

Optimal Design of Selective Excitation Pulses in Magnetic Resonance Imaging using Genetic Algorithms

Mohammed A. Alolfe, Abou-Bakr M. Youssef and Yasser M. Kadah

Abstract—The proper design of RF pulses in magnetic resonance imaging (MRI) has a direct impact on the quality of acquired images, and is needed for many applications. Several techniques have been proposed to obtain the RF pulse envelope given the desired slice profile. Unfortunately, these techniques do not take into account the limitations of practical implementation such as limited amplitude resolution. Moreover, implementing constraints for special RF pulses on most techniques is not possible. In this work, we propose to develop an approach for designing optimal RF pulses under theoretically any constraints. The new technique will pose the RF pulse design problem as a combinatorial optimization problem and uses efficient techniques from this area such as genetic algorithms (GA) to solve this problem. In particular, an objective function will be proposed as the norm of the difference between the desired profile and the one obtained from solving the Bloch equations for the current RF pulse design values. The proposed approach will be verified using analytical solution based RF simulations and compared to previous methods such as Shinnar-Le Roux (SLR) method, and analysis, selected, and tested the options and parameters that control the Genetic Algorithm (GA) can significantly affect its performance to get the best improved results and compared to previous works in this field. The results show a significant improvement over conventional design techniques, select the best options and parameters for GA to get most improvement over the previous works, and suggest the practicality of using of the new technique for most important applications as slice selection for large flip angles, in the area of unconventional spatial encoding, and another clinical use.

Keywords—selective excitation, magnetic resonance imaging, combinatorial optimization, pulse design.

I. INTRODUCTION

MAGNETIC resonance imaging (MRI) is an imaging technique using primarily in medical setting to produce high quality images of the inside of the human body. It offers true volumetric acquisition, ability to visualize and quantify flow, and spectroscopic imaging to image both anatomy and function. This technique relies on collecting the signal from an excited slice or volume within the human body. This

excitation is achieved using special RF pulses that are designed to provide the required localization within the imaged volume. The proper design of RF pulses is important to avoid artifacts such as cross-talk in the acquired images. The design of RF pulses is a rather difficult problem mathematically [1]. The basic goal of this design is to enable the desired slice profile to be achieved using the available RF pulse generation hardware. The practical implementation of RF pulse systems consists of a computer that stores the array of digital values representing the RF pulse envelope amplitudes. These values are converted using a digital-to-analog converter (DAC) into actual voltage levels. This DAC has a limited resolution in both amplitude and time. As a result, the generated envelope voltages appear like a piecewise constant curve with a fixed time step and limited stepwise amplitudes. These levels modulate the amplitude of the output of an RF generator before applying this output to the RF coils. The RF coils may be either linear (i.e., allowing only the real component to be applied) or quadrature (i.e., allowing both the real and imaginary components to be used). The actual frequency of the RF generator and the applied slice selection magnetic field gradient determine the position of excited slice. On the other hand, the amplitudes of the RF pulse envelope points determine the shape of the excitation profile as well as its flip angle.

Development of such pulses has been a topic of interest to researchers for over 20 years [2] and many methods have been developed. Hoult showed that at small tip angles (30 or less), the characteristic Bloch equations are nearly linear in nature [3]. As a result, assuming linear response in the spectrometer transmitter chain, the Fourier transform (FT) of the desired magnetization profile is a reasonable choice for the RF waveform. Pulses derived in this manner can produce acceptable results at larger tip angles, but as the tip angle approaches and exceeds 90, the Bloch equations become increasingly nonlinear, with significant distortion in both phase and magnitude [4].

Researchers have extensively investigated both direct and inverse approaches to RF pulse optimization. Hoult [3] and Mansfield *et al.* [6] were pioneers in the direct solution of the Bloch equations for shaped pulse design, whose work was verified numerically by Locher [7]. Techniques for analytical inversion of the Bloch equations were also proposed by

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Caprihan [8] and Silver *et al.* [9]. Caprihan concluded that numerical methods are the key to effective selective pulse synthesis. Conolly *et al.* [10] and Murdoch *et al.* [11] explored optimal control adaptations to RF pulse refinement. This work was reinforced by Ngo and Morris [12], who showed that the Bloch equations respond linearly to large excitations if they are treated as a superposition of perturbations of small tip angle. Among the many design methodologies that have been proposed in the last decade, the Shinnar-Le Roux (SLR) method is probably the most widely used [13]. This method works by transforming the problem into one of designing a finite impulse response (FIR) filter. The solution of this problem is obtained as an FIR filter coefficients and subsequently transformed back into the desired RF pulse envelope.

Given the extensive literature on FIR filter design, the strength of the SLR technique is that it taps into some of the most powerful FIR filter design techniques to solve the original problem of RF pulse design [13]. Nevertheless, it still has some limitations that did not enable its performance to be optimal in practice. In particular, this technique does not take into consideration the limited amplitude resolution in designing the RF filter. As it is well known in FIR filter design literature, the limited precision (i.e., quantization or limited word length effects) in implementing the digital filter may substantially deteriorate its performance [14]. Even if the FIR filter design technique is modified to take care of this problem and provides optimal filter coefficients for a given precision, there is no guarantee that the backward transformation to RF pulse coefficients would preserve this property for RF pulse coefficients. In other words, the characteristics of the SLR transformation do not allow such constraints to be imposed. In fact, it is generally difficult to impose any type of constraints on the solution (like for example adiabatic constraints). As a result, the obtained design may in fact be suboptimal in many cases that are common in practical use. An example where difficulty to obtain accurate slice profiles is reported is the use of unconventional spatial encoding techniques such as wavelet encoding and pseudo-Fourier imaging [15]. The implementation of such techniques had to compromise between the need to use low flip angles to obtain accurate slice profiles for correct encoding and the need for high flip angles for better signal-to-noise ratio. Therefore, a new RF pulse design technique that can incorporate practical constraints thus offering a true optimal performance under the practical implementation constraints would be rather helpful to solve these problems.

In this work, we formulate the problem of RF pulse design as a combinatorial optimization problem with an arbitrary number of constraints and uses efficient techniques from this area such as genetic algorithms (GA) to solve this problem. This formulation takes into account the limited precision of RF pulse generation and provides the optimal results at any given precision. Unlike SLR technique, the objective function will be proposed as the norm of the difference between the

desired profile and the one obtained from solving the Bloch equations for the current RF pulse design values, which offers a feedback loop to improve the results. The proposed approach will be verified using analytical solution based RF simulations and compared to previous methods such as Shinnar-Le Roux (SLR) method, and analysis, selected, and tested the options and parameters of genetic algorithms to get the best improved results and compared to previous works in this field. We provide the detailed implementation details for each and present their results compared to those of the SLR technique.

