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. Zhicheng , Hao Li , Jufeng Dai and Sashuang Wang[7] proposed image watermarking based genetic algorithm. In order to improve the robustness and imperceptibleness 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 en 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

$$cimage = [\ c_{11},\ c_{12}, \ldots \ldots \ldots c_{ij} \ldots \ldots \ldots \ldots c_{mc\ x\ nc}] \qquad (1)$$
$$where\ 1 <= i <= mc\ and\ 1 <= j <= nc$$

Step 2 : cimage is now reshaped into row vector containing mc*nc entries

$$cimage((i\text{-}1)*nc+j) = cimage(i,j, $$
$$where,\ 1 <= i <= mc\ and\ 1 <= j <= nc \qquad (2)$$

This produces a row vector

$$cimage(c_1, c_2, \ldots \ldots c_i, \ldots \ldots c_{mc*nc}) \qquad (3)$$

The size of the cover image is given as s1=mc*nc

Step 3:   Let the watermark be given as

$w=[w_{11},w_{12},.........w_{ij},........w_{mn}]$ *(4)*
where 1<=i<=m and 1<=j<=n

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

 fitness=[0,0,0,0...pop_size times]   *(5)*

Step 5:   The array population is created randomly as

Population = [p_{11},p_{12,},.........p_{ij}...,p_{popsize*no_of_genes}]   *(6)*

where 1<=i<=pop_size and i<j<=no_of_genes And p_{ij}=0 or 1 (randomly assigned)

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

$W_{m1}=[w_1,w_2,...w_i,...w_{m*n}]$ *(7)*
The total number of watermark locations is given by m*n.

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

$chromosomes[k]=[p_{k1},p_{k2},...p_{ki},.....p_{kno\_of\_genes}]$ *(8)*
where, 1<=k<=pop_size and $p_{k1},p_{k2},...p_{ki}$,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.

$$x(i) = \sum chromosomes(y+j) \times 2^{-j} \qquad (9)$$

where 1<=i<=watermark_location and 1<=j<=no_of_genes/watermark_location, y=0
then
$x(i) = 1+ fix((variable\_range-1)*x(i)/(1-2^{-no\_of\_genes/watermark\_location}))$ *(10)*
where 1<=i<=watermark_location

Step 9:   The Pixel intensity value of the cover image as modified at the selected location specified by x(i),
(where 1<=i<=watermark_location) according to the following procedure.

*new_cimage(x(i)) = cimage(x(i)) + multi * cimage(x(i))*   *(11)*
where 1<=i<=watermark_location and $W_{m1}(i)=1$

*new_cimage(x(i)) = cimage(x(i)) - multi * cimage(x(i))*   *(12)*
where 1<=i<=watermark_location and $W_{m1}(i)=0$
where multi is embedding strength

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

*f(i) = 10 * log 10 ((max_value)^2/ psnrsum)*   *(13)*
where 1<=i<=pop_size and max_value = Max[cimage(c_1,c_2,.........c_{mc*nc})]

and psnrsum is given by

$$psnrsum = \sum_{var=1}^{mc*nc}(new\_cimage(var) - cimage(var))^{\wedge}2 \qquad (14)$$

Step 11: Now maxfitness and bestindividual index k is derived

$$F(i) < f(k) \quad \forall i \therefore 1 <= 1 <= pop\_size \ and \ i <> k \ , \ 1 <= k <= pop\_size \qquad (15)$$

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 I1 and I2 are selected

$$I1 \ = \quad itemp1 \qquad\qquad if \ f(itemp1) > f(itemp2)$$

$$itemp2 \qquad\qquad if \ f(itemp2) > f(itemp1) \qquad (16)$$

where r< tournamentselectionparameter and itemp1 and itemp2 are two randomly generated index such that.

