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Acknowledgements

The GOSET software package is a direct result of two research awards from the Office of Naval Research. The software itself had its beginnings prior to any formal research support, at that time it was known as ENEGAT (ESAC Non-Encoded Genetic Algorithm Toolbox). Later, a substantial revision and expansion of the software were made under Office of Naval Research (ONR) support through the effort “Polytopic Model Based Stability Analysis and Genetic Design of Electric Warship Power Systems,” contract N00014-02-1-0990. In this regard I sincerely appreciate the support of both Katherine Drew, our program manager at ONR, and Ed Zivi, a Professor at the US Naval Academy, whose support of the vision of this effort was critical. Contractually, another important source of this effort was the effort “National Naval Responsibility for Naval Engineering: Education and Research for the Electric Naval Engineer,” contract N00014-02-1-0623. This award paid for the development of this manual, as well as a short course to go with it. I would like to express our appreciation to Sharon Beerman-Curtin for supporting the pedagogical and technology transfer efforts.

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Scott D. Sudhoff
Professor of Electrical and Computer Engineering
Purdue University
Chapter 1

Introduction

1.1 The Genetic Optimization System Engineering Tool (GOSET)
1.2 System requirements
1.3 Installing GOSET
1.4 GOSET license
1.1 The Genetic Optimization System Engineering Tool (GOSET)

The Genetic Optimization System Engineering Tool (GOSET) is a MATLAB®-based code for solving optimization problems. In the course of its development, it was extensively used to solve a variety of engineering problems – particularly those related to magnetics, electric machinery, power electronics, and entire power and propulsion systems. It has been used to automatically design inductors, brushless dc motors, power supplies, and inverters and for the parameter identification of synchronous machines, induction machines, gas turbines, etc. It is meant primarily as an engineering tool, although it is quite generic in its ability to solve both single-objective and multi-objective optimization problems. Because it solves these problems using evolutionary algorithms it is very robust in its ability to seek global rather than local optimum, as well as in its ability to contend with functions that are not ‘friendly’ in that they are, for example, discontinuous. GOSET provides the means for the user to either be blissfully unaware of the algorithms and parameters used, or to become intimately involved in the exact algorithms as well as the parameters used in these algorithms. It also allows the user to either work from a text-based environment or to utilize a graphical user interface. In short, it provides the user with a powerful tool for the automation of the engineering design process.

1.2 System Requirements

GOSET runs on MATLAB Version 6.5 Release 13 and up, and you can refer to the system requirements for corresponding versions of MATLAB.

For the MATLAB 6.5.1 or later versions running on Microsoft Windows, DLL version of GOSET is also provided to improve the computational speed. If you are using MATLAB 6.5 on Microsoft Windows, you can download the following file and install this functionality.

http://www.mathworks.com/support/solutions/files/s33513/GenericDll_1p1.exe

The detailed installation procedure is provided in the following link.

http://www.mathworks.com/support/solutions/data/1-1ABRP.html?solution=1-1ABRP
GOSET DLL version is marked by the letter ‘D’ in the GOSET version. For example, DLL version of ‘goset 2.0’ is ‘goset 2.0D’.

1.3 Installing GOSET

GOSET is MATLAB based toolbox and the installation is a simple process of adding the GOSET path to the MATLAB paths.

It is strongly advised not to change the default folder name of GOSET. For the GOSET provided with this manual, the default folder name is ‘goset 2.x’ or ‘goset 2.xD’ for the DLL version.

Installation Instruction

1. Copy the ‘goset 2.x(D)’ and ‘goset 2.x examples’ folders in a convenient place.

2. In MATLAB menu, go to ‘File’ and select ‘Set Path’.

3. Then, click ‘Add Folder’.
4. Locate 'goset 2.x (D)' folder and click 'OK' to add 'goset 2.x (D)' folder to the MATLAB search paths.

![Browser For Folder](image)

5. Click 'Save' and 'Close' to finish.

![Set Path](image)

6. Now, you are ready to use GOSET.

**1.4 GOSET License**
Each version of GOSET is subject to the license control. The license of GOSET expires after certain period of time from the date of release. This is to prevent the unlawful distribution of GOSET and also to mandate the users to update their GOSET to the latest version.

When there is less than a week left in the GOSET license, you will get the following warning message:

There are only $n$ days left in GOSET 2.x License.

