

# FIR Filter Design via Linear Complementarity Problem, Messy Genetic Algorithm, and Ising Messy Genetic Algorithm

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**Abstract**—In this paper the design of maximally flat linear phase finite impulse response (FIR) filters is considered. The problem is handled with totally two different approaches. The first one is completely deterministic numerical approach where the problem is formulated as a Linear Complementarity Problem (LCP). The other one is based on a combination of Markov Random Fields (MRF's) approach with messy genetic algorithm (MGA). Markov Random Fields (MRFs) are a class of probabilistic models that have been applied for many years to the analysis of visual patterns or textures. Our objective is to establish MRFs as an interesting approach to modeling messy genetic algorithms. We establish a theoretical result that every genetic algorithm problem can be characterized in terms of a MRF model. This allows us to construct an explicit probabilistic model of the MGA fitness function and introduce the Ising MGA. Experimentations done with Ising MGA are less costly than those done with standard MGA since much less computations are involved. The least computations of all is for the LCP. Results of the LCP, random search, random seeded search, MGA, and Ising MGA are discussed.

**Keywords**—Filter design, FIR digital filters, LCP, Ising model, MGA, Ising MGA.

## I. INTRODUCTION

THE linear phase finite impulse response (FIR) filters are very important since they are highly required in applications where the linear phase restriction is crucial. Due to the linear phase restriction the design of these filters is converted to real approximation problem. The problem of designing such types of filters has been studied extensively and solved using a number of different methods [1]–[12]. Vaidyanathan and Nguyen [2] used a minimization of a quadratic measure of the error in the pass-band and stop-band. This method is based on the computation of eigenvector of an appropriate symmetric and positive definite matrix. In reference [3] the Lagrange multipliers were applied in the design of FIR filters. Er and Siew [4] applied a quadratically constrained quadratic programming method. In this method the mean-square error between the desired response and the

filter response over the pass-band of interest is subject to a mean-square stop-band constraint. In the previous methods the numerical techniques were iterative. The bulk of the design computation in these methods is concerned with a matrix inversion in order to solve a system of equations. One of the methods used in the present paper is the formulation of the problem as a Linear Complementarity Problem (LCP). The given rise problem can be solved with iterative algorithms [27] or a direct algorithm such as Lemke's algorithm [26].

In designing of optimal FIR filters, it is necessary to optimize a desired frequency response by minimizing an error norm. The mean-square error in the pass-band and stop-band are combined through a convex combination in order to obtain the objective function of the minimization problem. The flatness conditions are applied to form the constraints of the optimization problem.

The filter coefficients are written as a difference of two nonnegative coefficients in order to formulate the problem in a compact form as a Linear Complementarity Problem (LCP). This extends the results of the work of Hanna [13] where the minimization problem is solved using Lagrange multipliers. The presented formulation can be solved using many different iterative algorithms (see [26]).

Markov Random Fields (MRFs) [14]–[17], on the other hand, are a class of probabilistic models. They have been applied for many years to the analysis of images specially pattern recognition and detection. Probabilistic information is used to characterize particular pixel values in terms of their neighbors. Moreover, MRF theory may be used for analyzing spatial or contextual dependencies. We investigate a MRF approach to modeling messy genetic algorithms (MGA's). The motivation behind this is the fact that chromosomes in the MGA population are, after all, a sequence of patterns that are controlled by the fitness function. Moreover, the order of the coefficients for the FIR filter is very important; any alteration in the coefficients sequence may change the whole characteristics of the filter. The most important thing is that patterns of order similarities are noticed among the FIR filter coefficients, especially for linear phase filters. These similarities require a fitness that is directly related to the structure of the chromosomes and not their phenotypes only. Messy genetic algorithms are different than standard genetic algorithms in their ability to deal with chromosomes with different lengths within a single population, and hence exploit various patterns and similarities. The least computations of all

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is that for the LCP. Results of the LCP, random search, random seeded search, MGA, and Ising MGA are discussed.

The paper is structured as follows. In section II we provide a description of the problem formulation necessary to build the cost function and its associated constraints. In section III, the LCP is formulated in a compact form, and in section IV the LCP is solved using Lemke algorithm. Examples solved with this method are shown. In section V, the second part of the paper is handled. Here, an MGA problem description as an instance of the Labeling Problem is presented. We also prove a theorem showing that every MGA encoding can be modeled as a Markov Random Field with respect to some neighborhood relation on the chromosome alleles. The theorem also establishes an explicit relationship between the MRF parameters and the MGA fitness function. In section V, we focus on MRF modeling of MGA, in section VI, we deduce the Ising MGA model. In section VII, we show some experiments on the FIR filter design using the Ising MGA model and standard MGA model. Discussions of these two methods and the LCP method are presented in section VIII.

