1	1
	2	(2)	(1)
	3	(3)	(1)
	4	(4)	(1)
	5	(5)	(1)

Appendix XI End-group for each of the 685 reference sites in the new GB-inclusive model, sorted by end-group (1-43) showing O/E ratios for NTAXA and ASPT.

Appendix XI End-group for each of the 685 reference sites in the new GB-inclusive model, sorted by end-group (1-43) showing O/E ratios for NTAXA and ASPT.

Country	Site Code	River name	Site name	End-Group	Most probable group by MDA	Obs TAXA	Exp TAXA	O/E TAXA	Obs ASPT	Exp ASPT	O/E ASPT
Scotland	SEPA_N01	Shetland: Upper Loch of Brouster	Brouster	1	1	18	16.11	1.117	5.39	5.36	1.006
Scotland	SEPA_N03	Shetland:South Burn of Burrafirth	East Burrafirth	1	1	13	16.11	0.807	5.31	5.36	0.991
Scotland	SEPA_N04	Shetland: Burn of Sandwater	Stromfirth	1	1	17	16.12	1.055	5.00	5.36	0.933
Scotland	SEPA_N05	Shetland:Laxo/Gossawater	Laxo	1	1	15	16.11	0.931	5.20	5.36	0.970
Scotland	SEPA_N06	Shetland: Burn of Laxdale	North Voxter	1	1	13	16.11	0.807	5.23	5.36	0.976
Scotland	SEPA_N07	Unst: Burn of Mailand/Caldback	Stackhoull	1	1	22	16.11	1.366	5.59	5.36	1.043
Scotland	SEPA_N08	Yell: Laxa Burn	u/s B9081	1	1	12	16.11	0.745	5.50	5.36	1.026
Scotland	SEPA_N09	Yell: Easter Burn of Bouster	Bouster	1	1	19	16.11	1.179	5.32	5.36	0.993
Scotland	SEPA_N10	Yell:Burn of Arisdale	Hamnavoe	1	1	16	16.11	0.993	5.69	5.36	1.062
Scotland	SEPA_N11	Orkney: Hillside/Rusht	Deasbreck	2	2	28	25.36	1.104	6.64	6.13	1.083
Scotland	SEPA_N12	Orkney: Hillside/Rusht	Millgeo	2	2	30	25.36	1.183	6.20	6.13	1.011
Scotland	SEPA_N13	Orkney:Burn of Woodwick	Neigarth	2	2	24	25.36	0.946	6.17	6.13	1.006
Scotland	SEPA_N14	Orkney: Unnamed	Garth	2	2	26	25.36	1.025	6.19	6.13	1.009
Scotland	SEPA_N15	Orkney: Etheriegeo	Whitemire	2	2	23	25.36	0.907	6.13	6.13	1.000
Scotland	SEPA_N16	Orkney: Burn of Swartabeck	Harabreck	2	2	31	25.36	1.222	6.16	6.13	1.004
Scotland	SEPA_N17	Orkney: Hillside/Rusht	Kirbuster	2	2	25	25.36	0.986	5.80	6.13	0.946
Scotland	SEPA_N18	Orkney: Burn of Corrigal	Corrigal	2	2	26	25.36	1.025	6.12	6.13	0.998
Scotland	SEPA_N21	Rousay:Suso Burn	Sourin	2	2	25	25.33	0.987	6.20	6.13	1.011
Scotland	SEPA_N56	Ledmore/Loin Duibh	A837	2	9	20	29.66	0.674	5.90	6.69	0.882
Scotland	SEPA_N57	Dornoch Burn	u/s Camore	2	8	21	25.95	0.809	5.95	6.48	0.918
Scotland	SEPA_N22	Skye:Sligachan	Sligachan	3	3	16	20.92	0.765	6.44	6.48	0.994
Scotland	SEPA_N31	Lewis: Tolsta Burn	B895	3	3	15	18.44	0.813	6.07	6.45	0.941
Scotland	SEPA_N32	Lewis: Abhainn a Loin	B8011	3	3	16	19.58	0.817	6.31	6.46	0.976

Scotland	SEPA_N34	Lewis: Abhainn Geiraha	Port Geiraha	3	3	20	18.32	1.092	6.35	6.45	0.984
Scotland	SEPA_N35	Lewis: Abhainn Dhubh	d/s Loch Beag	3	3	19	20.26	0.938	6.37	6.46	0.986
Scotland	SEPA_N36	North Harris: Meavaig River	Meavaig	3	3	15	19.26	0.779	6.53	6.48	1.008
Scotland	SEPA_N37	North Harris: Scaladale River	A859	3	3	15	18.2	0.824	6.27	6.45	0.972
Scotland	SEPA_N39	South Harris: Laxdale	A859	3	3	21	19.48	1.078	6.57	6.49	1.012
Scotland	SEPA_W17	Jura:Corran River	A846 Br	3	3	17	18.6	0.914	6.59	6.45	1.021
Scotland	SEPA_W18	Jura:Lussa River	Ardlussa Br	3	3	26	19.01	1.368	6.77	6.46	1.047
Scotland	SEPA_W22	Allt Maol Ruainidh	u/s A82 Bridge (Allt Maol)	3	8	20	22.61	0.884	6.70	6.77	0.990
Scotland	SEPA_N20	Hoy: Withigill/Bailiefea	Burnhouse	4	2	21	25.24	0.832	6.29	6.12	1.027
Scotland	SEPA_N41	Dionard	Drochaidmhor	4	4	24	23.4	1.026	6.42	6.56	0.979
Scotland	SEPA_N48	Clachan/nan Laogh	Unamed	4	10	23	25.89	0.888	6.96	6.62	1.052
Scotland	SEPA_N64	Moidart	u/s Brunery	4	3	21	21.47	0.978	6.67	6.54	1.020
Scotland	SEPA_W05	Islay: Duich/Torra	Torra Bridge	4	3	25	20.96	1.193	6.72	6.49	1.035
Scotland	SEPA_W06	Islay: Duich/Torra	Drochaid Bheag	4	4	25	23.85	1.048	6.56	6.57	0.999
Scotland	SEPA_W12	Mull:Forsa	u/s Gaodhail	4	4	23	23.63	0.973	6.91	6.60	1.047
Scotland	SEPA_W15	Mull:Coladoir River	A849 Bridge	4	4	22	24.17	0.910	6.27	6.60	0.951
Scotland	SEPA_W35	Barr Water	Arnicle	4	4	22	23.94	0.919	6.64	6.63	1.001
Scotland	HI05	Unnamed	Mon	5	5	22	21.93	1.003	6.45	6.48	0.996
Scotland	SEPA_N29	Lewis:Airigh Sgridhe/Greeta/Abhainn Ghrioda	A859	5	5	21	21.98	0.955	6.43	6.47	0.994
Scotland	SEPA_N30	Lewis:Airigh Sgridhe/Greeta/Abhainn Ghrioda	A858	5	5	22	22.52	0.977	6.18	6.47	0.956
Scotland	SEPA_N33	Lewis: nan Torcan/Laxay	u/s Loch Valtos	5	5	25	21.81	1.146	6.36	6.48	0.982
Scotland	SEPA_N40	South Uist: Abhainn Roag	Snishival	5	4	24	24.88	0.965	6.54	6.55	0.998
Scotland	SEPA_N42	Hope	Hope	5	5	24	23.4	1.026	6.83	6.47	1.056
Scotland	SEPA_N47	Meadie Burn	d/s Loch Meadie	5	5	19	23.5	0.808	6.74	6.48	1.041
Scotland	SEPA_N60	Ewe/Kinlochewe River/Abhainn Bruach	Poolewe	5	5	24	23.4	1.026	6.38	6.48	0.985
Scotland	SEPA_N61	Beauly/Glass/Affric/Cam-ban	Forest Walk	5	5	27	23.44	1.152	6.41	6.51	0.984
Scotland	SEPA_W26	Orchy/Water of Tulla	d/s Loch Tulla	5	5	28	23.54	1.190	6.36	6.48	0.982
Scotland	8913	Brora	d/s Loch Brora	6	11	27	26.69	1.012	6.48	6.67	0.972
Scotland	9009	Laxford	d/s Loch Stack	6	6	30	27.61	1.087	6.60	6.52	1.012
Scotland	HI10	Conon/Bran	Moy Bridge	6	15	25	23.59	1.060	6.72	6.76	0.994
Scotland	SEPA_N24	Skye:Snizort	Skeabost	6	6	31	27.72	1.118	6.19	6.50	0.952
Scotland	SEPA_N26	Skye:Broadford River	Suardal	6	7	29	27.95	1.038	6.38	6.41	0.995
Scotland	SEPA_N49	Kirkaig/Ledbeg	Inverkirkaig	6	13	27	25.36	1.065	6.22	6.64	0.936
Scotland	SEPA_N54	Kirkaig/Ledbeg	Rhisalach	6	6	33	29.37	1.124	6.88	6.51	1.057
Scotland	SEPA_N55	Ledmore/Loin Duibh	d/s Loch Borralan	6	6	34	26.84	1.267	6.56	6.57	0.999
Scotland	SEPA_N28	Skye:Ord River	Minor Road	7	7	28	26.88	1.041	6.50	6.48	1.003

