Optimization of Fidelity with Adaptive Genetic Watermarking Algorithm using Tournament Selection

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Abstract

Water making is the process of embedding data called a watermark into a multimedia object such that watermark can be detected or extracted later to make an assertion about the object. Earlier techniques based on spatial and frequency domain had the problems of a poor fidelity especially with higher payloads of watermark image. Unsatisfactory value of Peak Signal to Noise Ratio (PSNR) of watermarked image resulting in image quality degradation was seen in varying degree, in various research works. This paper is an attempt to employ genetic algorithms to find suitable locations for watermark insertion within a cover image, to focus on the issue of optimizing fidelity. The paper provides a comprehensive discussion of using a tournament selection strategy in genetic algorithm for this purpose and investigates the variation of maximum fitness which reflects the higher PSNR of the watermarked image with respect to embedding strength, number of genes, crossover probability, and number of generations consisting of binary matrix. With the proper understanding and analysis of the results of this paper, a successful watermarking scheme can be obtained using Genetic algorithms, which may be useful when optimizing the fidelity aspect of digital watermarking is the principal concern.

Keywords: Digital watermarking, genetic algorithm, fidelity, tournament selection.

1. Introduction

Digital watermarking should provide the qualities like imperceptibility, robustness, security of cover image. A large number of techniques have been developed in spatial domain and frequency domain like manipulating the bit plane of Least Significant Bit (LSB) [1]. Deng and wang[2] propose a novel algorithm to Embed a watermark into a still host image in DCT domain. Cox et al. [3] pointed that, in order for a watermark to be robust to attack, it must be placed in perceptually significant areas of the image. Kundur and Hatzinakos [4] embedded the watermark in the wavelet domain where the strength of watermark was decided by the contrast sensitivity of the original image. Huang at el[5] paper used a concept of DCT and proposed a Progressive watermarking Techniques with genetic algorithm. Dengeun Lee, Takeyung Kim, Seongwon and Joonki Paik [6] present a novel watermark extraction algorithm based on DWT and Genetic algorithm. Zhichen, Hao Li, Jufeng Dai and Sashuang Wang[7] proposed image watermarking based genetic algorithm. In order to improve the robustness and imperceptibility of the image spread spectrum watermark algorithm, a new approach for optimization in 8x8 domain using genetic algorithm. Chien-Chang chen and Chien-Shian Lin [8] propose Genetic algorithm based image authentication approach to improve the image quality of a protected image. Z.wai[9] et al. was proposed new embedding and extracting method with genetic algorithm. The proposed embedding and extracting method was employed to accelerate the genetic watermarking. B. Sikandar[10]
proposed method use genetic algorithm to optimize the strength of the watermark for mid-band DCT coefficient.

This paper proposes a technique which employs genetic algorithm to find a suitable location for watermark insertion within a cover image for optimizing fidelity without consideration the aspect of robustness.

Section II discusses the concept of genetic algorithm. Section III discusses the Algorithm for optimization of Fidelity using genetic algorithms. Section IV show Experimental Result and Conclusion is given in section V.

2. Genetic Algorithm

Genetic algorithms [11, 12] are search algorithms based on mechanics of natural selection and natural genetics. They combine survival of fittest among string structures with a structured yet randomized information exchange to form search algorithms with some of the innovative flair of human search. In every search, a new set of artificial creatures (strings) is created using bits and pieces of fittest of the old creatures. Conventional search techniques are not very suitable for optimizing non-linear functions with multiple variables. However, genetic algorithms this can be conveniently done.

In the genetic algorithms, the parameters are represented by an encoded binary string called the “chromosome” and the elements in the binary strings or the “genes” are adjusted to maximize or minimize the fitness values. The fitness function has to be carefully selected specific to a particular application and the kind of optimization required. Thus, the entire process of genetic algorithm starts with a set of proposed solutions randomly generated and try to produce further possible solutions to achieve the desired optimization.

