Optimisation of Multiplier-less FIR Filter Design Techniques

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ABSTRACT

This thesis is concerned with the design of multiplier-less (ML) finite impulse response (FIR) digital filters. The use of multiplier-less digital filters results in simplified filtering structures, better throughput rates and higher speed. These characteristics are very desirable in many DSP systems. This thesis concentrates on the design of digital filters with power-of-two coefficients that result in simplified filtering structures.

Two distinct classes of ML FIR filter design algorithms are developed and compared with traditional techniques. The first class is based on the sensitivity of filter coefficients to rounding to power-of-two. Novel elements include extending of the algorithm for multiple-bands filters and introducing mean square error as the sensitivity criterion. This improves the performance of the algorithm and reduces the complexity of resulting filtering structures.

The second class of filter design algorithms is based on evolutionary techniques, primarily genetic algorithms. Three different algorithms based on genetic algorithm kernel are developed. They include simple genetic algorithm, knowledge-based genetic algorithm and hybrid of genetic algorithm and simulated annealing. Inclusion of the additional knowledge has been found very useful when re-designing filters or refining previous designs. Hybrid techniques are useful when exploring large, N-dimensional searching spaces. Here, the genetic algorithm is used to explore searching space rapidly, followed by fine search using simulated annealing. This approach has been found beneficial for design of high-order filters. Finally, a formula for estimation of the filter length from its specification and complementing both classes of design algorithms, has been evolved using techniques of symbolic regression and genetic programming. Although the evolved formula is very complex and not easily understandable, statistical analysis has shown that it produces more accurate results than traditional Kaiser's formula.

In summary, several novel algorithms for the design of multiplier-less digital filters have been developed. They outperform traditional techniques that are used for the design of ML FIR filters and hence contributed to the knowledge in the field of ML FIR filter design.

To my precious wife Martina and daughter Alexandra.

This work would not exist without their support and sacrifice.

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Symbols and abbreviations

ACF	amplitude change function
ADC	analogue to digital converter
B	coefficient wordlength
B_{gene}	number of bits to encode genes
CSD	canonical signed-digit
$D(e^{j\omega})$	desired frequency response
DFT	discrete Fourier transform
δ_1, δ_2	pass-band and stop-band ripples
$E(e^{j\omega})$	frequency response error function
Δf	transition band width
ELS	evolutionary local search
FIR	finite impulse response
FWL	finite wordlength

$h(n)$	filter coefficients
$h_0(n)$	infinite precision filter coefficients
$H(e^{j\omega})$	frequency response
$H(z)$	transfer function
IDFT	inverse discrete Fourier transform
IIR	infinite impulse response
ILP	integer linear programming
MAE	mean absolute error
MSE	mean square error
MILP	mixed integer linear programming
ML	multiplier-less
N	filter length
N_{Coeff}	number of folded coefficients
N_{pop}	size of population
N_p	number of pass-bands
N_s	number of stop-bands
N_{fs}	size of frequency step
N_{genes}	number of genes
N_{xover}	number of crossover points
(N-1)	filter order
o(H)	order of schema
PTV-SS	periodically time-varying state space structures
PWR2	power-of-two

2PWR2	sum of two powers-of-two
$P_{chromosome}$	probability that a population contains a valid chromosome
p_c	crossover probability
p_m	mutation probability
PRP	proportional relation-preserve method
SD	signed digit
S_n	coefficient sensitivity
SR	simple rounding
SSS	simple symmetric sharpening method
$x(n)$	discrete signal sequence
$X(e^{j\omega})$	discrete-time Fourier transform of $x(n)$
$Y(e^{j\omega})$	output sequence of digital filter
$W(e^{j\omega})$	weight function
ω	normalised frequency
ω_p, ω_s	normalised pass-band and stop-band cut-off frequencies

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Chapter 1

Introduction

"An engineer can build a better mousetrap, but evolution can create a cat."

Andy Singleton

1.1 Introduction

The evolution of human society has been always closely tied with the effective communication and exchange of information enabling to pass human knowledge and skills from generation to generation. The last three decades of the twentieth century, in particular, are often termed as "information age". The way in which information are transmitted, stored and processed has changed entirely with the availability of powerful and fast computers and the rapid advances in telecommunications fueled by the growth of Internet and multimedia. One of the key enabling technologies in the development of communication infrastructure was*signal processing*.

The field of signal processing embodies the algorithms and hardware that allow processing of signals produced by natural or artificial means. These signals might be speech, audio, video, images, seismic signals, satellite and weather data, etc. Processing of these signals can involve acquisition, conversion, coding, compression, transmission, display, etc. When signals are represented in the discrete form and processed by computers or special purpose digital hardware, we identify an exciting and rapidly expanding field of *Digital Signal Processing* (DSP). In recent years, DSP has been spreading rapidly both in new software algorithms and hardware implementations.

Digital filters form an essential component in many DSP systems. They are simple algorithms that can be implemented either in software or in a hardware. Their task is to change signal properties that will satisfy a desired goal, for example shaping of signals, noise removal, edge sharpening in images, etc. Several commercial products make use of digital filtering and digital filters, including digital compact cassette, video-phones, NICAM TVs, CD players, tape-less telephone answering machines, cellular and satellite-based mobile telephony, etc.

The main component in a digital filter is a multiplier. As the requirements for higher speed and throughput rates are increasing, they can be best met by using a hardware multiplier. However, the hardware multiplier is the most power consuming and area occupying component in the filter structure. Hence the need to optimise multiplier structures and to reduce computational complexity is essential. This can be achieved by specific arrangements and alternations of the multiplier structures to reduce the size of multipliers. Alternatively, an elimination of multipliers from filtering structures is possible. This is generally accomplished by restricting the filter coefficients to powers-of-two exploiting the fact that powers-of-two coefficients reduce the multiplication operation to the simple shift and add operation. The approach to the design of digital filters with no multipliers is often referred to as a multiplier-less (or multiplier-free) approach.

Digital filters are the most researched topic in DSP. The multiplier-less (ML) subclass is coming to the forefront as a result of increased demand for further reduction in multiplier hardware. Despite the increased research effort in past years, no methodology or design approach for multiplier-less digital filters has been formalised. This is a consequence of limitations of calculus-based methods, a quasi non availability of software tools for the design of multiplier-less digital filters and the NP-complete nature of the multiplier-less filter design problem. The design of ML digital filters has been recognised as a hard optimisation problem, because the approximation of infinite precision coefficients by powers-of-two coefficients yields a very poor performance [Ben92] and methods developed for discrete coefficient filters are very slow in the case of high order filters.

This thesis is concerned with the design of multiplier-less finite impulse response digital filters based on evolutionary algorithms. Evolutionary algorithms are powerful search optimisation algorithms, which imitate the process of the biological evolution in the nature. Genetic algorithms (GAs) particularly have emerged as a powerful technique for searching in high dimensional spaces, capable of solving problems despite their lack of knowledge of the problem being solved. They have been shown to be robust optimisation algorithms for real-valued functions, whilst their application to the combinatorial optimisation (the precise nature of the digital filter design with PWR2 coefficients) possesses several obstacles [Ree94, Suh87].

The aims of this research are:

(i) to investigate and develop novel design techniques based on classical methods and evolutionary algorithms for the design of multiplier-less digital filters,

(ii) to establish and develop a solid framework for the design of ML digital filters. This would alleviate the designer from the burden of evaluating the appropriate

method for a particular application and to provide him/her with a powerful evolution-based tool applicable to a broad range of filter design tasks.

(iii) to instigate research in the area of "Genetic Design & Synthesis", what could represent a way of designing and synthesising electronic circuits in the foreseeable future.

1.2 Contribution of the research

The work presented in this thesis is concerned with the design of multiplier-less finite impulse response (ML FIR) digital filters. The use of multiplier-less digital filters results in simplified filtering architectures, better throughput rates and higher operational speed - highly desirable characteristics in a number of DSP systems. The review of classical design techniques demonstrates that despite the intense research effort in past years, no design approach for the design of ML FIR digital filters has been formalised and the problem is far from being solved.

The core of this research work presents two distinct approaches to the design of ML FIR digital filters. Following the study of classical design techniques, one of the best performing methods based on the sensitivity of filter coefficients has been selected and further improved. A novel algorithm uses a different approach to the calculation of the coefficient sensitivity that is based on the mean square error (MSE) between the desired and the actual frequency response of the filter. The novel coefficient sensitivity criterion originates from the theoretical analysis of the original sensitivity criterion that has identified its deficiency. It is shown that the mean square error sensitivity criterion is more accurate measure of the influence of filter coefficients' quantisation on the frequency response. Theoretical foundations of the novel algorithm and the novel criterion are strengthened by the numerical analysis that shows that the MSE criterion outperforms the original sensitivity criterion [Sha91].

Filters designed using the novel criterion benefit from a lower complexity, simplified architectural implementations and shorter design times than those designed using other techniques. The only disadvantage of the proposed algorithm is that optimal designs cannot be guaranteed. Indeed, better filter designs can be achieved using evolutionary algorithms. Evolutionary design techniques represent the second approach to the ML FIR filter design investigated in this thesis.

The theoretical analysis of genetic algorithms shows that they are very suitable for combinatorial optimisation problems, the very nature of the ML filter design with coefficients limited to the set of power-of-two values. As a result, a design technique based on genetic algorithms is proposed. The distinct feature of the novel design technique is that no prior knowledge of infinite precision filter coefficients is required. The algorithm is not restricted to approximating of infinite precision coefficients to power-of-two (PWR2) terms. Instead, the entire space of discrete PWR2 coefficients is open for exploration by genetic algorithms. Benefits of this approach are numerous. The calculation of infinite precision coefficients is not required and this part can be removed from the design method thus resulting in shorter design times. Further, sub-optimal (possibly optimal) solutions can be attained. The GA-based technique has been favorably compared with other techniques, including the improved coefficient sensitivity criterion based method. The designs that have been realised could not be accomplished using other reported techniques [Sha91, Cem93a, Cem93c]. Further improvements of the basic algorithm have been achieved by introducing advanced genetic operators and hybrid evolutionary techniques.

GA-based and classical techniques can further benefit from the prior knowledge of minimum number of discrete power-of-two coefficients, i.e. the filter length, that is required to satisfy the filter design constraints. The prior knowledge of the filter length would decrease a number of iterations that is required for a particular technique to converge to the solution. Empirical formula that would predict the minimum number of discrete power-of-two coefficients from the filter's specification

is not known yet. No research work attempting to devise such formula has been known to the author in time of writing up this thesis. Hence the concluding part of this research work presents an empirical formula that has been evolved from a large number of realised filter designs using the technique of genetic programming. Although the devised formula is very complex and difficult to understand it can achieve better predictions of filter length for ML FIR filters than classical Kaiser's formula. However, further research in this area is required to obtain a formula that is both simple and accurate.

To summarise, the design of ML FIR digital filters is very complex problem involving many factors that have to be considered. This work concentrates on development of novel design techniques that reduce the computational complexity of filtering structures and well outperform classical design methods. The improvements that have been achieved justify the relevance of the research that has been undertaken.

1.3 Outline of the thesis

This thesis is organised as follows:

Chapter 1 presents the research described in this thesis and briefly introduces the reader to the problem of multiplier-less digital filter design. Genetic algorithms are briefly highlighted as a powerful procedures for solving complex problems. This chapter also lists the contributions of the thesis.

The background to the field of digital filters and a survey of related design methods is provided in **Chapter 2.** Two classes of design methods are distinguished. Algorithmic methods focus on filter design algorithms that would produce filter coefficients with a low complexity thus resulting in simplified filter architectures,

while architecture-optimising methods concentrate solely on optimisation of hardware structures.

Two new algorithms are presented in **Chapter 3.** The first algorithm describes an evolutionary local search, which produces better results than simple rounding of infinite precision Remez coefficients to power-of-two terms. The second algorithm is an improvement of the coefficient sensitivity based method [Sha91], used for efficient rounding of infinite precision Remez coefficients to the single power-of-two terms (PWR2) or sums/differences of two power-of-two terms (2PWR2).

The background on genetic algorithms is introduced in **Chapter 4.** GAs are explained in depth, concentrating on various methods of encoding, selection, reproduction and fitness assignment and their implications. The application of genetic algorithms to the multiplier-less digital filter design and the experimental results are described in the second part of the chapter. Chapter 4 also presents further improvements of the basic GA-based filter design technique, including a knowledge-based genetic algorithm and hybrid techniques.

Chapter 5 describes the research concerned with estimating a formula characterising the relationship between the required number of single power-of-two coefficients and the filter's specification. The application of genetic programming and symbolic regression to evolve the empirical formula is illustrated.

Finally, conclusions and further work related to improving of the multiplier-less filter design algorithms are presented in **Chapter 6.**

Chapter 2

Review of multiplier-less FIR digital filters

This chapter presents current development in multiplier-less digital filter design. The basic theory and principles of digital filtering are briefly explained in section 1 together with advantages and disadvantages of digital filters. Section 2 presents an extended review of multiplier-less FIR digital filters. Two approaches to multiplier-less FIR filter design are identified namely, an algorithmic approach and an architecture-optimising approach. The main methods used for both approaches are reviewed. The chapter concludes with the results of a comparative study of algorithmic design methods.

2.1 Digital filtering

Digital filtering algorithms were developed from computer simulations of algorithms describing analogue filters. As the technology advanced and provided essential

hardware components (ADC converters, memories, multipliers, adders) with a reasonable speed and price, those algorithms were implemented in hardware. Over the years, digital filters replaced analogue filters in most applications because of their numerous advantages:

- digital filters can be designed with an exactly linear phase
- they do not suffer from the degradation mechanisms of passive and active components of analogue filters
- digital filters have better stability, reproducibility and higher orders of precision
- it is possible to realise filters with very low cut-off frequencies
- they can be realised as integrated circuits.

Digital filtering in the frequency domain can be easily considered as a multiplication of the signal $X(e^{j\omega})$ with a specific "mask" $H(e^{j\omega})$ that allows certain frequencies to pass through a filter and discriminates other frequencies. The "mask" $H(e^{j\omega})$ is called a *frequency response* and describes the change in magnitude and phase of the filter at the frequency ω.

A convenient and useful form of describing the behaviour of filters in terms of their frequency response is by using the *z-transform*. To obtain a z-transform of a digital filter, the term $e^{j\omega}$ is replaced by a complex number z. The z-transform of the unit-impulse response is also called the *transfer function* of the filter. The generalised expression of the transfer function is given by:

$$H(z)=\frac{b_0+b_1z^{-1}+...+b_Nz^{-N}}{1+a_1z^{-1}+...+a_Mz^{-M}} \tag{2.1}$$

Digital filters can be classified into two main categories by considering the length of unit-impulse response. If all the coefficients a_i in the denominator of (2.1) are set to zero, then the filter has a *finite impulse response* and is referred to as FIR filter. The output of the FIR filter depends on the input signal and filter coefficients only. When some of the coefficients $a_i \neq 0$, then the filter has an *infinite impulse response* and is referred to as IIR filter. The output of the IIR filter depends on the input signal, filter coefficients and past output values. FIR filters are preferred because of a number of their advantages over IIR filters:

- an exactly linear-phase response can be achieved to preserve the shape of the input signal
- they are inherently stable (unless they are implemented with recursive blocks)
- excellent design methods are available
- the output round-off noise is generally very low
- multidimensional FIR filters can be easily designed from one-dimensional filter prototypes
- they allow easy implementation of multirate signal processing algorithms.

The main disadvantage of FIR digital filters is that they usually require a large number of coefficients and hence the overall group delay is large for higher order filters. The overall amount of hardware components required to implement a FIR filter is also much higher than the one for an implementation of IIR filters.

2.1.1 FIR digital filters

Finite impulse response digital filters of length N are described in the time domain by the following equation:

$$y(k) = \sum_{n=0}^{N-1} h(n)x(k-n) \tag{2.2}$$

The corresponding frequency response of the FIR filter is given as:

$$H(e^{j\omega}) = \sum_{n=0}^{N-1} h(n)e^{-j\omega n} \tag{2.3}$$

The transfer function of FIR filter in z-domain based on its frequency response is a polynomial:

$$H(z) = h(0) + h(1)z^{-1} + \ldots + h(N-1)z^{-(N-1)} \tag{2.4}$$

The process of designing FIR filters is to select a set of filter coefficients $h(n)$, so that the frequency response $H(e^{j\omega})$ approximates a desired frequency response $D(e^{j\omega})$ with a minimum error function $E(e^{j\omega})$. The frequency response error function is defined as:

$$\left\| E(e^{j\omega}) \right\| = \left\| H(e^{j\omega}) - D(e^{j\omega}) \right\| \tag{2.5}$$

where the symbol $\| \ \|$ represents one of the following approximation criteria:

- **LS approximation** is based on the average squared error and is therefore suitable for the design of noise separating filters as the energy of a signal is related to the square of the signal,

- **Chebyshev (or minimax) approximation** minimises the maximum error between the approximating and the desired frequency response,

- **maximally flat approximation** is suitable when smoothness of the frequency response is required.

There are a number of available design methods in the design of digital FIR filters based on these approximations. Amongst them, windowing [Par87, Kin89], McClellan-Parks-Rabiner algorithm [MC73a, MC73b] and linear programming [Kin89, Rab72] have established themselves as traditional FIR filter design methods.

(i) Windowing: one of the earliest design techniques for FIR filters. The technique is based on the inverse discrete Fourier transform (IDFT) of the desired frequency response $D(e^{j\omega})$. The infinite series of corresponding impulse response coefficients obtained by the IDFT is subsequently truncated to the finite-length sequence by multiplying with the *window function.* Windowing techniques attempt to reduce the error between the desired frequency response and the actual frequency response. However, they do not guarantee that designed filters will be optimal (i.e. that they will have a minimum length for a given specification). Another disadvantage is that they do not allow control of pass-band and stop-band errors separately, which are restricted to be approximately equal. Therefore, design of multiple band filters with different attenuation in different bands may be difficult to realise.

(ii) McClellan-Parks-Rabiner (MPR) algorithm: probably the most popular and widely used technique for the design of FIR digital filters. MPR algorithm was advanced by Parks and McClellan [Par72] and further improved by McClellan, Parks, and Rabiner [MC73a, MC73b]. The algorithm can design linear-phase FIR filters which satisfy given specifications (cut-off frequencies and the maximum deviation from the desired frequency response) with a minimum filter order. The Chebyshev approximation, exploiting the *alternation theorem,* is used to approximate the desired frequency response.

Alternation theorem.

Let F be an interval $\langle 0,\pi \rangle$. Let $P(e^{j\omega})$ be a linear combination of cosines:

$$P(e^{j\omega}) = \sum_{n=0}^{M} \alpha(n)\cos(\omega n) \tag{2.6}$$

and $D(e^{j\omega})$ the desired frequency response defined on the interval F. Let $W(e^{j\omega})$ be a positive weight function defined on the interval F. To design a linear-phase FIR filter we want to minimise the weighted error function $E(e^{j\omega})$:

$$E(e^{j\omega}) = W(e^{j\omega}) \cdot [D(e^{j\omega}) - P(e^{j\omega})] \tag{2.7}$$

by choice of $\alpha(n)$ in (2.6).

The alternation theorem states that $P(e^{j\omega})$ is the unique, best weighted Chebyshev approximation to a given function $D(e^{j\omega})$ on F if and only if weighted error function (2.7) exhibits at least M+2 extremal frequencies. The extremal frequencies are points $\omega_i \in F$ such that $\omega_1 < \omega_2 < \ldots \omega_{M+2}$ and such that

$$E(e^{j\omega_i}) = -E(e^{j\omega_{i+1}}) \tag{2.8}$$

for i =1, 2, ..., M+1, and

$$\left|E(e^{j\omega_i})\right| = \max\left|E(e^{j\omega})\right| \tag{2.9}$$

for i=1,2,...,M+2 and $\omega_i \in F$.

Because of the alternation theorem, filters designed using Chebyshev approximation necessarily exhibit an equiripple behaviour in their frequency response. Hence, they are often referred in a literature as *equiripple* filters or *optimum Chebyshev* filters.

The alternation theorem does not determine how to choose the filter coefficients, so how can it help to design optimal FIR filters? The answer is that the alternation theorem precisely characterises the optimum solution by the M+2 extremal frequencies. If they are known, the impulse-response coefficients can be easily determined by interpolation. The problem of finding filter coefficients is thus reduced to the problem of finding the extremal frequencies. The Remez multiple exchange algorithm [Rem57] is the most powerful algorithm to find these extremal frequencies, from which the filter coefficients$h(n)$ can be determined.

(iii) Linear programming techniques: they were originally introduced by Rabiner *et al.* [Rab72]. They allow linear constraints in the time or the frequency domain to be imposed on a design. These constraints can be a fixed pass-band error, a flatness constraint on frequency response in a pass-band, etc. Under these circumstances the Remez exchange algorithm is not applicable.

The general linear programming problem can be considered as a set of M linear equations:

$$\sum_{i=1}^{N} c_{ij} x_i \le b_j \qquad j = 1,2,...,M \text{ and } i = 1,2,...,N \tag{2.10}$$

where $\{x_i\}$ is a set of unknowns. The objective of linear programming is to find values of $\{x_i\}$ such that the objective function

$$\sum_{i=1}^{N} a_i x_i \tag{2.11}$$

is maximised (minimised). It means that from the infinite number of solutions of (2.10) we have to select a solution that maximises (minimises) the objective function (2.11). Equations (2.10) are the constraints of the system and a_i, b_j, c_{ij} are given constants.

The linear programming problem and constraint lines (2.10) can be easily understood from the following example in two dimensions. Suppose that we have the following set of inequalities:

$$\begin{aligned} c_{11}x_1 + c_{21}x_2 &\le b_1 \\ c_{12}x_1 + c_{22}x_2 &\le b_2 \\ c_{13}x_1 + c_{23}x_2 &\le b_3 \\ c_{14}x_1 + c_{24}x_2 &\le b_4 \end{aligned} \tag{2.12}$$

and the objective function is

$$f(x) = a_1x_1 + a_2x_2 \tag{2.13}$$

Each of the constraints (2.12) will divide x_1x_2 plane into two sections. The section below the constraint line (inclusive) is permissible region for the objective function (2.13), whereas the section above the constraint line is not permissible. Several constraint lines will form a polygon with each point of the polygon including its boundaries satisfying constraints. Graphical representation of the polygon formed by constraints (2.12) is in Figure 2.1. Dashed line represents the objective function (2.13).

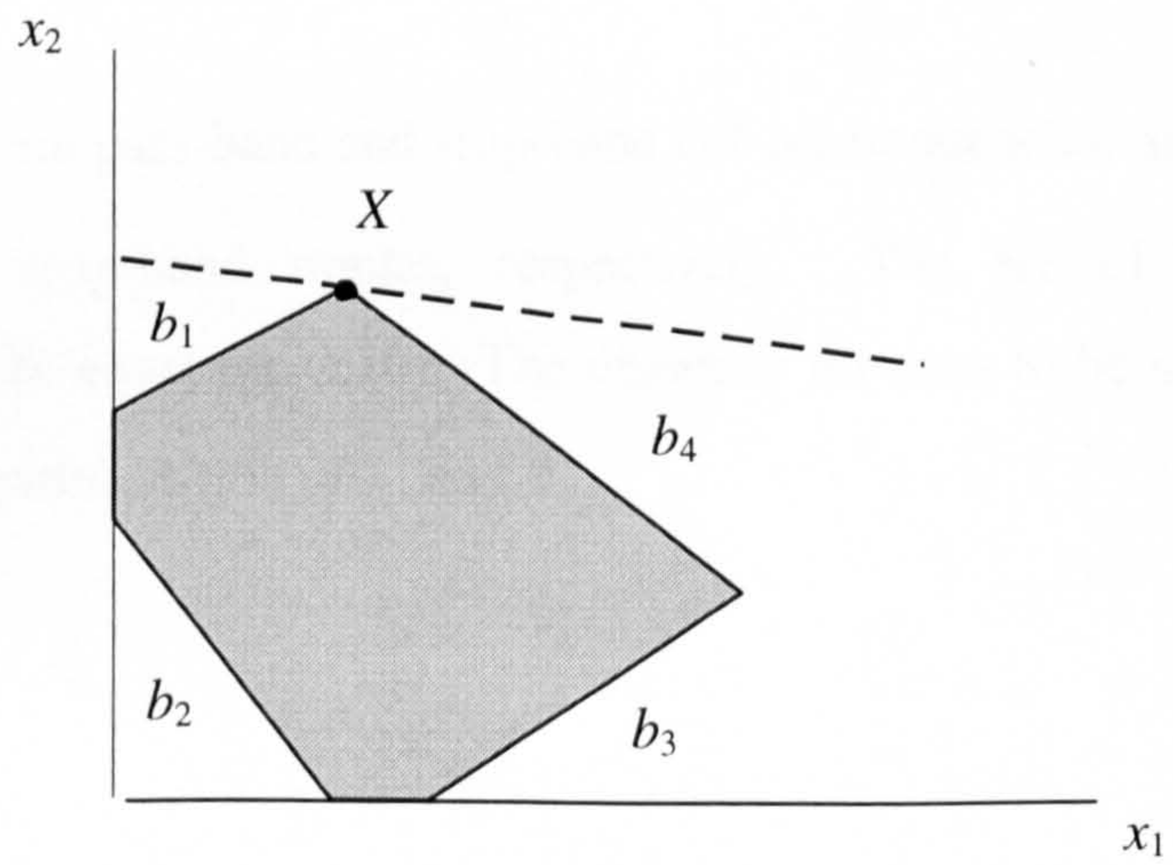


Fig. 2.1 A graphical representation of linear programming

The objective here is to find values of $\{x_i\}$ which are within the polygon and maximise the objective function (2.13) that is depicted by the dashed line. A solution of the above problem is trivial in two-dimensional case, but becomes more difficult when solving problems in N dimensions. An analytic solution to the N-dimensional linear programming problem has not been found yet. A number of different techniques to solve the general linear programming problem has been devised. They are mostly iterative procedures. An important characteristic of linear programming techniques is that if there exists a solution, it is guaranteed to be a unique solution to the problem. In other words, filters designed using linear programming techniques are guaranteed to be optimal.

