Studies on Automatic Termination Criteria for Evolutionary Computation

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Preface

Optimization can be seen as one of the oldest sciences exerted, consciously or not, by living creatures or matter that is subject to the physical laws. The famous quotation "*mens sana in corpore sano*" for example, written around the late first century AD by the Roman poet Juvenal, reminds us to strive for what is considered by many as an optimal health condition, that is to say, "a sound mind in a healthy body". The quest for an optimal condition is also pursued by much more fundamental systems than creatures blessed with judgment. The second law of thermodynamics, for instance, teaches us that an isolated physical system without any external exchange will see its differences in temperature, pressure, and chemical potential reach equilibrium over time. In other words, at equilibrium, the entropy of the system will be maximized. In modern economy, a firm usually tries to maximize its profit and minimize the costs.

For all these more or less abstract concepts, the search for an optimal state or condition can be reformulated as a mathematical problem. Global optimization is the branch of applied mathematics and numerical analysis that focuses on that problem. Formally, it refers to finding the extreme value of a given nonconvex function given a certain feasible region and constraints.

There exist numerous kinds of optimization methods and an infinite amount of problems all having their own specificities. Roughly speaking, approaches adopted in mathematical optimization that deal with those problems can be classified in two main classes; the deterministic and the stochastic approaches. The main difference is that stochastic approaches introduce randomness into the search process to obtain more robust algorithms. Unfortunately, a single optimization method that would be able to solve any kind of problem does not exist yet, and it is commonly believed that such algorithm cannot possibly exist. Nevertheless, practical considerations urge researchers and practitioners to develop increasingly versatile solvers for global optimization problems. Metaheuristics designates those methods that do not require any assumptions about the problem being optimized. A wide class of metaheuristics heavily takes inspiration from natural behavior or implement intelligent learned procedures. Those concepts are the foundation of the Evolutionary Computation field.

Evolutionary Computation search techniques use a population of candidate solutions that

evolve using mechanisms inspired by concepts of biological evolution. Although other theories exist, it is the theory of evolution by natural selection that was formulated by Darwin in the 19th century that influenced the most the Evolutionary Algorithms, one of the major classes of the Evolutionary Computation field. If we consider the generally adopted idea that evolution is about changes across successive generations through inheritance of the characteristics of biological populations, one can realize that in nature, there is no mechanism that would interrupt the evolutionary process of a species on its own volition. Arguably, interruption is fundamentally different from extinction, the latter meaning that an entire species simply came to an end. But when solving an optimization problem, it is not a good idea to eradicate the whole population of candidate solutions since the outcome should be a particular individual of that population. Hence, what Evolutionary Computation practitioners usually do is to force the evolutionary process to stop when some conditions are met and get hold of the available information at that instant. This highlights an important dissimilarity between biological evolution and Evolutionary Computation.

Termination of the search in Evolutionary Computation is mainly motivated by practical reasons. Indeed, many real world applications for example have limited computational resources. However, there is no guarantee that stopping the search for such motives can lead to satisfactory results, nor does it guarantee that the search is cost-effective. This study is devoted to the development of Evolutionary computing techniques that would terminate automatically without *a priori* knowledge of the problem to solve and without any kind of computational budget. In this study, we propose novel mechanisms designed to equip the search with an automatic termination criterion, accelerate the search process and increase its accuracy and reliability. We also design new hybrid Evolutionary Computation methods that make use of the proposed mechanisms and we show that they can terminate the search process without negative impact on the quality of the solution obtained and without undue computational resources.

The author hopes that this work can be helpful for further research and contribute to the field of Evolutionary Computation. He also wishes it opens the door to the development of more intelligent methods to solve various real-world problems.

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Chapter 1

Introduction

Evolutionary Computation (EC) is a subfield of Computational Intelligence that embraces a wide range of stochastic optimization techniques inspired by concepts of biological evolution. EC techniques use a population of candidate solutions that evolves towards globally optimal solutions. Nowadays, these techniques are widely applied to real-world applications in industry and commerce and to cutting edge scientific research. Many companies all over the world, specialized in providing optimized business solutions, offer their services by using EC methods.

In this study, two subsets of EC are considered to develop our proposed methods. The first subset is the Evolutionary Algorithms (EA). EAs highly draw inspiration from processes of biological evolution such as reproduction, crossover, mutation, natural selection and survival of the fittest for problem solving. The population of individuals evolves through repetition of the above mentioned mechanisms in an attempt to mimic the life cycles of living species (Back et al., 1997; Konar, 2005). The second subset is known as Swarm Intelligence (SI). SI systems consist of a population of agents that move through some multidimensional search space and interact with one another and with their environment in an attempt to converge towards the global optima.

EC methods do not require specific assumptions about the problem to optimize. Consequently, they are particularly suitable for the category of global optimization problems characterized by one or more of the following properties (frequently met in most real-world applications):

- The calculation of the objective function is computationally expensive or time consuming.
- The exact or approximate gradient of the objective function is not available.
- The objective function is noisy.

Although present EC techniques are successfully applied and show impressive performance in many real-world and theoretical optimization problems, they suffer from the following two major drawbacks; slow convergence in the vicinity of local minima and unlearned termination criteria. Indeed, because of their stochastic nature, EC methods suffer from slow convergence. They do not exploit much local information to guide their search. In this research, we address this problem by combining EC techniques with local search methods. During the search, local search methods are invoked in order to take advantage of their fast convergence. In addition, the randomness inherent to EC techniques prevents them from being entrapped in local optima. Also, an essential difference between natural evolution and problem solving is that in natural evolution, species do not usually seek for termination. In problem solving, on the other hand, at some point and under a given budget, we deliberately need to stop the life cycle process. When to stop is not a trivial question. It is admitted that in many real world applications, saving computational resources is of prime importance. Complex optimization problems for instance endure an intensive function evaluation process. By stopping the search right before unnecessary function evaluations are performed, it is the algorithmic efficiency that is increased. This study is devoted to the development of novel EC methods that would terminate without *a priori* knowledge of any desirable or available solution range, and of any specific number of iterations or function evaluations. It is desired that the termination instant after completion of adequate exploration and exploitation is determined by the algorithm itself.

In the remaining text of this introduction, we first present the global optimization problem that is addressed in this study. Then, we provide some definitions commonly used in the EC literature for better understanding of the subsequent sections. The last three sections are dedicated to the description of two EAs (Genetic Algorithms and Differential Evolution) and one SI method (Particle Swarm Optimization) used throughout this research.

1.1 Nonconvex Global Optimization Problems

In this study, we consider the nonconvex global optimization problem

$$\min_{x \in D} f(x), \tag{1.1.1}$$

where f is a real-valued function defined on the search domain $D \subseteq R^n$ with variables $x \in D$.

A lot of EC methods and other heuristics have been proposed to deal with this problem, see for instance (Hansen, 2006; Hedar et al., 2011; Ong and Fukushima, 2011a,b,c) and the references therein. We do not make any assumption about the landscape of the problem being optimized and hence, we do not assume the differentiability, or even the continuity of the objective function. Let us note that maximization problems can easily be transformed into minimization problems by a simple transformation of their objective functions.

1.2 EC Terminology

For better understanding of later arguments, some notions commonly found in the EC literature are defined in this section.

1.2.1 Phenotype and Genotype

Phenotypic traits are physical and behavioral characteristics of an individual. The phenotype of an individual is determined by its genotype which represents the genetic state of an individual and contains all the information concerning its attributes and traits. An individual interacts with the environment by its phenotypic traits, determining its fitness. If the fitness of an individual is high, then its phenotypic traits will have a high probability to be propagated to further generations.

1.2.2 Representation

Representation consists in creating a correspondence between genotypes and phenotypes. In the original problem, an object is represented by the phenotype but in the algorithm itself, the encoding of such an object is the genotype. The genotype space might differ largely from the phenotype space but it is worth to precise that the algorithm works with the genotype and a candidate solution is evaluated by its phenotype after termination.

1.2.3 Evaluation Function

To evaluate a solution, an evaluation function (or fitness or objective function) is used. Its role is to establish a quality measure to genotypes and to phenotypes.

1.3 Genetic Algorithms

Genetic algorithm (GA) is one of the oldest and most popular EAs (Holland, 1975). Pioneered by Holland (1975), it largely imitates genetic inheritance from parents to children and natural selection procedures until a termination criterion is satisfied.

GA starts by randomly generating an initial population of strings called “chromosomes” in the genotype space. A chromosome consists of a fixed number of variables called “genes”. The population evolves in generations through the repetition of three operators; the selection, the recombination and the mutation operators. Based on their fitness, the selection operator stochastically selects some individuals from the current population to form a new population. The recombination operator selects pairs of individuals from the new population and mates them to produce the offspring. Then, the mutation operator randomly mutates some individuals by altering one or more of their genes. Finally, another type of selection

mechanism selects individuals from the current and the new populations to constitute the population for the next generation. The algorithm stops when a predefined criteria is met. A formal algorithm of GA is stated in Algorithm 1.3.1 (Hedar, 2004), before describing the main components that compose a standard GA.

Algorithm 1.3.1. *Genetic Algorithm*

1. ***Initialization.*** *Generate an initial population P_0. Set the crossover and mutation probabilities $\pi_c \in (0,1)$ and $\pi_m \in (0,1)$, respectively. Set the generation counter $t := 1$.*
2. ***Selection.*** *Evaluate the fitness function F at all chromosomes in P_t. Select an intermediate population P'_t from the current population P_t. Set the parents pool set S_t^P and the children pool set S_t^C to be empty.*
3. ***Crossover.*** *Associate a random number from $(0,1)$ with each chromosome in P'_t and add this chromosome to the parents pool set S_t^P if the associated number is less than π_c. Repeat the following Steps 3.1 and 3.2 until all parents in S_t^P are mated:*
   3.1. *Choose two parents p_1 and p_2 from S_t^P. Mate p_1 and p_2 to reproduce children c_1 and c_2.*
   3.2. *Update the children pool set S_t^C through $S_t^C := S_t^C \cup \{c_1, c_2\}$ and update S_t^P through $S_t^P := S_t^P - \{p_1, p_2\}$.*
4. ***Mutation.*** *Associate a random number from $(0,1)$ with each gene in each chromosome in P'_t, mutate this gene if the associated number is less than π_m, and add the mutated chromosome to the children pool S_t^C.*
5. ***Stopping Conditions.*** *If stopping conditions are satisfied, then terminate. Otherwise, select the next generation P_{t+1} from $P_t \cup S_t^C$. Set $t := t + 1$ and go to Step 2.*

1.3.1 Representation

The representation of candidate solutions is made by defining a mapping between the search space and the problem space. Then, the link between genotypes and phenotypes can be established. In the following, the most commonly used representations are described (Herrera et al., 1998).

Binary Representation

One of the most intuitive representations is the binary representation. It consists of a bit string for the genotype. One must ensure that all possible solutions have its equivalent in the genotype space and that all genotypes represent a feasible solution.

Integer Representation

The integer representation consists in representing a solution by a set of variables. These variables are integers that may possess a relation between the different values of a variable, such as ordinal attributes for example.

Real-valued Representation

The real-valued representation, or floating-point representation, is useful when one wants to represent solutions that come from a continuous distribution. It consists of a string of real values.

Permutation Representation

The permutation representation is based on the representations previously described. Most often, problems that use the permutation representation are based on the integer representation but the difference is that a value can occur only once. There are two classes of problems adapted for the permutation representation; the problems that depend on some order and the problems that depend on adjacency.

1.3.2 Mutation Operators

Depending on the adopted representation, the form of this variation operator changes as well as its associated parameter, called the mutation rate or mutation probability π_m (Herrera et al., 1998).

Binary Representations

In the case of binary representations, the most used mutation form consists in considering each gene separately and flipping their values with probability π_m.

Integer Representations

For integer representations, two main schemes are used (sometimes in combination); the random resetting and the creep mutation. The random resetting uses the mutation rate π_m to change the value of a gene into another permissible value. This technique is commonly used when there is no relation between the different values of a variable. The creep mutation adds to each gene a randomly sampled slight value with probability π_m.

Floating-point Representations

The mutation operators for floating-point representations are very similar to the methods used for integer representations. Two schemes are used; the uniform mutation and the

nonuniform mutation with a fixed distribution. In both cases, a gene is randomly replaced by a new one according to a probability distribution within its permissible domain given by lower and upper bounds. In uniform mutation, each new value is drawn randomly within the domain. However the nonuniform representation is largely more used. It consists in adding to each gene a randomly drawn value, and ensuring that the resulting value stays within the permissible domain.

Permutation Representations

For permutation representations, the general method is different since the genes cannot be altered freely without taking into consideration that some configurations can be proscribed. Hence, the mutation parameter is seen here as the probability that the entire string is modified. We briefly describe four common procedures for this operator; the swap mutation, the insert mutation, the scramble mutation and the inversion mutation. The swap mutation takes two genes and substitutes their values. The insert mutation considers two random genes, moves one next to the other and translates the others genes into the free spaces. The scramble mutation takes two random positions, and scrambles the genes that lie between the two selected positions. Similar to the scramble mutation, the inversion mutation chooses two random positions and inverses the order of the genes that lie between the selected positions.

1.3.3 Recombination

Recombination, also called crossover, is the most specific operator of GAs. This variation operator uses two or more parent solutions to generate one or more child solutions. A crossover rate π_c determines whether or not two or more parent solutions are combined to generate new solutions. The mechanism works as follows: First, two or more parent solutions are selected. Then, a random value is drawn and compared to the crossover rate π_c. If the random value is below the crossover rate, a "recombination" is applied and two or more child solutions are generated. Depending on the adopted representation, the form of the recombination differs (Back et al., 2000; Eiben and Smith, 2003).

Binary and Integer Representations

For binary and integer representations, the three most common forms use two parents to generate two children. They are the one-point crossover, the ρ-point crossover and the uniform crossover.

The one-point crossover first selects a random value within the range of the encoding's length. That value is used to determine the point where the genotype of both parents are cut in two parts. Two children are created by exchanging the tails of the parents.

The ρ-point crossover is similar to the one-point crossover except that ρ random values are drawn. The genotype of both parents are then cut in $(\rho + 1)$ parts and alternative parts are exchanged to form the children.

The uniform crossover considers each gene separately. For each gene, a random value is compared to the probability π_c. If the value is below π_c, then the first child takes the value of the considered gene from the first parent. Otherwise, it takes the value of the gene of the second parent. The second child is built with the inverse mapping.

Floating-point Representations

For this representation, two forms are commonly used; the discrete recombination and the arithmetic representation. The discrete recombination uses the same operators as for the binary representation. Hence, new solutions cannot appear without mutation operators.

With the arithmetic recombination, each gene is considered separately and the gene of a child is generated by setting its value between the values of the genes of the parents.

Permutation Representations

Because of the permutation property, the recombination operator must here obey to specific rules. Many operators have been designed and we describe here the most common; the partially mapped crossover, the edge crossover, the order crossover and the cycle crossover. They all aim at maintaining as much as possible of the common information contained in the parents.

The partially mapped crossover is a widely used recombination operator for adjacency-type problems. It was first designed to solve a particular problem that consists in finding the shortest path connecting a number of locations. The general idea is as follows: Two random values are first chosen in the encoding length's range of the parents. Between these two points, the values of the first parent are copied into the child. Then, the second parent is considered and all values that are not contained in the child are transferred. The major problem of this technique is that information commonly contained in both parents is not systematically transferred to the child.

To restore this property, the edge crossover works by constructing an edge table where each element is linked with the other elements contained in both parents.

The order crossover is very similar to the partially mapped crossover except that after the copy of the segment between the two random values, the non-copied values present in the second parent are written into the child with the intention to conserve the relative order contained in the second parent.

The cycle crossover is slightly different from the operators described above in the fact that it aims at maintaining the absolute position of the elements of the parents.

1.3.4 Parent and Survivor Selection

Variation operators aim to create a new generation of individuals. Among these new individuals, one can decide that they will entirely replace the old generation (the generational model) or that only some of them will take part in the next generation (the steady-state model). Commonly, in both cases the population size is constant. Those considerations are highly related to the survivor selection mechanisms and to the parent selection mechanisms (Back et al., 2000; Eiben and Smith, 2003).

Parent Selection

There are basically four mechanisms for the parents selection; the fitness proportional selection, the ranking selection, the implementing selection probabilities, and the tournament selection.

With the proportional selection, the probability that a solution will be used as a parent to create offspring depends on its absolute fitness compared to the absolute fitness of the population. However, this method has some drawbacks. When a solution is far better than the other solutions, the algorithm might converge prematurely (see Section 2.1). On the other hand, if solutions have about the same fitness, the algorithm might converge very slowly after some iterations.

The ranking selection is similar to the proportional selection but the probability that a solution will be used as a parent depends on its rank in the whole population rather than on its absolute fitness.

Implementing selection probabilities is achieved by the roulette wheel algorithm. The idea of this stochastic algorithm is to give to each individual a set of values depending on its fitness. Then, a random number is generated and the individual that matches the random number is selected. The procedure is repeated until the number of desired parents is reached.

The tournament selection has the advantage that one does not have to possess any information about the entire population. The algorithm first picks a given number of individuals. Then, it selects the individual that has the highest fitness and repeats the procedure until the number of desired parents is reached.

Survivor Selection

The survivor selection mechanism is analogous to the parent selection with the difference that it occurs at a different stage in the evolutionary cycle. Instead of selecting individuals for reproduction, the survivor selection determines the parents and the offspring individuals that will remain for the next generation. This mechanism is sometimes also called replacement. We distinguish two types of replacements; the age-based replacement and the fitness-based replacement.

The age-based replacement is a very simple mechanism. An individual exists only for a determined number of GA cycle. It is thus independent of the fitness of the individuals.

With the fitness-based replacement, two schemes are commonly encountered. The first is the replace worst scheme, which consists in selecting for replacement individuals of the population with the worst fitness until the number of individuals inside the population equals the initial population. The second is the elitism scheme, which aims at maintaining in the next generation the individual with the highest fitness even if it is selected for replacement.

1.4 Differential Evolution

Differential Evolution (DE) is a very competitive EA for solving real-parameter optimization problems that first appeared in 1995 in a technical report written by R. Storn and K. Price (Storn and Price, 1995). Since then, DE has attracted particular attention and yielded a significant number of research articles.

Practitioners particularly appreciate the relative simplicity to implement and efficiency for many optimization problems in real-world applications (Joshi and Sanderson, 1999; Price et al., 2005; Zhang et al., 2008). Another advantage of DE compared with other EAs is that the number of control parameters is very low (three for the classical DE, namely, the population size μ, the crossover rate π_c and the scaling factor F). A number of papers in the literature extensively study the influence of these parameters on the performance of the algorithm (Gämperle et al., 2002).

As other EAs, DE is population-based and uses common features of EAs such as recombination and selection operators. However, one of the distinctive features of DE lies in the fact that it exploits the information about differences between trial solutions, the latter being identified as "parameter vectors", to explore the search space. Basically, in DE, the mutation operator considers two parameter vectors and adds a weighted difference vector to create a third parameter vector. Different flavors of the mutation operator have been investigated. Coupled with different kinds of crossover operators, various DE schemes can be designed (Das and Suganthan, 2011).

1.4.1 Basic Concepts

In DE, a population is represented by n-dimensional vectors $x^i, i \in \{1, \ldots, \mu\}$, where n is the dimension of the problem and μ is the population size. Like other EAs, DE starts with an initial population that is generated randomly. It is followed by the mutation, crossover and selection operators. We emphasize that, in DE, the mutation, crossover and selection operations are mutually dependent and are performed sequentially for every individual x^i in the population.

Mutation

At each generation, the parameter vectors undergo mutation to create new vectors v^i according to the formula

$$v^i = x^{r0} + F \times (x^{r1} - x^{r2}), \tag{1.4.1}$$

where $r0$, $r1$, $r2$ are distinct integers taken from the set $\{1, 2, \ldots, \mu\}\backslash\{i\}$ and F is a positive real constant that represents the mutation factor used to control the effect of the difference vector $(x^{r1} - x^{r2})$. The parameter F is commonly referred to as the amplification factor or scale factor. Depending on the number of difference vectors being considered, different strategies can be implemented.

Crossover

The crossover operator is called right after the mutation operation. During this process, the vector $u^i = (u^i_1, u^i_2, \ldots, u^i_n) \in R^n$ is generated by

$$u^i_j = \begin{cases} v^i_j, & \text{if } U_j \leq \pi_c \text{ or } j = j_{rand}, \\ x^i_j, & \text{otherwise,} \end{cases} \tag{1.4.2}$$

where U_j is a uniform random number from the interval $(0, 1)$, and $\pi_c \in [0, 1]$ is a parameter that represents the crossover rate. For each j and each i, the number U_j is independently generated, and for each i, j_{rand} is a random integer from $[1, n]$.

Equation (1.4.2) is in fact the scheme used for what is called the *binomial* crossover. In DE, there are mainly two types of crossovers that can be used; the *binomial* and the *exponential* crossovers (Price et al., 2005).

Selection

During the selection process, the parameter vector u^i generated by the crossover operator competes with the vector x^i according to its value of the function $f(\cdot)$. Specifically, the offspring of x^i is determined by

$$\tilde{x}^i = \begin{cases} u^i, & \text{if } f(u^i) \leq f(x^i), \\ x^i, & \text{otherwise.} \end{cases} \tag{1.4.3}$$

The population size thus remains constant and its fitness is assured to never decline.

Those three operators, mutation, crossover and selection, can have many different variants, and when assembled together, they form different kinds of DE that can be classified by the following commonly used notation: DE/x/y/z, where “DE” stands for “Differential Evolution”, x denotes the base parameter vector to be perturbed, y represents the number of difference vectors to consider, and z is the type of crossover employed.

1.5 Particle Swarm Optimization

Particle Swarm Optimization (PSO) is a population-based stochastic approach for solving optimization problems. It was introduced by Kennedy and Eberhart in 1995 (Kennedy and Eberhart, 1995; Eberhart and Kennedy, 1995) and is today one of the most important SI paradigms. Inspired by the social behavior of bird flocking and fish schooling, a population of agents, called particles, moves through some multidimensional search space in an attempt to converge towards the global optima.

During the evolutionary process, the position of each particle in the search space as well as its historical best position it could achieve so far are stored. The latter is often referred to as the personal best value of a particle, or *pbest*, in the literature. The global best solution so far reached by the swarm is also tracked and designated as *gbest*. This information represents the cognitive (*pbest*) and social (*gbest*) components that adjust, during the search, the velocities of each particle which then determine their positions in the subsequent iterations.

Nowadays, PSO is widely and successfully applied in many real-world optimization problems (Eberhart and Yuhui, 2001; Franken and Engelbrecht, 2005; Krohling and dos Santos Coelho, 2006; Li and Engelbrecht, 2007). However, like other population-based stochastic algorithms, accelerating the convergence speed as well as avoiding getting trapped in local optima is still an important subject of research for PSO (Liang et al., 2006), as confirmed by numerous works dealing with these issues (Ciuprina et al., 2002; Liang et al., 2006; Liu et al., 2007; Ho et al., 2008). Yet, it is still arduous to increase both convergence speed and reliability simultaneously.

1.5.1 Basic Concepts

In PSO, each particle p^i represents a potential solution in an n-dimensional space and is associated with two vectors that determine its position and velocity with which it navigates through the search space. Specifically, the position of particle p^i is represented by the position vector $x^i = (x_1^i, x_2^i, \ldots, x_n^i)$ and the speed by the velocity vector $v^i = (v_1^i, v_2^i, \ldots, v_n^i)$.

Initially, the position and the velocity of each particle are generated randomly within the corresponding range of each coordinate. During the evolutionary process, the positions and velocities of particle p^i are iteratively updated using the following rules that take into account the trajectory of each particle according to its own experience, information on the performance of the *gbest* as well as on the performance of other individuals in its neighborhood:

$$x^{i,k+1} := x^{i,k} + v^{i,k}, \tag{1.5.1}$$

$$v^{i,k+1} := w \times v^{i,k} + c_1 \times rand_1^k \times (p^{i,k} - x^{i,k}) + c_2 \times rand_2^k \times (p^{g,k} - x^{i,k}), \tag{1.5.2}$$

where $rand_1^k$ and $rand_2^k$ are two random numbers uniformly distributed in the range $[0, 1]$,

w, c_1 and c_2 are parameters that represent the inertia weight, the cognition weight and the social weight, respectively, $x^{i,k}$ and $v^{i,k}$ are the position and the velocity vectors of particle p^i in iteration k, respectively, $p^{i,k}$ is the *pbest* vector of particle p^i in iteration k, and $p^{g,k}$ is the *gbest* vector in iteration k. The classical PSO is illustrated in Algorithm 1.5.1, where N denotes the size of the swarm and $f(x^i)$ represents the objective function value of particle p^i located at position x^i.

Algorithm 1.5.1. *PSO Pseudocode*

1. ***Initialization.*** *For each particle p^i, $i = 1, \ldots, N$, in the swarm, do the following:*
   - ***1.1.*** *Initialize x^i and v^i randomly.*
   - ***1.2.*** *Evaluate $f(x^i)$.*
   - ***1.3.*** *Initialize* pbest^i *associated to p^i.*
2. ***Main loop.*** *Repeat Steps 2.1 to 2.3 until a stopping criterion is met.*
   - ***2.1.*** *Locate* gbest.
   - ***2.2.*** *For each particle p^i, set* pbest$^i := x^i$ *if $f(x^i) \leq f(\text{pbest}^i)$.*
   - ***2.3.*** *For each particle p^i, update x^i and v^i by applying Equations (1.5.1) and (1.5.2), and evaluate $f(x^i)$.*

1.5.2 PSO Variants and Improvements

PSO has rapidly gained popularity among researchers and is now a widely used optimizer for practical problem solving. One of the first improvements made to PSO was related to its strong parameter dependency. Indeed, one can find in the literature much work on improving its performance via self-adaptation (Clerc, 1999; Shi and Eberhart, 2001; Yasuda et al., 2003; Zhang et al., 2003) or by using hybrid techniques (Angeline, 1998b; Reynolds et al., 2003; Higashi and Iba, 2003; Esquivel and Coello, 2003). Theoretical studies have mainly focused on convergence and stability analysis (Clerc and Kennedy, 2002; Trelea, 2003; Kadirkamanathan et al., 2006; van den Bergh and Engelbrecht, 2006).

Hybridization of PSO with other techniques or evolutionary paradigms is also a very active research trend. In order to increase diversity within the swarm and thus to avoid premature convergence, many researchers have considered introducing operators inspired from Genetic Algorithms (GA) within PSO, such as selection (Angeline, 1998b), crossover (Chen et al., 2007) and mutation (Andrews, 2006). For instance, to include within PSO a natural selection mechanism can help increasing the general fitness of the swarm at each generation. It is explained by the fact that the selection mechanism allows the swarm to change the current search area or to jump towards another one, which makes the algorithm convergent faster (EL-Dib et al., 2004). EL-Dib et al. proposed to modify the positions and the velocities of randomly selected particles using formulas inspired from the reproduction system of species with the following crossover rules. Let x^1 and x^2 be the positions of two

particles randomly selected (the parents), and let v^1 and v^2 be their respective velocities. Then the positions and velocities of two created candidate particles (the offspring), denoted x^3, x^4 and v^3, v^4, respectively, are determined by arithmetic crossover, for the position of the offspring, and as the sum of the velocity vectors of the parents normalized to the original length of each parent velocity vector, for the velocity:

$$x^3 := r \times x^1 + (1 - r) \times x^2,$$

$$x^4 := r \times x^2 + (1 - r) \times x^1,$$

$$v^3 := \frac{|v^1|}{|v^1 + v^2|} \times (v^1 + v^2),$$

$$v^4 := \frac{|v^2|}{|v^1 + v^2|} \times (v^1 + v^2),$$

where r is a random number from the interval $[0, 1]$ and $|\cdot|$ is some vector norm.

Other variations include the incorporation of techniques such as local search (Liang and Suganthan, 2005), cooperative approaches (van den Bergh and Engelbrecht, 2004) and DE (Zhang and Xie, 2003). In (Zhang and Xie, 2003) for example, the hybridization of PSO with DE is proposed to speed up the convergence. This method uses Equations (1.5.1) and (1.5.2) at the odd iterations, while it uses the following mutation operation rule at the even iterations with a trial point $T^i := p^i$:

$$\text{If } (rand < \pi_c \text{ or } n = k) \text{ then } T^i := p^g + \vec{\delta},$$

where k is a random integer chosen from $[1, n]$, which ensures that at least one component will eventually participate in the mutation, π_c (≤ 1) is the crossover rate, p^g is the *gbest* vector and $\vec{\delta} := (\vec{\Delta}_1 + \vec{\Delta}_2)/2$, where $\vec{\Delta}_1 = p^a - p^b$ and $\vec{\Delta}_2 = p^c - p^d$ represent the difference vectors between two *pbests* p^a and p^b and two *pbests* p^c and p^d, respectively, selected randomly from the *pbest* set. The resulting trial point T^i replaces p^i if its fitness value is better than the fitness value of p^i.

1.6 Organization and Contributions

In the subsequent chapters, we will describe the original EC methods that we have developed to address the problem of the termination criteria. Our main objective is to demonstrate that the novel mechanisms developed in this research can effectively provide the search process with the ability to stop automatically, without external intervention. In addition, we ensure that the automatic termination does not have a negative impact on the quality of the solution obtained.

In Chapter 2, we illustrate some of the main drawbacks of EC that have led us to develop the Gene Matrix (GM). The GM, described in this chapter, is the core mechanism common to our proposed methods in this study, and developed to equip the search with a termination tool. We also describe the mutagenesis operator, a new type of mutation that works in combination with the GM. Moreover, we overview the main concepts of the Nelder-Mead (NM) method, a local search algorithm used to accelerate the search in the final stage of the search process.

In Chapter 3, we introduce the Genetic Algorithms Combined with Accelerated Mutation and Automatic Termination (G3AT) method. G3AT is the first method that is embedded with the GM. The competitiveness of G3AT against existing methods is demonstrated and the influence of the GM on the search is extensively analyzed.

In Chapter 4, an improvement of G3AT is presented. It addresses several drawbacks of the GM by calling the novel Space Decomposition (SD) and Space Rotation (SR) mechanisms. The enhanced method is named Genetic Algorithm with Automatic Termination and Search Space Rotation (GATR). We show through extensive numerical experiments that the solutions obtained do not suffer from premature termination and that GATR is comparable or superior to many state-of-the-art EAs.

In Chapter 5, we show that the GM, SD and SR mechanisms can also be applied to DE, as an illustration of another EA. We present the Differential Evolution with Automatic Termination (DEAT) method and demonstrate that DEAT can also terminate the search automatically and be equal or superior to other DE methods.

In Chapter 6, we combine the Principal Component Analysis (PCA) technique with the GM and implement it on the PSO paradigm in order to compose the Automatically Terminated Particle Swarm Optimization with Principal Component Analysis (AT-PSO-PCA) method. The performance of AT-PSO-PCA is discussed through several numerical experiments and the impact of PCA is analyzed.

Finally, Chapter 7 summarizes the main contributions of this dissertation and discusses possible opportunities for further research.

Chapter 2

Gene Matrix, Mutagenesis and Intensification

The novel EC methods that we propose in this study are equipped with new directing strategies. The common elements are the Gene Matrix (GM), the mutagenesis operator and the final intensification process. The GM is a matrix constructed to represent subranges of the possible values of each variable and consequently reflects the distribution of the genes over the search range. Its role is to assist the exploration process in two different ways. First, the GM can provide the search with new diverse solutions by applying the mutagenesis operator. The mutagenesis operator is a new type of mutation that works in combination with the GM. It alters some individuals in order to accelerate the exploration and exploitation processes by guiding the search specifically towards unexplored areas. Also, the GM is the key to let the search know how far the exploration process has been performed in order to determine an adequate termination instant. To further accelerate the search process, a local search method is used in the final intensification process to improve the best candidate solution obtained upon GM termination.

In this chapter, the concepts of premature convergence and slow convergence are reviewed, before providing an overview of the commonly adopted termination criteria in EC. Then, the advantages of having automatic termination criteria are discussed. Finally, the GM, the mutagenesis operator as well as the Nelder-Mead local search method are described in detail.

2.1 Premature Convergence

When the diversity of the population decreases below a certain level, the population may converge to a suboptimal similar individual. EC techniques have been initially designed so that they can focus their search on promising areas of the search space discovered during the exploration phase. Consequently, diversity among individuals of the population tends to

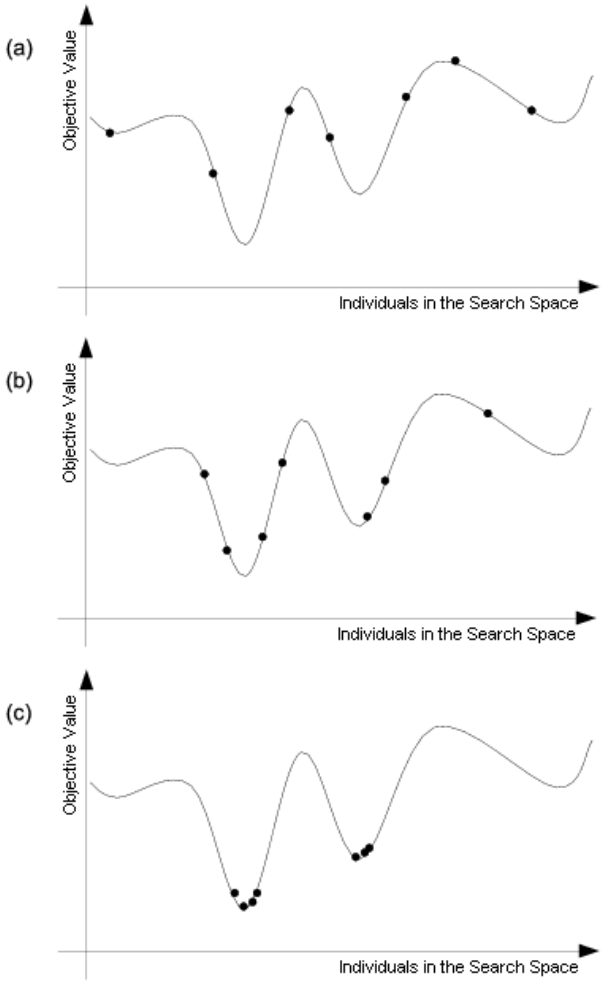


Figure 2.1: Objective function evolution at different stages of the search.

decrease and to concentrate around individuals with high fitness (Fogel, 1994). As a result of this behavior, EC techniques tend to get trapped in the vicinity of local optima. This phenomenon is known as "premature convergence".

2.2 Slow Convergence

Figure 2.1 depicts the objective function evolution for a minimization problem at three different stages of the search (Eiben and Smith, 2003). At the first stage, represented in Figure 2.1(a), the population is randomly distributed over the search space. As the evolutionary search progresses, the population tends to concentrate around valleys, as depicted in Figure 2.1(b). At the end of the search, the whole population lies on a few valleys as shown in Figure 2.1(c). Hopefully, the individuals are gathering around a global optimum.

