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GENETIC CHROMODYNAMICS FOR MULTIMODAL OPTIMIZATION

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Abstract. An improved Genetic Chromodynamics strategy, with simulated annealing characteristics is proposed. The main idea of Genetic Chromodynamics is a local interaction scheme, that forces the formation and maintenance of subpopulations of solutions. The subpopulations co-evolve and will converge towards different optimal solutions. Very similar individuals are merged. At convergence the number of subpopulations equals the number of optimal solutions. A simulated annealing like heuristic may be considered to conserve population diversity and to prevent premature convergence of the search process. But the simulated annealing acceptance of worse offspring causes some loss of the optimum points. To drawback this difficulty the local interaction scheme is modifying through time by decreasing the interaction radius.

1.Introduction

Genetic chromodynamics (GC) (see [3],[4],[5][6]) is an evolutionary strategy designed to prevent premature local convergence and to detect multiple optimal solutions. GC uses a variable sized population and a local mating scheme. The main idea of the GC is to force the formation and maintenance of subpopulations of solutions. Subpopulations co-evolve and converge towards different optimal problem solutions. The number of individuals in the population decreases with the generations. There is a high probability that each new generation will contain some individuals better than the individuals in the previous generation. Only local chromosome interactions are allowed. The role of the mating scheme can be summarised as follows (see [3]):

(i) to ensure early subpopulation formation and stabilisation;
(ii) to avoid massive migration between subpopulationns approximating different optimum points
(iii) to prevent destruction of some useful subpopulations
(iv) to ensure a high probability of obtaining each optimal solution

Very similar individuals are merged. At convergence the number of subpopulations equals the number of optimal solutions. Each final subpopulation will contain a single individual representing an optimum point. Every chromosome in each generation is selected for crossover and mutation.

The crossover mate of a given chromosome is selected from a determined mating region, this region of a given c chromosome is the closed ball V(c,r) of center c and radius r. The radius r can be interpreted as the interaction radius of the individual c. Let m be a chromosome in the interaction domain.

The probability p(m) that the m is selected as the mate of c can be defined as

$$p(m) = \frac{f(m)}{\sum_{a \in V(c,r)} f(a)}.$$

A (2,1) crossover mechanism is used. The first parent is dominant and the second one is recessive. The unique offspring is labelled as the descendent of its dominant parent. If the closed ball V(c,r) is empty, then the chromosome c will be selected for mutation. By mutation chromosomes are forced towards one of the existing subpopulations.

In usual genetic algorithms (see [2]) mutations are generally unconditionally accepted. To improve the convergence of GC techniques we may consider a more sophisticated acceptation mechanism. Within this mechanism a mutated chromosome which is better than its parent is unconditionally accepted in the new generation. Otherwise we associate to each chromosome worse than its parent an acceptance probability p.

A simulated annealing (SA) (see [1],[7]) scheme is used to control the mutated chromosome acceptance according to the probability value p. Let d be an offspring of c. Probability of accepting d in the new generation will be:

$$p = e^{-\frac{\Delta f}{kT}},$$

where

$$\Delta f = f(d) - f(c),$$

k>0 and T is the actual system temperature.

The values of k and T controlling the acceptance probability are chosen depending on the specific problem. By subsequently lowering the temperature, the acceptance probability decreases over time. In the final stages very small acceptation probabilities of worse solutions are needed. By this acceptance mechanism the chromosomes will generally get closer to the points corresponding to small cost values. This acceptance mechanism does not ensure the system reaches thermodynamic equilibrium at each generation, like in the Metropolis algorithm (see [7]) normally used in simulated annealing. We may suppose the equilibrium will be achieved only at the end of the search process. We may consider for temperature the decreasing rule

$$T_g = \frac{T_1}{1 + \ln g},$$

where T_1 is the initial temperature and g>1 is the generation index.

To implement this mechanism a random number R from a uniform probability distribution in [0,1] is generated. If R<p then the offspring is accepted in the new generation. Otherwise its parent is accepted.

Short range interactions permit early chromosome clustering in subpopulations, and local interactions will allow subpopulation stabilisation.

As a side effect, after a few generations, some chromosomes might overlap or become very close, as two or more subpopulations might evolve towards the same optimum point. If distance between two chromosomes is less than an appropriate threshold, then the two chromosomes will be merged. This verification will be done at

each insertion of a chromosome in the new generation. We obtain the number of optimum points as the number of chromosomes in the population. Each chromosome in the final population corresponds to a global or local optimum point.

As GC strategy uses solution population of changing sizes, its population dynamics is more complicated than in usual evolutionary optimisation algorithms. Therefore the corresponding search process may be also supposed to be more powerful. This feature makes GC based searching methods appealing for solving difficult tasks, like multi-modal optimisation problems.

Various termination conditions can be identified. Some of them are formulated according to the considered particular problem. Other stop conditions are problem independent. A good general, problem independent heuristics is to stop the search process if the chromosome population remains unchanged for a fixed number of generations.

2.GC with controlled migration

In this paper we propose a slight modification of the standard GC strategy. The goals of the proposed approach is to improve the GC behaviour for multi-modal optimisation problems. A modified local mating scheme will stabilise the subpopulations, avoiding massive migrations between subpopulations in the final search stages. It also prevents the destruction of some useful subpopulations, and ensure a high probability of obtaining each optimal solution.

2.1 Recombination

Each individual c will have a different radius of interaction ir_c :

$$ir_c = k_1 \frac{ir_s}{(1+\ln g) f(c)},$$

where ir_s is the starting interaction radius of the system, $k_1 > 0$, g the generation index, and f(c) is the fitness value of c. The mate of c is selected from the closed ball V(c,r).

This mechanism gives a higher probability that individuals worse than their parents to generate better offspring, while the 'purest' individuals will interact with only the 'purest' ones (an individual is pure if it is in the neighbourhood of a peak). Each population will have a more independent evolution, and the flexibility of the procedure increases significantly.

2.2 Acceptance scheme

A modified acceptance is introduced. An offspring obtained by crossover will be accepted only if it lies in a definite acceptance region of the dominant parent c. The acceptance region is a closed ball of center c and radius cr_c. The acceptance radius cr_c is defined as:

$$cr_c = k_2 \frac{cr_s}{(1+\ln g) f(c)},$$

where cr_s is the initial acceptance radius of the system, $k_2 > 0$, g is the generation index, and f(c) is the fitness value of c.

If the offspring resulted from crossover is not in the closed ball $V(c, cr_c)$, then it will not be accepted in the new generation. Otherwise it will be considered for the SA like acceptance scheme (see section 1).

2.3 Mutation

For the mutation we also consider a similar acceptance mechanism. The mutation radius of the chromosome c is considered to be:

$$mr_c = k_3 \frac{mr_s}{(1+\ln g) f(c)},$$

where mr_s is the crossover radius of chromosome c, $k_3 > 0$, g is the generation index, and f(c) is the fitness value of c.

If the offspring resulted from mutation of c is not in the region $V(c, mr_c)$, then it will not be accepted in the new generation. Otherwise it will be proposed for the SA like acceptance scheme. This mechanism prevents the vanishing of some optimum points in the final stages of the search process.

2.4 Other heuristics

For some particular problems we may admit migrations between different interaction domains, leading to better solutions by increasing the population diversity. In such situations the search time can be longer, and also the accuracy of results could be affected. Using this mechanism, migrations are allowed only in the first search stages and possibly can detect new optimum points. In the final stages there will be no losses of 'pure' individuals, as may happen while using the simple SA acceptance scheme. The use of the proposed mechanism tunes up the search from the first stages.

For speeding up the search process, an offspring can be generated within its parent's crossover or mutation acceptance radius.

3.The algorithm

A general outline of the modified genetic chromodynamics algorithm is

GC() {

k←1; initialise(P_k ,*param*);

while (*stop criterion has not been met*) do

for i←1 to n do

if hasmate(a_i) then

a_j ←selectmate(P_k , a_i);

$a_i' \leftarrow$crossover (a_i, a_j);

$a_i'' \leftarrow$crossoveracceptance(a_i, a_i');

else

$a_i' \leftarrow$mutate (a_i);

$a_i'' \leftarrow$mutationacceptance(a_i, a_i');

$a_i''' \leftarrow$SAacceptance(a_i'', a_i);

od

mergesimilar(P_k);

k←k+1;

od

}.

crossoveracceptance(a_i, a_i') {

if $a_i' \in V(a_i, cr_{a_i})$ then return a_i' else return a_i;

}.

mutationacceptance(a_i, a_i') {

if $a_i' \in V(a_i, mr_{a_i})$ then return a_i' else return a_i;

}.

For this algorithm we use the following notation. The set P_k is the population in generation k. The set *param* is the set of parameters : $T_1, ir_s, cr_s, mr_s, K, k, k_1, k_2, k_3$. The *initialise* procedure initialises the initial generation and the parameters. The stop criterion is met, if for a number of generation the chromosomes does not change. The *hasmate* function returns true, if the chromosome has at least a mate. The *selectmate* function selects one from the mates. The *crossover* function performs the crossover. The *crossoveracceptance* function accepts the offspring if it is in the crossover acceptance radius of the parent. The *mutate* function performs the mutation. The *mutationacceptance* function accepts the offspring, if it is in the mutation acceptance radius of the parent. The Saacceptance function performs the SA acceptance. The *mergesimilar* function merges all similar chromosomes in the generation P_k.

4.Implementational issues

In this section a study case will be considered to exemplify the effect of parameter values on the searching process.

Effects of the parameters.

Consider the function

$$f(X) = \frac{(\sin X)^2 - 0.5}{\left(1 + 10^{-3} \cdot X^2\right)^2}$$

$$f : [-100,100] \times [-0.55,0.6].$$

In the specified domain the function has 64 local optima. For this function we will exemplify the effect of the changing the parameter values. We consider a set of standard values given in Table 1.

similarity radius	0.30517578125
interaction radius	3.125
crossover acceptance radius	3.125
mutation acceptance radius	3.125
starting temperature	1
starting chromosome number	200
SA acceptance modifier (k)	0.00001.
minimal fitness value (K)	1
interaction radius modifier	1
crossover acceptance radius modifier	1
mutation acceptance radius modifier	1
search stop after 10 generation if no change	

Table 1. The set of standard parameter values.

The value of a single parameter will be changed at once. The values of changed parameters and the corresponding results are given in Table 2.