Linear programming can be easily adapted for a design of digital FIR filters. The frequency response of FIR filter and the desired frequency response are written as a set of linear inequalities on a dense grid of frequencies. The following example shows the set of inequalities for a low-pass filter:

$$\begin{aligned} H(e^{j\omega}) &\le 1+\delta_1 \qquad 0 \le \omega \le \omega_p \\ H(e^{j\omega}) &\ge 1-\delta_1 \qquad 0 \le \omega \le \omega_p \\ H(e^{j\omega}) &\le \delta_2 \qquad \omega_r \le \omega \le \pi \end{aligned} \tag{2.14}$$

where ω_p, ω_s, are pass-band and stop-band cut-off frequencies, and δ_1, δ_2 are the pass-band and stop-band ripples, respectively. The set of equations (2.14) corresponds to the equation (2.10). The objective function to be minimised (2.11) is usually a linear combination of δ_1 and δ_2.

2.2 Design techniques of multiplier-less linear-phase FIR digital filters

Despite the large number of algorithms developed for the design and implementation of infinite precision FIR filters, no closed-form design formulas for the multiplier-less FIR filter design have been developed yet. The main methods for optimal FIR filter design, such as the Remez exchange algorithm and linear programming, are not suitable because they do not allow an inclusion of discrete coefficient set constraint.

Essentially, there are two possible approaches to the design of multiplier-less FIR digital filters. We have denoted these approaches as *algorithmic methods* and *architecture-optimising methods*.

The concept of algorithmic methods is to design multiplier-less digital filters with discrete coefficients selected from the discrete domain of powers-of-two. Therefore, a multiplication operation is converted to simple shift and add operations. As a result of that, multipliers can be removed from the filtering structures. Algorithmic methods are not limited to a particular filter structure and are suitable for any implementation of the filtering structure (direct form, transposed form, cascades, etc.). Algorithmic methods are mostly iterative procedures based on the algorithms which have been established as the main techniques in the design of FIR digital filters with infinite precision coefficients.

A different design philosophy can be seen in architecture-optimising methods. These methods attempt to optimise the hardware realisation of filtering structures so that some (or all) of the multipliers can be removed. Architecture-optimising methods include design of FIR filters using various number systems [Kin71], recursive architectures [Ram89], numerous arrangements of filter structures [Gre85, Sha87, Sar91, Bul91], systems with the filtering operation distributed in time and space [Gha93], etc.

2.2.1 Algorithmic methods

Algorithmic methods focus on design of filter coefficients with lower complexity rather than on the optimisation of hardware structures. This in turn leads to lower implementation complexity of filtering structures. There are two categories of algorithms to solve an approximation problem for FIR filters with powers-of-two coefficients (PWR2): exact and approximate. Exact algorithms guarantee the optimal filter design, i.e. a minimum order of the filter for a given specification. An example of exact algorithms is an *exhaustive search* (examines all possibilities) and a *branch-and-bound* algorithm [Lim83a]. Approximate algorithms do not guarantee the optimality of the design, although they can deliver near-optimal designs in less time than exact algorithms. The majority of algorithms for the multiplier-less FIR filter design belongs to the category of approximate algorithms.

The following sections list and explain design methods and techniques used in the design of multiplier-less digital filters as they chronologically appeared. Benefits and restrictions for each method are explained.

2.2.1.1 Rounding of infinite precision filter coefficients

Rounding of infinite precision filter coefficients to nearest powers-of-two is the simplest method for the multiplier-less FIR filter design. It is often used as a benchmark to test performance of other more complex algorithms. The rounding algorithm is relatively simple:

Step 1) obtain infinite precision filter coefficients for a given filter specification and a given length of filter$N$ by any of the methods described in 2.1.1,

Step 2) round the infinite precision coefficients to the nearest power-of-two (or a sum/difference of two powers-of-two),

Step 3) evaluate the frequency response,

Step 4) if the frequency response satisfies the desired frequency response $D(e^{j\omega})$ then finish, otherwise increment the length of filter and go to the Step 1.

The advantage of this method is its simplicity and the possibility to utilise any of the methods described earlier in the process of designing infinite precision coefficients, thus allowing to choose a preferred approximation criterion. However, filters designed by rounding of optimal infinite precision coefficients are not guaranteed to be optimal. This is because of the fact that the domain of powers-of-two is not searched for a solution. Instead, searching is conducted in the real domain and subsequently mapped onto powers-of-two domain. In general, most of the methods described below are able to design multiplier-less FIR filters with a smaller deviation from the desired frequency response or fewer coefficients for a fixed error.

2.2.1.2 Mixed Integer Linear Programming

Linear Programming has been shown beneficial in the design of infinite precision FIR filters (see section 2.1.1) as it is able to handle additional linear constraints. Unfortunately, linear programming cannot be applied to the design of discrete (PWR2) coefficient filters, since it does not allow the inclusion of this type of constraint. When the coefficient domain is discrete and uniformly distributed, the integer linear programming (ILP), an extension of linear programming techniques, can be used. ILP techniques were successfully applied to the design of FIR digital filters with integer coefficients to minimise finite wordlength (FWL) effects by Kodek [Kod80].

The design problem is more difficult when considering FIR filters with powers-of-two coefficients since powers-of-two are non-uniformly distributed. General integer linear programming techniques cannot be used for optimisation in a domain that is non-uniformly distributed, unless they are modified. Modified integer linear programming techniques applicable to the design of FIR filters with PWR2 coefficients in the minimax sense has been first reported in [Lim79] and then subsequently in [Lim82, Lim83a, Lim83b, Lim88, Lim90]. Lim proposed mixed integer linear programming (MILP), a combination of ILP techniques with a branch-and-bound algorithm, to solve the design problem in non-uniformly distributed coefficient domain.

The branch-and-bound algorithm limits the number of solutions needing to be examined by calculating upper and lower bounds on partial solution of the problem. The algorithm creates an enumeration tree starting with an unsolved problem $P(0)$. A solution of the problem $P(0)$ is $S(0)$. The problem $P(0)$ is resolved into smaller problems $P(i)$ with solutions $S(i)$ satisfying the following condition:

$$\forall i: \cup S(i) = S(0) \tag{2.15}$$

This process is further continued by resolving subproblems $P(i)$ into smaller subproblems. Bounds are used to prune a search tree as the enumeration process proceeds. The process continues until the problem $P(0)$ is solved. An illustration of Branch-and-bound algorithm is shown in Fig. 2.2.

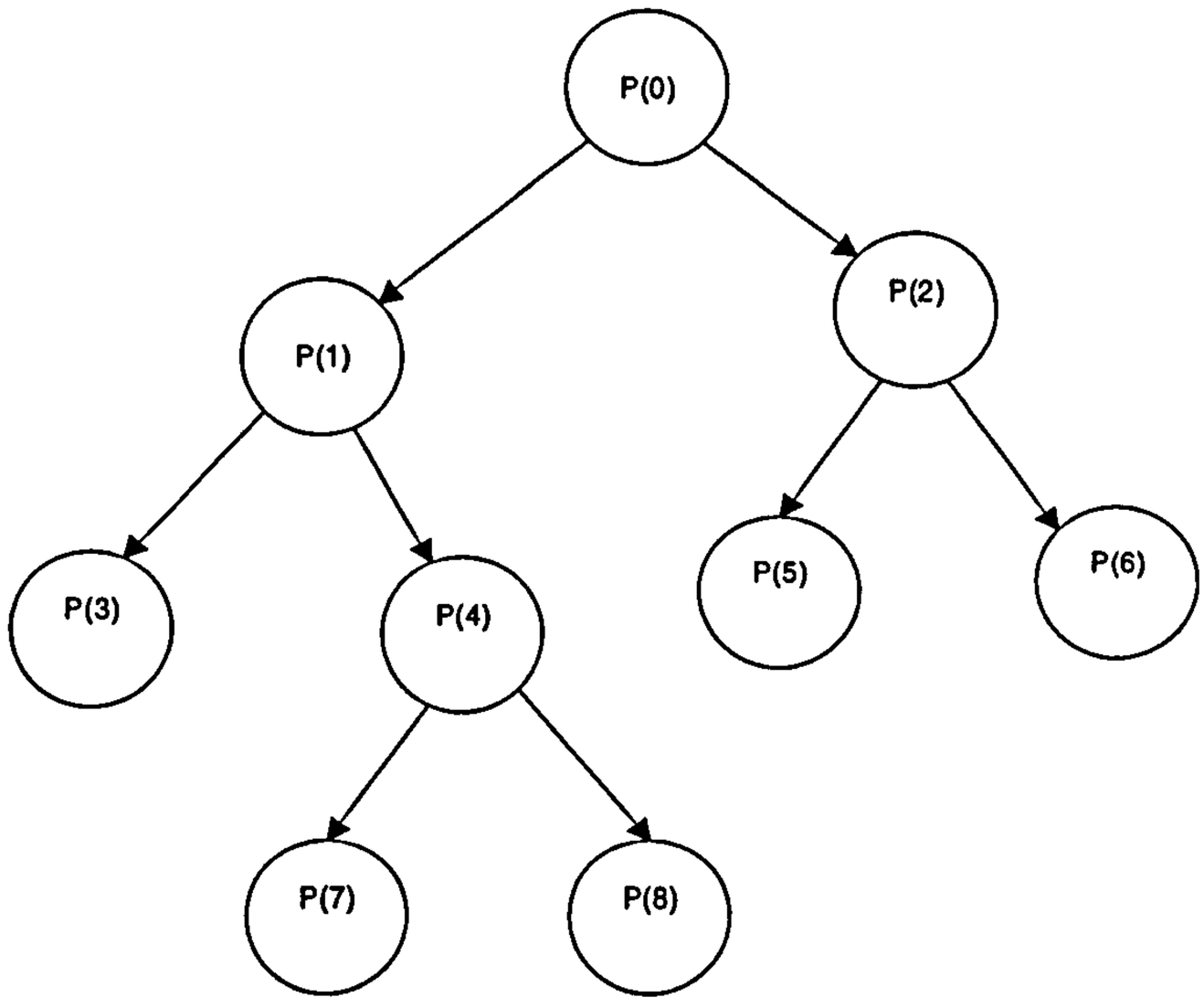


Fig.2.2 Branch-and-bound algorithm

The design procedure proposed by Lim starts with the infinite precision coefficient vector obtained by the Remez exchange algorithm or linear programming techniques. In the next step, a coefficient $h(n)$ whose value is not a power-of-two is selected. If 2^j and 2^k are two consecutive power-of-two values such that

$$2^j \le h(n) \le 2^k \tag{2.16}$$

then, since the value of $h(n)$ rounded to the power-of-two cannot fall between 2^j and 2^k, two problems $P(1)$ and $P(2)$ may be generated by imposing the constraints:

$$h(n) \le 2^k \tag{2.17}$$

$$h(n) \ge 2^j \tag{2.18}$$

as shown in Fig. 2.2. Problems $P(1)$ and $P(2)$ are solved individually and further branching is performed on $P(1)$ and $P(2)$. The process of branching continues until the problem $P(0)$ is completely solved. The number of branches required can be reduced by removing those branches, where no improvements can be predicted (only subproblems with better subsolutions are selected for further branching).

The MILP algorithm is at the present the only known algorithm to guarantee the optimal design of FIR filters with powers-of-two coefficients in the minimax sense, i.e. minimising a peak weighted error function in the frequency domain using:

$$\max_{\omega_i}\left\{W(\omega_i)\cdot\left[D(\omega_i)-H(\omega_i)\right]\right\} \tag{2.19}$$

If the LMS approximation is required, it can be achieved by minimising the mean squared weighted error function:

$$\sum_{\omega_i} W(\omega_i)\cdot\left|D(\omega_i)-H(\omega_i)\right|^2 \tag{2.20}$$

Minimising of (2.20) is an integer quadratic programming problem, which is also capable to produce optimal designs.

Frequency responses of filters designed by the MILP algorithm have been shown superior to those obtained by simply rounding of infinite precision coefficients [Lim83a]. Unfortunately, a very high computation cost of the MILP algorithm prohibits its practical application to the design of high-order PWR2 FIR filters. The upper bound on the filter length was found to be less than 70 in order to converge in reasonable times [Lim90].

The design of high-order PWR2 has been presented in [Lim83b]. This has been achieved by incorporating the least mean square (LMS) criterion into the MILP algorithm. The LMS approach can be also used to design FIR filters in the minimax sense, approximating the minimax criterion by adjusting the least squares weighting. PWR2 filters with the filter length $N \leq 90$ were realised. However, the LMS criterion algorithm does not guarantee an optimal solution.

2.2.1.3 Local search

A useful alternative to the branch-and-bound algorithm, particularly when designing high-order FIR filters with PWR2 coefficients is the local search algorithm. It has been applied to the design of finite wordlength filters [Kod81], but can be also applied to the design of PWR2 filters. The local search algorithm iteratively explores a neighbourhood of a given starting point for improvements until a local optimum is found. Hence, the local search algorithm requires a good choice of starting point and a good searching strategy. A starting point is usually an infinite precision coefficient vector obtained by the Remez exchange algorithm or linear programming.

There are generally two types of searching strategies:

a) changing each coefficient, one at a time, in both directions and repeating the process until no further improvement is registered,

b) changing two or more coefficients over all possible pairs of coefficients, thus allowing to analyse searching space in more extensive manner.

Local search can yield to substantial improvements of the frequency response when compared with rounding of infinite precision coefficients to their nearest neighbours. A performance of the local search can be severely reduced when the landscape of frequency response contains deep local minima, as local search tends to be easily trapped in those minima.

2.2.1.4 Proportional relation-preserve/ simple symmetric sharpening method

A simple suboptimal algorithm for the design of PWR2 filters enabling sharp cut-off frequencies and capable to design filters with filter length $N > 200$ was proposed by Zhao and Tadokoro [Zha88]. The algorithm embodies two methods. The first method is a suboptimal design that determines PWR2 coefficients from the set of infinite precision coefficient vectors. The method, referred to as the *proportional relation-preserve* (PRP) method, preserves a proportional relation between the optimal infinite precision coefficients and the PWR2 coefficients. When filters designed using the PRP method cannot satisfy given filter specifications, the second method, referred to as *simple symmetric-sharpening* (SSS) method, is employed.

The PRP method minimises the maximum error with a constraint on coefficients $h(n)$, allowing coefficients to be single power-of-two or powers-of-two values only. The design strategy is as follows:

(1) The infinite precision filter coefficients $h_0(n)$ are calculated by the Remez algorithm.

(2) The filter gain A of the filter with PWR2 coefficients is determined by varying the gain A from 0.5 to 1.0 to minimise error function $E(A)$:

$$E(A) = \sum_{n=0}^{(N-1)/2} \left(h_0(n) - \frac{[A \times h_0(n)]}{A} \right)^2 \tag{2.21}$$

where the symbol [ ] represents rounding to PWR2 values: $\pm 2^{-p_n} \pm 2^{-q_n}$. A set of coefficients $h_A(n)$, which minimises $E(A)$ of (2.21) is defined.

(3) The filter coefficients $h(n)$ of the PWR2 filter are determined by local optimisation to preserve, as far as possible, the proportional relation between the

coefficients $h_0(n)$ and $h(n)$. This is accomplished by selecting the optimum combination of n_1 adjacent coefficients $h_A(n)$ and n_2 discrete values of these coefficients to minimise the maximum error δ. The optimal values of n_1 and n_2 have been experimentally found to be 4 and 5, respectively.

(4) The previous operation is carried out recursively for all coefficients and the maximum error δ is recorded.

(5) The same operation is continued using coefficient values obtained from the previous operation as initial values. If the maximum error δ is larger than error in the previous operation, the local optimisation is stopped.

(6) If the designed filter does not satisfy the given specification on the maximum error δ, the filter length N is incremented and the algorithm starts again.

The SSS method on the other hand, can greatly improve the approximation errors of the PRP method. It is based on the sharpening of the frequency response of the symmetric FIR filter by multiple use of the same filter, a technique described by Kaiser in [Kai77]. The filter designed by the PRP method is considered as a subfilter $H_s(z)$ of the filter $H(z)$ designed by SSS method. The SSS method is applied when the filter length N becomes greater than $N_{max} = 59$.

2.2.1.5 Samueli's method

A technique of rounding infinite precision filter coefficients to their nearest power-of-two values described in section 2.2.1.1 has been adopted by Samueli for the design of multiplier-less FIR filters with the *canonical signed-digit* (CSD) coefficients [Sam88]. To define canonical signed-digit numbers, signed-digit numbers must be explained first.

Signed-digit (SD) numbers were formally defined by Hwang [Hwa79]:

Given a radix r, each digit of an SD number can assume the following $2\alpha+1$ values:

$$\sum_{r}\{-\alpha,\ldots,-1,0,1,\ldots,\alpha\} \tag{2.22}$$

where the maximum digit magnitudeα must be within the following region:

$$\left\lceil\frac{r-1}{2}\right\rceil \le \alpha \le r-1 \tag{2.23}$$

In (2.23), the symbol $\lceil x\rceil$ represents the smallest integer that is more than or equal to the real number x. Because integer α must be bigger or equal to one, the minimum radix r bigger or equal to two must be assumed.

The radix-r signed-digit representation of a fractional number$x$ has the general form

$$x=\sum_{k=1}^{L}\alpha_k r^{-p_k} \tag{2.24}$$

where L is the number of nonzero digits, $p_k \in \{0,1,\ldots,B-1\}$ determines positions of nonzero bits and B is the total number of bits.

A minimal signed-digit representation that contains no adjacent nonzero digits α_k is called a **canonical signed-digit representation.** The CSD representation has some interesting properties. For example, a number of adders/subtracters required to realise a CSD coefficient is one less than the number of nonzero digits in the code. The added redundancy and the added flexibility of negative digits allows most

numbers to be represented with fewer nonzero digits. This can be used in the design of totally parallel adders and fast hardware multipliers.

The starting point for the Samueli's algorithm is an infinite precision coefficient vector obtained by the Remez exchange algorithm. Infinite precision coefficients are scaled prior to rounding to avoid a possible overflow and also to minimise the error introduced by rounding. Scaled coefficients must satisfy a condition:

$$\sum_{n=0}^{N-1}|h(n)| \leq 1. \tag{2.25}$$

Samueli has found, that the best results are achieved when the filter coefficients are scaled so that the largest coefficient can be represented exactly by two-bit CSD coefficient. Scaled filter coefficients $h(n)$ are rounded to the nearest sum or difference of at most two powers-of-two and represented by a CSD numbers with at most two nonzero bits. This resulted in at most one adder required to implement each coefficient.

An improved, two-stage optimisation algorithm has been presented in [Sam89]. In the first stage, a search for an optimum scale factor is performed. The algorithm allocates one additional nonzero digit in the CSD representation to those coefficients whose magnitudes exceed 0.5. This is to compensate for the very non uniform distribution of the CSD coefficient set. When the optimum scale factor is found, a set of infinite precision filter coefficients is scaled and rounded to the nearest CSD coefficients.

The process of scaling and rounding of coefficients is followed by a *bivariate local search* [Kod81] in the neighbourhood of CSD coefficients. All possible pairs of coefficients are varied by one quantisation step size in both directions and the resulting peak ripple δ is calculated. A coefficient vector resulting in the minimum

value of δ is selected for further optimisation. The bivariate local search is repeated with this coefficient vector as the starting point. The process of bivariate local search stops when no further improvement is obtained. Filters with CSD coefficients designed using Samueli's algorithm were found to have nearly optimal performances when compared with the ideal infinite precision filters.

2.2.1.6 Coefficient sensitivity method

An improved optimisation algorithm based on Samueli's algorithm [Sam89] was presented in [Sha91]. The improved algorithm replaces a scaling procedure by evaluating the sensitivity S_n of the coefficients $h(n)$ rounded to the nearest power-of-two.

Prior to the optimisation procedure, the optimal infinite-precision coefficient vector is obtained by one of the conventional design methods (Remez exchange algorithm or linear programming). The optimisation procedure evaluates the sensitivity S_n of the frequency response to each of the coefficients $h(n)$.

The sensitivity S_n is calculated as follows:

- each coefficient, in turn, is set to its nearest power-of-two, yielding in each case a response $A_n^{'}(\omega)$,
- the sensitivity is calculated as the sum of the increase in the pass-band ripple and the increase in the stop-band ripple:

$$
\begin{aligned}
S_n = & \left(\left| A_n'(\omega) \right|_{\max} - \left| A_n'(\omega) \right|_{\min} \right)_{passband} \\
& - \left(\left| A(\omega) \right|_{\max} - \left| A(\omega) \right|_{\min} \right)_{passband} \\
& + \left(\left| A_n'(\omega) \right|_{\max} \right)_{stopband} - \left(\left| A(\omega) \right|_{\max} \right)_{stopband}
\end{aligned}
\tag{2.26}
$$

All coefficients are then set to their nearest power-of-two. If the frequency response at this stage does not satisfy a prescribed specification, the coefficients are set one after another, in the decreasing order of sensitivity, to the nearest sum or difference of two powers-of-two. The frequency response is evaluated after each change of coefficient and the entire process is repeated until the frequency response does not satisfy a given filter specification. When all coefficients are changed and the given filter specifications are not met, the design procedure may be repeated with an increased filter length.

An alternative approach is to re-calculate the coefficient sensitivity S_n with each coefficient set to the nearest sum or difference of two powers-of-two. Then all coefficients are set to the nearest sum or difference of two powers-of-two and the frequency response is evaluated. If the frequency response is not within the prescribed specification, the coefficients are set one after another, in the decreasing order of sensitivity, to the nearest sum or difference of three powers-of-two. The frequency response is evaluated at each stage and the optimisation procedure continues until a satisfying frequency response is obtained.

The coefficient sensitivity method has been compared with other algorithms described in the literature (rounding to the nearest power-of-two, Samueli's algorithm, etc.). Superiority of the improved algorithm has been demonstrated in terms of savings of the number of PWR2 coefficients required to realise a given filter specification.

2.1.1.7 Design of multiplier-less FIR filters using genetic algorithms

Research into the design of multiplier-less digital filters using genetic algorithms has been initiated by Suckley in [Suc91]. Suckley described synthesis of FIR filter structures by cascading of simple elements from a library of primitive filters. All primitives in the library were computationally simple blocks with a multiplication reduced to shift-and-add operations, hence producing multiplier-less FIR structures. A genetic algorithm was used to select the best combination of primitives. Suckley's method is a further development of integer linear programming techniques applied to the synthesis of cascades of primitive elements described by Wade *et al.* [Wad90]. Recently, Wade *et al.* also reported a synthesis technique for multiplier-less FIR filter design using genetic algorithms [Wad94]. A drawback of the above techniques is that a filtering structure is determined at the same time as the filter coefficients. Therefore filters designed using these methods are not suitable to implement with direct or transposed filtering structures.

Schaffer *et al.* presented a software tool Fil-E using a genetic algorithm to evolve digital filters with PWR2 coefficients [Sch93]. The approach used in Fil-E to design ML FIR filters is similar to that of Suckley's and Wade's work: cascades of FIR filters. Schaffer suggests that the 3-stage cascades are suitable for most designs. If the frequency response is not within the specified boundaries, either the number of cascades or number of coefficients in each cascade is changed and a population of filter structures is re-evaluated. Fil-E uses Gray coding with only four bits to encode PWR2 coefficients onto chromosomes. To estimate the order of the filter, heuristics formulas used for the design of infinite-precision coefficients have been applied.

Gentilli *et al.* described an evolutionary design of ML FIR filters that introduces the pass-band gain G criterion [Gen94] as the additional parameter of the optimisation problem. The pass-band G preserves a proportionality between the power-of-two and infinite-precision coefficients similar to that described by Zhao *et al.* in [Zha88]. The pass-band gain G is relevant when rounding infinite-precision coefficients to

powers-of-two using heuristics methods, yet it limits searching space for the genetic algorithm.

2.2.2 Architecture-optimising methods

Architecture-optimising methods focus rather on the optimisation and implementation aspects of filter structures than on the design and optimisation of filter coefficients. They are usually associated with specific architectures, what does not make them very practical when considering, for example, implementation of digital filtering algorithms using digital signal processors (DSP).

One of the first multiplier-less architectures was proposed by Greenberger [Gre85] and improved by Shah [Sha87]. It was achieved by rearranging the order of convolution operations so that the convolution has been replaced with simple SHIFT and ADD operations. Although the proposed architecture is multiplier-less, the final number of gates was approaching the complexity of filter structures using multipliers. In addition, the proposed arrangement does not have an advantage of higher speed than multiplier based filter structures.

Filter structures using the logarithmic system [Kin71] do not require multipliers as the multiplication of two operands is achieved by adding their logarithms. On the other hand, the addition operation is fairly complex and there is also a need to convert numbers between binary and logarithmic representations.