However, Figure 2.2 characterizes the convergence behavior of an evolutionary search by

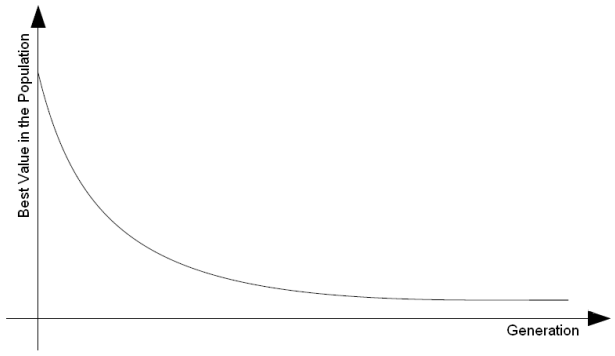


Figure 2.2: Convergence behavior of an evolutionary search.

plotting the best value of the objective function in time. We can observe a rapid descendant progression of the objective value during the beginning of the search. Later on, progresses in terms of objective value deteriorate and it could be insignificant to let the search run after a certain time. As a result, compared to local search techniques, EC methods suffer from slow convergence. Indeed, due to their random constructions, they do not exploit much local information to guide their search. Typically, these techniques cover a large frontier in the search space in the early stage of the search but explore it in a less directional approach. Thus when dealing with stopping criteria, one should also pay meticulous attention to the balance between exploration and exploitation.

2.3 Automatic Termination

Basically, EC methods cannot decide when or where they can terminate the search and usually a user should prespecify the maximum number of generations or function evaluations as termination criteria. There are only a few recent works on termination criteria for EAs (Giggs et al., 2006; Kwok et al., 2007; Jain et al., 2001). In (Giggs et al., 2006), an empirical study is conducted to detect the maximum number of generations using the problem characteristics. In (Kwok et al., 2007), the particle swarm optimization algorithm is stopped using a termination condition based on statistics. The hypothesis testing non-parametric sign-test method is considered as a decision making process using a list of the stored highest fitness values in each iteration. The search stops when the hypothetical test indicates that no significant improvement in terms of solution quality is going to occur. In (Jain et al., 2001), eight termination criteria have been studied with an interesting idea of using clustering techniques to examine the distribution of individuals in the search space at a given generation.

The most commonly employed termination criteria for EC methods can be enumerated as the T_{Fit} *Criterion*, the T_{Pop} *Criterion*, the T_{Bud} *Criterion* and the T_{SFB} *Criterion*. The

T_{Fit} *Criterion* uses convergence measures of the best fitness function values over generations. This criterion is used for instance in (Hansen and Kern, 2004; Tsai et al., 2004; Zhong et al., 2004; Ong et al., 2006), where the goal is to get as close as possible to the known global minima. In (Leung and Wang, 2001), the search stops after reaching the maximum number of consecutive generations without improvement. When used alone, however, T_{Fit} *Criterion* may easily lead the search towards local minima, especially if the algorithm tends to reach in early stages a deep local minimum (Jain et al., 2001; Safe et al., 2004; Hedar and Fukushima, 2006b). The T_{Pop} *Criterion* uses convergence measures of the population over generations. This criterion is not particularly efficient though, since having one individual to reach a global minimum is enough. Moreover making the whole population or a part of it convergent can be expensive. The T_{Bud} *Criterion* uses a prespecified budget, that can be the number of generations or function evaluations (Yao et al., 1999; Lee and Yao, 2004; Ong and Keane, 2004; Tu and Lu, 2004; Koumousis and Katsaras, 2006; Ong et al., 2006; Zhou et al., 2007). The drawback is that it requires prior information about the test problem and is also highly problem dependent. Finally, the T_{SFB} *Criterion* checks the progress of the exploration and exploitation processes by using search feedback measures. Unfortunately, the use of search feedback may bring a complexity problem due to the need to save and check historical search information that can be huge and is also very sensitive to the dimensionality.

Good automatic termination criteria should assure that the search avoids premature termination but also indicates the point in time when further computations becomes unnecessary. This feature is of key importance in some real-world applications such as in "evolutionary testing" (O'Sullivan et al., 1998; McMinn, 2004). Indeed, during the development of embedded systems, testing is one of the most important quality assurance measure. A huge amount of effort and budget is allocated for testing. In evolutionary testing, EAs are used for test data generation and to verify the logical and temporal correctness of a system. Most testing methods are specialized in the logical correctness. However, for real-time systems, it is also essential to check the temporal correctness. Evolutionary testing fills this gap by testing the timing constraints where a temporal error occurs when outputs are produced too early or if the computational time is too long. In such situations, it is crucial to have reliable automatic termination criteria for EAs.

Multi-start methods may also benefit from automatic termination criteria. Among the main components of a multi-start method, we note the stopping criterion used within the generation mechanism of candidate solutions. The stopping criterion, in this case also referred to as the restarting criterion, is prespecified by the user and has a big impact on the overall computational cost of the method. Consequently, a reliable automatic termination criterion may have a positive effect on multi-start methods, by reducing the cost of generating candidate solutions, thereby more iterations can be allowed with a fixed budget. In the same way, automatic termination criteria may also be used effectively for dynamic EA

(Koo et al., 2010) where the convergence is very dependent on the behavior of the dynamic problem.

2.4 Gene Matrix and Termination

To achieve a wide exploration and to keep track of the progress of the exploration, we propose the concept of the GM. Each individual x in the search space consists of n variables. The range of each variable is divided into m sub-ranges in order to check the diversity of the variable values. Then, we define a solution counter matrix C of size $n \times m$, in which entry c_{ij} represents the number of generated solutions such that the i-th variable lies in the sub-range j, where $i = 1, \ldots, n$, and $j = 1, \ldots, m$. The GM is initialized to be the $n \times m$ zero matrix in which each entry of the i-th row refers to a sub-range of the i-th variable. GM is a 0–1 matrix and while the search is processing, the entries of GM are updated from zeros to ones if new values for variables are generated within the corresponding sub-ranges. After having a GM full, i.e., with no zero entry, the search learns that an advanced exploration process has been achieved and is stopped. In this way, the principal use of the GM is to equip the search process with a practical termination tool. Moreover, the GM assists in providing the search with diverse solutions as will be shown in Subsection 2.4.1. By keeping track of explored area of the search space in order to concentrate on parts that have not been considered yet, the GM yields some similarities with tabu search ideas (Glover, 1986; Ting et al., 2009). We define the GM completion ratio, referred to as CP, as the number of non-null entries divided by the total number of entries of GM. We have considered two types of GM as follows.

Simple Gene Matrix (GM^S)

GM^S does not take into account the number of solutions lying within each sub-range. During the search, the solution counter matrix C is updated. Let x_i be the representation of the i-th variable, $i = 1, \ldots, n$. Once variable i gets a value corresponding to a non-explored sub-range j, i.e., $c_{ij} > 0$, then GM is updated by flipping the zero into one in the corresponding (i, j) entry. Therefore, the updating process for GM^S can be defined as

$$(\mathrm{GM}^S)_{ij} = \begin{cases} 0, & \text{if } c_{ij} = 0 \\ 1, & \text{if } c_{ij} > 0, \end{cases} \tag{2.4.1}$$

where $i = 1, \ldots, n$, $j = 1, \ldots, m$, and $(\mathrm{GM}^S)_{ij}$ is the (i, j) entry of the gene matrix GM^S.

Figure 2.3 shows an example of GM^S in two dimensions, i.e., $n = 2$. In this figure, the range of each variable is divided into ten sub-ranges. We can see that for the first gene x_1, no individual has been generated inside the sub-ranges 1, 7 and 10, i.e., $c_{1,1} = c_{1,7} = c_{1,10} = 0$. Consequently, the $(1, 1)$, $(1, 7)$ and $(1, 10)$ entries of GM^S are equal to zero. For the second

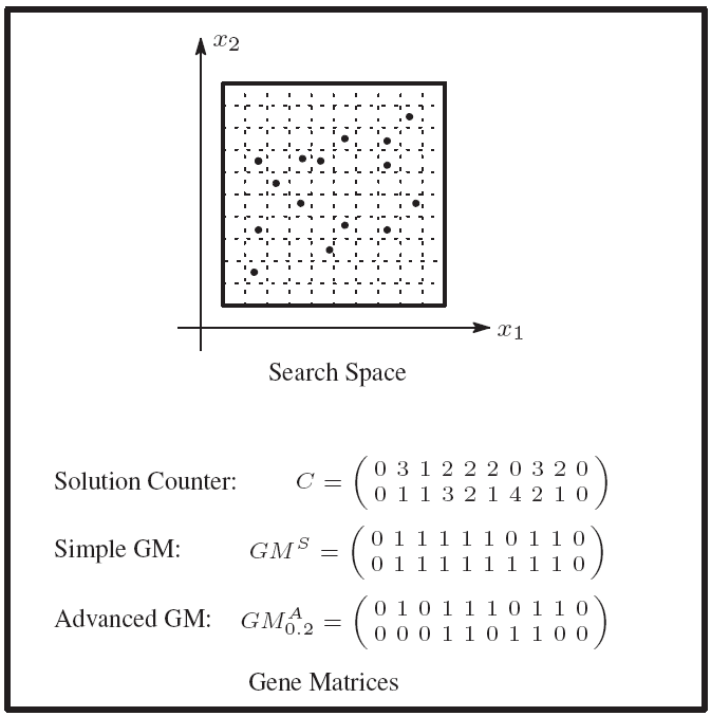


Figure 2.3: An example of the GM in R^2.

gene x_2, only the first and the last sub-ranges are unvisited, hence entries $(2,1)$ and $(2,10)$ of GM^S are null.

Advanced Gene Matrix (GM^A_α)

GM^A_α comes along with a ratio α predefined by the user. Unlike GM^S, GM^A_α is not immediately updated, unless the ratio of the number of individuals that have been generated inside a sub-range and m equals or exceeds α. Therefore, the updating process for GM^A_α can be defined as

$$(\mathrm{GM}^A_\alpha)_{ij} = \begin{cases} 0, & \text{if } c_{ij} < \alpha m \\ 1, & \text{if } c_{ij} \geq \alpha m, \end{cases} \tag{2.4.2}$$

where $i = 1, \ldots, n$, $j = 1, \ldots, m$, and $(\mathrm{GM}^A_\alpha)_{ij}$ is the (i,j) entry of the gene matrix GM^A_α.

An example of GM^A_α with $\alpha = 0.2$ in two dimensions can be found in Figure 2.3. Like GM^S, no individual has been generated inside sub-ranges 1, 7 and 10 for gene x_1. However, unlike GM^S, entry $(1,3)$ is equal to 0 in $\mathrm{GM}^A_{0.2}$ since there is only one individual lying inside the third sub-range, that is, $c_{1,3} = 1 < \alpha m = 2$. For the same reason, x_2 has six zero-entries corresponding to six sub-ranges in which the number of generated individuals divided by m is less than α. This example refers to the first generation of individuals. In a succeeding generation, if one or more individuals are generated inside the third sub-range for x_1 for example, then entry $(1,3)$ will be set equal to one.

2.4.1 Mutagenesis

After computing all children in each generation, we may want to give a chance to some characteristic children to improve themselves by modifying their genes. This is done by using a more artificial mutation operation called "mutagenesis". Specifically, two different types of mutagenesis operation are defined; the *Gene Matrix Mutagenesis* (GM-*Mutagenesis*) and the *Best Child Inspiration Mutagenesis* (BCI-*Mutagenesis*). These mutagenesis schemes alter some of the worst individuals of the current population. Specifically, the mutagenesis operation sorts the current population of size μ, then selects the worst μ_w ($< \mu$) individuals. GM-*Mutagenesis* and BCI-*Mutagenesis* alter μ_1 and μ_2 out of these μ_w worst individuals, respectively, as described below, where $\mu_1 + \mu_2 \leq \mu_w$.

GM-*Mutagenesis*

In order to preserve the diversity in the search process and accelerate the exploration process, GM-*Mutagenesis* is used to alter μ_1 from the μ_w worst individuals selected for the next generation. Instead of waiting for the crossover operation to generate new diverse solutions in some unexplored search space partitions, GM-*Mutagenesis* operations do this by guidance of the GM. Specifically, a zero-position in GM is randomly chosen, say position (i, j), i.e., the variable x_i has not yet taken any value in the j-th partition of its range. Then, a random value for x_i is chosen within this partition to alter one of the chosen individuals for mutagenesis. GM is updated since a new partition has been visited. The formal procedure for GM-*Mutagenesis* is given as follows.

Procedure 2.4.1. GM−Mutagenesis(x, GM)

1. *If there is no zero-position in GM, then return; otherwise, go to Step 2.*
2. *Choose a zero-position (i, j) in GM randomly.*
3. *Update x by setting $x_i = l_i + (j - r)\frac{u_i - l_i}{m}$, where r is a random number from $(0, 1)$, and l_i, u_i are the lower and upper bounds of the variable x_i, respectively.*
4. *Update GM and return.*

BCI-*Mutagenesis*

μ_2 individuals from the μ_w worst children are modified by considering the best child's gene values in the children pool. For each of the μ_2 worst children, one gene from the best child is randomly chosen and copied to the same position of the considered bad child as stated formally in the following procedure.

Procedure 2.4.2. BCI−Mutagenesis(x, x^{Best})

1. *Choose a random gene position i from $\{1, 2, \ldots, n\}$.*
2. *Alter x by setting $x_i := x_i^{Best}$, and return.*

2.5 Nelder-Mead Method

The methods proposed in this research invoke a local search (LS) method at the end of the search to produce an improved final solution from the best solution found upon automatic termination. The LS method used in our methods is based on the Nelder-Mead method (Nelder and Mead, 1965). The Nelder-Mead method is a derivative-free nonlinear optimization method. To avoid the computation of the derivative information for minimizing an objective function of several variables, this local search method uses the concept of a simplex. A simplex is the convex hull of a set of $n+1$ vertices, $x_1, x_2, \ldots, x_{n+1}$ in n dimensions; the geometric figure of nonzero volume is for instance a line segment on a line or a triangle on a plane.

At each iteration, the Nelder-Mead method maintains a non-degenerate simplex, i.e., a generalized triangle in n dimensions, as well as the function value of each vertex. Typically, new points (and their function values) are computed by reflecting the worst point through the remaining points considered as a plane. Then, the new worst point is replaced to form a new simplex. A sequence of simplex is thus created and the function value at each vertex decreases.

In order to create a sequence of simplices, some rules are applied; reflection, expansion, contraction and shrinkage. They possess the coefficients ρ, χ, γ and σ, respectively, such that:

$$\rho > 0, \quad \chi > 1, \quad 0 < \gamma < 1, \quad 0 < \sigma < 1.$$

Let $B = (x_1, y_1)$, $G = (x_2, y_2)$ and $W = (x_3, y_3)$ be the three vertices of a triangle as in (Mathews and Fink, 2004). Given $f(x, y)$, the function to be minimized, let us evaluate each vertices and order them such that $f(B) \leq f(G) \leq f(W)$. With this notation, point B conveniently stands for "best", G for "good" and W for "worst". M is the midpoint between B and G:

$$M = \frac{B+G}{2} = \left(\frac{x_1 + x_2}{2}, \frac{y_1 + y_2}{2} \right).$$

2.5.1 Reflection

If the function value decreases while moving along the vertex from W to B and from W to G, then the algorithm computes a test point R located on the opposite side from W of the line joining B and G as in Figure 2.4. Specifically, $R = 2M - W$ is found by reporting the length d of the line segment joining W and M and extending the same distance from M on the opposite side.

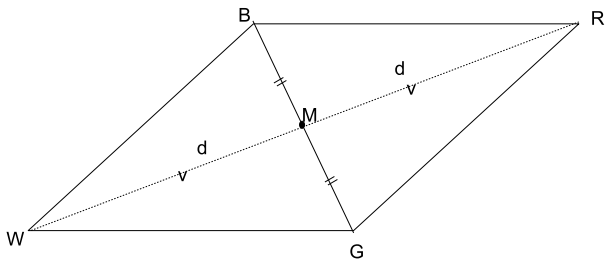


Figure 2.4: Reflection point for a simplex in two dimensions.

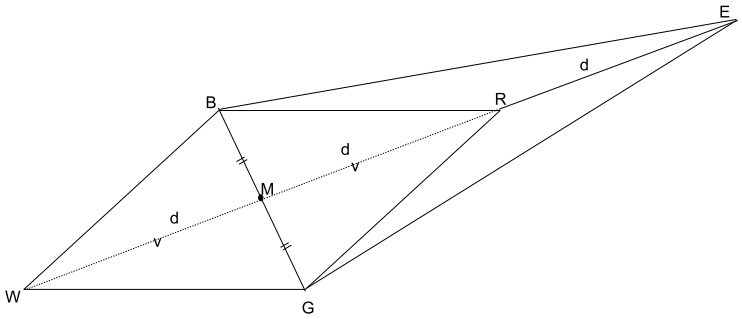


Figure 2.5: Expansion point for a simplex in two dimensions.

2.5.2 Expansion

If the vertex R has a function value smaller than B, then R is extended again through the line segment between W and R by the distance d from R to reach the point $E = 2R - M$ as in Figure 2.5.

2.5.3 Contraction

Contraction is used when the computed point R is not better than G. When it happens, the algorithm generates two points C_1 and C_2 located on the line segment $\overline{WR}$ and $\overline{WM}$, with C_1 inside the triangle BGW and C_2 inside the triangle BRG as drawn in Figure 2.6. Afterwards, the algorithm tries to locate between C_1 and C_2 a point C that would be better than R and W. If such point is found, it becomes the new point to be tested instead of R.

2.5.4 Shrinkage

After contraction, if the function value of the vertex C is bigger than W, then W and G are moved closer to B. This is achieved by replacing them by two new points S and M located in the middle of the line segments $\overline{WB}$ and $\overline{GB}$, respectively, as depicted in Figure 2.7.

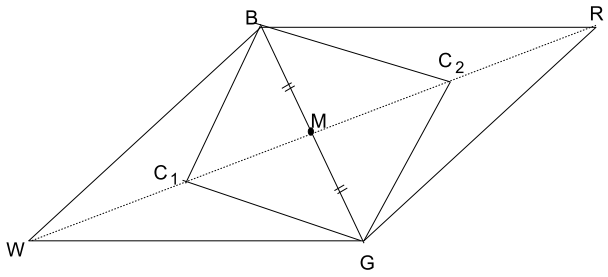


Figure 2.6: Contraction points for a simplex in two dimensions.

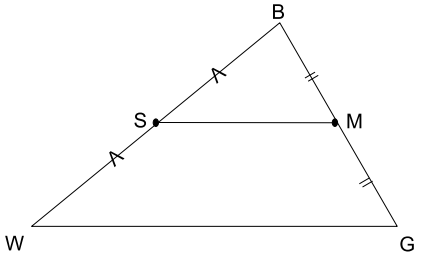


Figure 2.7: Shrinkage points for a simplex in two dimensions.

2.5.5 Kelley's Modification

It has been shown that the Nelder-Mead method can stagnate and converge to a non-optimal point, even for very simple problems (Mckinnon, 1999). Nevertheless, under certain conditions, convergence of the Nelder-Mead method to a stationary point can be guaranteed. Indeed, Kelley (Kelley, 1999) proposes a test for sufficient decrease and this modification of the Nelder-Mead method is the one we employ in the final stage of our proposed methods.

Chapter 3

Genetic Algorithms Combined with Accelerated Mutation and Automatic Termination

EAs are general problem solvers that show powerful performance in solving various problems. There have been many attempts to enhance the structure of EAs. However, EAs still have no automatic termination criterion. This chapter introduces our first attempt to equip GA, as an example of EAs, with new automatic termination criteria and acceleration elements. The proposed method is called Genetic Algorithm with Accelerated Automatic Termination (G3AT). In the G3AT method, the GM is constructed to equip the search process with a self-check to judge how much exploration has been done and to maintain the population diversity. Moreover, the mutagenesis operation is used to achieve more efficient and faster exploration and exploitation processes. The computational experiments show the efficiency of the G3AT method with the proposed termination criteria and the mutagenesis operation.

3.1 Introduction

In this chapter, we introduce a new hybrid GA that implements an automatic T_{SFB} termination criterion (see Section 2.3) with low complexity structure. Specifically, a new version of GAs called G3AT is proposed. In the G3AT method, a new GA method is designed and equipped with automatic termination criteria and new accelerating elements in order to achieve better performances.

The G3AT method is composed by modifying GAs with some directing strategies. First, an exploration and exploitation scheme is invoked to equip the search process with accelerated automatic termination criteria. Specifically, this role is carried out by the GM. The role of GM is to assist the exploration process in two different ways. First, GM can provide the search with new diverse solutions by applying the mutagenesis operator. The mutagenesis

operator alters some survival individuals in order to accelerate the exploration and exploitation processes. In addition, GM is used to let G3AT know how far the exploration process has gone in order to judge a termination point. The mutagenesis operation lets G3AT behave like a so-called "Memetic Algorithm" (Moscato, 1999) in order to achieve faster convergence (Ong and Keane, 2004; Ong et al., 2006). The numerical results presented later show that mutagenesis is effective and much cheaper than a local search. Then, the final intensification process can be started in order to refine the elite solutions obtained so far. The numerical results indicate that the proposed G3AT method is competitive with some other versions of GAs.

The rest of this chapter is structured as follows. In Section 3.2, we highlight and describe the main components of the G3AT method. The formal algorithm of G3AT is also provided in this section. In Section 3.3, numerical experiments aiming at analyzing the performance of G3AT and its novel operators are discussed. The effects that have GM and mutagenesis on the algorithm is also examined. Numerical comparisons with several advanced GAs and state-of-art EAs are carried out in Section 3.4. Section 3.5 contains a comparison between G3AT and the GA included in the MATLAB toolbox. Finally, the conclusion makes up Section 3.6.

3.2 G3AT Mechanisms

In this section, a new modified version of GAs called G3AT is presented. Before presenting the details of G3AT, we highlight some remarks on GAs to motivate the proposed G3AT.

Keeping diversity and elitism is an important issue in GAs. A key factor in composing GAs is to define genetic operators that can maintain the balance between diversity and elitism. Those considerations lead us to compose the mutagenesis operator. Mutagenesis alters some survival individuals while maintaining diversity and elitism and accelerates the diversification and intensification processes.

EAs are not equipped with automatic termination criteria. Actually, EAs may obtain an optimal or near-optimal solution in an early stage of the search but they are not learned enough to judge whether they can terminate. To counter this weakness, G3AT is built with termination measures that can check the progress of the exploration process through successive generations. Then, an exploitation process refines the best candidates obtained so far in order to achieve faster convergence.

In designing G3AT, we have considered the above-mentioned remarks. The standard GA is modified with the Simple GM and termination mechanisms, described in Section 2.4. The selection, crossover and mutation operators that compose G3AT are described in this section.

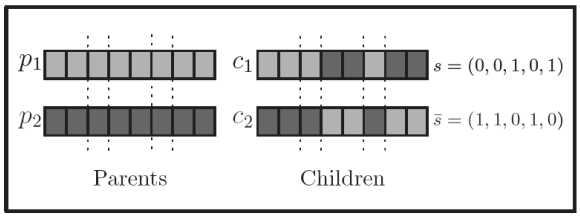


Figure 3.1: An example of the crossover operation.

3.2.1 Parent Selection

The parent selection mechanism first produces an intermediate population P' from the initial population P, i.e., $P' \subseteq P$, as in the canonical GA. For each generation, P' has the same size as P but an individual can be present in P' more than once. The individuals in P are ranked with their fitness function values based on the *linear ranking selection mechanism* (Baker, 1985; Hedar and Fukushima, 2003). Indeed, individuals in P' are copies of individuals in P depending on their fitness ranking; the higher fitness an individual has, the more the probability that it will be copied is. This process is repeated until P' is full while an already chosen individual is not removed from P.

3.2.2 Crossover

The crossover operation has an exploration tendency, and therefore it is not applied to all parents. First, for each individual in the intermediate population P', the crossover operation chooses a random number from the interval $(0, 1)$. If the chosen number is less than a prespecified crossover probability $\pi_c \in (0, 1)$, the individual is added to the parent pool. After that, two parents from the parent pool are randomly selected and mated to produce two children c_1 and c_2, which are then placed in the children pool. These procedures are repeated until all parents are mated. The crossover operator used in G3AT method is a ρ-point operator with random $\rho \leq n$. Therefore, a recombined child is calculated to have ρ partitions. Both parents genotypes are cut in ρ partitions and the randomly chosen parts are exchanged to create two children. Let us note that a parent is selected only once, and if the total number of parents inside the parent pool is uneven, then the last parent that was added into the pool is not considered for the mating procedure. As an example, Figure 3.1 shows two parents p_1 and p_2 partitioned into five partitions at the same positions (after the second, third, fourth and sixth genes). Then, a recombined child c_1 is generated to inherit partitions from the two parents according to a random sequence of zeros and ones, $(0, 0, 1, 0, 1)$ in this example, meaning that its first, second and fourth partitions will be inherited from p_1 and third and fifth partitions from p_2. The other partition sequence of the recombined child c_2 is the complementary of the sequence of c_1, namely $(1, 1, 0, 1, 0)$. The following procedure

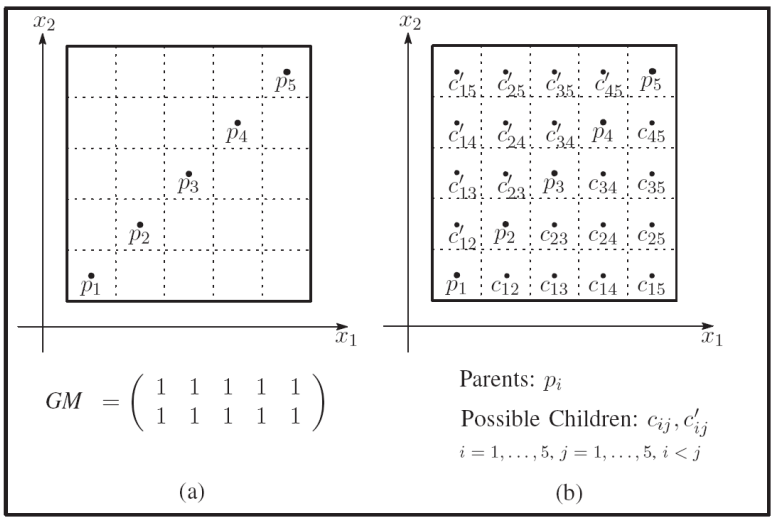


Figure 3.2: The role of crossover operation and GM.

describes the G3AT crossover operation precisely.

Procedure 3.2.1. Crossover(p_1, p_2, c_1, c_2)

1. *Choose an integer* ρ $(2 \leq \rho \leq n)$ *randomly.*
2. *Partition each parent into* ρ *partitions at the same positions, i.e.* $p_1 = [X_1^1\ X_2^1\ \ldots\ X_\rho^1]$ *and* $p_2 = [X_1^2\ X_2^2\ \ldots\ X_\rho^2]$.
3. *Choose a random mask (binary string)* s *of size* ρ*, i.e.* $s = o_1 o_2 \ldots o_\rho$*, where* $o_i \in \{0, 1\}$*,* $i = 1, \ldots, \rho$.
4. *Set* $c_1 = p_1$ *and* $c_2 = p_2$.
5. *Swap partitions* X_i^1 *and* X_i^2 *in* c_1 *and* c_2 *if the corresponding digit* o_i *of mask* s *is equal to 1, where* $i = 1, \ldots, \rho$*, and return.*

Actually, this type of crossover is chosen to support the G3AT exploration process. Specifically, there is no information related to different sub-ranges of different variables saved in GM in order to escape from the complexity of high dimensional problems. Therefore, there is a possibility of having misguided termination of the exploration process as in the example shown in Figure 3.2(a), where GM is already full although genes x_1 and x_2 have not their search spaces entirely covered. However, invoking this type of crossover operation as in Procedure 3.2.1 can easily overcome the drawback as shown in Figure 3.2(b). Actually, the mutagenesis operation cooperates with this type of crossover operation by combining new generated genes by mutagenesis with other existing genes of the current population individuals. Moreover, the numerical simulations presented in Section 3.3 demonstrate that G3AT can explore the search space widely.

3.2.3 Mutation

The mutation operator uses information contained in GM. For each individual in the intermediate population P' and for each gene, a random number from the interval $(0, 1)$ is associated. If the associated number is less than a prespecified mutation probability π_m, then the individual is copied to the intermediate pool IP_M. The number of times the associated numbers are less than the mutation probability π_m is counted. Let num_m denote this number. Afterward, the mutation operation makes sure that the total number num_m of genes to be mutated does not exceed the number of zeros in the GM, denoted num_{zeros}. Otherwise, the number of genes to be mutated is reduced to num_{zeros}. Finally, a zero from GM is randomly selected, say in position (i, j), and a randomly chosen individual from IP_M has its gene x_i modified by a new value lying inside the j-th partition of its range. The formal procedure for mutation is analogous to Procedure 2.4.1.

Procedure 3.2.2. Mutation(x, GM)

1. *If GM is full, then return; otherwise, go to Step 2.*
2. *Choose a zero-position (i, j) in GM randomly.*
3. *Update x by setting $x_i = l_i + (j - r)\frac{u_i - l_i}{m}$, where r is a random number from $(0, 1)$, and l_i, u_i are the lower and upper bounds of the variable x_i, respectively.*
4. *Update GM and return.*

3.2.4 G3AT Formal Algorithm

G3AT starts with an initial population of size μ. As in a standard GA, G3AT evaluates the population members, and then, parent selection, crossover and mutation operations are applied to generate the offspring. Following memetic algorithm features, G3AT invokes a local search method to improve some promising children. Since applying a local search might be expensive, G3AT alternatively uses mutagenesis operation. Therefore, to avoid the redundance of applying two intensification schemes for the same purpose, either the local search step or the mutagenesis step is invoked. This pattern is repeated until the termination criteria are satisfied. Specifically, G3AT is terminated when η generations have elapsed after getting a full GM. The reason for waiting η generations after having a full GM is to allow the crossover operation, which is the main exploration operation, to explore corresponding partitions found by the last update of GM. It is worthwhile to mention that the main role of GM is to guide the search process towards unexplored regions, not to explore them since the exploration is the main role of the crossover operation. Finally, G3AT uses a complete local search method as final intensification in order to refine the best solutions found so far. The formal detailed description of G3AT is given in the following algorithm.

Algorithm 3.2.3. *G3AT Algorithm*

1. ***Initialization.*** *Set values of m, μ, η, and (l_i, u_i), for $i = 1, \ldots, n$. Set the crossover and mutation probabilities $\pi_c \in (0, 1)$ and $\pi_m \in (0, 1)$, respectively. Set the generation counter $t := 0$. Initialize GM as an $n \times m$ zero matrix, and generate an initial population P_0 of size μ.*
2. ***Parent Selection.*** *Evaluate the fitness function F of all individuals in P_t. Select an intermediate population P'_t from the current population P_t.*
3. ***Crossover.*** *Associate a random number from $(0, 1)$ with each individual in P'_t and add this individual to the parent pool SP_t if the associated number is less than π_c. Repeat Steps 3.1 and 3.2 until all chosen parents from SP_t are mated.*
   3.1. *Choose two parents p_1 and p_2 from SP_t. Mate p_1 and p_2 using Procedure 3.2.1 to reproduce children c_1 and c_2.*
   3.2. *Update the children pool SC_t by $\mathrm{SC}_t := \mathrm{SC}_t \cup \{c_1, c_2\}$, update SP_t by $\mathrm{SP}_t := \mathrm{SP}_t \setminus \{p_1, p_2\}$, and update GM.*
4. ***Mutation.*** *Associate a random number from $(0, 1)$ with each gene for each individual in P'_t. Mutate the individuals which have an associated number less than π_m by applying Procedure 3.2.2. Add the mutated individual to the children pool SC_t, and update GM.*
5. ***Local Search.*** *Apply a local search method to improve the best child (if exists), and then update GM.*
6. ***Stopping Condition.*** *If η generations have passed after getting a full GM, then go to Step 9. Otherwise, go to Step 7.*
7. ***Survivor Selection.*** *Evaluate the fitness function of all generated children SC_t, and choose the μ best individuals in $P_t \cup \mathrm{SC}_t$ for the next generation P_{t+1}.*
8. ***Mutagenesis.*** *Apply Procedures 2.4.1 and 2.4.2 to alter the μ_w worst individuals in P_{t+1}, set $t := t + 1$, update GM, and go to Step 2.*
9. ***Intensification.*** *Apply a local search method starting from each solution from the μ_{elite} elite ones obtained in the previous search stage.*

There are three main versions of Algorithm 3.2.3. These versions are composed by considering only one intensification scheme; mutagenesis or Local Search (Step 5 or Step 8). $\mathrm{G3AT}_L$ version is composed by invoking Local Search and discarding Step 8, while $\mathrm{G3AT}_M^S$ and $\mathrm{G3AT}_M^A$ discard Step 5 and invoke mutagenesis using Simple and Advanced GM (see Section 2.4), respectively. Actually, the main difference between the local search version $\mathrm{G3AT}_L$ and mutagenesis versions $\mathrm{G3AT}_M^S$ and $\mathrm{G3AT}_M^A$ is that the latter replaces the exact local search method with the defined heuristic local search mutagenesis. The difference between an exact local search method with a heuristic local search is that the former has a convergence guarantee under tractable time while the latter does not (Noman and Iba, 2005). Therefore, $\mathrm{G3AT}_L$, $\mathrm{G3AT}_M^S$ and $\mathrm{G3AT}_M^A$ can be considered as memetic algorithms or hybrid global-local search algorithms. The difference in these proposed algorithms is the use

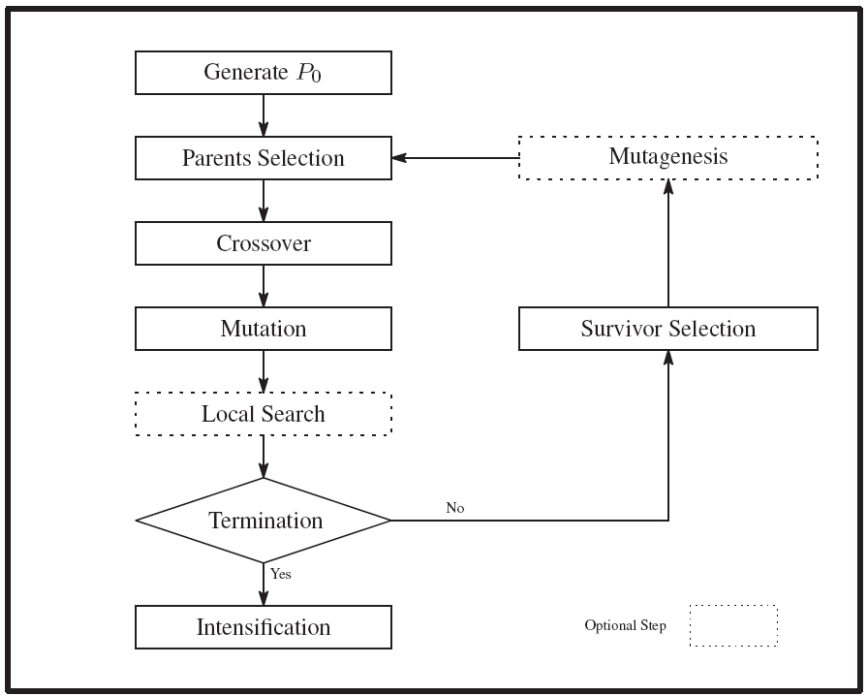


Figure 3.3: G3AT flowchart.

of a heuristic local search known here as mutagenesis as opposed to an exact local search. The general flowchart of Algorithm 3.2.3 is represented in Figure 3.3.