Scotland	SEPA_W01	Islay:Laggan/Barr	Storakaig	7	8	32	25.86	1.237	6.56	6.58	0.997
Scotland	SEPA_W04	Islay:Laggan/Barr	u/s Duich confluence	7	7	37	28.06	1.318	6.43	6.39	1.006
Scotland	SEPA_W13	Mull:Forsa	u/s A849 Bridge	7	13	25	25.69	0.973	6.28	6.56	0.958
Scotland	SEPA_W19	Barbreck	A816 Bridge	7	7	23	27.77	0.828	6.43	6.41	1.003
Scotland	SEPA_W38	Carradale Water	B842 Bridge	7	4	24	25.19	0.953	6.04	6.53	0.925
England	0301	Exe	Warren Farm	8	26	21	32.05	0.655	6.67	6.59	1.012
England	0381	Barle	Goat Hill	8	25	31	32.58	0.952	6.84	6.61	1.035
England	3153	Wheat Beck	Dale Head	8	28	23	27.95	0.823	6.65	6.34	1.049
England	3581	South Tyne	South Tyne Head	8	8	32	24.57	1.302	6.84	6.69	1.023
Scotland	3781	Caorainn Achaidh Burn	Comer	8	14	18	21.96	0.820	6.39	6.82	0.937
Scotland	3783	Allt Tairbh	Teapot	8	14	18	21.96	0.820	7.11	6.79	1.047
Scotland	3785	Green Burn	Dalmary	8	8	18	23.64	0.762	6.28	6.73	0.933
Scotland	3791	Balvag/Larig	Blaircreich	8	9	20	27.57	0.725	7.05	6.71	1.051
Scotland	4381	Carron	u/s Loch Sgamhain	8	8	22	23.73	0.927	6.55	6.70	0.977
Scotland	4881	Unnamed	Achavanich	8	2	25	25.35	0.986	5.80	6.21	0.933
Scotland	7001	Conon/Bran	Ledgowan	8	15	24	22.36	1.073	6.79	6.80	0.998
Scotland	7205	Cree	Wheeb Bridge	8	5	27	23.01	1.173	6.93	6.62	1.047
Scotland	7305	Strontian	Ariundle Oakwood NNR	8	15	25	22.53	1.110	6.72	6.82	0.985
Scotland	7405	Cnocloisgte Water	u/s Loch Caluim	8	10	26	26.22	0.991	6.54	6.67	0.981
Scotland	7505	Burn of Latheronwheel	Den Moss	8	10	27	24.32	1.110	6.56	6.64	0.987
Scotland	7511	Burn of Latheronwheel	Landhallow	8	10	27	24.67	1.095	7.15	6.59	1.085
Wales	WE01	Cynfal	Pont Newydd	8	16	22	26.32	0.836	6.86	6.71	1.023
England	2711	Ribble/Gayle Beck	Horton in Ribblesdale	9	22	25	30.23	0.827	6.64	6.37	1.042
England	3303	Swale	Oxnop	9	22	25	29.86	0.837	6.84	6.43	1.064
Scotland	4307	Carron	d/s Loch Damhain	9	14	30	23.8	1.261	6.87	6.76	1.017
Scotland	4311	Carron	Balnacra	9	14	30	22.89	1.311	6.53	6.80	0.961
Scotland	4403	Loanan	d/s Loch Awe	9	9	31	28.19	1.100	6.94	6.72	1.032
Scotland	4405	Loanan	Inchnadamph	9	9	27	29.84	0.905	6.63	6.65	0.997
Scotland	4407	Inver	Little Assynt	9	9	37	29.87	1.239	6.62	6.69	0.989
Scotland	4807	Thurso	Sordale	9	10	32	27.23	1.175	6.44	6.69	0.963
Wales	5613	Wye	Dolhelfa	9	17	30	32.11	0.934	7.07	6.39	1.106
Wales	5701	Usk	u/s Usk Reservoir	9	26	37	31.04	1.192	6.70	6.64	1.010
Scotland	7217	Cree	Newton Stewart	9	12	28	30.24	0.926	6.57	6.52	1.008
Scotland	7311	Strontian	Anaheilt	9	13	29	25.5	1.137	6.83	6.62	1.032
England	2709	Ribble/Gayle Beck	Cam End	10	16	27	27.29	0.989	7.11	6.61	1.075
Scotland	3903	Dee	Braemar	10	11	22	26.57	0.828	7.27	6.74	1.078

Scotland	4001	Spey	Garva Bridge	10	15	20	22.19	0.901	6.50	6.84	0.950
Scotland	4101	Stinchar	Highbridge	10	8	24	24.53	0.978	6.54	6.71	0.975
Scotland	4301	Allt Coire Crubaidh	Allt Coire Crubaidh	10	14	18	22.43	0.802	6.72	6.77	0.992
Scotland	4303	Lair	Achnashellach Lodge	10	14	25	23.43	1.067	6.96	6.72	1.036
Scotland	4305	Fionn Abhainn	Fionn-Abhainn	10	14	18	22.86	0.788	6.44	6.76	0.952
Scotland	4309	Carron	Craig	10	10	20	24.31	0.823	6.60	6.75	0.977
Scotland	4313	Carron	New Kelso	10	13	23	25.51	0.902	6.70	6.63	1.011
Scotland	4401	Traligill	Glenbain	10	10	25	26.48	0.944	6.60	6.65	0.993
Scotland	4701	Halladale	Forsinard Lodge	10	10	21	23.98	0.876	6.43	6.71	0.958
Scotland	4703	Halladale	Forsinain	10	10	28	24.26	1.154	7.07	6.74	1.049
Scotland	4705	Halladale	Millburn	10	10	25	26.09	0.958	7.00	6.69	1.046
Scotland	4707	Halladale	Golval	10	13	29	26.51	1.094	6.76	6.63	1.020
Scotland	4801	Burn of Aultachleven	u/s Loch Rangag	10	10	26	24.02	1.082	6.46	6.72	0.962
Scotland	4803	Little River	Tacher	10	10	30	27.38	1.096	6.70	6.66	1.006
Scotland	4805	Thurso	Westerdale	10	10	28	25.25	1.109	6.82	6.72	1.014
Scotland	4905	Tweed	Kingledores	10	22	24	29.68	0.809	6.42	6.49	0.989
England	3305	Swale	Grinton	11	22	23	30.18	0.762	6.91	6.36	1.087
England	3307	Swale	u/s Richmond	11	22	24	30.31	0.792	6.96	6.32	1.102
England	3401	Tees	Moorhouse	11	11	24	27.1	0.886	6.46	6.70	0.964
England	3403	Tees	Cauldron Snout	11	12	22	28.49	0.772	5.77	6.62	0.871
Scotland	3905	Dee	Balmoral	11	11	23	26.79	0.859	6.83	6.70	1.019
Scotland	3907	Dee	d/s Ballater	11	11	22	26.96	0.816	6.45	6.69	0.964
Scotland	3911	Dee	Potarch Bridge	11	11	26	27.59	0.942	7.04	6.63	1.062
Scotland	4003	Spey	Laggan Bridge	11	11	28	26.76	1.046	6.68	6.75	0.990
Scotland	4005	Spey	Newtonmore	11	11	24	26.57	0.903	7.25	6.74	1.075
Scotland	4009	Spey	Boat of Garten	11	11	32	26.72	1.197	7.12	6.73	1.058
Scotland	4011	Spey	Grantown	11	11	28	26.68	1.049	6.75	6.73	1.003
Scotland	4017	Spey	Garmouth	11	18	26	28.41	0.915	6.69	6.36	1.052
Scotland	4103	Stinchar	d/s Dalquhairn	11	11	27	28.11	0.961	6.78	6.59	1.029
Scotland	4205	Annan	Newton Bridge	11	22	26	29.95	0.868	6.38	6.46	0.988
Wales	5615	Wye	Llanwrthwl	11	17	29	30.87	0.939	6.79	6.39	1.063
Scotland	8909	Brora	u/s Balnacoil	11	14	33	24.2	1.364	6.94	6.77	1.026
Scotland	HI07	Shiel	Shiel Bridge	11	13	23	25.13	0.915	6.78	6.65	1.019
Scotland	SEPA_N44	Naver/Mudale/Meadie	Skelpick	11	5	28	24.18	1.158	6.96	6.58	1.058
Scotland	SEPA_N45	Naver/Mudale/Meadie	Syre	11	5	30	23.43	1.281	6.93	6.53	1.061
Scotland	SEPA_N46	Naver/Mudale/Meadie	Altnaharra	11	15	25	25.08	0.997	7.00	6.65	1.053

Wales	ST01	Severn	Llandinam	11	17	27	31.96	0.845	6.81	6.42	1.061
England	3376	Cowside Beck	Arncliffe	12	16	29	27.79	1.044	6.72	6.63	1.013
England	3381	Wharfe	Hubberholme	12	22	30	30.78	0.975	6.30	6.41	0.984
Scotland	4971	Whiteadder Water	Cranshaws	12	19	31	29.88	1.038	6.19	6.43	0.962
England	9603	Coquet	Carshope	12	16	30	28.46	1.054	6.60	6.56	1.006
Scotland	9703	Bladnoch	Glassoch Bridge	12	5	26	22.92	1.134	6.62	6.60	1.002
Scotland	9711	Bladnoch	Spittal	12	12	28	30.46	0.919	5.82	6.49	0.897
Scotland	NE01	Lossie	Cloddach	12	12	25	27.71	0.902	6.96	6.58	1.058
Scotland	SEPA_E04	Tay/Dochart/Fillan/Cononish	1.5km u/s A9 Road Bridge	12	11	29	27.88	1.040	6.69	6.59	1.016
Scotland	SEPA_E07	Tay/Dochart/Fillan/Cononish	Haugh of Kercock	12	18	29	28.85	1.005	6.72	6.44	1.043
Scotland	SEPA_E09	North Esk	Edzell	12	11	34	27.31	1.245	6.74	6.68	1.009
Scotland	SEPA_W03	Islay:Laggan/Barr	Laggan Bridge	12	7	33	28.02	1.178	6.82	6.48	1.052
Scotland	SO01	Urr Water	Corsock	12	14	37	24.31	1.522	6.38	6.75	0.945
Scotland	TA01	Earn	Forteviot	12	22	31	31.55	0.983	6.71	6.33	1.060
Scotland	TA04	Braan	u/s Tay Confluence	12	12	30	29.38	1.021	6.47	6.56	0.987
Scotland	SEPA_N19	Hoy: South Burn	Glen	13	2	21	25.32	0.829	6.10	6.13	0.995
Scotland	SEPA_N23	Skye:Ose	Ose	13	7	29	27.45	1.056	6.52	6.44	1.012
Scotland	SEPA_N25	Skye:Snizort	B885	13	6	28	28.11	0.996	6.32	6.55	0.965
Scotland	SEPA_N27	Skye:Brittle	Leachd Thuilm	13	6	23	26.39	0.872	7.00	6.56	1.067
Scotland	SEPA_N52	Carron/Abhainn a Ghlinne Mhoir	Amat	13	15	24	22.81	1.052	7.00	6.83	1.024
Scotland	SEPA_N53	Carron/Abhainn a Ghlinne Mhoir	Gledfield	13	13	27	25	1.080	7.00	6.69	1.047
Scotland	SEPA_N66	Croe	Innis a Chrotha	13	13	26	24.35	1.068	6.81	6.70	1.016
Scotland	SEPA_W02	Islay:Laggan/Barr	d/s Cattadale	13	13	32	26.75	1.196	6.56	6.54	1.004
Scotland	SEPA_W08	Arran: Machrie Water	Machriewater Foot	13	13	27	26.03	1.037	6.74	6.57	1.026
Scotland	SEPA_W10	Arran:Sliddery Water	Slidderywater Foot	13	13	26	25.86	1.006	6.58	6.60	0.997
Scotland	SEPA_W11	Mull:Aros River	u/s A848 Bridge	13	13	25	26.26	0.952	6.36	6.55	0.971
Scotland	SEPA_W20	Allt Bragleenmore	Bragleenmore Farm Bridge	13	13	24	24.7	0.972	6.58	6.70	0.982
Scotland	SEPA_W21	Eachaig	Eckford	13	13	21	25.26	0.831	6.57	6.69	0.983
Scotland	SEPA_W28	Orchy/Water of Tulla	Dalmally	13	15	24	22.92	1.047	6.88	6.72	1.024
Scotland	SEPA_W33	Ruel	A886 Bridge	13	14	22	23.8	0.924	6.45	6.73	0.958
Scotland	SEPA_W34	Ruel	A8003 Bridge	13	13	25	26.82	0.932	6.92	6.56	1.054
Scotland	SEPA_W36	Barr Water	Glenbarr	13	13	24	25.77	0.931	6.67	6.62	1.008
England	3301	Swale	Keld	14	16	20	27.99	0.715	6.60	6.60	1.000
England	3501	South Tyne	Dipper Bridge	14	16	22	25.64	0.858	6.68	6.71	0.996
England	3505	South Tyne	d/s Knarsdale	14	22	21	30.13	0.697	6.86	6.39	1.073
Scotland	4105	Stinchar	d/s Barr	14	12	25	29.29	0.854	6.36	6.50	0.978