II. METHODOLOGY

A. Theoretical background

Given the definition of the RF pulse, it is possible to compute the expected slice profile using the solution to the Bloch equations. This solution relies on using the analytical form for the slice profile from a single rectangular pulse of arbitrary magnitude given in [1]. In traditional practical cases, the gradient is kept constant and the relaxation times (T_1 & T_2) are neglected. The Bloch equations relate magnetization values with these assumptions is given by:

$$\frac{d}{dt} \begin{bmatrix} Mx \\ My \\ Mz \end{bmatrix} = \gamma \cdot \begin{bmatrix} 0 & G.z & -By \\ -G.z & 0 & Bx \\ By & -Bx & 0 \end{bmatrix} \begin{bmatrix} Mx \\ My \\ Mz \end{bmatrix} = A \cdot \vec{M} \quad (1)$$

Here, B_x and B_y are the two quadrature components of the RF pulse, γ is the gyromagnetic ratio, and $G.z$ is the slice selection gradient. The gradient is assumed to lie along the +z axis. For a rectangular pulse, the solution can be simply computed as,

$$\vec{M}(z) = \vec{M}_0(z) \cdot \text{Exp}(-A.t), \quad (2)$$

Where t is the duration of the rectangular RF pulse and the matrix exponent can be computed analytically for this problem as in [1].

Keeping in mind the practical implementation of RF pulses in the form of piecewise constant envelope pulses (i.e., a sequence of rectangular pulses of arbitrary amplitudes), the output magnetization from one piece serves as the initial condition for the next. Hence, given any design for the RF pulse, the slice profile can be computed this method. Given that the amplitudes of the RF pulses must be represented within a certain number of bits, the problem now becomes the one of finding the optimal combination of amplitudes that would give a slice profile closest to the desired. This problem description shows that this problem is indeed a combinatorial optimization problem. Using the rich literature of this area, the solution can be obtained efficiently and accurately. In this work, we explore one of the most prominent techniques in this area, namely, genetic algorithm (GA).

B. Methods

We use one of the most prominent techniques in the area of

a combinatorial optimization problem, namely, genetic algorithm (GA). The Genetic algorithm (GA) is an optimization and search technique based on the principles of genetics and natural selection. A GA allows a population composed of many individuals to evolve under specified selection rules to a state that maximizes the "fitness" (i.e., minimizes the cost function) [16]. GA accommodate all the facets of soft computing, namely uncertainty, imprecision, non-linearity, and robustness. Some of the attractive features include:

- a. Learning: GA are the best known and widely used global search techniques with an ability to explore and exploit a given operating space using available performance (or learning) measures. Moreover, genetic operators such as crossover, mutation, and reproduction allow express simulations of an extensive learning process of nature.
- b. Generic code structure: operate on an encoded parameter string and not directly on the parameters. This enables the user to treat any aspect of the problem as an optimizable variable.
- c. Optimality of the Solutions: In many problems, there is no guarantee of smoothness and unimodality. Traditional search techniques often fail miserably on such search spaces. GA is known to be capable of finding near optimal solutions in complex search spaces.
- d. Advanced Operators: This includes techniques such as niching (for discovering multiple solutions), combinations of Neural, Fuzzy, and chaos theory, and multiple objective optimizations.

The Figure (1) and following outline summarize how the genetic algorithm works:

1. The algorithm begins by creating a random initial population.
2. The algorithm then creates a sequence of new populations, or generations. At each step, the algorithm uses the individuals in the current generation to create the next generation. To create the new generation, the algorithm performs the following steps:
 - a. Scores each member of the current population by computing its fitness value.
 - b. Scales the raw fitness scores to convert them into a more usable range of values.
 - c. Selects parents based on their fitness.
 - d. Produces children from the parents. Children are produced either by making random changes to a single parent – mutation – or by combining the vector entries of a pair of parents – crossover.
 - e. Replaces the current population with the children to form the next generation.
 - f. The algorithm stops when one of the stopping criteria is met.

A solution is encoded as a string of genes to form a chromosome representing an individual. In many applications the gene values are [0, 1] and the chromosomes are simply bit strings. An objective function, f , is supplied which can decode the chromosome and assign a fitness value to the individual

the chromosome represents.

Given a population of chromosomes the genetic operator's crossover and mutation can be applied in order to propagate variation within the population. Crossover takes two parent chromosomes, cuts them at some random gene/bit position and recombines the opposing sections to create two children. Mutation is a background operator, which selects a gene at random on a given individual and mutates the value for that gene (for bit strings the bit is complemented).

The use of GA is robust in that they are not affected by spurious local optima in the solution space. Nevertheless, the parameters that control the GA can significantly affect its performance, and there is no guidance in theory as to how properly select them but in this work we are analysis, select, and test the options and parameters of genetic algorithms to get the best improved results and compared to previous works in this field. The most important parameters are the population size, the fitness scaling, the selection function, the crossover function, and the mutation function. The following are the proposed algorithm details.

- 1) *Population of the chromosomes*: Population represents the size of the solutions that we are working with and specifies how many individuals there are in each generation. With a large population size, the genetic algorithm searches the solution space more thoroughly, thereby reducing the chance that the algorithm will return a local minimum that is not a global minimum. However, a large population size also causes the algorithm to run more slowly. Some research also shows that best population size depends on encoding, on size of encoded string. It means, if you have chromosome with 32 bits, the population should be say 32, but surely two times more than the best population size for chromosome with 16 bits [17].
- 2) *Population Initialization*: The populations of chromosomes are initialized randomly by the GA. A chromosome that represents the SLR solution is added to the initial population to produce the initial population that we are working with. This means that we start with the best solution in the literature and try to get a more optimal solution that produces a better slice profiles.
- 3) *Chromosome structure*: Binary chromosome is used. The RF pulse is encoded into the chromosome as follows. The real RF pulse values are converted into discrete ones according to the resolution of the D/A of the MRI machine (12 or 16 bit for example). Every bit represents a gene. The most significant bits of all values are placed adjacent to each other, then the second most bits and so on until placing the least significant bits together at the end. Hence, the chromosome size equals the number of the RF pulse envelope values times the bit resolution (usually 12 or 16).
- 4) *Fitness criterion*: The chromosome is decoded to obtain the corresponding RF pulse envelope amplitudes and its slice profile is computed by solving the Bloch equations. Then, an error measure is calculated for the difference