3.3 Numerical Experiments

Algorithm 3.2.3 was programmed in MATLAB and applied to 25 well-known test functions (Yao et al., 1999; Leung and Wang, 2001), listed in Appendix A. These test functions can be classified into two classes; functions involving a small number of variables (f_{14}–f_{23}), and functions involving arbitrarily many variables (f_1–f_{13}, f_{24}, f_{25}). In addition, another class of hard test functions has been considered, referred to as h_1–h_{17}, taken from the CEC 2005 (Liang and Suganthan, 2005). These hard functions are modified versions of some classical test functions by shifting and/or rotating the decision variables and also by adding noise, as reported in Appendix B, see (Liang and Suganthan, 2005) for more details. For each function, the G3AT MATLAB codes were run 50 times with different initial populations. The main results are reported in Table 3.5 as well as in Figures 3.6, 3.7, 3.8 and 3.9. Before discussing these results, we summarize the setting of the G3AT parameters and performance.

Table 3.1: G3AT Parameter Setting

Parameter	Definition	Value
μ	Population size	$\min\{50, 10n\}$
π_c	Crossover probability	0.6
π_m	Mutation probability	0.1
m	No. of GM columns	$50n$
μ_1	No. of individuals used by GM-*Mutagenesis*	2
μ_2	No. of individuals used by BCI-*Mutagenesis*	2
μ_{elite}	No. of starting points for intensification	1
α	Advanced GM percentage for G3AT_M^A	$3/m$
NM_{maxIt}	No. of maximum iterations used by Local Search in G3AT_L	$5n$

3.3.1 Parameter Setting

First, the search domain for Problem (1.1.1) is defined as

$$[L, U] = \{x \in R^n : l_i \leq x_i \leq u_i,\ i = 1, \ldots, n\}\,.$$

This search domain is essential for constructing the GM and it can be easily determined for many application problems. However, the construction of the GM can be modified if the actual search domain is not specified. The user can start with a sufficiently large initial search domain and then new partitions of the GM can be added whenever new regions are reached outside the initial search domain.

In Table 3.1, we summarize all G3AT parameters with their assigned values. These values are based on the common setting in the literature or determined through our preliminary numerical experiments.

We used the scatter search diversification generation method (Laguna and Marti, 2003; Hedar and Fukushima, 2006a) to generate the initial population P_0 of G3AT. In that method, the interval $[l_i, u_i]$ of each variable is divided into four sub-intervals of equal size. New points are generated and added to P_0 as follows.

1. Choose one sub-interval for each variable randomly with a probability inversely proportional to the number of solutions previously chosen in this sub-interval.

2. Choose a random value for each variable that lies in the corresponding selected sub-interval.

We tested three mechanisms for local search in the intensification process based on two methods; the Kelley's modification (Kelley, 1999) of the Nelder-Mead (NM) method (Nelder and Mead, 1965), and a MATLAB function named "`fminunc.m`". These mechanisms are

1. *method*$_1$: to apply $10n$ iterations of Kelley-NM method,

Table 3.2: Results of Local Search Strategies

		Initial	Local Search Strategy		
f	n	$\bar{f}$	$\bar{f}_{method_1}$	$\bar{f}_{method_2}$	$\bar{f}_{method_3}$
f_{18}	2	46118	371.3246	23.8734	13.0660
f_{19}	3	–0.9322	–2.6361	–2.8486	–3.6695
f_{15}	4	8.8e+5	1998.5	0.0120	0.0309
f_2	30	2.2e+20	1.2+e19	1.1e+13	340.6061
f_9	30	551.7739	256.0628	91.5412	193.4720

2. *method*$_2$: to apply $10n$ iterations of MATLAB `fminunc.m` function, and

3. *method*$_3$: to apply $5n$ iterations of Kelley-NM method, then apply $5n$ iterations of MATLAB `fminunc.m` function.

Five test functions shown in Table 3.2 were chosen to test these three mechanisms. One hundred random initial points were generated in the search space of each test function. Then the three local search mechanisms were applied to improve the generated points. The average results are reported in Table 3.2. The last mechanism *method*$_3$ could improve the initial values significantly and is better than the other two mechanisms. Therefore, G3AT employs *method*$_3$ for the local search in Step 4 of Algorithm 3.2.3. Moreover, *method*$_3$ was used with a bigger number of iterations as the final intensification method in Step 9 of Algorithm 3.2.3.

For the parameter m, several preliminary numerical experiments have been done to set its value and check its sensitivity. In these preliminary numerical experiments, different values of m were tested and some of them are shown in Figure 3.4. Three terminations were applied for each test problem; at $m = 10n$, $m = 30n$ and $m = 50n$. Figure 3.4 shows that premature termination has clearly occurred with $m = 10n$. We can observe that this parameter is not sensitive for small changes but setting it equal to too small a value may lead to premature termination. The best problem-free value found was $m = 50n$. Actually, no further significant exploration of the search domains of the tested functions can be expected for $m > 50n$.

It is worthwhile to mention that the extra cost for maintaining GM and applying mutagenesis, which is not required in the standard GA, is still within a polynomial time of the population size (μ), the variable dimension (n) and the maximum number of generations ($G_{\max}$). Actually, mutagenesis is $O(G_{\max})$ and GM updating is $O(\mu n G_{\max})$ for a whole run of G3AT$_M^S$.

3.3.2 G3AT Performance

Extensive numerical experiments were carried out to examine the efficiency of G3AT and to give an idea on how it works. First, several preliminary experiments were done to analyse

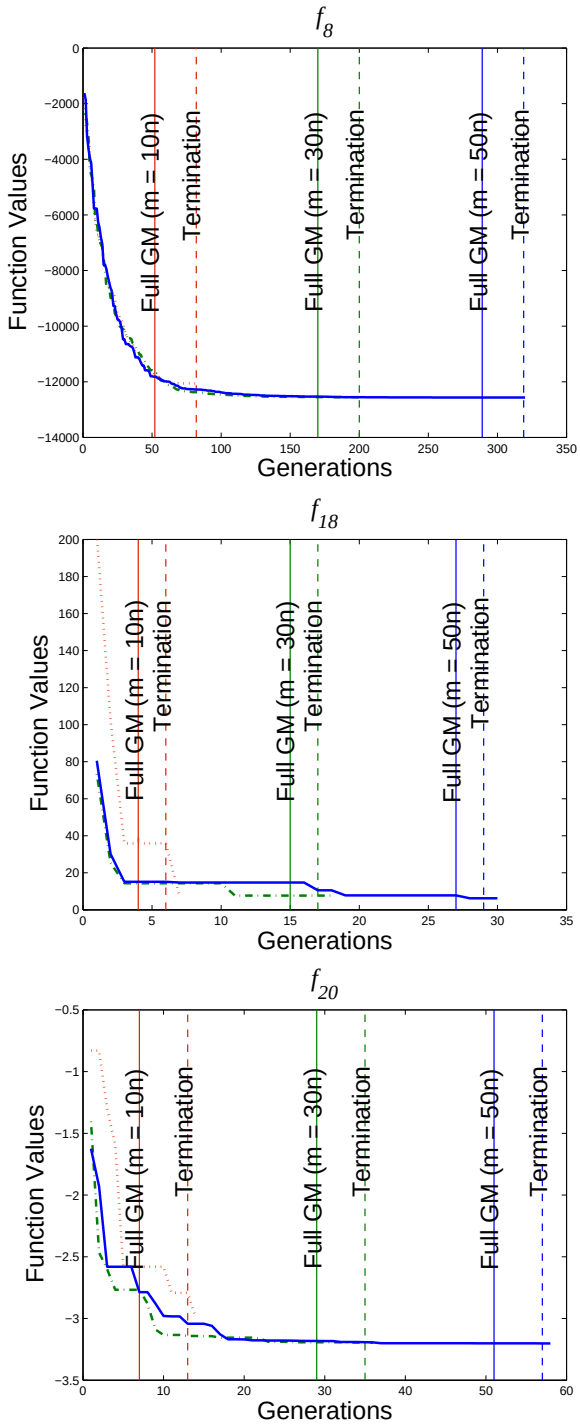


Figure 3.4: Tuning of the number of GM columns m.

G3AT operations and some of them are summarized in Figure 3.5 and Table 3.3. Each graph of Figure 3.5 shows the results of the following three algorithms:

- G3AT^S_M, which is G3AT with mutagenesis and Simple GM.
- G3AT^S_M without mutagenesis, i.e., GA with the crossover and mutation operations stated in Procedures 3.2.1 and 3.2.2.
- GA, with the crossover operation stated in Procedure 3.2.1 and uniform random mutation.

Figure 3.5 reveals that the proposed mutation and mutagenesis operations can improve the performance of GA. Moreover, Table 3.3 shows that the number of function evaluations needed by G3AT^S_M without mutagenesis to reach the same accuracy obtained by G3AT^S_M is higher than those needed by G3AT^S_M. Therefore, mutagenesis operation helps reducing the solution costs. However, these reduction percentages vary for one test problem to another as stated in the last column of Table 3.3.

More preliminary experimental results are depicted in Figures 3.6, 3.7 and 3.8 to show the role of the exploration and automatic termination by using GM within G3AT^S_M. In these figures, the solid vertical line "Full GM" refers to the generation number at which a full GM is obtained, while the dotted vertical line "Termination" refers to the generation number at which the exploration process terminates. The G3AT^S_M code still kept running after reaching the dotted line without applying the final intensification in order to check the efficiency of the automatic termination. As we can see, no more significant improvement in terms of function values can be expected after the dotted line for all test functions. Thus, we can conclude that our automatic termination played a significant role. Even in runs that failed for some difficult test problems, the genetic operators in G3AT^S_M could not achieve any significant progress after the automatic termination line as shown in Figure 3.8. Moreover, these figures show the robustness of the proposed method, in the sense that it obtains nearly optimal solutions even without the final intensification. On the other hand, the final intensification phase in Step 9 of Algorithm 3.2.3 can accelerate the convergence in the final stage instead of letting the algorithm run for several generations without much significant improvement of the objective value as shown in Figure 3.9. This figure represents the general performance of G3AT (using G3AT^S_M as an example) on functions f_{12}, f_{15} and f_{23} by plotting the values of the objective function versus the number of function evaluations. We can observe in this figure that the objective value decreases as the number of function evaluations increases. This figure also highlights the efficiency of using a final intensification phase in Step 9 of Algorithm 3.2.3 in order to accelerate the convergence in the final stage. The behavior in the final intensification phase is represented by dotted lines in Figure 3.9, in which a rapid decrease of the function value during the last stage is clearly observed.

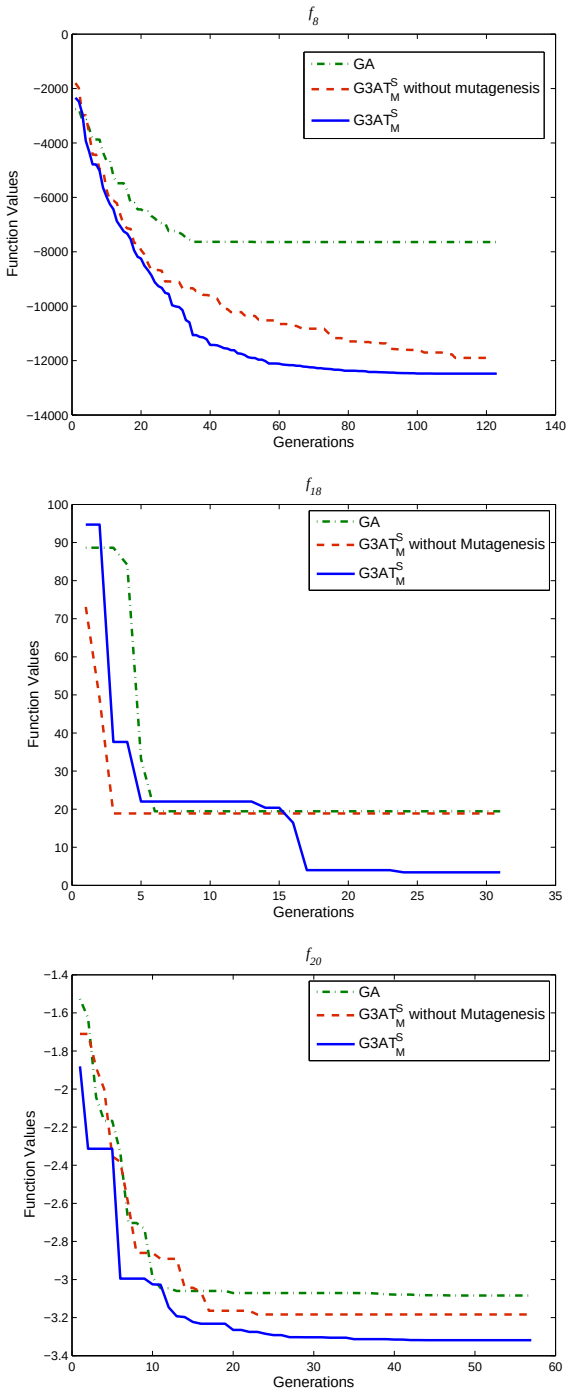


Figure 3.5: Performance of G3AT$_M^S$ operations.

Table 3.3: Efficiency of Mutagenesis Operation

f	Function Evaluations		%
	G3AT^S_M	G3AT^S_M without Mutagenesis	
f_8	13,021	14,992	13.15%
f_{20}	2,504	5,889	57.48%
f_{18}	612	13,494	95.46%

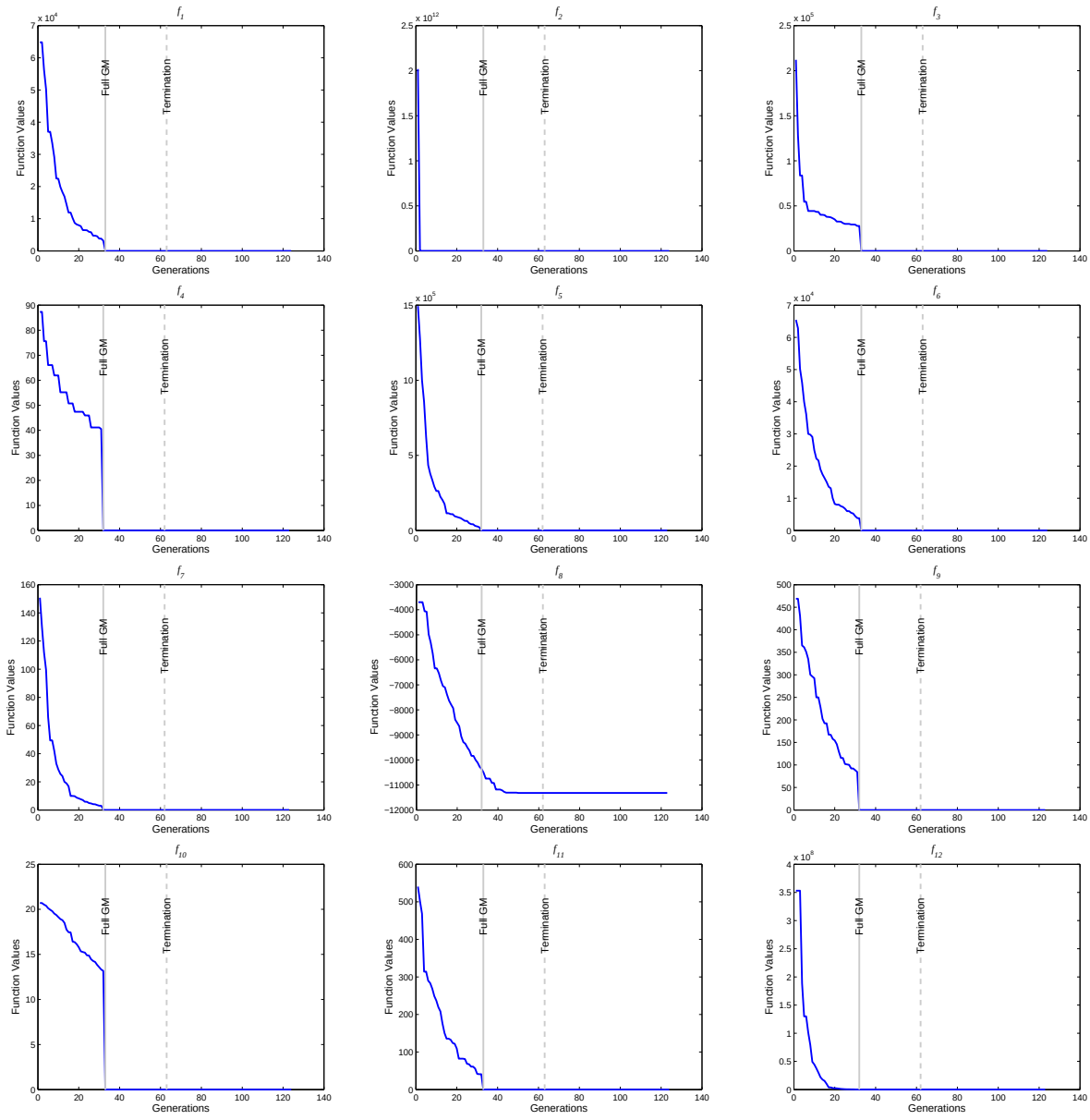


Figure 3.6: Automatic termination performance of G3AT^S_M without the final intensification (f_1–f_{12}).

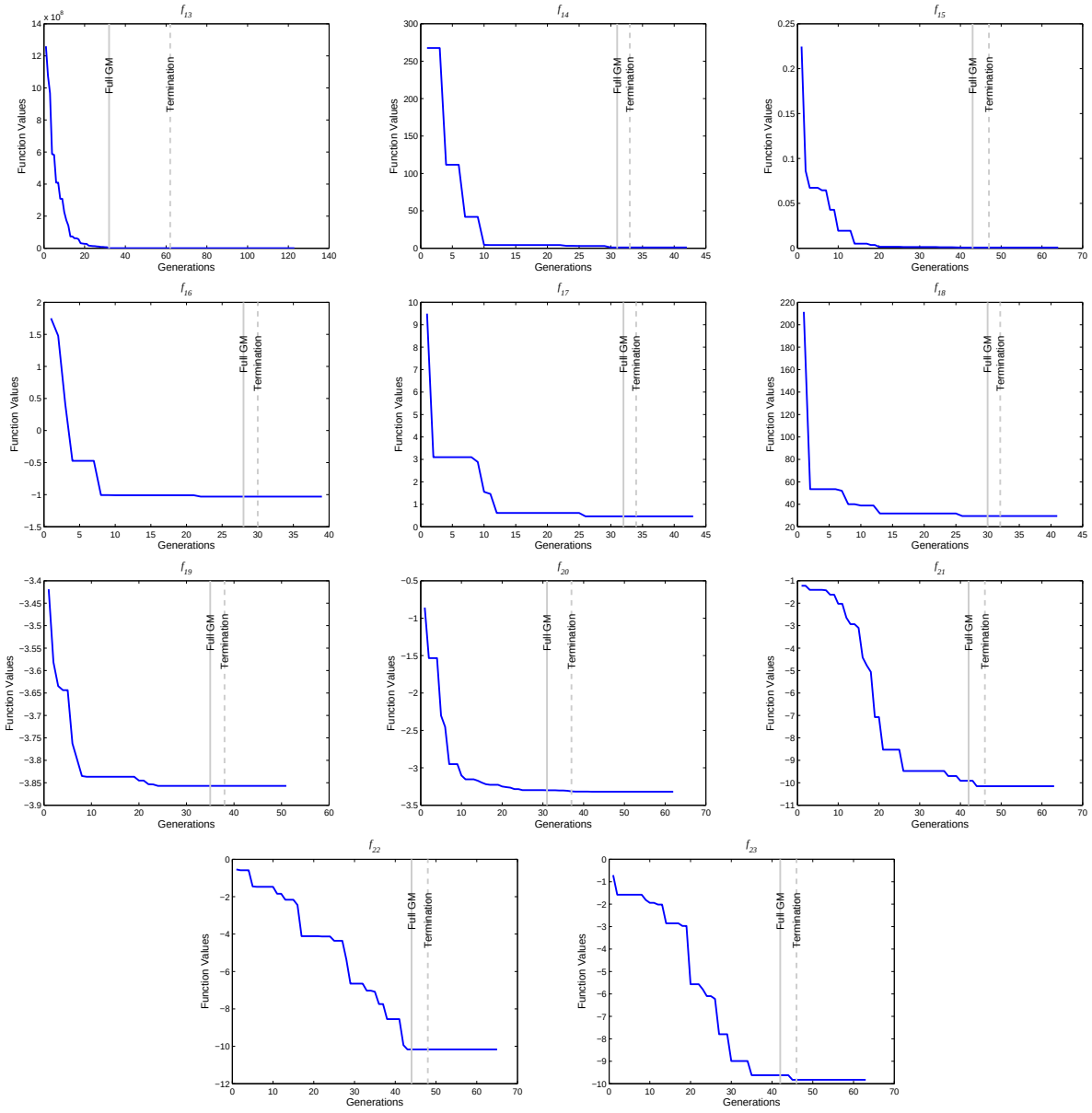


Figure 3.7: Automatic termination performance of G3AT^S_M without the final intensification (f_{13}–f_{23}).

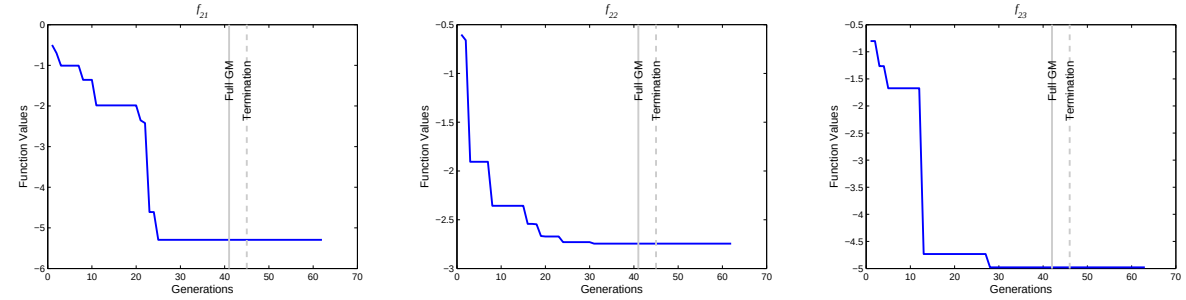


Figure 3.8: Performance of the automatic termination in failure runs.

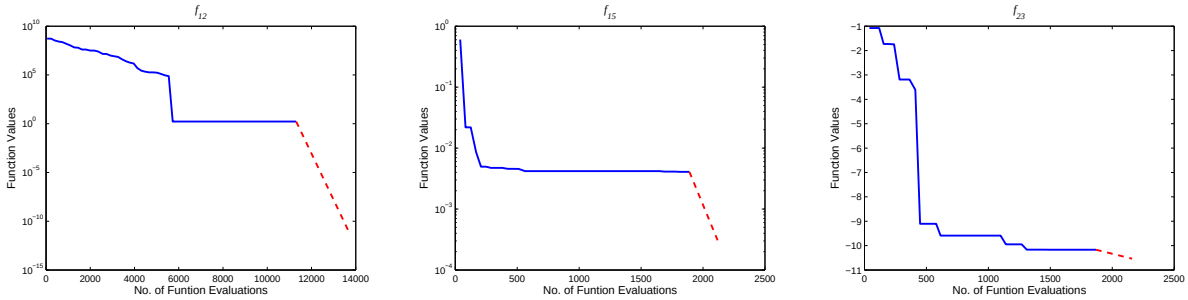


Figure 3.9: Performance of the final intensification.

Table 3.4: Three Versions of G3AT

Version	Description
G3AT_L	G3AT with Local Search
G3AT_M^S	G3AT with Mutagenesis and Simple GM
G3AT_M^A	G3AT with Mutagenesis and Advanced GM

Three versions of the G3AT (G3AT_L, G3AT_M^S and G3AT_M^A, see Table 3.4) were compared with each other. The comparison results are reported in Table 3.5. It contains the mean and the standard deviation (SD) of the best solutions obtained for each function as the measure of solution qualities and the average number of function evaluations as the measure of solution costs. These results were obtained from 50 runs. Figure 3.10 summarizes the results presented in Table 3.5.

In order to check the significance of the difference between the results of the compared methods, we use the Wilcoxon Rank-Sum test. This test is a non-parametric procedure employed in a hypothesis testing situation involving a design with two samples (Sheskin, 2003; García et al., 2009). It is a pairwise test that aims at detecting significant differences between the behavior of two algorithms. In the following, we describe its procedure. Let d_i be the difference between the performance scores of two algorithms on i out of N results. The differences are ranked according to their absolute values; average ranks are assigned in case of ties. Let R^+ be the sum of ranks for the results on which the first algorithm outperformed the second, and R^- the sum of ranks for the opposite. Ranks of $d_i = 0$ are split evenly among the sums and if there is an odd number of them, one is ignored. Therefore, R^+ and R^- can be mathematically defined as

$$R^+ = \sum_{d_i>0} rank(d_i) + \frac{1}{2}\sum_{d_i=0} rank(d_i),$$
$$R^- = \sum_{d_i<0} rank(d_i) + \frac{1}{2}\sum_{d_i=0} rank(d_i),$$

where $rank(d_i)$ is the rank value of the difference value d_i. The rank-sum test is used for pairwise comparisons and the p-value is independent from one comparison to another. Therefore, the new statistical significance for combining pairwise comparisons between the winner method A against other k methods is given by

$$p = 1 - \prod_{i=1}^{k}(1 - p_i), \tag{3.3.1}$$

where p_i is the p-value calculated for comparing method A against the method numbered i for $i = 1, \ldots, k$ (García et al., 2009). For all comparisons done in the rest of this chapter, the reported results of the rank-sum test show significant differences between the compared methods at significance level 0.05.

Based on the statistical test figures shown in Table 3.6 for the results in Table 3.5, we can conclude that solutions obtained by G3AT$_L$ and G3AT$_M^S$ are roughly similar. Nevertheless, the numbers of function evaluations required by G3AT$_L$ were much larger than those required by G3AT$_M^S$. We estimate that this relatively high cost in terms of function evaluations required by G3AT$_L$ does not justify the slight advantage in terms of function values. Therefore, we decided to use G3AT$_M^S$ instead of G3AT$_L$ for our further comparisons. At this stage, we may conclude that the mutagenesis operation is as efficient as the local search but the latter is more expensive. In other words, applying local search methods frequently during the exploration process is costly, and invoking a cheaper method such as the proposed mutagenesis yields similar results. However, applying a complete local search method as final refinement intensification is essential in order to achieve higher accuracy as illustrated in Figure 3.9.

In order to explore the sub-ranges of each gene's search space more than once, the parameter α of GM_α^A allows G3AT$_M^A$ to revisit sub-ranges until the ratio α is achieved. For our experiments, a sub-range is considered to be visited if it is visited at least three times, i.e., $\alpha = 0.3$. The results shown in Table 3.5 and discussed below indicate that increasing the value of α will produce an augmentation of the number of function evaluations without much significant improvement of solution qualities. We compared these two versions of GM and the numerical results are also reported in Table 3.5. Based on the statistical test results available in Table 3.6, there is no significant difference between G3AT$_M^A$ and G3AT$_M^S$ in terms of solution qualities. However, the number of function evaluations required by G3AT$_M^A$ is relatively large compared to the number needed by G3AT$_M^S$ for all functions. Furthermore, the results in Table 3.6 show that G3AT$_M^S$ is significantly superior to G3AT$_L$ and G3AT$_M^A$ in terms of solution costs with a p-value of

$$p = 1 - [(1 - 0.0052) \cdot (1 - 0.0121)] = 0.0172.$$

Consequently, we judge that the best version of G3AT among G3AT$_L$, G3AT$_M^S$ and G3AT$_M^A$ is G3AT$_M^S$.

Table 3.5: Solution Qualities and Costs for G3AT$_L$, G3AT^S_M and G3AT^A_M

		Solution Qualities						Solution Costs		
		G3AT$_L$		G3AT^S_M		G3AT^A_M		G3AT$_L$	G3AT^S_M	G3AT^A_M
f	n	Mean	SD	Mean	SD	Mean	SD	Mean	Mean	Mean
f_1	30	0	0	0	0	0	0	3.1e+4	1.4e+4	2.6e+4
f_2	30	0	0	0	0	0	0	2.9e+4	1.1e+4	2.3e+4
f_3	30	0	0	0	0	0	0	2.7e+4	1.4e+4	2.6e+4
f_4	30	0	0	0	0	0	0	2.8e+4	1.2e+4	2.4e+4
f_5	30	6.3e–11	2.9e–12	6.4e–11	3.1e–12	6.5e–11	2.8e–12	3.2e+4	1.4e+4	2.9e+4
f_6	30	0	0	0	0	0	0	2.8e+4	1.1e+4	2.3e+4
f_7	30	2.0e–4	2.1e–4	2.0e–4	1.6e–4	2.1e–4	1.9e–4	3.0e+4	1.2e+4	2.4e+4
f_8	30	–1.0e+4	7.8e+2	–1.2e+4	194.04	–1.2e+4	1.9e–11	2.9e+4	1.3e+4	2.5e+4
f_9	30	0	0	0	0	0	0	3.0e+4	1.2e+4	2.4e+4
f_{10}	30	8.8e–16	0	8.8e–16	0	8.8e–16	0	2.9e+4	1.2e+4	2.4e+4
f_{11}	30	0	0	0	0	0	0	2.9e+4	1.3e+4	2.5e+4
f_{12}	30	3.9e–12	2.9e–12	1.1e–11	7.7e–12	2.2e–2	5.2e–2	3.0e+4	1.3e+4	2.6e+4
f_{13}	30	1.36	1.48	1.90	1.37	3.2e–1	8.9e–1	3.2e+4	2.1e+4	5.3e+4
f_{14}	2	1.37	1.28	2	2.26	1.03	1.9e–1	1.6e+3	5.5e+2	1.4e+3
f_{15}	4	3.9e–4	2.6e–4	3.3e–4	1.3e–4	3.8e–4	2.4e–4	3.9e+4	2.1e+3	5.2e+3
f_{16}	2	–1.03	8.5e–15	–1.03	3.8e–14	–1.03	9.0e–15	1.7e+3	5.9e+2	1.4e+3
f_{17}	2	0.39	1.5e–13	0.397887	8.8e–14	0.397887	3.6e–14	1.6e+3	5.9e+2	1.3e+3
f_{18}	2	3	7.4e–14	3	2.6e–13	3	7.4e–14	1.7e+3	6.1e+2	1.4e+3
f_{19}	3	–3.86	5.5e–13	–3.86	2.2e–14	–3.86	3.1e–14	2.6e+3	1.1e+3	2.8e+3
f_{20}	6	–3.27	5.7e–2	–3.28	5.5e–2	–3.27	5.7e–2	4.3e+3	2.5e+3	6.3e+3
f_{21}	4	–7.14	3.27	–6.90	3.71	–5.70	3.46	3.8e+3	2.1e+3	5.3e+3
f_{22}	4	–7.64	3.20	–7.86	3.58	–8.23	3.36	3.9e+3	2.1e+3	5.3e+3
f_{23}	4	–7.98	3.49	–8.36	3.38	–7.97	3.48	3.8e+3	2.1e+3	5.3e+3

Table 3.6: Rank-sum Test for G3AT_L and G3AT_M^S Results

Compared Methods		Solution Qualities				Solution Costs			
Method 1	Method 2	R^+	R^-	p-value	Best Method	R^+	R^-	p-value	Best Method
G3AT_L	G3AT_M^S	144	132	0.9822	–	0	276	0.0052	G3AT_M^S
G3AT_L	G3AT_M^A	140	136	1	–	57.5	218.5	0.0861	–
G3AT_M^S	G3AT_M^A	167.5	108.5	0.9556	–	276	0	0.0121	G3AT_M^S

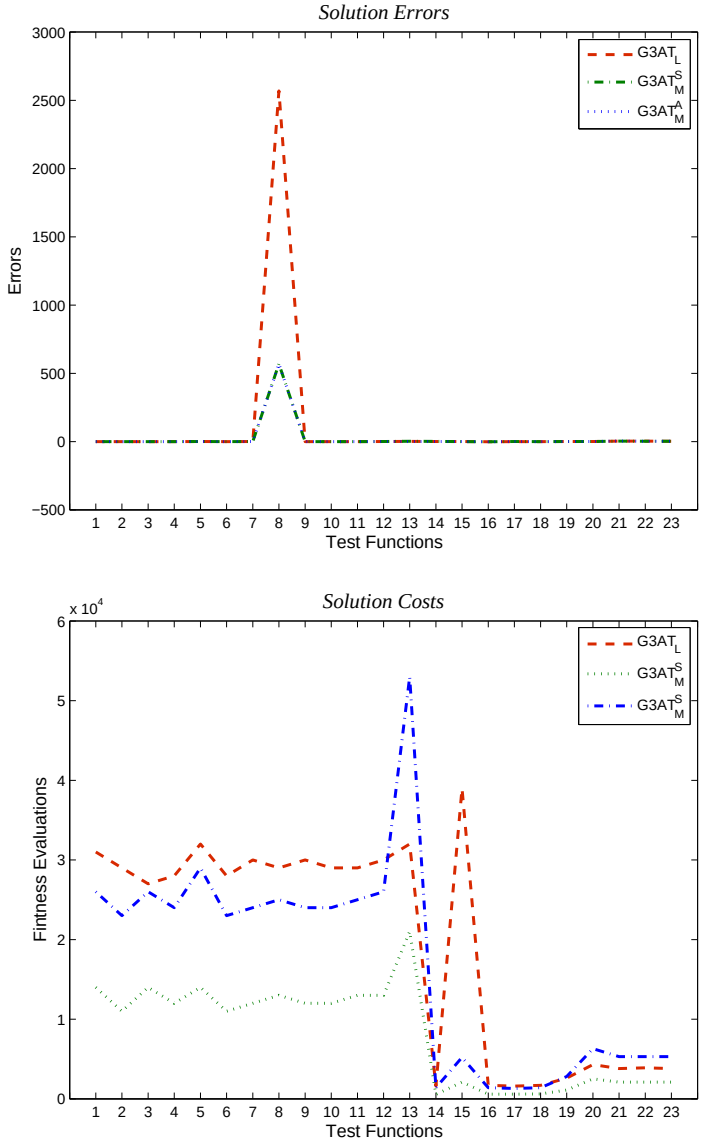


Figure 3.10: Results of Table 3.5.