## II. PROBLEM FORMULATION

An FIR filter with length  $N$  has a frequency response given by

$$H(\omega) = \sum_{n=0}^{N-1} h(n)e^{-jn\omega} \quad (1)$$

where the values of impulse responses  $h(n)$  may be complex or real numbers. In this paper, the impulse responses are assumed to be real. If  $h(n)$  satisfies some symmetry constraints, then  $H(\omega)$  has linear phase response and can be written as

$$H(\omega) = A(\omega)e^{-jM\omega} \quad (2)$$

where  $A(\omega)$  is a real-valued amplitude. Real coefficients linear phase filters are classified into four types. These types depend on symmetry of the impulse responses and on whether the filter length is even or odd [24-25]. For each type the amplitude function  $A(\omega)$  can be expressed as follows

$$A(\omega) = \sum_{n=0}^{N-1} a_n \Phi_n(\omega) \quad (3)$$

where  $\Phi_n(\omega)$  is a set of appropriate trigonometric functions depends on the filter type and  $M$  is the number of the independent coefficients in the filter. The filter design problem is approximated to a given frequency response. That is, to find the coefficients  $a_n$  such that the amplitude response  $A(\omega)$  is close to a given amplitude response  $A_d(\omega)$ . If the performance of the filter is controlled precisely for obtaining a good approximation for maximally flat frequency response the following flatness condition is applied

$$\frac{d^k}{d\omega^k} A(\omega_m) = \frac{d^k}{d\omega^k} A_d(\omega_m) \quad (4)$$

for  $k = 0, 1, \dots, K - 1$  at a given frequency point  $\omega_m$  where  $K$  is called the degree of flatness. The constraints obtained from equation (4) can be expressed in compact form as follows:

$$\mathbf{C}\mathbf{a} = \boldsymbol{\eta} \quad (5)$$

where  $\mathbf{C} \in \mathbb{R}^{K \times M}$ ,  $\mathbf{a} = [a_0 \ a_1 \ \dots \ a_M]^T$  represents the independent coefficients vector of the filter. The weighted mean-square error in the passband can be expressed as

$$E_p = \int_p W(\omega) |A(\omega) - A_d(\omega)|^2 d\omega \quad (6)$$

where  $W(\omega)$  a positive weighting function and the subscript  $p$  denotes pass-band. Using (3) and (6) the weighted mean-square error in the stop-band can be written as follows:

$$E_p = \mathbf{a}^T \mathbf{Q}_p \mathbf{a} \quad (7)$$

The weighted mean-square error in the stop-band is given by the relation

$$E_s = \int_s W(\omega) |A(\omega)|^2 d\omega \quad (8)$$

where the subscript  $s$  denotes stop band. Using (3) and (8) the weighted mean-square error in the stop-band can be expressed as

$$E_s = \mathbf{a}^T \mathbf{Q}_s \mathbf{a} \quad (9)$$

The mean-square errors in the pass-band and stop-band can be combined through a convex combination. Let  $\alpha \in [0, 1]$ , the convex combination is given by [13]

$$E = \alpha E_s + (1 - \alpha) E_p \quad (10)$$

Substituting (7) and (9) in (10), the following is obtained

$$E = \mathbf{a}^T \mathbf{Q} \mathbf{a} \quad (11)$$

where

$$\mathbf{Q} = \alpha \mathbf{Q}_s + (1 - \alpha) \mathbf{Q}_p \quad (12)$$

For the convenience of formulation the coefficient vector  $\mathbf{a}$  can be written as a difference of two nonnegative vectors

$$\mathbf{a} = \mathbf{a}^+ - \mathbf{a}^- \quad (13)$$

where

$$\mathbf{a}^+ = \frac{\mathbf{a} + |\mathbf{a}|}{2} \geq 0, \text{ and } \mathbf{a}^- = \frac{\mathbf{a} - |\mathbf{a}|}{2} \geq 0$$

Using equations (5) and (13) the flatness constraints can be written as follows:

$$\mathbf{B}\mathbf{x} = \boldsymbol{\eta} \quad (14)$$

where

$$\mathbf{B} = [\mathbf{C} \quad -\mathbf{C}] \text{ and } \mathbf{x} = [\mathbf{a}^+ \quad \mathbf{a}^-]$$

Substituting (13) in (11) the total mean-square error can be written as follows:

$$E = \mathbf{x}^T \mathbf{D} \mathbf{x} \tag{15}$$

Here

$$\mathbf{D} = \begin{bmatrix} \mathbf{Q} & -\mathbf{Q} \\ -\mathbf{Q} & \mathbf{Q} \end{bmatrix}$$

The constraints equation (14) can be written as inequality constraints

$$\mathbf{G} \mathbf{x} \leq \mathbf{F} \tag{16}$$

Here

$$\mathbf{G} = \begin{bmatrix} \mathbf{B} \\ -\mathbf{B} \end{bmatrix}, \mathbf{F} = \begin{bmatrix} \boldsymbol{\eta} \\ -\boldsymbol{\eta} \end{bmatrix}$$

### III. LINEAR COMPLEMENTARITY PROBLEM (LCP) FORMULATION

The minimization problem defined by (15) and (16) can be written now

$$\begin{aligned} \text{Minimize } & \mathbb{J}(\mathbf{x}) = \mathbf{x}^T \mathbf{D} \mathbf{x} \\ & \mathbf{G} \mathbf{x} \leq \mathbf{F} \\ & \mathbf{x} \geq \mathbf{0} \end{aligned}$$

The necessary and sufficient KKT optimality conditions for this minimization problem are

$$\begin{aligned} 2 \mathbf{D} \mathbf{x} + \mathbf{G}^T \mathbf{u} - \mathbf{y} &= \mathbf{0} \\ \mathbf{G} \mathbf{x} - \mathbf{F} &\leq \mathbf{0} \\ \mathbf{u} \geq \mathbf{0}, \mathbf{y} &\geq \mathbf{0} \\ \mathbf{u}^T (\mathbf{G} \mathbf{x} - \mathbf{F}) &= 0, \mathbf{y}^T \mathbf{x} = 0 \end{aligned}$$

By introducing the vector of slack variables  $\mathbf{v}$  the previous problem can be written in the form of a linear complementarity problem (LCP) [26]