Scotland	CL05	Leven/Loch Lomond/Falloch	Keilator	14	14	17	22.11	0.769	7.06	6.81	1.036
Scotland	HI02	Foyers	Dalcrag	14	14	18	22.2	0.811	7.17	6.84	1.048
Scotland	SEPA_E01	Water of Ruchill	u/s Auchinner Bridge	14	14	24	23.32	1.029	6.88	6.78	1.014
Scotland	SEPA_E02	Invervar Burn	Invervar	14	14	17	22.02	0.772	7.12	6.82	1.044
Scotland	SEPA_N43	Hope	Strathmore	14	4	19	24.06	0.790	7.00	6.56	1.068
Scotland	SEPA_N58	Applecross/Allt Coire Attadale	Applecross	14	13	22	24.74	0.889	6.59	6.66	0.990
Scotland	SEPA_N59	Abhainn Bhuachaig	Tullich House	14	14	20	22.4	0.893	6.95	6.77	1.026
Scotland	SEPA_N62	Enrick	Corrimony	14	14	26	21.63	1.202	6.69	6.84	0.978
Scotland	SEPA_N67	Spean/Pattack/Chaoil-reidhe	Kinloch Laggan	14	14	21	22.02	0.954	6.90	6.84	1.009
Scotland	SEPA_N68	Coe	Pass of Glencoe	14	15	17	21.91	0.776	6.76	6.77	0.999
Scotland	SEPA_W09	Arran:Sliddery Water	u/s Glenscorrodale	14	8	27	23.63	1.143	6.96	6.74	1.033
Scotland	SEPA_W16	Mull: Allt an Lon Biolaireich	Allt an Lon Biolaireich	14	6	28	26.41	1.060	7.04	6.56	1.073
Scotland	SEPA_W23	Etive	Kingshouse Hotel	14	14	22	21.8	1.009	6.64	6.84	0.971
Scotland	SEPA_W25	Etive	u/s Allt Mheuran	14	5	20	22.96	0.871	6.55	6.55	1.000
Scotland	SEPA_W30	Orchy/Water of Tulla	A82 Bridge	14	14	18	22.57	0.797	7.33	6.83	1.073
Scotland	SEPA_W31	Abhainn Shira	Victoria Bridge	14	15	26	22.25	1.168	6.88	6.84	1.007
Scotland	SEPA_W37	Carradale Water	u/s Auchenbreck	14	5	20	21.46	0.932	6.80	6.47	1.052
England	2901	Derwent	Grange-in-Borrowdale	15	11	21	28.28	0.742	6.71	6.63	1.012
Scotland	8905	Brora	Dalnessie	15	10	21	23.25	0.903	6.48	6.78	0.956
Scotland	8925	Black Water	Pollie	15	10	25	23.67	1.056	7.04	6.78	1.038
Scotland	HI01	Finnan	Glen Finnan	15	3	20	19.29	1.037	6.80	6.51	1.044
Scotland	HI03	Fechlin/Killin	Killin Lodge	15	15	17	22.31	0.762	6.71	6.84	0.980
Scotland	HI04	Spean	Corrie Coille	15	14	22	22.85	0.963	7.09	6.82	1.039
Scotland	HI06	Unnamed	Craig Ghobhair	15	3	22	18.56	1.185	6.59	6.47	1.018
Scotland	HI08	Arkaig/Dessarry	Strathan	15	15	25	22.45	1.113	7.20	6.85	1.051
Scotland	HI09	Meig	Bridgend	15	15	28	22.5	1.244	7.11	6.82	1.043
England	NH07	Balder	u/s Balderhead Reservoir	15	16	21	25.84	0.813	6.81	6.71	1.015
Scotland	SEPA_W07	Arran: Machrie Water	Monyquil	15	15	25	23.29	1.073	6.84	6.71	1.019
Wales	0007	Aber/Rhaeadr-fawr	Abergwyngregyn	16	29	27	30.41	0.888	6.70	6.62	1.011
England	3372	Cowside Beck	Nab End	16	16	27	27.35	0.987	6.48	6.66	0.973
Scotland	4201	Annan	Above Ericstane	16	16	22	25.63	0.859	6.68	6.66	1.004
Scotland	4203	Annan	Moffat	16	12	24	27.98	0.858	6.25	6.57	0.952
Scotland	4901	Tweed	Fingland	16	16	23	26.18	0.878	6.78	6.66	1.018
Scotland	4903	Tweed	Nether Rigs	16	16	21	28.14	0.746	6.48	6.58	0.985
Wales	5705	Usk	Trecastle	16	26	28	30.91	0.906	7.11	6.59	1.079
Wales	5848	Unnamed	Glasnant	16	16	31	28	1.107	6.97	6.62	1.053

Wales	5850	Unnamed	Crinfynydd	16	26	26	28.72	0.905	6.85	6.60	1.037
England	8705	Fowey	Codda Ford	16	25	29	35.29	0.822	6.76	6.63	1.020
England	9205	Millburn Beck/Knock Ore Gill	Green Castle	16	16	23	25.49	0.902	6.70	6.71	0.999
England	9481	Walkham	Merrivale	16	25	27	35.46	0.762	6.70	6.63	1.011
England	NH09	Wooler Water/Harthope Burn	Coronation Wood	16	16	28	26.01	1.077	6.68	6.70	0.997
Scotland	SEPA_N50	Allt nam Uamh	u/s River Loanan	16	10	20	24.48	0.817	6.30	6.70	0.940
Scotland	SO03	Southwick Burn/Boreland Burn	Nr. Southwick House	16	16	25	26.48	0.944	6.52	6.59	0.989
Scotland	TA05	Prosen Water	Prosen Bridge	16	11	26	27.27	0.953	7.27	6.67	1.091
Wales	WE03	Afon Caseg	Braichmelyn	16	16	32	29.2	1.096	6.84	6.68	1.024
England	0307	Exe	Exebridge	17	17	33	33.47	0.986	6.36	6.41	0.993
England	0311	Exe	Bramford Speke	17	17	29	33.84	0.857	6.31	6.34	0.995
England	0407	Torridge	Hele Bridge	17	17	32	34.23	0.935	6.69	6.36	1.051
England	0409	Torridge	Beaford Bridge	17	17	28	33.69	0.831	6.64	6.41	1.037
England	0411	Torridge	Great Torrington Town Mills	17	17	33	33.72	0.979	6.30	6.38	0.987
Wales	1605	Teifi	Pont Gogoyan	17	17	43	32.63	1.318	6.60	6.40	1.032
Wales	1609	Teifi	Bangor Tyfi	17	17	37	32.44	1.140	6.24	6.38	0.979
England	2207	Dove	u/s Rocester	17	32	35	33.59	1.042	6.34	6.00	1.057
England	2209	Dove	Sudbury	17	32	36	33.36	1.079	6.44	6.03	1.068
England	2907	Derwent	Cockermouth	17	19	33	29.27	1.128	6.45	6.40	1.008
England	2909	Derwent	Ribton Hall	17	18	30	29.41	1.020	6.47	6.32	1.023
England	2911	Derwent	Workington	17	18	31	29.4	1.055	5.87	6.31	0.930
Wales	5617	Wye	Hafodygarreg	17	17	42	30.74	1.366	6.50	6.39	1.017
England	5619	Wye	Bredwardine	17	17	29	31.38	0.924	6.69	6.37	1.049
England	5695	Arrow	Folly Farm	17	24	35	33.7	1.039	6.40	6.22	1.029
England	0107	Camel	Brocton	18	17	35	33.81	1.035	6.60	6.43	1.026
England	0309	Exe	Lythecourt	18	17	32	33.62	0.952	6.53	6.40	1.020
England	3003	Ehen/Liza	u/s Keekle	18	19	21	30.53	0.688	6.33	6.30	1.004
England	3007	Ehen/Liza	Braystones	18	19	26	31.44	0.827	5.73	6.23	0.919
England	3409	Tees	Gainford	18	19	25	30.55	0.818	6.44	6.28	1.025
England	3513	Tyne/North Tyne	Corbridge	18	18	30	29.81	1.006	6.20	6.30	0.985
Scotland	3701	Teith	Teith Bridge, Callander	18	11	35	26.41	1.325	6.37	6.73	0.946
Scotland	3703	Teith	Laighlands	18	12	26	28.04	0.927	6.19	6.62	0.936
Scotland	3909	Dee	d/s Aboyne	18	11	34	27.7	1.227	6.56	6.61	0.992
Scotland	3913	Dee	d/s Banchory	18	18	27	28.74	0.939	6.30	6.43	0.980
Scotland	3915	Dee	Cults	18	18	22	29.26	0.752	6.32	6.33	0.998
Scotland	4013	Spey	Marypark	18	11	27	26.99	1.001	6.81	6.64	1.025