It has been observed that better frequency responses can be achieved by multiple use of the same filter. This has been described by Kaiser *et al.* as the Amplitude Change Function (ACF) technique [Kai77]. Ramakrishnan *et al.* [Ram89] adopted this technique for the multiplier-less filter design by choosing a recursive running sum (RRS) filter as the prototype filter for cascading. As a result, their filter structure uses fewer multipliers and adders. However, the number of delay units has doubled

when compared to conventional methods and the technique assumes a prefixed filter architecture.

Tai *et al.* has further improved Ramakrishnan's technique by using the cascade of a cosine function (CCOS) as the prototype filter [Tai92]. The resulting filter structure in [Tai92] does not use any multipliers. However, this method also assumes a prefixed architecture for the filter implementation.

Other multiplier-less filter design approaches include the use of primitive operators described by Bull *et al.* [Bul87, Bul88, Bul91], or periodically time-varying state-space structures (PTV-SS) distributing the filtering operation over space and time. The principle of the primitive operator method exploits the redundancy in the direct-form filter structure. This has been achieved by decomposition of each product in the convolution operation into a number of primitive arithmetic operations and reusing of partial results to form other product terms.

The use of periodically time-varying state-space structures using ternary coefficients ($\{0, \pm 1\}$) and therefore multiplier-less, has been described by Ghanekar in [Gha93]. Because PTV-SS structures use upsampling and downsampling and therefore effectively operate at N times the input signal rate, where N is the rate of upsampling, they are not practical for high-speed applications. The PTV-SS structures are applicable also to the design of multiplier-less IIR filters [Gha94].

2.3 Conclusion

A number of design techniques and algorithms used for the design of multiplier-less digital filters have been presented. Each method has its advantages and disadvantages. For instance, architecture-optimising methods are generally not suitable for software implementation. Some of these architectures need a special hardware to convert between different number systems. However, they do not need specific algorithms for the design of filter coefficients, as they can usually operate with Remez coefficients.

Algorithmic methods are not limited by implementation issues. They use infinite precision coefficients calculated by Remez algorithm as an initial coefficient vector and iteratively search for a coefficient vector that is composed from power-of-two terms only. Apart from mixed integer linear programming incorporating the branch-and-bound algorithm, and the enumerative search, which is not practical, they are not optimal in the minimax sense. To date, the MILP algorithm developed by Lim is the only method that guarantees an optimal solution in minimax sense. However, the MILP algorithm is not practical for higher order filters as the computational cost becomes excessive. The summary of the algorithmic methods is in Table 2.1.

We conclude this chapter with the observation that Shaffeu *et al.* [Sha91] presented a method that outperformed other classical techniques used in multiplier-less FIR filter design. Shaffeu's method is simple, it has a relatively short design time when compared to MILP and authors claim that a minimum filter length required to satisfy the desired frequency response is shorter than with other methods. We will analyse this method in more detail and investigate further improvements in the next chapter.

Table 2.1 Algorithmic methods for the multiplier-less digital filter design

Method	Initial set of coefficients	Optimal	Max. length of filter N	Features and limitations
Rounding (nearest PWR2)	Remez	No	unlimited	simple
MILP (branch-and-bound)	Remez	Yes	$N \leq 70$	to date this is the only optimal method
MILP (LMS criterion)	Remez	No	$N \leq 90$	
Local search	Remez	No		
PRP/SSS method	Remez	No	N≤59 (PRP only) N>200 (PRP+SSS)	
Samueli's method	Remez	No		uses CSD coefficients
Coefficient sensitivity method	Remez	No	not limited	produces best results from non-opt. methods

Chapter 3

Novel techniques of multiplier-less FIR filter design

This chapter presents two novel design methods for ML FIR digital filters based on classical design methods. First, a modification of a local search algorithm, an *evolutionary local search* is described [Cem93c]. The evolutionary local search is very simple, but it can produce better results than simple rounding of infinite precision coefficients to nearest power-of-two numbers. An advantage of the evolutionary local search is that there is no need to calculate Remez coefficients.

The rest of this chapter is devoted to two novel algorithms based on Shaffeu's method of rounding of filter coefficients based on coefficient sensitivity. The first algorithm is an improvement of the coefficient sensitivity criterion for filters with multiple bands. The improved sensitivity criterion yields better frequency responses and lesser complexity of filter coefficients (i.e. more coefficients are represented as

single PWR2 and less coefficients as 2PWR2). The second algorithm replaces Shaffeu's sensitivity criterion with a novel sensitivity criterion that is based on a mean square error (MSE) or a mean absolute error (MAE). The novel coefficient sensitivity criterion yields better frequency responses and lesser complexity of coefficients for all types of filters, including filters with multiple bands. The most significant contribution of the novel sensitivity criterion is that it can result in shorter filter lengths than the original Shaffeu's criterion. A shorter filter length represents a number of advantages, e.g. shorter design times, lesser complexity and a smaller group delay.

3.1 Evolutionary local search

A modification of the local search algorithm, an evolutionary local search (ELS), is presented in this section. The evolutionary local search for the design of multiplier-less FIR filters uses sequential and modified sequential searching methods. The minimum solution is acquired from a set of power-of-two coefficients and does not pre-empt the filter architecture prior to the calculation of the coefficients, thus supporting a variety of alternative implementations. It also eliminates the use of sensitivity procedures to map real coefficients to their nearest power of two coefficients as no standard procedure is used to obtain the initial real coefficients. Evolutionary local search guarantees the optimal solution for low-order filters and suboptimal for higher orders.

An alternative approach to the Remez-based technique could search for a suitable coefficient vector from the possible arrangement of the values over the range defined by the coefficient wordlength. This suggestion is impractical as the complexity of the searching process increases beyond the capability of existing computing machines. However, since we are interested in multiplier-less FIR filters, the restriction of the coefficients to power of two values reduces dramatically the number of possible arrangements of coefficients.

The proposed coefficient approximation procedure uses the following concept. Initially, a basic set of possible power of two coefficients is defined. The band tolerances are then entered, and the minimum length filter is evaluated using Kaiser's formula. Starting from this order, all possible arrangements of coefficients extracted from the basic set have their frequency responses computed and compared with the desired frequency response. When a satisfactory solution is obtained, the algorithm terminates, otherwise the next arrangement is used until all combinations have been evaluated. When no solution is found, the order of the filter is increased and the process is repeated. The nature of this sequential search guarantees minimum order multiplier-less filters.

For more complex filters that require a large number of coefficients to approximate the desired frequency response, this method has shortcomings due to the excessive amount of computations resulting from the complexity of the search process. A modified procedure is proposed for these categories. The pseudo-code of the modified procedure is illustrated in Figure 3.1. The source code written in Pascal is included on the accompanying disk.

The minimum length is evaluated again by Kaiser's formula and the coefficients' values randomly assigned. The procedure searches through all possible powers of two for the best value for each coefficient. The value that provides the best frequency response approximation is saved and the procedure continues with the next coefficient. This procedure is repeated until no further improvements in the approximation of the desired frequency response are obtained. If no solution is found, the order of filter is increased and the process repeated. This approach adopts the principle of keeping the best and rejecting the rest through sequential exchange. The method is faster than the sequential searching, and computer simulations have shown better results compared to conventional methods of simple rounding (SR) to nearest power-of-two.

```
Evolutionary local search ()
begin
  evaluate the minimum length of filter
  initialise coefficient values randomly
  repeat
    for each coefficient do
      search all PWR2 values
      evaluate frequency response
      keep the best coefficient
    end for
    if unsatisfactory frequency response then
      increment the length of filter
    end if
  until satisfactory frequency response
end
```

Fig. 3.1 Pseudo-code of the evolutionary local search

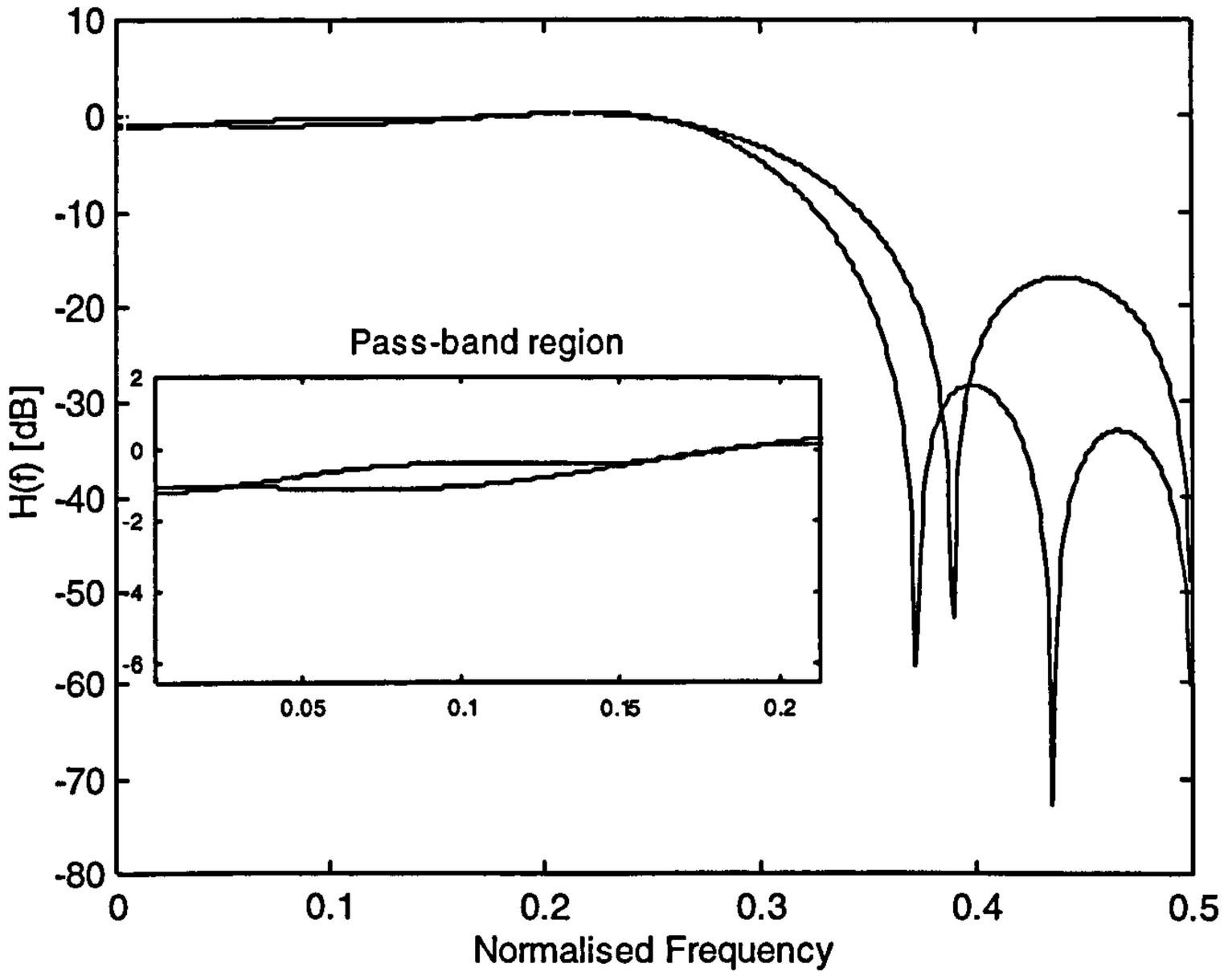
A more powerful method that produces better results can be obtained when the discrete space of the coefficients to be explored is extended. This is done by a small variation of the searching procedure when the coefficients are arranged into groups of two or three. Thereafter, all possible combinations of powers of two terms for each group of coefficients are explored. There are three possible modes of arrangements of these coefficients into groups: randomly, sequentially and according to their fitness. The arrangement of the coefficients that gives the least mean square error in the frequency response is saved and the searching procedure continued with another group of coefficients.

The evolutionary local search (ELS) algorithm has been compared with the conventional rounding of infinite precision coefficients. The conventional rounding

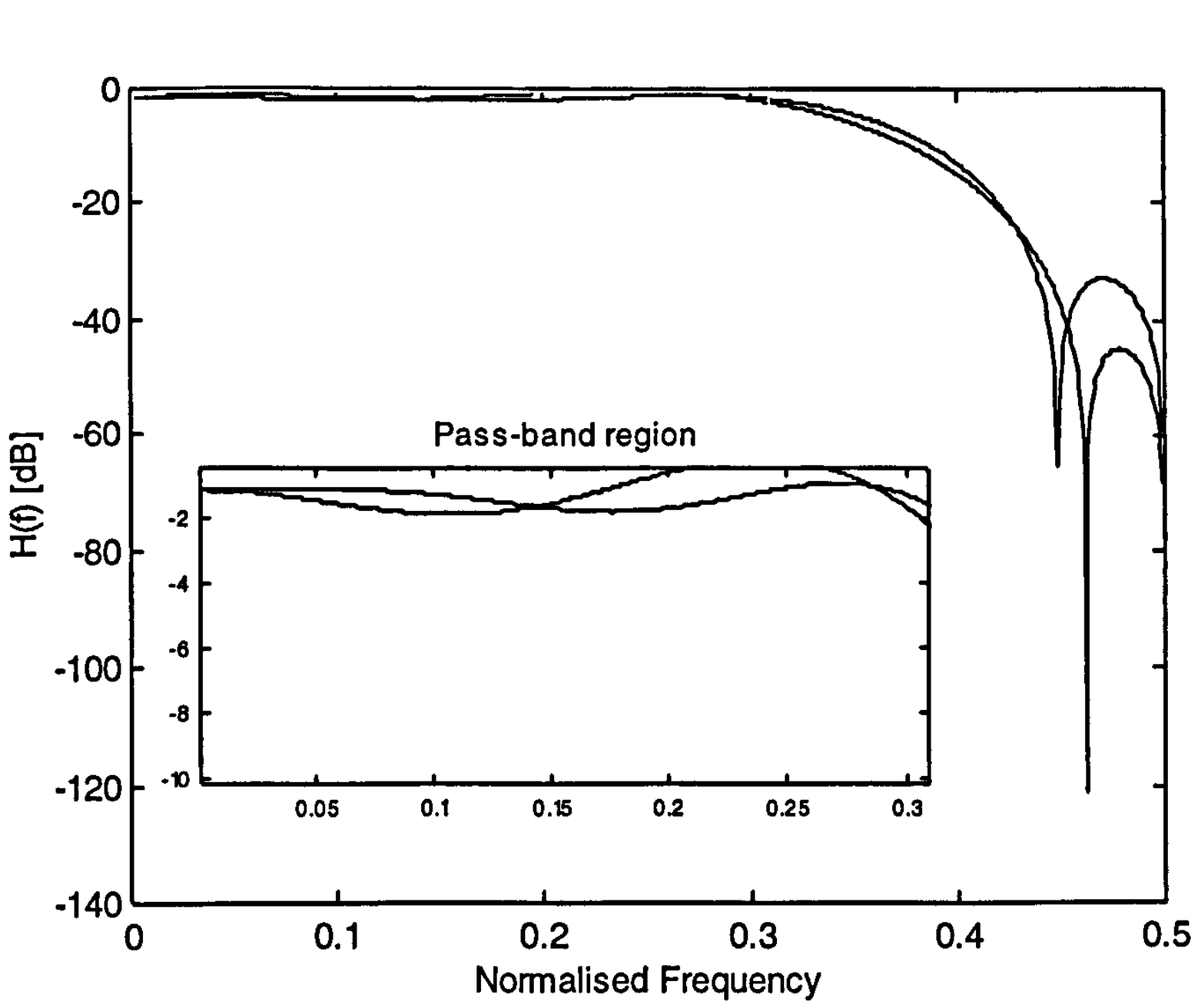
method uses McClellan - Parks algorithm to obtain an initial set of coefficients and then this set is approximated to the nearest power of two coefficients. The ELS algorithm is shown to produce superior results to the more conventional approach. Results obtained using the evolutionary local search algorithm are compared to the conventional rounding to nearest power-of-two coefficients in Table 3.1. Typical frequency responses for filters from Table 3.1 are shown in Figure 3.2.

Table 3.1 Comparison between simple rounding (SR) to the nearest PWR2 and evolutionary local search (ELS) algorithm

Filter No.	**Frequency Bands**	**Desired response**	**Max. error allowed**	**Filter Length (SR)**	**Filter Length (ELS)**	**Coeffs. saving**
1	0 - 0.05 0.20 - 0.30 0.45 - 0.50	band-pass	0.1	13	13	0
2	0 - 0.30 0.45 - 0.50	high-pass	0.1	15	11	27 %
3	0 - 0.25 0.37 - 0.50	low-pass	0.15	14	8	43 %
4	0 - 0.30 0.45 - 0.50	low-pass	0.1	10	8	20 %
5	0 - 0.10 0.20 - 0.30 0.40 - 0.50	band-pass	0.2	13	10	23 %



(a) frequency response of the filter No.3



(b) frequency response of the filter No.4

Fig.3.2 Comparison of simple rounding (SR) and evolutionary local search (ELS)

Figure 3.2 (a) depicts the frequency responses for the filter No.3 with the solid line representing the conventional method and the dotted line representing the ELS algorithm. Both frequency responses are well within the specification, however, the filter designed using the ELS algorithm requires only eight coefficients in comparison with fourteen coefficients required when the conventional method of infinite-precision coefficients is used. This represents 43% saving in the number of coefficients. Figure 3.2 (b) shows the frequency responses for the filter No.4. While the saving in terms of the number of coefficients required is less (20%), the filter designed using the ELS algorithm has better attenuation in the stop-band than the filter designed using the conventional approach.

The ELS algorithm is applicable to any filter type, and because it does not assume a prefixed architecture for the implementation, it could be implemented on any processor that can perform a Multiply-Accumulate function. Furthermore, the elimination of multipliers makes the resulting structure ideal for fast, low area, high throughput rate ASIC implementations.

3.2 Rounding of filter coefficients based on coefficient sensitivity

3.2.1 Coefficient sensitivity

The coefficient sensitivity reflects the degree of influence on the frequency response of digital filter resulting from rounding of infinite precision coefficient to the nearest power-of-two. The sensitivity of each coefficient as defined by Shaffeu in [Sha91] was calculated as the sum of the increase in the pass-band and stop-band ripples:

$$\begin{aligned} S_n = & \left(\left|A_n^{'}(\omega)\right|_{max} - \left|A_n^{'}(\omega)\right|_{min}\right)_{passband} \\ & -\left(\left|A(\omega)\right|_{max} - \left|A(\omega)\right|_{min}\right)_{passband} \\ & +\left(\left|A_n^{'}(\omega)\right|_{max}\right)_{stopband} - \left(\left|A(\omega)\right|_{max}\right)_{stopband} \end{aligned} \tag{3.1}$$

where $A(\omega)$ is the amplitude response of infinite precision coefficient vector and $A_n^{'}(\omega)$ is the amplitude response with n-*th* coefficient changed to the nearest power-of-two. As we will show later, this sensitivity measure does not yield a minimum number of canonical coefficients (having more than one power-of-two term). It is also not suitable for the design of multiple-band filters with power-of-two coefficients. This is because in equation 3.1 the sensitivity is calculated using only six extremes of the frequency response, ignoring extremes in different bands.

3.2.2 Modified coefficient sensitivity

We propose two novel approaches for the evaluation of the sensitivity criterion, both maximising the number of single power-of-two coefficients and therefore reducing the overall complexity of the filter. The first approach is a generalised version of the sensitivity criterion in (3.1). The sensitivity is calculated using local maxima and minima in each band, while Shaffeu used only global extrema. The improved coefficient sensitivityS_n is calculated as follows:

$$S_n = \sum_{i=1}^{N_p} \left(\left| A_{ni}^{'}(\omega) \right|_{max} - \left| A_{ni}^{'}(\omega) \right|_{min} \right)_{passband}$$
$$- \left(\left| A(\omega) \right|_{max} - \left| A(\omega) \right|_{min} \right)_{passband} \qquad (3.2)$$
$$+ \sum_{j=1}^{N_s} \left(\left| A_{nj}^{'}(\omega) \right|_{max} \right)_{stopband} - \left(\left| A(\omega) \right|_{max} \right)_{stopband}$$

where N_p and N_s represent the number of pass-bands and stop-bands, respectively. The improved sensitivity criterion (3.2) has been shown superior to the original sensitivity criterion (3.1), when designing PWR2 filters with multiple bands. Its performance has been verified on several filter designs. Examples of the filter specifications (band-pass and multiple-band filters) that have been used to evaluate the performance of the modified sensitivity criterion are given in Table 3.2.

Comparisons of frequency responses for the band-pass filter BP1 are illustrated in Figures 3.3 (a) and 3.3 (b), respectively. Solid lines represent frequency responses of filters that have been designed using the original sensitivity measure, while frequency responses of filters that have been designed using the improved criterion are represented by the dashed line. Solid and dashed lines in Figure 3.3 (a) and 3.3 (b) are aligned as frequency responses for both methods are approximately the same. However, the design based on the improved sensitivity criterion cuts the total number of canonical coefficients by 4 %. This results in a lower complexity of the filter implementation.

Figures 3.3 (c) and 3.3 (d) show frequency responses of the filter with multiple bands (example MB1). The improved sensitivity criterion resulted in smaller errors in the pass-bands and slightly increased errors in the stop-bands. However, the number of canonical coefficients has been decreased by more than 30 %. The results comparing the minimum filter length and the total number of single PWR2 coefficients that are required to satisfy frequency response constraints are summarised in Table 3.3.

Table 3.2 Examples of filters designed using modified sensitivity criterion

Filter type	Number of bands	Cutoff frequencies (f)	Desired freq. resp. (D)	Attenuation [dB]	Maximum error allowed (δ)
Bandpass BP1	3	0 - 0.22, 0.24 - 0.26, 0.28 - 0.5	0, 1, 0	> -26 dB	0.05, 0.03, 0.05
Multiple bands MB1	6	0 - 0.05, 0.10 - 0.15, 0.20 - 0.23, 0.27 - 0.30, 0.35 - 0.4, 0.45 - 0.5	1, 0, 1, 0, 1, 0		0.1, 0.1, 0.1, 0.1, 0.1, 0.1
Multiple bands MB2	7	0 - 0.04, 0.08 - 0.12, 0.16 - 0.22, 0.245 - 0.275, 0.30 - 0.34, 0.38 - 0.42, 0.46 - 0.5	1, 0, 1, 0, 1, 0, 1		0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1
Lowpass LP1	2	0 - 0.27, 0.31 - 0.5	1, 0		0.02, 0.02
Lowpass LP2	2	0 - 0.24, 0.25 - 0.5	1, 0		0.05, 0.05

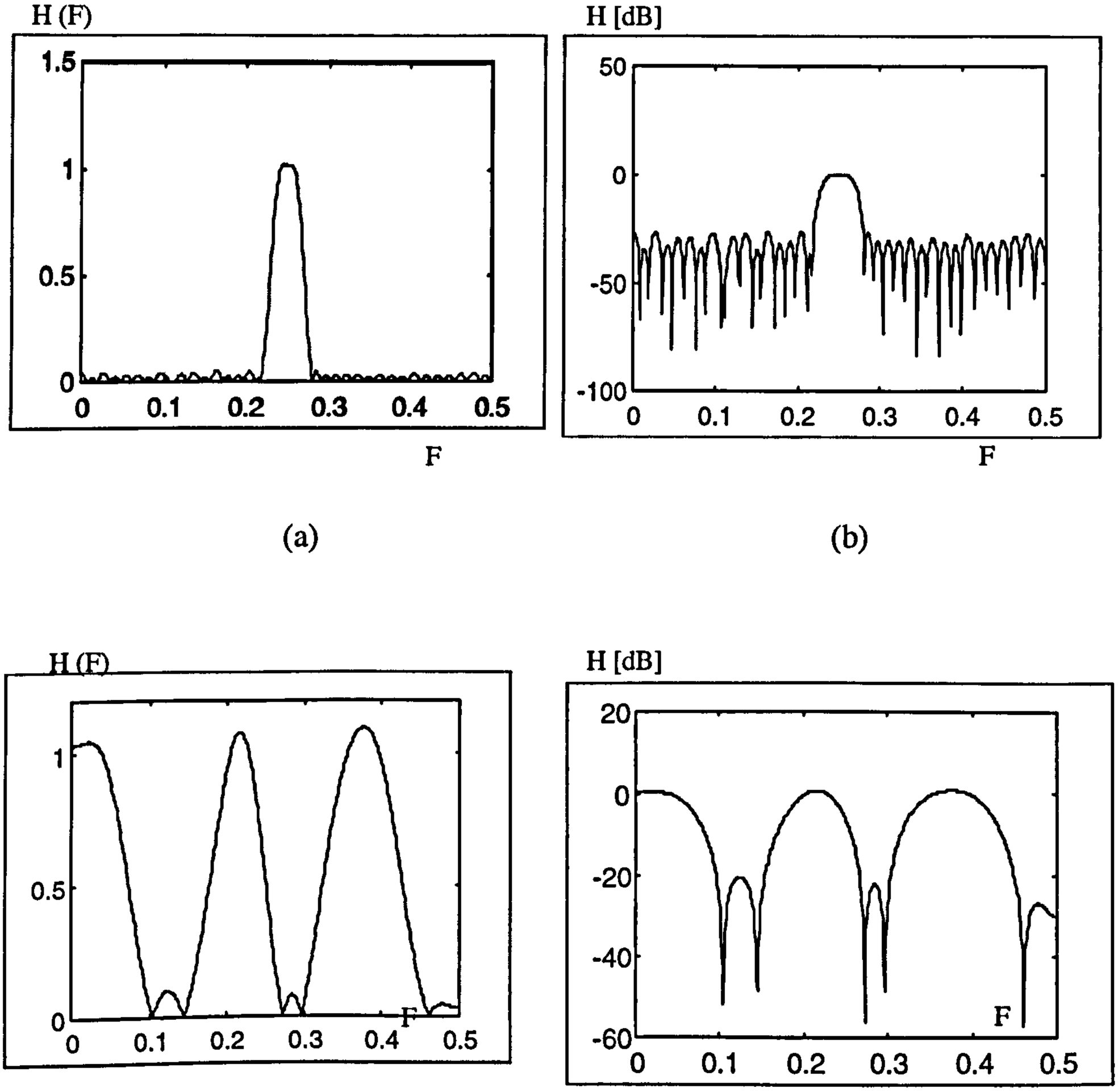


Fig. 3.3 Comparison of the original and improved sensitivity criterion:

(a) frequency response of band-pass filter BP1,

(b) as (a), but in logarithmic scale,

(c) frequency response of the multiple-bands filter MB1,

(d) as (c), but in logarithmic scale.