1<=itemp1<=pop_size and 1<=itemp2<=pop_size and r is randomly generated between 0<=r<1.

$$I2 \ = \quad itemp2 \qquad\qquad if \ f(itemp1) > f(itemp2)$$
$$itemp1 \qquad\qquad if \ f(itemp2) > f(itemp1) \qquad (17)$$

where r> tournamentselectionparameter and itemp1 and itemp2 are two randomly generated index such that

1<=itemp1<=pop_size and 1<=itemp2<=pop_size and r is randomly generated between 0<=r<1.

The chromosome corresponding to the selected indices I1 and I2 are generated

$$chromosome1 = population(I1,J)$$
$$where \ 1 <= J <= no\_of\_genes \qquad (18)$$
$$chromosome2 = population(I2,J)$$
$$where \ 1 <= J <= no\_of\_genes \qquad (19)$$

Step 13: The crossover point is selected randomly such that
$$1 <= crossoverpoint < no\_of\_genes$$

Now crossover between chromosome1 & chromosome2 is performed as per following equation and new chromosome
pair called newChromosome_pair is generated.

$$newChromosome\_pair(1,j) = chromosome1(j) \qquad (20)$$
$$newChromosome\_pair(2,j) = chromosome2(j) \qquad (21)$$

$$\forall j \therefore, \ 1 <= j <= crossoverpoint$$

OR

$$newChromosome\_pair(1,j) = chromosome2(j) \qquad (22)$$
$$newChromosome\_pair(2,j) = chromosome1(j) \qquad (23)$$

$$\forall j \therefore, \ crossoverpoint < j <= no\_of\_genes$$

Step 14 : new population is defined as
$$new\_population(i,j) = newChromosome\_pair(1,j) \qquad (24)$$
$$new\_population \ (i+1,j) = newChromosome\_pair(2,j) \qquad (25)$$

$\forall j \therefore, \ 1 <= j <= no\_of\_genes$ *and r<crossoverprobabilty, where r is random number generated between 0<=r<1*

If r> crossoverprobability then crossover is not performed and new_population is given by

$$new\_population(i,j) = chromosome1 \text{ and} \qquad (26)$$
$$new\_population (i+1,j)=chromosome2 \qquad (27)$$
$$\forall j \because, 1<=j<=no\_of\_genes$$

Step 15 : The new_population is redefined such that each chromosome in the new_population is mutated depend on the mutation probability.

$$new\_population(i,j) = 1- (new\_population(i,j)) \qquad (28)$$

$\forall i, j \because 1<=i<=pop\_size$ and $1<=j<=no\_of\_genes$ and $r<mutation\_probability,$
where r is random number
generated between $0<=r<1$

Step 16 : gen_count = gen_count+1
Step 17 : population= new_population
Repeat all step 7 to 16   for gen_count<=no_of_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.

Fig.1 Cover Image (Lena Image)