Acceptance modifier	**Generations until convergence**	**Number of detected optimal points**
0.00001	70	64
0.0001	170	64
0.001	>3000	64
0.01	>3000	62
0.1	>3000	40
Initial temperature	**Generations until convergence**	**Number of detected optimal points**
1	70	64
2	70	64
4	110	64~
8	130	64~
16	480	64~
Similarity radius	**Generations until convergence**	**Number of detected optimal points**
0,1953125	70	64
0,91552734375	70	64~

1,52587890625	80	64~
Initial chromosome number	**Generations until convergence**	**Number of detected optimal points**
64	65	40
128	80	60
196	85	64~
Interaction radius	**Generations until convergence**	**Number of detected optimal points**
1,5625	80	64
3,125	70	64
6,25	65	63
12,5	85	64
Crossover acceptance radius	**Generations until convergence**	**Number of detected optimal points**
1,5625	80	64
3,125	70	64
6,25	70	64
12,5	75	64~
Mutation acceptance radius	**Generations until convergence**	**Number of detected optimal points**
1,5625	120	63
3,125	70	64
6,25	60	62
12,5	50	38

~ = less suitable solution or very rarely an optimum has been lost

Table 2. The effect of changing a parameter.

The similarity radius parameter. The optimal value of this parameter is smaller than the minimal distance between two peaks of the function. However, bigger its value is, longer the search process is, and 'pure' individuals may be loosed.

The interaction radius parameter. This parameter controls the formation and stabilisation of the subpopulations. The optimal value of this parameter is the minimal distance between two peaks of function. However, bigger its value is, bigger is the possibility of losing subpopulations, and the search process it is faster.

The crossover acceptance radius. This parameter controls the splitting of subpopulations. If its value is bigger than the interaction radius, then gives higher probability of mutation in the next generation. The optimal value of this parameter is the minimal distance between two peaks of function.

The mutation acceptance radius. This parameter assures, that in the final stages no individual will be lost. Also leads to detection of new peaks of the function. Its value

must be sufficiently small to assure these, an optimal value may be the minimal distance between two peaks of function.

Initial temperature. Higher its value is, bigger is the possibility in the search process to accept offspring worse than their parents. Bigger it is, longer the search process is, and the quality of solutions is poorer.

Initial chromosome number. The initial population must be sufficiently numerous to detect all peaks (generally 2x-2.5x the number of peaks).

SA acceptance modifier. Smaller its value is, smaller is the possibility to accept offspring worse than their parents. Its value is optimal, when $Tk \approx 1$.

Minimal fitness value. Must be chosen such that f(c)<K, for every chromosome.

Interaction radius modifier. Bigger its value is, bigger will be the interaction radius in the search process.

Crossover acceptance modifier. Bigger its value is, bigger will be the crossover acceptance radius in the search process.

Crossover acceptance modifier. Bigger its value is, bigger will be the mutation acceptance radius in the search process.

5.Experimental results

The proposed method is compared with standard GC and with GC allowing simple SA acceptance. The considered examples emphasise that the method proposed in this paper gives better results than the other two methods.

The number of the optimum points as well as their positions are correctly detected. However the quality of the results depend on the correct choice of the parameters.

Example 1.

Consider the function

$$f(X) = \frac{(\sin X)^2 - 0.5}{\left(1 + 10^{-3} \cdot X^2\right)^2}$$

$$f : [-100,100] \times [-0.55,0.6].$$

The values of parameters are:

Similarity radius	0.30517578125
Interaction radius	3.125
Crossover acceptance radius	3.125
Mutation acceptance radius	3.125
Initial temperature	1
Initial chromosome number	200
SA acceptance modifier (k)	0.00001
Minimal fitness value (K)	1
Interaction radius modifier	1
Crossover acceptance radius modifier	1
Mutation acceptance radius modifier	1
Search stop after 10 generation if no change	

a) simple GC

The initial population is depicted in figure 1.

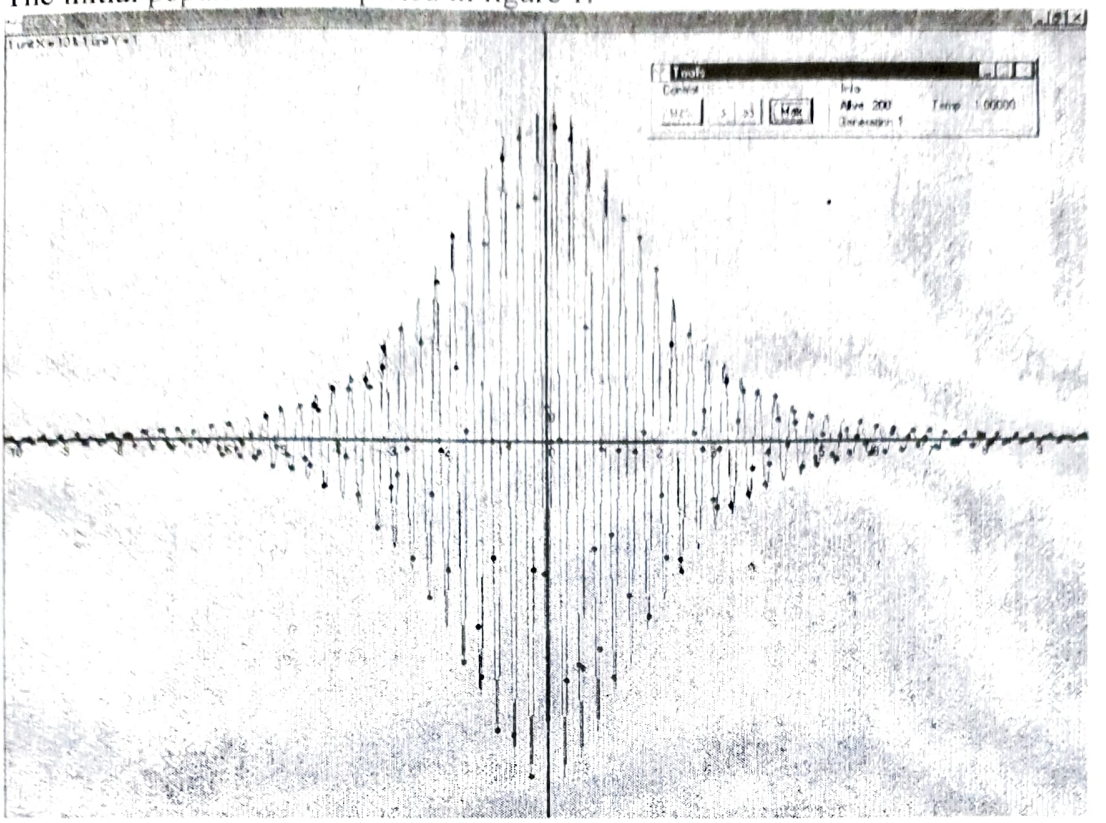

Figure 1. Objective function and initial population

After 10 generations the 55 chromosomes depicted in figure 2 remained.

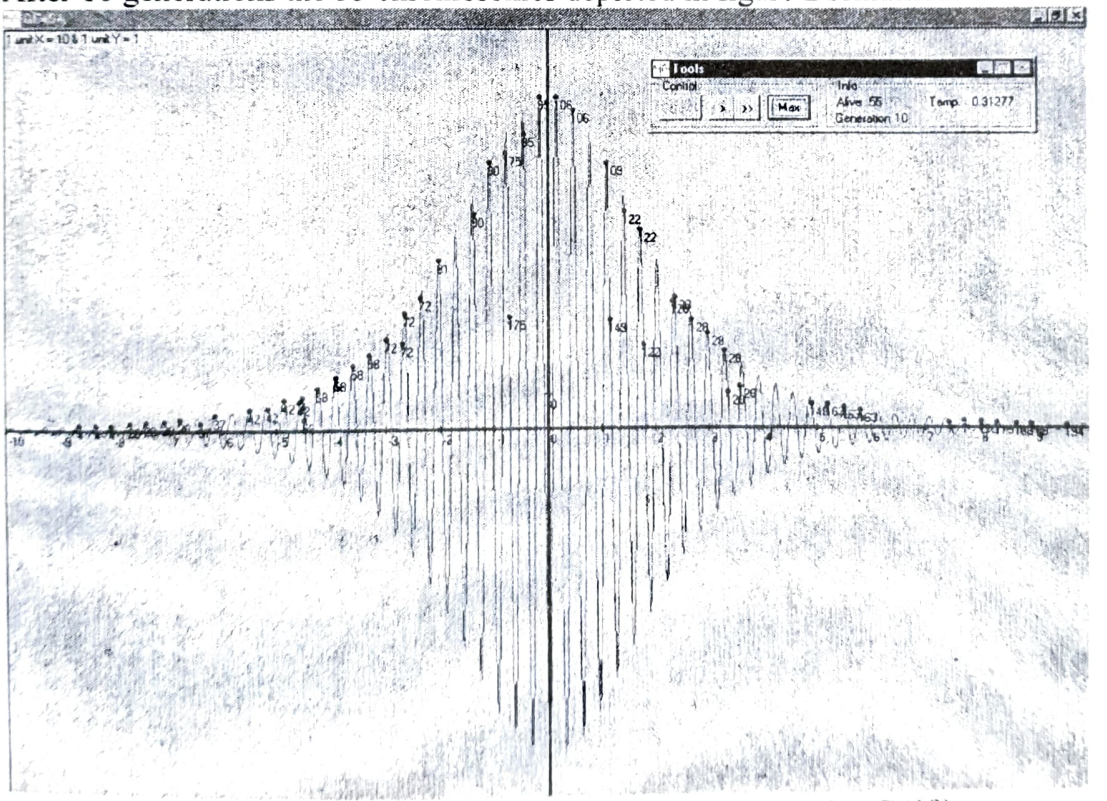

Figure 2. The 55 chromosomes in generation P(10).

After 20 generations the 35 chromosomes depicted in figure 3 remained.