The core components of the GA [11] are as under.
1. Fitness Value
2. Selection
3. Crossover
4. Mutation

Fitness Function: A Measurement of how well the chromosome fit the search space.
Selection: Selection is based on the survival-of-the-fittest mechanism. Chromosome is selected based on the fitness value.
Cross Over: The Chromosome with the higher fitness values generate more offspring.
Mutation: After Crossover, the strings are subjected to mutation. Mutation of a bit involves flipping it changing 0 to 1 and vice versa with a small probability.

3. Algorithm for Optimization of Fidelity Using Genetic Algorithm

Step 1: Let the cover image used to embed the watermark be given as

\[ \text{cimage} = \{c_{11}, c_{12}, \ldots, c_{ij}, \ldots, c_{mc \times nc}\} \]

where \(1 \leq i \leq mc\) and \(1 \leq j \leq nc\)

Step 2: \(\text{cimage}(i-j*nc+j) = \text{cimage}(i,j)\),

\(\text{where}, \ 1 \leq i \leq mc\) and \(1 \leq j \leq nc\)

This produces a row vector

\[ \text{cimage}(c_1, c_2, \ldots, c_i, \ldots, c_{mc*nc}) \]
The size of the cover image is given as \( s_1 = m \times c \times n_c \)

**Step 3:** Let the watermark be given as

\[
w = \{ w_{11}, w_{12}, \ldots, w_{ij}, \ldots, w_{nm} \}
\]

where \( 1 \leq i \leq m \) and \( 1 \leq j \leq n \)

**Step 4:** The array fitness is initialized with all zeros.

\[
\text{fitness} = [0, 0, 0, \ldots \times \text{pop_size times}]
\]

**Step 5:** The array population is created randomly as

\[
\text{Population} = \{ p_{11}, p_{12}, \ldots, p_{ij}, \ldots, p_{\text{pop_size} \times \text{no_of_genes}} \}
\]

where \( 1 \leq i \leq \text{pop_size} \) and \( i < j \leq \text{no_of_genes} \)

**Step 6:** The watermark is converted into a single dimension vector \( W_{m1} \) as

\[
W_{m1} = \{ w_1, w_2, \ldots, w_i, \ldots, w_{mn} \}
\]

The total number of watermark locations is given by \( m \times n \).

**Step 7:** The individual chromosomes from the population are extracted.

\[
\text{chromosomes}[k] = \{ p_{k1}, p_{k2}, \ldots, p_{ki}, \ldots, p_{\text{no_of_genes}} \}
\]

where, \( 1 \leq k \leq \text{pop_size} \) and \( p_{k1}, p_{k2}, \ldots, p_{ki}, \ldots, p_{\text{no_of_genes}} \) are the genes of the population.

**Step 8:** The individual chromosomes are brought into variable range as following.

First of all, the watermark locations in the cover image \( x(i) \) are found.

\[
x(i) = \sum \text{chromosomes}(y + j) \times 2^j
\]

where \( 1 \leq i \leq \text{watermark_location} \) and \( 1 < j < \text{no_of_genes}/\text{watermark_location} \), \( y = 0 \) then

\[
x(i) = 1 + \text{fix}((\text{variable_range}-1) \times x(i)/(1-2^{\text{no_of_genes}/\text{watermark_location}}))
\]

where \( 1 \leq i \leq \text{watermark_location} \)

**Step 9:** The Pixel intensity value of the cover image as modified at the selected location specified by \( x(i) \),

(\( 1 \leq i \leq \text{watermark_location} \)) according to the following procedure.

\[
\text{new_cimage}(x(i)) = \text{cimage}(x(i)) + \text{multi} \times \text{cimage}(x(i))
\]

\[
\text{new_cimage}(x(i)) = \text{cimage}(x(i)) - \text{multi} \times \text{cimage}(x(i))
\]

where \( 1 \leq i \leq \text{watermark_location} \) and \( W_{m1}(i) = 1 \)

where \( 1 \leq i \leq \text{watermark_location} \) and \( W_{m1}(i) = 0 \)

where \( \text{multi} \) is embedding strength

**Step 10:** The similarity between the modified cover image and the original cover image is termed as fitness \( f(i) \) calculated as per following equation.