Table 3.7: GM within a Simple GA

Function	f_8	f_{18}	f_{20}
GM Zeros Percentage	80.50%	82.22%	84.97%

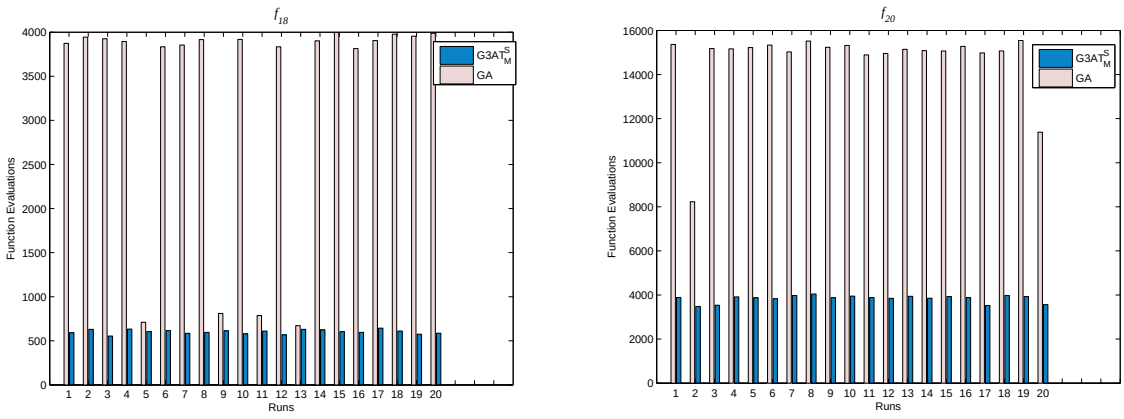


Figure 3.11: Results of 20 independent runs of G3AT^S_M and GA (with GM).

In order to analyze the impact that the introduction of GM has on a simple GA, GM has been implemented within a canonical GA, without any additional operator (such as mutagenesis). GM is initialized as in G3AT^S_M and is updated after generating the offspring in each generation. Three test functions are used in this experiment as shown in Table 3.7. For each test function, GA is terminated at the same generation number as in G3AT^S_M. At the end of each run, the percentage of zero entries to all entries of GM are reported in Table 3.7. Even if the maximum number of generations used for terminating GA is doubled, these percentages will not be significantly improved. This indicates that there are many partitions of the search space that are not well explored with a simple GA and this may explain the low success rates of GA, as shown later in Table 3.22. Moreover, this highlights the significant role of the proposed mutation and mutagenesis operations that enforce G3AT^S_M to explore the search space widely. In addition, results of 20 independent runs of G3AT^S_M and GA are shown in Figure 3.11. For test functions f_{18} and f_{20}, Figure 3.11 shows that G3AT^S_M tends to save function evaluation costs. For test function f_8, GA could not achieve the objective function value obtained by G3AT^S_M within a computational budget of 100,000 function evaluations although it is almost 8 times the budget needed by G3AT^S_M.

3.4 Numerical Comparisons

The best version G3AT^S_M was compared with two other advanced GAs; the Orthogonal GA (OGA/Q) (Leung and Wang, 2001), and the Hybrid Taguchi-Genetic Algorithm (HTGA) (Tsai et al., 2004), as well as four other EAs; the Covariance Matrix Adaptation Evolution

Strategy (CMA-ES) (Hansen and Kern, 2004; Hansen, 2006) and its global restart version G-CMA-ES (Hansen et al., 2005a,b), the Real-Coded Memetic Algorithms (RCMA) (Lozano et al., 2005), and the Restart q-Gaussian mutation Evolution Strategy (RqGES) (Tinós and Yang, 2011). More details about these methods are stated below.

- *Orthogonal GA with Quantization (OGA/Q)* (Leung and Wang, 2001). It is a modified version of a classical GA (CGA). OGA/Q is identical to CGA, except that it uses the orthogonal design to generate the initial population and the offspring of the crossover operator.

- *Hybrid Taguchi-Genetic Algorithm (HTGA)* (Tsai et al., 2004). HTGA combines the traditional GA with the Taguchi method (Taguchi et al., 2000), which can exploit promising offspring. Taguchi method is incorporated in the crossover operations to select better genes to achieve crossover and enhance the genetic algorithm.

- *Covariance Matrix Adaptation Evolution Strategy (CMA-ES)* (Hansen and Kern, 2004; Hansen, 2006). CMA-ES is an evolution strategy method that invokes an adaptation process of the covariance matrix. The main advantage of using the covariance matrix is to detect a second order model of the underlying objective function similar to the approximation of the inverse Hessian matrix in the Quasi-Newton method in classical optimization.

- *Global restart Covariance Matrix Adaptation Evolution Strategy (G-CMA-ES)* (Hansen et al., 2005a,b). G-CMA-ES is a modified version of CMA-ES in which premature convergence can be detected and then a restart strategy is launched by doubling the population size on each restart. By increasing the population size, the search characteristic becomes more global after each restart, which empowers the operation of the CMA-ES on multi-modal functions. G-CMA-ES is the winner of the CEC 2005 optimization competition.

- *Real-Coded Memetic Algorithms (RCMA)* (Lozano et al., 2005). RCMA uses the individual fitness to decide when local search is applied and how much effort should be made. The individuals of the population are divided into three different categories based on their fitness values. Local search parameters are set according to the category to which an individual belongs.

- *Restart q-Gaussian mutation Evolution Strategy (RqGES)* (Tinós and Yang, 2011). RqGES uses a Gaussian mutation with self-adaptation of the shape of the mutation distribution in evolutionary algorithms. The shape of the Gaussian mutation distribution is controlled by a real parameter q which is encoded in the chromosomes in order to evolve during the evolutionary process.

Table 3.8: Solution Qualities for G3AT^S_M, HTGA and OGA/Q

		Solution Qualities					
		G3AT^S_M		HTGA		OGA/Q	
f	n	Mean	SD	Mean	SD	Mean	SD
f_1	30	0	0	0	0	0	0
f_2	30	0	0	0	0	0	0
f_3	30	0	0	0	0	0	0
f_4	30	0	0	0	0	0	0
f_5	100	2.2e–010	0	0.7	0	0.752	0.114
f_7	30	2.0e–4	1.6e–4	1.0e–3	0	6.3e–3	4.1e–4
f_8	30	–12155.34	194.04	–12569.46	0	–12569.45	6.4e–4
f_9	30	0	0	0	0	0	0
f_{10}	30	8.8e–16	0	0	0	4.4e–16	4.0e–17
f_{11}	30	0	0	0	0	0	0
f_{12}	30	1.1e–11	7.7e–12	1.0e–6	0	6.0e–6	1.2e–6
f_{13}	30	1.90	1.37	1.0e–4	0	1.9e–4	2.6e–5
f_{24}	100	–93.31	1.14	–92.83	0	–92.83	2.6e–2
f_{25}	100	–72.68	1.46	–78.3	0	–78.3	6.3e–3

The results of these compared methods are taken from their original papers. These results were obtained from 50 runs. It is worthwhile to mention that the reported results for G3AT^S_M are based on achieving a full GM termination.

3.4.1 G3AT^S_M against Other GAs Using Classical Test Functions

The comparison results for G3AT^S_M, HTGA and OGA/Q are reported in Tables 3.8 and 3.9 along with Figure 3.12. They contain the mean and the standard deviation (SD) of the best solutions obtained for each function and the average number of function evaluations. All the compared methods (G3AT^S_M, HTGA and OGA/Q) are neutral on 7 out of 14 problems in terms of solution qualities. Moreover, we observe that G3AT^S_M outperforms the other two methods on 4 problems, while HTGA and OGA/Q outperform G3AT^S_M on 3 problems in terms of solution qualities. On the other hand, G3AT^S_M consistently outperforms the other two methods in terms of solution costs. Actually, G3AT^S_M is cheaper than HTGA and much cheaper than OGA/Q. The results of the rank-sum test shown in Table 3.10 confirm these conclusions. Specifically, there is no significant difference between each pair of G3AT^S_M, HTGA and OGA/Q in terms of solution qualities. However, G3AT^S_M is significantly cheaper than the other two methods in terms of solution costs with a p-value of

$$p = 1 - [(1 - 0.0307) \cdot (1 - 7.0 \times 10^{-6})] = 0.0307067851.$$

Table 3.9: Solution Costs for G3AT^S_M, HTGA and OGA/Q

		Solution Costs		
f	n	G3AT^S_M	HTGA	OGA/Q
f_1	30	1.41e+4	1.43e+4	1.13e+5
f_2	30	1.17e+4	1.28e+4	1.13e+5
f_3	30	1.40e+4	1.54e+4	1.13e+5
f_4	30	1.23e+4	1.46e+4	1.13e+5
f_5	100	3.88e+4	3.93e+4	1.68e+5
f_7	30	1.22e+4	1.28e+4	1.13e+5
f_8	30	1.35e+4	1.11e+5	3.02e+5
f_9	30	1.20e+4	1.51e+4	2.25e+5
f_{10}	30	1.20e+4	1.41e+4	1.12e+5
f_{11}	30	1.36e+4	1.61e+4	1.34e+5
f_{12}	30	1.38e+4	3.43e+4	1.35e+5
f_{13}	30	2.05e+4	2.06e+4	1.34e+5
f_{24}	100	4.49e+4	2.19e+5	3.03e+5
f_{25}	100	5.07e+4	2.05e+5	2.46e+5

Table 3.10: Rank-sum Test for G3AT^S_M, HTGA and OGA/Q Results

Compared Methods		Solution Qualities				Solution Costs			
Method 1	Method 2	R^+	R^-	p-value	Best Method	R^+	R^-	p-value	Best Method
G3AT^S_M	HTGA	56.5	48.5	0.9421	–	105	0	0.0307	G3AT^S_M
G3AT^S_M	OGA/Q	56.5	48.5	0.9809	–	105	0	7.0×10^{-6}	G3AT^S_M
HTGA	OGA/Q	18	87	0.7899	–	105	0	3.5×10^{-6}	HTGA

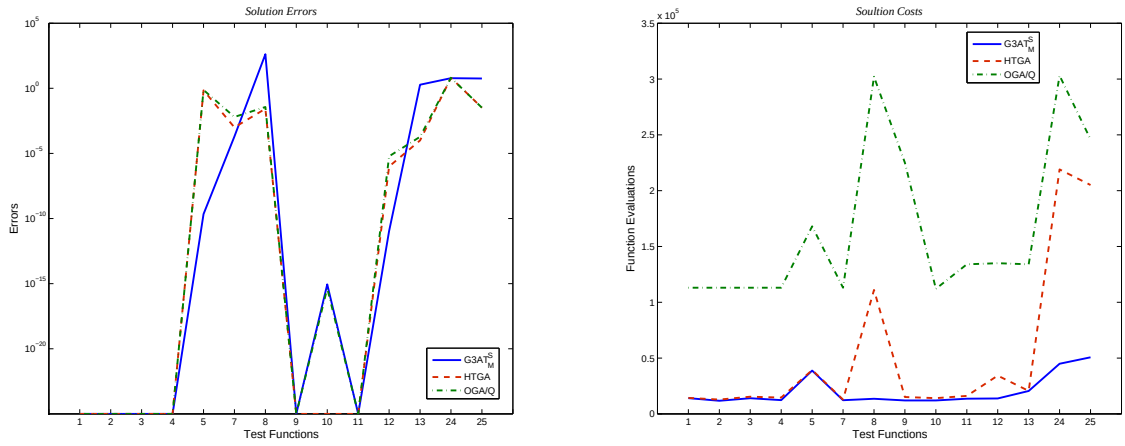


Figure 3.12: Results of Tables 3.8 and 3.9.

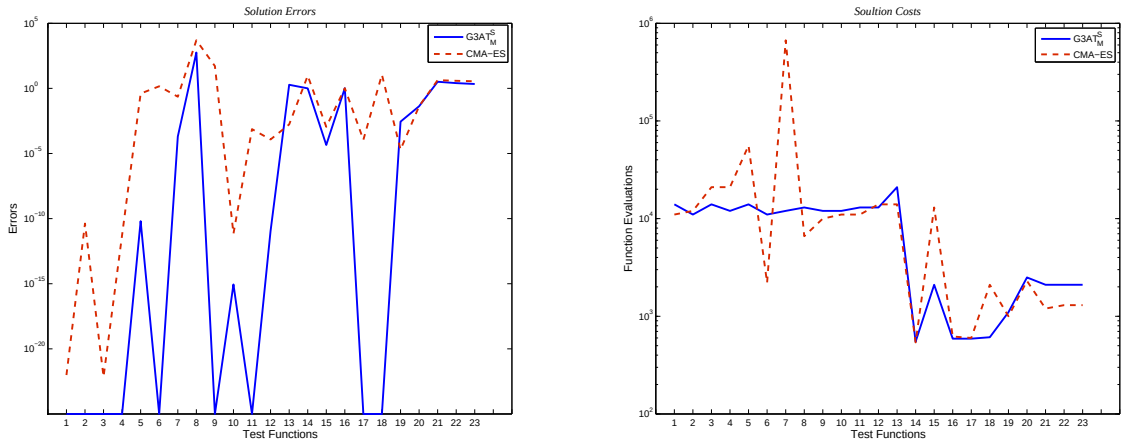


Figure 3.13: Results of Table 3.11.

3.4.2 G3AT^S_M against CMA-ES and Its Variants

One of the most promising and efficient modifications of evolution strategies (ESs) is CMA-ES (Hansen and Kern, 2004; Hansen, 2006). In the following, we discuss the results of G3AT^S_M against CMA-ES and its global restart version G-CMA-ES using the figures shown in Tables 3.11 and 3.13. The results reported in Table 3.11 contain the success rate of a trial judged by means of the condition

$$|f^* - \hat{f}| < \epsilon, \tag{3.4.1}$$

where f^* refers to the known exact global minimum value, $\hat{f}$ refers to the best function value obtained by the algorithm, and ϵ is a small positive number, which is set equal to 10^{-3} in our experiments. Condition (3.4.1) is only used to check the success of the result obtained from each run. The results of Table 3.11 are summarized in Figure 3.13.

The percentages between parentheses in Table 3.11 represent the success rate under condition (3.4.1). To make fair comparisons between G3AT^S_M and CMA-ES, the latter is terminated after reaching the same number of function evaluations needed by G3AT^S_M. Therefore, both of them have the same solution costs. In terms of solution qualities or success rates, CMA-ES did not outperform G3AT^S_M except for function f_{13}. Actually, the rank-sum test results shown in Table 3.12 indicate that there is no significant difference between G3AT^S_M and CMA-ES in terms of solution qualities. However, G3AT^S_M obtained significantly better success rates compared to those obtained by CMA-ES.

The results of CMA-ES can be improved by using its restart version G-CMA-ES (Hansen et al., 2005a,b). Table 3.13 shows the results of G-CMA-ES with two restarts for the functions for which CMA-ES fails at reaching comparable success rates against G3AT^S_M. Table 3.14 presents the rank-sum test figures for the results presented in Table 3.13. From these statistical results, we can observe that there is no significant difference between G3AT^S_M and

Table 3.11: Solution Qualities for G3AT^S_M and CMA-ES

		G3AT^S_M		CMA-ES	
f	n	Mean	SD	Mean	SD
f_1	30	0 (100%)	0	4.43e–21 (100%)	1.17e–21
f_2	30	0 (100%)	0	1.51e–09 (100%)	3.45e–09
f_3	30	0 (100%)	0	6.66e–08 (100%)	1.63e–07
f_4	30	0 (100%)	0	3.79e–06 (100%)	4.46e–06
f_5	30	6.40e–11 (100%)	3.1e–12	1.85e+01 (0%)	1.77e+00
f_6	30	0 (100%)	0	2.80e–01 (80%)	6.14e–01
f_7	30	2.00e–4 (100%)	1.6e–4	2.14e–01 (0%)	6.62e–02
f_8	30	–1.2e+4 (0%)	194.04	–7.61e+03 (0%)	8.56e+01
f_9	30	0 (100%)	0	4.86e+01 (0%)	1.36e+01
f_{10}	30	8.80e–16 (100%)	0	5.04e–11 (100%)	8.44e–12
f_{11}	30	0 (100%)	0	1.08e–03 (88%)	3.11e–03
f_{12}	30	1.10e–11 (100%)	7.7e–12	1.24e–02 (88%)	3.44e–02
f_{13}	30	1.90 (4%)	1.37	4.39e–04 (96%)	2.20e–03
f_{14}	2	2 (74%)	2.26	1.46e+01 (0%)	1.89e–13
f_{15}	4	3.30e–4 (100%)	1.3e–4	4.98e–03 (48%)	1.78e–02
f_{16}	2	–1.03 (100%)	3.8e–14	–1.03e+00 (100%)	3.51e–16
f_{17}	2	0.397887 (100%)	8.8e–14	3.98e–01 (100%)	1.69e–14
f_{18}	2	3 (100%)	2.6e–13	6.24e+00 (88%)	8.95e+00
f_{19}	3	–3.86 (100%)	2.2e–14	–3.86e+00 (100%)	7.08e–16
f_{20}	6	–3.28 (70%)	6.0e–2	–3.27e+00 (60%)	5.96e–02
f_{21}	4	–6.90 (56%)	3.71	–4.65e+00 (16%)	2.69e+00
f_{22}	4	–7.86 (66%)	3.58	–4.80e+00 (20%)	3.01e+00
f_{23}	4	–8.36 (70%)	3.38	–4.67e+00 (28%)	3.74e+00

Table 3.12: Rank-sum Test for G3AT^S_M and CMA-ES Results in Table 3.11

Comparing Criterion	Compared Methods		R^+	R^-	p-value	Best Method
Solution Qualities	G3AT^S_M	CMA-ES	259.5	16.5	0.1131	–
Success Rates	G3AT^S_M	CMA-ES	233.5	42.5	0.0233	G3AT^S_M

Table 3.13: Improved Results of G-CMA-ES with Two Restarts

		G3AT^S_M		G-CMA-ES	
f	n	Avg. f	Costs	Avg. f	Costs
f_5	30	6.40e–11(100%)	1.4e+4	6.35e–15(100%)	2.02e+05
f_6	30	0(100%)	1.1e+4	0.00e+00(100%)	1.45e+04
f_7	30	2.00e–4(100%)	1.2e+4	6.29e–02(0%)	3.12e+04
f_9	30	0(100%)	1.2e+4	1.29e+02(0%)	3.99e+04
f_{11}	30	0(100%)	1.3e+4	1.02e+02(0%)	2.52e+04
f_{12}	30	1.10e–11(100%)	1.3e+4	5.98e–15(100%)	4.26e+04
f_{13}	30	1.90(4%)	2.1e+4	7.32e–15(100%)	4.47e+04
f_{14}	2	2(74%)	5.5e+2	2.05e+01(0%)	2.33e+03
f_{15}	4	3.30e–4(100%)	2.1e+3	3.07e–04(100%)	8.21e+03
f_{18}	2	3(100%)	6.1e+2	3.00e+00(100%)	3.01e+03
f_{20}	6	–3.28(70%)	2.5e+3	–3.28e+00(64%)	7.66e+03
f_{21}	4	–6.90 (56%)	2.1e+3	–6.36e+00(48%)	5.67e+03
f_{22}	4	–7.86(66%)	2.1e+3	–5.77e+00(39%)	5.51e+03
f_{22}	4	–8.36(70%)	2.1e+3	–6.37e+00(48%)	5.61e+03

Table 3.14: Rank-sum Test for G3AT^S_M and G-CMA-ES Results in Table 3.13

Comparing Criterion	Compared Methods		R^+	R^-	p-value	Best Method
Solution Qualities	G3AT^S_M	G-CMA-ES	78	27	0.4340	–
Solution Costs	G3AT^S_M	G-CMA-ES	105	0	0.0323	G3AT^S_M
Success Rates	G3AT^S_M	G-CMA-ES	86.5	18.5	0.1098	–

G-CMA-ES in terms of solution qualities and success rates. However, G-CMA-ES needs more function evaluations to reach such solution qualities and success rates. Actually, G3AT^S_M is cheaper than G-CMA-ES in terms of solution costs. Thus, we may conclude that G3AT^S_M is more reliable than CMA-ES and cheaper than G-CMA-ES.

3.4.3 Comparisons Using the Hard Functions Benchmark CEC 2005

The final comparisons in this section are done using a new class of modified test problems taken from the CEC 2005 (Liang and Suganthan, 2005). Some well-known test functions have been modified by shifting and/or rotating their decision variables and also by adding noise to them (Liang and Suganthan, 2005). These modifications bring higher challenge in testing newly proposed methods on functions with different properties, since they avoid the easiness of some well-known functions such as the separability in the variables, the symmetry of the global optimum or its center position in the search space. These modified test functions represent randomly distributed landscapes and their structures are closer to those found in real-world applications, see Appendix B for their description. These test functions are used for a harder level of testing G3AT^S_M and their results are presented in Tables 3.15, 3.17, 3.18

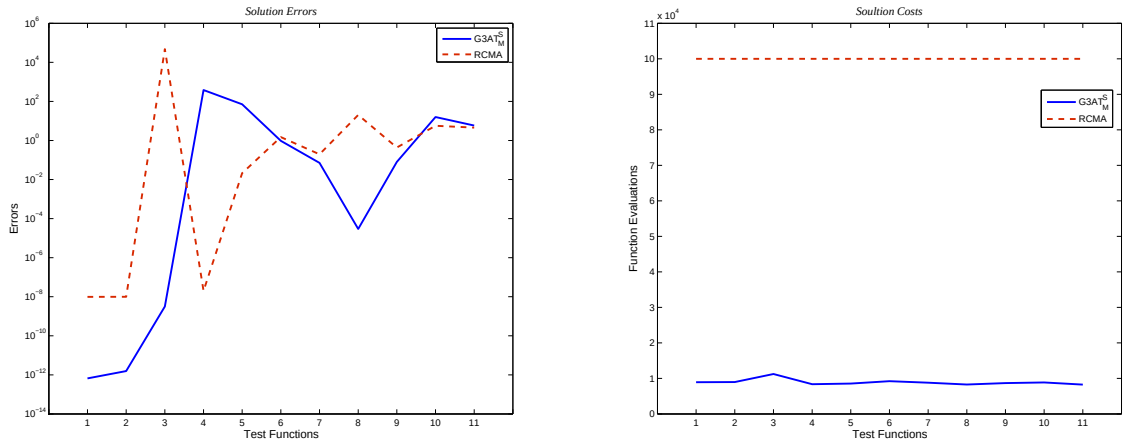


Figure 3.14: Results of Table 3.15 for test functions h_1–h_{11} with $n = 10$.

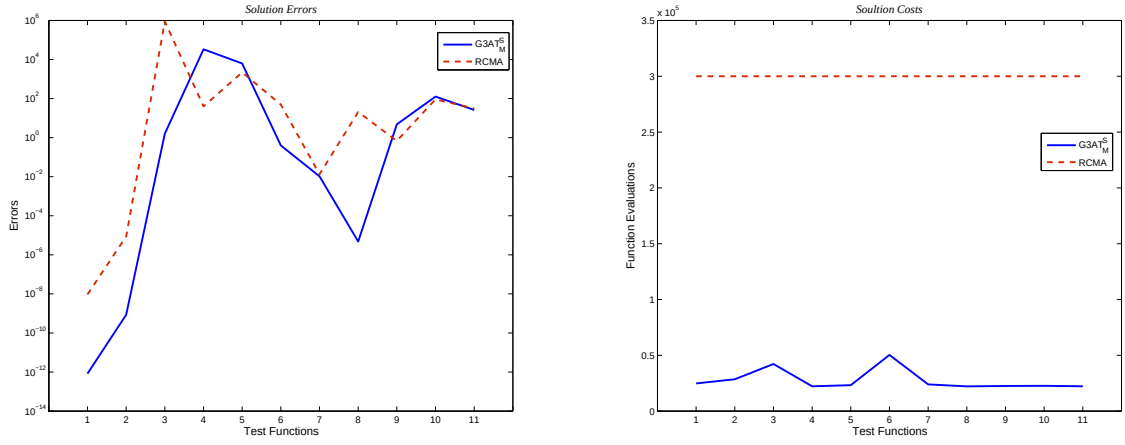


Figure 3.15: Results of Table 3.15 for test functions h_1–h_{11} with $n = 30$.

and 3.19.

The results of Real-Coded Memetic Algorithm (RCMA) (Lozano et al., 2005) are also presented in Table 3.15 to discuss the efficiency of the proposed method. The convergence performance of G3AT^S_M and that of RCMA are almost the same. However, the accelerated automatic termination enables G3AT^S_M to achieve cheaper function evaluations than RCMA. The statistical results of the rank-sum test shown in Table 3.16 confirm these conclusions.

Other comparisons are presented here to test the performance of G3AT^S_M against G-CMA-ES, the winner of CEC 2005 competition, and against the recently proposed RqGES method. The results of these comparisons are reported in Tables 3.17, 3.18 and 3.19. They are summarized in Figures 3.16, 3.17 and 3.18, and statistically analyzed in Tables 3.20 and 3.21. All these results yield the same conclusions as above. Namely, G3AT^S_M could obtain competitive solution qualities with cheaper costs. Actually, G3AT^S_M requires significantly

Table 3.15: Results for Shifted and Shifted-Rotated Functions

Function No.	n	Solution Qualities (Errors)				Solution Costs		
		$G3AT_M^S$		RCMA		Average no. of function evaluations		
		Mean	SD	Mean	SD	$G3AT_M^S$	RCMA	
h_1	10	6.594e–13	2.990e–13	9.869e–9	6.617e–25	8926	100,000	
h_2	10	1.573e–12	1.448e–12	9.936e–9	0	8968	100,000	
h_3	10	3.166e–9	1.582e–8	4.771e+4	6.496e+3	11252	100,000	
h_4	10	3.835e+2	6.401e+2	1.997e–8	2.526e–9	8379	100,000	
h_5	10	7.143e+1	1.070e+2	2.124e–2	1.879e–2	8543	100,000	
h_6	10	9.568e–1	1.738e+0	1.490e+0	5.402e–2	9217	100,000	
h_7	10	7.120e–2	5.928e–2	1.971e–1	2.066e–2	8791	100,000	
h_8	10	2.957e–5	1.015e–4	2.019e+1	1.376e–2	8273	100,000	
h_9	10	7.960e–2	2.755e–2	4.378e–1	9.876e–2	8681	100,000	
h_{10}	10	1.588e+1	6.836e+0	5.643e+0	3.618e–1	8864	100,000	
h_{11}	10	5.843e+0	1.169e+0	4.557e+0	5.243e–1	8270	100,000	
h_1	30	8.242e–13	4.564e–13	9.364e–9	1.899e–10	24770	300,000	
h_2	30	8.516e–10	4.564e–10	8.717e–6	7.474e–7	28523	300,000	
h_3	30	1.604e+0	2.727e+0	8.775e+5	5.810e+4	42183	300,000	
h_4	30	3.333e+4	1.026e+4	3.966e+1	8.554e+0	22190	300,000	
h_5	30	6.277e+3	1.734e+3	2.183e+3	7.831e+1	23249	300,000	
h_6	30	3.987e–1	1.261e+0	4.955e+1	1.933e+1	50331	300,000	
h_7	30	1.040e–2	1.000e–3	1.329e–2	1.272e–3	23908	300,000	
h_8	30	4.791e–6	1.133e–5	2.071e+1	3.766e–2	22143	300,000	
h_9	30	4.776e+0	2.428e+0	6.806e–1	1.214e–1	22510	300,000	
h_{10}	30	1.269e+2	2.221e+1	9.058e+1	4.892e+0	22655	300,000	
h_{11}	30	2.621e+1	1.7243e+0	3.114e+1	1.525e+0	22186	300,000	

Table 3.16: Rank-sum Test for $G3AT_M^S$ and RCMA Results in Table 3.15

			Solution Qualities				Solution Costs			
n	Compared Methods		R^+	R^-	p-value	Best Method	R^+	R^-	p-value	Best Method
10	$G3AT_M^S$	RCMA	34	32	0.7427	–	66	0	2.5377×10^{-5}	$G3AT_M^S$
30	$G3AT_M^S$	RCMA	36	30	0.4307	–	66	0	2.5377×10^{-5}	$G3AT_M^S$
All	$G3AT_M^S$	RCMA	133	120	0.4047	–	253	0	8.4593×10^{-9}	$G3AT_M^S$

Table 3.17: Results for the Hard Functions h_1–h_{17} with $n = 10$

	G3AT$_M^S$		G-CMA-ES		RqGES	
Function	Error	Cost	Error	Cost	Error	Cost
h_1	1.60e–12	8611	5.20e–09	10,000	3.77e–08	100,000
h_2	2.95e–09	9,170	4.70e–09	10,000	3.76e–08	100,000
h_3	7.53e–04	10,026	5.60e–09	10,000	1.55e+05	100,000
h_4	1.21e+03	14,152	5.02e–09	10,000	6.29e–08	100,000
h_5	1.92e+02	9,878	6.58e–09	10,000	1.05e–04	100,000
h_6	6.38e–01	10,058	1.17e+01	10,000	8.23e+02	100,000
h_7	1.57e–01	9,508	2.27e–03	10,000	1.40e–03	100,000
h_8	2.00e+01	9,270	2.05e+01	10,000	2.04e+01	100,000
h_9	5.93e–13	8,469	6.21e+00	10,000	1.49e+00	100,000
h_{10}	1.81e+01	8,563	7.16e+00	10,000	1.72e+00	100,000
h_{11}	5.09e+00	8,868	4.42e+00	10,000	1.69e–01	100,000
h_{12}	3.00e+02	9,070	2.98e+03	10,000	1.05e+03	100,000
h_{13}	4.42e–01	8,968	9.71e–01	10,000	1.09e+00	100,000
h_{14}	3.52e+00	10,509	3.91e+00	10,000	2.91e+00	100,000
h_{15}	1.23e+02	8,630	2.99e+02	10,000	1.98e+02	100,000
h_{16}	1.28e+02	8,943	1.11e+02	10,000	9.37e+01	100,000
h_{17}	1.60e+02	14,184	1.95e+02	10,000	9.59e+01	100,000

reduced solution costs compared to G-CMA-ES and RqGES with a p-value of

$$p = 1 - [(1 - 1.0101 \times 10^{-9}) \cdot (1 - 1.9276 \times 10^{-18})] = 1.010100003639991 \times 10^{-9}.$$

3.5 G3AT$_M^S$ against GA MATLAB Toolbox

In this section, the G3AT$_M^S$ method is compared with GA MATLAB included in "MATLAB Genetic Algorithm and Direct Search Toolbox". The algorithm implemented in the GA

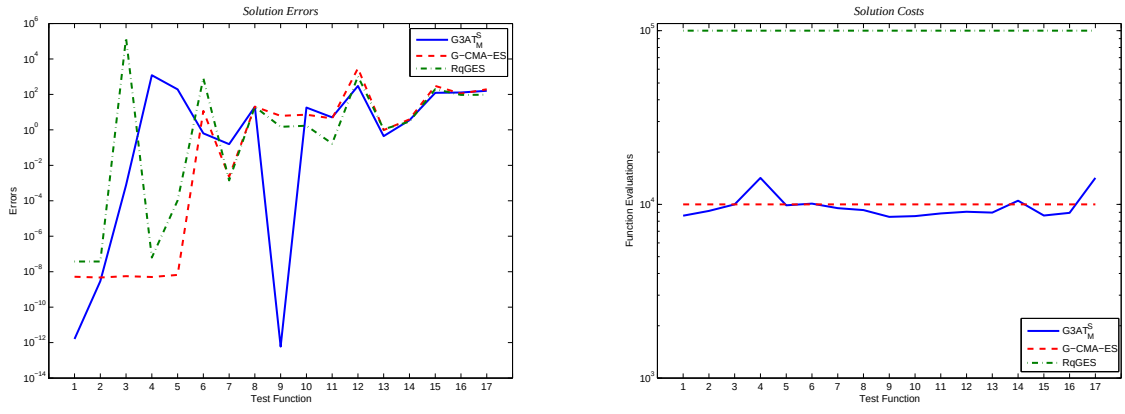


Figure 3.16: Results of Table 3.17 for test functions h_1–h_{17} with $n = 10$.

Table 3.18: Results for the Hard Functions h_1–h_{17} with $n = 30$

	G3AT$_M^S$		G-CMA-ES		RqGES	
Function	Error	Cost	Error	Cost	Error	Cost
h_1	6.96e–12	23,654	5.42e–09	100,000	1.54e–06	300,000
h_2	8.24e–08	27,896	6.22e–09	100,000	1.74e–06	300,000
h_3	3.36e+00	34,865	5.55e–09	100,000	9.43e+05	300,000
h_4	3.81e+04	43,251	1.27e+04	100,000	4.58e–01	300,000
h_5	6.12e+03	30,388	1.08e–07	100,000	2.31e+03	300,000
h_6	7.07e–01	36,288	4.78e–01	100,000	1.75e+03	300,000
h_7	1.06e–02	28,291	5.31e–09	100,000	2.69e–03	300,000
h_8	2.00e+01	28,021	2.07e+01	100,000	2.10e+01	300,000
h_9	4.74e+00	23,132	6.89e+00	100,000	9.74e+00	300,000
h_{10}	1.14e+02	23,415	6.96e+00	100,000	9.24e+00	300,000
h_{11}	2.32e+01	24,268	9.10e+00	100,000	3.60e+00	300,000
h_{12}	1.60e+03	27,076	5.95e+04	100,000	8.90e+03	300,000
h_{13}	1.98e+00	29,069	2.89e+00	100,000	3.26e+00	300,000
h_{14}	1.28e+01	38,136	1.35e+01	100,000	1.24e+01	300,000
h_{15}	3.33e+02	24,534	2.25e+02	100,000	3.37e+02	300,000
h_{16}	1.92e+02	25,108	5.34e+01	100,000	1.77e+02	300,000
h_{17}	2.79e+02	43,321	2.92e+02	100,000	1.04e+02	300,000

Table 3.19: Results for the Hard Functions h_1–h_{17} with $n = 50$

	G3AT$_M^S$		G-CMA-ES		RqGES	
Function	Error	Cost	Error	Cost	Error	Cost
h_1	3.52e–11	37,116	5.87e–9	100,000	7.21e–03	500,000
h_2	2.24e–07	47,262	7.86e–9	100,000	2.16e–03	500,000
h_3	8.63e+00	65,952	4.84e+01	100,000	1.13e+06	500,000
h_4	1.03e+05	73,537	6.16e+05	100,000	7.85e+02	500,000
h_5	1.45e+04	49,725	1.21e+03	100,000	6.38e+03	500,000
h_6	1.11e+02	66,398	3.74e+01	100,000	6.74e+02	500,000
h_7	7.10e–03	47,020	7.22e–9	100,000	1.43e–02	500,000
h_8	2.00e+01	44,754	2.11e+01	100,000	2.11e+01	500,000
h_9	1.94e+01	36,233	2.19e+01	100,000	5.89e+01	500,000
h_{10}	2.83e+02	36,685	2.61e+01	100,000	2.40e+01	500,000
h_{11}	4.47e+01	38,166	2.12e+01	100,000	1.28e+01	500,000
h_{12}	6.29e+03	45,919	4.84e+05	100,000	4.31e+04	500,000
h_{13}	4.28e+00	55,248	5.48e+00	100,000	5.63e+00	500,000
h_{14}	2.24e+01	66,316	2.30e+01	100,000	2.18e+01	500,000
h_{15}	3.17e+02	39,465	2.50e+02	100,000	3.53e+02	500,000
h_{16}	2.43e+02	42,570	6.50e+01	100,000	4.99e+01	500,000
h_{17}	3.83e+02	73,528	2.36e+02	100,000	3.20e+01	500,000

Table 3.20: Rank-sum Test for Solution Qualities Reported in Tables 3.17–3.19

n	Compared Methods		R^+	R^-	p-value	Best Method
10	G3AT_M^S	G-CMA-ES	85	68	0.8363	–
	G3AT_M^S	RqGES	78	75	0.9725	–
	G-CMA-ES	RqGES	49	104	0.5816	–
30	G3AT_M^S	G-CMA-ES	54	99	0.4084	–
	G3AT_M^S	RqGES	74	79	0.9177	–
	G-CMA-ES	RqGES	95	58	0.2416	–
50	G3AT_M^S	G-CMA-ES	65	88	0.8633	–
	G3AT_M^S	RqGES	79	74	0.7566	–
	G-CMA-ES	RqGES	79.5	73.5	0.7176	–
All	G3AT_M^S	G-CMA-ES	584	742	0.4028	–
	G3AT_M^S	RqGES	666	660	0.8122	–
	G-CMA-ES	RqGES	667.5	667.5	0.1907	–

Table 3.21: Rank-sum Test for Solution Costs Reported in Tables 3.17–3.19

n	Compared Methods		R^+	R^-	p-value	Best Method
10	G3AT_M^S	G-CMA-ES	153	0	0.0118	G3AT_M^S
	G3AT_M^S	RqGES	153	0	1.1467×10^{-7}	G3AT_M^S
	G-CMA-ES	RqGES	153	0	1.0363×10^{-8}	G-CMA-ES
30	G3AT_M^S	G-CMA-ES	153	0	1.1467×10^{-7}	G3AT_M^S
	G3AT_M^S	RqGES	153	0	1.1467×10^{-7}	G3AT_M^S
	G-CMA-ES	RqGES	153	0	1.0363×10^{-8}	G-CMA-ES
50	G3AT_M^S	G-CMA-ES	153	0	1.1467×10^{-7}	G3AT_M^S
	G3AT_M^S	RqGES	153	0	1.1467×10^{-7}	G3AT_M^S
	G-CMA-ES	RqGES	153	0	1.0363×10^{-8}	G-CMA-ES
All	G3AT_M^S	G-CMA-ES	1285.5	40.5	1.0101×10^{-9}	G3AT_M^S
	G3AT_M^S	RqGES	1326	0	1.9276×10^{-18}	G3AT_M^S
	G-CMA-ES	RqGES	1326	0	3.0707×10^{-13}	G-CMA-ES

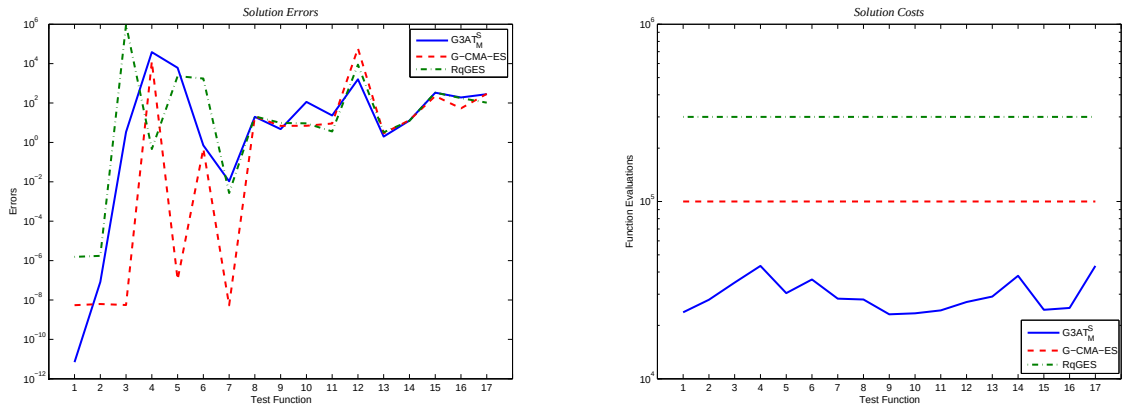


Figure 3.17: Results of Table 3.18 for test functions h_1–h_{17} with $n = 30$.