Scotland	4107	Stinchar	Pinmore Bridge	18	18	24	30.38	0.790	6.00	6.33	0.948
Scotland	4109	Stinchar	d/s Colmonell	18	18	30	29.96	1.001	6.10	6.34	0.962
Scotland	4207	Annan	Millhouse Bridge	18	22	26	29.83	0.872	6.08	6.36	0.956
Scotland	4209	Annan	Williamwath Bridge	18	18	29	29.66	0.978	6.10	6.34	0.962
Scotland	4211	Annan	Brydekirk	18	18	27	29.44	0.917	6.59	6.33	1.041
Scotland	4913	Tweed	Dry Grange Bridge	18	18	25	28.64	0.873	6.52	6.34	1.028
Wales	5711	Usk	Llandetty	18	17	23	32.48	0.708	6.74	6.34	1.063
Wales	5713	Usk	Crickhowell	18	17	31	32.46	0.955	6.55	6.33	1.034
Wales	5715	Usk	Llanellen Bridge	18	17	27	33.09	0.816	6.44	6.27	1.026
Scotland	CL04	Ayr	Mainholm Ford	18	32	27	31.61	0.854	5.96	6.19	0.963
England	2703	Hodder	Slaidburn	19	19	29	30.84	0.940	6.83	6.35	1.075
England	2705	Hodder	d/s Langden Brook	19	19	32	30.87	1.036	6.44	6.30	1.022
England	2707	Hodder	Higher Hodder Bridge	19	19	32	31.19	1.026	6.69	6.21	1.077
England	2717	Ribble/Gayle Beck	Sawley Bridge	19	32	38	31.77	1.196	6.03	6.16	0.979
England	2903	Derwent	High Stock Bridge	19	19	28	31.03	0.902	6.25	6.37	0.981
England	3001	Ehen/Liza	Ennerdale Bridge	19	19	24	30.96	0.775	6.08	6.41	0.948
England	3005	Ehen/Liza	d/s Keekle	19	19	24	30.47	0.788	5.62	6.29	0.893
England	3205	Esk	Lealholm	19	19	33	30.72	1.074	6.45	6.40	1.009
England	3207	Esk	Briggswath	19	19	30	31.47	0.953	6.70	6.17	1.087
England	3511	South Tyne	Warden Bridge	19	22	27	30.87	0.875	6.56	6.29	1.043
England	3515	Tyne/North Tyne	Wylam	19	18	26	30.2	0.861	5.69	6.24	0.912
England	3605	Wansbeck	Meldon	19	19	30	31.15	0.963	6.70	6.22	1.077
England	3609	Wansbeck	Bothal	19	32	30	33.52	0.895	5.97	5.94	1.004
Scotland	3705	Teith	Bridge of Teith, Doune	19	12	28	28.65	0.977	6.21	6.54	0.950
Scotland	3709	Forth	Aberfoyle Bridge	19	12	33	27.75	1.189	6.52	6.62	0.985
Scotland	3805	Tyne	Easter Pencaitland	19	32	31	31.97	0.970	5.74	6.20	0.925
Scotland	4111	Stinchar	Ballantrae	19	18	28	30.73	0.911	5.89	6.32	0.932
Scotland	4911	Tweed	Old Tweed Bridge	19	18	33	29.69	1.111	6.06	6.34	0.956
England	0403	Torridge	Woodford Bridge	20	25	34	35.05	0.970	6.35	6.57	0.967
England	3101	Derwent	Langdale End	20	24	30	32.15	0.933	6.03	6.28	0.960
England	3601	Wansbeck	Kirkwhelpington	20	23	31	29.45	1.053	6.65	6.42	1.036
England	3603	Wansbeck	Middleton	20	20	31	31	1.000	6.68	6.35	1.051
Scotland	4907	Tweed	Crownhead Bridge	20	22	31	31.25	0.992	6.03	6.36	0.947
England	5003	Otter	Bidwell Farm	20	26	34	32.78	1.037	6.41	6.51	0.985
England	5005	Otter	Monkton	20	25	37	33.64	1.100	6.35	6.45	0.984
England	5605	Lugg	Mortimer's Cross	20	33	42	34.24	1.227	6.50	6.06	1.073

Scotland	7413	Forss Water	Achalone	20	6	31	28.07	1.104	6.52	6.58	0.990
Scotland	7417	Forss Water	Crosskirk	20	13	35	26.65	1.313	6.51	6.52	0.999
England	0105	Camel	Helland Bridge	21	25	35	34.74	1.008	6.71	6.59	1.018
England	0303	Exe	Exford	21	26	32	32.12	0.996	6.28	6.54	0.960
England	0305	Exe	Edbrooke	21	25	29	33.12	0.875	6.69	6.50	1.029
England	0505	Avill	Dunster	21	21	30	32.59	0.920	6.43	6.32	1.017
Wales	1703	Clwyd	Nantclwyd Hall	21	20	35	32.47	1.078	6.43	6.37	1.009
Wales	1705	Clwyd	Above Ruthin	21	32	30	33.36	0.899	5.77	6.13	0.941
Wales	1707	Clwyd	Glan-y-Wern	21	32	35	34.28	1.021	6.29	6.05	1.039
Wales	1709	Clwyd	Pont Llanerch	21	32	37	34.05	1.087	6.16	6.00	1.027
England	2201	Dove	Glutton Bridge	21	26	34	30.77	1.105	6.35	6.60	0.961
England	2203	Dove	Hartington	21	24	31	32.78	0.946	6.00	6.22	0.965
England	2205	Dove	Dove Dale	21	32	36	33.06	1.089	6.31	6.12	1.032
Scotland	3803	Tyne	Ormiston	21	23	26	31.17	0.834	5.85	6.28	0.932
Wales	5709	Usk	Brecon Town Bridge	21	17	33	32.47	1.016	6.42	6.37	1.008
England	3385	Wharfe	Grassington	22	19	32	30.54	1.048	6.50	6.31	1.031
England	3389	Wharfe	Addingham	22	19	26	31	0.839	6.65	6.26	1.062
Scotland	4975	Whiteadder Water	Preston Haugh	22	19	34	30.54	1.113	6.12	6.26	0.977
England	9607	Coquet	Linshiels	22	22	28	29.69	0.943	6.36	6.43	0.990
England	9611	Coquet	Sharperton	22	22	33	30.2	1.093	6.36	6.38	0.997
Scotland	NE03	Bervie Water	Inverbervie G.S.	22	23	24	29.16	0.823	6.17	6.33	0.974
England	NW01	Lune	Old Tebay	22	18	32	29.87	1.071	6.53	6.35	1.029
England	NW02	Lune	Rigmaden	22	18	28	30.17	0.928	6.32	6.31	1.001
England	NW03	Lune	Forge Wear	22	18	33	30.96	1.066	5.73	6.23	0.920
England	NW04	Eden	Temple Sowerby	22	32	35	32.43	1.079	5.77	6.11	0.944
England	NW05	Eden	Appleby	22	32	32	32.46	0.986	6.09	6.15	0.991
Scotland	SEPA_E03	Tay/Dochart/Fillan/Cononish	Tayview House	22	18	35	29.52	1.185	6.40	6.35	1.008
Scotland	SEPA_E05	Tay/Dochart/Fillan/Cononish	Pitnacree	22	11	30	27.35	1.097	6.23	6.67	0.934
Scotland	SEPA_E06	Tay/Dochart/Fillan/Cononish	Boat of Murthly	22	18	32	28.66	1.117	6.59	6.47	1.019
Scotland	SEPA_E08	Tay/Dochart/Fillan/Cononish	Taymount Mains	22	18	36	29.31	1.228	6.11	6.37	0.960
Scotland	SEPA_E10	North Esk	Galley Farm	22	22	37	29.98	1.234	6.57	6.38	1.030
Scotland	SO02	Urr Water	Haugh of Urr	22	22	36	30.78	1.169	6.61	6.36	1.039
Scotland	TA02	Isla	Wester Cardean	22	22	32	31.39	1.020	6.56	6.37	1.030
Scotland	TA03	South Esk	Stannochy Bridge	22	22	31	29.76	1.042	6.58	6.37	1.032
Scotland	TW02	Tarth Water	Tarth Water Foot	22	20	28	31.98	0.876	6.54	6.39	1.023
England	3395	Gordale Beck	Gordale Bridge	23	16	25	26.67	0.937	6.44	6.68	0.964