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

| S.No	Watermark Bits	No. 0f Genes	Maximum Fitness when Generation=50	Maximum Fitness when Generation= 100	Maximum Fitness when Generation= 200	Maximum Fitness when Generation= 300	Maximum Fitness when Generation =500
1	16	80	61.9310	64.4573	64.9461	64.9461	64.9461
2	20	100	58.9103	62.3282	63.6407	63.6407	64.2557
3	24	120	57.8990	59.2114	60.8304	60.8304	61.7380
4	28	140	57.8538	59.5180	60.4116	61.4265	63.4265
5	32	160	55.9495	58.1732	58.4176	61.1590	63.3970
6	40	200	55.5363	57.4926	57.8345	57.9638	58.4462
7	56	280	54.8160	55.3195	55.9454	55.9608	56.3282
8	112	560	51.7359	51.9656	52.1840	52.1840	52.3330
9	128	640	51.8106	51.9309	52.3851	52.4891	52.4891
10	256	1280	50.7029	50.7522	50.8348	50.8523	50.8523
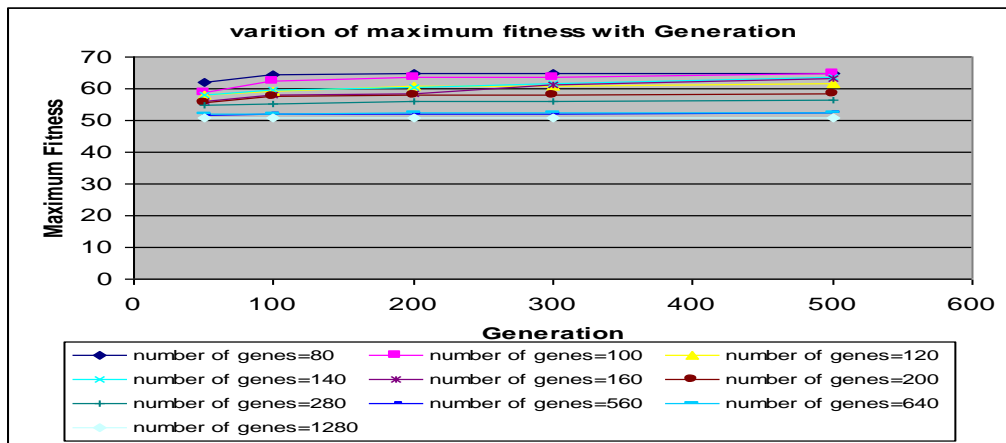
Fig. 2 Maximum Fitness Vs Generation when No. of Genes Varies from 80 to 1280

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
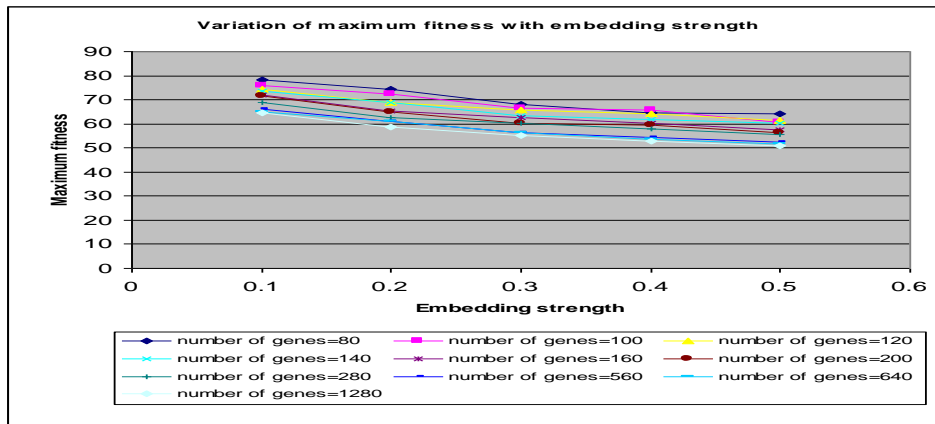

Fig. 3 Maximum fitness Vs Embedding Strength when No. of Genes Varies from 80 to 1280

Table 2. Variation of Maximum Fitness with Embedding Strength

S. No	Water mark Bits	No. 0f Gen es	Maximum Fitness when Embedding Strengths=0.1	Maximum Fitness when Embedding Strengths= 0.2	Maximum Fitness when Embedding Strengths= 0.3	Maximum Fitness when Embedding Strengths= 0.4	Maximum Fitness when Embedding Strengths= 0.5
1	16	80	78.1907	74.2013	68.1523	64.4774	64.3328
2	20	100	75.9836	72.3153	66.3448	65.7418	60.7591
3	24	120	74.4120	68.6929	65.7568	64.3524	61.3901
4	28	140	73.6137	68.8274	63.2830	61.7785	60.3328
5	32	160	71.9436	65.4888	62.6579	60.2618	57.4112
6	40	200	71.7780	64.9562	60.4088	59.5264	56.4498
7	56	280	69.027	62.7078	60.2377	57.8788	55.6938
8	112	560	66.2833	61.2312	56.3472	54.2084	52.5103
9	128	640	65.1021	60.9102	56.1604	53.6875	51.6456
10	256	128 0	64.7346	58.7120	55.1922	52.9507	50.7522