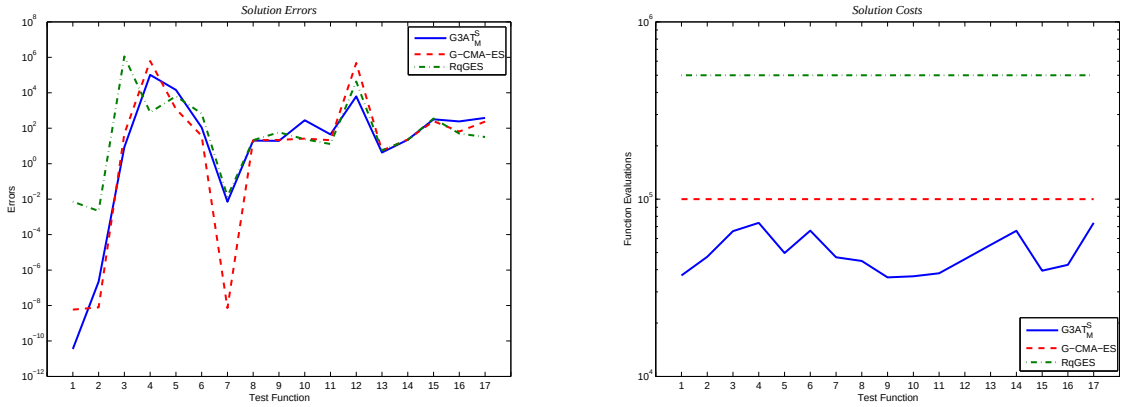


Figure 3.18: Results of Table 3.19 for test functions h_1–h_{17} with $n = 50$.

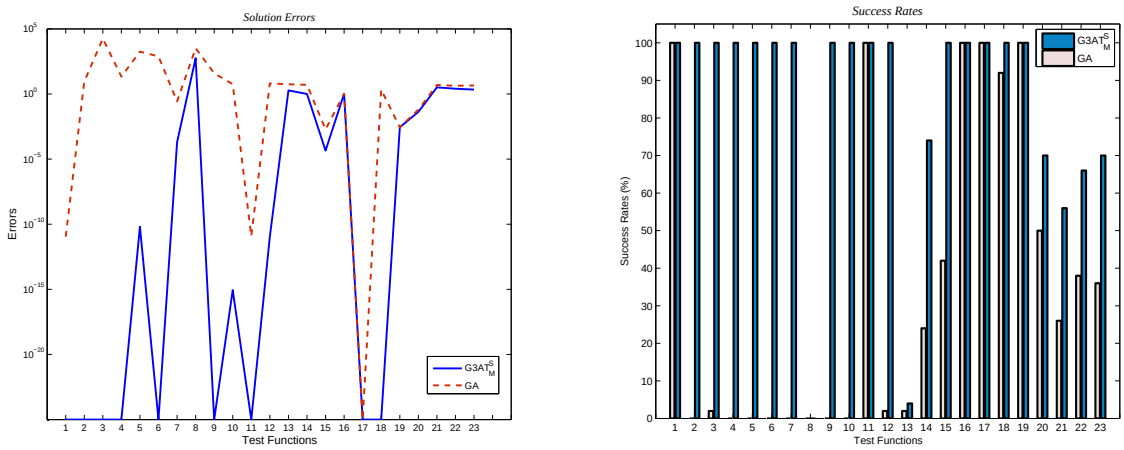


Figure 3.19: Results of Table 3.22.

MATLAB toolbox is a basic GA. We compared it with our best version of G3AT using the same number of function evaluations and the same GA parameters. To refine the best solution found by GA MATLAB, a built-in hybrid Nelder-Mead method is used to keep an equal level of search strategies between GA MATLAB and G3AT^S_M. The success rate of a trial is judged by means of condition (3.4.1).

From the results shown in Table 3.22 and summarized in Figure 3.19, we can conclude that using the mutagenesis operation can help a simple GA (such as the one found in the GA MATLAB toolbox) to achieve better results with faster convergence. This is confirmed by the statistical results presented in Table 3.23. Indeed, the difference between the two methods in terms of both solution qualities and success rates is statistically significant.

Actually, it seems that GA MATLAB was sometimes trapped in local minima even for some easy functions like f_{18}. As shown in Figure 3.20, the global minimum of f_{18} lies in a widespread valley. Therefore, it is not difficult for a search method with an efficient

Table 3.22: Solution Qualities for G3AT^S_M and GA MATLAB

		G3AT^S_M		GA MATLAB	
f	n	Mean	SD	Mean	SD
f_1	30	0(100%)	0	1.1e–11(100%)	4.9e–11
f_2	30	0(100%)	0	8.88(0%)	1.78
f_3	30	0(100%)	0	1.8e+4(2%)	5.1e+3
f_4	30	0(100%)	0	21.62(0%)	11.08
f_5	30	6.4e–11(100%)	3.1e–12	1.8e+3(0%)	2.4e+3
f_6	30	0(100%)	0	769.34(0%)	225.71
f_7	30	2.0e–4(100%)	1.6e–4	0.27(0%)	8.9e–2
f_8	30	–1.2e+4(0%)	194.04	–9.3e+3(0%)	7.1e+3
f_9	30	0(100%)	0	38.90(0%)	10.58
f_{10}	30	8.8e–16(100%)	0	5.64(0%)	0.66
f_{11}	30	0(100%)	0	1.2e–11(100%)	1.1e–11
f_{12}	30	1.1e–11(100%)	7.7e–12	6.55(2%)	2.64
f_{13}	30	1.90(4%)	1.37	5.62(2%)	2.23
f_{14}	2	2(74%)	2.26	6.04(24%)	5.41
f_{15}	4	3.3e–4(100%)	1.3e–4	2.3e–3(42%)	1.8e–3
f_{16}	2	–1.03(100%)	3.8e–14	–1.03(100%)	2.3e–14
f_{17}	2	0.397887(100%)	8.8e–14	0.397887(100%)	3.1e–13
f_{18}	2	3(100%)	2.6e–13	6.48(90%)	21.06
f_{19}	3	–3.86(100%)	2.2e–14	–3.86(100%)	1.5e–14
f_{20}	6	–3.28(70%)	6.0e–2	–3.26(50%)	6.0e–2
f_{21}	4	–6.90 (56%)	3.71	–5.19(26%)	3.13
f_{22}	4	–7.86(66%)	3.58	–6.13(38%)	3.44
f_{23}	4	–8.36(70%)	3.38	–5.99(36%)	3.53

Table 3.23: Rank-sum Test for G3AT^S_M and GA MATLAB Results

Comparing	Compared Methods					
Criteria	Method 1	Method 2	R^+	R^-	p-value	Best Method
Solution Qualities	G3AT^S_M	GA MATLAB	273	3	0.0185	G3AT^S_M
Success Rates	G3AT^S_M	GA MATLAB	265.5	10.5	1.5663×10^{-4}	G3AT^S_M

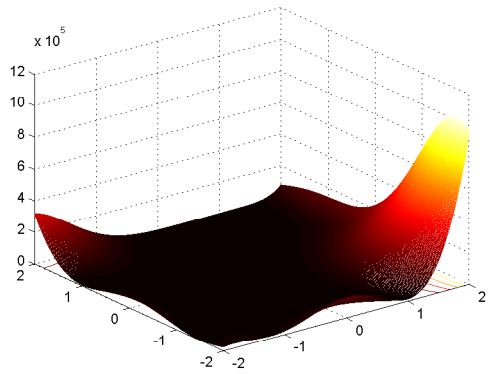


Figure 3.20: Goldstein & Price Function f_{18}.

exploration process to reach the global minimum. However, GA MATLAB failed to reach the global minimum in 10% of the trials.

3.6 Conclusion

In this chapter, we have introduced a new GA that is equipped with the GM, mutagenesis and a final intensification process. We have shown that G3AT is robust and able to reach global minima or at least be very close to them in many test problems. The use of GM effectively assists the algorithm to achieve wide exploration and deep exploitation before stopping the search. This indicates that our main objective, which is to equip evolutionary algorithms with automatic accelerated termination criteria, has largely been fulfilled. Moreover, the proposed intensification schemes based on mutagenesis of GM and Best Child Inspiration have proved to be more efficient in our experiments than local search based on the Nelder-Mead method. Among the three versions of G3AT, G3AT^S_M is the one showing the best general performance. The comparison results indicate that G3AT^S_M undoubtedly outperforms the GA MATLAB toolbox and is much cheaper than some advanced versions of GAs as well as some other EAs. Moreover, even though the proposed method uses a classical type of crossover, it is very competitive with some state-of-art methods. Therefore, the newly added elements in the proposed method contribute in achieving good performance. Finally, we may conclude that using mutagenesis could improve the solution quality and using the GM to determine termination criteria could reduce the amount of function evaluations.

Chapter 4

Genetic Algorithm with Automatic Termination and Search Space Rotation

In the last two decades, numerous EAs have been developed for solving optimization problems. However, only a few works have focused on the question of the termination criteria. Indeed, EAs still need termination criteria prespecified by the user. In this chapter, we develop another GA with automatic termination and acceleration elements which allow the search to end without resort to predefined conditions. We call this algorithm Genetic Algorithm with Automatic Termination and Search Space Rotation, abbreviated as GATR. This algorithm utilizes the GM to equip the search process with a self-check in order to judge how much exploration has been performed, while maintaining the population diversity. The algorithm also implements the mutagenesis operation to achieve more efficient and faster exploration and exploitation processes. Moreover, GATR improves the performance of G3AT by fully exploiting the structure of the GM by calling a novel search space decomposition mechanism combined with a search space rotation procedure. As a result, the search operates strictly within two-dimensional subspaces irrespective of the dimension of the original problem. The computational experiments and comparisons with some state-of-the-art EAs demonstrate the effectiveness of the automatic termination criteria and the space decomposition mechanism of GATR.

4.1 Introduction

We propose in this chapter an improved version of G3AT presented in Chapter 3. G3AT is originally a GA with new directing strategies. The key elements of G3AT are the GM, the mutagenesis operator and a final intensification process. The GM is a matrix constructed to represent subranges of the possible values of each variable and consequently reflects the

distribution of the genes over the search range. Its role is to assist the exploration process in two different ways. First, GM can provide the search with new diverse solutions by applying the mutagenesis operator. Mutagenesis operator is a new type of mutation that works in combination with GM. It alters some individuals in order to accelerate the exploration and exploitation processes by guiding the search specifically towards unexplored areas. Also, GM is the key component to let G3AT know how far the exploration process has been performed in order to determine an adequate termination instant. By definition, however, although numerical experiments lead to positive results, the GM is a two-dimensional structure and there is no evidence that it is able to represent the distribution of individuals in the multi-dimensional search space accurately, especially in high-dimensional, multi-modal and highly epistatic problems. We thus provide in this chapter a response to those considerations, while attempting to improve the performance of the G3AT algorithm. We keep focused, however, on the main objective of this study, that is, on the automatic termination. We would like to stress out that our main objective is not to outperform existing results, although we will show that the method proposed in this chapter is competitive.

The response is a rotation-based version of the G3AT method, designated as GATR, which stands for Genetic Algorithm with Automatic Termination and Search Space Rotation. The main new elements are the Space Decomposition (SD) and the Space Rotation (SR). SD and SR work in combination in order to create a two-dimensional environment for the GM irrespective of the original dimension of the problem to be solved. In this environment, the GM goes through a series of rotations which allow the search to avoid premature convergence and termination due to specificities of the problems. As a hybrid GA, GATR first emphasizes on exploring the whole search space using the GM. Afterward, the exploitation process is invoked through a local search method in order to refine the best candidates obtained so far. GATR thus behaves like a "Memetic Algorithm" (Moscato, 1999; Le et al., 2009) in order to achieve faster convergence (Ong and Keane, 2004; Ong et al., 2006; Jakob, 2010; Kramer, 2010).

The performance of the algorithm is evaluated in 10, 30 and 50 dimensions on the set of 25 test problems of the CEC 2005 real-parameter optimization contest (Suganthan et al., 2005) and compared against a number of existing algorithms such as G3AT, a Real-Coded Memetic Algorithm (RCMA) (Lozano et al., 2005), a version of the Evolution Strategy with Covariance Matrix Adaptation method (which is a well-known state-of-the-art method for adaptive mutation) that is combined with a restart strategy (L-CMA-ES) (Hansen and Kern, 2004; Hansen, 2006) as well as the recent Non-Revisiting Genetic Algorithm with Parameter-less Adaptive Mutation (NrGA) (Yuen and Chow, 2009), a Differential Evolution method using an adaptive local search (DEahcSPX) (Noman and Iba, 2008) and the winner of the CEC 2005 competition, the Restart CMA Evolution Strategy With Increasing Population Size (G-CMA-ES) (Hansen et al., 2005b).

The rest of the chapter is organized as follows. Section 4.2 provides a review of the mechanisms implemented in GATR. It includes the GM and the mutagenesis operator as well as the new concepts developed to reinforce the GM model. The SD and SR are also described in this section. The effects of the introduction of the new mechanisms are discussed in Section 4.3. In Section 4.4, components and the formal algorithm of GATR are detailed. In Section 4.5, the methodology adopted for the numerical experiments is explained and results in dimensions 10, 30 and 50 are presented with the benchmark functions from CEC 2005. A comparative study against other methods from the literature is also conducted. A summary with conclusions is provided in Section 4.6.

4.2 GATR Mechanisms

GATR uses the Simple GM and mutagenesis operator described in Section 2.4. However, in GATR, the SD and SR mechanisms create solely two-dimensional environments that affect the GM. For that reason, the definition of the GM undergoes a slight adaptation, described in this section. Also, new concepts that reinforce the GM model are presented here. G3AT and GATR are methods that aims to determine a stopping point without knowledge about the problem. However, we also want GATR to be a method that not only possesses a proper stopping judgement but also exhibits more accurate and versatile performance than G3AT against a wider class of problems.

4.2.1 Gene Matrix and Termination

GATR adopts the real-coding representation of individuals. Hence in the search space, every individual x consists of n variables or genes. The range of each gene is divided into m subranges in order to check the diversity of the gene values. In GATR, GM is initialized as a $2 \times m$ zero matrix in which each entry of the i-th row refers to a subrange of the i-th gene. Indeed, in GATR, GM deals solely with two-dimensional subspaces, although the problem being optimized can be of any dimension $n \geq 2$. While the search is processing, the entries of GM are updated if new values for genes are generated within the corresponding subranges. Those entries are granted with a non-null value. Specifically, during the search, the value of each gene is considered in order to extract the number associated with the subrange where the considered gene is located, say $v \in \{1, \ldots, m\}$. Let x_i be the representation of the i-th gene, $i = 1, \ldots, n$. Once a gene gets a value corresponding to a non-explored subrange, GM is updated by flipping a zero into a one in the corresponding (i, v) entry. Let us note that, with this mechanism, GM is not sensitive to the number of genes lying inside each subrange.

After having a GM full, i.e., with no zero entry, the search judges that an advanced exploration process has been achieved and can be stopped. In this way, the principal use

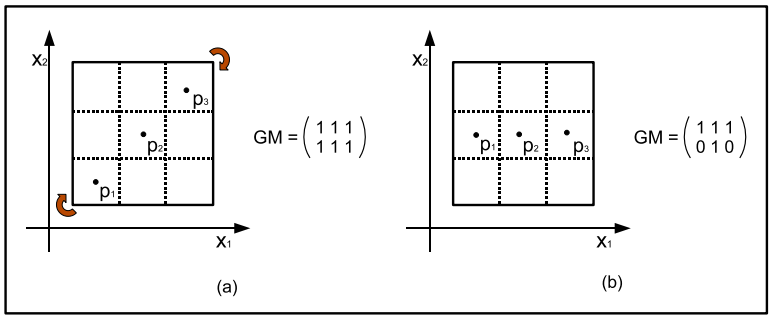


Figure 4.1: Diagonal distribution of individuals before and after rotation and the associated GM.

of GM is to equip the search process with a practical termination tool. Other versions of GM, sensitive to the number of genes within each subrange, have been investigated. However, our comparative study has revealed that the zero-one GM mechanism presented here (and implemented in GATR) yields the best performances in terms of number of function evaluations versus solution quality.

4.2.2 High-dimensional Search Space

By definition, GM has a two-dimensional structure, i.e., a matrix of indicator variables for subranges in each dimension of the search space. Consequently, it may face some difficulties in representing the distribution of individuals in a high-dimensional search space. Basically, for m subranges and n dimensions, we can count m^n hyperrectangles in the search space. However the GM can become complete with less than $m \times n$ points. Therefore, there is a possibility of having a misguided termination of the exploration process, as depicted in a simple example in Figure 3.2(a), where the GM is already full although the search space is far from being entirely covered. The crossover operation can overcome this drawback as shown in Figure 3.2(b). As a matter of fact, numerical simulations show that GM explores the search space widely. However, although it is easy to comprehend in two dimensions, it is difficult to admit whether such mechanism can perform a sufficient exploration of the search space when the dimension of the problem increases, which is one of the reasons why we introduce the SR and SD mechanisms.

4.2.3 Space Rotation

Those considerations on GM prompt us to develop the space rotation mechanism. As depicted in Figure 4.1(a), a particular distribution of the individuals may lead to premature completion of GM. Indeed in this case, it is clear that the entire search space has not been fully covered. In Figure 4.1(b), after applying to the search space a clockwise 45 degrees rotation, the same distribution of the explored areas is seen by GM from a different angle.

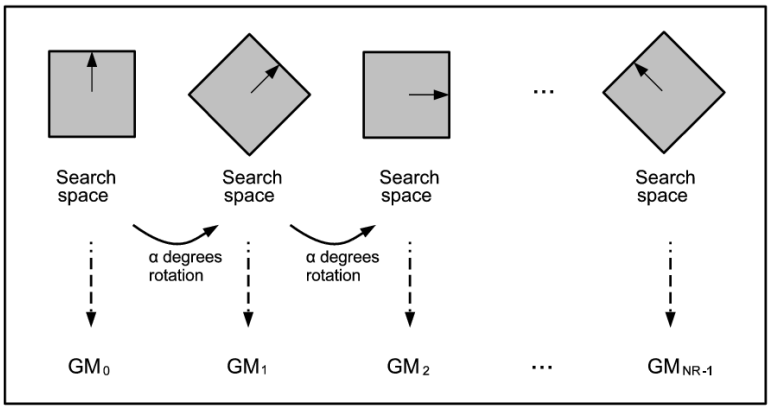


Figure 4.2: *NR* rotations of the search space by angle α and the associated GM.

Recomputing the GM then reveals unexplored regions (i.e., the matrix is not complete any more). Thus in order to escape from premature termination of the search, the idea is to "rotate" the search space and attach to the resulting spaces a GM that do not necessarily have the same configuration as the original one at a given instant.

Let us consider the optimization problem (1.1.1) defined in Section 1.1. The search domain D can be seen as an n-dimensional rectangle in R^n. The edges of this rectangle are given by the lower bounds l_i and upper bounds u_i of the variables x_i with $l_i \leq x_i \leq u_i$ $(i = 1, ..., n)$.

The rotation of the rectangle is depicted in Figure 4.2. Rotation is defined by the rotation angle α, which is a divisor of 360, as well as the number of rotations, $NR = 360/\alpha$. To each rotation is associated a GM, namely GM_l, $l = 0, \ldots, NR - 1$. They are independently fed by their respective rotated spaces.

During the search process, SR applies the rotation operator, named $Rot_\alpha[x]$, to each individual x using angle α such that $x' = Rot_\alpha[x]$, where x' represents the rotated individual. Then the original objective function can be recomputed by $f(x) = f(Rot_\alpha^{-1}[x'])$. Formal description of SR is given in Procedure 4.2.1, where x_i represents the i-th gene of each individual x within the population X, and X' is the population in the rotated subspace associated with its GM that will be denoted as GM$'$. Each population is of size μ.

Procedure 4.2.1. *Rotation*(X', GM')

1. *Set values of* α. *Set* $Rot_\alpha := \begin{bmatrix} \cos\alpha & -\sin\alpha \\ \sin\alpha & \cos\alpha \end{bmatrix}$.
2. *For each individual* x *in* X, *let* $x'_i := (Rot_\alpha[x])_i$, $i = 1, ..., n$.
3. *Update* GM' *using all individuals* x', *and return.*

The SR mechanism can be compared to a previous work by Schwefel that first appeared in (Schwefel, 1974) and also later in (Beyer and Schwefel, 2002). In that work, Schwefel introduces the idea of correlated mutation based on rotation of the solution space by using

a rotation matrix for a variant of EA, namely, the Evolution Strategies (ES) (Rechenberg, 1965; Beyer and Schwefel, 2002). One of the peculiarities of ES is that individuals not only comprise the decision variables but also a set of strategy parameters. Among them, we can find those of the mutation operator. Hence, the decision variables along with the strategy parameters evolve simultaneously during the evolution process. However, in essence this strategy is different from SR. Indeed, the rotation matrix introduced by Schwefel aims at improving the mutation operation by controlling the area of the search space where are generated individuals. SR, on the other hand, do not aim at composing new individuals but rather ensuring that GM has explored a widespread area of the search space and detecting unexplored regions.

4.2.4 Space Decomposition

GM and SR are by nature two-dimensional mechanisms. For problems in higher dimensions, we invoke the space decomposition mechanism. Its role is to transform a high-dimensional search space of a problem into several two-dimensional subspaces. In order to do so, before the search process, SD selects two variables, say x_a and x_b, among $\{x_1, x_2, \ldots, x_n\}$, which will be referred to as the current "active variables". During the generation process, only x_a and x_b are directly treated as the variables to be manipulated. The other variables, referred to as "passive variables", momentarily hold their values fixed (i.e., they will not participate in the improvement for a moment). The upper and lower bounds of x_a and x_b are used to define the edges of the rectangle that will be considered by SR. At the end of the search, all genes of the best individual found (both active and passive variables) are given a chance to be improved in an intensification phase. The resulting candidate (individual) is referred to as x^{elite}. At this point, we end the search using the GM information, but obviously the obtained x^{elite} does not announce the end of the entire process since we have only considered a portion of variables. Thus, if "enough" genes have not participated yet in the search as active variables, the current ones are set as passives and two other genes are selected as new actives. The search is then resumed, as what we will call a new "era". It is important to understand that the entire process will end when enough active variables have participated in their own eras. However, it is the role of the GM to terminate adequately each era. The efficiency of the whole algorithm is thus under the influence of the performance of the automatic termination. At the beginning of each era, the whole population is randomly generated. However, once the passive variables are designated, the values of all individuals' passive variables (or genes) are transformed in such a way that their values are aligned with those of the previously obtained x^{elite}.

4.3 Effects of the GATR Mechanisms

Although GATR is used as an optimization tool, its parameters cannot be set to be optimal for all problems at the same time. Since GATR is not a self-adaptive method, in order to observe the guideline proposed by the CEC 2005, we have decided to run preliminary experiments on the test bed and observe which parameter values would give the best results on a large set of test functions. In particular, we here discuss the effects of the introduction of each component of GATR and how the parameter values have been determined and used in this work.

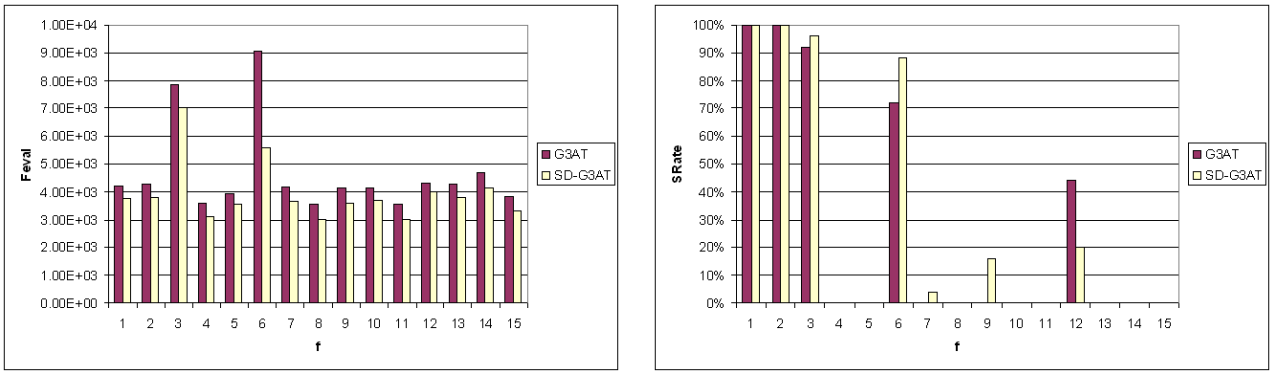
4.3.1 Number of Subranges of the GM

The parameter m regulates the size of the sub-regions and its suitable value appears to be very problem dependent. The number of function evaluations, abbreviated as Feval, is directly proportional to m in any dimension, but the success rates, referred to as SRate and defined later in Subsection 4.5.1, have unpredictable behaviors. For our numerical experiments, the convergence speed has been given more importance, since the Feval with m varying from 50 to 300 can dramatically increase, while SRate keeps fluctuating and does not necessarily increase significantly. It is thus favorable to keep m as small as possible. In our experiments, $m = 100$ was the value demonstrating the most satisfactory results on a large set of functions in terms of SRate, with moderate Feval.

4.3.2 Effect of the Space Decomposition

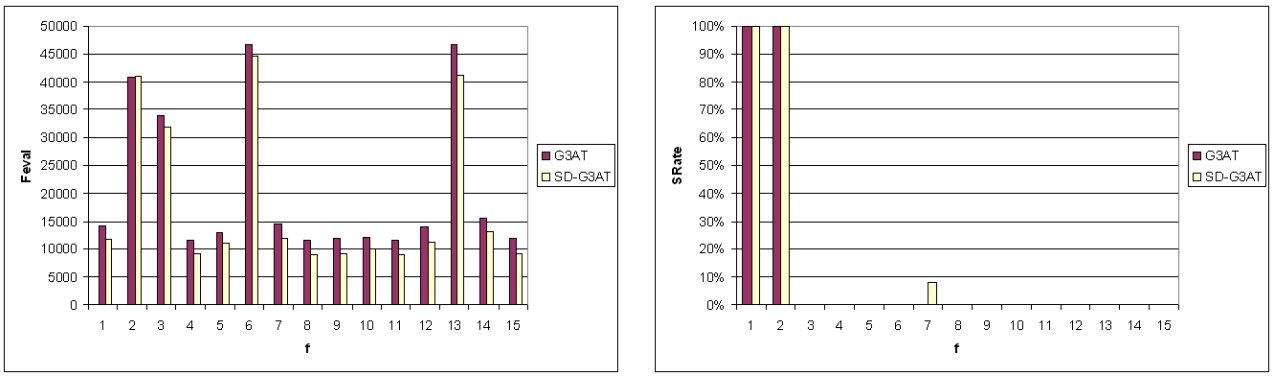
Here we discuss the effects of the introduction of SD into G3AT. To do so, a variant of G3AT, referred to as SD-G3AT, has been implemented. This variant employs SD with G3AT, but using a single GM without rotations, and only one intensification phase during the final era, as in G3AT. SD-G3AT is compared against G3AT in terms of SRate and Feval in 10 and 30 dimensions.

As shown in Figure 4.3(a) and 4.4(a) for functions f_1–f_{15} in 10 and 30 dimensions, respectively, the use of SD (through SD-G3AT), i.e., using solely $n = 2$ during the search, tends to slightly decrease the required Feval before termination (except function f_2 in 30 dimensions, for which Feval is slightly higher). Performance in terms of SRate in 10 dimensions, as shown in Figure 4.3(b), is advantageous for SD-G3AT. Functions that could be solved by G3AT were also solved by SD-G3AT. Moreover, SD-G3AT could perform better for functions f_3 and f_6, and could also solve functions f_7 and f_9. Figure 4.4(b) depicts the results achieved in 30 dimensions. We can observe that SRate stays around the same order. Functions f_1 and f_2 could be solved by both variants. We also note that function f_7 could not be solved by G3AT, but could be handled (with a small SRate) by SD-G3AT.



(a) (b)

Figure 4.3: Comparison of Feval and SRate for G3AT vs SD-G3AT on functions f_1–f_{15} in 10 dimensions.



(a) (b)

Figure 4.4: Comparison of Feval and SRate for G3AT vs SD-G3AT on functions f_1–f_{15} in 30 dimensions.

Thus, in terms of Feval and SRate, the introduction of SD could slightly accelerate the convergence of the algorithm, and obtain equivalent or better SRate.

4.3.3 Number of Space Rotations

In GATR, the role of the rotations is to lower the possibility of premature termination at a non-optimal solution, which is caused by insufficient exploration of the search space due to the structure of the GM. We have tested GATR with different numbers of space rotations NR ranging between 0 and 4, where $NR = 0$ means no rotation. Thus only the impact of SD was measured, as in Subsection 4.3.2. We could observe that Feval is directly proportional to NR. It can be estimated that the introduction of one rotation in 30 dimensions increases the Feval by around 5.4% on average, while in 10 dimensions it increases the Feval by around 10%. Also high NR tends to slow down the algorithm. Starting with no rotation, after 3 rotations, the functions that could not be solved before came with positive results. Thus,

to keep an acceptable convergence speed, we have decided to adopt $NR = 3$ as the default value in our numerical experiments.

4.3.4 Combination List

The CL is a list that keeps track of the pairs of variables that are designated to participate during the eras. Let us consider the pair $\{x_a, x_b\}$. Obviously x_a and x_b should not be identical. One of the easiest and most intuitive way to construct the CL is to select randomly x_a and x_b from the set of all possible variables $\{x_1, x_2, \ldots, x_n\}$ with the only condition that x_a is different from x_b. However, experiments show that selecting the active variables in a sequential manner (i.e., starting with x_1 and x_2, then x_3 and x_4, etc.) could provide equal or better results for all functions. Although there is no theoretical proof to support this finding, we decided to adopt the "sequential" way of creating the CL (as opposed to the random construction) in GATR.

Now, we are concerned about the length of the CL (CL_length) (i.e., the number of eras), which has a direct impact on the convergence speed of the search. According to our preliminary experiments, it is without surprise that the cost in Feval increases proportionally with the length of the CL. Intuitively, one can expect better SRate with a longer CL, since more eras would be allowed to refine a solution. However, the results show that SRate increases slowly or fluctuates with CL_length for many functions. Moreover, a length of 5 and 15 in 10 and 30 dimensions, respectively, provided in general good performance in terms of SRate on a large set of problems. Increasing those values may improve slightly the SRate, but the Feval will considerably increase at the same time. According to those results, in GATR, CL_length has been set equal to $round(n/2)$, where the operation $round$ rounds towards the nearest integer. This value aims at good SRate with acceptable Feval. Note that setting $CL\_length = round(n/2)$ guarantees that each variable is given a chance to participate in the search as an active variable at least once.