England	5861	Hindwell Brook/Summergil Brook	Combe	23	24	27	33.31	0.811	6.37	6.34	1.005
Scotland	9903	Lusragan Burn	Cluny Villa	23	7	36	26.77	1.345	6.58	6.50	1.012
Scotland	CL02	Ayr	Nether Wellwood	23	22	32	30.5	1.049	6.50	6.44	1.009
Scotland	FO01	Cocklemill Burn	Kill Conquhar Mill	23	23	24	28.27	0.849	5.42	6.29	0.862
Scotland	NE02	Lossie	u/s Blackburn	23	23	30	29.32	1.023	6.73	6.34	1.062
Scotland	NE05	Carron Water	Tewel Ford	23	23	25	28.12	0.889	6.52	6.44	1.012
Scotland	NE06	Carron Water	Stonehaven	23	23	30	28.12	1.067	6.37	6.30	1.011
Scotland	TA06	Vinny Water	Pitmuies	23	23	27	28.45	0.949	6.19	6.29	0.984
England	WE05	Morlas Brook	d/s Glyn Morlas	23	27	25	30.04	0.832	5.88	6.37	0.923
England	3166	Rye	Nunnington	24	32	32	33.13	0.966	6.28	6.09	1.032
Scotland	4991	Blackadder Water	Fogo	24	32	34	32.44	1.048	6.06	6.22	0.974
Wales	5675	Monnow	Great Goytre	24	24	40	33.19	1.205	6.45	6.28	1.027
England	5854	Back Brook	Kington	24	24	27	32.92	0.820	6.04	6.29	0.960
Wales	5895	Western Cleddau	Crow Hill	24	31	40	37.57	1.065	6.30	6.25	1.008
England	8213	Teme	Brampton Bryan	24	24	36	33.4	1.078	6.19	6.32	0.980
England	8285	Clun	Purslow	24	26	36	32.56	1.106	6.44	6.46	0.996
England	9581	Lathkill	Alport	24	35	30	32.3	0.929	6.63	6.01	1.102
England	ST04	Sence	Newton Linford	24	26	34	31.09	1.094	6.44	6.19	1.040
England	ST05	Derwent	Baslow	24	24	34	32.93	1.032	6.38	6.29	1.015
England	ST07	Wye	Ashford	24	24	31	33.65	0.921	6.58	6.17	1.067
England	0181	DeLank River	Bradford	25	25	43	34.98	1.229	6.81	6.62	1.028
England	0185	DeLank River	Keybridge	25	25	30	35.22	0.852	7.03	6.63	1.061
England	0385	Barle	Cow Castle	25	25	35	35.32	0.991	6.74	6.63	1.017
England	0389	Barle	South Hill	25	25	32	35.34	0.905	7.03	6.62	1.061
England	0393	Barle	Pixton Hill	25	25	37	35.28	1.049	6.54	6.62	0.988
England	0401	Torridge	Fordmill Farm	25	25	42	34.68	1.211	6.71	6.61	1.015
England	0801	Avon Water	Wootton Bridge	25	40	31	37.05	0.837	6.35	6.03	1.053
Wales	1601	Teifi	Strata Florida	25	25	29	34.07	0.851	6.66	6.62	1.006
England	5303	Ober Water	Puttles Bridge	25	40	42	36.76	1.143	6.45	6.18	1.044
England	5307	Lymington	Balmer Lawn	25	40	40	35.37	1.131	6.55	6.20	1.056
Wales	5801	Eastern Cleddau	Plasymeibion	25	25	39	33.75	1.156	6.72	6.61	1.017
Wales	5803	Eastern Cleddau	West of Llandissilio	25	25	40	34.03	1.175	6.45	6.47	0.997
Wales	5891	Western Cleddau	Treffgarne	25	31	39	35.04	1.113	6.51	6.31	1.032
Wales	5901	Dwyfach	Pant Glas	25	25	36	30.03	1.199	6.53	6.66	0.981
Wales	5903	Dwyfach	Pont y Felin	25	25	34	34.05	0.998	6.18	6.63	0.932
Wales	5905	Dwyfach	Bont Fechan	25	25	35	34.03	1.029	6.57	6.61	0.995

England	8281	Clun	Whitcott Keysett	25	26	32	31.86	1.004	6.91	6.56	1.053
England	8609	Teign	Fingle Bridge	25	25	29	35.33	0.821	6.79	6.63	1.024
England	8613	Teign	Whetcombe Barton	25	25	38	34.39	1.105	6.66	6.49	1.026
England	8709	Fowey	Draynes Bridge	25	25	33	35.34	0.934	7.00	6.63	1.056
England	8713	Fowey	Leball Bridge	25	25	28	35.44	0.790	6.61	6.63	0.997
England	9485	Walkham	Grenofen	25	25	33	35.42	0.932	6.61	6.63	0.997
England	SW04	Poltesco River	Poltesco Bridge	25	29	39	29.43	1.325	6.05	6.56	0.922
England	0101	Camel	Pencarrow Bridge	26	25	32	34.47	0.928	6.62	6.61	1.001
England	0103	Camel	Tuckingmill	26	25	28	34.89	0.803	6.75	6.61	1.022
England	0227	Yarty	Crawley Bridge	26	21	31	32.58	0.951	6.10	6.45	0.946
England	0501	Avill	Wheddon Cross	26	27	29	30.27	0.958	6.97	6.38	1.093
England	0503	Avill	Timberscombe	26	27	35	31.53	1.110	6.63	6.30	1.052
Wales	1701	Clwyd	Melin-y-Wig	26	16	31	29.48	1.051	6.35	6.58	0.965
England	2801	Dane	Hug Bridge	26	26	32	32.12	0.996	6.62	6.49	1.020
England	3160	Pickering Beck	Levisham	26	28	32	31.15	1.027	7.12	6.33	1.125
England	3162	Seph	Laskill	26	26	30	31.74	0.945	6.90	6.39	1.079
England	3391	Gordale Beck	Seaty Hill	26	16	29	27.95	1.038	6.59	6.66	0.989
Scotland	3801	Tyne	Crichton	26	23	29	28.34	1.023	6.93	6.27	1.105
England	5001	Otter	Fairhouse Farm	26	26	35	31.36	1.116	6.14	6.54	0.939
Wales	5601	Lugg	Monaughty	26	26	31	32.18	0.963	6.74	6.52	1.034
England	5603	Lugg	Combe	26	24	40	33.83	1.182	6.78	6.21	1.093
England	5671	Monnow	Llanveynoe	26	26	34	31.71	1.072	6.47	6.58	0.983
England	5673	Monnow	Clodock	26	26	35	32.52	1.076	6.63	6.44	1.030
Wales	5681	Lugg	Crug	26	26	30	30.7	0.977	6.67	6.61	1.010
Wales	5691	Arrow	Kesty	26	26	23	30.59	0.752	6.65	6.52	1.020
England	5693	Arrow	Kington Urban	26	26	31	32.32	0.959	6.71	6.48	1.036
Wales	5703	Usk	d/s Usk Reservoir	26	26	35	31.16	1.123	6.89	6.64	1.037
Wales	5707	Usk	Trallong	26	17	35	31.32	1.118	6.69	6.39	1.046
Wales	5881	Wern	Mynachlog-Ddu	26	8	33	25.32	1.303	6.27	6.69	0.937
Scotland	7705	Lunan Burn	Forneth	26	23	28	28.52	0.982	6.54	6.40	1.021
Wales	8205	Teme	Felindre	26	26	33	31.34	1.053	6.58	6.61	0.996
Wales	8209	Teme	Pennant Pound	26	26	27	32.66	0.827	6.67	6.47	1.031
England	8605	Teign	Leigh Bridge	26	25	33	35.28	0.935	6.67	6.63	1.006
England	NH05	Gate Burn	Framlington Gate	26	8	27	25.45	1.061	6.52	6.56	0.993
England	0221	Synderford	Venn Hill	27	26	31	31.89	0.972	6.16	6.40	0.962
England	0223	Blackwater	Beerhall	27	27	32	32.08	0.997	5.94	6.47	0.918

England	0225	Kit Brook	Kit Bridge	27	27	35	31.03	1.128	6.31	6.24	1.012
England	1083	Rother	Hawkley Mill	27	38	31	31.52	0.983	6.19	5.40	1.146
Wales	1501	Gwendraeth Fach	Garn-Lwyd	27	26	34	31.29	1.087	6.53	6.48	1.007
England	2401	Great Eau	Ruckland	27	38	26	31.36	0.829	6.35	5.51	1.153
Scotland	4601	Durness Stream	u/s Durness	27	2	25	25.37	0.986	5.92	6.13	0.965
Scotland	4885	Unnamed	Westerdale	27	8	29	24.09	1.204	6.07	6.70	0.906
England	5101	Frome	Chantmarle	27	39	36	30.61	1.176	5.97	5.69	1.049
England	5201	Axe	Wookey Hole	27	27	24	30.11	0.797	6.33	6.28	1.008
England	5305	Highland Water	Millyford Bridge	27	40	34	36.76	0.925	6.79	6.15	1.105
England	5383	Bratley Water	Bratley	27	27	30	31.2	0.961	6.60	6.42	1.028
England	5385	Highland Water	Ocknell	27	27	29	30.07	0.964	6.17	6.33	0.974
Wales	6501	Mounton Brook	Bully Hole Bottom	27	27	29	29.48	0.984	6.66	6.31	1.056
England	6693	Dowles Brook	u/s Dowles Manor	27	26	26	31.23	0.832	6.62	6.45	1.026
England	6701	Cannop Brook	Speculation	27	27	30	29.95	1.002	6.50	6.35	1.024
Wales	5851	Unnamed	Hill House Dingle	28	26	28	30.31	0.924	6.50	6.52	0.996
England	6691	Dowles Brook	d/s Lem Brook	28	26	26	31.06	0.837	6.50	6.54	0.994
England	8805	Coombevalley Stream	Kilkhampton	28	29	30	30.12	0.996	6.40	6.55	0.977
Scotland	FO02	Crail Burn	A917 Road Bridge	28	23	23	28	0.822	5.87	6.26	0.938
Scotland	FO03	Boghall Burn/Keil Burn	Pitcruvie Castle	28	23	29	28.16	1.030	6.17	6.31	0.978
England	NH04	Glanton Burn	Rothill	28	28	28	28.14	0.995	5.57	6.21	0.897
England	NH06	Kilton Beck	Lodge Wood	28	28	29	29.55	0.982	6.34	6.36	0.997
England	ST03	Sher Brook	Shugborough	28	28	31	29.53	1.050	6.32	6.38	0.990
Scotland	TW03	Eden Water	A6089 Bridge	28	28	26	29.87	0.870	6.08	6.18	0.985
England	3150	Cowhouse Beck	Snaper House	29	27	29	28.84	1.006	6.59	6.28	1.050
England	6840	Unnamed	Gasper	29	27	28	29.5	0.949	6.68	6.32	1.057
England	8809	Coombevalley Stream	Coombe	29	25	31	33.04	0.938	6.55	6.57	0.997
England	SW01	Bodilly Stream	Bodilly Bridge	29	29	28	29.48	0.950	6.46	6.56	0.984
England	SW02	Drift/Newlyn River	Skimmel Bridge	29	29	26	29.66	0.877	6.42	6.57	0.978
England	SW05	Stithians Stream	Searaugh Moor	29	29	26	29.49	0.882	6.38	6.57	0.972
England	SW06	Trevaylor Stream	Trythogga	29	29	31	29.37	1.056	6.29	6.56	0.958
England	SW07	Gweek River	Mether-uny-Mill Bridge	29	29	32	29.37	1.090	6.94	6.56	1.057
England	SW08	Manaccan River	Polkanoggo	29	29	33	29.39	1.123	6.76	6.56	1.030
England	1081	Hammer's Pond Tributary	Carter's Lodge	30	30	26	21.88	1.188	6.04	6.02	1.003
England	3141	Mill Beck	Bathingwell Wood	30	30	18	21.86	0.824	6.11	6.02	1.015
England	3144	Long Gill	Newgate Foot	30	30	22	21.86	1.007	5.64	6.02	0.937
England	3145	Halleykeld Spring Stream	Halleykeld Rigg	30	30	18	21.86	0.824	5.67	6.02	0.942