Please contact the distributor for the latest version of GOSET.
Chapter 2

An Overview of Single-Objective Genetic Algorithms

This section is devoted to a brief overview of Genetic Algorithms (GAs) focused on the canonical genetic algorithm.

2.1 Introduction to genetic algorithms
2.2 Canonical genetic algorithm
2.3 Other genetic operators
2.1 Introduction to genetic algorithms

Genetic algorithms are optimization methods that are inspired by biological evolution. GAs operate on a population of candidate solutions and apply the principle of survival of the fittest to evolve the candidate solutions towards the desired optimal solutions.

In GAs, candidate solutions are referred to as *individuals*. The defining properties of these individuals (parameters) are encoded to chromosomes that consist of a string of genes. According to the representation rule, a gene can be a symbol from an alphabet (in a canonical GA), a binary number, integer, real-value, etc. A *population* refers to the group of individuals.

The *fitness* of an individual is a metric that tells us how good each individual is as the solution to the given problem. Using a fitness function, individuals are assigned corresponding fitness values. The individuals with better fitness values are more likely to survive and reproduce.

With the representation rule and the fitness function determined for the given optimization problem, an initial population is randomly generated and fitness values are evaluated. Then a pair of *parent* chromosomes is selected from the current population. The probability of selection increases with increasing fitness. Genetic operators such as *crossover* and *mutation* are applied to these parent chromosomes to generate children. The children are used to create a new population, for which fitness values are evaluated and assigned. This process of selection, crossover, mutation, and fitness evaluation is repeated until a stopping criterion is satisfied. Each iteration of this procedure is called a generation.

From the above description of a GA, it is clear that GAs are radically different from the classical optimization approaches. Some of the most significant differences are:

- GAs operate encodings of the parameter values, not necessarily the actual parameter values
- GAs operate on a population of solutions, not a single solution
- GAs only uses the fitness values based on the objective functions and do not require derivative information or other knowledge
- GAs uses probabilistic computations, not deterministic ones
- GAs are efficient in handling problems with a discrete search space
2.2 Canonical genetic algorithm

In this section, a canonical GA is introduced to illustrate the fundamental mechanisms of GAs. A flow chart of canonical GA is shown in Figure 2.1. There in, the GA begins with an initialization step, followed by a repeated sequence of fitness evaluation, selection, crossover and mutation.

![Flow chart of a typical GA](image)

**Figure 2.1 Flow chart of a typical GA**

**Initialization**

In the initialization step, initial solutions are randomly generated and encoded into individuals according to the predefined representation rule. Binary coding is employed in canonical GAs. The generation number $k$ is set to 0 and the initial population is denoted $P_0$.

**Fitness Evaluation**

The fitness value is a figure of merit for an individual. In the fitness evaluation step, each individual is assigned with its fitness value. Generally, higher fitness value corresponds to a more optimal individual.
Selection

In nature, the individuals that are better suited to the environment are more likely to survive and reproduce. The selection operator emulates this situation by ensuring that individuals with larger fitness values are more likely to survive to reproduce. Among the several different selection methods, the roulette wheel and tournament selection algorithms are commonly used to form a mating pool $M_k$.

a. Roulette wheel selection

Roulette wheel selection is one of the most popular selection methods. Let’s assume that all the individuals are evaluated and assigned with their fitness values. Then one can imagine a roulette wheel with sections whose number is same as the number of individuals and whose areas are proportional to the fitness values of the corresponding individuals. Then the wheel is turned and a chromosome is selected and copied to the mating pool. This process is repeated until the mating pool is full.

![Roulette wheel selection](image)

b. Tournament selection

As the name states, two or more individuals are randomly chosen from the population and the one with better fitness value is selected and copied in the mating pool. This method is simpler than the roulette wheel method.

![Tournament selection](image)
Crossover

Crossover emulates the reproduction of living organs by exchanging gene among the chromosomes. Crossover generates new individuals that share the characteristics of their parents. Crossover is performed on the mating pool $M_k$ to form population $P_{k+1}$ as a first step in forming the next generation $P_{k+1}$. The single-point crossover and the multiple-point crossover operators are list below.

a. Single-point crossover

A crossover point is randomly selected and the genes of the parents are exchanged after the crossover point as depicted in Figure 2.5.

```
Crossover point

Parent 1  1 0 1 1 1
Parent 2  0 1 1 0 1

Child 1  1 0 1 0 1
Child 2  0 1 1 1 1
```