4.3.5 Intensification

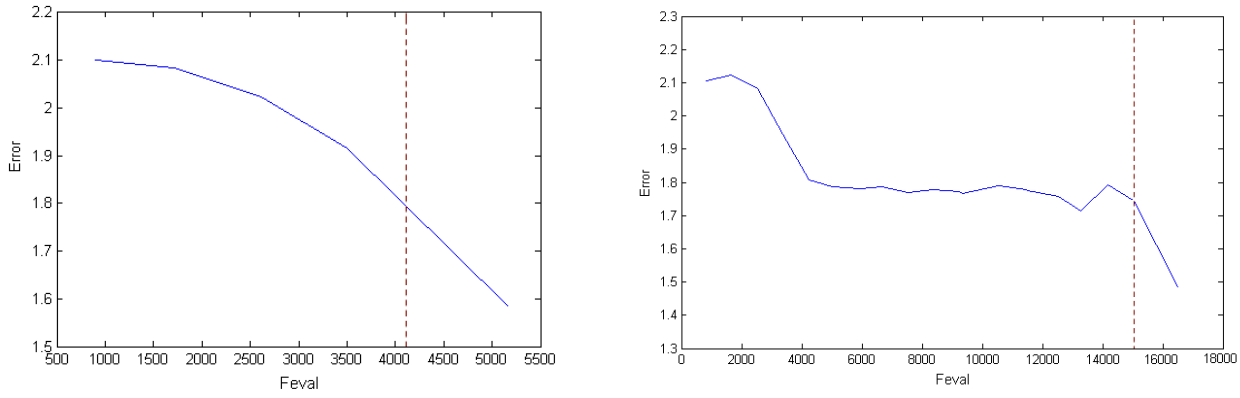
Intensification is the process whose purpose is to refine the elite solution obtained at the end of an era. In GATR as well, intensification calls a local search process based on the Kelley's modification (Kelley, 1999) of the Nelder-Mead (NM) method (Nelder and Mead, 1965). The use of systematic intensification at the end of each era, however, can be expensive in terms of Feval. In GATR, intensification is therefore sparingly called by specific eras since it yields positive effects when called at intermediate stages of the search. We should remark, however, that the final refinement by intensification at the end of the search is most important to achieve higher accuracy. Indeed, GM combined with the SD and SR can be seen as the components that will explore the search space widely in order to find promising

individuals. Those individuals will be given a chance to improve further through an exploitation phase handled by intensification. The numbers designating the eras that will go through an intensification step are stored in the intensification list (IL). Preliminary experiments, using the terminology introduced in Subsection 4.5.1 concerning the test functions and methodology, show that the best results are obtained when the first and last eras are subject to intensification. Various patterns to select the remaining eras have been studied. However, no significative differences can be observed when compared to a random selection of the intermediate intensified eras. The total number of eras that go through intensification (i.e., the length of IL) has also been studied. Intensification calls a local search method at the end of an era. Consequently, it relatively requires a considerable amount of additional computational resources. As a matter of fact, experiments show that a longer IL considerably increase Feval. However, SRate does not necessarily increase for all functions. Thus, in order to keep a good balance between exploration and exploitation, the length of IL in GATR has been set equal to $n/5$.

It should also be noted that although GATR relies on intensification when it comes to the exploitation phase, intensification alone cannot reach the results obtained by GATR. Indeed, experiments on some functions, such as f_9 for instance, revealed that the success rate for that function could reach 36% using GATR over the 25 trials. On the same function, the use of intensification only and using random starting points led to a success rate of 0%. From this simple experiment, we may observe that intensification has an important part to play in GATR. However, if used alone, the results are not satisfactory compared to GATR. It is thus in combination with GATR that superior results could be achieved.

4.3.6 Termination

In order to estimate whether the GMs are able to provide the search with a correct termination point, the automatic termination has been compared for each function with the same run in the same conditions, as described in Subsection 4.5.1, but with an artificially maintained higher number of generations and only one final intensification occurring during the last era. For function f_{10} in 10 dimensions for instance, Figure 4.5(a) represents the evolution of the error with Feval using GATR and only one final intensification, referred to as Short-GATR. We can observe that around 5,100 Fevals were required to reach an error level of around 1.6. The dotted vertical line represents the instant at which the algorithm decided to stop and launch the final intensification phase. Intensification could improve the results by reducing the error from roughly 1.8 to 1.6. Figure 4.5(b) depicts the evolution of the error over Feval obtained by a modified version of GATR, called Long-GATR, whose termination instant was artificially delayed. To do so, CL_length has been set equal to 15 instead of 5 (i.e., $round(n/2)$) in the original setting. More eras were thus allowed to explore the search



(a) (b)

Figure 4.5: Comparison of termination instant after intensification (vertical dotted line) for function f_{10} using Short-GATR (a) and Long-GATR (b).

space. Also, CP was set equal to 100% instead of 90% in order to obtain longer eras and let the search refine the obtained solutions further. In Long-GATR, around 16,500 Fevals were necessary before termination, which is slightly more than 3 times the short version. We can see that after around 4,000 Fevals, which is the instant at which Short-GATR decided to stop, the improvement in terms of error begins to stagnate at around 1.8. After 10,000 function evaluations, the error improvement is still not significative. Finally, intensification could reduce the error from around 1.75 to 1.5. This experiment reveals that letting the search run after the original termination instant does not necessarily improve the best solution obtained, considering the substantial amount of additional Feval required to improve a solution further.

4.4 GATR Operators and Formal Algorithm

Before stating the formal algorithm of GATR, basic components that compose a GA and that are used by GATR are briefly described in this section.

4.4.1 GA Operators

The parent selection mechanism implemented in GATR is based on the *linear ranking selection mechanism* (Baker, 1985; Hedar and Fukushima, 2003). This mechanism ranks the initial population P according to the fitness function value of each individual. From P, an intermediate population P' is produced by copying repeatedly individuals based on their fitness ranking until P' becomes full. Note that an already chosen individual can be selected more than once. In GATR, since $n = 2$ during the search, the crossover operation is straightforward. The procedure consists in swapping the active variables of two parents p_1

and p_2, and create two children c_1 and c_2. The mutation operator is designed to take advantage of the information contained in the GM. Indeed, existing zeros from GM are randomly selected, say in the position (i, j), and a randomly chosen individual from the intermediate pool IP_M has its variable x_i modified by a new value lying inside the j-th partition of its range. For each individual in the intermediate population P' and for each gene, a random number from the interval $(0, 1)$ is associated. If the associated number is less than a prespecified mutation probability π_m, then the individual is copied to the intermediate pool IP_M. The number of times the associated numbers are less than the mutation probability π_m is counted, and let num_m denote this number. Afterward the mutation operation ensures that the total number num_m of genes to be mutated does not exceed the number of zeros in the GM, denoted num_{zeros}. Otherwise the number of genes is reduced to num_{zeros}. The formal procedure for mutation is analogous to Procedure 2.4.1, where m represents the number of each gene's subranges. Parents and children then compete together for survival, making GATR a steady-state GA.

Procedure 4.4.1. Mutation(x, GM)

1. *If GM is full, then return; otherwise, go to Step 2.*
2. *Choose a zero-position (i, j) in GM randomly.*
3. *Update x by setting $x_i = l_i + (j - r)\frac{u_i - l_i}{m}$, where r is a random number from $(0, 1)$, and l_i, u_i are the lower and upper bounds of the variable x_i, respectively.*
4. *Update GM and return.*

4.4.2 GATR Formal Algorithm

The search process in GATR is repeated several times, with different active variables taking part in distinct eras. Each search can be considered to be a G3AT run for a two-dimensional problem, taking advantage of GM and SR to terminate adequately. Preliminaries consist in SD whose role is to transform an n-dimensional search space into several two-dimensional subspaces. During an era, GATR starts by generating an initial population of size μ and dimension n. Two variables, x_a and x_b, are chosen as active variables. They will participate in the current era's evolution, while the other genes have their values replicated from x^{elite}'s respective gene values. In the very first era, however, each gene of x^{elite} is pre-initialized as $x_i^{elite} := (\frac{u_i + l_i}{2})$, where l_i and u_i are the lower and upper bounds of gene x_i, respectively. For any n-dimensional problem, CL_length eras are carried out with distinct pairs of active variables, and the values of passive genes remain unchanged during each era.

As a GA based method, GATR evaluates the population members, and then generates offsprings by applying parent selection, crossover and mutation operations. The role of SR is to manipulate the two-dimensional space in which the active variables are evolved by executing NR rotations of angle α. NR distinct GMs are updated, each corresponding to

one of the NR rotated subspaces. Mutagenesis is invoked until the GM completion ratio CP, which may be set as different from 1, is reached. An era terminates when all NR GMs reach CP. Eventually, it is guaranteed that the GMs will reach CP since mutagenesis makes sure that new individuals are generated within unvisited areas. It is worthwhile to mention that the main role of GM and SR is to guide the search towards unexplored regions, while exploration by itself is conducted by the crossover and mutagenesis operations. The termination of the algorithm is thus guaranteed. Finally, an era ends with a final intensification phase that uses a local search method in order to refine the best solution found so far. Let us emphasize that each era consecutively improves the current best solution x^{elite} by using the active variables. However, intensification improves all genes, actives and passives. The solution x^{elite} is then used in the starting point for the next era, where a different couple of active variables is selected and the remaining ones become passive. When all the pairs of variables in CL have actively participated in some eras, GATR terminates with the last refined solution. A formal description of GATR is given below.

Algorithm 4.4.2. *GATR Algorithm*

1. ***Initialization.*** *Set values of* m, μ, μ_w, NR, α, CP, *and* (l_i, u_i) *for* $i = 1, \ldots, n$. *Set the crossover and mutation probabilities* $\pi_c \in (0,1)$ *and* $\pi_m \in (0,1)$, *respectively. Set the Intensification List IL as described in Subsection 4.3.5. Set the Combination List* $CL := \{x_1, x_2, \ldots, x_n\}$. *If the number of elements in* CL *is odd, add a randomly chosen element from* $\{x_1, x_2, \ldots, x_n\}$. *Set the generation counter* $t := 1$. *Compute* x^{elite} *by* $x_i^{elite} := \frac{u_i + l_i}{2}$ *for* $i = 1, \ldots, n$.
2. *Set all variables to be passive. Select* x_a *and* x_b *from* CL. *Update* CL *by* $CL := CL \backslash \{x_a, x_b\}$ *and designate* x_a *and* x_b *as active variables.*
   2.1. *Generate an initial population* P_0 *of size* μ *and update each individual* x^k *in* P_0 *so that* $x_i^k := x_i^{elite}$ *for* $i \in \{1, \ldots, n\} \backslash \{a, b\}$.
   2.2. *Initialize Gene Matrices* GM_l, $l = 1, ..., NR$, *as* $2 \times m$ *zero matrices, where* GM_l *corresponds to the* l*-th space rotation.*
3. ***Parent Selection.*** *Evaluate the fitness function* F *for all individuals in* P_t. *Select an intermediate population of parents* P_t' *from the current population* P_t. *Let the initial parent pool* SP_t *and children pool* SC_t *be empty.*
4. ***Crossover.*** *Associate a random number from* $(0,1)$ *with each individual in* P_t' *and add this individual to the parent pool* SP_t *if the associated number is less than* π_c. *Repeat the following Steps 4.1 and 4.2 until all chosen parents from* SP_t *are mated:*
   4.1. *Choose two parents* p_1 *and* p_2 *from* SP_t. *Mate* p_1 *and* p_2 *by swapping their active variables to create children* c_1 *and* c_2.
   4.2. *Update the children pool* SC_t *by* $\mathrm{SC}_t := \mathrm{SC}_t \cup \{c_1, c_2\}$ *and update* SP_t *by* $\mathrm{SP}_t := \mathrm{SP}_t \setminus \{p_1, p_2\}$.
5. ***Mutation.*** *Associate a random number from* $(0,1)$ *with each gene in each individual in* P_t'. *Let* num_m *be the number of genes whose associated number*

is less than π_m, and let num_{zeros} be the number of zero elements in GM. If $num_m \geq num_{zeros}$, then set $num_m := num_{zeros}$. Mutate num_m individuals among those which have an associated number less than π_m by applying Procedure 4.4.1. Add the mutated individual to the children pool SC_t. Update GM_l, $l = 1, ..., NR$ with SR by applying Procedure 4.2.1.

6. *If all GMs have reached the completion ratio CP, go to Step 9. Otherwise go to Step 7.*
7. ***Survivor Selection.*** *Evaluate the fitness function for all generated children SC_t, and choose the μ best individuals in $P_t \cup \mathrm{SC}_t$ for the next generation P_{t+1}.*
8. ***Mutagenesis.*** *Apply Procedure 2.4.1 to alter the μ_w worst individuals in P_{t+1}, set $t := t+1$, update GM_l, $l = 1, ..., NR$ with SR by applying Procedure 4.2.1, and go to Step 3.*
9. ***Intensification.*** *If the current era is in IL, then go to Step 9.1. Otherwise go to Step 9.2.*
   9.1. *Apply a local search method starting from the best solution obtained in the previous search stage using all variables, and go to Step 9.2.*
   9.2. *Let x^{elite} be the best solution obtained so far. If $CL \neq \emptyset$, go to Step 2. Otherwise, terminate with x^{elite}.*

4.5 Numerical Results

Numerical experiments were carried out to evaluate the performance of GATR. Before presenting the results, we describe the methodology adopted to conduct the numerical study of GATR.

4.5.1 Methodology

The numerical study is based on a test bed of 25 standard test functions from the special session on real-parameter optimization in the IEEE Congress on Evolutionary Computations, CEC 2005 (Suganthan et al., 2005). The set was carefully built based on classic benchmark functions in an attempt to cover a diverse set of problem properties. The first 5 functions are unimodal functions while the 20 other functions are multimodal, with functions f_{13} to f_{25} being hybrid composition functions. The mathematical form of the 25 test problems can be found in (Suganthan et al., 2005).

Before proceeding to the description of the test settings and results, some remarks should be stated in order to emphasize the particularity of the proposed GATR method. This is to clarify the dissimilarities in the way we present and compare the data with other methods, which does not exactly follow the evaluation guideline suggested in CEC 2005. When conducting numerical experiments, the CEC 2005 guideline recommends the use of

Table 4.1: GATR Parameter Setting

Parameter	Definition	Value
μ	Population size	30
π_c	Crossover probability	0.6
π_m	Mutation probability	0.1
m	No. of GM subranges	100
μ_w	No. of individuals used by mutagenesis	2
NR	Number of space rotations	3
α	Space rotation angle	45^o
CP	Completion ratio of GM	90%

common evaluation criteria such as the initialization scheme, the size of problems, a common termination criterion, etc. The guideline in particular indicates that the search should be stopped when reaching a pre-specified maximum number of function evaluations $(10,000 \times n)$ or if the error in the function value becomes lower than a given threshold (10^{-8}). Solution quality is measured through the function error value given by $(f(x) - f(x^*))$, where $f(x)$ represents the best function value obtained by the algorithm and $f(x^*)$ is the known exact global minimum value. Also, when evaluating the amount of function evaluations needed, the search is stopped as soon as a fixed accuracy level is achieved. It is clear that GATR cannot fully comply with those termination criteria, since the point here is to let the search terminate automatically. Consequently, the results of the numerical experiments are not reported exactly as suggested in CEC 2005, but comparison is still possible and realistic, as done in this section, where interesting findings are discussed.

Table 4.1 summarizes the GATR parameters with their assigned values. GATR was programmed using MATLAB and the code for each test function was run 25 times in 10, 30 and 50 dimensions, in accordance with the guideline proposed in CEC 2005. Also, a run is considered successful when the fixed accuracy level is achieved within the pre-specified maximum number of function evaluations (before 100,000 Fevals in 10 dimensions, 300,000 Fevals in 30 dimensions and 500,000 Fevals in 50 dimensions). The success rate (SRate) is defined as the number of successful runs divided by the total number of runs.

In this study, the Wilcoxon matched-pairs signed-ranks non-parametric test is used for directly comparing the results of two methods. This test, as described in (García et al., 2009), does not assume that the data are sampled from a normal distribution. It assumes however that the data are symmetrically distributed around the median. We employ the Wilcoxon non-parametric test because, for the methods that follow the framework suggested by the CEC 2005, the authors report their achieved average results using the same conditions for each algorithm and test problem. In particular, we consider in this work the function error values obtained by each method.

4.5.2 Discussion from the Benchmark Results

The 25 test functions of the CEC 2005 can be classified according to their characteristics. Hence, we will discuss here the performance of GATR by taking into account the nature of the functions. Results are available in Table 4.2 for GATR, where the mean error values are reported for each functions as well the SRate, in parentheses, when not null. To begin with, the first five functions are unimodal functions and the others are multimodal. Functions f_1 and f_2 are relatively easy to solve, in 10, 30 and 50 dimensions. The increase in dimensionality did not affect substantially the performance of the algorithm in terms of mean error value. Function f_3 is the shifted rotated high conditioned elliptic function and the optima could be found only in 10 dimensions. Function f_4 is similar to f_2 but shifted with noise. The addition of noise seems to have affected the performance. Function f_6 could be solved in all dimensions with decent success rates, due to the local search capability of GATR through intensification. Function f_7 is a shifted rotated version of Griewank's function and does not have predefined bounds. It was easy to solve even in high dimensions. Function f_8 has a "needle in a haystack" profile and is thus very challenging to solve for most methods. GATR got stuck at the same mean error value order in all dimensions. Functions f_9 and f_{10} are shifted and rotated shifted versions of the Rastrigin function, respectively, and f_{11} is also a shifted rotated function. The global optimum was missed in all runs for f_{10} and f_{11}. Function f_{12} is Schwefel's problem and it could be solved in 10 dimensions. Function f_{13} and f_{14} are expanded functions and could not be solved. Functions f_{15}–f_{25} are hybrid composition functions based on basic functions. In particular, comparing functions f_{21} and f_{23} that have the same error order, we see that the algorithm did not seem affected when discontinuity is introduced. In general, functions f_{15}–f_{25} are designed to be very hard to solve for any algorithm. Except f_{15} in 10 dimensions with low success rate, GATR as well could not locate a global optimum for them under the requirements set by the CEC 2005 guideline.

4.5.3 Comparison with G3AT

With the intention of improving the G3AT method, the SD and SR mechanisms have been developed and implemented within the GATR method. The aim of this section is to study the impact of those new mechanisms within GATR against G3AT by comparing their results.

We first try to determine whether there is any significant difference between the two methods using the Wilcoxon non-parametric test over the 25 benchmark functions of the CEC 2005. Table 4.3 summarizes the results of the test in 10, 30 and 50 dimensions. The signed ranked statistics are reported ($R-$ for GATR and $R+$ for the compared method, here G3AT) along with the indication of the significantly superior method at significance level 0.05 (for this test bed, the Wilcoxon critical value is equal to 89). The highest values of the test

Table 4.2: Solution Qualities for GATR and G3AT with Significant Method in Bold and SRate in Parentheses

	$n = 10$		$n = 30$		$n = 50$	
	GATR	G3AT	GATR	G3AT	GATR	G3AT
f	Error Mean	Error Mean	Error Mean	Error Mean	Error Mean	Error Mean
f_1	6.84e–13 (100%)	6.21e-13 (100%)	1.12e-12 (100%)	2.01e-12 (100%)	6.539e-12 (100%)	9.779e-12 (100%)
f_2	2.54e–12 (100%)	2.23e-12 (100%)	1.45e-09 (100%)	4.32e-06 (100%)	4.676e-08 (100%)	3.844e-03 (96%)
f_3	4.73e–12 (100%)	1.20e-03 (92%)	**2.11e+02**	6.89e+04	**6.790e+02**	1.395e+05
f_4	1.02e+04	**1.54e+03**	1.03e+05	**4.27e+04**	5.066e+05	**1.227e+05**
f_5	2.28e+02	1.38e+02	**2.29e+03**	5.79e+03	**5.473e+03**	1.614e+04
f_6	**3.19e–01** (92%)	1.50e+00 (72%)	**5.91e-01** (96%)	9.57e+01	**2.718e+00** (56%)	4.677e+02
f_7	**9.72e–02** (12%)	2.25e-01	**3.22e-04** (100%)	1.12e-02	**1.102e-03** (100%)	8.689e-03 (60%)
f_8	2.00e+01	2.00e+01	2.00e+01	2.00e+01	**2.000e+01**	2.001e+01
f_9	**3.98e–13** (88%)	2.83e+00	**2.61e-12** (36%)	2.17e+01	**4.975e+00**	7.053e+01
f_{10}	4.63e+01	**1.83e+01**	**5.53e+01**	1.20e+02	**1.830e+02**	3.161e+02
f_{11}	1.12e+01	**7.59e+00**	3.10e+01	2.98e+01	7.572e+01	**5.704e+01**
f_{12}	**9.48e–12** (100%)	3.09e+02 (44%)	3.94e+01	2.06e+03	**3.535e+03**	9.016e+03
f_{13}	**4.92e–01**	7.34e-01	**1.73e+00**	4.66e+00	**3.092e+00**	1.813e+01
f_{14}	4.01e+00	3.94e+00	1.32e+01	1.30e+01	2.257e+01	2.254e+01
f_{15}	**3.79e+01** (8%)	1.48e+02	3.67e+02	3.88e+02	**2.726e+02**	4.470e+02
f_{16}	1.46e+02	1.34e+02	**7.47e+01**	1.83e+02	**8.559e+01**	2.147e+02
f_{17}	2.10e+02	1.89e+02	2.77e+02	3.31e+02	**3.528e+02**	4.219e+02
f_{18}	9.00e+02	8.71e+02	9.00e+02	9.00e+02	9.000e+02	9.000e+02
f_{19}	9.00e+02	**8.84e+02**	9.00e+02	9.00e+02	9.000e+02	**9.000e+02**
f_{20}	9.00e+02	**8.43e+02**	9.00e+02	**9.00e+02**	9.000e+02	9.000e+02
f_{21}	**4.78e+02**	8.86e+02	8.82e+02	**5.70e+02**	7.439e+02	7.446e+02
f_{22}	8.38e+02	8.13e+02	**5.30e+02**	7.92e+02	5.007e+02	5.144e+02
f_{23}	**7.86e+02**	9.99e+02	7.40e+02	6.77e+02	7.529e+02	7.522e+02
f_{24}	2.91e+02	2.48e+02	2.24e+02	2.96e+02	**3.189e+02**	8.712e+02
f_{25}	**4.37e+02**	6.54e+02	**2.22e+02**	2.98e+02	**3.230e+02**	8.259e+02

Table 4.3: Wilcoxon's Test for GATR against G3AT (at level 0.05)

n	GATR ($R-$)	G3AT ($R+$)	Significant Method
10	147	178	–
30	236	89	GATR
50	261	64	GATR

statistics represent the best results. From Table 4.3, we note that in dimension 10, GATR and G3AT are not significantly different. In higher dimensions however, for dimensions 30 and 50, GATR significantly outperforms G3AT, the gap getting bigger as the dimension increases. The introduction of the SD and SR mechanisms thus seems particularly effective in higher dimensions.

Since both G3AT and GATR are under automatic termination, it is possible to empirically compare their results using the framework proposed in CEC 2005 and get a better insight of the performance of GATR on a *function-level* rather than on a *method-level*. We support our findings by the paired Student's t-test (Montgomery and Runger, 2003) using the mean error as well as the error standard deviation (not reported). Table 4.2 reports the results of G3AT and GATR in 10, 30 and 50 dimensions using the same test bed as for the Wilcoxon's test. The results of a significantly superior method at level 0.05 for each function are reported in bold font. The Feval, reported in Table 4.4, indicates that GATR is on average around 1.4 times more expensive in terms of function evaluations in 10 dimensions. In 30 and 50 dimensions, the computational cost in Feval approximately doubles on average. The introduction of SD and SR mechanisms is however not the principal cause of the raise of Feval. It is the increase of frequency of the local searches during the intensification phase, which has a more predominant weight in the total Feval cost of GATR. In 10 dimensions, t-tests indicate that GATR gives significantly better solutions than G3AT in terms of solution quality on 9 functions, while G3AT is significantly better on 5 functions. The gap gets bigger in 30 and 50 dimensions. In 30 dimensions, GATR performs significantly better on 10 functions while G3AT performs better on 3 functions. In 50 dimensions, out of the 25 problems, G3AT achieves significantly better results for only 3 problems, while GATR outperforms G3AT in 14 problems. Those improved results, especially in higher dimensions, demonstrate the efficiency of the SD and SR mechanisms, especially when the problem complexity increases. In addition, it is worth pointing out that the SD and SR mechanisms themselves do not increase the running time of the algorithm. The additional running time in GATR when compared to G3AT comes from the intensification steps. Roughly speaking, the running time is proportional to Fevals in both GATR and G3AT. Experiments carried out using a computer with 3 GHz Intel Core 2 Duo processor and 3 GB of RAM reveals that for function f_1 in 50 dimensions for instance, the measured CPU time was around 37 seconds for G3AT and 95 seconds for GATR.

Table 4.4: Solution Costs for GATR and G3AT

	$n = 10$		$n = 30$		$n = 50$	
	GATR	G3AT	GATR	G3AT	GATR	G3AT
f	Feval Mean	Feval Mean	Feval Mean	Feval Mean	Feval Mean	Feval Mean
f_1	6.24e+03	4.22e+03	3.05e+04	1.41e+04	7.347e+04	2.836e+04
f_2	6.31e+03	4.28e+03	1.41e+05	4.08e+04	5.258e+05	7.841e+04
f_3	1.26e+04	7.87e+03	1.50e+05	3.40e+04	5.535e+05	7.888e+04
f_4	4.63e+03	3.60e+03	1.46e+04	1.16e+04	2.571e+04	2.357e+04
f_5	5.72e+03	3.91e+03	1.99e+04	1.30e+04	3.721e+04	2.562e+04
f_6	1.17e+04	9.05e+03	2.03e+05	4.66e+04	4.437e+05	7.988e+04
f_7	6.21e+03	4.18e+03	3.41e+04	1.44e+04	4.537e+04	2.657e+04
f_8	4.01e+03	3.52e+03	1.30e+04	1.16e+04	2.245e+04	2.346e+04
f_9	5.41e+03	4.14e+03	1.57e+04	1.19e+04	3.066e+04	2.365e+04
f_{10}	5.61e+03	4.16e+03	1.79e+04	1.21e+04	3.135e+04	2.402e+04
f_{11}	4.51e+03	3.55e+03	1.47e+04	1.16e+04	2.634e+04	2.345e+04
f_{12}	6.39e+03	4.30e+03	3.16e+04	1.39e+04	3.121e+04	2.367e+04
f_{13}	6.01e+03	4.28e+03	1.67e+05	4.66e+04	1.686e+05	7.910e+04
f_{14}	6.13e+03	4.67e+03	3.89e+04	1.56e+04	8.994e+04	2.927e+04
f_{15}	5.12e+03	3.85e+03	1.60e+04	1.21e+04	2.842e+04	2.440e+04
f_{16}	5.34e+03	3.87e+03	1.89e+04	1.24e+04	3.206e+04	2.472e+04
f_{17}	5.02e+03	3.64e+03	1.66e+04	1.18e+04	2.916e+04	2.379e+04
f_{18}	6.12e+03	4.10e+03	2.25e+04	1.22e+04	4.674e+04	2.492e+04
f_{19}	6.25e+03	4.24e+03	2.41e+04	1.32e+04	5.067e+04	2.511e+04
f_{20}	6.26e+03	4.23e+03	2.24e+04	1.22e+04	4.854e+04	2.578e+04
f_{21}	6.94e+03	4.10e+03	2.16e+04	1.45e+04	4.417e+04	2.527e+04
f_{22}	5.15e+03	3.77e+03	1.99e+04	1.22e+04	5.154e+04	2.847e+04
f_{23}	5.24e+03	3.72e+03	2.00e+04	1.24e+04	4.041e+04	2.497e+04
f_{24}	5.27e+03	4.65e+03	1.99e+04	1.25e+04	3.499e+04	2.410e+04
f_{25}	4.83e+03	3.67e+03	1.80e+04	1.23e+04	3.195e+04	2.415e+04

Table 4.5: Wilcoxon's Test for GATR against RCMA (at level 0.05)

n	GATR (R–)	RCMA (R+)	Significant Method
10	131	194	–
30	162	163	–

Table 4.6: Wilcoxon's Test for GATR against L-CMA-ES (at level 0.05)

n	GATR (R–)	L-CMA-ES (R+)	Significant Method
10	154	171	–
30	191	134	–
50	199	126	–

4.5.4 Comparison with a Real-Coded Memetic Algorithm

Performance of GATR is now compared against a Real-Coded Memetic Algorithm (RCMA) introduced in (Lozano et al., 2005). As Memetic Algorithms (MA) are GAs combined with a local search (LS) process to refine individuals (Moscato, 1999), RCMA is a Real-Coded GA combined with LS techniques. "Real-Coded" means that the structure of an individual is based on the real number representation (in opposition with the binary coding for example), as it is the case for GATR. This representation seems particularly natural when dealing with variables in a continuous domain. In (Lozano et al., 2005), the authors propose an RCMA that uses an adaptive LS process with a high diversity global exploration. The LS process depends on the individual fitness, which is used to compute a probability to decide whether LS is applied or not and also to determine the LS intensity.

Numerical experiments described in (Lozano et al., 2005) follow the guideline of CEC 2005 (consequently it should be reminded that the required optimal number of function evaluations is defined under some specific termination conditions, i.e., when the maximum number of Feval is reached or when the optimal accuracy is obtained). Results of the Wilcoxon's test in 10 and 30 dimensions are presented in Table 4.5 (RCMA was not tested for 50 dimensions in (Lozano et al., 2005)). It reveals that the two methods are not significantly different in any dimension, although RCMA seems to have a slight advantage in lower dimensions. Let us note however that in 10 dimensions, the precision obtained by RCMA was mostly achieved after 10^5 function evaluations, while GATR decided to stop before 10^4 function evaluations. In 30 dimensions, similar performance was obtained after around 10 times less function evaluations for GATR, thus showing the effectiveness of the automatic termination of GATR.

4.5.5 Comparison with CMA-ES

In this subsection, GATR is compared against the Evolution Strategy with Covariance Matrix Adaptation (CMA-ES) method (Hansen and Kern, 2004; Hansen, 2006), which is a

state-of-the-art method recommended by experts for adaptive mutation (Lobo et al., 2007). CMA-ES has been designed to improve the local search performance of ES (Hansen and Ostermeier, 1996). An important property of CMA-ES is its invariance under linear transformations of the search space. The CMA-ES version considered for our comparisons also implements the so-called rank-μ-update, abbreviated as L-CMA-ES (Hansen et al., 2005a) which reduces significantly the needed number of generations to reach a certain function value (Hansen et al., 2003).

Results of the Wilcoxon's statistical test are shown in Table 4.6. In 10, 30 and 50 dimensions, the test does not reveal any statistically significant difference at level 0.05. Nevertheless, we may notice that L-CMA-ES shows slightly higher quality solution in 10 dimensions, but the situation is opposite in 30 and 50 dimensions. Thus, we may conclude that the SR and SD mechanisms seem to enhance the performance of GATR particularly in higher dimensions.

4.5.6 Comparison with State-of-the-Art GA

In this section, GATR is compared against a recent GA that is equipped with a memory and designed in such a way that positions that have already been searched are never revisited. This version of GA is named Non-Revisiting Genetic Algorithm with Parameter-less Adaptive Mutation (NrGA) (Yuen and Chow, 2009) and makes use of a binary space partitioning (BSP) tree which is dynamically constructed and designed to reflect the evolution history of the search by remembering the positions already explored and avoid the reevaluation of the fitness of those positions. The BSP search history is also employed to guide the search towards unvisited positions through a new adaptive mutation mechanism (Yuen and Chow, 2009).

In order to compare GATR with NrGA, we use the numerical results reported in (Yuen and Chow, 2009) for NrGA and the paired Student's t-test. The authors of the NrGA method (Yuen and Chow, 2009) tested the performance of their algorithm by using a set of 19 well-known benchmark functions. Among those 19 functions, five are taken from the CEC 2005 contest. They were however slightly modified by removing the shift of the positions of global optima. For this reason, although the difference is minor, the numerical results reported here for GATR might be slightly different from those reported elsewhere in this chapter.

The functions used for the comparison are the Rotated high conditioned elliptic function (f_3), the Rotated Griewanks function (f_7), the Rotated Rastrigins function (f_9), the Rotated Weierstrasss function (f_{11}) and the Hybrid Composition function (f_{15}) (Suganthan et al., 2005). Simulation settings for G3AT have been slightly adjusted in order to correspond with NrgA's and allow a fair competition. In NrGA, the search has been set to stop after

Table 4.7: Comparison of GATR and NrGA on the Best Fitness Values Found and Feval in 10 and 30 Dimensions: f_3,f_7 and f_9

Method		f_3		f_7		f_9	
		$n = 10$	$n = 30$	$n = 10$	$n = 30$	$n = 10$	$n = 30$
NrGA	mean	2.56e+06	1.15e+08	0.00e+00	0.00e+00	3.98e+00	2.89e+01
	std. dev.	1.50e+06	5.51e+07	0.00e+00	0.00e+00	6.49e+00	1.36e+01
	Feval	40100	40100	40100	40100	40100	40100
GATR	mean	2.23e-12	2.31e+03	9.72e-02	2.88e-04	1.59e-01	1.89e+00
	std. dev.	4.13e-12	4.90e+02	1.01e-01	5.63e-04	4.70e-01	1.75e+00
	Feval	12620.6	39448.5	6208.6	34123.7	5410.1	15657.3
Significant Method (at level 0.05)		GATR	GATR	NrGA	NrGA	GATR	GATR

Table 4.8: Comparison of GATR and NrGA on the Best Fitness Values Found and Feval in 10 and 30 Dimensions: f_{11} and f_{15}

Method		f_{11}		f_{15}	
		$n = 10$	$n = 30$	$n = 10$	$n = 30$
NrGA	mean	9.00e-02	5.40e-01	3.83e+03	4.41e+03
	std. dev.	8.00e-02	4.10e-01	6.34e+02	2.79e+02
	Feval	40100	40100	40100	40100
GATR	mean	1.07e+01	4.25e+01	3.79e+01	4.09e+02
	std. dev.	1.57e+00	3.09e+00	3.35e+01	1.73e+01
	Feval	4513.6	14725.7	5116	15959.2
Significant Method (at level 0.05)		NrGA	NrGA	GATR	GATR

exactly 40,100 function evaluations in 10 and 30 dimensions. GATR stopped according to its own automatic termination criteria. Except for function f_3 in 30 dimensions, the Fevals for all functions in 10 and 30 dimensions were less than 40,100 for GATR. Function f_3 in 30 dimensions required more Fevals and therefore has been artificially stopped when Feval reached 40,100.

The results are reported in Tables 4.7 and 4.8, where NrGA's data for those five common benchmark functions in 10 and 30 dimensions are taken from (Yuen and Chow, 2009). It is worthwhile to note that, except for function f_3 in 30 dimensions, GATR stopped automatically with notably less Fevals than NrGA. Comparisons based on 100 independent runs for each test function indicate that GATR performs quite well, compared to NrGA. In particular, it significantly outperformed NrGA on 3 out of 5 functions, namely functions f_3, f_9 and f_{15}.

Table 4.9: Wilcoxon's Test for GATR against DEahcSPX (at level 0.05)

n	GATR (R–)	DEahcSPX (R+)	Significant Method
10	95	115	–
30	109	101	–
50	127	83	–

Table 4.10: Wilcoxon's Test for GATR against G-CMA-ES (at level 0.05)

n	GATR (R–)	G-CMA-ES (R+)	Significant Method
10	61	264	G-CMA-ES
30	131	194	–
50	227	98	GATR

4.5.7 Comparison with State-of-the-Art MA

Here we confront GATR with one of the current best MA for continuous optimization: the DEahcSPX method (Noman and Iba, 2008). It combines differential evolution (DE) with a crossover-based local search (XLS) that adaptively determines the length of the LS using a hill-climbing heuristic and feedback from the search. The crossover operator in DEahcSPX is based on the simplex multi-parent crossover, described in (Tsutsui et al., 1999). According to the authors, DEahcSPX is superior or at least comparable to other well-known MAs.

The DE algorithm has been proposed by Storn and Price (Storn and Price, 1997). It is one of the most recent EAs and is known to be a relatively simple but powerful population-based stochastic search technique. DE uses a limited number of parameters but they may greatly influence the performance of the algorithm. In particular, we note the population size, the scaling factor and the crossover rate.