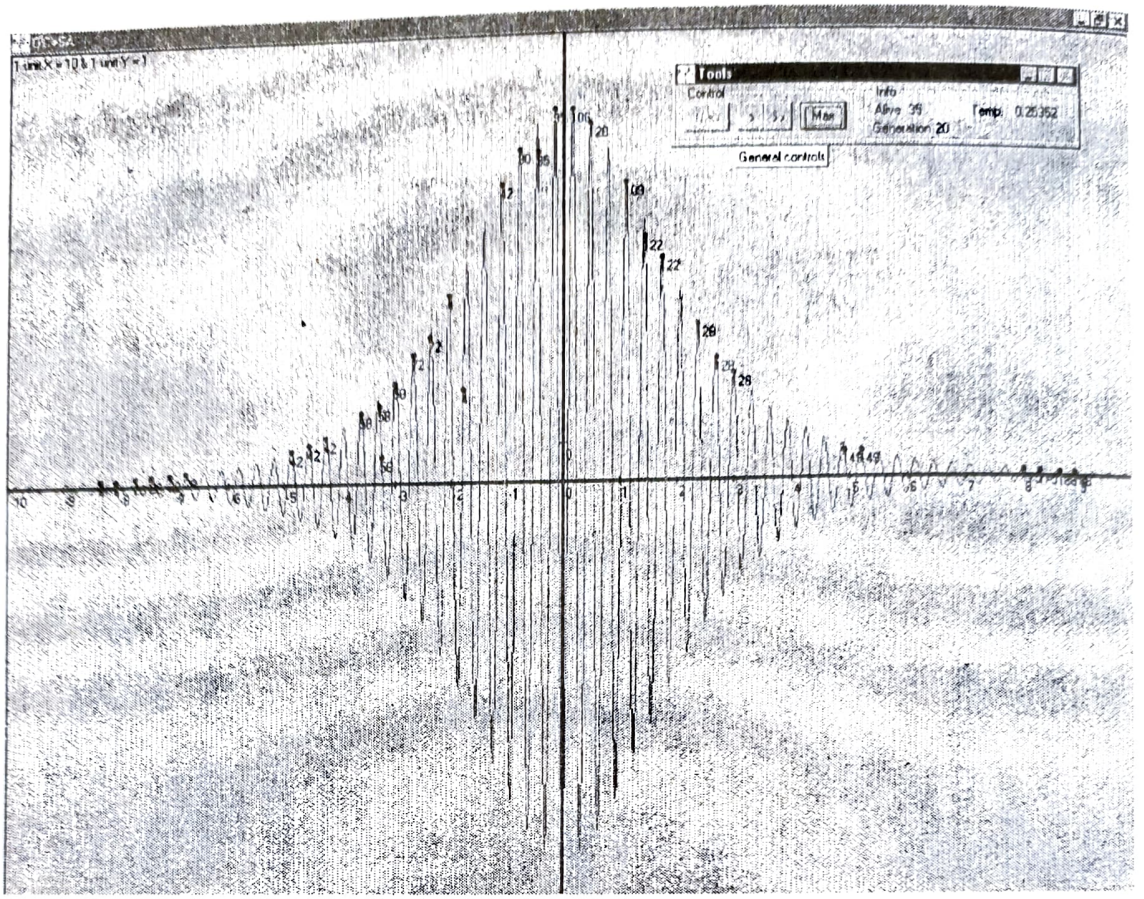

Figure 3. The 35 chromosomes in generation P(20).

The final generation contains the 16 chromosomes depicted in figure 4.

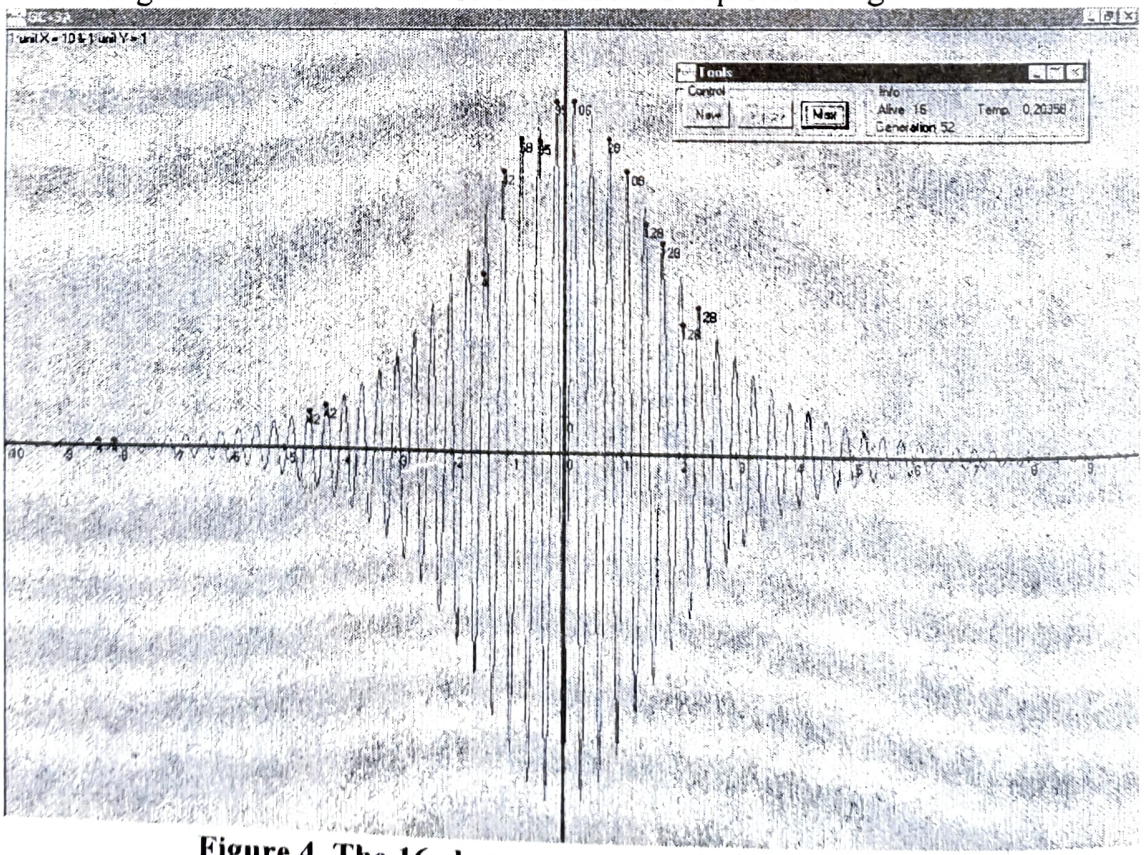

Figure 4. The 16 chromosomes in final generation P(52).

b) GC with SA acceptance

The first generation population is depicted in figure 5.

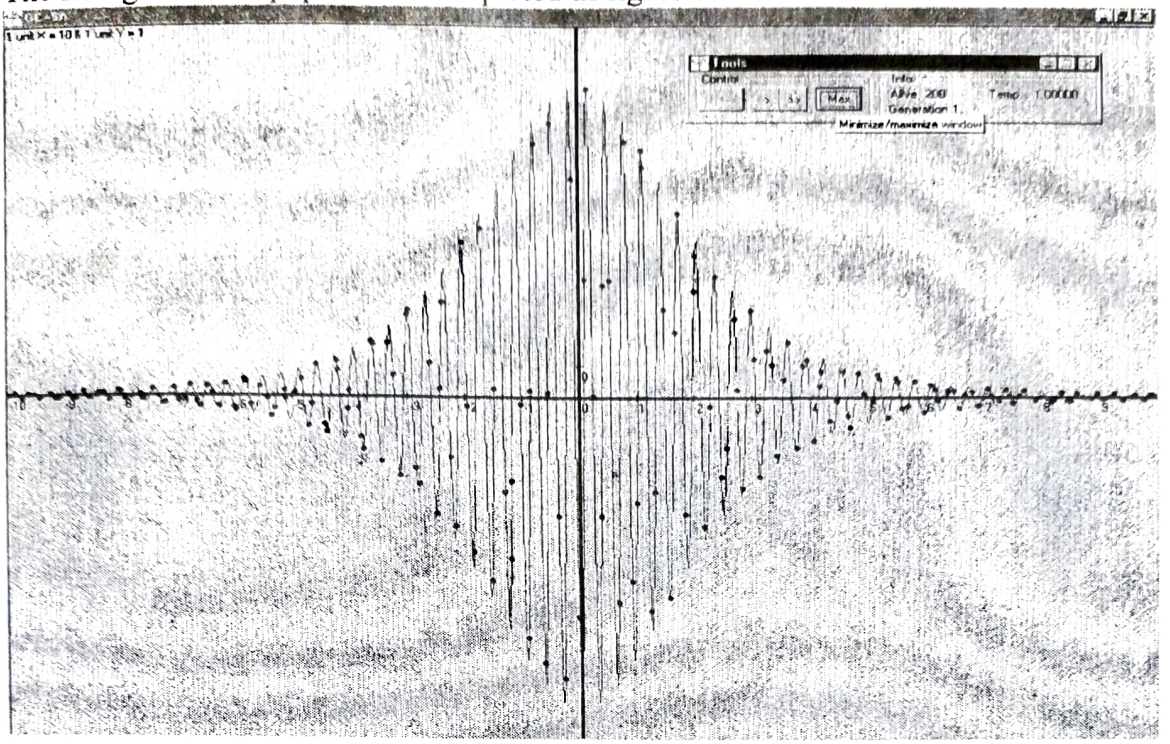

Figure 5. Objective function and initial population.

After 10 generations the 55 chromosomes depicted in figure 6 remained.

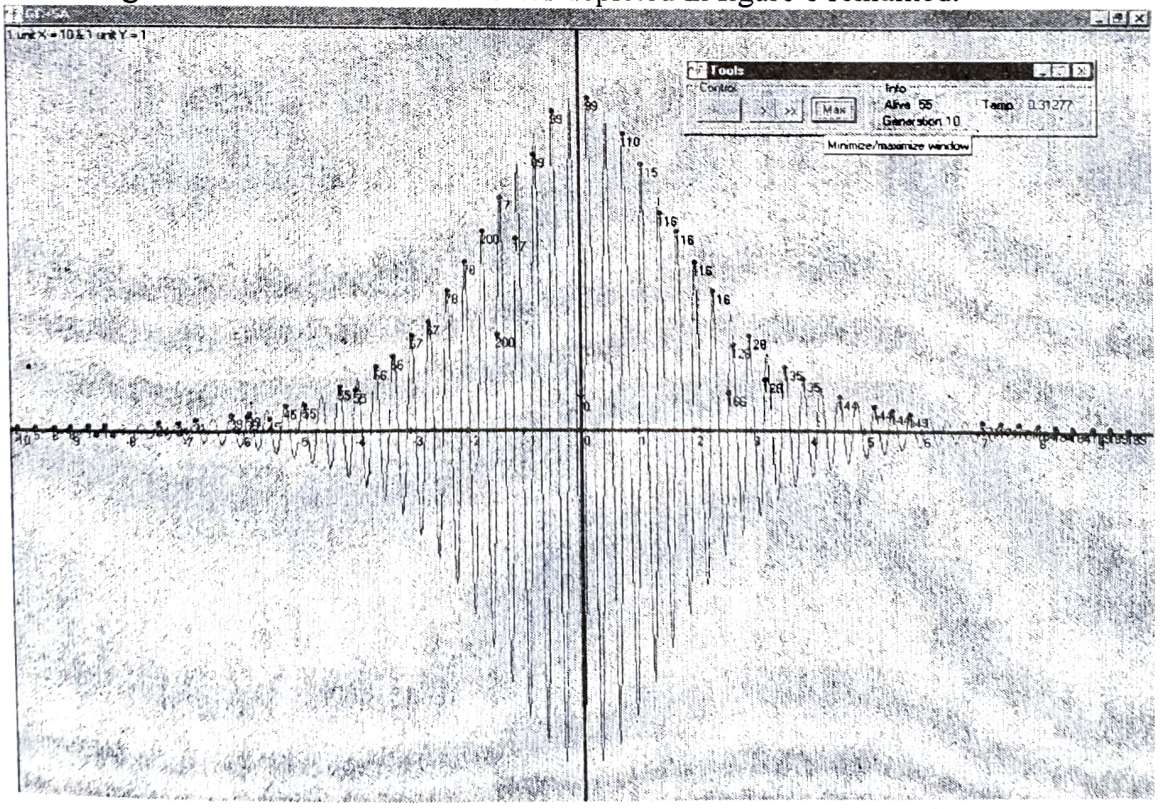

Figure 6. The 55 chromosomes in generation P(10).