Table 3.3 Comparison of the original and improved sensitivity criterion

Filter	**Filter length**		**Number of canonical coeffs.**	
	with the criterion:		with the criterion:	
	original	improved	original	improved
BP1	74	74	50	48
MB1	31	31	17	11
MB2	41	41	39	23

3.2.3 Mean square error and mean absolute error sensitivity criterion

Although the sensitivity criterion (3.2) reflects the changes in the frequency response for each band, it still overlooks the fact that by approximating infinite precision coefficients with power-of-two terms, the entire frequency response is influenced at more than few isolated points. Therefore, we propose a novel sensitivity criterion, based either on a mean square error (MSE) or on a mean absolute error (MAE). Both criteria make use of the entire information acquired within the process of searching for extrema of the frequency response. The MSE criterion is more suitable for the design of noise separating filters as the energy of signal is related to the square of the signal. The MAE criterion can be used when a minimax design is preferred. As we will show later in this section, MSE and MAE based sensitivity criteria maximise further the number of coefficients that are single power-of-two [Cem93a].

Better interpretation and visualisation of the coefficient sensitivity as proposed by Shaffeu in [Sha91] can be achieved by re-arranging individual sensitivity terms in equation 3.1. The re-arranged sensitivity criterion S_n is given as follows:

$$
\begin{aligned}
S_n = &\left(\left|A_n^{'}(\omega)\right|_{max} - \left|A(\omega)\right|_{max}\right)_{passband} \\
&+\left(\left|A(\omega)\right|_{min} - \left|A_n^{'}(\omega)\right|_{min}\right)_{passband} \\
&+\left(\left|A_n^{'}(\omega)\right|_{max} - \left|A(\omega)\right|_{max}\right)_{stopband}
\end{aligned}
\tag{3.3}
$$

where $A(\omega)$ is the infinite precision coefficients' frequency response, and $A^{'}_n(\omega)$ is the frequency response with the *n-th* coefficient changed to the nearest power-of-two. The first term in (3.3) represents the difference between maximum ripples in the pass-band for a filter with infinite precision coefficients and a filter with the *n-th* coefficient changed to the nearest power-of-two. The second term represents the difference between the smallest errors in the pass-band. The last term depicts the difference between maximum ripples in the stop-band. Graphic interpretation of individual sensitivity terms is illustrated for a low-pass filter in Figure 3.4.

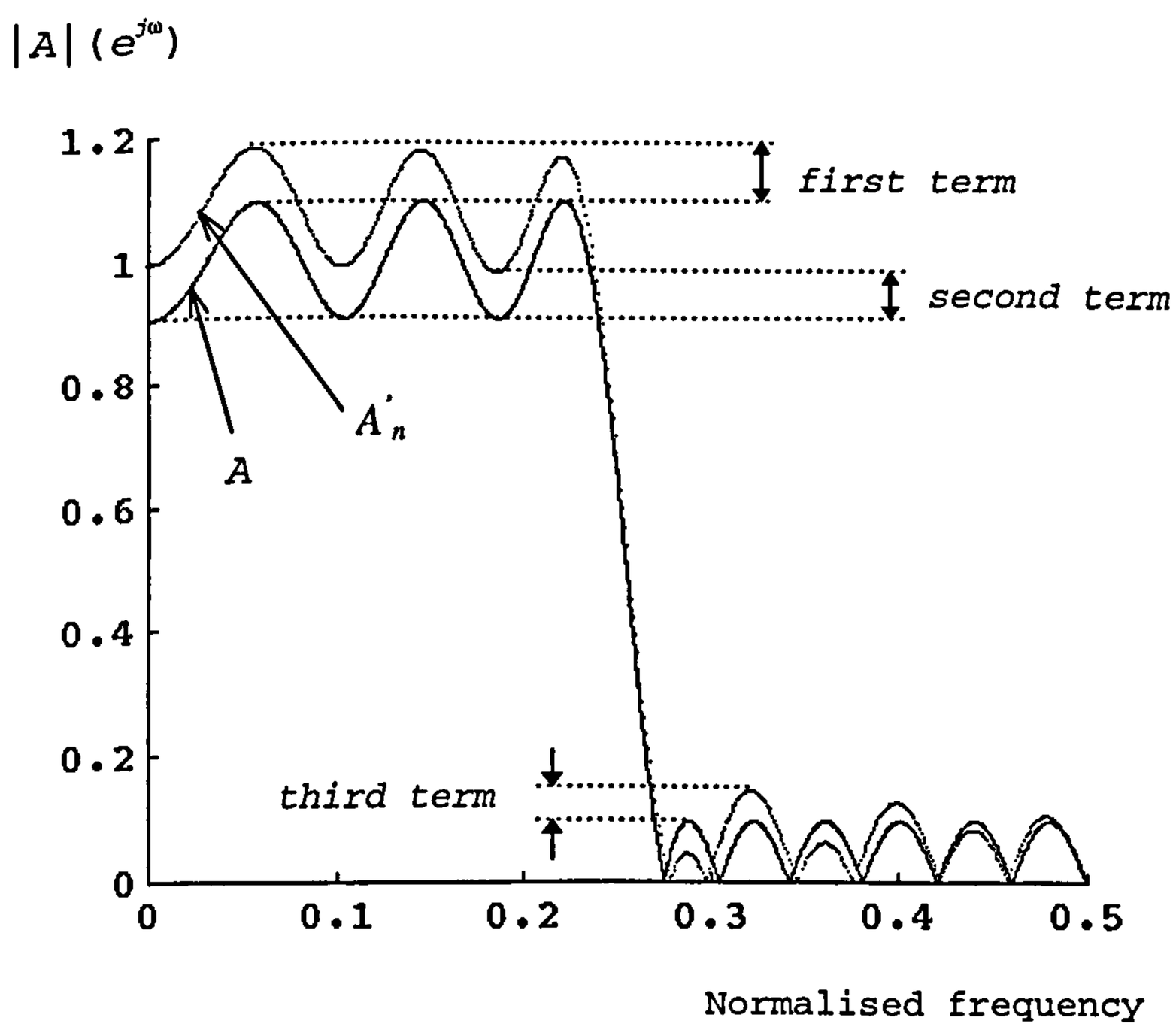


Fig. 3.4 Graphic interpretation of sensitivity

Because the sensitivity is calculated using the global extrema in both bands, it is necessary to seek their location across the whole frequency range. When searching for maxima and minima in (3.1) and (3.2), the frequency response at each discrete frequency point is evaluated. Except for the global extrema, this information is later disregarded. In fact, the calculation of coefficients' sensitivity does not consider that rounding of infinite precision coefficients to nearest powers-of-two influences the frequency response across the whole range and not only in extrema points.

The MSE sensitivity criterion is based on the mean square error between the frequency response of the filter with infinite precision coefficients and the frequency response of the filter with the *n-th* coefficient changed to the nearest power-of-two. The MSE criterion embodies every discrete frequency point across the entire frequency range that has been evaluated. The MSE coefficient sensitivity is calculated as follows:

$$S_{MSE}(n) = \frac{1}{L}\sum_{i=1}^{L}\left[A_n^{'}(\omega_i) - A(\omega_i)\right]^2 \tag{3.4}$$

Equally, the MAE criterion is based on the mean absolute error between the frequency response of the filter with infinite precision coefficients and the frequency response of the filter with the *n-th* coefficient changed to the nearest power-of-two:

$$S_{MAE}(n) = \frac{1}{L}\sum_{i=1}^{L}\left|A_n^{'}(\omega_i) - A(\omega_i)\right| \tag{3.5}$$

where ω_i is a set of discrete frequency points:

$$\omega_i = \left\{0, \frac{N_{fs}}{2N}, \frac{2\cdot N_{fs}}{2N}, \frac{3\cdot N_{fs}}{2N} \ldots, \omega_p, \omega_s, \ldots, 0.5\right\} \tag{3.6}$$

where ω_p, ω_s are normalised pass-band and stop-band cut-off frequencies, respectively and L is the number of discrete frequency points for evaluating the frequency response given as:

$$L = \left\lfloor \frac{2N \cdot \omega_p}{N_{fs}} \right\rfloor + \left\lfloor \frac{2N \cdot (0.5 - \omega_s)}{N_{fs}} \right\rfloor \tag{3.7}$$

In equation (3.7), N represents the length of filter and N_{fs} is the size of desired frequency step. The symbol $\lfloor x \rfloor$ means an integer less than or equal to the real number x. By varying N_{fs} we can adjust the precision for the calculation of the mean square error or the mean absolute error. The pseudo-code of the improved design algorithm is shown in Figure 3.5, while the Matlab source code is included on the accompanying disk.

```
Rounding of filter coefficients based on coefficient sensitivity ()
begin
  read initial specification of filter
  repeat
      calculate infinite precision coefficients
      evaluate frequency response
      choose criterion (MSE or MAE)

  /* evaluate sensitivity of each coefficient using MSE(MAE) criterion */
  for each coefficient do
      round i-th coefficient to PWR2
      evaluate frequency response with changed  i-th coefficient
      calculate sensitivity Si
  end for

  /* round to the nearest PWR2 */
  round all coefficients
  repeat
      evaluate frequency response
      if  unsatisfactory frequency response then
          /* round to the combination of two PWR2 */
          round next coefficient with the highest sensitivity
      end if
  until satisfactory frequency response
  increment filter length
      until satisfactory frequency response
end
```

Fig.3.5 Pseudo-code of the rounding algorithm using the improved sensitivity

The MSE/MAE sensitivity criterion has been verified on more than 700 various filter specifications. Some of the specifications were shown in Table 3.2. The novel criterion clearly outperformed the original Shaffeu's sensitivity criterion. Filters designed using the MSE criterion had often lower complexity with either fewer coefficients represented as canonical or with a lesser number of coefficients. In some instances, the number of canonical coefficients was reduced even more when the MAE criterion has been used.

The first example illustrated here addresses the design of a low-pass filter (Filter LP1) with relatively strict requirements on the pass-band and stop-band errors. Using the original sensitivity criterion, the minimum number of PWR2 coefficients required to satisfy the prescribed specification has been found equal to 58. When the MSE sensitivity criterion has been applied, the length of filter equal to 54 has been found to be sufficient. We failed to meet the prescribed specification with the original criterion for filter lengths less than 58 even when all the coefficients were changed to 2PWR2 values. Frequency responses for the filter LP1 are illustrated in Figure 3.6, where dotted line represents the original criterion and the solid line depicts the novel sensitivity criterion.

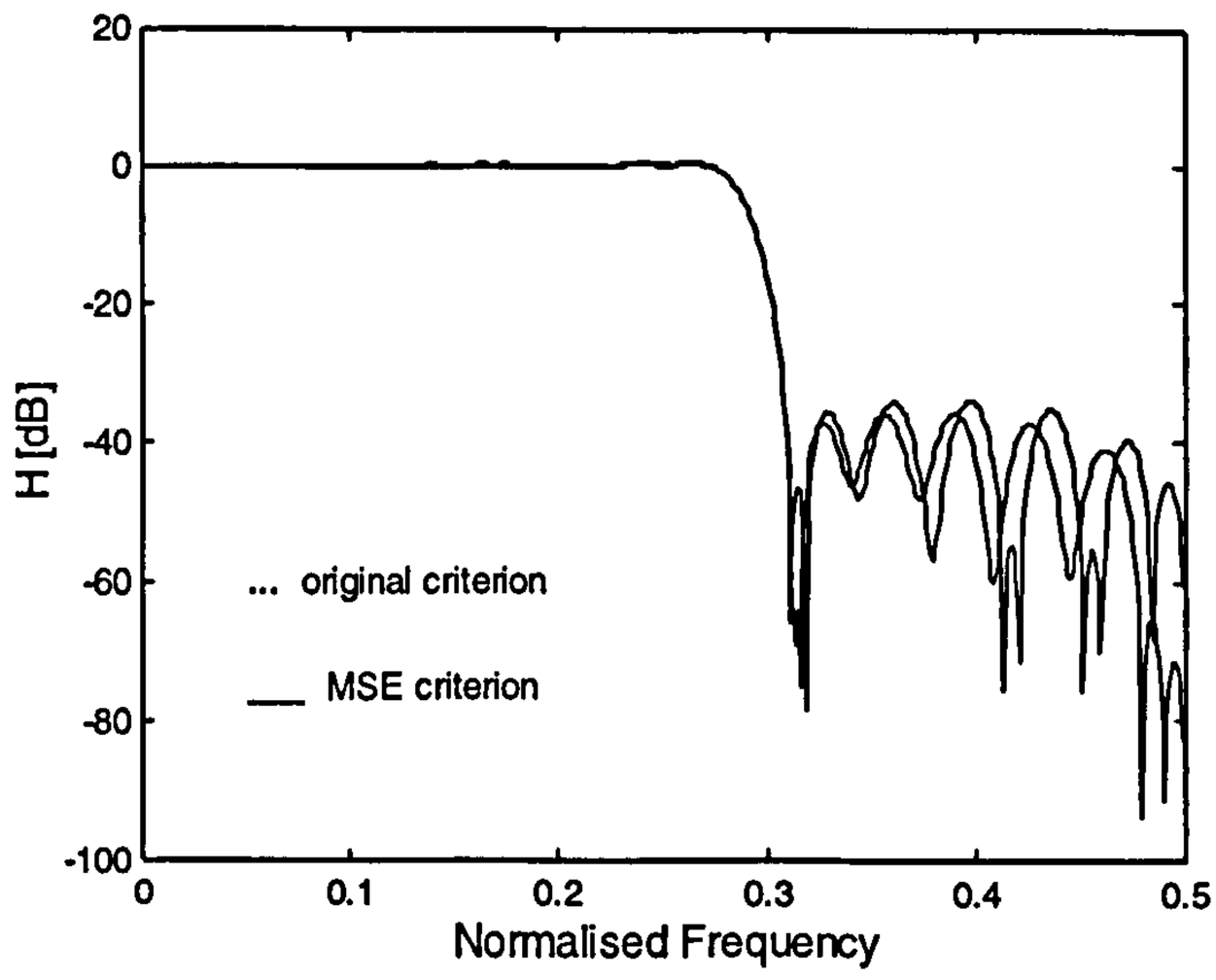


Fig. 3.6 Frequency response of the low-pass filter LP1

The next example illustrates the design of low-pass filter (Filter LP2) with very narrow transition band, where the MSE sensitivity criterion failed to deliver expected results. This can be caused by the fact, that the amplitude of ripples attributed to the narrow transition band is averaged with other ripples when using the mean square error approach. This is not the case of the original sensitivity criterion that emphasises maximum error peaks. Bearing this in mind, we can conclude that in the majority of cases the mean square error sensitivity criterion is superior to the original sensitivity criterion proposed by Shaffeu. Frequency responses for the filter LP2 are illustrated in Figure 3.7. They are almost aligned as there was very small difference between both responses. However, the minimum number of coefficients when using the MSE criterion has been found to be higher.

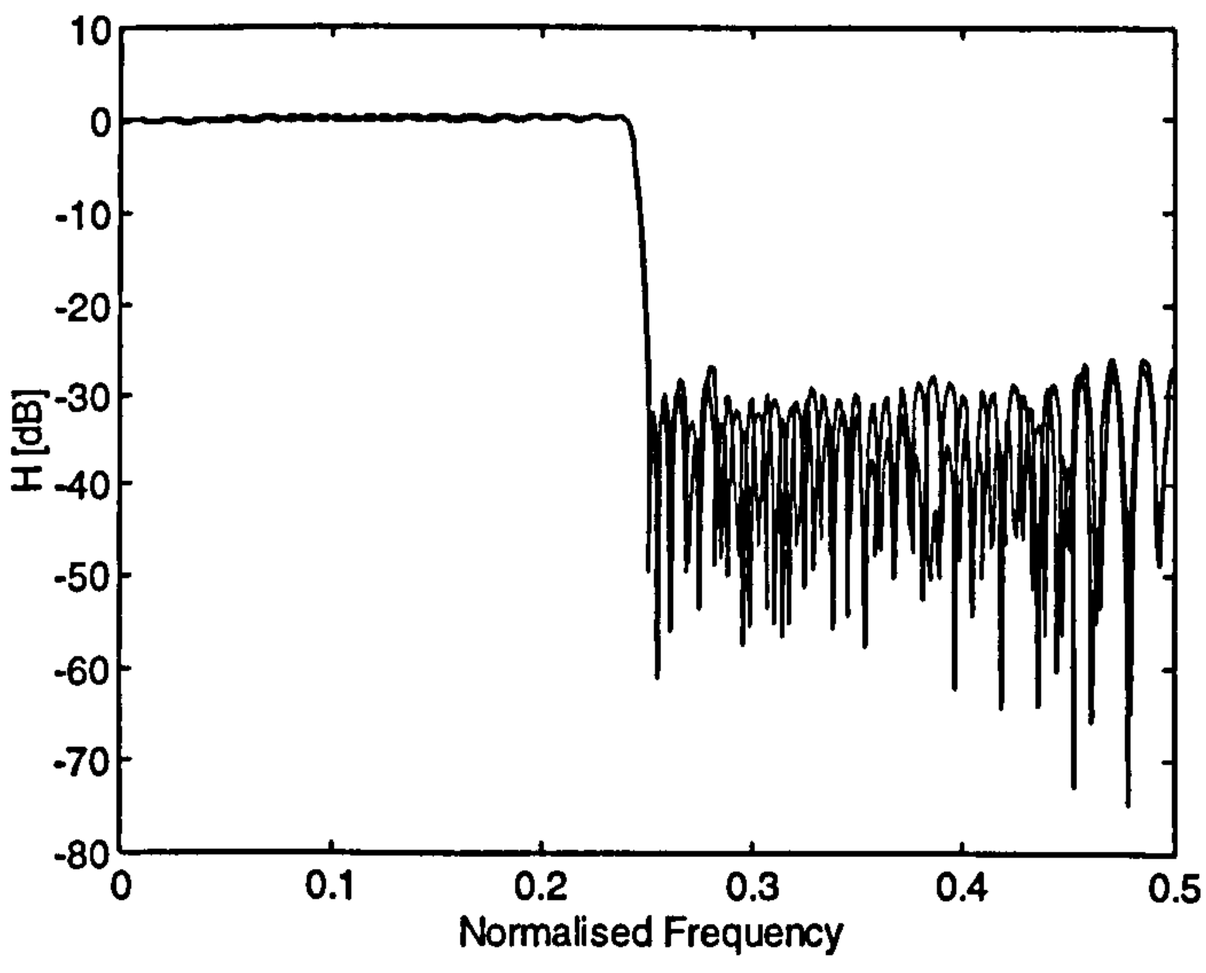


Fig. 3.7 Frequency response of the low-pass filter LP2

Results for all five filter examples using the original , MSE and MAE criteria are summarised in the Table 3.4.

Table 3.4 Comparison of Shaffeu's and novel (MSE based) sensitivity criterion

Filter	Filter length			Single PWR2 coefficient		
	Shaffeu	MSE	MAE	Shaffeu	MSE	MAE
BP1	74	74	74	24	28	28
MB1	31	31	31	14	20	20
MB2	41	41	41	2	18	18
LP1	58	54	54	16	18	18
LP2	133	141	141	82	64	39

3.3 Conclusion

In this chapter, we analysed the problem of designing multiplier-less digital FIR filters. We presented three novel algorithms that are based on classic rounding of infinite precision filter coefficients. They include evolutionary local search, modified coefficient sensitivity and mean squared error coefficient sensitivity for rounding filter coefficients, respectively. These algorithms outperformed their counterparts and the results are particularly encouraging for the MSE based method for rounding filter coefficients.

However, there are still number of issues that have not been addressed. For instance, the design of filters with phase requirements other than linear cannot be realised in a straightforward manner. The algorithms are not suitable for the design of IIR digital filters and they cannot guarantee the optimal design in the minimax sense. In fact, none of the algorithms previously described can guarantee that the coefficients are optimal (except the exhaustive search and mixed integer linear programming). Let us summarise the observations and draw some conclusions for the multiplier-less FIR filter design.

(i) The algorithms presented in previous chapters are essentially searching algorithms approximating infinite-precision coefficients by the discrete coefficients (powers-of-two) that would satisfy the desired frequency response. They use either the Remez algorithm or linear programming to obtain the initial infinite-precision coefficient vector and they explore only the vicinity of infinite-precision coefficients.

(ii) The set of discrete filter coefficients obtained by rounding of infinite-precision coefficients is suboptimal. This is because the Remez algorithm and linear programming methods can design filters that are optimal in the minimax sense only with infinite-precision coefficients. By approximating these coefficients with powers-of-two, we are ignoring a vast searching space where potential optimal filter designs might occur. We still know very little about properties of filters with power-of-two coefficients and no closed analytical solutions for the design of multiplier-less filters with powers-of-two coefficients have been developed yet.

(iii) Essentially, the problem of discrete coefficient filter design is a combinatorial optimisation problem of an enormous computational complexity. For example, let us consider a design of linear-phase FIR digital filter with 50 coefficients, using 16 bit wordlength. By restricting the coefficients to single power-of-two numbers and reserving one bit as a sign bit, we have 30 possible values for each coefficient. Because of the symmetry of the impulse response, the number of unknown variables is halved from 50 to 25. To find an optimal coefficient vector, we are dealing with the 25-dimensional combinatorial optimisation problem. The total number of coefficient combinations is given as:

$$C_t = B^{N/2} = 30^{25} = 8.472886 \cdot 10^{36} \tag{3.7}$$

where B is the number of all possible discrete values for each coefficient and N is the length of filter.

Imagine now, that we have extremely powerful computer facilities able to calculate the frequency response and to evaluate one combination of coefficients each picosecond. The time t that is needed to evaluate all combinations would be

$$t = \frac{8.472886 \cdot 10^{36}}{1ps} = 8.4 \cdot 10^{24} \text{ sec} = 2.7 \cdot 10^{17} \text{ years } !!!$$

Simple analysis of (3.7) will show that the time t increases exponentially with increasing filter length N. When the filter coefficients would be sums/ differences of two (or more) power-of-two numbers, the total number of combinations would be even bigger. Problems where the computing cost increases exponentially with the dimension of the problem are in complexity theory denoted as *NP-complete problems* (non-deterministic polynomial time complete problems). For solving of NP-complete problems we need robust searching algorithms that will handle combinatorial optimisation problems efficiently.

Natural algorithms, primarily genetic algorithms, offer themselves as ideal candidates. They are powerful searching and optimisation algorithms, based on natural processes and systems. An advantage of genetic algorithms is that the computing cost of GA's grows linearly with the size of problem. Therefore we suggest that the kernel of techniques for the design of ML FIR filters should be based upon natural algorithms, primarily genetic algorithms. In the next chapter, we will show how genetic algorithms can be applied to the design of multiplier-less FIR digital filters.

Chapter 4

Design of multiplier-less FIR filters using genetic algorithms

This chapter presents a new robust technique for the design of multiplier-less FIR digital filters based on natural algorithms. Natural algorithms are problem solving methods based on natural processes and systems. They are an alternative to traditional optimisation techniques for solving complex optimisation problems. They tend to perform well where the traditional (calculus-based) techniques failed to deliver successful results. Natural algorithms include *neural networks, simulated annealing and evolutionary algorithms* based on natural selection and evolution principles. Amongst evolutionary algorithms, *Genetic Algorithms* have emerged as very powerful searching and optimisation techniques. They are capable of solving problems with no previous knowledge. This makes them very attractive in the design of digital filters.

The structure of this chapter is as follows. First, the principles of genetic algorithms are thoroughly explained. The emphasis is placed on a thorough understanding of how genetic algorithms work. This is vital for further improvements of the basic implementation of the genetic algorithm (simple genetic algorithm). In the following section we develop and test our proposed genetic filter design method, that represents foundations for advanced techniques that are presented in the second part of the chapter. This chapter closes with conclusions.

4.1 Genetic Algorithms

Genetic algorithms (GAs) are robust search and optimisation algorithms based on genetic processes of biological organisms. They combine the mechanics of natural selection with the Darwinian principle of *"the survival of the fittest"*. GAs have been developed by John Holland in 1975, but have only been considered by few researchers for 15 more years (primarily because of the complexity of Holland's book [Hol75]). The breakthrough came after the distinguished work of Goldberg [Gol89a], that sparked intense research in the field of genetic algorithms and, more importantly, their applications to real world problems.

What makes genetic algorithms so attractive is that they really work very well for broad range of problems. This is because they emulate the process of natural evolution that has been exercised and proven in nature for millions of years. In nature, living creatures have to compete with each other for resources for survival. If they want to reproduce themselves, they must also attract a mate. They must be also able to adapt to the ever changing environment. Thus they can have a large number of offsprings and naturally increase their numbers. Individuals unable to provide enough resources will produce either weak offsprings or only few offsprings and will gradually degenerate.