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} - \begin{bmatrix} 2\mathbf{D} & \mathbf{G}^T \\ -\mathbf{G} & \mathbf{0} \end{bmatrix} \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix} = \begin{bmatrix} \mathbf{0} \\ \mathbf{F} \end{bmatrix}$$

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix} \geq \mathbf{0}, \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix} \geq \mathbf{0} \text{ and } \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix}^T \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix} = 0 \tag{19}$$

In compact form the LCP can be written as

$$\begin{aligned} \mathbf{w} - \mathbf{M} \mathbf{z} &= \mathbf{b} \\ \mathbf{w} \geq \mathbf{0}, \mathbf{z} \geq \mathbf{0}, \mathbf{w}^T \mathbf{z} &= 0 \end{aligned}$$

Here

$$\mathbf{M} = \begin{bmatrix} 2\mathbf{D} & \mathbf{G}^T \\ -\mathbf{G} & \mathbf{0} \end{bmatrix}, \mathbf{w} = \begin{bmatrix} \mathbf{y} \\ \mathbf{v} \end{bmatrix}, \mathbf{z} = \begin{bmatrix} \mathbf{x} \\ \mathbf{u} \end{bmatrix}, \mathbf{b} = \begin{bmatrix} \mathbf{0} \\ \mathbf{F} \end{bmatrix}$$

It is clear that  $\mathbf{D}$  is PSD matrix then  $\mathbf{M}$  is PSD matrix [26].

**Theorem** [26]: If  $\mathbf{D}$  is PSD and  $\mathbf{x}$  is a KKT point of (17),  $\mathbf{x}$  is an optimum feasible solution of (17).

### IV. DESIGN EXAMPLES

In this section a design examples of maximally flat FIR filters using the LCP formulation are presented. The performance characteristics of the proposed design approach are demonstrated by the presented examples.

**Example 1:** In this example, design of 9th-order (10th-length) linear phase low-pass FIR filter with pass-band and stop-band cover the intervals  $[0, 0.318\pi]$  and  $[0.477\pi, \pi]$  is considered. The used  $\alpha$  in this example was 0.8 and flatness degree was 3. Fig.1 shows the amplitude response. Fig.2 shows the phase response. It can be shown that the proposed method is able to give linear phase property.

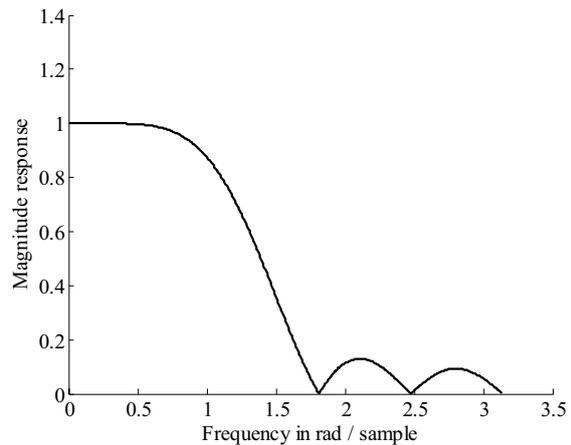


Figure 1: Amplitude response for example 1

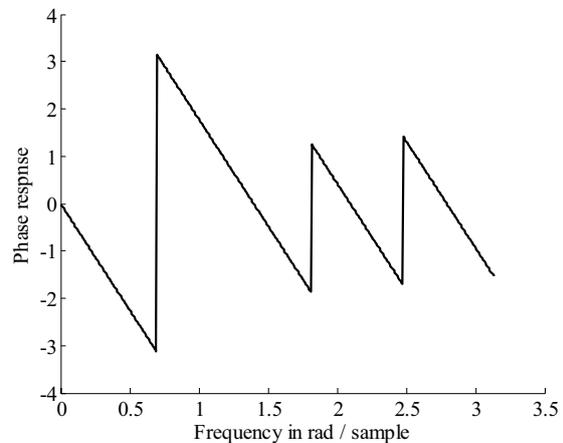


Figure 2: Phase response for example 1

**Example 2:** 78th-order (79th-length) linear phase low-pass FIR filter will be designed in this example. The used  $\alpha$  in this example was 0.8 and flatness degree was 3. The pass-band and stop-band cover the intervals  $[0, 0.4\pi]$  and  $[0.45\pi, \pi]$ . Fig.3 shows the magnitude response. The phase response is shown in Fig.4 which is also very close to linear phase property.