\[
f(i) = 10 \times \log 10 \left( \frac{(\text{max_value})^2}{\text{psnrsum}} \right)
\]

where \( 1 \leq i \leq \text{pop_size} \) and \( \text{max_value} = \text{Max} \{ \text{cimage}(c_1, c_2, \ldots, \ldots, c_{mc \times nc}) \} \)

and \( \text{psnrsum} \) is given by

\[
\text{psnrsum} = \sum_{\text{var}=1}^{\text{mc} \times \text{nc}} \left( \text{new_cimage(var)} - \text{cimage(var)} \right)^2
\]

**Step 11:** Now maxfitness and bestindividual index \( k \) is derived
\[ F(i) < f(k) \quad \forall i : 1 \leq i \leq pop\_size \text{ and } i \neq k, \ 1 \leq k \leq pop\_size \quad (15) \]

Repeat step 12 to 14 for each value of \( i \) varying from 1 to \( pop\_size \) in increment of 2

Step 12: Tournament selection is done, index \( I_1 \) and \( I_2 \) are selected

\[
I_1 = \begin{array}{ll}
itemp1 & \text{if } f(itemp1) > f(itemp2) \\
itemp2 & \text{if } f(itemp2) > f(itemp1)
\end{array} \quad (16)
\]

where \( r < \text{tournamentselectionparameter} \) and \( itemp1 \) and \( itemp2 \) are two randomly generated indices such that

\[ 1 \leq itemp1 \leq pop\_size \text{ and } 1 \leq itemp2 \leq pop\_size \text{ and } r \text{ is randomly generated between } 0 \leq r < 1. \]

\[
I_2 = \begin{array}{ll}
itemp2 & \text{if } f(itemp1) > f(itemp2) \\
itemp1 & \text{if } f(itemp2) > f(itemp1)
\end{array} \quad (17)
\]

where \( r > \text{tournamentselectionparameter} \) and \( itemp1 \) and \( itemp2 \) are two randomly generated indices such that

\[ 1 \leq itemp1 \leq pop\_size \text{ and } 1 \leq itemp2 \leq pop\_size \text{ and } r \text{ is randomly generated between } 0 \leq r < 1. \]

The chromosome corresponding to the selected indices \( I_1 \) and \( I_2 \) are generated

\[
\begin{align*}
\text{chromosome}_1 &= \text{population}(I_1,J) \quad \text{where } 1 \leq J \leq \text{no\_of\_genes} \\
\text{chromosome}_2 &= \text{population}(I_2,J) \quad \text{where } 1 \leq J \leq \text{no\_of\_genes}
\end{align*}
\quad (18, 19)
\]

Step 13: The crossover point is selected randomly such that

\[ 1 \leq \text{crossoverpoint} < \text{no\_of\_genes} \]

Now crossover between \( \text{chromosome}_1 \) & \( \text{chromosome}_2 \) is performed as per following equation and new chromosome pair called \( \text{newChromosome\_pair} \) is generated.

\[
\begin{align*}
\text{newChromosome\_pair}(1,j) &= \text{chromosome}_1(j) \quad (20) \\
\text{newChromosome\_pair}(2,j) &= \text{chromosome}_2(j) \quad (21)
\end{align*}
\]

\[ \forall j \ni 1 \leq j \leq \text{crossoverpoint} \]

\[ OR \]

\[
\begin{align*}
\text{newChromosome\_pair}(1,j) &= \text{chromosome}_2(j) \quad (22) \\
\text{newChromosome\_pair}(2,j) &= \text{chromosome}_1(j) \quad (23)
\end{align*}
\]

\[ \forall j \ni \text{crossoverpoint} < j \leq \text{no\_of\_genes} \]