Genetic algorithms are direct analogy of the process of natural evolution. They work with a population of *chromosomes* that represent encoded potential solutions to a given problem. Unlike calculus based algorithms, genetic algorithms work with the encoded unknown variables, not with the variables themselves. Chromosomes are built up of *genes,* which represent particular parameters of the problem. The values of genes are called *alleles* and the position of the gene is referred to as *locus.* The chromosomes in genetic algorithms are represented as strings of symbols, most often as binary strings. Each chromosome is assigned a *fitness* value that reflects the performance of the chromosome as a potential solution of the problem.

In genetics terms, the chromosome is often called the *genotype* (an encoded potential solution), while the solution itself is referred to as the *phenotype.* In nature, an analogy of genotype is the DNA (deoxyribonucleic acid, the main constituent of the chromosomes of all organisms), while humans, animals or plants are various examples of phenotypes. A gene is a piece of DNA that is expressed as a particular feature (e.g. hair) in the phenotype and can have a number of possible values (alleles). A particular gene can characterize a human's hair color, for example, and the allele value can be black.

Chromosomes are selected for a recombination according to their fitness values. Those having a high fitness are more likely to be selected and have better chances to reproduce than others. Hence, the genes of the fittest chromosomes will survive and spread themselves in further generations, while the genes of the chromosomes with a low fitness will gradually die out. The process of natural selection therefore leads not only to the "survival of the fittest" individuals, but also to the survival of their genes. The "fittest genes" will propagate themselves from population to population. *Therefore, what natural evolution actually selects for is genes with high fitness.*

The process of selection is followed by the recombination process, where the exchange of a genetic material occurs. Parent chromosomes swap sections of DNA

to form offsprings and as a result they pass their genetic information to the offsprings. This is the very moment, when the evolution process begins. An analogous operation in genetic algorithms is a *crossover* operation, when the selected chromosomes are recombined. The crossover operator randomly generates a crossover point (site) and sections of parent chromosomes before and after the crossover point are swapped to form offsprings. Parents' genetic information is propagated to the offsprings. Offspring chromosomes combine the information gained in previous cycles to direct subsequent moves in the searching space. This is a very important aspect, distinguishing genetic algorithms from the random search. Figure 4.1 illustrates the most simple, one-point crossover.

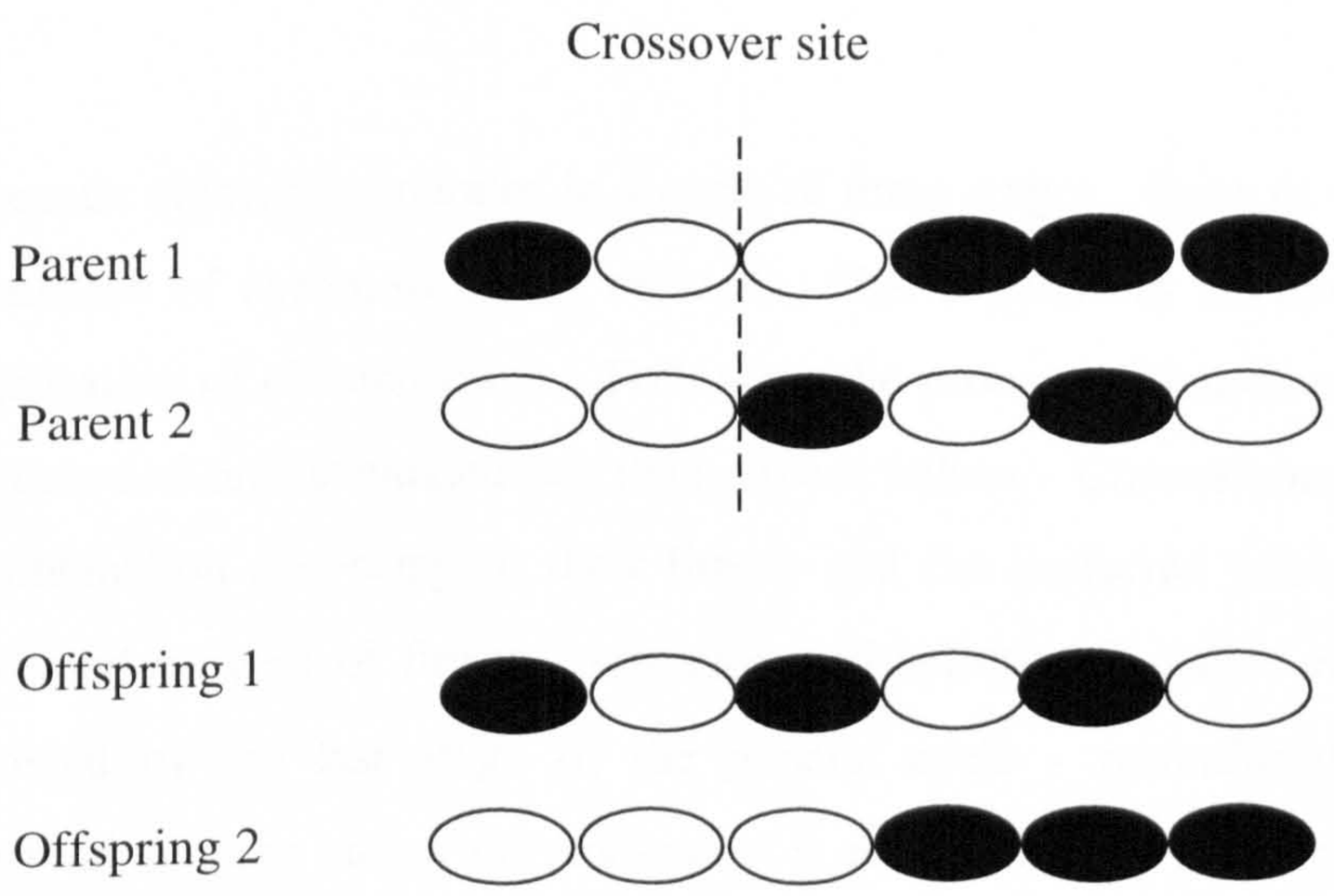


Fig. 4.1 Crossover

The operation of crossover is followed by a mutation. In the process of mutation, every allele of each chromosome in the population is randomly mutated (altered) with a certain probability. The mutation probability p_m is generally very low, hence producing only few changes. The role of the mutation is to regenerate a lost genetic material and to introduce new genetic structures. This allows us to explore the regions of the searching space which are not represented by chromosomes in the current population. For example, if all chromosomes in the population have the same

allele at the n-th locus and this allele is wrong, the mutation can regenerate the correct allele. This cannot be realised by the crossover. Figure 4.2 illustrates the mutation of the allele at the second locus.

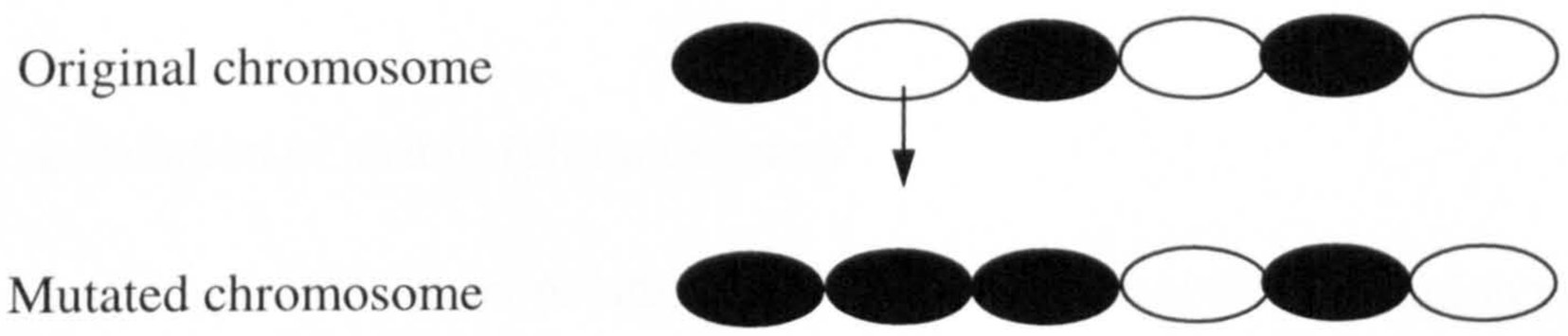


Fig. 4.2 Mutation

A genetic algorithm operates in a cycle of three stages. Prior to this cycle, an initial population of chromosomes is created. This is generally accomplished by random initialisation of chromosomes. Following the process of initialisation, chromosomes are decoded and evaluated for their fitness values. Chromosomes are selected for recombination according to their fitness and the preferred selection method. The combined process of fitness evaluation and selection is called *reproduction* and is followed by the last stage of the genetic cycle - *recombination.* The genetic information from parent chromosomes is recombined to form offsprings using the crossover and mutation operators. The process of fitness evaluation, reproduction and recombination is repeated for a given number of generations. We may wish to stop the evolution process when the entire population has converged (reached a certain degree of homogeneity).

4.1.1 Model of genetic algorithm

Goldberg's Genetic Algorithm (Simple Genetic Algorithm) consists of the following components:

- population of strings (chromosomes)
- control parameters (population size, crossover probability, mutation probability)
- genetic operators (crossover, mutation)
- fitness function

and the following operations are defined on the GA components:

- encoding/decoding of strings
- fitness evaluation
- selection
- recombination (crossover and mutation)

We have implemented Goldberg's Simple Genetic Algorithm in Matlab and further in this thesis it is referred to as the SGA model. This model also creates a basic framework for the implementation of more complex genetic algorithms that are built upon this model. The pseudo-code of the Simple Genetic Algorithm (SGA) is illustrated in Figure 4.3:

```
Simple Genetic Algorithm ( )
begin
        /* initialisation process */
        initialise population_size, p_c , p_m
        initialise population of chromosomes
        evaluate fitness of each chromosome

        /*evolution process */
        while not converged do
                for each generation do
                        selection
                        /* recombination *
                        crossover
                        mutation
                        /* evaluate fitness of offsprings */
                        evaluate fitness
                end for
        end while
end
```

Fig. 4.3 Pseudo-code of Simple Genetic Algorithm

4.1.2 How does the genetic algorithm work?

To illustrate stages of the genetic algorithm and to demonstrate the role of all components and operations involved we will use similar approach of "simulation by hand" as has been used by Goldberg [Gol89a]. Let us apply the SGA from Figure

4.3 to find a maximum of the function $f(x) = sin(x) + \sqrt[5]{x^3}$, where x is an integer number from the interval $\langle 0,63 \rangle$.

Depending on the nature of the problem, the control variables *population_size,* crossover probability p_c and mutation probability p_m must be suitably chosen. In this example a rather small population size of six strings has been used for illustration purposes only. In fact, the size of the population varies from 30 (Goldberg's SGA) to several hundreds up to thousands strings for some real world problems. The encoding method must be also decided before the initialisation. A six-bit unsigned binary coding was chosen in this example to encode integers from 0 (000000) to 63 (111111). The selection of the optimal control variables and an appropriate encoding method is very important for efficient implementation of a genetic algorithm and is a subject of the intense research [Gre86, Sch89, DeJ90, Gol92, Aru93]. The next step is to create an initial population of strings. This is done usually by random initialisation of strings. The initial population of six strings is shown in Table 4.1 in the first column.

The initialisation is followed by a process of reproduction which combines the processes of fitness evaluation and selection. Strings are selected according to their normalised fitness values $f_i / \overline{f}$ and reproduced for the next population. Normalised fitness values and the actual number of strings to be reproduced are shown in Table 4.1. with the symbol f_i denoting the fitnes of the i-th string and the symbol $\overline{f}$ representing the average fitness of the entire population. String 110011 will be reproduced twice, because it has the highest fitness. String 001011 will not be reproduced at all, because of its low fitness, and the remaining strings will be assigned one copy each, to maintain a constant size of the population. The reproduced population is shown in the first column of Table 4.2.

Table 4.1 GA's initial population, normalised fitness values and actual number of strings selected for recombination

Initial population	x	f(x)	$f_i / \overline{f}$	Number of selected strings
001001	9	4.1493	0.5907	1
010110	22	6.3805	0.9084	1
110011	51	11.2516	1.6019	2
011111	31	7.4450	1.0599	1
001011	11	3.2154	0.4578	0
101100	44	9.7021	1.3813	1

Table 4.2 First generation of GA computer simulation

Reproduced population	Mate	Crossover site	Offsprings	New population	x	f(x)
001001	3	2	000011	000011	3	2.0743
010110	6	4	010100	010000	16	4.9901
110011	1	2	111001	111001	57	11.7478
110011	5	5	110011	110010	50	10.1940
011111	4	5	011111	011111	31	7.4450
101100	2	4	101110	101110	46	10.8479

Following the process of reproduction, the crossover operator is applied in two steps. In the first step, strings are randomly mated, using coin tosses to pair mates. In this example, the first string was paired with the third, the second with the sixth and fourth with fifth string. In the second step, a biased coin toss will decide if the crossover will occur. If the result is heads, the strings swap their parts before and after a randomly chosen crossover site (shown in the third column of Table 4.2), thus generating offsprings. If the result is tails, the offsprings are the exact copies of parent strings. After crossover, the mutation operator is applied, mutating randomly string's bits with the probability p_m. String 010100 was mutated at the fourth locus (position) creating thus the string 010000 and string 110011 was mutated at the sixth locus, creating the string 110010. Mutated strings are shown as the new population in fifth column of Table 4.2. In this example, the SGA after first generation produced a string 111001 which when decoded, returns higher value of the function to be maximised, than the best string from the initial population (the string, its decoded value and the function value is shown in italics in Table 4.2). Subsequent generations would produce "better" strings, eventually a global maxima of the function is attained. The algorithm terminates, when the total number of generations has exceeded a specified amount or when the population has converged. The population is converged, when all of the genes have converged. A gene is said to be converged, when 95% of the population have identical value [DeJ75]. But why is the Genetic Algorithm able to produce better strings by just selecting, copying and crossing strings together?

The first explanations how GAs work was given by Holland's *schema theorem* [Hol75]. A schema is a pattern of gene values describing a subset of chromosomes which have similarities at certain positions. A chromosome contains a particular schema if it matches that schema. For example, when using a binary coding with the three symbols 1, 0 and * (the symbol * can represent either 1 or 0), the string 111001 from the previous example contains schemata 11****, 11*0*1, **1001, etc. Goldberg [Gol89a] introduces the following two properties for schemata: defining length and order. The *defining length* δ of a schema H is the distance between the

outermost chromosome's position that are fixed (in this example, δ = 1, 5, and 3, respectively). The *order* of a schema, denoted in GA literature as $o(H)$, is the total number of fixed positions. Schema theorem states:

Schema theorem.

The optimum way to explore a searching space is to allocate chances to individuals to reproduce proportionally to their fitness relative to the average fitness of the population. Good schemata are then exponentially increasing in numbers in successive generations.

Holland also showed that the number of schemata processed in each generation is of the order N_{pop}^3, where N_{pop} is the size of the population. This is very important and powerful feature of genetic algorithms known as*implicit parallelism.*

The proof of the schema theorem and a theoretical analysis of the effect of reproduction, crossover and mutation on a particular schema H was shown by Goldberg in [Gol89a]. We will repeat the proof here as it is a foundation for understanding how genetic algorithms work. Let's suppose that in the discrete time step t there are m examples of a schema H in a current population. We will denote this as $m= m(H,t)$, meaning that there are different numbers of different schemata H at different times t. Each discrete time step represents one generation. An expected number of schemata H in the next generation is therefore denoted as $m= m(H, t + 1)$.

The first step is to determine the effect of reproduction. Let's suppose that a population contains n strings and the average fitness of all strings representing schema H at time t is $f(H)$. The expected number of schemata H at time $t + 1$ is then given by the following equation:

$$m(H,t+1) = m(H,t) \cdot n \cdot \frac{f(H)}{\sum f_i} \tag{4.1}$$

As the average fitness of the population was defined as $\overline{f} = \Sigma f_i / n$, equation (4.1) can be rewritten as

$$m(H,t+1) = m(H,t) \frac{f(H)}{\overline{f}} \tag{4.2}$$

Equation (4.2) states that, during reproduction, schemata with fitness values above the population average will receive increased number of copies for the next generation and schemata with low fitness values will decrease in numbers (and gradually will die off). To complete the proof of the schema theorem Goldberg has also shown in [Gol89a] that good schemata are increasing in their numbers exponentially.

Suppose that a schema H has an above average fitness $f(H) = \overline{f} + C \cdot \overline{f}$, where C is a constant. Equation (4.2) after substituting $f(H)$ and assuming a stationary value of C becomes:

$$m(H,t+1) = m(H,t) \frac{(\overline{f} + C \cdot \overline{f})}{\overline{f}} = (1+C) \cdot m(H,t) \tag{4.3}$$

and this can be rewritten as:

$$m(H,t+1) = m(H,0) \cdot (1+C)^t \tag{4.4}$$

This equation is also known as a discrete form of an exponential function. Hence, we have a proof that good schemata during reproduction are increasing in numbers exponentially.

To analyse the effect of crossover, suppose a binary string of length L that contains a particular schema H with defining length $\delta(H)$. Schema H will be destroyed (disrupted) by crossover, whenever a crossover point falls between any two bits corresponding to schema H. Generally, the probability that a schema H will be destroyed is:

$$p_d = p_c \cdot \frac{\delta(H)}{L-1} \tag{4.5}$$

where p_c is the probability of crossover. The probability that a schema H will survive crossover is defined as the mutation survival probabilityp_{sc}

$$p_{sc} \geq 1 - p_d = 1 - p_c \cdot \frac{\delta(H)}{L-1} \tag{4.6}$$

Because the crossover operation is independent of the reproduction and follows the reproduction stage, equation (4.2) can be multiplied by the survival probability p_{sc} to obtain a combined effect of reproduction and crossover:

$$m(H,t+1) \geq m(H,t) \cdot \frac{f(H)}{\bar{f}} \left[1 - p_c \cdot \frac{\delta(H)}{L-1}\right] \tag{4.7}$$

The last step is to determine the effect of mutation. Mutation randomly alters each allele of the string with the probability p_m. If a schema H has the $o(H)$ fixed alleles, each allele has to survive in order for a schema H to survive. The probability that an allele survives mutation is (1 - p_m). Because there is no correlation between mutations, the probability that a particular schema H with the $o(H)$ fixed alleles survives mutation is:

$$p_{sm} = (1 - p_m)^{o(H)} \tag{4.8}$$

Multiplying equation (4.7) with equation (4.8) and ignoring one small cross-product term, the combined effect of reproduction, crossover and mutation is given by the following equation:

$$m(H,t+1) \geq m(H,t) \cdot \frac{f(H)}{\bar{f}} \left[1 - p_c \cdot \frac{\delta(H)}{L-1} \right] \cdot (1-p_m)^{o(H)} \tag{4.9}$$

Equation (4.9) states that schemata of short defining length and fitness values above the average are receiving exponentially increasing numbers of copies in subsequent generations. Crossover can be a very disruptive operation, but has a little disruptive effect on schemata with short defining length. However, as we have shown before (Table 4.1 and Table 4.2), the exchange of information occurring during crossover is of greater importance than disruptive effects.

Goldberg in [Gol89a] explains how GAs work by the building *block hypothesis*. Building blocks are schemata of short defining length and above average fitness values. They are propagating themselves from generation to generation and increasing exponentially in numbers according to the schema theorem. When combined together, they result in the improved performance. For example, the string 111001 in the example shown in Table 4.2 has been obtained by combining schemata 11**** and **10**. An analogy of the building blocks hypothesis in real life can be building a model from Lego pieces, or designing a complex microprocessor from blocks like adders, registers, buses, etc. In both cases, by combining small components (equivalent of the short defining length) with exactly defined function within the entity (high fitness) we can create amazing things. Goldberg concluded that:

Genetic algorithms seek near optimal performance through the juxtaposition of short, low-order, highly fit building blocks.

The formation of building blocks can be encouraged by a suitable coding method. A good coding method will encode genes that are related to each other so that they will appear close on the chromosome and the interaction between them will be as low as possible. The crossover and mutation operations should also support a formation of building blocks, with a minimum disruption. We will follow these principles in our implementation of a simple genetic algorithm that is presented next.

4.2 Simple genetic algorithm for the FIR filter design

A mapping of the discrete combinatorial optimisation problem onto a genetic algorithm is not a straightforward task. A thorough analysis of the optimisation problem has to precede the mapping of the problem onto a genetic algorithm. When this is omitted, the performance of genetic search is low and the results are more-less random. This is in agreement with previous claims that genetic algorithms can find a solution without any knowledge about the problem. This is true, yet the genetic algorithm must:

- perform the searching process in a domain where the problem is defined,
- know whether chromosomes represent good or poor potential solutions to the problem.

The first requirement can be satisfied by a choice of an appropriate *encoding scheme* and the second requirement is accomplished by constructing of a specific *problem-related fitness function*.

The process of mapping the filter design problem onto the genetic algorithm is shown next. The filter coefficients are encoded onto a population of chromosomes as they are the parameters that need to be designed. The chromosomes can have any data structure, in case of the simple genetic algorithm they are just binary strings. The filter coefficients are evolved by the genetic manipulating of chromosomes.

When designing digital FIR filters the following considerations must be known:

- the desired frequency response, i.e. magnitude and phase response
- the filter order (N-1)
- coefficient wordlength

In case of multiplier-less FIR digital filters, additional restrictions on the range of coefficient values must be also taken into account. These considerations greatly influence the chromosome structure and the associated encoding method and also the fitness function. The chromosome structure and the fitness function vary for each particular filter.

The algorithm proposed here (further referred as GA-1) employs the SGA model and can design linear-phase ML FIR filters of the following types: low-pass, high-pass, band-pass, band-stop, multiple-band filters or filters with an arbitrary frequency response. No other magnitude or phase constraints can be realised with the GA-1 algorithm. The filter coefficients are restricted to the PWR2 or 2PWR2. The source code of GA-1 algorithm written in Matlab is included on the accompanying disk.

4.2.1 Encoding

In living organisms, the DNA carries an important genetic information of organisms by the information onto the chromosomes. Genetic algorithms must have also a similar system to encode parameters of the problem to be solved. Each individual parameter (representing an individual gene) is encoded and genes are concatenated to form chromosomes (strings of values). Encoding of the problem's parameters must be decided before genetic algorithm can be considered to solve any problem. A particular method of encoding depends on the nature of the problem and is very critical to the performance of genetic algorithms.

The traditional way of coding is *binary coding*, where individual parameters are coded as binary numbers and concatenated to form chromosomes. The main disadvantage of binary coding is the large Hamming distances between the binary codes of adjacent numbers (Hamming cliffs). For example, when the gene's value is 3 and the required value is 4, we need to flip three bits to arrive to the solution. To avoid Hamming cliffs, *Gray coding* has been proposed [Hol71, Gol89a]. Other coding methods include dynamic parameter encoding (DPE) proposed by Schraudolph in [Sch91], which increases the resolution search as the evolution process proceeds, and coding methods that use *high-cardinality alphabets*. Using high-cardinality alphabets, genes can be represented as integers or real numbers. However, special crossover and mutation operators must be used, for example arithmetic crossover [Ife93], averaging crossover, geometric mean crossover, random replacement mutation, etc.

Encoding scheme for GA-1 algorithm.

To satisfy the linear-phase condition, the filter coefficients must be symmetrical. This can be achieved by folding of the filter coefficients, i.e. the number of coefficients N_{Coeff} evolved during the design process is:

$$N_{Coeff} = \begin{cases} N/2, & \text{if N is even} \\ (N-1)/2+1, & \text{otherwise} \end{cases} \tag{4.10}$$

where N is the length of the filter. Before calculating the frequency response the filter coefficients must be unfolded, i.e.:

$$h(N-i+1) = h(i) \tag{4.11}$$

Hence, the number of parameters that need to be encoded onto chromosomes is equal to N_{Coeff}. Each parameter, i.e. each folded coefficient represents one gene,

therefore the chromosomes will have N_{Coeff} genes in total. The values of the filter coefficients h_i (alleles) are assumed to be either single power-of-two values (PWR2):

$$h_i \in \left\{\alpha:\ \alpha = c_i \cdot 2^{-b_i}, c_i \in \{-1,\ 1\}, b_i \in \{1,2,\ldots,B-1\}\right\} \tag{4.12}$$

or the sum (or the difference) of two power-of-two values (2PWR2):

$$h_i \in \left\{\beta:\beta = \sum_{i=1}^{2} d_i \cdot 2^{-b_i}, d_i \in \{-1,0,1\}, b_i \in \{1,\ldots,B-1\}\right\} \tag{4.13}$$

where B is the coefficient wordlength. For example, when the coefficient wordlength $B = 16$, the filter coefficients can be any of the following values:

a) <u>PWR2</u>

$$\{-2^{-1},-2^{-2},\ldots,-2^{-15},+2^{-15},\ldots,+2^{-2},+2^{-1}\} \tag{4.14}$$

b) <u>2PWR2</u>

$$\begin{Bmatrix} -2^{-1}-2^{-1},\ -2^{-1}-2^{-2},\ldots,-2^{-15}, \\ +2^{-15},\ldots,\ +2^{-1}+2^{-2},\ +2^{-1}+2^{-1} \end{Bmatrix} \tag{4.15}$$

When designing ML FIR filters, the choice of filter coefficients is limited to discrete values with highly non-uniform distribution. The distribution of PWR2 coefficients in the interval $\langle -0.5,+0.5\rangle$ is shown in Figure 4.4.