After 20 generations the 25 chromosomes depicted in figure 7 remained.

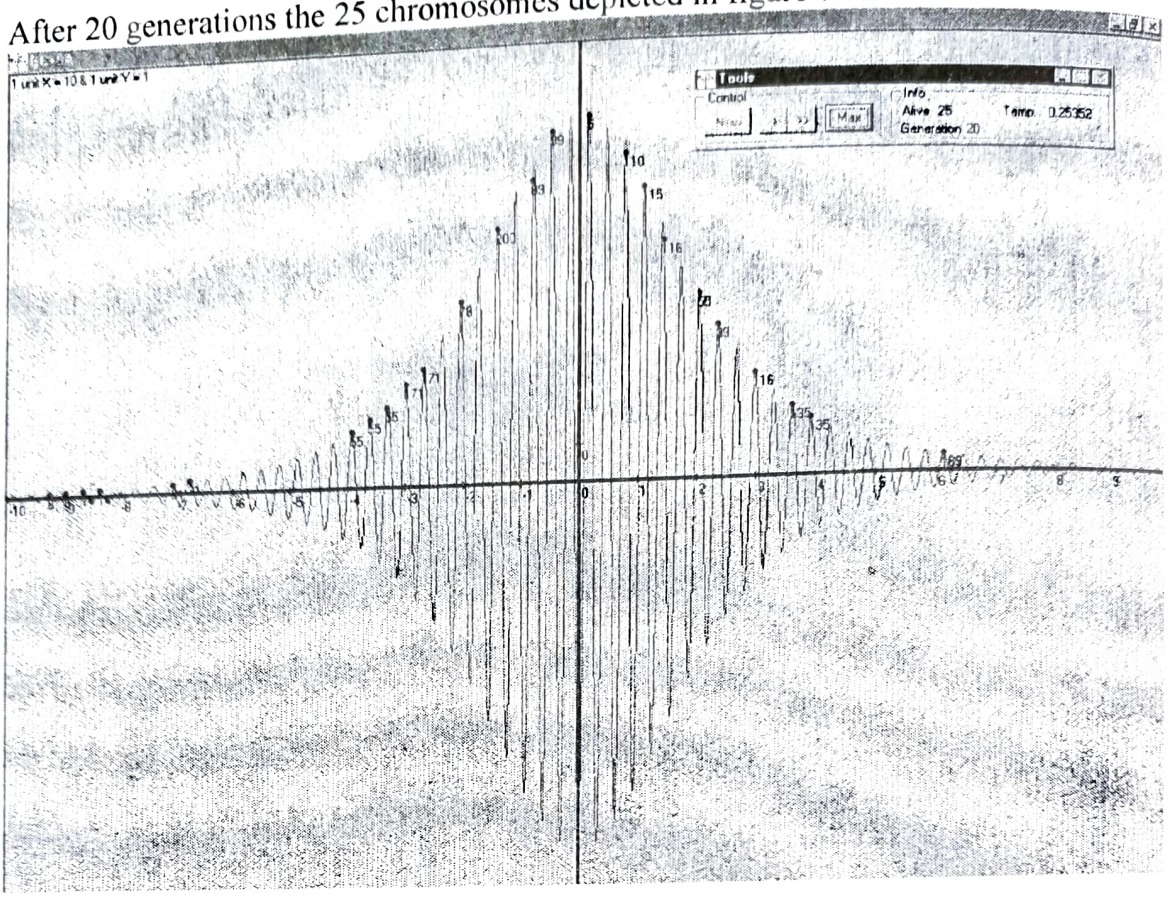

Figure 7. The 25 chromosomes in generation P(20).

The final generation contains the 14 chromosomes depicted in figure 8.

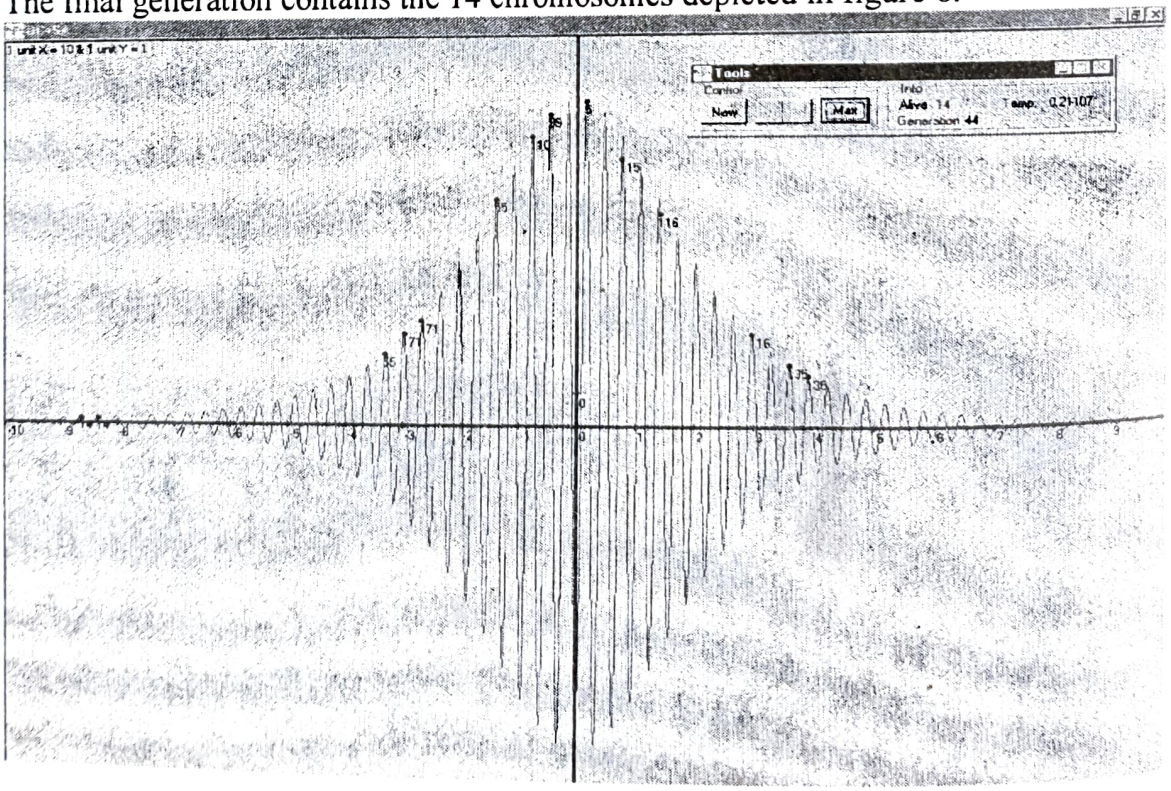

Figure 8. The 14 chromosomes in final generation P(44).

c) GC with controlled migrations

The first generation population is depicted in figure 9.

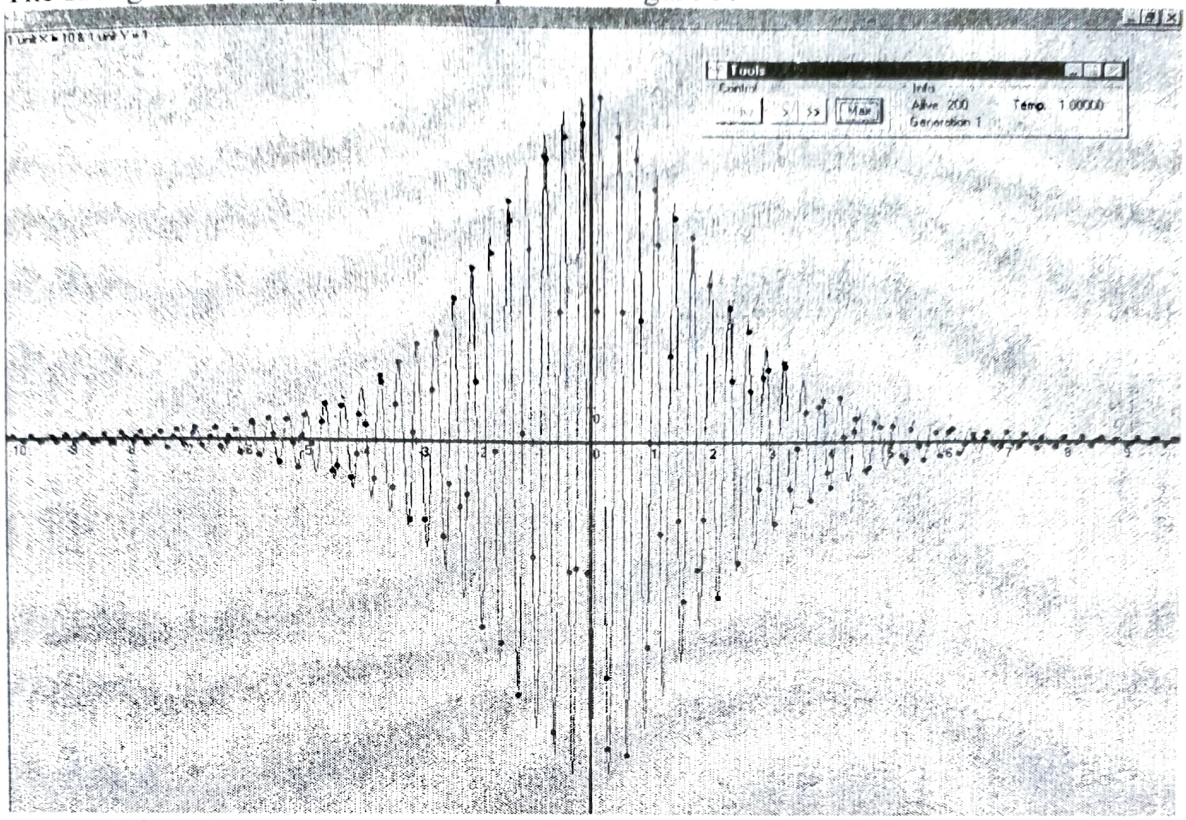

Figure 9. Objective function and initial population.