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
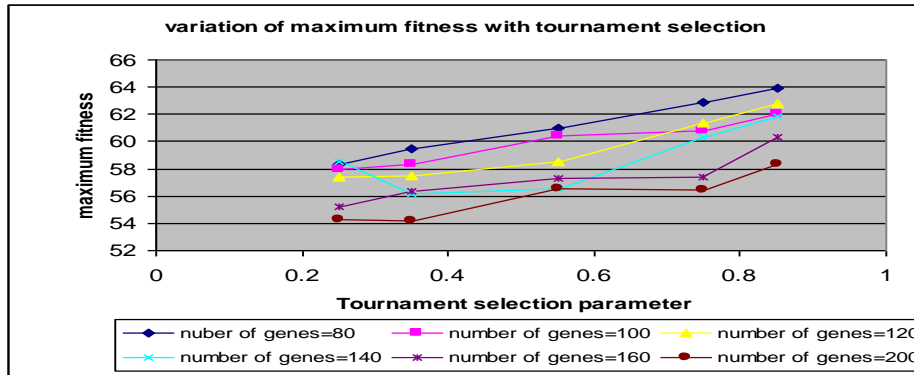

Fig. 4 Maximum Fitness Vs Tournament Selection when No. of Genes Varies from 80 to 200

Table 3. Variation of Maximum Fitness with Tournament Selection

S.No	Water mark Bits	No. 0f Genes	Maximum Fitness when Tournament Selection Parameter =0.85	Maximum Fitness when Tournament Selection Parameter= 0.75	Maximum Fitness when Tournament Selection Parameter= 0.55	Maximum Fitness when Tournament Selection Parameter= 0.35	Maximum Fitness when Tournament Selection Parameter= 0.25
1	16	80	63.9049	62.9154	61.0021	59.4803	58.3133
2	20	100	62.0085	60.7591	60.4590	58.3012	57.9418
3	24	120	62.8015	61.3901	58.5553	57.5210	57.4341
4	28	140	61.8801	60.3328	56.5739	56.1203	58.5293
5	32	160	60.3620	57.4112	57.3141	56.3305	55.2330
6	40	200	58.3017	56.4498	56.4956	54.2014	54.2780
7	56	280	55.9115	55.6938	54.0437	53.4652	53.7661
8	112	560	52.8044	52.5103	52.3429	51.4017	51.4208
9	128	640	52.0643	51.6456	51.9407	51.4927	50.0112
10	256	1280	51.1618	50.7522	50.8161	51.1154	50.8581

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
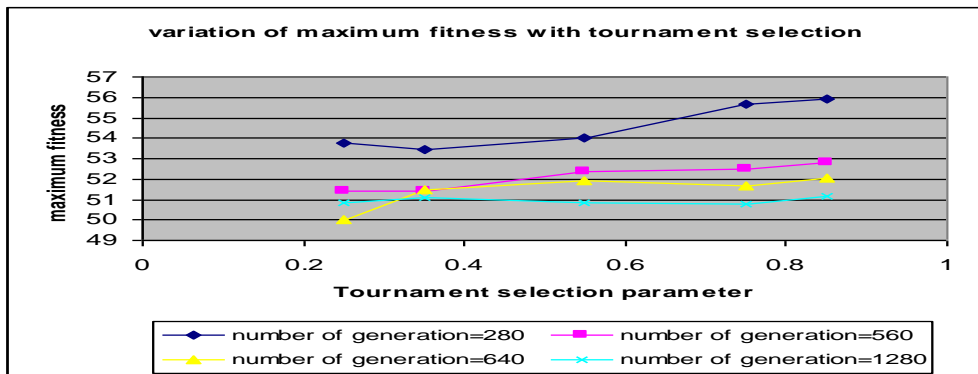