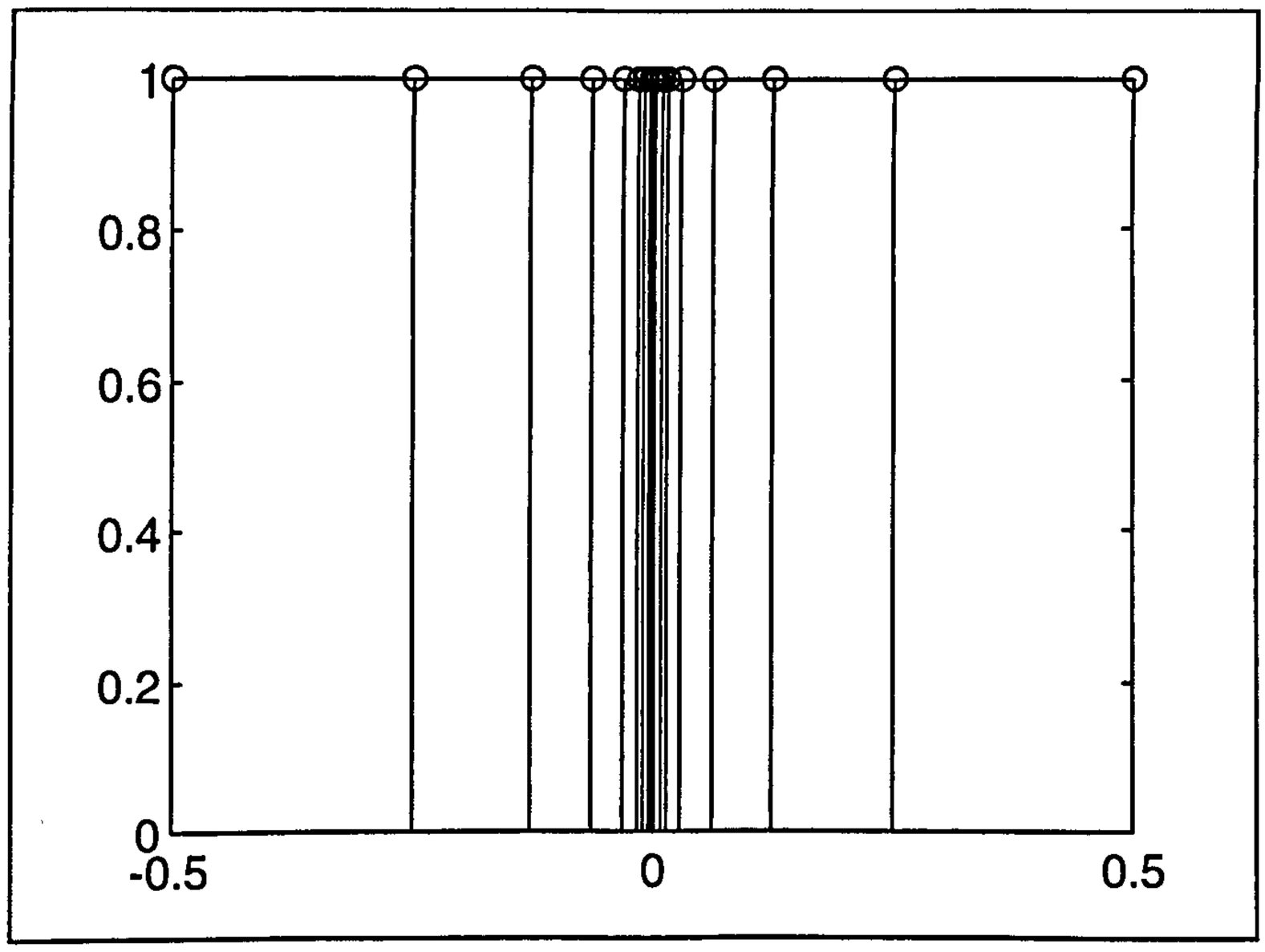


Fig 4.4 Distribution of PWR2 coefficients in the interval $\langle -0.5,+0.5 \rangle$

Because of the non-linear distribution of filter coefficients and therefore also the non-linear distribution of the gene alleles, the encoding procedure for the simple genetic algorithm is not straightforward. Binary coding of filter coefficients cannot be used because of its redundancy. Suppose that the filter coefficients are represented by the 16-bit binary word with one bit reserved as a sign bit and limited to power-of-two numbers. Then each filter coefficient can have only 31 valid different values (including zero value). However, with 16-bit binary word there is $2^{16} = 65\ 536$ possible combinations, therefore the probability that a random initialisation of the 16-bit binary string to produce a valid coefficient is equal to (31/65536) = 0.00047. Suppose that the chromosome consists only of 10 genes, then the probability that the chromosome is valid, i.e. each gene is valid, is equal to $(31/65536)^{10} = 5.6081\text{e-}34$. Therefore the probability that a random initialisation of the population of chromosomes would produce a valid chromosome is :

$$P_{chromosome} = N_{pop}\left(\frac{2B-1}{2^B}\right)^{N_{genes}} \tag{4.16}$$

where N_{pop} is the size of the population (number of chromosomes) and N_{genes} is the number of genes in each chromosome:

$$N_{genes} = \begin{cases} N_{Coeff}, & \text{for PWR2 coefficients} \\ 2 \cdot N_{Coeff}, & \text{for 2PWR2 coefficients} \end{cases} \tag{4.17}$$

This redundancy produces a number of invalid strings that need to be removed from the population in each generation. As a consequence, the performance of genetic algorithm radically deteriorates.

Because of the redundancy problems we propose a different coding method. It follows from the analysis of (4.14) and (4.15) that only the exponents of power-of-two coefficients and the signs of coefficients need to be encoded. The exponent signs can be ignored as they are always minus. As only 30 different coefficients are to be encoded (when B= 16), only 5-bit binary word is needed where one bit is reserved for the sign. The chromosome length L_{chrom} is a product of the number of genes N_{genes} and the number of bits B_{gene} required to encode each allele:

$$L_{chrom} = N_{genes} \cdot B_{gene} \tag{4.18}$$

The encoding method is demonstrated by the following example.

Example:

We will demonstrate the encoding procedure using a 10-th order FIR filter with PWR2 coefficients and the coefficient wordlength B equal to 16, thus restricting the coefficient values to be power-of-two values in the range $\langle -2^{-15}, +2^{-15} \rangle$. A set of the filter coefficients can have, for example, the following values:

$$h = \{2^{-5}, 2^{-4}, 2^{-15}, -2^{-2}, 2^{-15}, 2^{-1}, 2^{-15}, -2^{-2}, 2^{-15}, 2^{-4}, 2^{-5}\} \tag{4.19}$$

The number of coefficients to be encoded is:

$$N_{Coeff} = (N-1)/2+1 = 10/2+1 = 6 \tag{4.20}$$

and the set of folded coefficients is:

$$h_{folded} = \left\{2^{-5}, 2^{-4}, 2^{-15}, -2^{-2}, 2^{-15}, 2^{-1}\right\} \tag{4.21}$$

Applying the encoding method proposed above, only the string {5,4,15,-2,15,1} needs to be encoded using 5-bit binary coding. The corresponding chromosome length L_{chrom} is:

$$L_{chrom} = N_{genes} \cdot B_{gene} = 6 \cdot 5 = 30 \tag{4.22}$$

and the chromosome representation of the filter coefficients from (4.19) is:

$$chromosome(i) = 001010010001111100100111100001$$

End of example.

When the population of chromosomes is encoded using the method described above, no invalid strings can be produced. The size of the initial population and the number of the genes depends on the filter specification and can be determined from the design constraints. There are several ways to create the initial population of chromosomes and to initialise their alleles, including a random initialisation, an equidistant sampling of the discrete power-of-two space and rounding of infinite-precision coefficients acquired from the Remez algorithm. The latter is accomplished just for one chromosome and represents very simple knowledge-inserting operator. When using this scheme the remaining chromosomes are initialised randomly .

Other representations of the encoded chromosomes can be also realised. For instance, Gray coding can be used to avoid Hamming cliffs, or gene alleles can be represented as integers or symbols, thus avoiding the creation of invalid strings.

There is an ongoing discussion between GA researchers concerning which representation of genes is better. Goldberg has shown in [Gol89a, Gol90] that the representation of genes with the minimal binary alphabet is more natural to genetic algorithms. Representation with the smallest alphabet allows better sampling of the searching space. This is because genes' alleles that can be either 0 or 1 effectively cut the searching space in half. Goldberg also investigated Gray coding and concluded that although it can help to avoid Hamming cliffs, it introduces non-linearity in the recombination process [Gol89b]. Davis [Dav91] argues in favour of nonbinary higher cardinality alphabets as the larger range of operators can be applied to the problem.

When using binary and Gray coding, crossover operator can have very disruptive effects on the overall performance of the algorithm. This occurs when the crossover point falls between any two bits of the gene that has converged to the genuine (and correct) value. Therefore, we have implemented non disruptive crossover methods, where the crossover point is guaranteed to be between outermost bits of the adjacent genes. The influence of various gene representations on a performance of genetic algorithm has been investigated, using the evolution speed as a criterion to measure the effects of various gene representation. We have defined the evolution speed as follows:

Definition 1.

Evolution speed is a number of generations that is necessary for genetic algorithm to produce a chromosome that represents an acceptable solution to the problem being solved.

Statistical analysis has shown that there is a little difference between results achieved with various gene representations for ML FIR filter design problems. Therefore we

conclude that the important decision that is strongly influencing the performance of genetic algorithms is taken when determining the encoding method. Effects of different gene representation on the performance of genetic algorithm has been found negligible. The evolution speed for various gene representations is shown in Table 4.3 (results shown are for the GA-LP2 example from Appendix A). Table 4.3 shows 10 runs of genetic algorithm for binary representation (with non-disruptive and disruptive crossover), Gray code representation (with non-disruptive and disruptive crossover) and integer representation, respectively. The last row represents the average evolution speed.

Table 4.3 Comparison of evolution speed for various gene representations

Binary representation	Binary representation (*disruptive*)	Gray representation	Gray representation (*disruptive*)	Integer representation
1	27	10	5	6
15	9	10	34	19
28	5	18	4	19
12	33	14	12	22
10	11	25	19	31
19	21	18	32	3
10	13	4	25	5
23	18	13	18	8
8	1	4	1	7
18	6	10	18	13
14.4	11.4	12.6	16.8	12.3

The decoding procedure is a reverse process of encoding. The chromosomes are split into the genes that are decoded creating thus folded filter coefficients. The filter coefficients are constructed by unfolding of the folded filter coefficients.

4.2.2 Fitness evaluation

The fitness function is the most important part of any genetic algorithm influencing its overall performance. GA assigns a fitness value to each string, reflecting a potential of the string to be a solution to the problem. To choose the fitness function is straightforward in many cases. For instance, when maximising (minimising) function $f(x)$, where $x \in \langle x_1, x_2 \rangle$, the fitness value can be simply a value of the function at a given point x (or a reciprocal function value). For complex design problems, when many parameters are to be optimised, the fitness function should reflect all these parameters. To construct a fitness function for multi-parameter optimisation problems is non trivial task. When the values of decoded chromosomes have no actual meaning for guiding a searching process, they cannot be used as a fitness measure. Therefore, the fitness function that describes how well are chromosomes progressing towards the local (global) optimum, must be constructed.

Fitness function for GA-1 algorithm.

The fitness function should express how accurately the desired frequency response is approximated by the frequency response of the potential solution (decoded chromosome) over the entire frequency range. The difference between both frequency responses can be expressed as the weighted error function $E(f_i)$:

$$E(f_i) = W(f_i) \cdot [H(f_i) - D(f_i)] \tag{4.23}$$

where $H(f_i)$ is the actual frequency response of the FIR filter, $D(f_i)$ is the desired frequency response and $W(f_i)$ is the weight function that controls the error ripples in different bands (see also (2.13) in Chapter 2).

The FIR filter design problem can be then viewed as a minimisation of the error function $E(f_i)$ over the frequency range $f \in \langle 0, \pi \rangle$ for a given filter specification :

$$\min \left\| E(f_i) = W(f_i) \cdot \left[H(f_i) - D(f_i) \right] \right\| \tag{4.24}$$

which must satisfy the filter specification

$$E(f_i) = W(f_i) \cdot \left[H(f_i) - D(f_i) \right] \leq \delta_{f_i} \tag{4.25}$$

The fitness function should guarantee that the genetic algorithm will minimise an error between the desired and actual frequency response, therefore it should be an inverse function of the error function. The error function can be calculated as a mean square error over the entire frequency range. Hence, the fitness function for the j-th chromosome is given as follows:

$$fitness_j = \frac{1}{1 + \frac{1}{N_{fs}} \sum_{f_i=1}^{N_{fs}} \left[D(f_i) - H_j(f_i) \right]^2} \tag{4.26}$$

where N_{fs} represents the number of frequency samples. Within the process of fitness evaluation, the frequency response is calculated and compared with the desired frequency response at N_{fs} discrete frequencies. The algorithm is terminated when the frequency response is within the specification. Considering four basic types of FIR filters, the fitness function (4.26) can be rewritten to reflect a specific frequency response of each filter type:

(a) odd filter length and symmetric coefficients

$$fitness_j = \frac{1}{1+\frac{1}{N_{fs}}\sum_{f_i=1}^{N_{fs}}\left[D(f_i)-\sum_{i=0}^{N-1}h_i\cos(2\pi f_i)\right]^2} \tag{4.27}$$

(b) even filter length and symmetric coefficients

$$fitness_j = \frac{1}{1+\frac{1}{N_{fs}}\sum_{f_i=1}^{N_{fs}}\left[D(f_i)-\cos\left(\frac{\omega}{2}\right)\sum_{i=0}^{N-1}h_i\cos(2\pi f_i)\right]^2} \tag{4.28}$$

(c) odd filter length and anti-symmetric coefficients

$$fitness_j = \frac{1}{1+\frac{1}{N_{fs}}\sum_{f_i=1}^{N_{fs}}\left[D(f_i)-\sin(\omega)\sum_{i=0}^{N-1}h_i\cos(2\pi f_i)\right]^2} \tag{4.29}$$

(d) even filter length and anti-symmetric coefficients

$$fitness_j = \frac{1}{1+\frac{1}{N_{fs}}\sum_{f_i=1}^{N_{fs}}\left[D(f_i)-\sin\left(\frac{\omega}{2}\right)\sum_{i=0}^{N-1}h_i\cos(2\pi f_i)\right]^2} \tag{4.30}$$

where N_{fs} is given as:

$$N_{fs} = n_p N \cdot \left[f_p + (0.5 - f_s)\right] \tag{4.31}$$

where f_p, f_s are the cut-off frequencies, n_p controls frequency sampling N is the filter length.

4.2.3 Implementation of GA-1 algorithm.

It follows from the analysis of (4.27-4.30) that a design of digital FIR filters of (N-1) order can be considered as N-dimensional combinatorial optimisation problem. The algorithm proposed here uses Goldberg's Simple Genetic Algorithm (SGA) to search in the discrete domain of powers-of-two for a combination of filter coefficients that best satisfy the filter specification.

The GA-1 algorithm starts with a random population of chromosomes. The length and the structure of chromosomes are determined by the filter length, filter type and the applied encoding method. The default size of the population is 40 and can be changed by the designer. Increasing of the size of the population N_{pop} greatly influences searching capabilities of the genetic algorithm, as the number of schemata processed in each generation is of the order N_{pop}^3 [Hol75]. Therefore a compromise between the size of the population, the available computer memory and the convergence speed of genetic algorithm has to be made.

In the next stage, the fitness values of chromosomes are evaluated. This is done in two steps. First, chromosomes are decoded and unfolded, thus creating vectors of filter coefficients. Then the frequency response of each coefficient vector is calculated. The fitness values are determined according to the equations (4.27), (4.28), (4.29) and (4.30).

Following the calculation of fitness values, offspring population is selected from the parent population according to the fitness values of parent chromosomes. Fitness-proportionate selection has been used in GA-1 algorithm. Half of the offspring population represents father chromosomes, while the other half represents mother chromosomes. Crossover sites are randomly choosen and the single point crossover operator is applied to father and mother chromosome pairs with the probability P_c, thus creating a population of child chromosomes. The crossover probability $P_c \leq 1$,

hence allowing to keep some parent chromosomes in children population with no changes.(default value of $P_c = 0.7$). The process of crossover is followed by the mutation. The probability of mutation P_m is kept very low (default value of P_m=0.001), otherwise genetic algorithms are reduced to a random search. During the process of crossover and mutation, the parent population is replaced with the population of offsprings.

Two generation replacement models have been tested with GA-1 algorithm. Initially, a model using only one father chromosome has been used. We have denoted this model as *one father model.* In one father model, the parent population is copied into the offspring population and the chromosome with the highest fitness in the parent population is selected as a father chromosome. This model preserves the best chromosome in successive generations (population elitism), therefore it can be used to refine the solution that has been found earlier or that has been found by other algorithms. The father chromosome is crossed with other chromosomes in the parent population (mothers) at every possible crossing point resulting in the creation of offspring chromosomes. The frequency response of every offspring chromosome is calculated, then compared with the desired frequency response and finally, the fitness value is calculated. When the offspring chromosome has better fitness than the chromosome with the worst fitness in the parent population, then it replaces the worst chromosome. This process is repeated until all possible combinations of [father | mother] crossing sites are exhausted. Following the process of selection and crossover, the *supervised mutation* operator is applied. This is accomplished by the inversion of every allele for each chromosome. A mutated chromosome is inserted into the offspring population when its fitness is better than the fitness of the worst chromosome. However, we have found that the one father model was very slow and did not produce better results than the traditional generation-replacement model.

The cycle of fitness evaluation, selection, crossover and mutation is repeated until no further improvements in the fitness function are achieved. If no solution is found, the filter length is incremented and the GA-1 algorithm is repeated. Pseudo-code of the proposed filter design algorithm is illustrated in Figure 4.5.

```
Genetic Filter Design ()
begin
        */ filter specification */
        specify the frequency response, filter type and coefficient type
        while no acceptable solution was found do
                create the initial population of chromosomes
                evaluate fitness of chromosomes
                while not converged do
                        for each generation do
                                select parent chromosomes for recombination
                                perform crossover
                                perform mutation
                                evaluate fitness of offspring chromosomes
                                /* generation replacement */
                                replace parent population with offsprings
                        end for
        end while
        /* increment the length of filter and run GA again */
        if no acceptable solution was found
                increment the length of filter
        end if
end while
end
```

Fig. 4.5 Pseudo-code of the GA-1 filter design algorithm

4.2.4 Experimental results

The GA-1 algorithm has been implemented in Matlab and compared with other methods of designing multiplier-less FIR filters. As the aim is to design a filter with the simplest coefficient set while satisfying the filter specification, the number of filter coefficients was choosen as a criterion to compare a performance of different algorithms. Results that have been achieved indicated the superior performance of GA-1 when compared with traditional approaches. Table 4.4 illustrates some of the results that have been achieved using the following methods:

SR: rounding of infinite precisionRemez coefficients to single power-of-two coefficients,

GA-1: single power-of-two coefficients designed by GA-1 algorithm as presented in [Cem93b],

SENS: MSE sensitivity criterion method for 2PWR2 coefficients as presented in [Cem93a],

GA-2PWR2: 2PWR2 coefficients designed by GA-1 algorithm.

Table 4.4 Comparison of the number of coefficients using simple rounding, simple genetic algorithm and coefficient sensitivity design methods

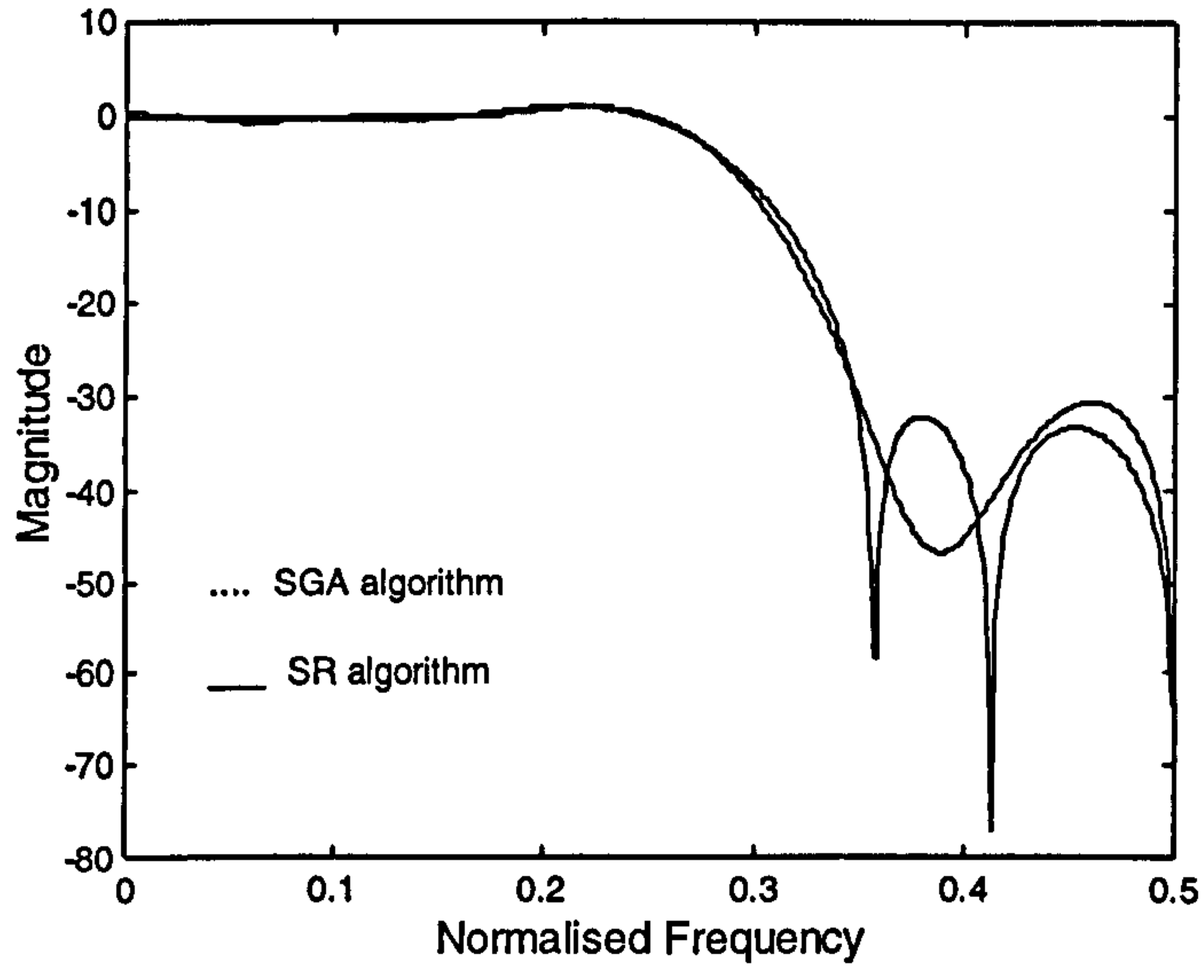
Deign method:	SR	GA-1	SENS	GA-2PWR2
GA-LP1	18	14	14	14
GA-HP1	11	7	5	3
GA-LP2	14	8	6	6
GA-BP1	13	10	9	5

The results in Table 4.4 indicate considerable savings of the total number of filter coefficients required to satisfy the desired frequency response when using the GA-1 algorithm for the filter design. GA-1 algorithm has outperformed the SR method in each case that has been tested.