After 10 generations the 64 chromosomes depicted in figure 10 remained.

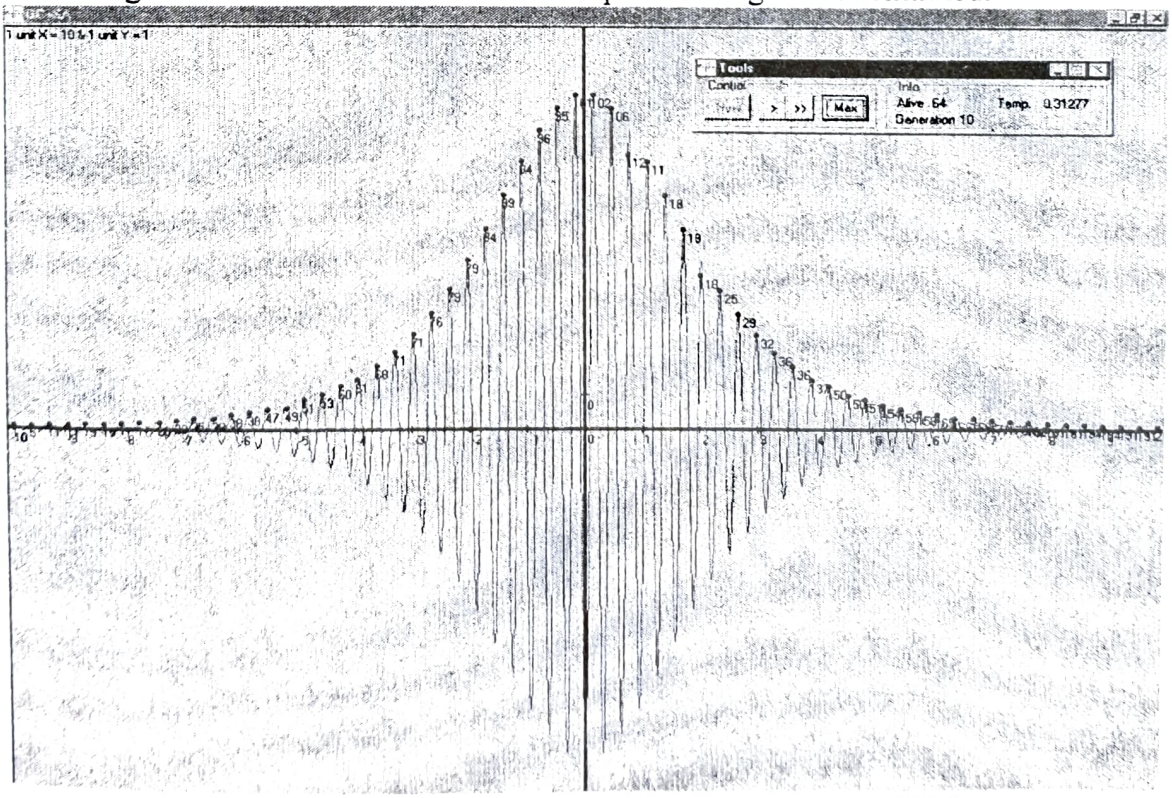

Figure 10. The 64 chromosomes in generation P(10).

After 20 generations the 64 chromosomes depicted in figure 11 remained.

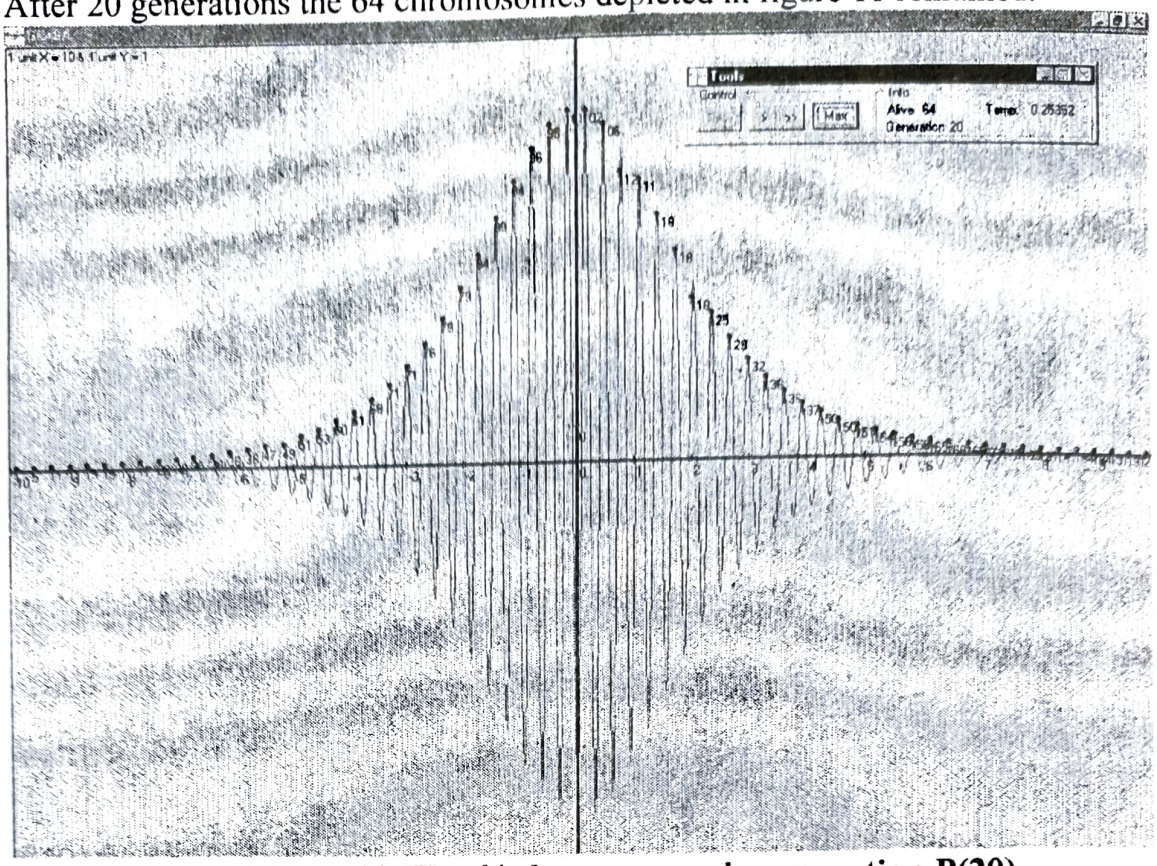

Figure 11. The 64 chromosomes in generation P(20).

The final generation contains the 64 chromosomes depicted in figure 12.

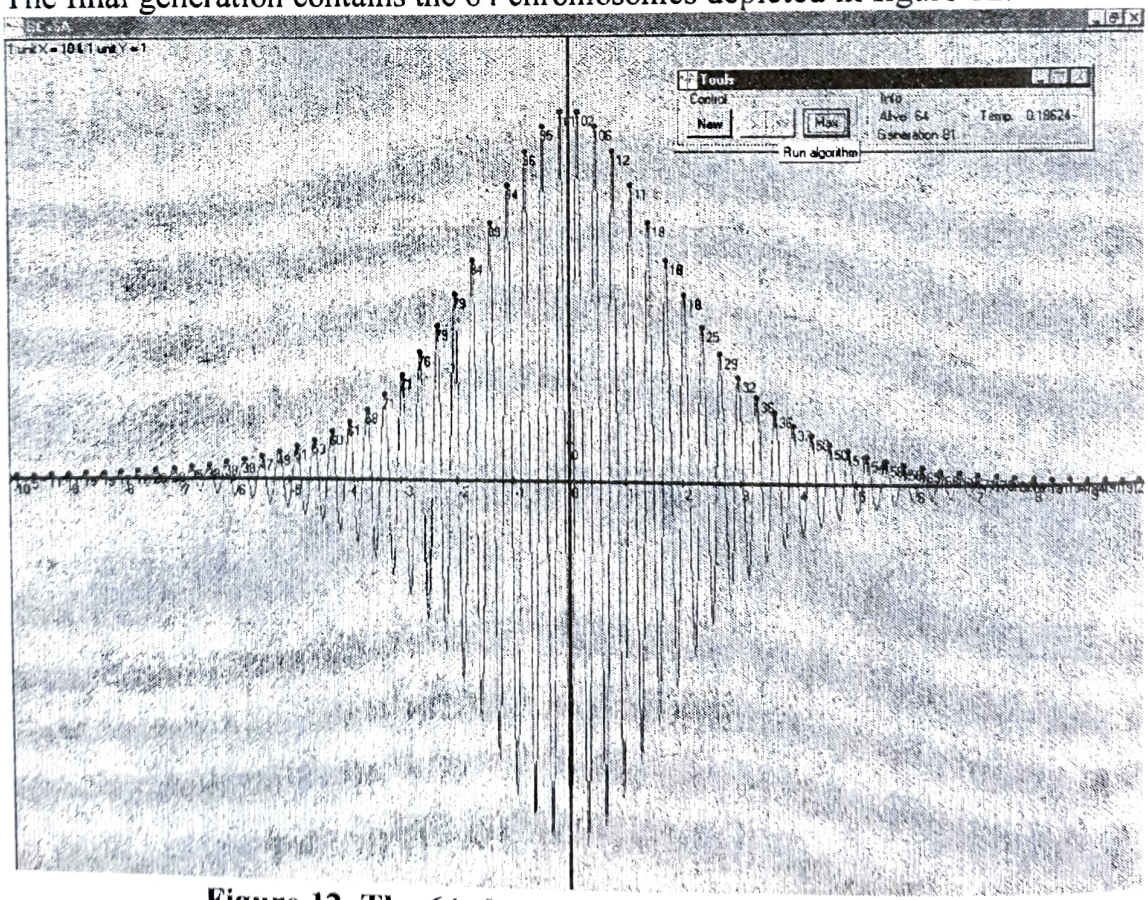

Figure 12. The 64 chromosomes in final generation P(81).