Figure 2.5 Single-point crossover

b. Multiple-point crossover

Several crossover points are randomly chosen and the genes of the parents are exchanged in between the crossover points. Figure 2.6 illustrates two point crossover.

```
Crossover points

Parent 1  1 0 1 1 1
Parent 2  0 1 1 0 1

Child 1  1 1 1 1 1
Child 2  0 0 1 0 1
```

Figure 2.6 Multiple-point crossover
**Mutation**

In natural evolution, mutation occurs as the result of an error in copying the gene information. As an analogy to this, mutation in GA is a process of changing some genes in chromosomes randomly. The main role of mutation operator is to maintain the diversity of the population.

In the canonical GA using binary representation, mutation operator flips the selected bit value as in Figure 2.7. The mutation operator is applied to $\hat{P}_{k+1}$ which yield $P_{k+1}$

![Mutation point]

Original chromosome 0 1 0 0 0 1 1 0 1 1
Mutated chromosome 0 1 0 0 1 1 1 0 1 1

Figure 2.7 Mutation in binary-coded GAs

### 2.3 Other genetic operators

Selection, crossover and mutation are the primary genetic operators. However, other genetic operators have been developed to improve the performance of GAs. We introduce some of them that are employed in GOSET.

**Elitism**

Elitism is a mechanism to protect the best individual from being altered and lost by genetic operations. The simplest way to implement elitism is to pass the current best individual to the next population without any genetic operations. By using elitism, it is guaranteed that maximum fitness in the population will never decrease.

![Elitism]

Old population New population
Best gene is preserved
GA operators

Figure 2.8 Elitism
**Migration**

This operator works only when multiple-region (or multiple-population) scheme is employed. By setting the number of regions, \( n \), greater than one, the population is divided into \( n \) different populations. Generally, these populations evolve without any interaction. Periodically, some of the individuals are redistributed and move from one region to other region.

![Migration operator](image)

Using multiple populations with migration can result in a better chance of finding the global optimum with less computation.

**Random search**

Random search is a way to extensively explore the neighborhood of the best individual for better solution by random mutation of the best individual. It can help reduce the time for the GA to converge to the optimal solution.

![Random search](image)

As shown in Figure 2.10, the best individual is randomly perturbed to generate mutants. Then, the fitness values of the generated individuals are evaluated. If the
best among the mutants has better fitness value than that of the current best individual, then the current best individual is replaced by the new best individual. Otherwise, the original best individual is placed back to the population.

**Diversity Control**

For some optimization problems, there are multiple optimal solutions (multi-modal problems). A naive application of GAs can result in convergence of the solutions to one optimal solution. Even in the problem with single optimal solution, it is not desirable for the many solutions exploring the same region in the solution space. Therefore, the diversity control is employed. By using diversity control, the underrepresented solutions are emphasized and similar solutions are penalized by adjusting their fitness values.

Figure 2.11 shows the effect of diversity control. Each circle on the curve represents a solution and its fitness value is shown by the vertical bar below it. Most of the solutions are close to the first optimal solution in (a). With the high probability of selecting a solution near the first optimum, it is likely to end up having all the solutions near the first optimum. However, when the diversity control is used, the fitness function values of the overrepresented solutions in the first optimum are penalized as in (b) and underrepresented solutions in the second optimum are less penalized and have better chance to survive.
An Overview of Multi-Objective Optimization

GOSET has the capability to perform multi-objective optimizations. A few fundamental notions on multi-objective optimization are introduced in this chapter.

3.1 Multi-objective optimization problems
3.2 GAs for multi-objective optimization problems
3.1 Multi-objective optimization problems

Definition

Multi-objective optimization problems involve more than one objective function. Each objective function is to be minimized or maximized. The general form of multi-objective optimization problem can be formally defined as

\[
\begin{align*}
\text{min/max } & \quad f_m(x), \quad m = 1, 2, \ldots, M \\
\text{subject to } & \quad g_j(x) \geq 0, \quad j = 1, 2, \ldots, J \\
& \quad h_k(x) = 0, \quad k = 1, 2, \ldots, K \\
& \quad x_j^{(L)} \leq x_j \leq x_j^{(U)}, \quad i = 1, 2, \ldots, n
\end{align*}
\]

The fundamental difference between single-objective optimization and multi-objective optimization is that in multi-objective optimization problem the desired result is a set of points that describe the best tradeoff between competing objectives rather than a single point representing the extrema of a single objective function.