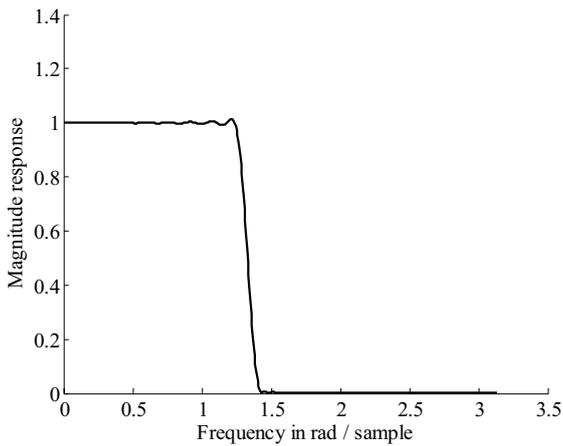


Figure 3: Amplitude response for example 2

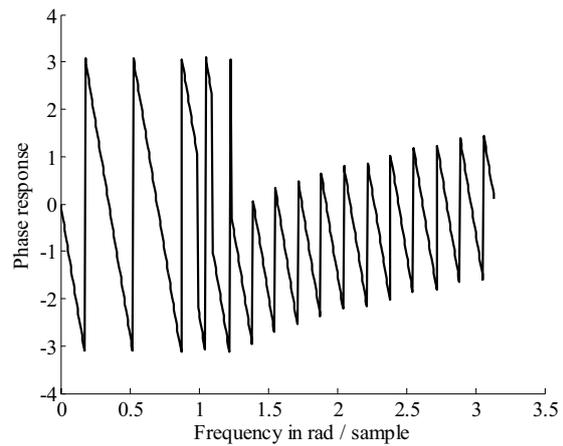


Figure 6: Phase response for example 3

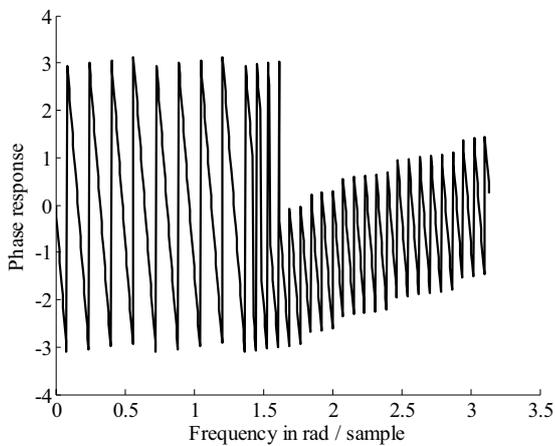


Figure 4: Phase response for example 2

**Example 3:** 36th-order (37th-length) linear phase low-pass FIR filter will be designed in this example. The used  $\alpha$  in this example was 0.8 and flatness degree was 3. The pass-band and stop-band cover the intervals  $[0, 0.156\pi]$  and  $[0.305\pi, \pi]$ . Fig.5 shows the magnitude response. Fig.6 shows the phase response. Again the proposed method is able to give a linear phase property.

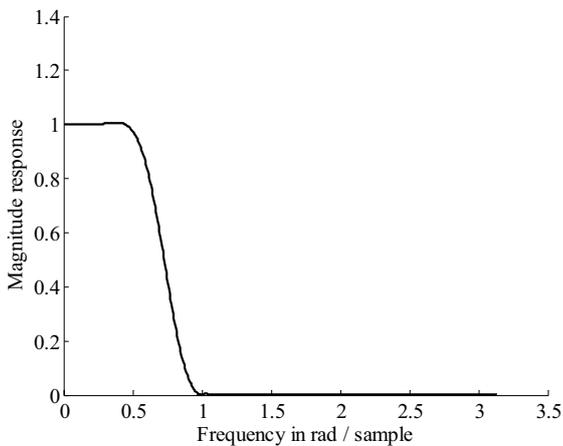


Figure 5: Amplitude response for example 3

### V. THE LABELING, THE MRF MODELING, AND THE ISING OF THE MGA

The second part of this work is concerned with using the MGA through MRF modeling and then building an Ising model for our MGA to be used in the proposed optimization problem. Assume we have a problem,  $G$ , to which messy genetic algorithms are to be applied.  $G$  consists of an encoding of chromosomes of length  $n$ , where  $n$  is a positive integer variable, with an associated fitness function  $f$ . The objective is to search for a chromosome that maximizes  $f$ .

Let  $A$  denote the set of chromosome alleles, and let  $L$  denote the set of possible allele values (bits). A particular chromosome  $c_n$  represents the assignment of an element of  $L$  to each element of  $A$ . In other words, each chromosome with length  $n$  is a labeling  $c_n: A \rightarrow L$ . Each labeling  $c_n$  has a fitness value  $f(c_n)$ , and we wish to find a chromosome that maximizes fitness. Thus we have the Labeling Problem for  $G$ :

Find a labeling  $c_n: A \rightarrow L$  which maximizes  $f(c_n)$

Encoding here is quite general, encompassing bit-string, other finite alphabet and floating-point encodings. In this section, we describe the MRF approach to the labeling problem. We begin with some notation and definitions.

Given a set  $A$  of locations, let us define the following:

1. Neighborhood system  $N$  on  $A$ .
2. A set of neighboring locations  $N_k$  for each location  $k$ .
3. A clique,  $k$ , is a single location or a set of mutual locations.
4. The set of all cliques are denoted by  $K$ .

Then it is important to say that Markov Random Field Modeling [15, 17, 18] regards locations as random variables and assigns each label  $c_n$  a non-zero probability  $P(c_n)$ . Now, for each clique  $k$ , we define a function  $V_k: k \rightarrow (-\infty, +\infty)$ . This function encapsulates information about related locations.

For any MRF with probability  $P$  the Hammersley-Clifford Theorem (HCT) [14] states that for any MRF, with probability function  $P$ , there is non-unique formulation:

$$P(c_n) = \frac{e^{-\frac{U(c_n)}{T}}}{Z} \tag{21}$$

Here

$$Z = \sum_c e^{-\frac{U(c_n)}{T}} \tag{22}$$

where  $T$  is cooling constant and set to 1. The energy function  $U$  is defined by:

$$U(c_n) = \sum_k V_k \tag{23}$$

**Theorem:** Let  $G$  be some encoding for messy Genetic algorithm MGA, and  $f$  is a given some fitness function, then  $G$  is an MRF with respect to neighborhood system  $N$ , if  $f(c_n) > 0$  for all members of the population of  $G$  that have labeling  $c_n$ .