Example 2.

Consider the function

$$f(X) = \sin(2 \cdot X^{\cos(2 \cdot X)})$$

$f : [-6.5,6.5] \times [-2,2]$.

The values of parameters are:

similarity radius	0,01983642578125
interaction radius	0,203125
crossover acceptance radius	0,203125
mutation acceptance radius	0,203125
starting temperature	1
starting chromosome number	200
SA acceptance modifier (k)	0.00001
minimal fitness value (K)	1
interaction radius modifier	2
crossover acceptance radius modifier	2
mutation acceptance radius modifier	2
search stop after 10 generation if no change	

a) simple GC

The first generation population is depicted in figure 13.

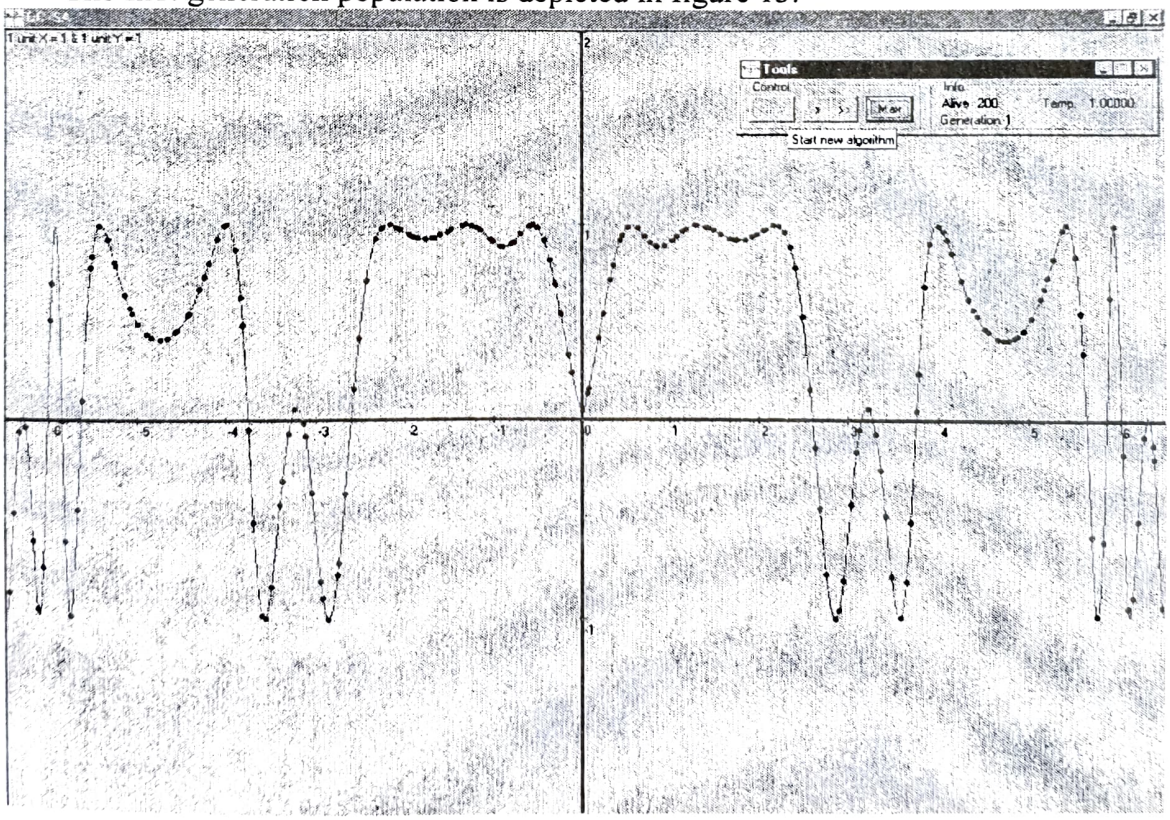

Figure 13. Objective function and initial population.

After 10 generations the 39 chromosomes depicted in figure 14 remained.

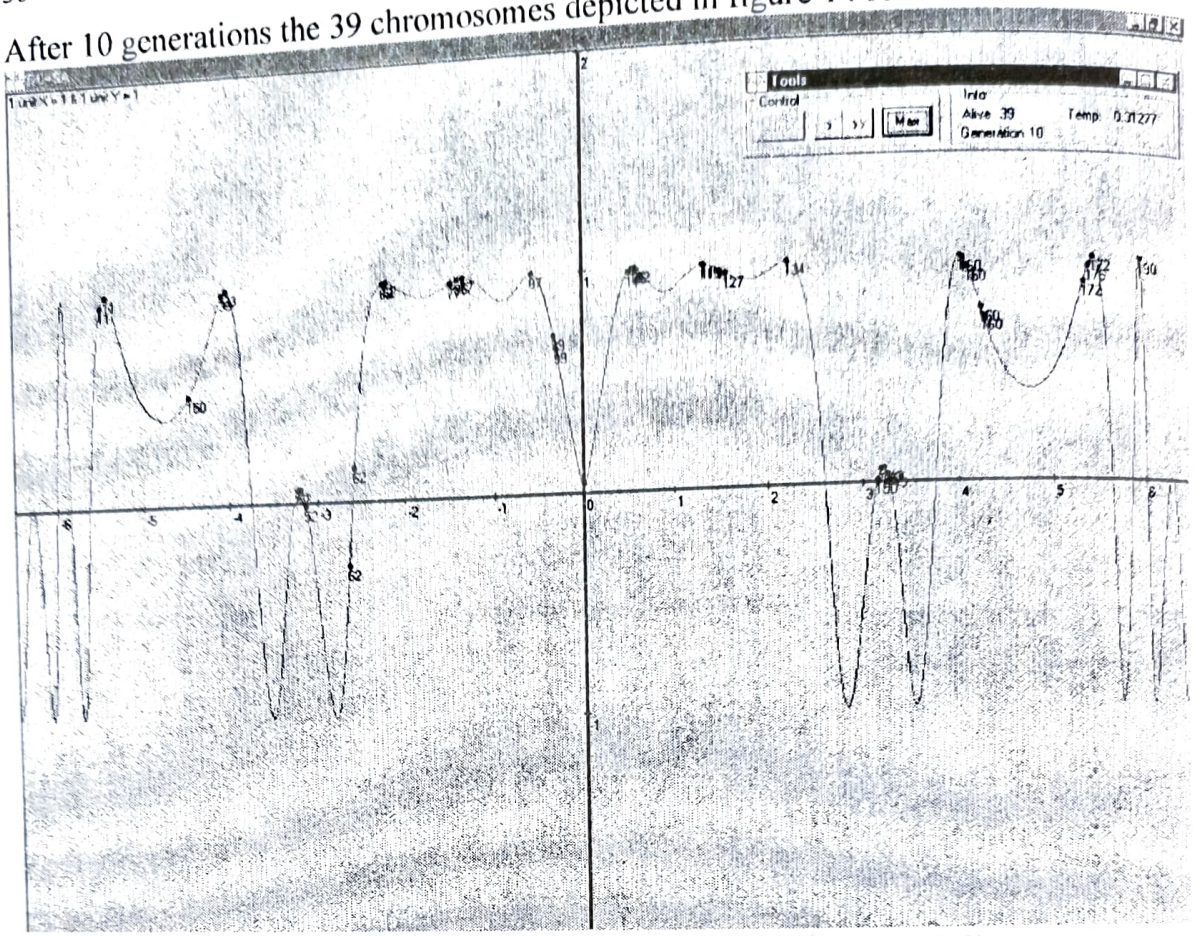

Figure 14. The 39 chromosomes in generation P(10).

The final generation contains the 9 chromosomes as depicted in figure 15.

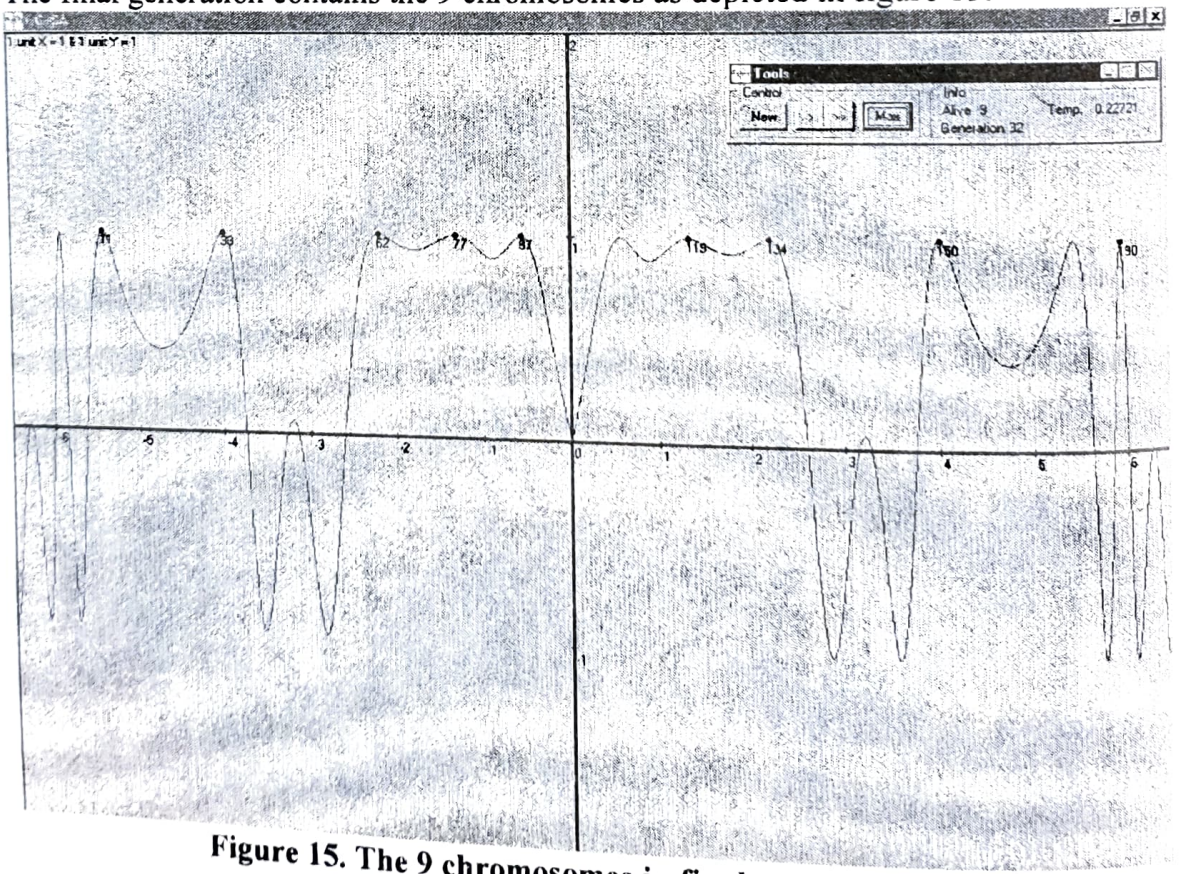

Figure 15. The 9 chromosomes in final generation P(32).

b) GC with SA acceptance

The first generation population is depicted in figure 16.