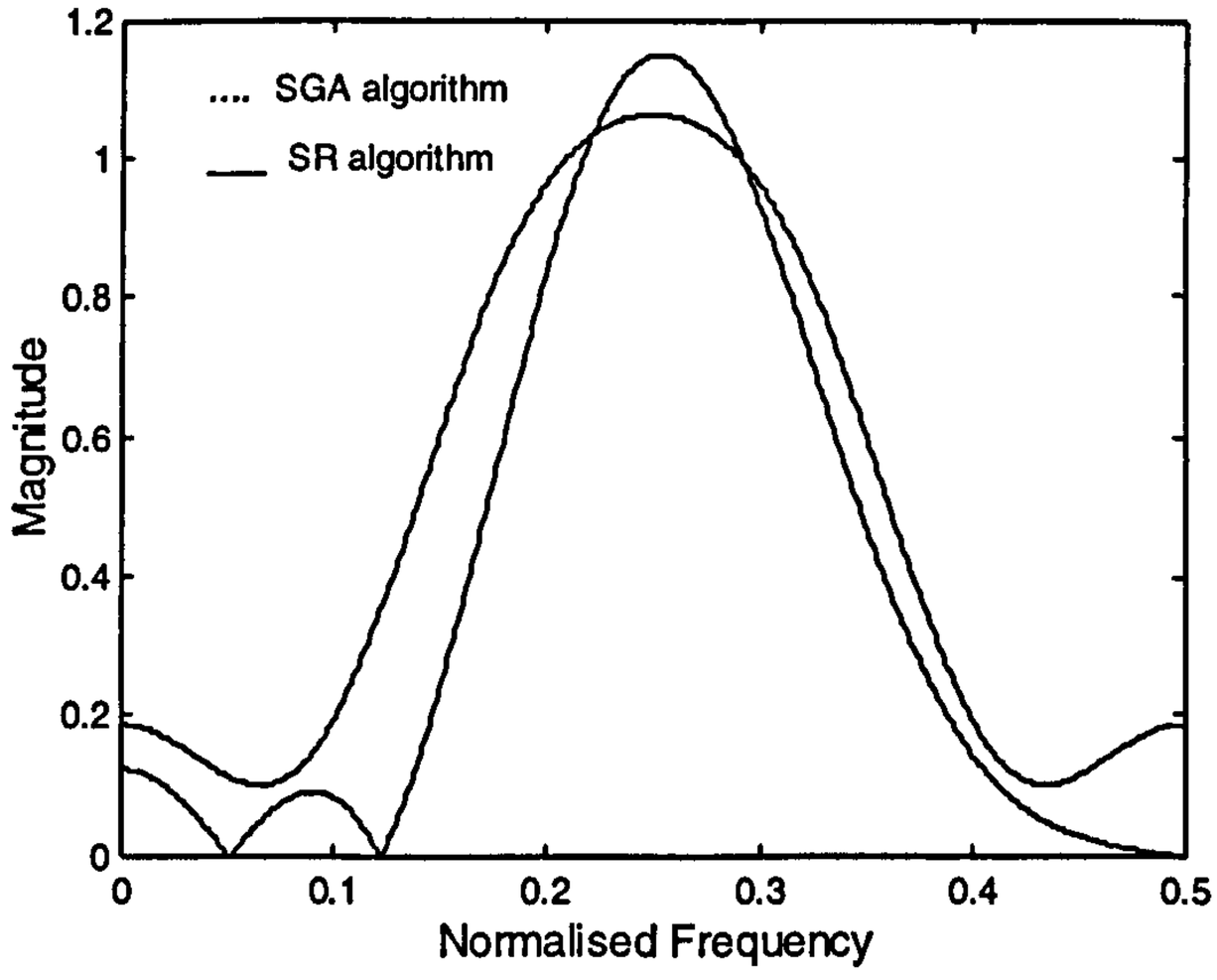
A comparison of the GA-1 algorithm and the sensitivity driven rounding of filter coefficients also shows remarkable results. For instance, the design constraints for the specification GA-LP1 were satisfied using the GA-1 algorithm when the filter length was equal to 14 (single power-of-two coefficients). When using the sensitivity driven rounding, the minimum filter length satisfying the constraints was found again to be 14, but with all coefficients changed to 2PWR2 values. The use of genetic algorithm to design the filter coefficients reduced the filter complexity by 50%. Even better results have been achieved when the GA-1 algorithm has been used to design the set of test filters with 2PWR2 coefficients. An example of the results that have been achieved are presented for filters GA-BP1 and GA-LP1. Table 4.5 illustrates filter coefficients for the filter GA-BP1 that have been designed using all four methods referred above, while the frequency responses for the filter specifications GA-LP1 and GA-BP1 are shown in Figure 4.6.

Table 4.5 Coefficient values for band-pass filter GA-BP1

SR method	GA-1 method	SENS method	GA-2PWR2 method
$h(1) = +2^{-5} = h(13)$	$h(1) = +2^{-4} = h(10)$	$h(1) = +2^{-4} = h(9)$	$h(1) = +2^{-4} = h(9)$
$h(2) = +2^{-15} = h(12)$	$h(2) = +2^{-3} = h(9)$	$h(2) = +2^{-15} = h(8)$	$h(2) = +2^{-15} = h(8)$
$h(3) = +2^{-4} = h(11)$	$h(3) = -2^{-3} = h(8)$	$h(3) = -2^{-2} = h(7)$	$h(3) = -2^{-2} = h(7)$
$h(4) = +2^{-15} = h(10)$	$h(4) = -2^{-2} = h(7)$	$h(4) = +2^{-15} = h\ 6)$	$h(4) = +2^{-14} = h\ 6)$
$h(5) = -2^{-2} = h(9)$	$h(5) = +2^{-2} = h(6)$	$h(5) = +2^{-1} - 2^{-3}$	$h(5) = +2^{-1} - 2^{-3}$
$h(6) = +2^{-15} = h(8)$			
$h(7) = +2^{-1}$			



(a)



(b)

Fig. 4.6 Frequency responses for the GA-LP1 and GA-BP1 filter specifications

4.3 Knowledge-based genetic algorithm

GA-1 algorithm based on SGA model that has been described in previous sections does not require any prior information about the problem being solved. However, in certain situations genetic algorithms can benefit from the additional knowledge that would support the evolution process. Considering the design of multiplier-less FIR filters, the knowledge can be inserted into the initial population in the form of knowledge-based chromosome. This chromosome can be a coefficient vector that has been designed using Remez algorithm or other suitable technique and rounded to the nearest single power-of-two coefficients. The rationale behind this approach is to refine the coefficient vectors that have been acquired by other techniques. Coefficient vector that has been inserted into the initial population can be refined during the evolution process, because genetic algorithm cannot converge to worse chromosome (with lower fitness) as the knowledge-based chromosome. However, the following requirements must be satisfied:

- genetic algorithm should propagate the best chromosome from population to population,
- suitable mechanisms to avoid premature convergence must be implemented.

The first requirement can be implemented within the generation replacement process that must guarantee that the best chromosome is copied from the parent population into the offspring population without changes. The proportion of strings in the population, which is replaced in each generation following the operation of selection, reproduction and recombination, is defined as the *generation gap*. Traditionally, researchers have used generation gap equal to 1 (Goldberg's Simple Genetic Algorithm). It means, that the entire population is replaced in each population. This method of replacement is often referred to as *generational-replacement*. It is not suitable for our purpose, because there is no guarantee that the best chromosome will be always propagated from generation to generation.

The other method, termed as *steady-state replacement* [Sys89, Whi89, Dav91] replaces only a part of the population, usually chromosomes with the lowest or below the average fitness, while preserving the best chromosomes. Preservation of best chromosomes for future generations is referred to as *population elitism*. The steady-state replacement might be a better model of what is happening in nature, because it allows coexistence of parents and offsprings. Goldberg and Deb examined [Gol91] both replacement methods and did not find any replacement method fundamentally better than other. However, for our purpose the steady-state replacement model is more suitable.

The problem of premature convergence is associated with the chromosomes with high fitness values that are well above the average fitness value of the population. These highly fit chromosomes can take over the entire population during the first few generations, causing a convergence to a local maximum (minimum). To avoid the premature convergence, various fitness re-mapping methods have been proposed, including fitness scaling and fitness ranking [Gol89a, Whi89]. Among several fitness scaling and ranking methods, we have choosen linear scaling because of its simplicity.

Linear fitness scaling ensures that the maximum value of the scaled fitness is only 1.5 to 2.0 times higher than the average fitness of the population. In this way, the maximum number of offsprings allocated to highly fit strings is two. The scaled fitness values are calculated as follows:

$$f_{scaled} = af + b \tag{4.32}$$

where a, b are constants which must be calculated in each generation. Constants a, b must be chosen to prevent negative fitness values to be generated.

The pseudo-code of the knowledge-based genetic algorithm for the design of FIR filters (further referred to as GA-2 algorithm) is shown in Figure 4.7. GA-2 algorithm has been tested on the set of filter specifications (Appendix A). Knowledge-based chromosomes were represented as Remez coefficients rounded to nearest single power-of-two terms. Results are shown in Table 4.6 (results shown are for the GA-LP2 example). The improvement of evolution speed has been achieved, when compared with Table 4.3 that shows results for the same experiment, but without the knowledge chromosomes inserted into the initial population. The last row represents the average evolution speed for various gene representation using knowledge-based chromosomes.

Table 4.6 Comparison of evolution speed (knowledge-based genetic algorithm)

Binary representation	Binary representation (*disruptive*)	Gray representation	Gray representation (*disruptive*)	Integer representation
7	9	9	6	5
5	1	10	4	5
8	5	14	13	3
16	7	15	17	17
7	12	7	5	8
10	12	13	19	19
19	4	6	21	30
9	22	19	8	9
4	5	2	16	14
15	8	7	19	20
10.0	8.5	10.2	12.8	13.0

```
Knowledge-based Genetic Filter Design ()
begin
        */ filter specification */
        specify the frequency response, filter type and coefficient type
        while no acceptable solution was found do
                /* create knowledge-based chromosome */
                calculate infinite precision coefficient vector
                round coefficients to nearest single power-of-two
                /* create the population of chromosomes */
                create the initial population of chromosomes
                insert the knowledge chromosome into the population
                evaluate fitness of  chromosomes
                while not converged do
                        for each generation do
                                select parent chromosomes for recombination
                                perform crossover
                                perform mutation
                                evaluate  fitness of offspring chromosomes
                                find elite chromosome
                                steady-state replacement
                                insert elite chromosome into new population
                        end for
                end while
                /* increment the length of filter and run GA again */
                if no acceptable solution was found
                        increment the length of filter
                end if
        end while
end
```

Fig. 4.7 Pseudo-code of the knowledge-based (GA-2) filter design algorithm

4.4 Hybrid GA-SA algorithm

In next section we describe the technique of Simulated Annealing and we discuss improvements that can be achieved by hybridising of Simulated Annealing with genetic algorithms.

4.4.1 Simulated annealing

Simulated Annealing (SA) is a stochastic optimisation technique based on modeling of the physical process of annealing and interactions between particles in systems that consist of a large number of atoms (typically of order 10^{23} atoms per cubic centimeter). Such systems have many degrees of freedom in thermal equilibrium at a finite temperature and the state dynamics of these systems behave according to the theory of statistical and thermal mechanics [Rei65] which states:

The probability that the system is in a state with energy E is proportional to the Boltzmann distribution, $e^{-E/k_B T}$*, where T is the temperature of the bath.*

This statement can be expressed in the equation form:

$$P(E) = exp(-E/k_B T) \tag{4.33}$$

where k_B is Boltzmann's constant.

According to equation (4.33), the system is in equilibrium with high probability when it is in a state of low energy. But this is not a sufficient condition to determine the states of matter. Kirkpatrick *et al.* [Kir83] have shown an analogy between the process of solidifying melted substances and the properties of combinatorial optimisation. For example, when growing a single silicon crystal from a melt, it must be done by careful annealing process which involves melting, lowering the

temperature slowly, allowing enough time to be spent in the vicinity of solidifying point. When this process is not realised properly, the resulting Si crystal will have many defects or will not form a crystalline structure at all.

Metropolis *et al.* [Met53] has developed an algorithm which simulates the process of annealing and uses Monte Carlo techniques. Metropolis algorithm generates a sequence of points in the searching space according to the annealing schedule and the energy values of generated points starting from the initial point x_0 describing the initial configuration of the system. In each step of the algorithm, a new point x_{new} is generated. This corresponds to the random displacement of the atom within the complex system of atoms and results in the change of the energy of the system ΔE. The new point x_{new} is accepted upon Monte Carlo criterion. If the new point x_{new} resulted in the change of energy $\Delta E \leq 0$, that places the system in a state of lower energy, the point x_{new} is always accepted and used as a starting point x_c in the next step. When the change of system's energy $\Delta E > 0$ and the system is placed in a state of higher energy, the new point is accepted with the probability $P(\Delta E)$, which depends on the difference between the energy states ΔE and the temperature T of the system described by:

$$P(\Delta E) = exp(-\Delta E/k_B T) \tag{4.34}$$

By repeating this procedure and lowering the temperature, Metropolis algorithm iteratively converges to the state with the lowest energy corresponding to the optimum point. The optimum point can be a global optimum, but because of the nature of the searching process, it cannot be guaranteed.

The Metropolis algorithm can be applied to the combinatorial optimisation problems, as there is an obvious connection between statistical mechanics and combinatorial optimisation shown by Kirkpatrick in [Kir83]. Hence, simulated annealing has been applied to various optimisation tasks, including VLSI routing and placement,

traveling salesman problem, etc. When applied to the optimisation problems, the change of the energy ΔE of the system is replaced by the cost function to be optimised. A new point x_{new} is accepted, if the Metropolis test [Kir83] is satisfied, i.e. if the cost function decreases:

$$f(x_{new}) \leq f(x_c) \tag{4.35}$$

where x_c is the current point.

However, if

$$f(x_{new}) > f(x_c) \tag{4.36}$$

x_{new} is accepted with the probability p equal to

$$p = exp\left(\frac{f(x_c) - f(x_{new})}{T}\right) \tag{4.37}$$

This corresponds to an uphill move under the control of probabilistic criterion, allowing the algorithm to escape from local minima. By analysing equation (4.37), we can distinguish two limit cases. If the temperature $T>>0$, the probability $p \approx 1$, irrespective of the cost function (system's energy). A new point x_{new} is practically always accepted. As the temperature T approaches zero, $T \approx 0$, states with higher energies are no longer accepted.

The pseudocode of the classic simulated annealing procedure is shown in Figure 4.8. The classic simulated annealing algorithm uses the Boltzmann distribution $exp(-E/k_BT)$. Variations of the classic SA have been reported, replacing the Boltzmann distribution in (4.33) to speed up the algorithm. Szu *et al.* [Szu87] proposed fast annealing algorithm, which replaces the Boltzmann distribution with the Cauchy distribution. Because of the properties of the Cauchy distribution, fast Cauchy

annealing (FCA) have an annealing schedule exponentially faster than classic Boltzmann annealing. Further improvement of FCA was proposed by Ingber [Ing92]. Ingber claims that his method of very fast simulated reannealing (VFSR) is exponentially faster than the fast Cauchy annealing and is also statistically guaranteed to find the function optima.

```
Simulated Annealing ()
begin
        initialise
        for each temperature do
                for number of search moves do
                        create new point x_new=x_c + step
                        if Metropolis test passed then
                                accept new point
                                compare with optimal point x_opt
                        end if
                        adjust step
                end for
                decrease temperature
        end for
        if termination test passed then
                return x_opt
        else
                restart SA from x_opt
        end if
end
```

Fig. 4.8 Pseudo-code of Simulated Annealing procedure

4.4.2 ML FIR filter design using simulated annealing

Because of its hill-climbing properties and the advantage to escape from local minima, several authors attempted to use simulated annealing for design of digital filters. Diethorn *et al.* [Die86] used simulated annealing for of finite wordlength digital filters and his work has been later extended by Benvenuto *et al.* [Ben89a, Ben89b]. Benvenuto *et al.* applied simulated annealing also in design of multiplier-less FIR digital filters [Ben90, Ben92]. However, their approach is based on refining of infinite precision coefficients obtained by Remez algorithm, that might limit searching space that is explored by simulated annealing. We have shown earlier, that genetic algorithm can produce better coefficient vectors than methods that use infinite precision coefficients as a starting point. Finally, Cemes *et al.* proposed simulated annealing as a technique for fine tuning of filter coefficients obtained by genetic algorithm [Cem93d].

We propose a hybrid technique for the design of ML FIR filters based on robust genetic algorithm kernel and simulated annealing operator. Genetic algorithm is used to rapidly explore the discrete space of power-of-two coefficients. We have implemented advanced genetic algorithms using tournament selection [Gol91], two-point crossover [Cav70], linear fitness scaling [Gol89a] and steady-state generation replacement [Dav91] that is retaining the elite chromosome. In each generation, the elite chromosome is selected and simulated annealing is applied. We follow the same annealing schedule as in [Ben92]. Pseudo-code of the proposed hybrid algorithm (GA-3) is shown in Figure 4.9.

```
Hybrid GA-SA Genetic Filter Design ()
    begin
        */ filter specification */
        specify the frequency response, filter type and coefficient type
        while no acceptable solution was found do
        create the initial population of chromosomes
        evaluate fitness of chromosomes
        while not converged do
            for each generation do
                select parent chromosomes for recombination
                perform crossover
                perform mutation
                evaluate fitness of offspring chromosomes
                find elite chromosome
                run simulated annealing on elite chromosome
                steady-state replacement
                insert elite chromosome into new population
            end for
        end while
        /* increment the length of filter and run GA again */
        if no acceptable solution was found
            increment the length of filter
        end if
        end while
    end
```

Fig. 4.9 Pseudo-code of the hybrid GA-SA filter design algorithm

The hybrid GA-3 algorithm was compared with both simple and knowledge-based genetic algorithms. Results have indicated that GA-3 algorithm is superior to GA-1 and GA-2 algorithms, especially for high-order filters. Figure 4.10 illustrates the frequency responses for the low-pass filter LP2 designed using GA-1 and GA-3 algorithms. The dotted line represents the frequency response that has been achieved by using GA-1 algorithm, while the solid line represents the frequency response that have been achieved by fine tuning of the coefficient vector using GA-3 algorithm. A similar frequency response to that obtained with the GA-1 algorithm has been obtained with the GA-2 algorithm.

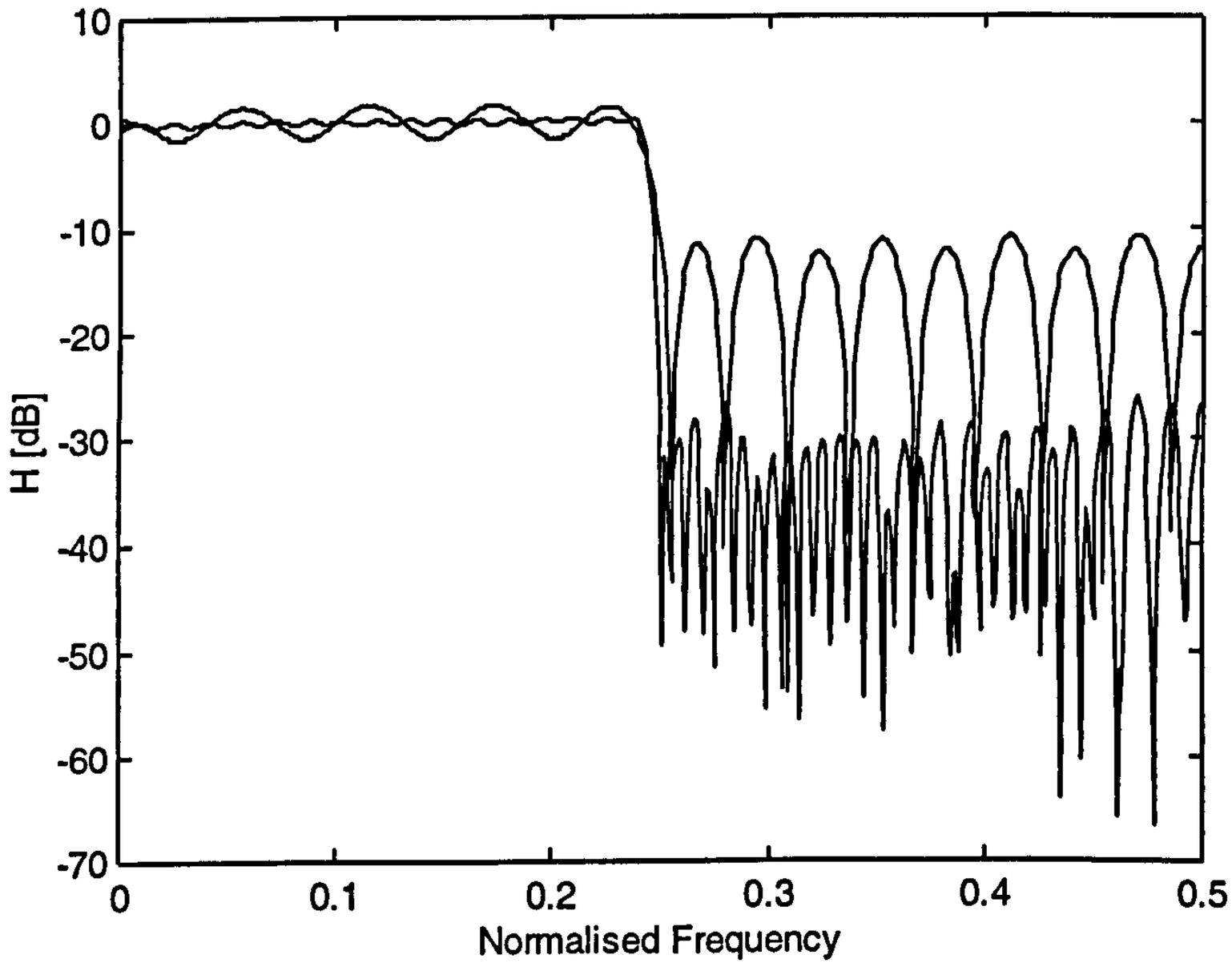


Fig.4.10 Frequency responses of the low-pass filter LP2 designed using GA-1 and GA-3 algorithms

4.5 Conclusions

The results presented in this chapter have shown the superiority of genetic algorithms for the design of FIR digital filters with discrete coefficients limited to power-of-two values. They confirmed our expectations and conclusions drawn in Chapter 3. Although limited to the simple genetic algorithm, the performance of the designed algorithm is dramatic when compared to conventional techniques. Further improvements of the basic technique have been also developed. They include knowledge-based genetic algorithm and hybrid technique based on genetic algorithm kernel using the simulated annealing operator that outperform design techniques based on a simple genetic algorithm mainly for high-order filters.

Chapter 5

Prediction of minimum filter length

Several methods for multiplier-less FIR filter design have been described in previous chapters. The majority of the design methods are iterative in a sense that the minimum filter length that is required to satisfy the filter specification is not known in advance. In this chapter, we attempt to fill-in this knowledge gap and to devise a formula that would predict the minimum number of power-of-two coefficients. The techniques of genetic programming and symbolic regression are used to evolve the formula describing the relationship between the filter length and its specification. The rest of this chapter is organised as follows. First, Kaiser's empirical formula that is used to estimate a number of infinite precision filter coefficients is described. The technique of genetic programming and symbolic regression is briefly introduced next. Section 6.3 describes our experiments and the results achieved. The chapter finishes with conclusions.

6.1 Kaiser's formula

A common drawback of all methods for the design of filters with power-of-two coefficients is that the filter length is not known prior to the design procedure. Therefore most designers adopted iterative design approach where design algorithms operate between lower and upper boundaries on the filter length. The upper boundary is set to the highest filter length that is still acceptable. The lower bound is estimated using the empirical formula that has been devised by Kaiser and can be found in classic DSP textbooks [Rab75]. Kaiser's formula has two different forms depending on whether the windowing design method (5.1) or equiripple design method (5.2) has been used:

$$N = \frac{-20\log_{10}\delta - 7.95}{14.36\Delta f} + 1 \tag{5.1}$$

$$N = \frac{-20\log_{10}\sqrt{\delta_1\delta_2} - 13}{14.6\Delta f} + 1 \tag{5.2}$$

where δ_1, δ_2 are the frequency response ripples (they might be different when the equiripple design method is used) and Δf is the width of the transition band.

It should be noted that Kaiser's empirical formulas (5.1) and (5.2) have been devised for infinite-precision coefficients. When filters are realised using power-of-two coefficients only, the minimum number of coefficients is usually much higher, rendering (5.1) and (5.2) only partially useful. Another disadvantage associated with the use of (5.1) and (5.2) in the design of PWR2 filters is that the widely adopted iterative approach starting from lower boundary on filter length is both time consuming and costly. If some formula estimating the minimum filter length from the filter specification would be known, it could save many unnecessary iterations independently of the design method. This would be particularly useful for higher

order filters. We attempt to evolve such formula using the techniques of genetic programming and symbolic regression that are described next.

5.2 Genetic programming and symbolic regression

Genetic programming (GP) can be thought as an extension of genetic algorithms into the space of computer programs. It has been devised and developed only recently by Prof. Koza [Koz92]. The thorough description and recent developments in the field of genetic programming can be found in [Koz92, Koz94 and Kin94]. Essentially, genetic programming is an evolution process in which computer programs are being evolved. The main difference between GAs and GP is that while genetic algorithms operate with fixed length linear chromosomes, genetic programming works with a population of computer programs that are represented as chromosomes of variable length having usually tree-like structure. The result of genetic programming is not a value (or a set of values), but a computer program that is able to solve some problem. Initially, a population of computer programs is created using the set of *terminals* (input and output variables and constants) and the set of *functions* (add, subtract, divide, multiply, sin, logarithm, etc.). No encoding and decoding functions are required as genetic programming operates directly with the population of computer programs. Each computer program in the population must satisfy the *closure* condition, i.e. situations that could result in errors (division by zero, etc.) must be avoided. Genetic programming does not require the fitness function. Instead, individual programs are executed to evaluate their fitness values that reflect "how well" particular programs are able to solve the problem. This is the most important and non trivial part when implementing genetic programming. The process of program execution and fitness evaluation is followed by selection and recombination. Genetic programming uses similar selection methods to those used in genetic algorithms. The recombination process in genetic programming differs from genetic algorithms as a crossover operator has been replaced by the tree structure crossover.

The process of program execution, fitness evaluation, selection and recombination is repeated for a given number of generations. With the exception of program execution stage, the process is identical to genetic algorithms. Pseudo-code of genetic programming is illustrated in Figure 5.1, while the tree structure crossover is shown in Figure 5.2.

```
Genetic Programming( )
begin
  identify set of functions and terminals
  randomly create population of computer programs
  while termination criterion is not satisfied do
     for each generation do
           execute each program to evaluate its fitness
           for each program do
              select genetic operator (crossover,mutation,reproduction)
              perform genetic operator
           end for
     end for
  end while
end
```

Fig. 5.1 Pseudo-code of genetic programming

Genetic programming has been successfully applied to a wide range of problems that are difficult to solve, including prediction of protein characteristics, forecasting of the weather, automatic programming, image compression, etc. Amongst a number of successful applications of genetic programming, we are particularly interested in *symbolic regression* (SR) described by Koza [Koz92]. Koza defines symbolic regression as "*seeking for a mathematical expression that would approximately fit a given sample of data*". Symbolic regression is different from the polynomial

regression where the function is known beforehand and only the polynomial coefficients are calculated. Symbolic regression attempts to construct a mathematical expression that would express the relationship between the input and output data (training set) as closely as possible. The application of symbolic regression to discover the relationship between the filter specification and the number of power-of-two coefficients is described in the next section.