**Proof:** Let us define:

$$P(c_n) = \frac{f(c_n)}{Z}$$

where  $Z = \sum_s f(s)$  is the sum of all chromosomes fitness. If we assume a clique potential function  $V_k: k \rightarrow (-\infty, +\infty)$  as follows:

$$V_k = \begin{cases} 0 & \text{if } k \text{ does not belong to } N \\ \ln\left(\frac{1}{f(c_n)}\right) & \text{if } k \text{ belongs to } N \end{cases}$$

If the cooling constant is set to 1 then  $P(c_n) = \frac{e^{-U(c_n)}}{Z}$  for all chromosomes  $c_n$  belongs to  $c$ . Using equation (22) one can found that  $P(c_n) = \frac{f(c_n)}{Z}$  for all  $k \in N$ . Invoking the converse of the HCT we deduce that  $G$  defines an MRF with respect to  $N$ . ■

It is worth telling that this  $G$  system is not unique.

### VI. THE ISING MGA MODEL

In a simple MGA chromosomes are encoded in binary bits. In a neighborhood system we assume that number of neighborhoods is equal to  $n$  2-cliques, where  $n$  is the length of the chromosome, and the 2-clique has the form  $\{k, k+1\}$  for each allele (bit) of the chromosome. It assumed that the last bit in each chromosome is a neighbor of the first bit (Fig. 7).

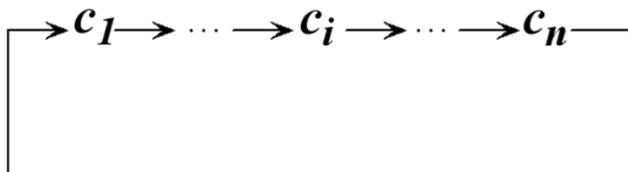


Figure 7: Chromosome bits configuration

The Ising model [17] is defined by assigning clique potential function as follows:

$$U(c_n) = \sum_k \alpha_k c_k + \beta_{k,k+1} c_k c_{k+1} \tag{25}$$

where  $\alpha$  and  $\beta$  are real coefficients called MRF parameters. Using equation (23), we will have for each chromosome  $c_n$  in the MGA population the following relation:

$$\ln(f(c_n)) = - \left\{ \sum_k \alpha_k c_k + \beta_{k,k+1} c_k c_{k+1} \right\} \tag{26}$$

Each chromosome at the MGA provides an equation of the form above. Since the length of the chromosomes is variable, it is essential to have a number of different chromosomes ( $>> 2nmax$ ), where  $nmax$  is the number of bits of the chromosome with highest length among the population. It is necessary to have  $2nmax$  equations in order to solve this set of linear equations and find values for the coefficients. Those coefficients are used to build the probabilistic model of the fitness based on the MRF theory. Note that we do not need to find the  $f(c_n)$  for the whole population, instead we need to find it for the  $2nmax$  equations only. In our case, finding the fitness function is costly since the binary bits need to be encoded into real coefficients and then those coefficients are passed to the model that designs the FIR filter and finds its amplitude response and its phase response. Then these responses are measured using some cost function against the desired filter characteristics to calculate the fitness. This is done for every chromosome in the population every generation.

With this Ising MGA model, once we have a model for the fitness, and a neighborhood system (with the coefficients that identify the cliques) we can now implement one step of the standard MGA (i.e. selection, crossover, and mutation) on the current population and move further to the next generation. The process is repeated until the maximum number of generations is reached or until the fitness saturates and the population consequently, converges to a group of different chromosomes that are less in number than  $2nmax$ . In that case, the set of equations described in (26) can not be solved and we have to stick with the last group of MRF parameters we found and go on with the MGA alone.

### VII. EXPERIMENTATIONS WITH STANDARD MGA AND ISING MGA

The chromosomes in MGA in general consist of varying number of bits. In a problem like the FIR filter design, major part of solving the problem is finding the optimum number of coefficients (degree of filter) that would accomplish the required characteristics. This requirement ultimately sets up the need for a variable length search parameter such as the variable length chromosomes in the MGA. The fitness function used for the MGA has to reflect the required criteria for both amplitude and phase transfer functions. A possible fitness function for the  $c_n$  (chromosome with length  $n$ ) may be given by:

$$f(c_n) = 1 - \left( \rho \sum_i (X_i - X'_i)^2 + \sigma \sum_i (Y_i - Y'_i)^2 \right) / \Lambda \tag{27}$$

where  $X_i$  and  $X'_i$  are the amplitude response values of the filters, the optimum one and the one generated from coefficients extracted from  $c_n$ , respectively and  $Y_i$  and  $Y'_i$  are the phase response values of the filters, the optimum one and the one generated from coefficients extracted from  $c_m$ , respectively.  $\rho$  and  $\sigma$  are weighting constants.  $i$  is frequency index.  $A$  is a normalization factor and is given by:

$$A = (\rho \sum_i X_i^2 + \sigma \sum_i Y_i^2) \quad (28)$$

In the random experiment we performed 10 runs with populations of 200 chromosomes. The chromosomes lengths varied between 24 bits and 80 bits, 8 bits per coefficient. The chromosomes were generated at random. The random experiments were implemented using the Random-Mutation Hill-Climbing algorithm (RMHC) on the Royal Road problem [20]. We recall RMHC method as follows:

1. Generate a chromosome  $c$  at random.
2. For  $N$  iterations, repeat:
  - i. Mutate an allele  $k$  chosen at random to produce  $c_o$ .
  - ii. If  $f(c_o) > f(c)$ , set  $c = c_o$ .
3. Terminate with answer  $c$ .