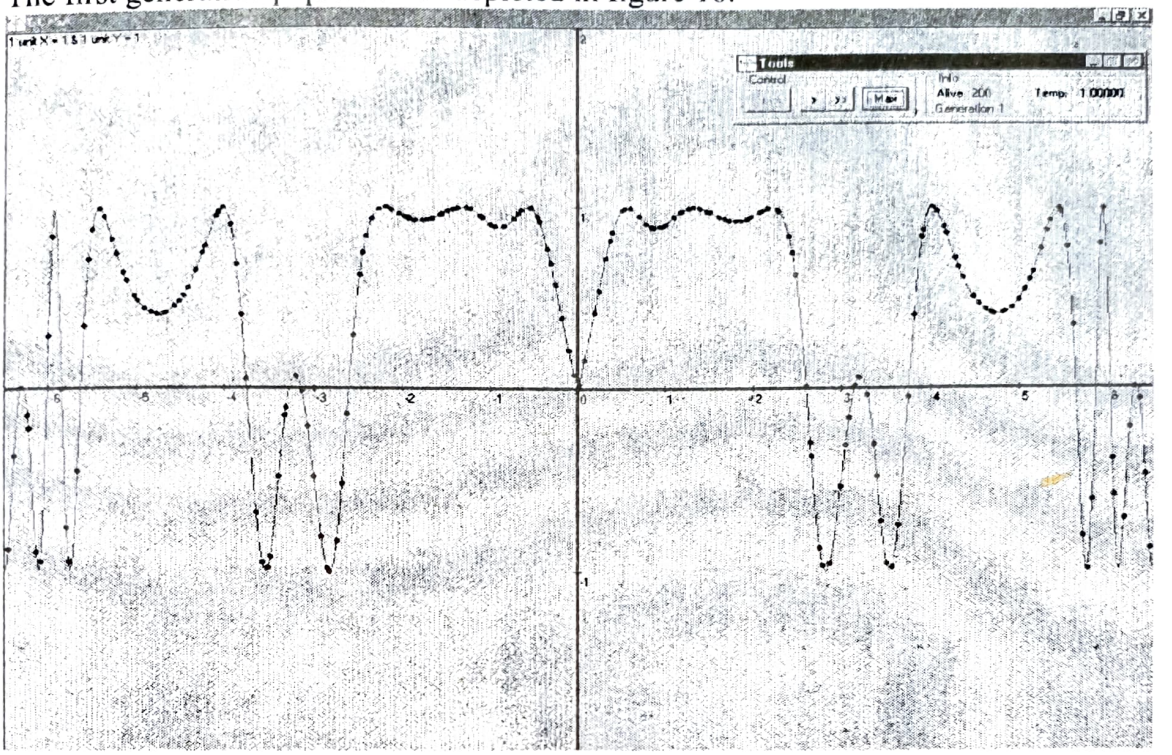

Figure 16. Objective function and initial population.

After 10 generations the 31 chromosomes depicted in figure 17 remained.

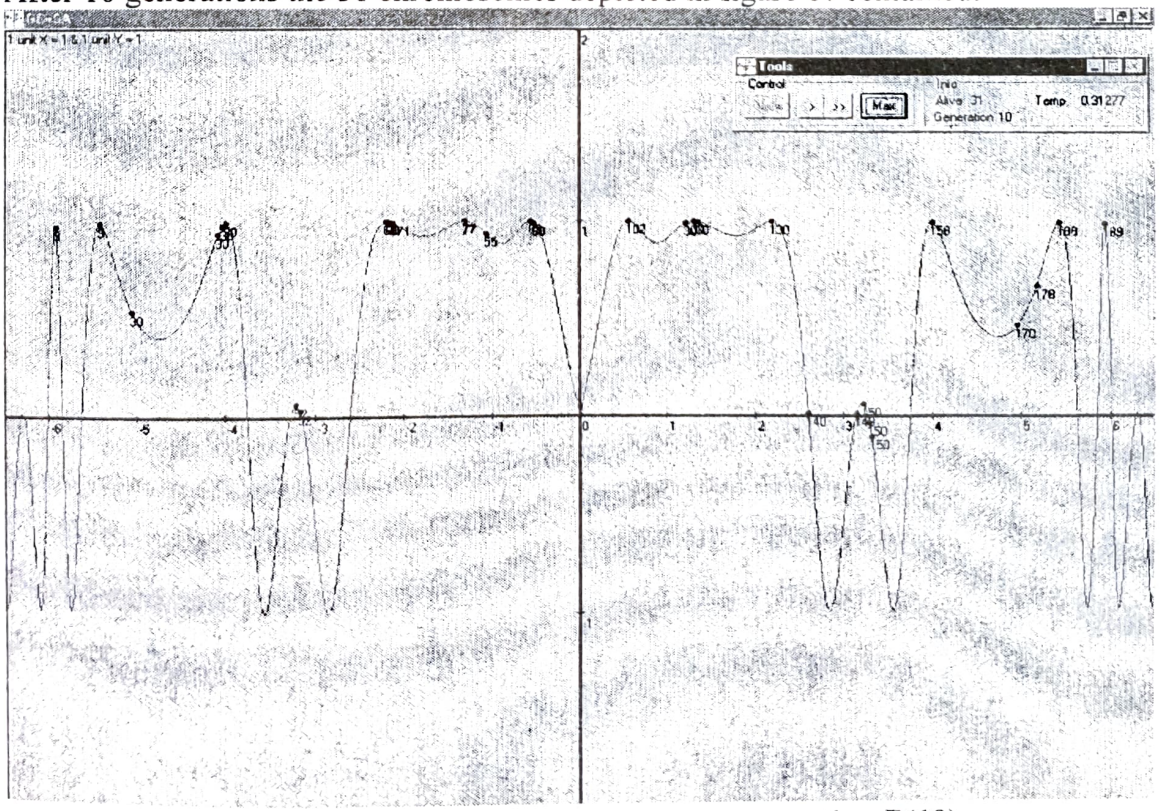

Figure 17. The 31 chromosomes in generation P(10).

The final generation contains the 12 chromosomes depicted in figure 18.

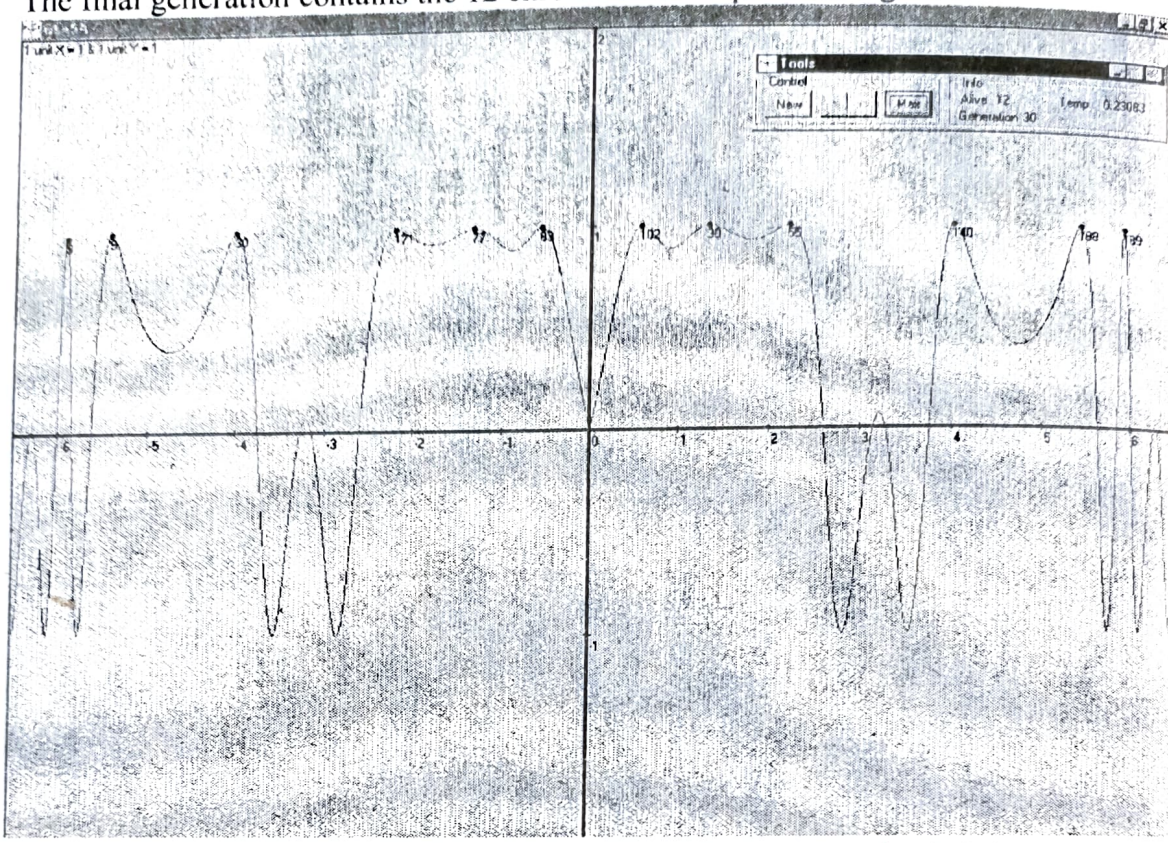

Figure 18. The 12 chromosomes in final generation P(30).

b) GC with controlled migrations

The first generation population is depicted in figure 19.