England	3151	Mire Falls Gill	Reins Wood	30	30	20	21.86	0.915	6.05	6.02	1.005
England	3152	Sledhill Gill	Yowlass Wood	30	30	24	22.56	1.064	7.04	6.03	1.168
England	5841	Unnamed	Bredenbury	30	30	23	21.87	1.051	6.00	6.02	0.997
England	5844	Unnamed	Dunhampton Farm	30	30	20	21.86	0.915	6.20	6.02	1.030
Wales	5852	Unnamed	Pen-Twyn	30	30	22	21.86	1.006	6.32	6.02	1.050
England	6381	Unnamed	Bonemills Hollow	30	30	21	24.89	0.844	5.52	5.85	0.944
England	6844	Unnamed	Lyon's Gate	30	30	20	21.86	0.915	5.90	6.02	0.980
England	6848	Unnamed	Woolland	30	30	23	21.87	1.052	6.00	6.02	0.997
England	7149	Unnamed	In wood, u/s tributary	30	30	22	22.01	1.000	5.77	6.02	0.959
England	AN07	Waithe Beck	Kirmond Le Mire	30	39	27	30.38	0.889	6.00	5.53	1.086
England	0405	Torridge	Kingsley Mill	31	17	39	34.02	1.146	6.33	6.39	0.991
England	1101	Dudwell	Burwash Weald	31	27	35	30.89	1.133	6.14	6.21	0.989
England	1109	Rother	Etchingham	31	41	33	33.94	0.972	6.06	5.51	1.100
Wales	1503	Gwendraeth Fach	Llangendeirne	31	31	42	34.92	1.203	6.10	6.12	0.996
Wales	1505	Gwendraeth Fach	u/s Kidwelly	31	24	39	33.49	1.164	6.33	6.19	1.023
Wales	1603	Teifi	Tregaron Bog	31	31	36	34.92	1.031	6.36	6.42	0.991
Wales	1607	Teifi	Alltyblacca	31	17	45	32.41	1.389	6.47	6.38	1.014
Wales	1611	Teifi	Llechryd	31	17	44	33.42	1.317	6.48	6.25	1.036
England	3311	Swale	Topcliffe	31	32	37	34.04	1.087	6.03	5.94	1.015
England	3607	Wansbeck	Mitford Gauging Station	31	32	34	32.12	1.059	6.47	6.16	1.051
Scotland	3704	Teith	Blackdub	31	31	35	37.12	0.943	6.29	6.27	1.004
Scotland	3711	Forth	Parks of Garden	31	31	39	37.28	1.046	6.38	6.27	1.017
Scotland	3713	Forth	Kippen Bridge	31	31	32	37.66	0.850	5.94	6.26	0.949
Scotland	3717	Forth	Drip Bridge	31	31	38	36.85	1.031	6.11	6.26	0.977
Wales	5805	Eastern Cleddau	Llawhaden	31	31	42	37.23	1.128	6.38	6.25	1.021
England	0203	Axe	Oathill Farm	32	35	32	31.84	1.005	6.16	5.80	1.063
England	0205	Axe	Broom	32	35	43	33.77	1.273	6.12	5.90	1.038
England	0207	Axe	Whitford Bridge	32	32	37	34.42	1.075	5.81	5.93	0.980
England	0229	Yarty	Gammons Hill	32	32	36	33.97	1.060	6.17	6.10	1.012
England	2007	Blithe	Newton	32	35	33	32.25	1.023	6.48	5.88	1.101
England	2713	Ribble/Gayle Beck	Cleatop Barns	32	32	39	31.98	1.219	6.00	6.19	0.969
England	2715	Ribble/Gayle Beck	Halton Bridge	32	32	35	31.59	1.108	5.94	6.19	0.959
England	2721	Ribble/Gayle Beck	Ribchester Bridge	32	32	30	32.5	0.923	5.77	6.09	0.947
England	2905	Derwent	Ouse Bridge	32	19	28	30.42	0.920	6.14	6.43	0.955
England	3393	Wharfe	Otley	32	32	33	33.48	0.986	6.00	6.01	0.998
England	3397	Wharfe	Wetherby	32	32	35	33.63	1.041	5.97	5.97	0.999

England	3413	Tees	Over Dinsdale	32	32	25	33.22	0.753	5.96	6.03	0.989
Scotland	3715	Forth	Gargunnock Bridge	32	31	33	37.31	0.885	5.79	6.26	0.925
Scotland	3807	Tyne	Haddington Weir	32	32	27	32.13	0.840	5.15	6.11	0.844
Scotland	3809	Tyne	East Linton	32	32	29	32.37	0.896	5.86	6.08	0.964
Scotland	4915	Tweed	d/s Birgham	32	32	36	32.06	1.123	5.61	6.08	0.922
Scotland	4917	Tweed	Canny Island	32	32	36	33.43	1.077	5.75	5.97	0.963
Scotland	4979	Whiteadder Water	u/s Allanton	32	32	31	31.73	0.977	5.16	6.15	0.838
Scotland	4983	Whiteadder Water	Chesterfield Ford	32	32	37	33.37	1.109	5.73	5.96	0.962
Scotland	4987	Blackadder Water	Halliburton Bridge	32	20	33	32.08	1.029	5.67	6.35	0.892
Scotland	4995	Blackadder Water	Blackadder Water Foot	32	32	29	33.38	0.869	5.24	5.99	0.875
England	5007	Otter	Colhayes Farm	32	21	36	33.5	1.074	5.86	6.38	0.919
Wales	5677	Monnow	Rockfield	32	33	30	34.99	0.857	6.30	5.93	1.062
Wales	5717	Usk	Llantrissant	32	32	37	35.05	1.055	6.49	6.09	1.065
England	5864	Lugg	Mordiford	32	33	35	34.45	1.016	5.77	5.99	0.964
Wales	5887	Western Cleddau	Wolf's Castle	32	21	40	33.83	1.182	6.30	6.39	0.986
England	9615	Coquet	Pauperhaugh	32	19	39	31.3	1.246	5.97	6.20	0.962
England	NH01	Till/Beamish	Etal	32	32	35	31.66	1.106	5.77	6.16	0.937
England	NH03	Glen	Ewart	32	32	28	31.1	0.900	5.96	6.33	0.942
England	NW06	Eden	Warwick Bridge	32	32	32	32.04	0.999	6.03	6.17	0.977
England	ST06	Derwent	Cromford Meadows	32	32	34	33.22	1.024	6.47	6.08	1.065
Wales	WE04	Braint	Pont Mynach	32	31	36	34.66	1.039	5.83	6.21	0.938
England	5009	Otter	Newton Poppleford	33	32	39	34.03	1.146	5.69	6.07	0.938
England	5607	Lugg	Marlbrook	33	33	38	34.01	1.117	6.32	5.97	1.059
England	5609	Lugg	Wergin'S Bridge	33	33	38	34.97	1.087	5.74	5.91	0.972
England	5621	Wye	Huntsham Bridge	33	33	39	34.9	1.118	5.85	5.94	0.985
England	5697	Arrow	Ivington	33	33	34	34.88	0.975	6.35	5.93	1.071
England	6858	Stour	Trill Bridge	33	37	34	34.64	0.981	5.41	5.62	0.962
England	8217	Teme	Tenbury	33	33	38	34.2	1.111	6.11	6.02	1.014
England	8221	Teme	Powick Bridge	33	33	35	35.33	0.991	5.89	5.88	1.002
England	NH02	Till/Beamish	Chatton	33	20	27	34.39	0.785	5.93	6.20	0.956
England	ST02	Severn	Isle Of Bicton	33	33	28	34.9	0.802	5.96	5.99	0.996
England	0605	Avon	Bulford	34	37	33	34.49	0.957	5.61	5.64	0.995
England	0607	Avon	Stratford-sub-Castle	34	34	37	35.65	1.038	6.05	5.74	1.054
England	0609	Avon	Breamore	34	34	36	38.58	0.933	5.72	5.83	0.980
England	0613	Avon	Christchurch	34	34	35	38.93	0.899	5.43	5.85	0.929
England	0903	Itchen	Chilland	34	36	39	34.64	1.126	5.72	5.51	1.038