Step 14: new population is defined as

\[
\begin{align*}
\text{new\_population}(i,j) &= \text{newChromosome\_pair}(1,j) \quad (24) \\
\text{new\_population}(i+1,j) &= \text{newChromosome\_pair}(2,j) \quad (25)
\end{align*}
\]

\[ \forall j \ni 1 \leq j \leq \text{no\_of\_genes} \text{ and } r < \text{crossoverprobability}, \text{ where } r \text{ is random number generated between } 0 \leq r < 1 \]

If \( r > \text{crossoverprobability} \) then crossover is not performed and \( \text{new\_population} \) is given by
\[ \text{new}_{-}\text{population}(i,j) = \text{chromosome1} \quad \text{and} \]
\[ \text{new}_{-}\text{population} (i+1,j) = \text{chromosome2} \]
\( \forall j \neq j < \text{no}_{-}\text{of}_{-}\text{genes} \) \tag{26}
\[ \text{new}_{-}\text{population}(i,j) = 1 - \text{new}_{-}\text{population}(i,j) \]
\( \forall i, j : 1 < i < \text{pop}_{-}\text{size} \text{ and } 1 < j < \text{no}_{-}\text{of}_{-}\text{genes} \text{ and } r < \text{mutation}_{-}\text{probability,} \]
where \( r \) is random number
\begin{equation*}
\text{generated between } 0 < r < 1
\end{equation*}
Step 15 : The \ new_{-}\text{population} \text{ is redefined such that each chromosome in the}
\ new_{-}\text{population} \text{ is mutated depend on the mutation probability.}
Step 16 : \text{gen}_{-}\text{count} = \text{gen}_{-}\text{count} + 1
Step 17 : \text{population} = \text{new}_{-}\text{population}
Repeat all step 7 to 16 for \text{gen}_{-}\text{count} < \text{no}_{-}\text{of}_{-}\text{generation}

Now the maxfitness and bestwatermark location is obtained.

4. Experimental Results

In order to investigate and study the GA based watermarking scheme using tournament selection which produces the desired locations for watermark insertion for fidelity optimization in a systematic way, four experiments were conducted. In all of these experiments, the cover images used is Lena size (512 X 512) Fig. (1) and the binary two dimensional matrix with varying length in different experiments as the watermark.

4.1. Experiment No. 1

In this experiment, the convergence of genetic algorithm is seen which is obtained when the most optimized value is reached. In the present case, this happens when the best fidelity is obtained for a given set of embedding locations within the cover image. The number of generations was gradually increased and the value of maximum fidelity was obtained in each case for varying number of genes in the selected chromosomes. The results are tabulated as Table no. : (1) and the fig (2). Show the variation of maximum fitness with respect to number of generations for different values of genes in the selected chromosomes.

It is observed that the value of maximum fitness increases fast when the numbers of generations change from 50 to 100 and then there is a slow improvement in fidelity for the number of generations between 100 and 500. This is due to attaining a significant improvement in fidelity in lesser number of generations. With increased number of generations, there is a trend of increased fidelity of watermarked image.
The various parameter settings for conducting this experiment of GA were as follows:
Embedding strength = 0.5, Crossover probability = 0.75, Mutation probability = 0.025, Tournament selection parameter = 0.75.

### Table 1. Variation of Maximum Fitness with Generation

<table>
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<tr>
<th>S.No</th>
<th>Watermark Bits</th>
<th>No. of Genes</th>
<th>Maximum Fitness when Generation=50</th>
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Fig. 2 Maximum Fitness Vs Generation when No. of Genes Varies from 80 to 1280

4.2. Experiment No. 2

In this experiment, the variation of maximum fitness corresponding to best fidelity of watermarked image is seen with respect to varying number of genes in the chromosome for different values of embedding strength. The embedding strength is varied from 0.1 to 0.5 and for each value of embedding strength, the number of genes is varied from 80 to 1280 and the results are tabulated as shown in table no (2) and chart show in fig. 3. The charts indicate that
for a given value of number of genes the maximum fitness reduces with increase in the value of the embedding strength

The best value of the maximum fitness obtained is 78.1907 corresponding to an embedding strength of 0.1 and number of genes equal to 80.