Numerical results of DEahcSPX for the CEC 2005 test suite functions f_6 to f_{25} are directly available in the literature (Noman and Iba, 2008). The performance comparison with GATR was carried out by means of the Wilcoxon's test. The results are reported in Table 4.9. We can see that in all dimensions, GATR achieves similar performance to DEahcSPX, the differences being not statistically significant. We can however point out a slight tendency of GATR to obtain better solution quality compared to DEahcSPX as the dimension increases. Specifically, in 10 dimensions, DEahcSPX is slightly superior, but it is outperformed by GATR in 50 dimensions.

4.5.8 Comparison with the Winner of the CEC 2005 Contest

G-CMA-ES (Hansen et al., 2005b) is the winner of the CEC 2005 competition (Langdon and Poli, 2007) and recognized as a very powerful algorithm for continuous optimization problems (Lunacek and Whitley, 2006; Langdon and Poli, 2007). G-CMA-ES is a restart CMA-ES that stops whenever some prespecified stopping conditions are met and repeats the search with the population size being doubled on each restart. Compared to the pure CMA-ES, G-CMA-ES is significantly superior in particular on multimodal functions.

The performance comparison was carried out by means of the Wilcoxon's test. The results in 10, 30 and 50 dimensions are reported in Table 4.10. We observe that G-CMA-ES clearly outperforms GATR in 10 dimensions. In 30 dimensions, G-CMA-ES still shows

better results but the difference is not statistically significant. In 50 dimensions, it is now the turn of GATR to exhibit significantly superior performance.

These results allow us to conclude again that the SD and SR mechanisms improve the search process of GATR particularly in higher dimensions. Also, the use of the automatic termination did not have negative effect on the quality of the solutions achieved by GATR, even outperforming G-CMA-ES in higher dimensions.

4.6 Conclusion

In this chapter, we have introduced a new EA, called GATR, that can terminate the search without conventional predefined criteria such as the maximum number of generations or function evaluations. It is based on the GM and implements new strategies; the SD and SR mechanisms. The SD and SR mechanisms provide an innovative way of handling problems by creating a two-dimensional environment in which several GMs evolve irrespective of the dimension of the original problem. In this environment, each GM goes through a series of rotations, which allow the search to avoid premature convergence and termination.

Numerical experiments were carried out on a set of 25 test functions presented at the CEC 2005 in 10, 30 and 50 dimensions. GATR was compared against G3AT, RCMA, a version of CMA-ES, the state-of-the-art NrGA and DEahcSPX as well as the CEC 2005 competition winner G-CMA-ES. The results indicate that GATR is competitive with state-of-the-art EAs. Especially in higher dimensions, the performance of GATR is comparable or superior to many of the well-known EAs. The competitive overall performance of GATR demonstrates that the quality of the solutions obtained did not suffer from premature termination. The proposed automatic termination thus enabled us to stop the search without undue objective function evaluations and without negative impact on the quality of the solution obtained.

Chapter 5

Global Optimization via Differential Evolution with Automatic Termination

EAs provide a very powerful tool for solving optimization problems. However, there is a lack of studies that tackle the question of the termination criteria. In this chapter, we propose to combine the DE method with our conceived GM, SD and SR mechanisms, in order to show that DE can also benefit from an automatic termination criterion without resort to predefined conditions. We name this algorithm Differential Evolution with Automatic Termination (DEAT). Numerical experiments using a test bed of widely used benchmark functions demonstrate the effectiveness of the proposed method.

5.1 Introduction

In Chapters 3 and 4, we have presented the G3AT and GATR methods, respectively. They are GAs that implement the GM and novel directing strategies. In particular, GATR addresses a major drawback of the GM by implementing the Space Decomposition (SD) and the Space Rotation (SR) mechanisms. In this Chapter, we show that the GM, SD and SR mechanisms can also be adopted effectively by other EAs. To do so, we combine DE with the GM, SD and SR mechanisms. Our developed mechanisms allow the search to accelerate its convergence and to determine automatically an adequate termination instant without prior knowledge about the problem. The GM is a matrix that represents subranges of the possible values of each variable. It gives an indication on the distributions of the variables over the search range. This information is used to provide the search with new diverse solutions and to let the search know how far the exploration process has been performed. SD and SR work in combination in order to create a two-dimensional environment for the GM irrespective of the original dimension of the problem to be solved. The role of SD is to manipulate

the original space in order to create two-dimensional spaces. SR then performs a series of rotations on the generated two-dimensional spaces, which allows GM to be more accurate. In that environment, it is possible to alleviate some drawbacks inherent to the construction of the GM and also to improve the performance of the algorithm in higher dimensions.

The performance of DEAT is evaluated through numerical experiments on a set of 15 test problems, in 10, 50 and 100 dimensions, taken from the CEC 2005 real-parameter optimization contest (Suganthan et al., 2005), and compared against the classical version of DE as well as the DE algorithm with ensemble of parameters and mutation strategies (EPSDE) (Mallipeddi et al., 2011).

The rest of this chapter is organized as follows. In Section 5.2, the GM, SD and SR operators are described before stating the formal algorithm of DEAT. Section 5.3 contains the results of numerical experiments of DEAT carried out for test problems of 10, 50 and 100 dimensions and of the comparisons with the classical DE and EPSDE. A summary with conclusions is provided in Section 5.4.

5.2 DEAT Mechanisms

DEAT belongs to the DE/rand/1/bin class, which is the variant of DE most commonly used in practice (Qin and Suganthan, 2005). In this case, the mutation operator deals with a randomly selected parameter vector and one weighted difference vector, coupled with the binomial crossover operator. In the rest of this section, we briefly review our developed mechanisms implemented in DETR.

5.2.1 Gene Matrix and Termination

The range of each component of the parameter vector is divided into several subranges in order to check the diversity of the values of the variable. As for GATR, the GM is also a two-dimensional matrix initialized as a $2 \times m$ zero matrix, where m is the number of subranges. Thus, GM deals solely with two-dimensional subspaces, although the problem being optimized can be of any dimension $n \geq 2$.

Each entry of the i-th row of GM refers to a subrange of the i-th variable. During the search, whenever parameter vectors are generated, the values of their variables are checked and the corresponding subranges are detected. The visited subranges are then granted with a non-null value in the GM. With a full GM, i.e., with no zero entry, the search considers that an advanced exploration process has been achieved and can be stopped.

The mutagenesis operator is described in Section 2.4.

Table 5.1: DEAT Parameter Setting

Parameter	Definition	Value
F	Scale factor	0.3
π_c	Crossover rate	0.5
μ	Population size	30
m	No. of GM columns	100
μ_w	No. of vectors used by mutagenesis	4
NR	Number of space rotations	3
α	Space rotation angle	45^o
CP	Completion ratio of GM	90%

5.2.2 Space Rotation and Space Decomposition

The SR and SD mechanisms in DEAT have the same implementation as in GATR. They are described in detail in Subsections 4.2.3 and 4.2.4, respectively.

5.2.3 Intensification

Intensification is the process whose purpose is to refine the elite solution obtained at the end of an era. Intensification calls a local search process based on the Kelley's modification (Kelley, 1999) of the Nelder-Mead (NM) method (Nelder and Mead, 1965). As discussed in GATR, the use of systematic intensification at the end of each era is avoided. Indeed, intensification is sparingly called by specific eras since it yields positive effects when called at intermediate stages of the search. The numbers designating the eras that will go through an intensification step are stored in the intensification list (IL).

5.2.4 DEAT Formal Algorithm

The algorithmic parameters with their assigned values are summarized in Table 5.1. The formal description of DEAT is given in Algorithm 5.2.1.

Algorithm 5.2.1. *DEAT Algorithm*

1. ***Initialization.*** *Set values of m, NR, α, μ_w and (l_j, u_j) for $j = 1, \ldots, n$. Set the scale factor F, crossover rate π_c, population size μ and completion ratio CP. Set the Intensification List IL. Set the Combination List $CL := \{x_1, x_2, \ldots, x_n\}$. If the number of elements in CL is odd, add a randomly chosen element from $\{x_1, x_2, \ldots, x_n\}$. Compute x^{elite} by $x_j^{elite} := \frac{u_j + l_j}{2}$ for $j = 1, \ldots, n$.*
2. *Set all variables to be passive. Select x_a and x_b from CL. Update CL by $CL := CL \backslash \{x_a, x_b\}$ and designate x_a and x_b as active variables.*
   2.1. *Generate an initial population P_0 of size μ. Set the values of all passive variables of each individual equal to the corresponding values of x^{elite}, i.e., $x_j^i := x_j^{elite}$ for $j \in \{1, \ldots, n\} \backslash \{a, b\}$ and $i = 1, ..., \mu$.*

2.2. *Initialize Gene Matrices GM_l, $l = 0, ..., NR-1$, as $2 \times m$ zero matrices, where GM_l corresponds to the l-th space rotation.*

3. *For every individual, repeat sequentially Steps 3.1 to 3.4.*
3.1. *Set the considered parameter vector x^i as the target vector.*
3.2. Mutation. *Generate a vector v^i using Equation (1.4.1) in two dimensions, as mentioned in Subsection 5.2.2.*
3.3. Crossover. *Generate a vector u^i using Equation (1.4.2) in two dimensions. Update GM_l, $l = 0, ..., NR-1$.*
3.4. Selection. *Compare vector u^i with vector x^i to generate the offspring $\tilde{x}^i$ using Equation (1.4.3). Update $x^i := \tilde{x}^i$.*

4. Mutagenesis. *Alter the μ_w worst individuals using Procedure 2.4.1 and update GM_l, $l = 0, ..., NR-1$. If all GMs have reached the completion ratio CP, then go to Step 5. Otherwise, go to Step 3.*

5. Intensification. *If the current era is in IL, then go to Step 5.1. Otherwise, go to Step 5.2.*
5.1. *Apply a local search method starting from the best solution obtained so far, and go to Step 5.2.*
5.2. *Let x^{elite} be the best solution obtained. If $CL \neq \emptyset$, go to Step 2. Otherwise, terminate with x^{elite}.*

5.3 Numerical Results

Before discussing the results, we describe the methodology adopted to conduct the numerical study of DEAT.

5.3.1 Methodology

A set of 15 benchmark functions provided by the special session on real-parameter optimization in the IEEE Congress on Evolutionary Computations CEC 2005 (Suganthan et al., 2005) was used to compare the performance of the proposed method DEAT against the classical DE (Storn and Price, 1997) and the EPSDE (Mallipeddi et al., 2011) methods. The original test set is composed of 25 test functions. However, for DEAT, only the first 15 functions (f_1–f_{15}) are considered. They are based on widely used benchmark functions and aim at covering a diverse set of problem properties and difficulties. Detailed description of those functions can be found in (Suganthan et al., 2005). They are all scalable and most of them are non-separable. In this chapter, to judge the success of each run, we use the relative error $(f(x^{best}) - f(x^*))/(1 + |f(x^*)|)$, where $f(x^{best})$ represents the best function value obtained by the algorithm and $f(x^*)$ is the known exact global minimum value. Specifically if this result is smaller than or equal to the accuracy level 10^{-1}, then a run is considered successful. In view of that, we define the success rate as the number of successful runs divided by the total number of runs, here equal to 25.

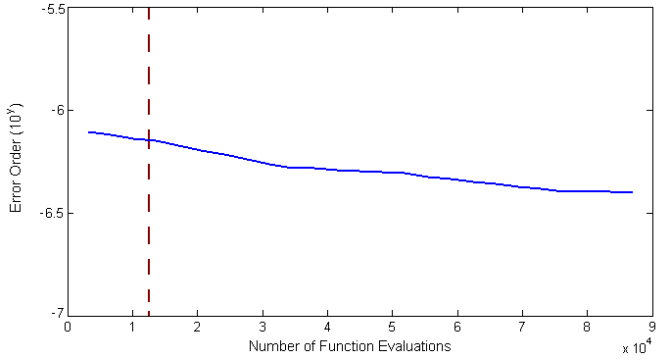


Figure 5.1: Termination instant (vertical dotted line) for function f_2.

Table 5.2: Number of Function Evaluations (Feval) and the Corresponding Success Rates for DEAT, DE and EPSDE with $n = 10$

f	Feval	DEAT	DE	EPSDE
f_1	4.972e+03	100%	100%	100%
f_2	4.574e+03	100%	100%	52%
f_3	8.349e+03	100%	88%	0%
f_4	2.806e+03	0%	0%	0%
f_5	4.442e+03	0%	0%	0%
f_6	7.753e+03	100%	100%	44%
f_7	6.325e+03	100%	100%	100%
f_8	2.400e+03	0%	0%	0%
f_9	4.531e+03	100%	100%	100%
f_{10}	3.920e+03	100%	100%	4%
f_{11}	2.719e+03	16%	20%	4%
f_{12}	6.100e+03	72%	76%	0%
f_{13}	5.838e+03	100%	100%	100%
f_{14}	3.588e+03	100%	100%	100%
f_{15}	3.695e+03	0%	0%	0%

5.3.2 Termination

In order to estimate whether the GMs are able to provide the search with a correct termination point for DE methods as well, the automatic termination has been compared for each function with the same run in the same conditions but with an artificially maintained higher number of generations. For function f_2 for instance, Figure 5.1 reveals that letting the search run after the termination instant does not significantly improve the best solution obtained. In Figure 5.1, the dotted line represents the instant, in the number of function evaluations, at which the search was stopped in DEAT. We can observe that, with almost 9 times more function evaluations, the improvement in terms of error order is not significant (still around 10^{-6}).

Table 5.3: Number of Function Evaluations (Feval) and the Corresponding Success Rates for DEAT, DE and EPSDE with $n = 50$

f	Feval	DEAT	DE	EPSDE
f_1	5.637e+04	100%	100%	100%
f_2	1.768e+05	100%	100%	100%
f_3	1.761e+05	0%	0%	0%
f_4	1.432e+04	0%	0%	0%
f_5	2.627e+04	0%	0%	0%
f_6	1.898e+05	40%	20%	76%
f_7	9.985e+04	100%	100%	100%
f_8	1.361e+04	0%	0%	0%
f_9	1.917e+04	100%	0%	0%
f_{10}	1.790e+04	0%	0%	0%
f_{11}	1.774e+04	0%	0%	0%
f_{12}	2.976e+04	0%	0%	0%
f_{13}	1.890e+05	100%	100%	100%
f_{14}	2.059e+04	100%	100%	100%
f_{15}	2.087e+04	0%	0%	0%

Table 5.4: Number of Function Evaluations (Feval) and the Corresponding Success Rates for DEAT, DE and EPSDE with $n = 100$

f	Feval	DEAT	DE	EPSDE
f_1	7.844e+04	100%	100%	100%
f_2	4.364e+05	100%	24%	100%
f_3	5.805e+05	0%	0%	0%
f_4	3.972e+04	0%	0%	0%
f_5	7.649e+04	0%	0%	0%
f_6	3.206e+05	96%	0%	0%
f_7	3.782e+05	100%	100%	100%
f_8	3.693e+04	0%	0%	0%
f_9	5.812e+04	100%	0%	0%
f_{10}	6.282e+04	0%	0%	0%
f_{11}	3.754e+04	0%	0%	0%
f_{12}	7.096e+04	0%	0%	0%
f_{13}	1.104e+05	100%	0%	0%
f_{14}	4.991e+04	0%	0%	0%
f_{15}	5.716e+04	0%	0%	0%

5.3.3 Comparison with DE

To evaluate the performance of DEAT against DE, we first let DEAT run until it terminates automatically and then compute its success rates for each function. Afterward, by using the same amount of objective function evaluations for each function as the termination condition, the success rates obtained by the compared method are determined. Results are reported in Tables 5.2, 5.3 and 5.4, in 10, 50 and 100 dimensions, respectively. For each test function, the numbers of function evaluations needed by DEAT and DE are shown as well as the success rate for each function.

In 10 dimensions, we can observe via Table 5.2 that both DEAT and DE could solve exactly the same functions, 11 out of 15. Only functions f_4, f_5, f_8 and f_{15} could not be solved under the specified accuracy level. Success rates are around the same order. In 50 dimensions, DEAT could reach or be close enough to a global optimum on 7 functions, while DE could find it on 6 functions out of 15, as reported in Table 5.3. In particular, function f_9 could be solved at each attempt by DEAT but never by DE. We note that all the other functions that DE could handle were also so by DEAT. Moreover, function f_6 has a success rate that is double for DEAT compared to DE. In 100 dimensions, as shown in Table 5.4, the gap between the two methods gets bigger. DEAT could work out a solution under the accuracy level on 6 functions, but DE could only do it for 3 functions out of the 15 functions. Additionally, the success rate for function f_2 is 4 times lower for DE, while DEAT could find the optimal solution at each run.

5.3.4 Comparison with EPSDE

In this section, DEAT is compared against a recent state-of-the-art algorithm called EPSDE that uses an ensemble of mutation strategies and parameter values with DE (Mallipeddi et al., 2011). This method makes use of a set of mutation strategies with different parameter settings and thus avoids unique parameter settings as in the classical DE. Since different strategies may become more effective during the evolution process than others depending on the problem, EPSDE keeps a pool of mutation strategies and parameters that have diverse characteristics in an attempt to adapt to different stage of the evolution process and to the nature of a particular problem. In (Mallipeddi et al., 2011), EPSDE is favorably compared to several well-known state-of-the-art DE methods.

Results are stated in Tables 5.2, 5.3 and 5.4, in 10, 50 and 100 dimensions, respectively. In 10 dimensions, we can observe that DEAT could solve more functions (functions f_4 anf f_{12}) and more efficiently (functions f_2, f_6, f_{10} and f_{11}) than EPSDE. In 50 dimensions, DEAT performed slightly better, since it could solve one more function (function f_9), although the success rate for function f_6 is higher for EPSDE. Success rates in 100 dimensions show, however, that DEAT clearly outperformed EPSDE by successfully solving 6 functions against

3 for EPSDE.

Those findings from the comparison of DEAT against DE and EPSDE indicate that SD and SR have beneficial effects on the performance of DE for high dimensional problems. Coupled with the GM, those mechanisms could determine a termination instant without deteriorating the performance of the algorithm.

5.4 Conclusion

In this chapter, we have proposed to combine DE with the GM, SR and SD mechanisms in order to equip DE with an automatic termination strategy that does not require any prescribed criterion such as the maximum number of generations or function evaluations. The search aims at exploring widely the whole search space, which is sequentially decomposed into two-dimensional subspaces that undergo a series of rotations, thereby avoiding premature convergence and termination of the search.

Numerical experiments conducted on a set of 15 test functions presented at the CEC 2005 in 10, 50 and 100 dimensions reveal that the results obtained by DEAT are equal or superior to those of the classical DE and the recent EPSDE, without undue objective function evaluations and without negative impact on the quality of the solution obtained.

Chapter 6

Automatically Terminated Particle Swarm Optimization with Principal Component Analysis

In this chapter, a hybrid PSO that features an automatic termination and better search efficiency than classical PSO is presented. The proposed method is combined with the GM to provide the search with a self-check in order to determine a proper termination instant. Its convergence speed and reliability are also increased by the implementation of the Principal Component Analysis technique and the hybridization with a local search method. The proposed algorithm is denominated as Automatically Terminated Particle Swarm Optimization with Principal Component Analysis (AT-PSO-PCA). The computational experiments demonstrate the effectiveness of the automatic termination criteria and show that AT-PSO-PCA enhances the convergence speed, accuracy and reliability of the PSO paradigm. Furthermore, comparisons with state-of-the-art evolutionary algorithms yield competitive results even under the automatically detected termination instant.

6.1 Introduction

Improving the performance of the GM has been performed in Chapter 4 by developing the SD and SR mechanisms. In this chapter, we show that implementing other techniques and taking advantage of the inner structure of the host EC method can also yield improved performance. Here, the PSO paradigm, as an example of SI method in considered. To materialize the automatic termination, we equip PSO with the GM, described in Section 2.4. The GM is a matrix that represents subranges of the possible values of each variable. It gives an indication on the distributions of the variables over the search range. This information is used to provide the search with new diverse solutions and let the search know how far the exploration process has been performed. Along with a self-check to determine a proper termination instant, the

proposed method also attempts to improve both convergence speed and reliability at the same time. To do so, we utilize the Principal Component Analysis (PCA) technique. At each iteration, PCA operates on each particle's *pbest* (that comprises a set of possibly correlated variables) in order to extract the eigenvectors that will be used to transform the original search space into an alternative space that possesses a new coordinate system wherein the swarm can navigate through uncorrelated dimensions. Finally, to further accelerate the search process, a local search method is used to improve the *gbest* candidate solution obtained upon GM termination. We call the proposed method Automatically Terminated Particle Swarm Optimization with Principal Component Analysis, abbreviated as AT-PSO-PCA. The performance of AT-PSO-PCA is evaluated through numerical experiments on a set of widely used test problems and compared against the classical PSO as well as a number of existing methods such as the Fully Informed Particle Swarm optimizer (FIPS) (Mendes et al., 2004), the state-of-the-art Comprehensive Learning Strategy PSO (CLPSO) (Liang et al., 2006), and the two state-of-the-art EAs called the Differential Evolution Algorithm with Ensemble of Parameters and Mutation Strategies (EPSDE) (Mallipeddi et al., 2011) and the Global and Local Real-Coded Genetic Algorithm based on Parent-Centric Crossover Operators (GL-25) (García-Martinez et al., 2008).

AT-PSO-PCA seeks an optimal or near-optimal solution of the nonconvex optimization problem defined in Section 1.1.

The rest of this chapter is organized as follows. In Section 6.2, the proposed techniques that compose AT-PSO-PCA are presented. Section 6.3 provides the experiments and comparative study conducted and discusses the results. The individual effect of PCA on the performance of PSO is analyzed in Section 6.4. The concluding remarks are given in Section 6.5.

6.2 AT-PSO-PCA Mechanisms

In AT-PSO-PCA, the GM and mutagenesis operator are implemented as in G3AT. Their description is provided in Section 2.4. The rest of this section reviews the PCA technique and describes the AT-PSO-PCA algorithm in detail.

6.2.1 Principal Component Analysis

PCA (Jolliffe, 1986) is a mathematical technique widely used in various fields such as neuroscience, pattern recognition and image compression. It employs an orthogonal linear transformation to extract a set of values of uncorrelated variables from a set of possibly correlated variables. The created set of variables is called the "principal components" and their number is less than or equal to the number of original variables. Applications take advantage of

PCA to reduce complex or confusing data sets into lower dimensions without much loss of information to simplify the identification of patterns in data or reveal their similarities and differences.

Let X be an $n \times \mu$ matrix with zero empirical mean that contains a data set of μ objects with n variables. We assume $n < \mu$. In our proposed PSO, X represents a swarm consisting of μ particles in R^n. More specifically, each column of X is the position of a particle. The singular value decomposition of X is expressed as

$$X = W\Sigma V^T, \tag{6.2.1}$$

where T denotes transpose, W is the $n \times n$ matrix of eigenvectors of XX^T, V is the $\mu \times \mu$ matrix of eigenvectors of X^TX,

$$\Sigma = \begin{pmatrix} \sigma_1 & & \\ & \ddots & 0 \\ & & \sigma_n \end{pmatrix}$$

is an $n \times \mu$ rectangular diagonal matrix with nonnegative diagonal entries $\sigma_1 \geq \sigma_2 \geq \ldots \geq \sigma_n \geq 0$. By defining the $n \times L$ matrix W_L as the matrix that consists of the first L ($\leq n$) columns of W, the operation

$$Y = W_L^T X \tag{6.2.2}$$

will project X onto the reduced subspace defined by W_L to form the $L \times \mu$ matrix Y. The reverse operation is performed with

$$X = W_L Y. \tag{6.2.3}$$

In the Euclidean space, PCA can be seen as an operator that rotates the original axes to new positions (called the principal axes) such that, among other properties, the covariance among each pair of the principal axes is zero.

6.2.2 AT-PSO-PCA Formal Algorithm

Our proposed method combines PSO with three distinct components (GM, PCA and a local search) to pursue the following three objectives. The first objective is to equip PSO with an intelligent automatic termination criterion. The second objective is to enhance the convergence speed of the search. At the same time, the last and third objective is to improve the reliability of the algorithm. To fulfill them, the proposed method is equipped with the Simple GM described in Section 2.4. When the GM indicates that a sufficient exploration has been performed (i.e., when all the entries of GM are non-null), the search is terminated. The GM also participates in fulfilling the second objective by providing some individuals with the ability to "jump" towards apparently unexplored area of the search space by using

mutagenesis. This mechanism is also a guarantee that the search will eventually stop. To further enhance the convergence speed, the final intensification process calls a local search method based on the Kelley's modification (Kelley, 1999) of the Nelder-Mead (NM) method (Nelder and Mead, 1965). The local search is initiated from the *gbest* obtained at the end of the search. AT-PSO-PCA thus behaves like a "Memetic Algorithm" (Moscato, 1999; Le et al., 2009) in order to achieve faster convergence (Ong et al., 2006; Kramer, 2010). For the third objective, the reliability of the algorithm is improved by creating a *gbest* of high quality after the automatic termination for undertaking the final intensification process. This role is carried out by the PCA operation described in Subsection 6.2.1 which operates during the search by transforming the coordinates of the search space into a different coordinate system of dimension L at every iteration. In AT-PSO-PCA, this is achieved by extracting the principal components of the set composed by all the *pbests*. Then, the new set of coordinates is created from an orthogonal transformation that uses the obtained principal components. Afterwards, the swarm navigates through the "distorted dimensions" and new positions are computed. Finally, the obtained positions are transformed back into the original space and form a candidate swarm S. Each particle of the swarm S is given a chance to undertake a random p-point ($p < n$) crossover operation of probability π_c with *gbest*. If the function value of the resulting particle is better than or equal to the function value of the *pbest* of the corresponding particle in the original space, then the obtained particle becomes the new *pbest*. The AT-PSO-PCA pseudocode is described in Algorithm 6.2.1.

Algorithm 6.2.1. *AT-PSO-PCA Pseudocode*

1. ***Initialization.*** *For each particle p^i in the swarm, $i = 1, \ldots, \mu$, do the following:*
   - ***1.1.*** *Initialize x^i and v^i randomly.*
   - ***1.2.*** *Evaluate $f(x^i)$.*
   - ***1.3.*** *Initialize* pbest^i *associated to p^i.*
   - ***1.4.*** *Initialize GM as the $n \times m$ zero matrix.*
2. ***Main loop.*** *Repeat Steps 2.1 to 2.7 until GM reaches the completion ratio CP.*
   - ***2.1.*** *Locate* gbest.
   - ***2.2.*** *For each particle p^i, set* $\text{pbest}^i := x^i$ *if* $f(x^i) \leq f(\text{pbest}^i)$.
   - ***2.3.*** *For each particle p^i, update x^i and v^i by applying Equations (1.5.1) and (1.5.2).*
   - ***2.4. GM.*** *Update GM and perform mutagenesis by applying Procedure 2.4.1 to alter the μ_w ($\leq \mu$) worst particles.*
   - ***2.5. PCA.*** *Apply Equation (6.2.1) with the set of pbests with zero empirical mean and extract the matrix W_L. Apply Equation (6.2.2) with the swarm X to form the matrix of particles Y. Update the position of each particle in Y with Equation (1.5.1). Apply Equation (6.2.3) to transform Y back into the original space and form the candidate swarm S.*

2.6. *Associate a random number from* $(0, 1)$ *with each particle* s^i *of* S*. If the associated number is less than* π_c*, perform a p-point crossover operation with* s^i *and* gbest *to alter* s^i*.*
2.7. *Evaluate* $f(x^i)$ *and* $f(s^i)$*. For each particle* s^i *in* S*, set* $\text{pbest}^i := s^i$ *if* $f(s^i) \leq f(\text{pbest}^i)$*.*

3. Intensification. *Apply a local search method starting from* gbest*.*

6.3 Numerical Experiments

To validate the performance of AT-PSO-PCA, we have selected a benchmark composed of 11 test functions that are taken from (Yao et al., 1999) and listed in Table 6.1. They provide a good balance of complexity and modality, and have been widely used by many researchers (Angeline, 1998a; Shi and Eberhart, 1998; Lovbjerg and Krink, 2002; Esquivel and Coello, 2003; Higashi and Iba, 2003; Richards and Ventura, 2003). Functions f_1–f_6 are unimodal functions and functions f_7–f_{11} are multimodal. Furthermore, existing state-of-the-art PSO and EAs, listed below, were selected to provide a comparison analysis with AT-PSO-PCA:

- SPSO (Kennedy and Eberhart, 1995) (PSO),
- FIPS (Mendes et al., 2004) (PSO),
- CLPSO (Liang et al., 2006) (PSO),
- EPSDE (Mallipeddi et al., 2011) (DE),
- GL-25 (García-Martinez et al., 2008) (GA).

The first PSO is the standard PSO (Kennedy and Eberhart, 1995) and is here abbreviated as SPSO. FIPS (Mendes et al., 2004) is a PSO that uses all the particles in the swarm to update the velocity vector. It is a so-called "fully informed" PSO. To improve its success rate, Mendes et al. recommend the use of a URing topology structure with weighted FIPS based on the goodness algorithm (Mendes et al., 2004). CLPSO (Liang et al., 2006) uses a "comprehensive learning strategy" that was developed to improve the performance of PSO on multimodal functions. EPSDE is a recent DE that uses an ensemble of mutation strategies and parameter values (Mallipeddi et al., 2011). This method makes use of a set of mutation strategies with different parameter settings and thus avoids unique parameter settings as in the classical DE. Since different strategies may become more effective during the evolution process than others depending on the problem, EPSDE keeps a pool of mutation strategies and parameters that have diverse characteristics in an attempt to adapt to different stages of the evolution process and to the nature of a particular problem. GL-25 (García-Martinez et al., 2008) is a GA with improved crossover operators with a male and female

Table 6.1: Test Functions

f	Function Name	n	Bounds	Global Min	Error Tol
$f_1(x) = \sum_{i=1}^{n} x_i^2$	Sphere Model	30	$[-100,100]^n$	0	0.01
$f_2(x) = \sum_{i=1}^{n} \lvert x_i \rvert + \Pi_{i=1}^{n} \lvert x_i \rvert$	Schwefel's P2.22	30	$[-10,10]^n$	0	0.01
$f_3(x) = \sum_{i=1}^{n} (\sum_{j=1}^{i} x_j)^2$	Schwefel's P1.2	30	$[-100,100]^n$	0	100
$f_4(x) = \sum_{i=1}^{n-1} \left[100 \left(x_i^2 - x_{i+1}\right)^2 + (x_i - 1)^2\right]$	Generalized Rosenbrock	30	$[-10,10]^n$	0	100
$f_5(x) = \sum_{i=1}^{n} (\lfloor x_i + 0.5 \rfloor)^2$	Step	30	$[-100,100]^n$	0	0
$f_6(x) = \sum_{i=1}^{n} i x_i^4 + random[0,1)$	Quartic with Noise	30	$[-1.28,1.28]^n$	0	0.01
$f_7(x) = -\sum_{i=1}^{n} \left(x_i \sin \sqrt{\lvert x_i \rvert}\right)$	Generalized Schwefel's P2.26	30	$[-500,500]^n$	-12569	-10000
$f_8(x) = 10n + \sum_{i=1}^{n} \left(x_i^2 - 10\cos\left(2\pi x_i\right)\right)$	Generalized Rastrigin	30	$[-5.12,5.12]^n$	0	50
$f_9(x) = \frac{1}{4000} \sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n} \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$	Generalized Griewank	30	$[-600,600]^n$	0	0.01
$f_{10}(x) = 20 + e - 20e^{-\frac{1}{5}\sqrt{\frac{1}{n}\sum_{i=1}^{n} x_i^2}} - e^{\frac{1}{n}\sum_{i=1}^{n} \cos(2\pi x_i)}$	Ackley	30	$[-32,32]^n$	0	0.01
$f_{11}(x) = \sum_{i=1}^{n-1} (z_1 - 1)^2 (1 + 10sin^2(\pi z_{i+1})) + \pi/30(10sin^2(\pi z_1) + (z_n - 1)^2) + \sum_{i=1}^{n} u(x_i, 10, 100, 4)$	Generalized Penalized	30	$[-50,50]^n$	0	0.01

where $z = 1 + 0.25(x_i + 1)$,

$$u(x_i, a, k, m) = \begin{cases} k(x_i - a)^m, & x_i > a; \\ 0, & -a \leq x_i \leq a; \\ k(-x_i - a)^m, & x_i < a. \end{cases}$$

Table 6.2: AT-PSO-PCA Parameter Setting

Parameter	Definition	Value
μ	Size of the swarm	40
w	Inertia weight	0.72
c_1	Cognition weight	1.2
c_2	Social weight	1.2
m	No. of GM subranges	500
μ_w	No. of individuals used by mutagenesis	2
CP	Completion ratio of GM	90%
L	Dimension of the reduced subspace	1
π_c	Crossover probability	0.6

differentiation process for each of the parents as well as some new male and female selection mechanisms. The crossover operators create the offspring in the neighborhood of one of the parents (the female parent) while the second parent (the male parent) defines the range of the neighborhood. By adjusting the number of female and male parents that participate in the differentiation process, GL-25 can act as a global search algorithm or as a local search algorithm with more or less reliability and accuracy. Throughout our numerical experiments, the population size is set at 40 for all methods and the adopted parameter settings are those recommended by their respective authors. The AT-PSO-PCA parameters with their assigned values are summarized in Table 6.2.

It should be noted that to conduct a fair comparison and due to the main goal of AT-PSO-PCA, which is to let the search stop automatically, we have adopted in this chapter a particular comparison framework. Indeed, the comparisons with the existing methods are conducted in two stages. In the first stage, of which results are reported in Table 6.3, we compare the best function value, abbreviated as Fmin, obtained by each algorithm for each function upon termination. In this stage, termination for each method took place with the number of function evaluations, referred to as Feval, that was required by AT-PSO-PCA to terminate automatically. It gives an indication on the accuracy and reliability of the solutions obtained by AT-PSO-PCA upon termination and thus, on the effectiveness of the proposed termination mechanism. The second stage allows the compared methods to run longer and show their performance with a predetermined Feval that is considerably bigger than that in the first stage. Namely, in the second stage, Feval is set equal to 2×10^5 for all functions and all methods but AT-PSO-PCA that preserves its automatic termination. Results are reported in Table 6.4. The objective is to detect whether AT-PSO-PCA suffered or not from premature termination when compared to existing algorithms. In both stages, the error tolerance levels specified in Table 6.1 (Error Tol) are used to judge if a run is successful or not. Specifically, a run is considered successful when the fixed error tolerance level is achieved at the end of the search. The success rate, abbreviated as SRate, is defined

as the number of successful runs divided by the total number of independent runs, here equal to 25 for all methods. Tables 6.3 and 6.4 report the mean Fmin and standard deviation (SD), as well as the SRate obtained for each test function by each algorithm.