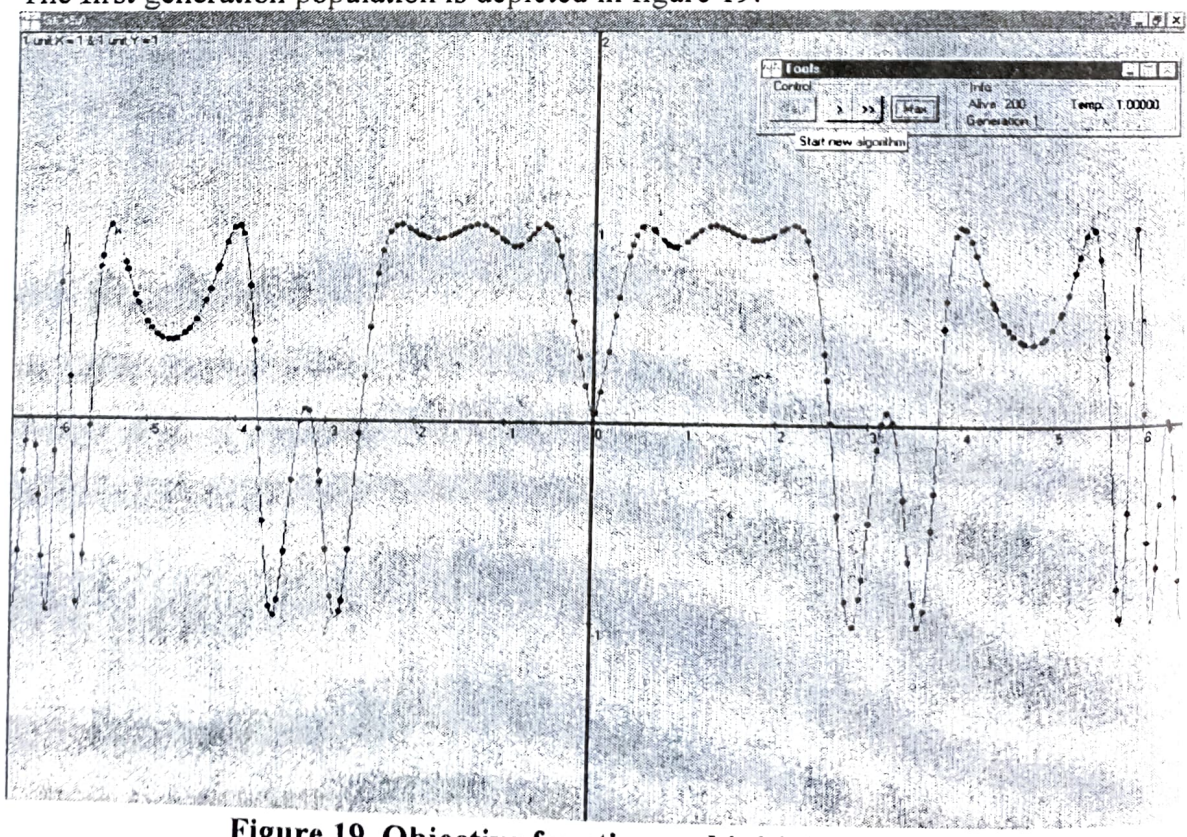

Figure 19. Objective function and initial population.

After 10 generations the 59 chromosomes depicted in figure 20 remained.

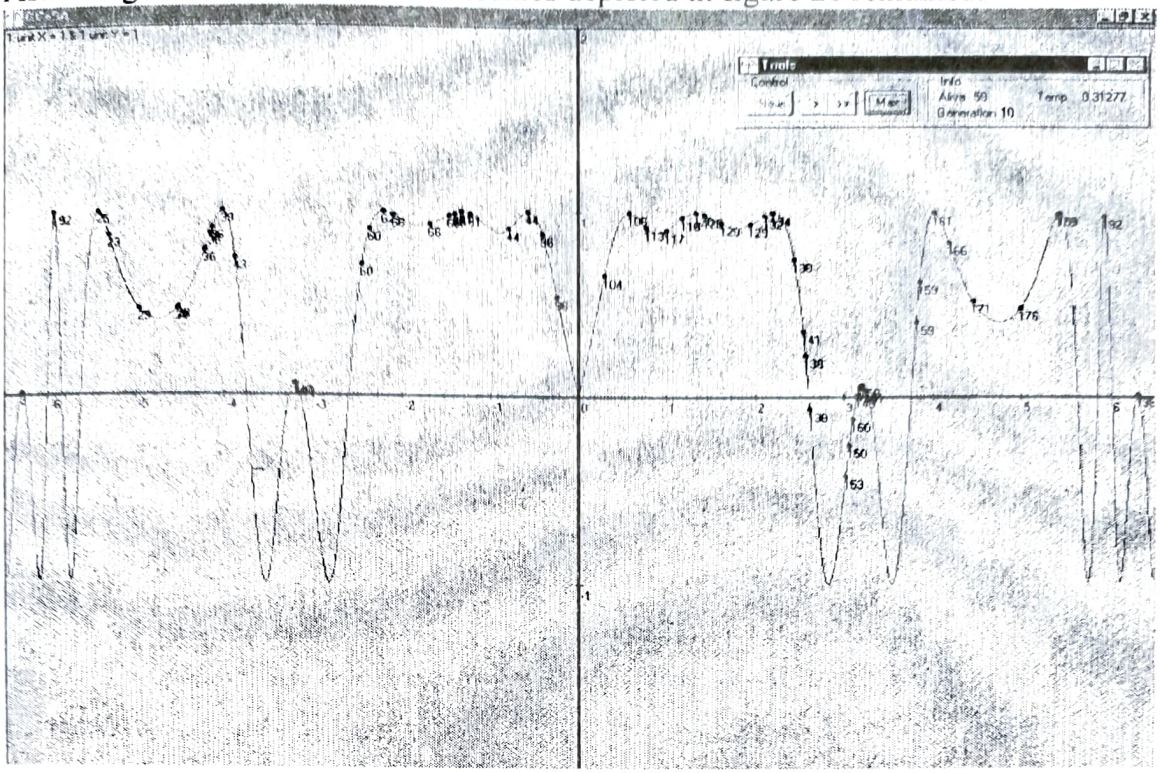

Figure 20. The 59 chromosomes in generation P(10).

The final generation contains the 16 chromosomes depicted in figure 21.

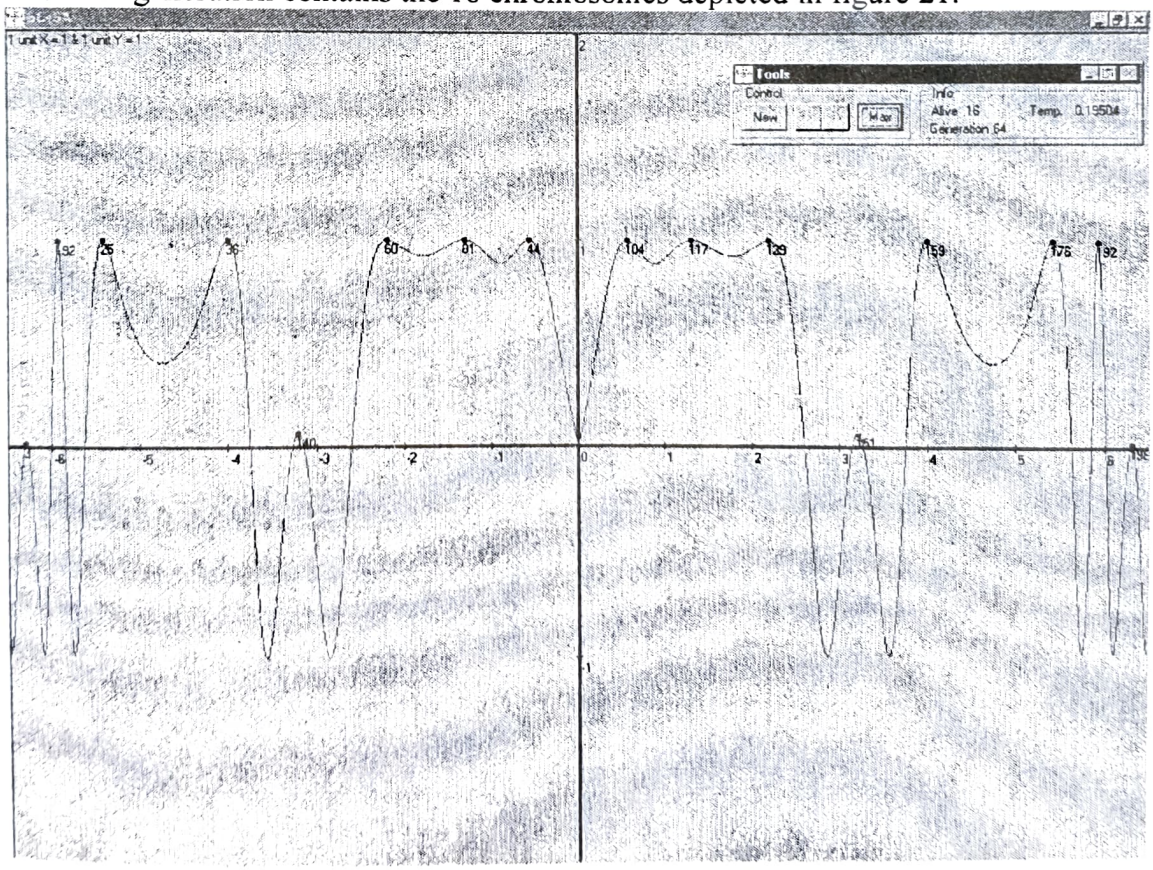

Figure 21. The 16 chromosomes in final generation P(64).

6. Conclusions

A modified Genetic Chromodynamics strategy is proposed in this paper. The method seems to work very well for solving multi-modal optimisation problems. By using this method, all local and global optima may be detected.

As examples proves, the simple GC finds numerous local optimum points in the first stages, but many of them will be lost until the final search stages. As the migrations may occur until the final search stages, only the highest local optima will be detected. The quality of solutions is not very good (detected points may not coincide with the peaks). The search process is fast.

The GC with SA acceptance finds more optima than the simple GC does. The SA acceptance mechanism enables us to detect local maximum points that are not very representative. The quality of solutions is good. The search process is slower than the simple GC.

The GC with controlled migration finds all optimums in the first search stages, the rest of the process can be considered as representing the tuning of the final solutions. Migration exists, but only in the first search stages. The migration process is controlled, preventing the loss of 'pure' populations (a population is pure, if its individuals are pure). The quality of solutions is very good. The search process is slower than the GC with SA acceptance.

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