between the response of this RF pulse and the desired response. This measure is usually taken as either the 1-norm or 2-norm of the difference vector. The results of this paper were obtained using the 1-norm. We use the evaluation function:

$$F = |D_x - M_x| + |D_y - M_y| + |D_z - M_z|, \quad (3)$$

5) *Fitness scaling*: Fitness scaling converts the raw fitness scores that are returned by the fitness function to values in a range that is suitable for the selection function. The range of the scaled values affects the performance of the genetic algorithm. If the scaled values vary too widely, the individuals with the highest scaled values reproduce too rapidly, taking over the population gene pool too quickly, and preventing the genetic algorithm from searching other areas of the solution space. On the other hand, if the scaled values vary only a little, all individuals have approximately the same chance of reproduction and the search will progress very slowly. We can specify options for fitness scaling in the GA:

- *Rank*: Rank, scales the raw scores based on the rank of each individual instead of its score. The rank of an individual is its position in the sorted scores. The rank of the fittest individual is 1, the next most fit is 2, and so on. Rank fitness scaling removes the effect of the spread of the raw scores.
 - *Proportional*: Proportional scaling makes the scaled value of an individual proportional to its raw fitness score.
 - *Top*: Top, scales the top individuals equally. Selecting Top displays an additional field, Quantity, which specifies the number of individuals that are assigned positive scaled values. Quantity can be an integer between 1 and the population size or a fraction between 0 and 1 specifying a fraction of the population size.
 - *Shift linear*: Shift linear, scales the raw scores so that the expectation of the fittest individual is equal to a constant multiplied by the average score. You specify the constant in the Max survival rate field, which is displayed when you select Shift linear.
- 6) *Selection*: Selection options specify how the genetic algorithm chooses parents for the next generation. You can specify options for selection in the GA:
- *Stochastic uniform*: stochastic uniform, lays out a line in which each parent corresponds to a section of the line of length proportional to its scaled value. The algorithm moves along the line in steps of equal size. At each step, the algorithm allocates a parent from the section it lands on. The first step is a uniform random number less than the step size.
 - *Remainder*: Remainder, assigns parents deterministically from the integer part of each individual's scaled value and then uses roulette selection on the remaining fractional part.

- *Uniform*: Uniform, chooses parents using the expectations and number of parents.
 - *Roulette*: Roulette, chooses parents by simulating a roulette wheel, in which the area of the section of the wheel corresponding to an individual is proportional to the individual's expectation. The algorithm uses a random number to select one of the sections with a probability equal to its area.
 - *Tournament*: Tournament selection chooses each parent by choosing Tournament size players at random and then choosing the best individual out of that set to be a parent. Tournament size must be at least 2.
 - *Reproduction*: Reproduction options specify how the genetic algorithm creates children for the next generation. You can specify options for reproduction in the GA:
 - *Elite count*: specifies the number of individuals that are guaranteed to survive to the next generation. Set Elite count to be a positive integer less than or equal to the population size. The default value is 2.
 - *Crossover fraction*: specifies the fraction of the next generation, other than elite children, that are produced by crossover. Set Crossover fraction to be a fraction between 0 and 1. The default value is 0.8.
- 7) *Crossover*: Crossover options specify how the genetic algorithm combines two individuals, or parents, to form a crossover child for the next generation. You can specify options for crossover in the GA:
- *Scattered*: creates a random binary vector and selects the genes where the vector is a 1 from the first parent, and the genes where the vector is a 0 from the second parent, and combines the genes to form the child.
 - *Single point*: chooses a random integer n between 1 and Number of variables and then
 1. Selects vector entries numbered less than or equal to n from the first parent.
 2. Selects vector entries numbered greater than n from the second parent.
 3. Concatenates these entries to form a child vector.
 - *Two point*: Selects two random integers' m and n between 1 and Number of variables. The function selects
 1. Vector entries numbered less than or equal to m from the first parent.
 2. Vector entries numbered from m+1 to n, inclusive, from the second parent.
 3. Vector entries numbered greater than n from the first parent.
 The algorithm then concatenates these genes to form a single gene.
 - *Intermediate*: Creates children by taking a weighted average of the parents. You can specify the weights by a single parameter, Ratio, which can be a scalar or a

row vector of length Number of variables. The function creates the child from parent1 and parent2 using the following formula. $Child = parent1 + rand \times Ratio \times (parent2 - parent1)$.

- *Heuristic*: returns a child that lies on the line containing the two parents, a small distance away from the parent with the better fitness value in the direction away from the parent with the worse fitness value. You can specify how far the child is from the better parent by the parameter Ratio, which appears when you select Heuristic. The default value of Ratio is 1.2. If parent1 and parent2 are the parents, and parent1 has the better fitness value, the function returns the child. $Child = parent2 + Ratio \times (parent1 - parent2)$.
- 8) *Mutation*: Mutation options specify how the genetic algorithm makes small random changes in the individuals in the population to create mutation children. Mutation provides genetic diversity and enables the genetic algorithm to search a broader space. You can specify options for mutation in the GA:
- *Gaussian*: Gaussian, adds a random number taken from a Gaussian distribution with mean 0 to each entry of the parent vector. The variance of this distribution is determined by the parameters Scale and Shrink, and by the Initial range setting in the Population options.
 - *Uniform*: Uniform mutation is a two-step process. First, the algorithm selects a fraction of the vector entries of an individual for mutation, where each entry has a probability Rate of being mutated. The default value of Rate is 0.01. In the second step, the algorithm replaces each selected entry by a random number selected uniformly from the range for that entry.