England	0907	Itchen	Otterbourne Water Works	34	34	39	38.65	1.009	6.08	5.82	1.044
England	0909	Itchen	d/s Chickenhall SDW	34	34	43	37.27	1.154	5.98	5.68	1.052
England	5105	Frome	Lower Bockhampton	34	34	38	36.36	1.045	5.74	5.76	0.996
England	5107	Frome	Moreton	34	34	43	38.33	1.122	6.12	5.86	1.045
England	5109	Frome	East Stoke	34	34	40	39.36	1.016	6.10	5.89	1.036
England	6856	Allen	Walford Mill	34	35	32	34.42	0.930	5.97	5.67	1.053
England	6863	Stour	Spetisbury	34	34	45	38.26	1.176	5.98	5.85	1.022
England	8421	Test	Lower Brook	34	41	45	35.52	1.267	6.04	5.50	1.098
England	8425	Test	Romsey	34	34	38	37.39	1.016	5.71	5.69	1.004
England	8429	Test	Skidmore	34	34	41	37.13	1.104	5.98	5.67	1.055
England	8517	Piddle	Wareham	34	34	41	36.5	1.123	5.85	5.63	1.040
England	TH01	Kennet	u/s Aldershot Water	34	34	46	38.01	1.210	6.11	5.79	1.056
England	0231	Corry Brook	Coryton	35	40	43	34.46	1.248	6.02	6.26	0.962
England	0603	Avon	Rushall	35	35	34	32.24	1.054	5.50	5.57	0.987
England	0701	Avon	Easton Grey	35	35	33	31.79	1.038	5.73	5.68	1.008
England	0703	Tetbury Avon	Brockenborough	35	35	29	31.95	0.908	6.07	5.71	1.063
England	0707	Avon	Great Somerford	35	35	24	32.07	0.748	6.38	5.73	1.113
England	0905	Itchen	Itchen St.Cross	35	34	38	36.62	1.038	5.61	5.69	0.986
England	1001	Rother	u/s Liss STW	35	35	30	33.24	0.902	5.90	5.82	1.015
England	1003	Rother	Stodham Park	35	35	36	33.07	1.089	6.14	5.86	1.049
England	1005	Rother	Durford Bridge	35	35	35	31.8	1.101	5.60	5.76	0.972
England	1007	Rother	Stedham	35	35	33	31.93	1.034	6.42	5.79	1.110
England	1009	Rother	Selham	35	35	35	32.73	1.069	5.91	5.66	1.045
England	1207	Evenlode	Fawler	35	37	24	35.66	0.673	5.58	5.64	0.990
England	1307	Wey	Tilford	35	41	24	33.42	0.718	5.12	5.35	0.956
England	1309	Wey	Eashing	35	36	29	33.3	0.871	6.10	5.52	1.104
England	1311	Wey	Burpham	35	36	27	33.63	0.803	5.67	5.60	1.012
England	1903	Perry	Rednal Mill	35	35	31	32.9	0.942	5.23	5.63	0.929
England	1909	Perry	Mytton	35	35	27	31.94	0.845	5.41	5.72	0.946
England	2003	Blithe	Cresswell	35	35	28	31.85	0.879	5.79	5.96	0.971
England	2009	Blithe	Hamstall Ridware	35	35	33	32.83	1.005	5.73	6.01	0.953
England	2505	Glen	Little Bytham	35	38	28	32.84	0.853	5.00	5.46	0.915
England	6005	Blythe	Temple Balsall	35	35	33	33.31	0.991	5.61	5.84	0.961
England	0610	Avon	Moortown	36	34	32	38.04	0.841	5.59	5.79	0.965
England	0705	Avon	Cow Bridge	36	35	37	32.37	1.143	5.16	5.73	0.901
England	0709	Avon	Kellaway'S Weir	36	34	32	36.39	0.879	5.78	5.68	1.017

England	0711	Avon	Lacock	36	35	30	35.03	0.856	5.43	5.74	0.945
England	1011	Rother	Hardham	36	36	42	33.04	1.271	6.05	5.62	1.077
England	1111	Rother	Udiam	36	36	34	33.56	1.013	5.65	5.50	1.027
England	1209	Evenlode	Cassington	36	36	33	35.04	0.942	5.61	5.55	1.011
England	1305	Wey	Wyck	36	35	31	32.53	0.953	5.10	5.59	0.912
England	2005	Blithe	Field	36	35	32	32.14	0.996	5.44	5.89	0.923
England	2109	Devon	Bottesford	36	37	36	34.11	1.056	5.28	5.61	0.941
England	2305	Colne	Earl's Colne	36	38	31	32.74	0.947	4.90	5.45	0.899
England	2307	Colne	Fordstreet Bridge	36	36	27	33.19	0.813	5.00	5.45	0.917
England	2611	Wensum	Taverham	36	36	29	33.45	0.867	5.21	5.34	0.975
England	2619	Yare/Blackwater	North of Barford	36	37	32	33.6	0.952	5.00	5.41	0.924
England	2621	Yare/Blackwater	Earlham	36	36	37	33.7	1.098	5.41	5.39	1.004
England	3105	Derwent	Yedingham	36	41	31	32.62	0.950	5.84	5.20	1.123
England	3107	Derwent	Norton	36	41	39	33.31	1.171	5.74	5.27	1.089
England	3109	Derwent	Stamford Bridge	36	41	41	33.11	1.238	5.66	5.27	1.075
England	3111	Derwent	Thorganby	36	41	38	32.71	1.162	5.79	5.20	1.114
England	5507	Stour/Great Stour	Milton Bridge	36	36	35	34.34	1.019	5.17	5.46	0.947
England	0775	By Brook	Ashley	37	37	30	34.72	0.864	5.63	5.66	0.995
England	3157	Holbeck	Hovingham Carrs	37	37	35	33.2	1.054	5.86	5.60	1.046
England	3163	Menethorpe Beck	Menethorpe	37	38	29	32.04	0.905	5.83	5.46	1.068
England	5103	Frome	Frampton	37	35	37	34.08	1.086	5.68	5.79	0.981
England	6285	Wissey	Linghills Farm	37	38	35	32.91	1.063	5.29	5.43	0.973
England	6289	Wissey	Didlington Lodge	37	36	42	33.56	1.251	5.74	5.48	1.047
England	6409	Brue	Wyke	37	35	32	32.97	0.971	5.56	5.65	0.984
England	6985	Loddon	Sherfield on Loddon	37	41	35	33.81	1.035	5.43	5.38	1.009
England	7122	Moors/Crane	King's Farm	37	41	39	32.35	1.206	5.67	5.27	1.075
England	8513	Piddle	Brockhill Bridge	37	34	45	37.83	1.190	6.00	5.78	1.038
England	9109	Hull/West Beck	Wansford	37	36	29	33.13	0.875	5.07	5.45	0.931
England	9121	Kelk Beck/Frodingham Beck	Harpham	37	38	28	32.42	0.864	4.93	5.65	0.873
England	AN02	Cringle Brook	Thunderbridge	37	37	41	32.9	1.246	5.73	5.51	1.040
England	AN08	Bain	Biscathorpe	37	38	34	31.8	1.069	5.74	5.46	1.051
England	TH02	Lambourn	Bagnor	37	37	42	34.86	1.205	6.02	5.53	1.089
England	TH03	Lyde River	Deanlands Farm	37	37	33	33.63	0.981	5.33	5.50	0.969
England	TH04	Coln	Fosse Bridge	37	37	43	33.95	1.267	5.72	5.71	1.002
England	TH05	Windrush	d/s Dickler	37	37	44	34.8	1.264	6.27	5.65	1.111
England	TH07	Ash	Easneye	37	37	39	33.77	1.155	5.59	5.47	1.021

England	TH08	Chess	u/s R. Colne	37	37	39	33.85	1.152	5.77	5.46	1.057
England	0201	Axe	Mosterton	38	39	34	29.88	1.138	5.59	5.58	1.002
England	0601	Avon	Patney	38	35	26	33.05	0.787	4.96	5.59	0.887
England	0803	Avon Water	Gordleton Mill	38	40	39	37.65	1.036	6.23	6.00	1.038
England	0805	Avon Water	Efford Bridge	38	40	33	38.58	0.855	5.94	6.08	0.977
England	0901	Candover Brook	Abbotstone	38	38	33	32.98	1.000	5.73	5.52	1.038
England	1203	Evenlode	Evenlode	38	38	32	32.89	0.973	5.19	5.48	0.947
England	1403	Mimram	Codicote Bottom	38	41	29	32.05	0.905	5.24	5.34	0.981
England	1405	Mimram	Panshanger	38	41	26	32.64	0.796	4.73	5.21	0.908
England	1807	Leadon	Ketford	38	38	26	33.13	0.785	5.08	5.54	0.916
England	1901	Perry	Perry Farm	38	37	30	32.71	0.917	5.13	5.53	0.927
England	2103	Smite	Colston Bassett	38	38	29	32.17	0.901	5.00	5.44	0.918
England	2301	Stambourne Brook	Great Yeldham	38	38	28	31.2	0.897	4.79	5.32	0.901
England	2403	Great Eau	Swaby	38	38	26	32.39	0.803	5.42	5.46	0.993
England	2405	Great Eau	Belleau	38	41	30	32.53	0.922	5.43	5.20	1.043
England	2513	Welland	Marston Trussel	38	38	25	31.93	0.783	4.88	5.44	0.898
England	2601	Wensum	South Raynham	38	38	31	31.62	0.980	5.42	5.33	1.016
England	3103	Derwent	West Ayton	38	39	30	33.68	0.891	5.13	5.59	0.918
England	5183	Wool Stream	Wool	38	38	30	30.93	0.970	5.13	5.41	0.949
England	5203	Axe	Bleadney	38	38	30	32.56	0.921	5.33	5.52	0.965
England	5503	Stour/Great Stour	Little Chart Forstal	38	35	34	31.56	1.077	5.03	5.53	0.910
England	6101	Thet	Red Bridge, Shropham	38	38	36	33.53	1.074	5.31	5.43	0.978
England	6103	Thet	East Harling	38	36	34	33.74	1.008	4.97	5.44	0.914
England	7116	Moors/Crane	Redmans Hill	38	38	41	32.86	1.248	5.54	5.52	1.003
England	0771	By Brook	Gatcombe Hill	39	37	27	32.97	0.819	5.78	5.59	1.035
England	0773	By Brook	Slaughterford	39	37	36	34.07	1.057	6.14	5.61	1.094
England	0781	Avon	Washpool Bridge	39	39	32	29.9	1.070	5.38	5.62	0.957
England	1201	Evenlode	Moreton-in-the-Marsh	39	39	26	29.84	0.871	5.00	5.57	0.897
England	1301	Tilling Bourne	Wotton	39	39	31	33.67	0.921	6.26	5.86	1.068
England	1303	Tilling Bourne	u/s Albury Village	39	40	24	37.99	0.632	5.79	6.05	0.956
England	2107	Devon	Knipton	39	39	28	31.75	0.882	5.71	5.75	0.993
England	5855	Curl Brook	Pembridge	39	24	30	33.48	0.896	6.13	6.14	0.999
England	5856	Main Ditch	Leominster	39	37	36	34.14	1.054	5.28	5.63	0.938
England	6201	Unnamed	u/s Brackley	39	39	21	29.12	0.721	5.10	5.61	0.909
England	6405	Brue	South Brewham	39	39	27	31.64	0.853	5.63	5.72	0.984
England	6801	Middlemarsh Stream	Grange Wood	39	27	33	30.33	1.088	5.91	6.23	0.949