We, also, performed two seeded experiments consisting of 10 runs and 200 chromosomes in which 175 chromosomes were generated in random, and 25 were seeded. Seeded chromosomes are chromosomes with high fitness values. In the MGA experiment, we made 10 runs using population of 200. Here, we used standard MGA with 0.6 probability of crossover and 0.01 probability of mutation. In the last experiment we made 10 runs using the Ising MGA with population of 200. The Ising MGA was implemented by solving the system of equations generated by (26).

In the random experiments, we observed the mean fitness, the best fitness for the population. We also observed the mean MRF (Markov Random Field) fitness and the best MRF fitness to investigate how these values are compared to associated values with the seeded, MGA, and Ising MGA experiments. Both the population fitness and the MRF values will have values not less than 0 and not more than 1 ( $\alpha$  and  $\beta$  are real positive coefficients in (26)). In the random experiments and in each generation, the chromosomes are selected randomly, without any regard for fitness, however, the chromosomes have variable lengths and at the end of every generation  $S$  number of chromosomes is selected, where  $S$  is the length of the chromosome with the maximum length in the population. If a selected chromosome has a length less than other chromosomes it is padded with 0's until it has the length of the maximum length chromosome. This will not affect the real fitness value which is calculated for each chromosome in the  $S$  group, equation (26) is formulated for every chromosome resulting in  $S$  linear equations system. This system of linear equations is solved using standard numerical method techniques [19]. If a problem of ill conditioned for a non-singular set of equations is faced, a new group  $S$  is selected from the population, and  $\alpha_i$  and  $\beta_{k,k+1}$  coefficients are calculated. As soon as, those coefficients are calculated, the MRF equation (i.e. equation (26)) is set and then it can be

used in calculating the MRF fitness for rest of the chromosomes in the population. The MRF equation is a probabilistic model for the fitness function that is based on a sample from the population. This model will be used as a qualitative measure for the goodness of chromosomes. The biggest advantage here is that we had to solve a linear system of equations for every generation one time and then calculate the MRF fitness directly for the rest of the population. This is much less exhaustive than finding the fitness for every chromosome, which implies designing an FIR filter for each chromosome, finding its responses (amplitude and phase) and then calculating the fitness.

In the random seeded experiment, the whole process is repeated except for initially inserting chromosomes with high fitness using some standard techniques for designing FIR filters [1]. For the MGA experiment, the initial population is randomly generated with chromosomes with different lengths. Applying the standard GA operations reproduction, crossover, and mutation will take us to the next generation. The process continues until the population converges to a set of a few distinct chromosomes. Finally, for the Ising MGA experiment the same steps applied by the MGA are applied here except that the MRF fitness coefficients are calculated using the previously described method. However, as the MGA draws close to convergence, the number of distinct chromosomes in the group  $S$  tends to become less than the number of coefficients. In other words, we will have under-specified system of equations to solve. In that case, we used the last set of coefficients we had to model the MRF fitness. This can be justified by the fact that as the MGA converges very little modifications is done on the labeling of the chromosomes and the MRF coefficients could also be considered stable.

The FIR filters being designed in this work are low-pass filters mostly suitable for medical applications where the range of the frequencies is relatively low and the phase response is required to be linear. The linearity of the phase is essential to avoid any distortions of the signals. For those reasons, FIR filters are more preferred in medical applications than IIR filters. The optimum amplitude response of the filter we are seeking is a step function that has value 1 for the pass-band range and 0 for the stop-band range, with linear phase response having  $-45^\circ$  degrees with  $x$ -axis. The pass-band ends where stop-band starts at a normalized frequency of  $\pi/4$ , no tolerance is specified. Definitely, this requirement is not realistic; it is only a theoretical criterion for this optimization problem. Also note that the order of the filter is not specified here, it is left open as long as the criterion is met. This, however, laid more burdens on the used optimization algorithm. The results of the experiments are shown in Table 1.

TABLE I  
SUMMARY OF FITNESS VALUES EXPERIMENTS DONE WITH THE FOUR ALGORITHMS

Experiment	Population Fitness	
	Mean Fitness	Best Fitness
Random	0.053	0.334
Seeded Random	0.346	0.677
MGA	0.798	0.899

Ising MGA	0.899	0.956
MRF Fitness		
Experiment	Mean Fitness	Best Fitness
Random	0.078	0.334
Seeded Random	0.413	0.756
MGA	-	-
Ising MGA	0.912	0.987

### VIII. DISCUSSIONS

In each experiment we used 500 chromosomes for population size. The purpose of the random and the seeded random experiments is to demonstrate how MRF fitness can reflect status of chromosomes under blind and totally unguided search.

MRF parameters are hypothesized to be able to detect the presence of preferred schemata in a population. The random and seeded experiments are considered first. In the random and seeded populations, the mean MRF fitness is better than population mean fitness in all cases. The best MRF fitness agrees closely with the best population fitness. In the random and seeded experiments it is likely to end up with some good members in the population, however, the average fitness of the population is not expected to be as good as in the MGA where all members of the population go through selection and evolution. The MGA works totally independent of any MRF's. It uses (27) and (28) to evaluate each member of the population independently.