III. RESULTS

The proposed Genetic Algorithm method was applied to design RF pulses with rectangular spatial profile at $\pi/2$ and π flip angle. The outcome of the Genetic method is compared to the outcome of the SLR technique. Firstly to get the best results from the genetic algorithm, you usually need to experiment with different options of GA. Selecting the best options for a problem involves trial and error. We used 64 points for RF pulse design and applied Genetic Algorithm to design RF pulses with rectangular spatial profile at π flip angle. The following describe some ways you can change options to improve results.

a. Population Size and Initial Range

One of the most important factors that determine the performance of the genetic algorithm performs is the diversity of the population. If the average distance between individuals is large, the diversity is high; if the average distance is small, the diversity is low. Getting the right amount of diversity is a matter of trial and error. If the diversity is too high or too low,

the genetic algorithm might not perform well. This section explains how to control diversity by setting the Initial range of the population, and also explains how to set the population size. The effects of the initial range and population size on the performance of the genetic algorithm are illustrated in table (1).

b. Fitness scaling

The range of the scaled values affects the performance of the genetic algorithm. If the scaled values vary too widely, the individuals with the highest scaled values reproduce too rapidly, taking over the population gene pool too quickly, and preventing the genetic algorithm from searching other areas of the solution space. On the other hand, if the scaled values vary only a little, all individuals have approximately the same chance of reproduction and the search will progress very slowly. The effects of the fitness scaling on the performance of the genetic algorithm are illustrated in table (2), and figure (2).

c. Selection function:

The effects of changing selection function on the performance of the genetic algorithm are illustrated in table (3), and figures (3).

d. Function of crossover:

The effects of changing selection function on the performance of the genetic algorithm are illustrated in table (4), and figures (4).

e. Change function of mutation:

The effects of changing the selection function on the performance of the genetic algorithm are illustrated in table (5), and figures (5).

Secondly, after the test options of GA to get the best results, we applied the genetic algorithm with the best parameters to design two RF pulses with rectangular spatial profiles at $\pi/2$ and π flip angles. The outcome of these experiments is compared to the outcome of the SLR technique, and compared the outcome of this work and the outcome of previous work (using the following options for GA: proportional scaling function, Roulette selection function, single point crossover function, probability of crossover is taken as 90%, uniform mutation function, and probability of mutation is taken as 1%). The results are shown in Table (6) and figures (6), and (7). As can be observed, the GA technique show a significant improvement over the design computed using the SLR technique. Also, the outcome of this work appears better and faster to reach the solution than that from previous work in the number of experiments we performed.

One of the most important applications for the proposed technique is in the area of unconventional spatial encoding where complex RF pulse are to be generate at high accuracy. The proposed technique is expected to enable better reconstruction accuracy, less image artifacts, and higher

signal-to-noise ratio. The study of this area requires the investigation of several of these techniques and the assessment of the results and is left to future work.

IV. CONCLUSIONS

In this paper, we present a new optimized RF pulse design in MRI using the GA. The new technique relies on posing the problem as a combinatorial optimization problem and uses GA to compute the solution under any type of constraints, and select the best options for parameters of GA to get the more improvement results. The results demonstrate the success of the new approach and suggest its potential for practical use in clinical magnetic resonance imaging.

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TABLE I BEST VALUES RESULTS FOR CHANGE POPULATION SIZE AND INITIAL RANGE

| No | Pop.Size | Norm-1 Errors(Best values) | | |
|----|----------|--------------------------------|----------------------------|--------------------------|
| | | Initial range [-0.0001,0.0001] | Initial range [-0.01,0.01] | Initial range [-0.1,0.1] |
| 1. | 16 | 4.9923 | 5.0223 | 8.557 |
| 2. | 32 | 4.9256 | 4.8973 | 5.1912 |
| 3. | 64 | 4.9951 | 4.9348 | 4.8993 |
| 4. | 128 | 4.986 | 5.026 | 5.0184 |
| 5. | 256 | 4.9337 | 4.935 | 6.6971 |

TABLE II BEST VALUES RESULTS FOR CHANGE FITNESS FUNCTION

| No. | Scaling Function | Norm-1 Errors (Best Values) |
|-----|------------------|-----------------------------|
| 1. | Rank | 4.8973 |
| 2. | Proportional | 4.9541 |
| 3. | Top | 4.9981 |
| 4. | Shift Linear | 4.927 |

TABLE III BEST VALUES RESULTS FOR CHANGE SELECTION FUNCTION

| No. | Selection Function | Norm-1 Errors (Best Values) |
|-----|--------------------|-----------------------------|
| 1. | Stochastic uniform | 4.8973 |
| 2. | Remainder | 5.0248 |
| 3. | Roulette | 5.0006 |
| 4. | Tournament | 4.9209 |

TABLE IV BEST VALUES RESULTS FOR CHANGE CROSSOVER FUNCTION

| No. | Crossover Function | Norm-1 Errors (Best Values) |
|-----|--------------------|-----------------------------|
| 1. | Scattered | 4.8973 |
| 2. | Single point | 5.0653 |
| 3. | Two point | 4.9948 |
| 4. | Intermediate | 5.2007 |

TABLE V BEST VALUES RESULTS FOR CHANGE MUTATION FUNCTION

| No. | Mutation Function | Norm-1 Errors (Best Values) |
|-----|-------------------|-----------------------------|
| 1. | Gaussian | 4.8973 |
| 2. | Uniform | 5.05 |

TABLE VI NORM-1 ERROR RESULTS FOR $\pi/2$ AND π FLIP ANGLE

| No. | Flip angle | Norm-1 Errors for 128 points | | Norm-1 Errors for 256 points | |
|-----|------------|------------------------------|----------|------------------------------|----------|
| | | previous work | Our work | previous work | Our work |
| 1. | $\pi/2$ | 1.304 | 1.2698 | 1.0979 | 0.88545 |
| 2. | π | 3.9839 | 3.8768 | 3.0929 | 2.7724 |