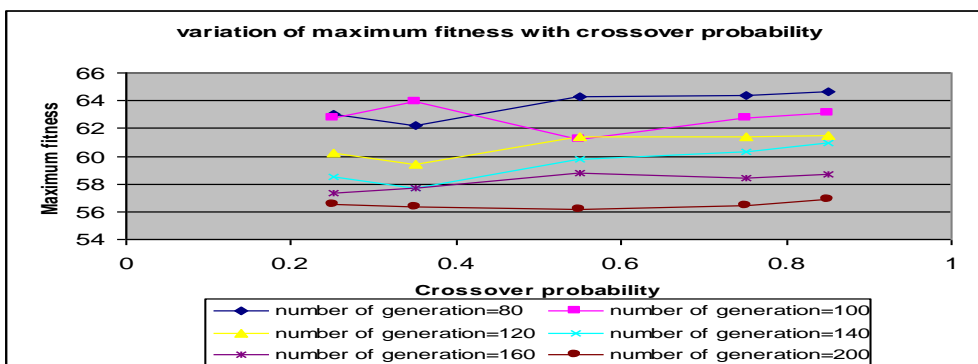**Fig. 5 Maximum Fitness Vs Tournament Selection when No. of Genes Varies from 280 to 1280**

Fig. 6 Maximum Fitness Vs Crossover Probability when No. of Genes Varies from 80 to 200
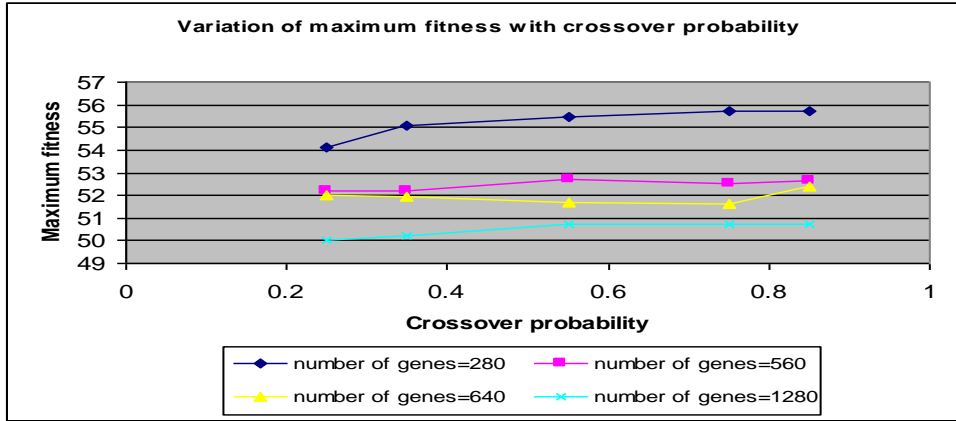
Fig. 7 Maximum Fitness Vs Crossover Probability when No. of Genes Varies from 280 to 1280

Table 4. Variation Maximum Fitness with Crossover Probability

S.No	Water mark Bits	No. 0f Genes	Maximum Fitness when CrossOver Probability= 0.85	Maximum Fitness when CrossOver Probability =0.75	Maximum Fitness when CrossOver Probability =0.55	Maximum Fitness when CrossOver Probability =0.35	Maximum Fitness when CrossOver Probability =0.25
1	16	80	64.6275	64.3328	64.2467	62.2245	63.0207
2	20	100	63.1429	62.7591	61.2108	63.8843	62.7595
3	24	120	61.4796	61.3901	61.4277	59.3993	60.1873
4	28	140	60.9268	60.3328	59.7797	57.7255	58.4802
5	32	160	58.7294	58.4112	58.7851	57.7153	57.3666
6	40	200	56.8708	56.4498	56.1753	56.3902	56.5701
7	56	280	55.7189	55.6938	55.4711	55.0555	54.1201
8	112	560	52.1760	52.5103	52.7104	52.1699	52.6286
9	128	640	51.6899	51.6456	52.3828	51.9229	51.9878
10	256	1280	50.7522	50.7522	50.7143	50.2012	50.0120

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.

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