In the Ising MGA, MRF's fitness helped to characterize a model for the fitness at every generation, therefore preventing costly usage of the FIR filter modules, and providing a qualitative helpful measure for the energy embedded within the labels of the population members. The mean fitness and the best fitness in Ising MGA are higher than those for the MGA. Those may be due to two major factors; the used MRF fitness function provides a better utility to evaluate the strings and classify them through the generations, the other factor is that in the MGA, calculating the fitness successively for each string in every generation involves an FIR filter design for each calculation of fitness, and this process itself has some approximations that will eventually result in accumulated errors. Moreover, equation (26) itself is a heuristic measure; there is no guarantee that it is the perfect measure to evaluate the strings.

The LCP method, on the other hand, is a totally different approach. It is not an iterative method that involves repetitive evaluations of some fitness function. It is based on formulating a constrained quadratic energy function and, consequently an LCP, then finding the minimum of this function by solving the associated LCP. It is required, as shown in the previous examples, to give some specifications such as the stop-band and the pass-band frequencies, and the order of the filter. As shown in Figures 1-6, the amplitude responses and the phase responses are acceptable.

Figures (8 - 11) show the magnitude and phase responses for the random method and the random seeded method respectively. It is obvious that the seeded method had a better performance than the random method. In Figs. (12 -15), the amplitude and frequency responses for the MGA, and the

Ising MGA are depicted. The order of the filter is kept open. It is part of the search space as the length of the string in the MGA is variable. The used cut off frequency was  $\pi/4$  and note that the filter order is not required here. The coefficients of all FIR filters are shown in Figs. (8-15) coming from the best strings in the population.