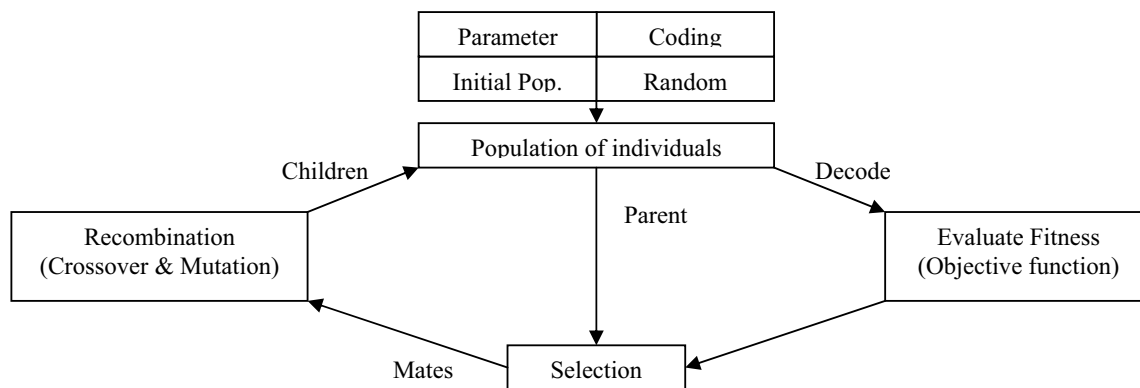
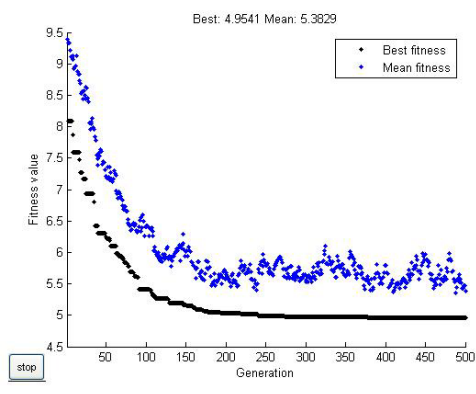
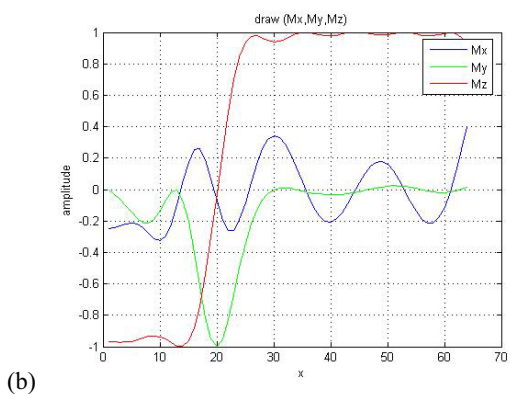
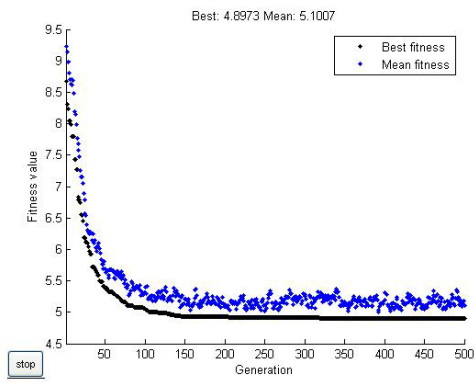
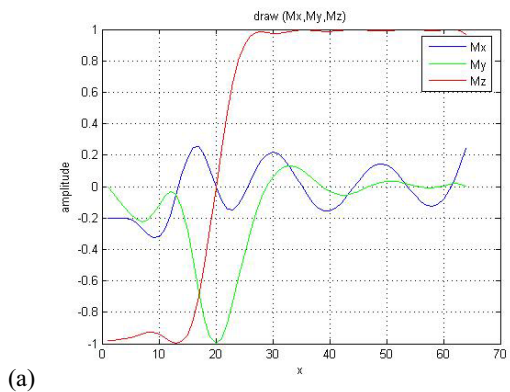


Fig. 1 Computational Flows in Genetic Algorithms



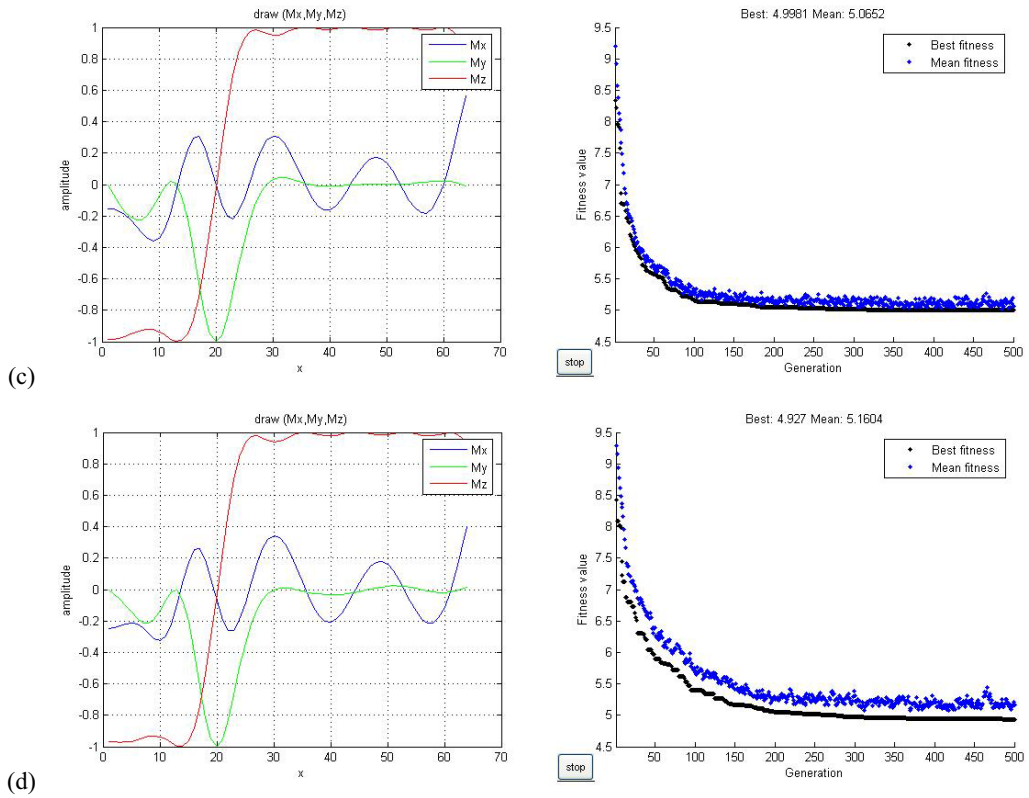
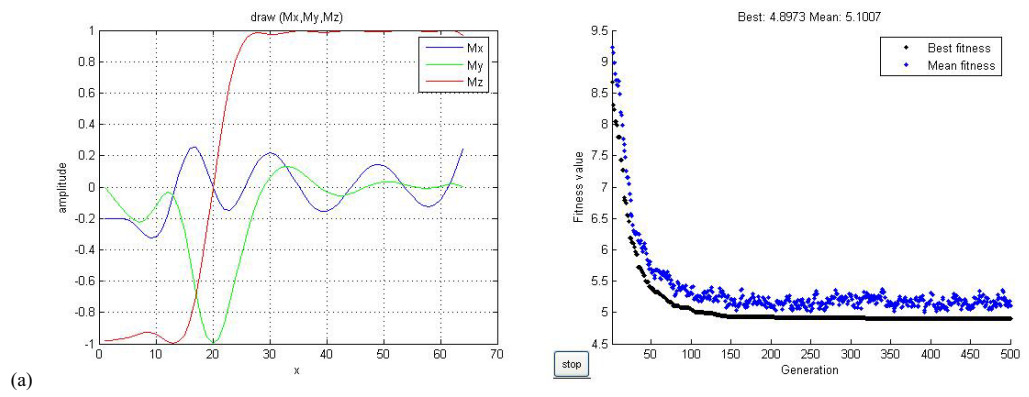