England	6841	Unnamed	Woodlands Manor	39	39	22	29.41	0.748	4.86	5.59	0.869
England	6847	Unnamed	Farrington	39	39	26	29.49	0.882	5.00	5.59	0.894
England	6849	Unnamed	Okeford Fitzpaine	39	39	30	29.26	1.025	6.03	5.88	1.025
England	7104	Moors/Crane	d/s Cranborne	39	39	29	30.89	0.939	5.45	5.54	0.984
England	7119	Moors/Crane	Verwood	39	39	34	31.75	1.071	5.50	5.52	0.997
England	7143	Ed	Upper Farm	39	39	34	27.61	1.231	5.18	5.70	0.909
England	7153	Unnamed	d/s Wood	39	30	28	22.06	1.269	5.89	6.02	0.978
England	8305	Bure	Corpusty	39	41	27	32.35	0.835	6.26	5.18	1.209
England	8309	Bure	Whitehouse Farm Ford	39	41	37	32.5	1.139	5.76	5.19	1.111
England	8505	Piddle	Piddletrenthide	39	39	27	29.98	0.901	5.00	5.55	0.900
England	8509	Piddle	Druce	39	39	32	33.35	0.960	5.53	5.63	0.982
England	8521	Bere Stream	Middle Bere	39	37	35	33.73	1.038	5.83	5.55	1.051
England	9105	Hull/West Beck	Little Driffield	39	27	24	29.88	0.803	5.00	6.29	0.795
England	AN06	Rase	Bully Hills	39	39	25	29	0.862	5.36	5.62	0.954
England	AN09	Goulceby Beck	Goulceby	39	39	27	31.47	0.858	5.41	5.58	0.970
England	SN02	Sutton Stream	Road Bridge	39	39	30	30.11	0.996	6.10	5.59	1.092
England	SW09	St.Keverne Stream	Porthoustock Bridge	39	29	34	29.36	1.158	6.09	6.56	0.929
Scotland	TA08	Kenly Water	Stravithie	39	23	30	28.06	1.069	5.53	6.37	0.868
England	0233	Umbourne Brook	Easy Bridge	40	40	38	37.17	1.022	6.37	6.13	1.039
England	1013	Arun	Magpie Bridge	40	27	35	33.61	1.041	5.74	6.16	0.931
England	5301	Ober Water	Mill Lawn	40	40	37	38.44	0.963	6.41	6.07	1.055
England	5381	Ober Water	Vereley	40	27	35	31.75	1.103	6.54	6.38	1.024
England	7107	Moors/Crane	Great Rhymes Copse	40	39	37	31.35	1.180	6.08	5.50	1.105
England	7110	Moors/Crane	Pinnocks Moor	40	39	41	32.13	1.276	5.98	5.53	1.081
England	7113	Moors/Crane	Romford Bridge	40	37	42	33.33	1.260	6.00	5.54	1.082
England	7145	Ed	Pains Moor	40	39	36	30.03	1.199	5.75	5.61	1.024
England	7189	Mannington Brook	Horton Heath	40	40	38	34.51	1.101	5.97	5.94	1.005
England	7192	Mannington Brook	Newman's Lane	40	40	43	36.73	1.171	6.16	5.95	1.036
England	7195	Mannington Brook	Penningston's Copse	40	40	44	38.4	1.146	5.98	6.07	0.986
England	0313	Exe	Flowerpot	41	33	33	35.17	0.938	5.30	6.13	0.865
England	0713	Avon	Staverton Weir	41	43	30	31.99	0.938	5.00	4.97	1.005
England	1411	Lee	Fisher's Green	41	36	34	34.94	0.973	5.35	5.54	0.965
England	1809	Leadon	Upleadon	41	41	33	35.29	0.935	4.91	5.51	0.890
England	2111	Devon	Hawton	41	41	28	32.21	0.869	4.68	5.08	0.921
England	2303	Colne	d/s Hedingham STW	41	38	30	33.03	0.908	5.13	5.40	0.950
England	2521	Welland	Tinwell	41	36	32	34.14	0.937	4.94	5.47	0.904

England	2605	Wensum	Great Ryburgh	41	41	25	32.51	0.769	4.76	5.18	0.919
England	2607	Wensum	Worthing	41	41	29	32.52	0.892	5.28	5.18	1.019
England	2609	Wensum	North of Elsing	41	41	31	32.84	0.944	5.00	5.24	0.955
England	3313	Ouse/Ure	Aldwark Toll Bridge	41	42	27	34.75	0.777	5.37	5.47	0.982
England	3315	Ouse/Ure	Nether Poppleton	41	42	30	34.52	0.869	5.00	5.42	0.923
England	3317	Ouse/Ure	Acaster Malbis	41	42	29	34.45	0.842	5.24	5.41	0.969
England	5309	Lymington	Boldre Bridge	41	40	39	38.49	1.013	5.85	6.06	0.965
England	5501	Stour/Great Stour	Stonebridge Green	41	41	25	32.15	0.777	4.56	5.13	0.888
England	5505	Stour/Great Stour	Wye	41	36	30	33.51	0.895	5.03	5.49	0.916
England	5509	Stour/Great Stour	Fordwich	41	41	29	33	0.879	4.72	5.27	0.896
England	5623	Wye	Redbrook	41	33	41	34.94	1.173	5.73	5.93	0.965
England	6105	Thet	Nuns Bridge, Thetford	41	41	39	32.39	1.204	5.59	5.16	1.084
England	6107	Little Ouse	Brandon	41	41	35	32.54	1.076	5.17	5.18	0.999
England	6242	Nine Wells Spring	Nine Wells	41	30	21	21.88	0.960	4.81	6.02	0.799
England	6258	Mill	Wendy	41	38	34	31.32	1.086	5.26	5.40	0.974
England	6264	Rhee	Harston	41	36	34	33.38	1.018	5.29	5.37	0.984
England	6265	Ouse/Cam	Hauxton Mill	41	36	31	33.68	0.921	4.94	5.37	0.921
England	6413	Brue	Tootle Bridge	41	34	38	38.1	0.997	5.37	5.79	0.927
England	6857	Cale	Syles Farm	41	37	40	34.52	1.159	5.22	5.48	0.953
England	6862	Lydden	Bagber Bridge	41	34	39	36.54	1.067	5.56	5.72	0.972
England	6981	Loddon	Oliver's Battery	41	41	33	32.27	1.023	4.70	5.29	0.889
England	6993	Enborne	Brimpton	41	41	33	33.65	0.981	5.79	5.41	1.070
England	7127	Moors/Crane	East Moors Farm	41	41	36	32.87	1.095	5.33	5.25	1.016
England	8313	Bure	Buxton Mill	41	43	33	31.48	1.048	5.30	4.85	1.094
England	8317	Bure	Coltishall Bridge	41	41	34	32.33	1.052	4.71	5.14	0.916
England	1409	Lee	Meadgate	42	41	30	33.09	0.907	5.37	5.24	1.024
England	1413	Lee	Enfield Weir	42	34	35	36.48	0.960	5.11	5.64	0.906
England	6009	Blythe	Blythe Bridge	42	42	32	33.69	0.950	5.28	5.32	0.992
England	6213	Great Ouse	Sharnbrook	42	41	35	33.39	1.048	5.17	5.28	0.979
England	6215	Great Ouse	Roxton Lock	42	36	30	34.79	0.862	5.27	5.49	0.960
England	6615	Severn	Stourport	42	42	38	35.02	1.085	5.63	5.49	1.026
England	6911	Thames/Isis	Malthouse	42	42	38	34.89	1.089	5.87	5.46	1.075
England	6913	Thames/Isis	Bablock Hythe	42	42	41	34.92	1.174	5.63	5.46	1.031
England	6915	Thames/Isis	Shillingford	42	42	42	34.94	1.202	5.60	5.46	1.025
England	6917	Thames/Isis	Reading	42	42	34	35.09	0.969	5.62	5.48	1.026
England	6919	Thames/Isis	Spade Oak	42	42	33	35.54	0.928	5.70	5.52	1.032

England	6921	Thames/Isis	Runnymede	42	42	32	35	0.914	5.41	5.47	0.989
England	1113	Rother	d/s Newenden	43	43	31	31.31	0.990	4.81	4.79	1.005
England	2409	Great Eau	Theddlethorpe-all-Saints	43	43	30	31.32	0.958	4.77	4.79	0.996
England	2509	Glen	South of Twenty	43	43	26	31.31	0.830	4.65	4.79	0.972
England	2523	Welland	Crowland	43	43	27	31.45	0.858	4.67	4.83	0.966
England	5207	Axe	Lower Weare	43	43	26	31.35	0.829	4.46	4.80	0.929
England	6109	Little Ouse	Brandon Creek	43	43	37	31.31	1.182	5.00	4.79	1.045
England	6111	Ouse/Cam	Hilgay Bridge	43	43	34	31.31	1.086	5.00	4.79	1.045
England	6261	Reach Lode	Upware Lock	43	43	31	31.31	0.990	4.74	4.79	0.991
England	6293	Wissey	Five Mile House	43	43	35	31.31	1.118	5.03	4.79	1.051
England	6417	Brue	Liberty Farm	43	43	32	31.32	1.022	4.59	4.79	0.958
England	AN03	Reach Lode	Hallards Fen Road	43	43	36	31.31	1.150	4.94	4.79	1.032
England	AN04	Monk's Lode	Eternity Hall Bridge	43	43	31	31.31	0.990	4.84	4.79	1.011
England	AN05	Sixteen Foot Drain	Horseways Corner	43	43	31	31.31	0.990	4.71	4.79	0.984