For conducting this experiment, the following parameter settings are taken in Genetic algorithm.

Crossover probability 0.75, Mutation probability = 0.025, Number of generations = 200, Tournament selection parameter = 0.75

![Graph showing variation of maximum fitness with embedding strength](image)

**Table 2. Variation of Maximum Fitness with Embedding Strength**

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<tr>
<th>S. No</th>
<th>Watermark Bits</th>
<th>No. of Genes</th>
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<th>Maximum Fitness when Embedding Strengths=0.3</th>
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4.3. Experiment no 3

In this experiment, the variation of maximum fitness corresponding to best fidelity of watermarked image is seen with respect to different value of tournament selection parameters ranging from 0.85 to 0.25. The experiment is conducted with number of genes varying from
80 to 1280 and a fixed embedding strength of 0.5. The results are tabulated as table no (3) and also as different charts shown in fig from (4) to fig (5).

The charts shown in fig from (4) to (5) indicate that the highest value of maximum fitness after convergence of GA is obtained when tournament selection parameter is 0.85 and gradually reduces with decrease in the value of tournament selection parameter from 0.85 to 0.25. The highest value of the maximum fitness is observed when the tournament selection parameter is taken as 0.85 and the number of genes is taken as 80. Thus, there is a trend of increase in the maximum fitness value with the increment in the tournament selection parameter for a given value of number of genes.

The various parameter settings for conducting this experiment of GA were as follows: Embedding strength = 0.5, Crossover probability = 0.75, Mutation probability = 0.025, Number of generations = 200

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<td>256</td>
<td>1280</td>
<td>51.1618</td>
<td>50.7522</td>
<td>50.8161</td>
<td>51.1154</td>
<td>50.8581</td>
</tr>
</tbody>
</table>
4.4. Experiment no 4

In this experiment, the variation of maximum fitness corresponding to best fidelity of watermarked image is seen with respect to different value of crossover probability ranging from 0.85 to 0.25. The experiment is conducted with number of genes varying from 80 to 1280 and a fixed embedding strength of 0.5. The results are tabulated as table no (4) and also as different charts shown in fig from fig no (6) to fig no(7).

The charts from (6) to (7) indicate that the highest value of maximum fitness (64.6275) after convergence of GA is obtained when the value of crossover probability is 0.85 and gradually reduces with decrease in the value of crossover Probability from 0.85 to 0.25 from 64.6275 to 63.0207 for the number of genes taken as 80.

The highest value of the maximum fitness is observed when the cross over probability is taken as 0.85 and the number of genes is taken as 80. Thus, there is a trend of increase in the maximum fitness value with the increment in the crossover probability for a given value of number of genes.

The various parameter settings for conducting this experiment of GA were as follows: Embedding strength = 0.5, Tournament selection parameter =0.75, Mutation probability = 0.025, Number of generations = 200

![Fig. 5 Maximum Fitness Vs Tournament Selection when No. of Genes Varies from 280 to 1280](image1)

![Fig. 6 Maximum Fitness Vs Crossover Probability when No. of Genes Varies from 80 to 200](image2)
5. Conclusions

In this paper has made a compressive study for the application of tournament selection strategy in genetic algorithm for digital watermarking application. The result obtained from the various experiment conducted as shown in the paper in the form of table and chat make it possible to understand the behavior of maximum fitness obtained after the convergence of genetic algorithms with various setting of number of genes, no of crossover probability, tournament selection parameter, Embedding strengths. While conducting of the experiment the primary concern has been taken to maximize a fidelity corresponding to high fitness value of GA without taking the consideration of robustness of inserted watermark under various attack and the inverse trade off between robustness and fidelity, so this work find special utility in watermarking application sole aim of obtaining high quality of watermark image. This work also can serve as a basis of inserting GA with other conventional watermarking algorithm to obtain maximum fidelity.
References


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