Fig. 2 (a) slice profile and Norm-1 Error with rank function, (b) slice profile and Norm-1 Error with proportional function, (c) slice profile and Norm-1 Error with top function, and (d) slice profile and Norm-1 Error with shift linear function



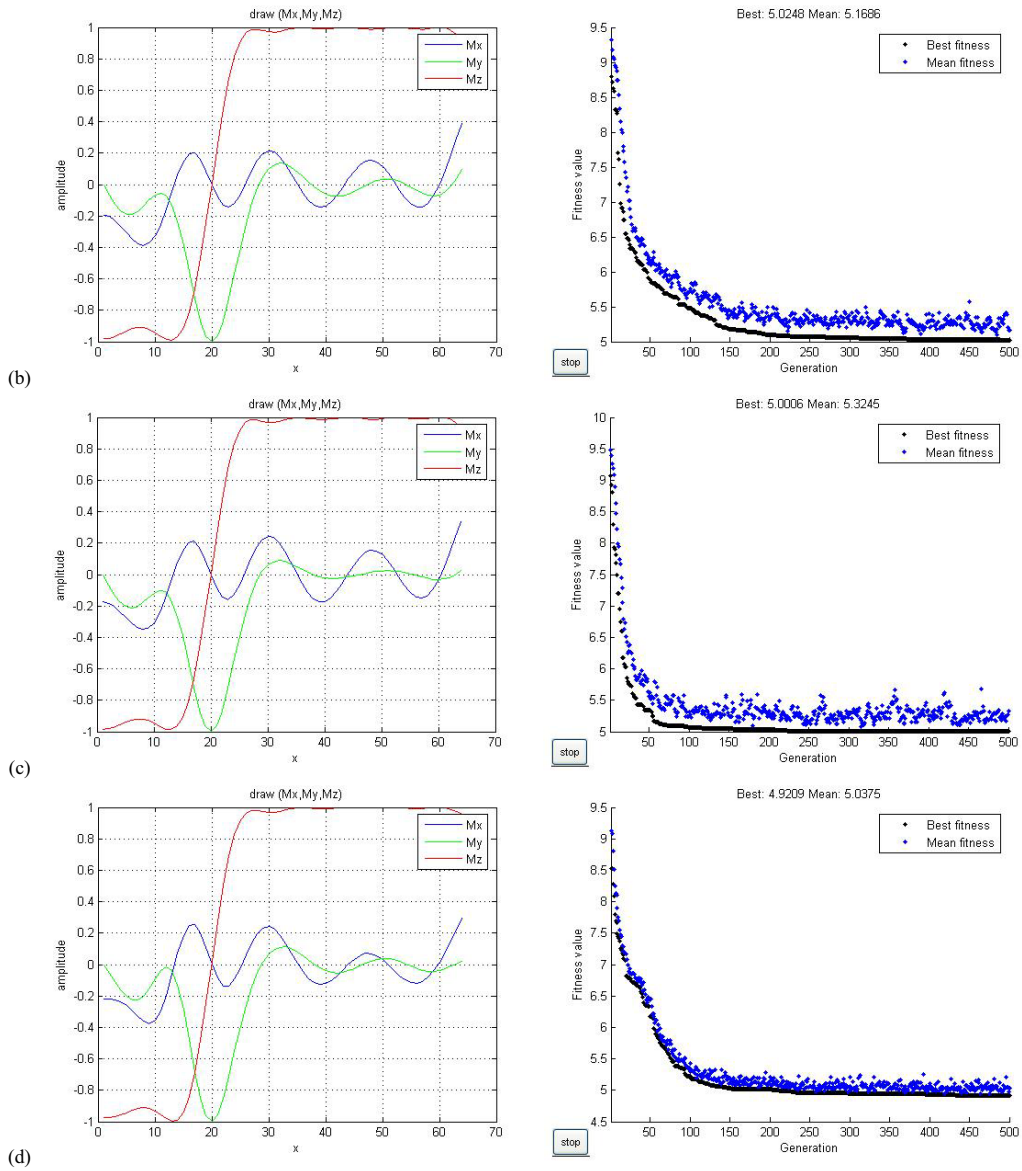


Fig. 3 (a) slice profile and Norm-1 Error with stochastic uniform function, (b) slice profile and Norm-1 Error with remainder function, (c) slice profile and Norm-1 Error with roulette function, and (d) slice profile and Norm-1 Error with tournament function