6.3.1 First Stage - Accuracy and Reliability

Table 6.3 lists the performance on the solution accuracy in terms of the mean Fmin, SD and SRate of each compared method. It can be observed that AT-PSO-PCA generally obtains quite accurate results upon (automatic) termination. Also, it could achieve the global optimum with 100% SRate on 10 out of 11 functions and with a non-null SRate for the remaining function f_7. By computing the mean SRate obtained over all test functions, it appears that AT-PSO-PCA has the highest overall SRate (94%), followed by EPSDE (89%) and CLPSO (82%). We note that AT-PSO-PCA performs relatively well on both unimodal functions f_1–f_6 and multimodal functions f_7–f_{11}. Actually, AT-PSO-PCA offers the best overall performance among all algorithms and only EPSDE, CLPSO and FIPS are superior when applied to the multimodal function f_7. It should also be noted that there is no problem that could not be solved at all by AT-PSO-PCA.

Those results show that the quality of the solutions obtained by AT-PSO-PCA after its automatic termination is very competitive. Actually, it achieves some of the best results in terms of accuracy and reliability on most test functions.

6.3.2 Second Stage - Premature Termination

The results in this stage, as displayed in Table 6.4, show that in terms of accuracy, some methods get more accurate solutions for some problems than AT-PSO-PCA (especially for unimodal functions). However, we may claim that, in spite of the fact that AT-PSO-PCA uses on average 60% less Feval than the other methods, it is still generally competitive. Furthermore, even though a considerably higher Feval is allowed to the other algorithms, AT-PSO-PCA with its relatively small Feval still has the best overall SRate (94%). Indeed, although the overall SRate of some of the rival methods (FIPS and GL-25) increased significantly, the second highest overall SRate is once again obtained by EPSDE with an overall SRate that is now of 91%. This demonstrates that the use of the automatic termination did not have negative effect on the quality of the solutions achieved by AT-PSO-PCA.

6.4 Impact of PCA

The impact of the GM and the intensification phase (local search) has been discussed in Section 4.3.5. It is shown that the use of GM effectively assists an algorithm to achieve wide exploration and deep exploitation before stopping the search. Moreover, the intensification

Table 6.3: Fmin Obtained by Each Method after the Same Feval as AT-PSO-PCA

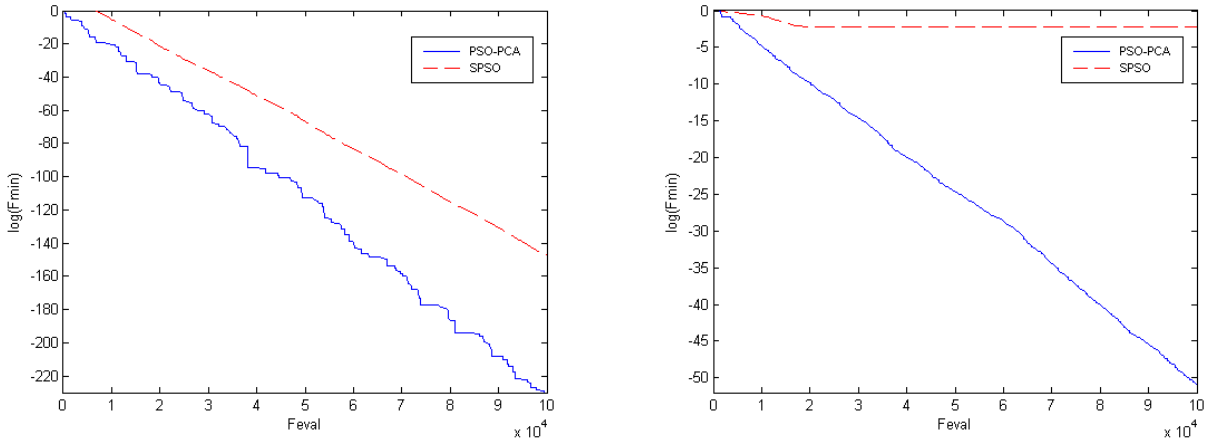
		Fmin mean (SRate)					
f	Feval mean	AT-PSO-PCA	SPSO	FIPS	CLPSO	EPSDE	GL-25
f_1	8.58e+04	1.95e-82 (100%)	4.78e-54 (100%)	2.39e-03 (100%)	1.17e-05 (100%)	9.06e-55 (100%)	7.00e-19 (100%)
f_2	8.60e+04	6.15e-43 (100%)	1.89e+00 (0%)	7.72e-03 (96%)	1.66e-04 (100%)	7.75e-27 (100%)	1.45e-10 (100%)
f_3	8.59e+04	2.67e-80 (100%)	1.14e-04 (100%)	2.43e+03 (0%)	2.83e+03 (0%)	6.02e+01 (96%)	1.56e+03 (0%)
f_4	8.73e+04	2.68e+01 (100%)	2.50e+01 (100%)	2.71e+01 (100%)	6.19e+01 (100%)	2.02e+00 (100%)	2.33e+01 (100%)
f_5	9.02e+04	0.00e+00 (100%)	1.08e+00 (40%)	0.00e+00 (100%)	0.00e+00 (100%)	1.60e-01 (84%)	8.40e-01 (36%)
f_6	8.62e+04	3.98e-02 (100%)	5.09e-01 (100%)	1.42e-02 (0%)	1.20e-02 (0%)	3.48e-03 (0%)	1.92e-02 (0%)
f_7	4.11e+04	-9.07e+03 (36%)	-7.03e+03 (0%)	-1.25e+04 (100%)	-1.26e+04 (100%)	-1.26e+04 (100%)	-4.08e+03 (0%)
f_8	8.63e+04	0.00e+00 (100%)	2.94e+01 (84%)	1.02e+02 (0%)	5.79e+00 (100%)	1.42e-16 (100%)	1.43e+02 (12%)
f_9	8.51e+04	0.00e+00 (100%)	6.99e-03 (76%)	2.83e-02 (12%)	4.55e-04 (100%)	0.00e+00 (100%)	2.96e-04 (100%)
f_{10}	8.49e+04	8.88e-16 (100%)	9.75e-01 (28%)	1.29e-02 (8%)	1.36e-03 (100%)	7.28e-15 (100%)	5.28e-10 (100%)
f_{11}	8.60e+04	2.39e-18 (100%)	4.15e-02 (72%)	1.15e-04 (100%)	4.99e-07 (100%)	4.15e-03 (96%)	8.23e-22 (100%)

Table 6.4: Comparison between Fmin Obtained by AT-PSO-PCA after Automatic Termination and Fmin Obtained by the Compared Methods after Feval = 2×10^5

	AT-PSO-PCA		Fmin (SRate) after Feval = 2×10^5				
f	Feval mean	Fmin mean (SRate)	SPSO	FIPS	CLPSO	EPSDE	GL-25
f_1	8.58e+04	1.95e-82 (100%)	8.42e-131 (100%)	4.59e-12 (100%)	3.53e-21 (100%)	1.02e-132 (100%)	1.24e-136 (100%)
f_2	8.60e+04	6.15e-43 (100%)	1.46e+00 (0%)	7.84e-08 (100%)	1.02e-13 (100%)	3.10e-66 (100%)	3.46e-35 (100%)
f_3	8.59e+04	2.67e-80 (100%)	8.36e-14 (100%)	3.27e+02 (0%)	1.08e+03 (0%)	2.48e-22 (100%)	2.82e+01 (96%)
f_4	8.73e+04	2.68e+01 (100%)	2.51e+01 (100%)	2.49e+01 (100%)	6.39e+00 (100%)	6.38e-01 (100%)	2.15e+01 (100%)
f_5	9.02e+04	0.00e+00 (100%)	8.80e-01 (52%)	0.00e+00 (100%)	0.00e+00 (100%)	4.00e-01 (96%)	0.00e+00 (100%)
f_6	8.62e+04	3.98e-02 (100%)	4.63e-01 (100%)	5.57e-03 (0%)	6.26e-03 (0%)	2.30e-03 (0%)	2.96e-03 (0%)
f_7	4.11e+04	-9.07e+03 (36%)	-7.84e+03 (0%)	-1.25e+04 (100%)	-1.26e+04 (100%)	-1.26e+04 (100%)	-8.65e+03 (0%)
f_8	8.63e+04	0.00e+00 (100%)	2.32e+01 (100%)	7.52e+01 (0%)	0.00e+00 (100%)	0.00e+00 (100%)	2.28e+01 (100%)
f_9	8.51e+04	0.00e+00 (100%)	8.06e-03 (76%)	1.92e-05 (100%)	5.45e-15 (100%)	2.96e-04 (100%)	8.97e-16 (100%)
f_{10}	8.49e+04	8.88e-16 (100%)	8.06e-01 (48%)	4.88e-07 (100%)	1.72e-11 (100%)	6.71e-15 (100%)	6.26e-14 (100%)
f_{11}	8.60e+04	2.39e-18 (100%)	3.73e-02 (84%)	1.74e-13 (100%)	1.17e-22 (100%)	1.57e-32 (100%)	7.82e-31 (100%)

Table 6.5: Fmin Obtained by SPSO and PSO-PCA after Feval = 10^5

		Fmin mean (SRate)	
f	Feval mean	SPSO	PSO-PCA
f_1	1.00e+05	2.02e-63 (100%)	1.05e-99 (100%)
f_2	1.00e+05	1.25e+00 (0%)	5.69e-51 (100%)
f_3	1.00e+05	1.26e-05 (100%)	1.11e-99 (100%)
f_4	1.00e+05	3.18e+01 (100%)	2.65e+01 (100%)
f_5	1.00e+05	5.20e-01 (48%)	0.00e+00 (100%)
f_6	1.00e+05	4.85e-01 (100%)	5.32e-01 (100%)
f_7	1.00e+05	-7.55e+03 (0%)	-9.01e+03 (40%)
f_8	1.00e+05	3.28e+01 (84%)	0.00e+00 (100%)
f_9	1.00e+05	4.83e-03 (68%)	0.00e+00 (100%)
f_{10}	1.00e+05	8.79e-01 (32%)	8.88e-16 (100%)
f_{11}	1.00e+05	2.49e-02 (76%)	6.98e-22 (100%)



(a) Function f_1 (b) Function f_{11}

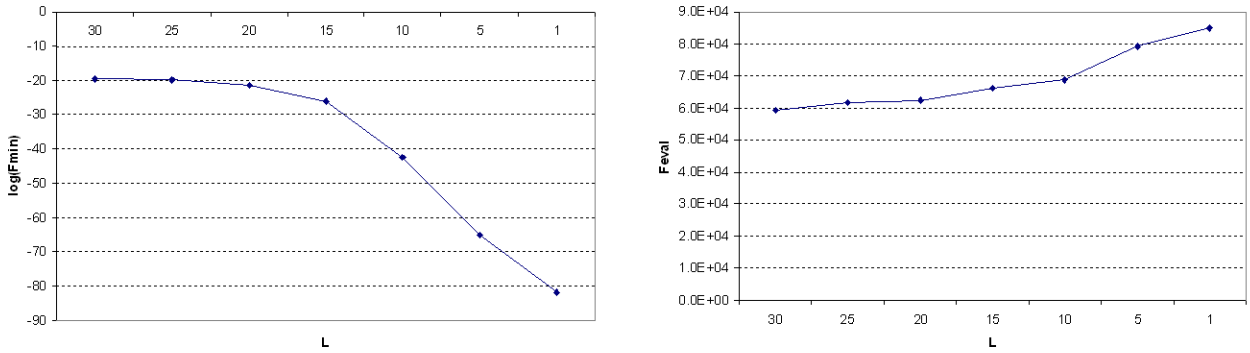
Figure 6.1: Convergence performance of SPSO and PSO-PCA on (a) function f_1 and (b) function f_{11}.

serves as a mechanism that increases the exploitation power of an algorithm, but when used alone, it cannot achieve the results obtained by its combination with its host algorithm.

Here, we investigate how the implementation of the PCA technique within the canonical PSO (SPSO) affects the performance of the method. We also analyze the influence of the parameter L that determines the number of dimensions in the new coordinate system generated by PCA.

6.4.1 PCA within SPSO

We carried out comparative experiments that consisted in confronting SPSO against the classical PSO with PCA, referred to as PSO-PCA. Compared to AT-PSO-PCA, PSO-PCA



(a) Accuracy

(b) Computational cost

Figure 6.2: Effect of the parameter L ranging between 1 and n (= 30) on function f_1 in terms of (a) Accuracy log(Fmin) and (b) Computational cost Feval.

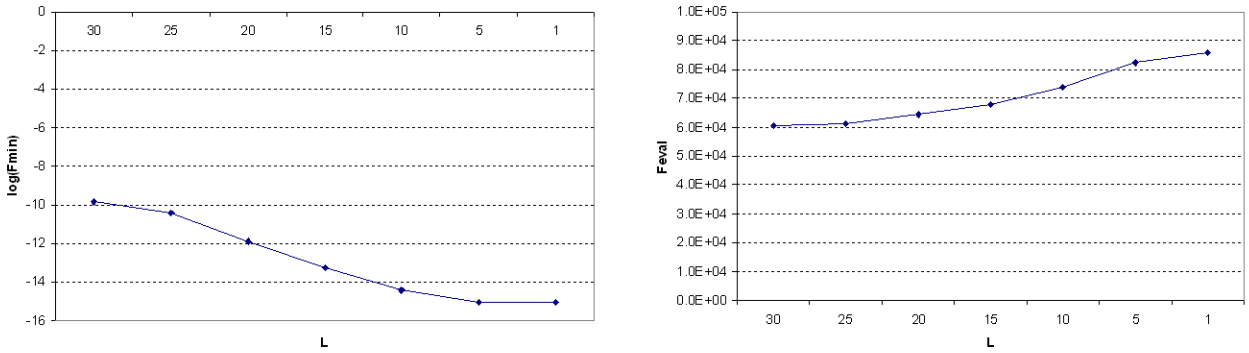
does not contain the GM, mutagenesis and the final intensification phase. Consequently, PSO-PCA is not equipped with an automatic termination.

Comparisons are made using the same benchmark functions listed in Table 6.1, as in Section 6.3. Both SPSO and PSO-PCA are terminated after 100,000 objective function evaluations. The average Fmin and SRate over 25 independent runs are reported in Table 6.5. Figure 6.1 graphically presents the comparisons in terms of log(Fmin) over Feval for functions f_1 and f_{11}, as examples of an unimodal function and a multimodal function, respectively. Figure 6.1(a) depicts the convergence speed of SPSO and PSO-PCA when minimizing f_1, a relatively easy unimodal function. The figure shows that PSO-PCA has a higher convergence speed than SPSO. Furthermore, in some cases such as the one depicted in Figure 6.1(b), where both methods are minimizing f_{11}, a complex multimodal function, it can be observed that SPSO got stuck at local minima after around 2×10^4 Fevals. On the other hand, PSO-PCA could easily escape from local optima and attain a global optimum. In terms of SRate, PSO-PCA evidently outperforms SPSO on the unimodal functions and also on the complex multimodal functions. In particular, a global optimum for function f_2 could not be found at all by SPSO, while the same problem was solved with a 100% success rate by PSO-PCA.

Those observations suggest that SPSO benefits from the use of PCA by attaining global minima for both unimodal and multimodal functions, with increased reliability. The use of PCA can increase the ability of SPSO to jump out of local optima and detect global optima.

6.4.2 Effect of Parameter L

In AT-PSO-PCA, the role of the parameter L is to control the number of dimensions of the space on which the swarm is projected. To assess the influence of L, we have tested



(a) Accuracy

(b) Computational cost

Figure 6.3: Effect of the parameter L ranging between 1 and n (= 30) on function f_{10} in terms of (a) Accuracy log(Fmin) and (b) Computational cost Feval.

AT-PSO-PCA with different numbers of L ranging between 1 and n. Figures 6.2 and 6.3 depict the results obtained for functions f_1 and f_{10}, respectively, as examples of an unimodal function and a multimodal function, with $n = 30$.

We can observe that both f_1 and f_{10} behave in a similar way in terms of Fmin and Feval. Indeed, in Figures 6.2(a) and 6.3(a), we see that log(Fmin) decreases as L decreases. For functions f_1 and f_{10}, log(Fmin) is equivalent to log(Error) and is thus an indicator of the accuracy of the search, i.e., the smaller log(Fmin), the higher the accuracy. The improvement in terms of accuracy is particularly high for the unimodal function f_1. However, Figures 6.2(b) and 6.3(b) reveal that Feval increases as L decreases. Nevertheless, the authors believe that the growth in Feval is relatively low when compared to the improvement achieved in terms of accuracy. In our experiments, there were no problems for which reducing L led to less accurate results. In the worst case, only Feval increased for the same accuracy. Those findings show that AT-PSO-PCA is able to take advantage of the principal components that have the highest variance to increase effectively the accuracy of the search under acceptable augmentation of the cost in terms of Feval.

6.5 Conclusion

In this chapter, we have introduced a new PSO, called AT-PSO-PCA, that is equipped with an automatic termination criterion based on the GM in order to terminate the search without conventional predefined criteria while avoiding premature termination. It also uses the PCA technique and a local search process to enhance the quality of the obtained solutions in terms of accuracy and reliability. PCA creates a search space based on the principal components of the set of all *pbests*. In that search space of possibly reduced dimension navigates the swarm to locate new promising areas. In the original set of coordinates, it forms a candidate

swarm that is given a chance to replace some of the *pbests* of the original swarm at each iteration.

Numerical experiments carried out on a set of widely used test functions and comparisons with state-of-the-art methods have shown that AT-PSO-PCA is competitive and that the main objectives have been fulfilled. Indeed, for all test functions, our proposed method could achieve very competitive results under a limited amount of function evaluations, without falling into premature termination or requiring undue objective function evaluations. In terms of accuracy and reliability, AT-PSO-PCA also clearly outperforms the canonical PSO and is comparable or superior to many of the well-known PSO and EAs. These results suggest that AT-PSO-PCA can contribute to real-world applications of PSO.

Chapter 7

Summary and Conclusions

In this dissertation, two subsets of EC have been considered to develop novel methods that answer the question of the termination criteria for EC. Namely, the proposed methods in this study are the G3AT, GATR, DEAT and AT-PSO-PCA methods, detailed in Chapters 3–6, respectively. They deal with the nonconvex global optimization problem defined in Section 1.1. The common elements in our proposed algorithms are the GM, the mutagenesis operator and the final intensification process. In addition, we have also developed the SD and SR mechanisms in GATR and implemented the PCA technique in AT-PSO-PCA. We have shown that our proposed methods can effectively terminate the search without conventional predefined criteria, without negative impact on the quality of the solution obtained and that they are comparable or superior to many well-known EC methods.

Specifically, in Chapter 3, we have shown that G3AT is robust and able to reach global minima or at least be very close to them in many of the selected test problems. The use of the GM effectively assists the algorithm to achieve wide exploration and deep exploitation before stopping the search. This indicates that our main objective to equip a GA with an automatic termination criterion has largely been fulfilled.

In Chapter 4, we have pointed out that as a two-dimensional structure, there is no evidence that the GM is able to represent the distribution of individuals in a multi-dimensional search space accurately. It has prompted us to develop the SR and SD mechanisms to alleviate this drawback and to implement them in GATR. We have shown that GATR can also terminate the search without conventional predefined criteria and that GATR is significantly superior to G3AT as well as to many other advanced EAs.

In Chapter 5, we have shown that the GM, SD and SR mechanisms can be successfully applied to DE, as an example of another EA. Numerical results have indicated that DE largely benefits from our developed mechanisms by stopping the search without undue objective function evaluations and without negative impact on the quality of the solution obtained.

In Chapter 6, we have shown that the GM can be combined with more traditional

mathematical tools to improve the performance of an EC method. The PSO paradigm was chosen and the GM was combined with the PCA mathematical technique. Our tests have shown that the resulting method was successfully equipped with an automatic termination criterion and could outperform the canonical PSO. Also, we have shown that AT-PSO-PCA is comparable or superior to many well-known PSO and EAs.

Although our main goal to develop automatic termination criteria for EC has been fulfilled, there remain topics that deserve further investigations. One of the main questions that remain unresolved is the number of subranges of the GM. The number of subranges is seen as a parameter, such as the crossover rate or the size of the initial population. However, we believe that its value can be determined during the search, for example, by letting the algorithm estimate the landscape of the function being optimized and by setting the number of subranges according to the estimated complexity of the function. Another question is the importance of the final intensification process. Finding a mechanism that would fully combine the local search with the GM is another interesting topic to explore in the future.

Appendix A

Standard Test Functions

Sphere Function (f_1)

Definition: $f_1(\mathbf{x}) = \sum_{i=1}^{n} x_i^2$.
Search space: $-100 \leq x_i \leq 100,\ i = 1, \ldots, n$
Global minimum: $\mathbf{x}^* = (0, \ldots, 0),\ f_1(\mathbf{x}^*) = 0$.

Schwefel Function (f_2)

Definition: $f_2(\mathbf{x}) = \sum_{i=1}^{n} |x_i| + \Pi_{i=1}^{n} |x_i|$.
Search space: $-10 \leq x_i \leq 10,\ i = 1, \ldots, n$
Global minimum: $\mathbf{x}^* = (0, \ldots, 0),\ f_2(\mathbf{x}^*) = 0$.

Schwefel Function (f_3)

Definition: $f_3(\mathbf{x}) = \sum_{i=1}^{n} (\sum_{j=1}^{i} x_j)^2$.
Search space: $-100 \leq x_i \leq 100,\ i = 1, \ldots, n$
Global minimum: $\mathbf{x}^* = (0, \ldots, 0),\ f_3(\mathbf{x}^*) = 0$.

Schwefel Function (f_4)

Definition: $f_4(\mathbf{x}) = \max_{i=1,\ldots n}\{|x_i|\}$.
Search space: $-100 \leq x_i \leq 100,\ i = 1, \ldots, n$
Global minimum: $\mathbf{x}^* = (0, \ldots, 0),\ f_4(\mathbf{x}^*) = 0$.

Rosenbrock Function (f_5)

Definition: $f_5(\mathbf{x}) = \sum_{i=1}^{n-1} \left[100 \left(x_i^2 - x_{i+1}\right)^2 + \left(x_i - 1\right)^2\right]$.
Search space: $-30 \leq x_i \leq 30,\ i = 1, 2, \ldots, n$.
Global minimum: $\mathbf{x}^* = (1, \ldots, 1),\ f_5(\mathbf{x}^*) = 0$.

Step Function (f_6)

Definition: $f_6(\mathbf{x}) = \sum_{i=1}^{n}(\lfloor x_i + 0.5 \rfloor)^2$.
Search space: $-100 \leq x_i \leq 100,\ i = 1, 2, \ldots, n$.
Global minimum: $\mathbf{x}^* = (0, \ldots, 0), f_6(\mathbf{x}^*) = 0$.

Quartic Function with Noise (f_7)

Definition: $f_7(\mathbf{x}) = \sum_{i=1}^{n} i x_i^4 + random[0, 1)$.
Search space: $-1.28 \leq x_i \leq 1.28,\ i = 1, \ldots, n$
Global minimum: $\mathbf{x}^* = (0, \ldots, 0),\ f_7(\mathbf{x}^*) = 0$.

Schwefel Functions (f_8)

Definition: $f_8(\mathbf{x}) = -\sum_{i=1}^{n}\left(x_i \sin\sqrt{|x_i|}\right)$.
Search space: $-500 \leq x_i \leq 500,\ i = 1, 2, \ldots, n$.
Global minimum: $\mathbf{x}^* = (420.9687, \ldots, 420.9687),\ f_8(\mathbf{x}^*) = -418.9829n$.

Rastrigin Function (f_9)

Definition: $f_9(\mathbf{x}) = 10n + \sum_{i=1}^{n}\left(x_i^2 - 10\cos(2\pi x_i)\right)$.
Search space: $-5.12 \leq x_i \leq 5.12,\ i = 1, \ldots, n$.
Global minimum: $\mathbf{x}^* = (0, \ldots, 0), f_9(\mathbf{x}^*) = 0$.

Ackley Function (f_{10})

Definition: $f_{10}(\mathbf{x}) = 20 + e - 20e^{-\frac{1}{5}\sqrt{\frac{1}{n}\sum_{i=1}^{n} x_i^2}} - e^{\frac{1}{n}\sum_{i=1}^{n}\cos(2\pi x_i)}$.
Search space: $-32 \leq x_i \leq 32,\ i = 1, 2, \ldots, n$.
Global minimum: $\mathbf{x}^* = (0, \ldots, 0); f_{10}(\mathbf{x}^*) = 0$.

Griewank Function (f_{11})

Definition: $f_{11}(\mathbf{x}) = \frac{1}{4000}\sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n}\cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$.
Search space: $-600 \leq x_i \leq 600,\ i = 1, \ldots, n$.
Global minimum: $\mathbf{x}^* = (0, \ldots, 0), f_{11}(\mathbf{x}^*) = 0$.

Levy Functions (f_{12}, f_{13})

Definition:

$$f_{12}(\mathbf{x}) = \frac{\pi}{n}\{10\sin^2(\pi y_1) + \sum_{i=1}^{n-1}\left[(y_i - 1)^2(1 + 10\sin^2(\pi y_i + 1))\right] + (y_n - 1)^2\}$$
$$+ \sum_{i=1}^{n} u(x_i, 10, 100, 4),\ y_i = 1 + \frac{x_i - 1}{4},\ i = 1, \ldots, n.$$
$$f_{13}(\mathbf{x}) = \frac{1}{10}\{\sin^2(3\pi x_1) + \sum_{i=1}^{n-1}\left[(x_i - 1)^2(1 + \sin^2(3\pi x_i + 1))\right] + (x_n - 1)^2(1 + \sin^2(2\pi x_n))$$
$$+ \sum_{i=1}^{n} u(x_i, 5, 100, 4),$$

$u(x_i, a, k, m) = \begin{cases} k(x_i - a)^m, & x_i > a; \\ 0, & -a \leq x_i \leq a; \\ k(-x_i - a)^m, & x_i < a. \end{cases}$
Search space: $-50 \leq x_i \leq 50,\ i = 1, \ldots, n.$
Global minimum: $\mathbf{x}^* = (1, \ldots, 1),\ f_{12}(\mathbf{x}^*) = f_{13}(\mathbf{x}^*) = 0.$

Shekel Foxholes Function (f_{14})

Definition: $f_{14}(\mathbf{x}) = \left[\frac{1}{500} + \sum_{j=1}^{25} \frac{1}{j + \sum_{i=1}^{2}(x_i - A_{ij})^6}\right]^{-1},$
$A = \begin{bmatrix} -32 & -16 & 0 & 16 & 33 & -32 & \ldots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & \ldots & 32 & 32 & 32 \end{bmatrix}.$
Search space: $-65.536 \leq x_i \leq 65.536,\ i = 1, 2.$
Global minimum: $\mathbf{x}^* = (-32, -32);\ f_{14}(\mathbf{x}^*) = 0.998.$

Kowalik Function (f_{15})

Definition: $f_{15}(\mathbf{x}) = \sum_{i=1}^{11} \left[a_i - \frac{x_1(b_i^2 + b_i x_2)}{b_i^2 + b_i x_3 + x_4}\right]^2,$
$a = (0.1957, 0.1947, 0.1735, 0.16, 0.0844, 0.0627, 0.0456, 0.0342, 0.0323, 0.0235, 0.0246),$
$b = (4, 2, 1, \frac{1}{2}, \frac{1}{4}, \frac{1}{6}, \frac{1}{8}, \frac{1}{10}, \frac{1}{12}, \frac{1}{14}, \frac{1}{16})$.
Search space: $-5 \leq x_i \leq 5,\ i = 1, \ldots, 4.$
Global minimum: $\mathbf{x}^* \approx (0.1928, 0.1908, 0.1231, 0.1358),\ f_{15}(\mathbf{x}^*) \approx 0.000375.$

Hump Function (f_{16})

Definition: $f_{16}(\mathbf{x}) = 4x_1^2 - 2.1x_1^4 + \frac{1}{3}x_1^6 + x_1x_2 - 4x_2^2 + 4x_2^4.$
Search space: $-5 \leq x_i \leq 5,\ i = 1, 2.$
Global minima: $\mathbf{x}^* = (0.0898, -0.7126),\ (-0.0898, 0.7126);\ f_{16}(\mathbf{x}^*) = 0.$

Branin RCOS Function (f_{17})

Definition: $f_{17}(\mathbf{x}) = (x_2 - \frac{5}{4\pi^2}x_1^2 + \frac{5}{\pi}x_1 - 6)^2 + 10(1 - \frac{1}{8\pi})\cos(x_1) + 10.$
Search space: $-5 \leq x_1 \leq 10,\ 0 \leq x_2 \leq 15.$
Global minima: $\mathbf{x}^* = (-\pi, 12.275),\ (\pi, 2.275),\ (9.42478, 2.475);\ f_{17}(\mathbf{x}^*) = 0.397887.$

Goldstein & Price Function (f_{18})

Definition: $f_{18}(\mathbf{x}) = (1 + (x_1 + x_2 + 1)^2(19 - 14x_1 + 13x_1^2 - 14x_2 + 6x_1x_2 + 3x_2^2))$
$* (30 + (2x_1 - 3x_2)^2(18 - 32x_1 + 12x_1^2 - 48x_2 - 36x_1x_2 + 27x_2^2)).$
Search space: $-2 \leq x_i \leq 2,\ i = 1, 2.$
Global minimum: $\mathbf{x}^* = (0, -1);\ f_{18}(\mathbf{x}^*) = 3.$

Hartmann Function (f_{19})

Definition: $f_{19}(\mathbf{x}) = -\sum_{i=1}^{4} \alpha_i \exp\left[-\sum_{j=1}^{3} A_{ij}\left(x_j - P_{ij}\right)^2\right]$,

$\alpha = [1, 1.2, 3, 3.2]^T$, $A = \begin{bmatrix} 3.0 & 10 & 30 \\ 0.1 & 10 & 35 \\ 3.0 & 10 & 30 \\ 0.1 & 10 & 35 \end{bmatrix}$, $P = 10^{-4} \begin{bmatrix} 6890 & 1170 & 2673 \\ 4699 & 4387 & 7470 \\ 1091 & 8732 & 5547 \\ 381 & 5743 & 8828 \end{bmatrix}$.

Search space: $0 \le x_i \le 1,\ i = 1, 2, 3.$

Global minimum: $\mathbf{x}^* = (0.114614, 0.555649, 0.852547)$; $f_{19}(\mathbf{x}^*) = -3.86278$.

Hartmann Function (f_{20})

Definition: $f_{20}(\mathbf{x}) = -\sum_{i=1}^{4} \alpha_i \exp\left[-\sum_{j=1}^{6} B_{ij}\left(x_j - Q_{ij}\right)^2\right]$,

$\alpha = [1, 1.2, 3, 3.2]^T$, $B = \begin{bmatrix} 10 & 3 & 17 & 3.05 & 1.7 & 8 \\ 0.05 & 10 & 17 & 0.1 & 8 & 14 \\ 3 & 3.5 & 1.7 & 10 & 17 & 8 \\ 17 & 8 & 0.05 & 10 & 0.1 & 14 \end{bmatrix}$,

$Q = 10^{-4} \begin{bmatrix} 1312 & 1696 & 5569 & 124 & 8283 & 5886 \\ 2329 & 4135 & 8307 & 3736 & 1004 & 9991 \\ 2348 & 1451 & 3522 & 2883 & 3047 & 6650 \\ 4047 & 8828 & 8732 & 5743 & 1091 & 381 \end{bmatrix}$.

Search space: $0 \le x_i \le 1,\ i = 1, \ldots, 6.$

Global minimum: $\mathbf{x}^* = (0.201690, 0.150011, 0.476874, 0.275332, 0.311652, 0.657300)$;

$f_{20}(\mathbf{x}^*) = -3.32237$.

Shekel Functions (f_{21}, f_{22}, f_{23})

Definition: $f_{21}(\mathbf{x}) = S_{4,5}(\mathbf{x})$, $f_{22}(\mathbf{x}) = S_{4,7}(\mathbf{x})$, $f_{23}(\mathbf{x}) = S_{4,10}(\mathbf{x})$,

where $S_{4,m}(\mathbf{x}) = -\sum_{j=1}^{m}\left[\sum_{i=1}^{4}\left(x_i - C_{ij}\right)^2 + \beta_j\right]^{-1}$, $m = 5, 7, 10$,

$\beta = \frac{1}{10}[1, 2, 2, 4, 4, 6, 3, 7, 5, 5]^T$, $C = \begin{bmatrix} 4.0 & 1.0 & 8.0 & 6.0 & 3.0 & 2.0 & 5.0 & 8.0 & 6.0 & 7.0 \\ 4.0 & 1.0 & 8.0 & 6.0 & 7.0 & 9.0 & 5.0 & 1.0 & 2.0 & 3.6 \\ 4.0 & 1.0 & 8.0 & 6.0 & 3.0 & 2.0 & 3.0 & 8.0 & 6.0 & 7.0 \\ 4.0 & 1.0 & 8.0 & 6.0 & 7.0 & 9.0 & 3.0 & 1.0 & 2.0 & 3.6 \end{bmatrix}$.

Search space: $0 \le x_i \le 10,\ i = 1, \ldots, 4.$

Global minimum: $\mathbf{x}^* = (4, 4, 4, 4)$;

$f_{21}(\mathbf{x}^*) = -10.1532$,

$f_{22}(\mathbf{x}^*) = -10.4029$,

$f_{23}(\mathbf{x}^*) = -10.5364$.

Function (f_{24})

Definition: $f_{24}(\mathbf{x}) = -\sum_{i=1}^{n} \sin(x_i) \sin^{20}(\frac{ix_i^2}{\pi})$.

Search space: $0 \le x_i \le \pi,\ i = 1, \ldots, n.$

Global minimum: $f_{24}(\mathbf{x}^*) = -99.2784$.

Function (f_{25})

Definition: $f_{25}(\mathbf{x}) = \frac{1}{n}\sum_{i=1}^{n}(x_i^4 - 16x_i^2 + 5x_i)$.
Search space: $-5 \leq x_i \leq 5,\ i = 1, \ldots, n$.
Global minimum: $f_{25}(\mathbf{x}^*) = -78.33236$.

Appendix B

Hard Test Functions

For the hard test functions h_1–h_{17}, their global minima and the bounds on the variables are listed in Table B.1. For more details about these functions, the reader is referred to Liang and Suganthan (2005).

Table B.1: Benchmark Hard Functions

h	Function name	Bounds	Global minimum
h_1	Shifted Sphere	[–100,100]	–450
h_2	Shifted Schwefel's 1.2	[–100,100]	–450
h_3	Shifted rotated high conditioned elliptic	[–100,100]	–450
h_4	Shifted Schwefel's 1.2 with noise in fitness	[–100,100]	–450
h_5	Schwefel's 2.6 with global optimum on bounds	[–100,100]	–310
h_6	Shifted Rosenbrock's	[–100,100]	390
h_7	Shifted rotated Griewank's without bounds	[0,600]	–180
h_8	Shifted rotated Ackley's with global optimum on bounds	[–32,32]	–140
h_9	Shifted Rastrigin's	[–5,5]	–330
h_{10}	Shifted rotated Rastrigin's	[–5,5]	–330
h_{11}	Shifted rotated Weierstrass	[–0.5,0.5]	90
h_{12}	Schwefel's 2.13	[–100,100]	–460
h_{13}	Expanded extended Griewank's + Rosenbrock's	[–3,1]	–130
h_{14}	Expanded rotated extended Scaffe's	[–100,100]	–300
h_{15}	Hybrid composition 1	[–5,5]	120
h_{16}	Rotated hybrid comp.	[–5,5]	120
h_{17}	Rotated hybrid comp. Fn 1 with noise in fitness	[–5,5]	120

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