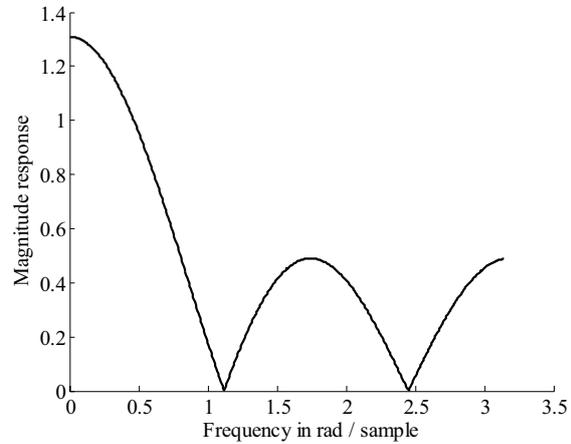


Figure 8: Magnitude response using random method

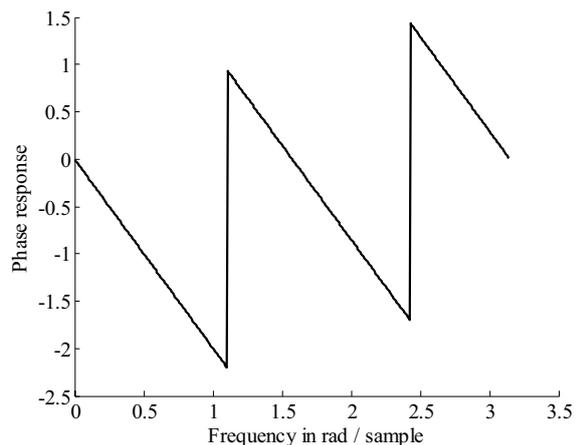


Figure 9: Phase response using random method

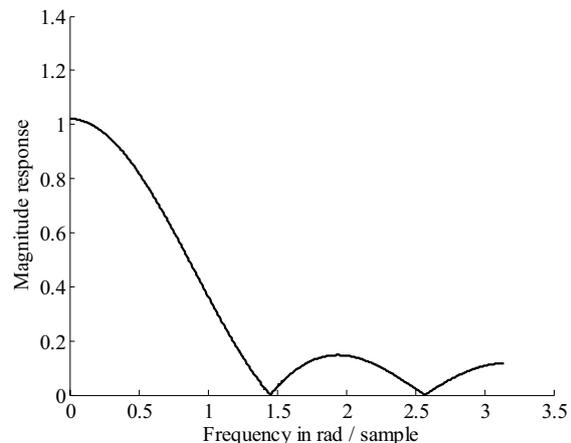


Figure 10: Magnitude response using random seeded method

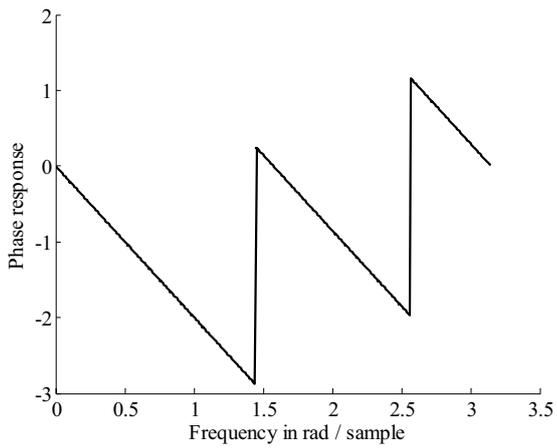


Figure 11: Phase response using random seeded method

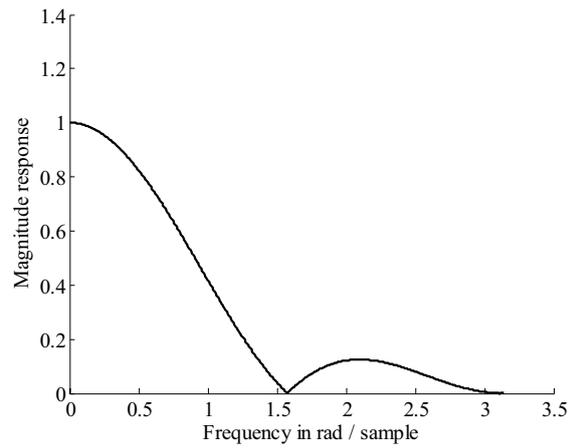


Figure 14: Magnitude response using Ising MGA method

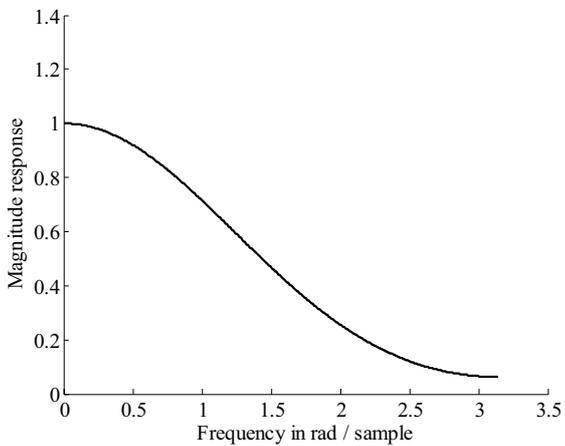


Figure 12: Magnitude response using MGA method

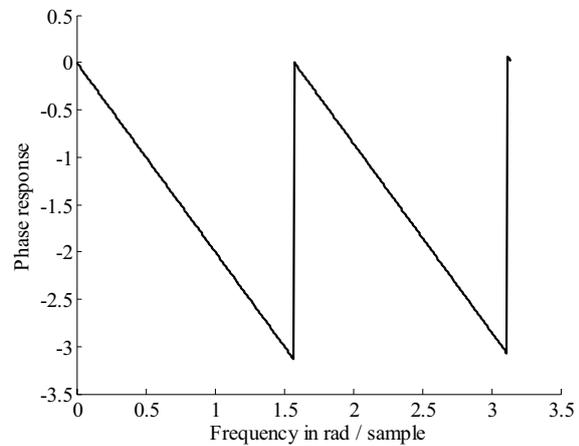


Figure 15: Phase response using Ising MGA method

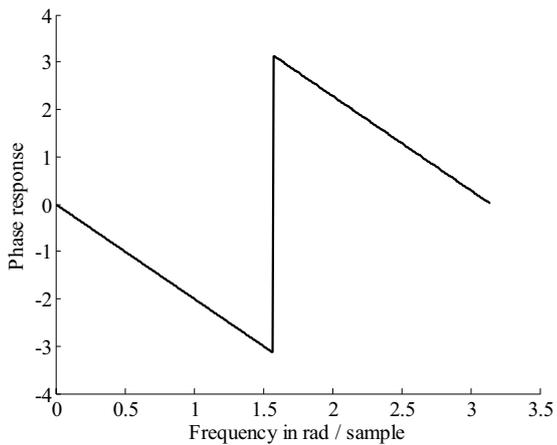


Figure 13: Phase response using MGA method

For what is shown, it is fair to conclude that the evolutionary based methods such as the MGA and Ising MGA gave good results in terms of the final outcome. However, we should bear in mind that the GA based techniques are far more computationally exhaustive than the other standard numerical techniques. Moreover, the LCP method does not require any FIR filter design stages during the optimization process, in the contrary to the GA based techniques which require substantial usage of the fitness function that implies the usage of external objective functions utilities ( i.e. the modules used to build the filter each time the fitness is calculated).

#### IX. CONCLUSION

A maximally flat FIR digital filter is presented. The problem is handled using two totally different approaches. The first one is completely deterministic method where the problem is formulated as LCP. The formulation is based on minimization of a suitable mean square error. Numerical

results show that the proposed method is effective. The other approach was based on a combination of MRF's approach with MGA.

In this paper we have demonstrated how a mathematical relation can be defined between a MGA fitness function and a MRF model of fitness, derived from the fitness of a population of chromosomes. Our theorem shows that such a link can always be defined for a very general class of MGA encodings. In practice, the strength of this link depends on the choice of neighborhood system, and the clique potential functions. We used a two neighbors system to build our potential function.

It should be noted that this approach is distinct from the work done in modeling the evolution of a GA using Markov chains. We do not model the evolution.

However, since the transition probabilities in the Markov chains models require the calculations of the fitness, then the MRF approach could be incorporated in the derivation of the Markov chains model.

The Bayesian Optimization Algorithm (BOA) developed in [21]-[22], and is applied to Probabilistic Model-Building Genetic Algorithms (PMBGA) [22]-[23], uses totally different approach than that of the MRF models, BOA approach is based on the inheritance of the alleles between the children and the parents, while the MRF model is based on the neighborhood between alleles. BOA calculates the fitness according to the objective of some external utility, while the MRF model does not assume that the fitness is directly related to the external objective function.

In general, iterative techniques that are adaptive give better results for the FIR filter design. Here, we present novel technique for optimizing multivariable functions based on labeling based genetic algorithm, and then we used it in solving a standard application such as the FIR filter design problem. We also managed to formulate an LCP for the FIR filter design problem and solve it using Lemke algorithm. Two basic approaches that are totally different were presented in this paper and used in solving a benchmark application. The Ising MGA, however, is less exhaustive than the MGA since less usage of the external objective function utility is used. Once the MRF model is established, it will be used in calculating the fitness for Ising MGA.

Future work will include further modeling of the Ising GA and using different labeling systems. More emphasis will be put in designing different types of digital filters, including two dimensional filters. Real life applications will be used to demonstrate the robustness of the designed filters.

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