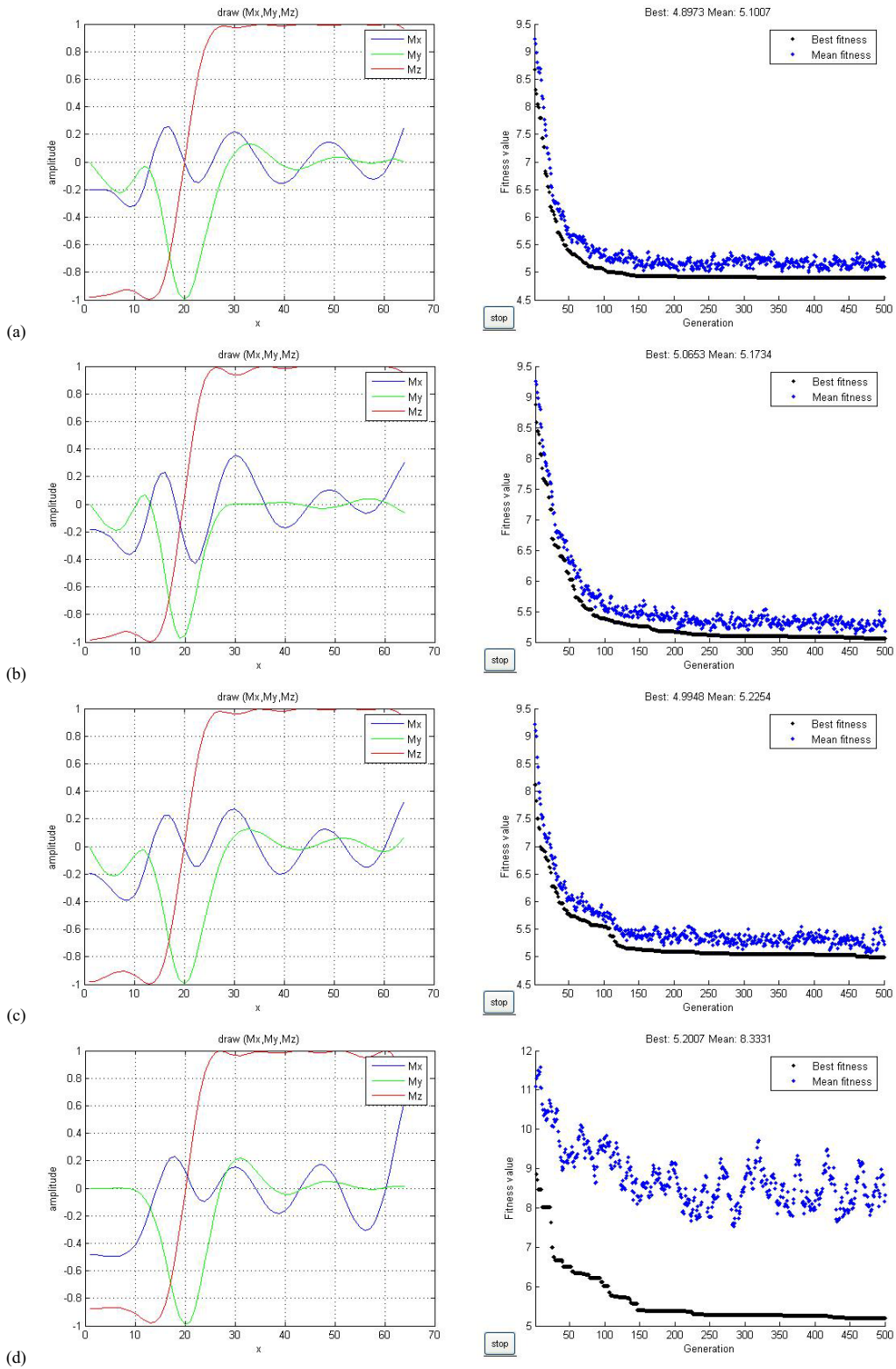


Fig. 4 (a) slice profile and Norm-1 Error with scattered function, (b) slice profile and Norm-1 Error with single point function, (c) slice profile and Norm-1 Error with two point function, and (d) slice profile and Norm-1 Error with Intermediate function

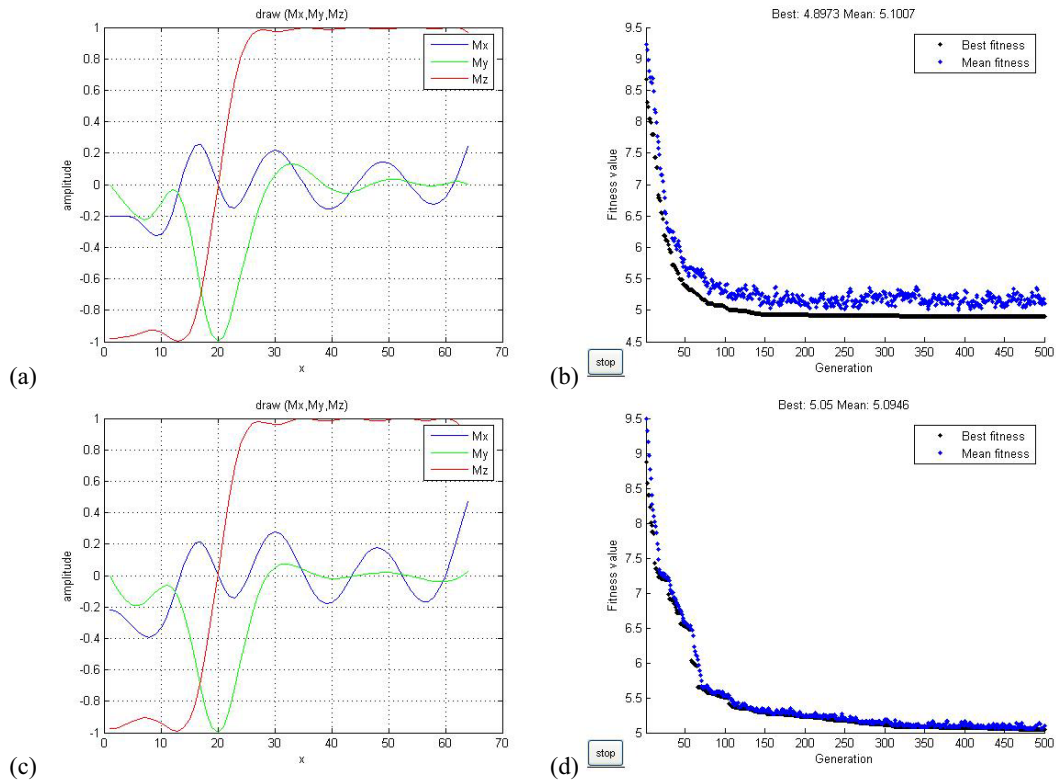
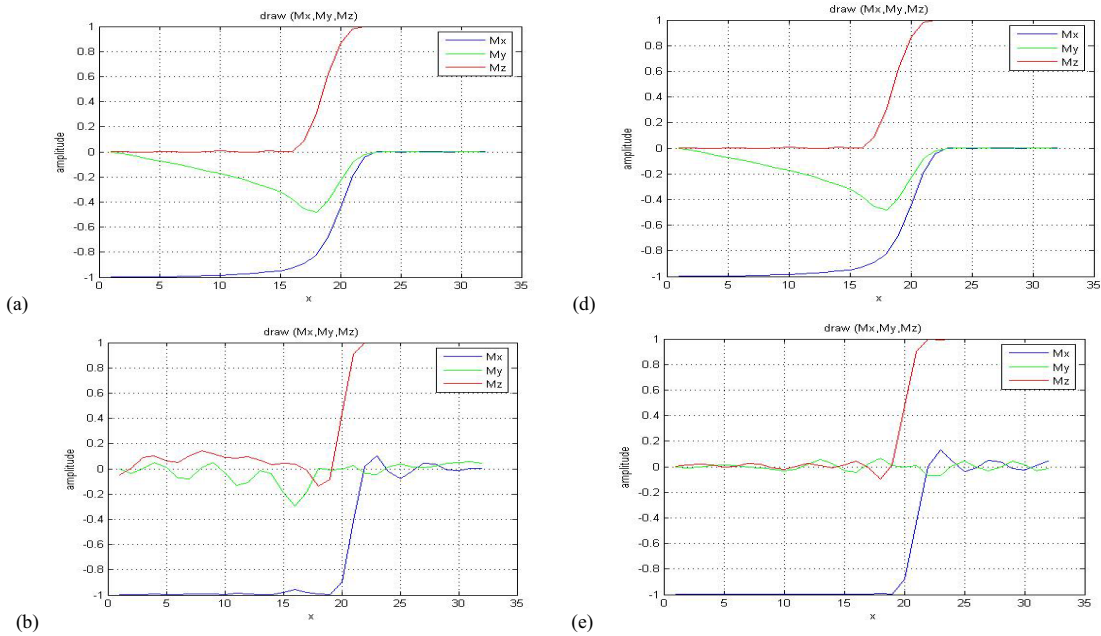