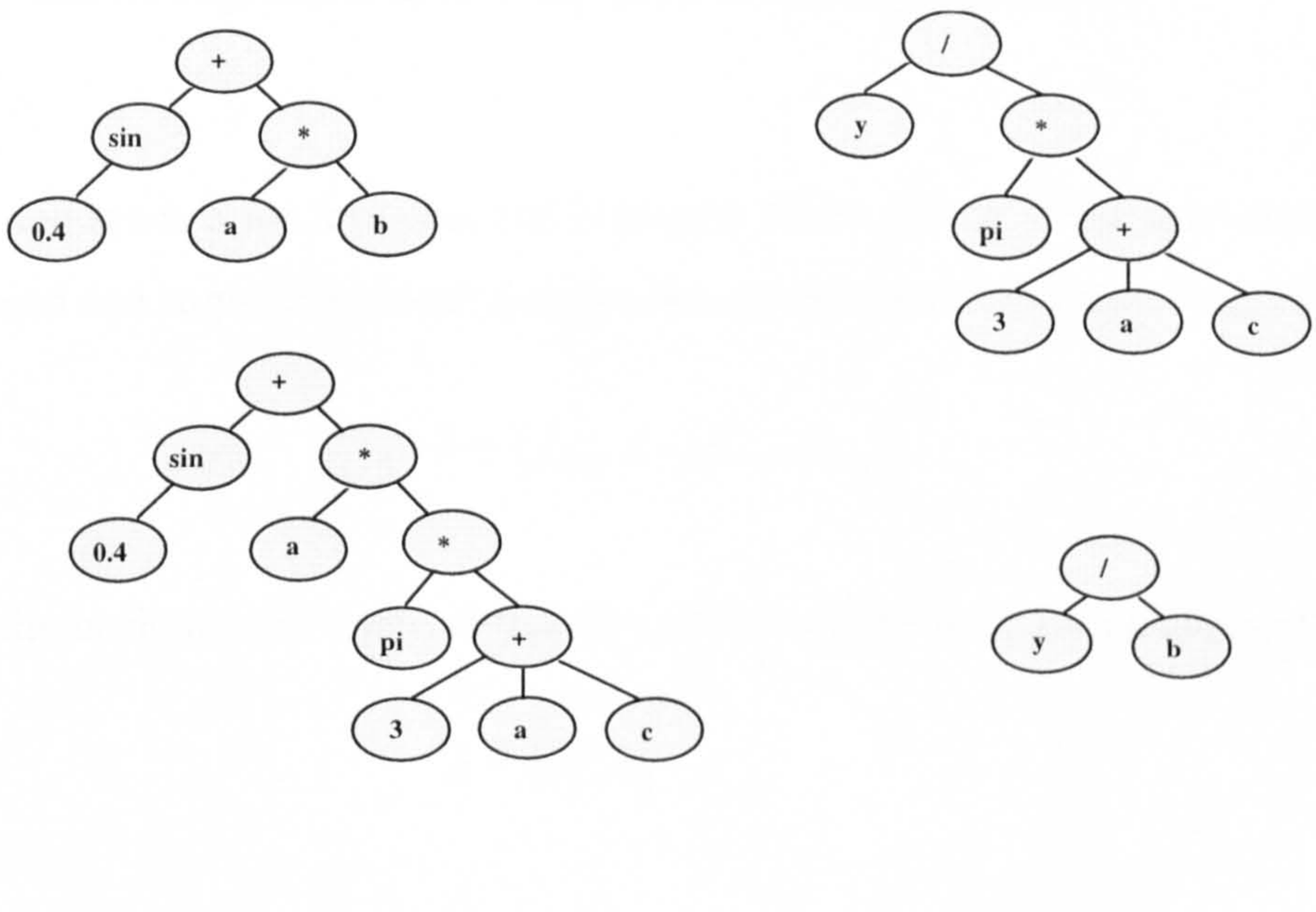


Fig. 5.2 Tree structure crossover

5.3 Implementation of experiments

The following requirements must be satisfied prior to the experiments with symbolic regression:

- a training set (sample of input and output data) must be designed
- genetic programming system must be compiled to perform N-dimensional symbolic regression.

As we are interested in an expression that would describe the relationship between the filter specification and its length, we must provide the symbolic regression system with the training set containing various examples of filter designs. We have chosen simple rounding of infinite precision Remez coefficients to the nearest single power-of-two coefficients as the design algorithm to construct the training set. The main criterion for choosing this algorithm was its simplicity and the speed, as extensive training sets are required to sample the space of filter specifications.

The design space S for low-pass and high-pass filters can be either four-dimensional (pass-band and stop-band cut-off frequencies and pass-band and stop-band ripples):

$$S = \left\{ f_{pass}, f_{stop}, \delta_{pass}, \delta_{stop} \right\} \tag{5.3}$$

or two-dimensional (the width of transition band and the max. ripple allowed):

$$S = \{ \Delta f, \delta \} \tag{5.4}$$

We have constructed three different training sets sampling the design space S of low-pass and high-pass filters in broad range of cut-off frequencies and band ripples. The set $S1$ contained 3,487 different low-pass filter specifications of type (5.3), the set $S2$ contained two-dimensional equivalent of the set $S1$ and the set $S3$ contained 3,018 different high-pass filter specifications of type (5.4). To construct these training sets we have performed 6,505 different filter designs in total. This took several days with the design algorithm written in Matlab running on Pentium 120 Mhz processor. The next step before the evolution process can be started is to choose and compile suitable symbolic regression system. We have chosen N-dimensional symbolic regression that has been compiled with the following set of functions: ADD, SUBTRACT, MULTIPLY and DIVIDE. For simplicity reasons, no other functions were realised at this time.

Upon completion of these preparatory steps, the process of five-dimensional (for the set $S1$) and three-dimensional (for the sets $S2$ and $S3$) symbolic regression has been performed. Symbolic regression in terms of memory and execution time is extremely costly process. The time to finish our experiments varied from 8 to 14 days as shown in Table 5.1. Each experiment has been repeated six times to produce more results that would allow us to choose the most suitable expression and to compare different runs. The results are analysed in the next section.

Table 5.1 Comparisons of SR runs

Dataset	*Training set cardinality*	*Training set size*	*Time to complete SR*
$S1$	5	3,487	14 days
$S2$	3	3,487	9 days
$S3$	3	3,018	8 days

5.4 Analysis of results

The mathematical expressions resulting from the application of symbolic regression to the training sets $S1$, $S2$ and $S3$ are rather complex. This is because symbolic regression does not simplify the evolved expressions from generation to generation. This does not constitute a problem as we were mainly interested whether the expression describing the relationship between the filter specification and its length could be attained using the symbolic regression. We have performed the error analysis of the resulting expressions to evaluate how close the evolved expressions approximate the given training sets. For this purpose, the error has been defined as the difference between the actual filter length and its estimated length.

The error analysis of six different expressions that have been evolved by the five-dimensional symbolic regression using the training set S1 is shown in Figure 5.3.

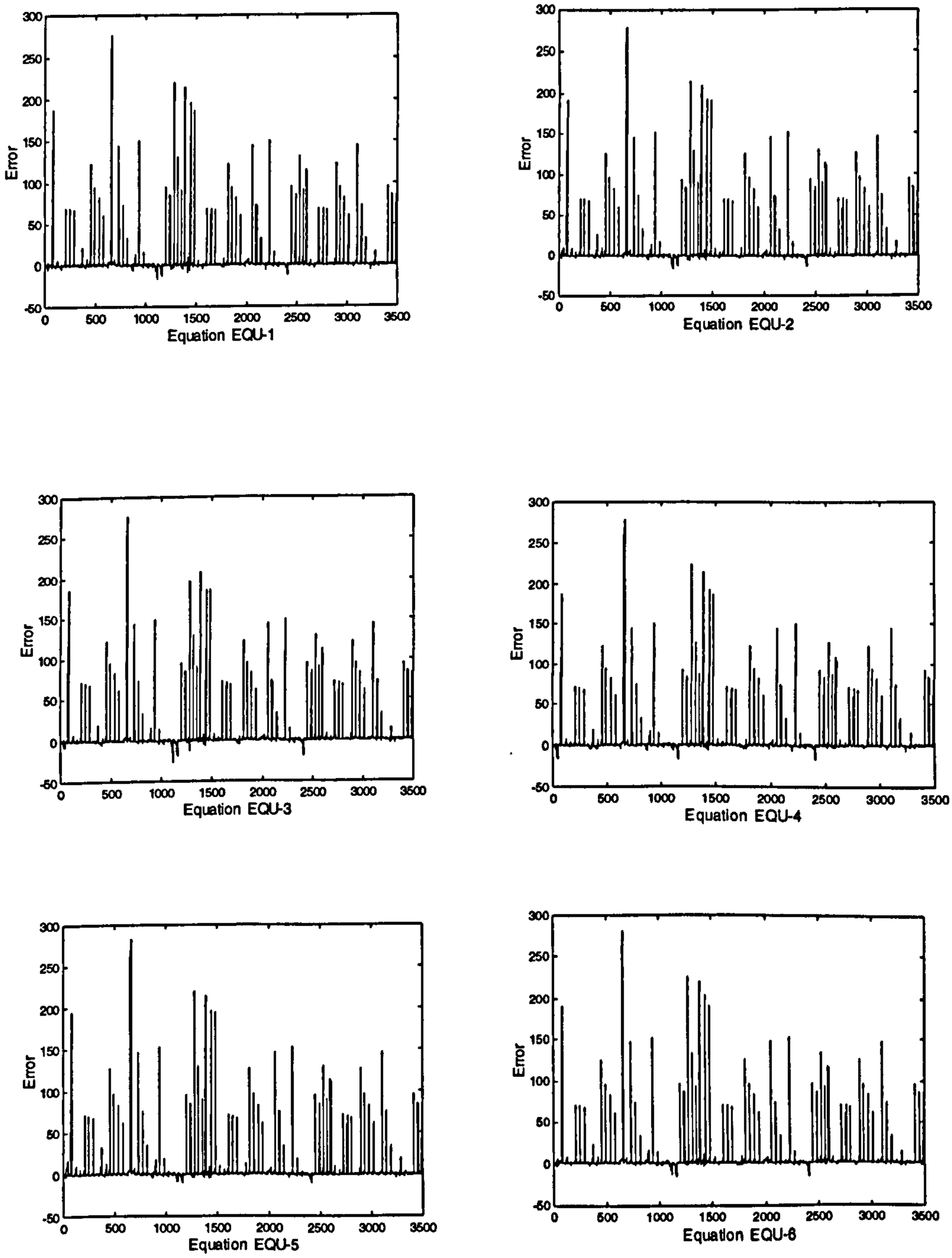


Fig. 5.3 Error analysis of expressions EQU-1 to EQU-6 for estimating the filter length for low-pass filters (five-dimensional training set)

Studies of the error analysis and the corresponding training sets have shown that large errors, represented as peaks in Figure 5.3, have occurred mainly for high-order filters. As the high-order filters (with the actual filter length bigger than 50) represented less than 5% of the entire training set, we have removed them from the training set $S1$ and re-evaluated the error analysis. In these circumstances the evolved expressions produced more realistic results. The maximum and average errors for the expressions EQU-1 to EQU-6 are shown in Table 5.2. The error analysis for the expression EQU-3 that yields in lowest errors is illustrated in Figure 5.4.

Table 5.2 Maximum and average errors following the removal of high-order filters

Expression	*Maximum error*	*Average error*
EQU-1	32.60	0.2162
EQU-2	33.35	0.2387
EQU-3	32.22	0.0988
EQU-4	32.76	0.1600
EQU-5	33.70	0.4355
EQU-6	34.31	2.3418

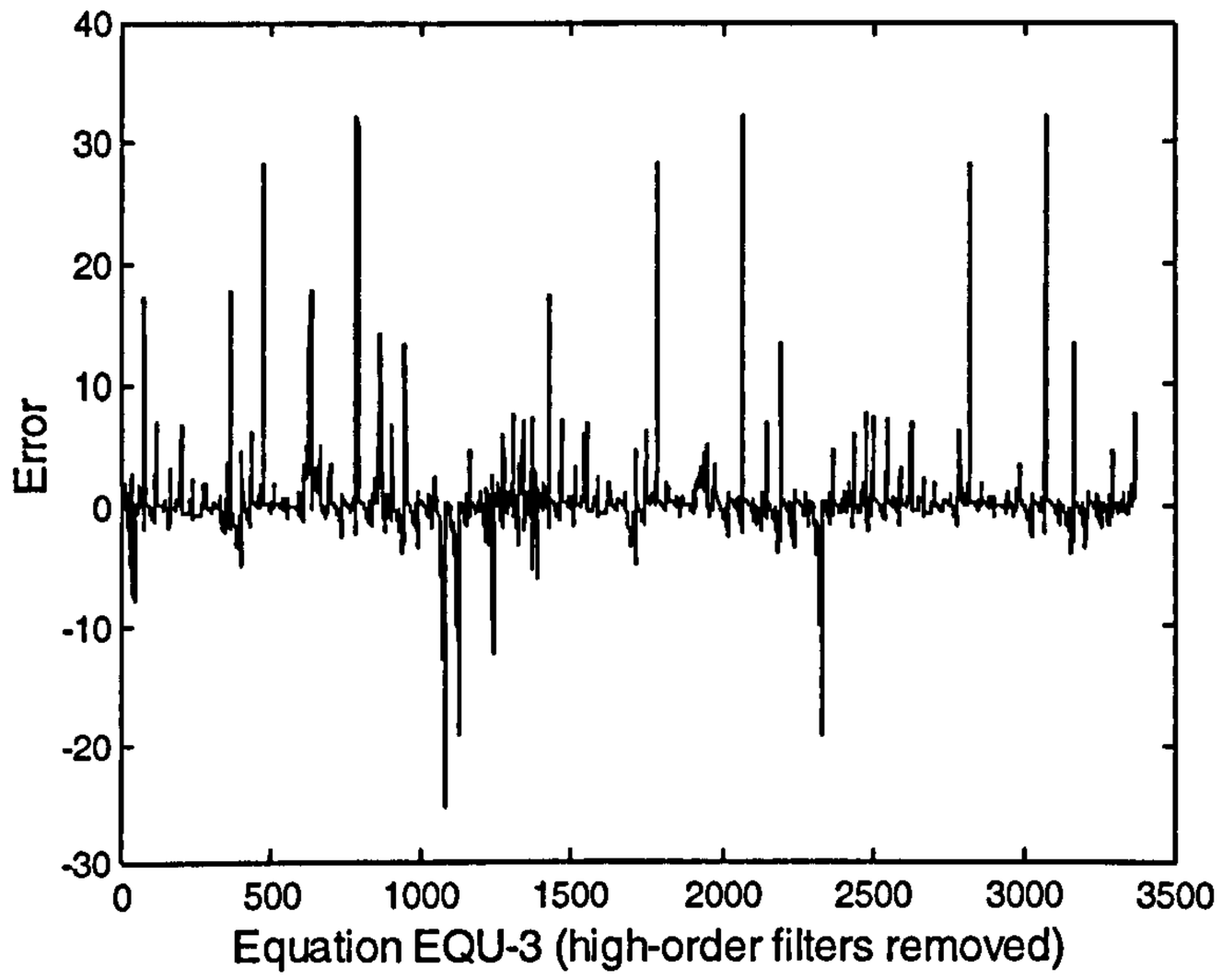


Fig 5.4 Error analysis of expression EQU-3 following the removal of high-order filters

The equation EQU-3 evolved by the five-dimensional symbolic regression using the training set *S*1 that contained 3,487 filter designs is as follows:

$$
\begin{aligned}
N_{estimated} = \; & (f_{stop}-f_{pass}) - (((f_{pass}/(2*(f_{stop}-f_{pass})))*f_{pass})/f_{stop}) + f_{stop} \\
& + (((f_{stop}-2*f_{pass})-(f_{pass}/\delta_s))-((f_{pass}/f_{stop})/(f_{stop}*f_{stop})))/6 \\
& + \; f_{pass}/(f_{stop}*\, f_{stop}*\delta_s) + 2*\delta_p - f_{pass}/f_{stop} \\
& + \delta_p/((f_{stop}-((f_{pass}/f_{stop})/(f_{stop}*f_{stop})))/f_{stop})) + (((f_{stop}*(f_{stop}/f_{pass}))-f_{pass}) \\
& + (((f_{pass}/(((f_{stop}-f_{pass})-(f_{stop}*f_{stop}))+\delta_s))*f_{pass})/(f_{stop}-f_{pass})) \\
& + ((\delta_s-((f_{pass}/\delta_s)*f_{pass}))-f_{stop})/(2*\delta_s)
\end{aligned}
\tag{5.5}
$$

The equation (5.5) has been tested with the set of filters not contained in the training set. Table 5.3 shows comparisons between the actual filter length, the filter length estimated using the Kaiser's formula and the equation (5.5) evolved using symbolic regression.

Table 5.3 Comparison of Kaiser formula, Maximum and average errors following the removal of high-order filters

f_{pass}	f_{stop}	δ_p	δ_s	N_{Kaiser}	$N_{estimated}$	N_{actual}
0.02	0.2	0.1	0.1	4	6	15
0.2	0.3	0.2	0.2	2	10	10
0.2	0.4	0.1	0.1	3	10	10
0.316	0.432	0.18	0.10	4	38	16
0.316	0.432	0.18	0.12	3	25	20
0.183	0.375	0.1	0.1	4	11	14

5.5 Conclusions

This chapter presents the application of symbolic regression to discovery of filter length when the filter coefficients are restricted to single power-of-two only. Several expressions describing approximate relationship between the filter specification and its length have been evolved. The error analysis has shown that the results are reasonably good for low-order filters (filter length $N \leq 30$). Although the training set for symbolic regression contained large amount of data, higher order filters ($N>30$) represented less than 5% of the training set. This could explain large difference

between the actual and estimated filter length for higher order filters. Further work is required to evolve a simplified expression that would achieve high accuracy. However, any of the evolved equation EQU-1 to EQU-6 can be included in any design technique for filters with single power-of-two coefficients in the present form. To increase the accuracy of the expressions, two alternatives are possible, including adding more functions into the function set and using better methods to generate the training set. This constitutes the aim of our future research.

Chapter 6

Conclusions and future work

The aim of this chapter is to review achievements that have been made and the contribution of this research work to the field of multiplier-less FIR filter design. Novel approaches to the design of multiplier-less FIR filters with coefficient vectors limited to power-of-two terms that have been proposed in this thesis can be classified into three separate classes:

- improvements of calculus-based design methods,
- design of ML FIR filters based on evolutionary algorithms,
- evolution of the formula for estimation of ML FIR filter length.

The advances that have been made and the limitations of the developed algorithms are analysed in the next section. The chapter concludes with a suggestions for further research to enhance proposed techniques.

6.1 Summary of the results

Two novel design techniques have been developed following the analysis of available calculus-based methods. The first technique has been referred to as *evolutionary local search* (ELS). ELS is a combination of exhaustive search with a refined local search technique. The algorithm differs from the majority of calculus-based techniques as it does not require the initial set of infinite-precision filter coefficients as a starting point. Although the algorithm is simple in its principle, it can design *optimal* low-order ML FIR and sub-optimal higher-order filters. It has outperformed the traditional rounding of infinite-precision filter coefficients.

The second technique has been termed as *MSE coefficient sensitivity based rounding*. In our view, this technique represents development of one of the best classic design techniques for ML FIR filter design available. We have suggested improvements to the basic technique to include among other types the design of filters with multiple-bands. Major improvements stem from the replacement of the original sensitivity criterion with the mean square error sensitivity criterion. The results that have been achieved and presented have demonstrated the superiority of this design technique. However, both ELS and MSE coefficient sensitivity based rounding techniques are able to produce only suboptimal designs as they limit searching to the vicinity of the starting vector.

Our work in the field of multiplier-less FIR filter design using genetic algorithms represents one of the earliest works in the field. Several novel algorithms, named as GA-1, GA-2 and GA-3, have been proposed. The kernel of these algorithms is based on a simple genetic algorithm model. The GA-1 algorithm uses unique encoding scheme that guarantees that each population contains only valid chromosomes without adverse effects on the performance of genetic algorithm. The GA-1 algorithm has been compared with other techniques, namely with the rounding of infinite precision coefficients based on MSE coefficient sensitivity criterion. Results have indicated that the GA-1 algorithm has greatly outperformed traditional ML FIR

filter design techniques as further reduction of the filter complexity has been achieved. It has to be stressed at this point that the filter vectors that have been designed using GA-1 algorithm could not be designed using other techniques that are based on rounding of infinite precision coefficients, as these techniques limit the searching space to the vicinity of infinite precision coefficients only. The power of the GA-1 algorithm to explore the entire searching space is its main advantage opposite calculus-based algorithms. Even better results have been achieved with GA-2 algorithm that uses inserting of knowledge-based chromosome into the initial population. Here, the knowledge based chromosome represents a Remez coefficient vector rounded to nearest single power-of-two coefficients. To overcome the problem of premature convergence, fitness scaling has been applied.

Hybrid evolutionary techniques are represented by GA-3 algorithm. The kernel of GA-3 algorithm embodies powerful genetic algorithm with a class of advanced genetic operators and simulated annealing. Here, the main genetic kernel is used to explore searching space rapidly, while simulated annealing is applied to refine the solution that has been obtained with genetic algorithms. GA-3 algorithm outperforms GA-1 and GA-2 mainly for higher-order filters. However, there is a price to be paid for the algorithm's ability to explore N-dimensional searching space as many control parameters have to be tuned.

A common drawback of all design methods that have been presented is that the filter length, i.e. the number of coefficients that is required to satisfy the filter specification, is not known beforehand. Instead, lower and upper boundaries on the filter length are specified and design techniques work iteratively within these boundaries. It would be advantageous to have a formula that would be able to estimate the filter length from its specification. In the last chapter, we have shown that it is possible to evolve such formula using the technique of genetic programming and symbolic regression. Although the expression that has been evolved is rather approximate, it does compare very well with Kaiser's formula that is used in majority of FIR filter design methods, either calculus-based or based on evolutionary algorithms. The

accuracy of the formula can by further improved either by extending the function set that is used by symbolic regression or using mixed integer linear programming to create a training set that would contain optimal coefficient vectors.

6.2 Further work

The aims of this research work as stated in Chapter 1 have been accomplished. However, the research has uncovered some problems that need to be addressed. We have shown that genetic algorithms are robust optimisation techniques, but they can suffer from undesired effects, such as premature or slow convergence. To overcome these problems, we suggest to use robust genetic kernels based on distributed genetic algorithms (DGA) described by Tanese in [Tan89]. Distributed genetic algorithms operate with several populations of chromosomes, with each population having different control parameters and using different genetic operators. Initially, there is no interaction between the populations. After a pre-specified number of generations, the average fitness values of different populations are compared and genetic operators that are related to the best performing population are selected for further evolution process.

Finally, the use of genetic programming for the design of multiplier-less FIR filters should lead to further improvements, as the filter coefficients and the filter architecture can be evolved at the same time. The approach using genetic programming would further benefit from variable length chromosome representation, effectively exploring the searching space between lower and upper boundaries in highly parallel fashion. The novel techniques that have been presented in this thesis can be also extended to the design of multiplier-less infinite impulse response filters.

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Appendix A

Filter specifications

Filter type	Number of bands	Cutoff frequencies (f)	Desired freq. resp. (D)	Attenuation [dB]	Maximum error allowed (δ)
Bandpass BP1	3	0 - 0.22, 0.24 - 0.26, 0.28 - 0.5	0, 1, 0	> -26 dB	0.05, 0.03, 0.05
Multiple bands MB1	6	0 - 0.05, 0.10 - 0.15, 0.20 - 0.23, 0.27 - 0.30, 0.35 - 0.4, 0.45 - 0.5	1, 0, 1, 0, 1, 0		0.1, 0.1, 0.1, 0.1, 0.1, 0.1
Multiple bands MB2	7	0 - 0.04, 0.08 - 0.12, 0.16 - 0.22, 0.245 - 0.275, 0.30 - 0.34, 0.38 - 0.42, 0.46 - 0.5	1, 0, 1, 0, 1, 0, 1		0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1
Lowpass LP1	2	0 - 0.27, 0.31 - 0.5	1, 0		0.02, 0.02
Lowpass LP2	2	0 - 0.24, 0.25 - 0.5	1, 0		0.05, 0.05

Table A.1 Some examples of filters designed using modified sensitivity criterion

Filter type	Number of bands	Cutoff frequencies (f)	Desired freq. resp. (D)	Weighting function W)	Maximum error allowed (δ)
Low-pass GA-LP1	2	0 - 0.25, 0.35 - 0.5	1, 0	1, 10	0.125, 0.032
High-pass GA-HP1	2	0 - 0.1218, 0.377 - 0.5	0, 1	1, 1	0.1, 0.1
Low-pass GA-LP2	2	0 - 0.1875, 0.4011 - 0.5	1, 0	1, 1	0.1, 0.1
Band-pass GA-BP1	3	0 - 0.1, 0.2 - 0.3, 0.4 - 0.5	0, 1, 0	1, 1, 1	0.2, 0.2, 0.2

Table A.2 Filter specifications used with simple genetic algorithm

Appendix B

List of published work

Cemes, R., and Ait-Boudaoud, D.: 'Modified sensitivity criterion for the design of powers-of-two FIR filters', *Electronics Letters*, Vol.29, No.16, August 1993, pp.1467-1469

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