Fig. 5 (a, b) slice profile and Norm-1 Error with Gaussian function, (c, d) slice profile and Norm-1 Error with uniform function



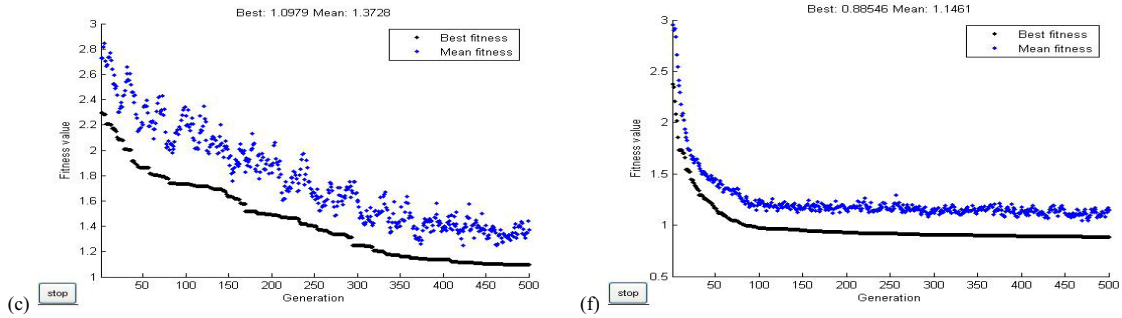


Fig. 6 (a, b, c) slice profile from SLR before GA, slice profile after GA, and Norm-1 Error for $\pi/2$ flip angle and 256 points from (previous work) , (d, e, f) slice profile before GA, slice profile after GA, and Norm-1 Error for $\pi/2$ flip angle and 256 points from our work

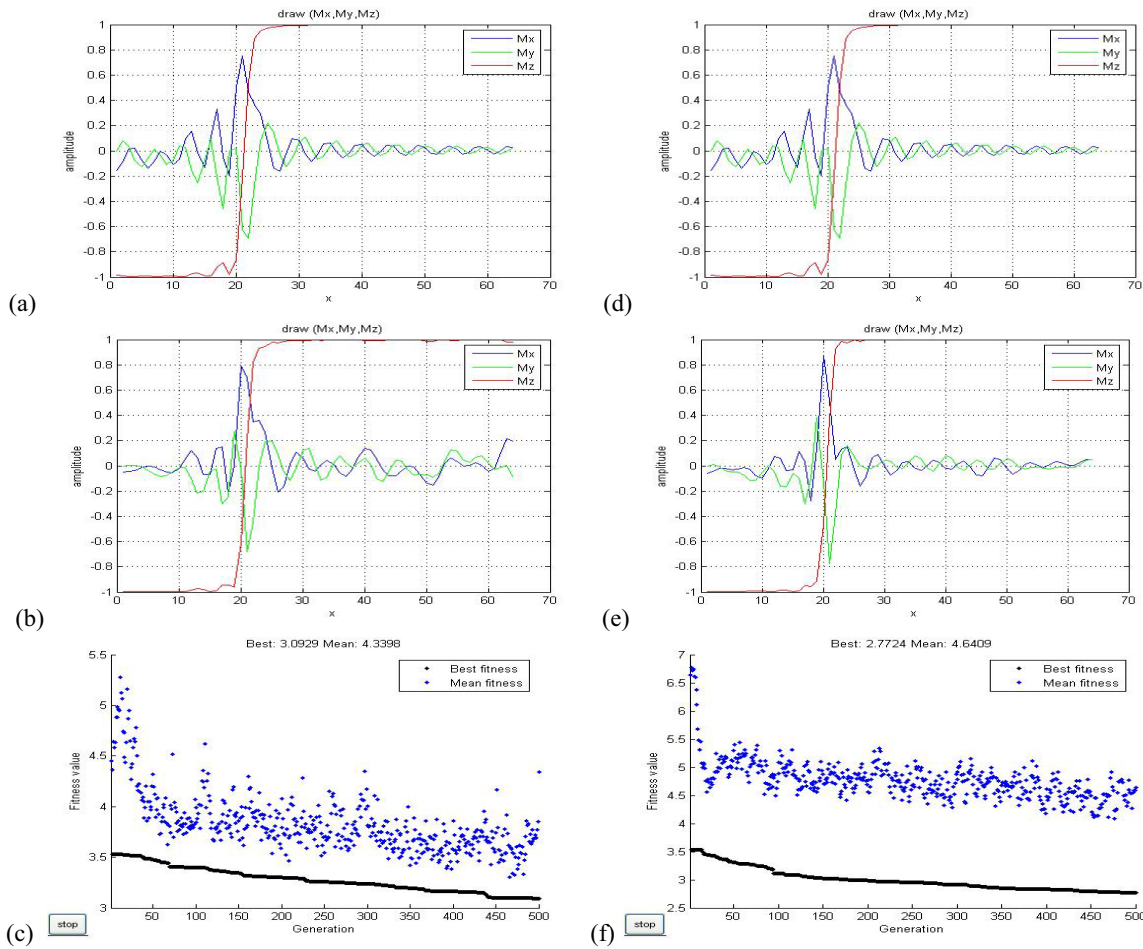


Fig. 7 (a, b, c) slice profile from SLR before GA, slice profile after GA, and Norm-1 Error for π flip angle and 256 points from (previous work) , (d, e, f) slice profile before GA, slice profile after GA, and Norm-1 Error for π flip angle and 256 points from our work