Pareto optimal solution

In the single-objective optimization problem, the superiority of a solution over other solutions is clearly determined by comparing their objective function values. However, in multiple-objective optimization problem, the goodness of a solution has to be redefined.

For this purpose, the concept of domination is introduced. Suppose there are two solutions \(x_1\) and \(x_2\). The solution \(x_1\) is said to dominate \(x_2\) (or \(x_2\) is dominated by \(x_1\)), if the following two conditions are satisfied,

<table>
<thead>
<tr>
<th>Dominance test conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. The solution (x_1) is no worse than (x_2) in all objectives.</td>
</tr>
<tr>
<td>2. The solution (x_1) is strictly better than (x_2) in at least one objective.</td>
</tr>
</tbody>
</table>

As an illustration of the concept of domination, let’s consider two-objective optimization problem with \(f_1\) and \(f_2\). We want to maximize \(f_1\) and minimize \(f_2\). Assume there are five solutions as in Figure 3.1.
First, compare the solution 1 and the solution 2. The solution 1 is better than the solution 2 for both of the objectives. Hence it is evident that the solution 1 dominates the solution 2.

Now look at the solution 1 and solution 5. They have same $f_2$ values, but solution 5 has bigger $f_1$ value than solution 1. Thus solution 5 dominates solution 1. As a final example, let’s check the dominance between the solution 1 and 4. The solution 4 is better for the first objective function, but the solution 1 is better for the second objective function. As neither solution satisfies the first condition for dominance test, we cannot say that either solution dominates the other.

Given a set of solutions, the non-dominated solution set is a set of all the solutions that are not dominated by any members of the solution set.

Each solution in the feasible decision space can be mapped to the feasible objective space. The non-dominated set of the entire feasible search space is called the Pareto-optimal solution set. In Figure 3.2, a bold line in the feasible objective space is...
called the **Pareto-optimal front** that is the set of all the points mapped from the Pareto optimal solution set. The Pareto-optimal front represents the best possible compromise between conflicting objectives. The Pareto-optimal front is the desired result of the multi-objective optimization.

**Diversity control**

There are multiple solutions for a given multi-objective optimization problem and any solution in the Pareto optimal solution set can be the best solution. Thus it is required to find not only as many Pareto-optimal solutions as possible, but also as diverse as possible solutions over the Pareto-optimal front.

![Diagram of Pareto-optimal fronts](image)

**Figure 3.3** Different distributions of solutions

In the Figure 3.3, there are five points in Pareto-optimal front for each case (a) and (b). While the solutions of (a) are concentrated on a specific part of the Pareto-optimal front, those of (b) are evenly distributed over the Pareto-optimal front. There are chances that the most appropriate solution for the given problem exists in the neglected portion of the Pareto-optimal front in case (a). Thus, it is very important to have diverse solutions.

There are several different techniques used to control the diversity of solutions. The interested is referred to [Deb01] or [Car02].

### 3.2 Genetic algorithms for multi-objective optimization problem

Genetic algorithm utilizes a population of solution candidates. It is possible for the genetic algorithms to find out multiple optimal solutions in one execution. Meanwhile,
a series of executions is required to find out multiple solutions in the classical optimization approaches. Therefore, genetic algorithms are highly suitable for solving multi-objective optimization problems.

Schaffer [Sch84] implemented the first multi-objective genetic algorithm in 1984 to find a set of non-dominated solutions. However, it is not until mid 1990’s that the researchers became actively involved in this area.

Several different multi-objective genetic algorithms have been developed over the years. The followings are some of those.

- Vector Evaluated GA (Schaffer, 1984)
- Non-Dominated Sorting GA (Goldberg, 1989)
- Niched-Pareto GA (Horn et al., 1994)
- Vector-optimized ES ((Frank Kursawe, 1990)
- Multiple objective GA (Fonseca & Fleming, 1993)
- Weighted-Based GA (Hajela and Lin, 1993)
- Random Weighted GA (Murata & Ishibuchi, 1995)
- Distance-based Pareto GA (Osyczka & Kundu, 1995)
- Strength Pareto EA (Zitzler & Thiele., 1998)
- Elitist NSGA (NSGA II) (Deb et al., 2000)
- Pareto-archived ES (Knowles & Corne., 2000)
- Rudolph’s elitist MOEA (Rudolph, 2001)

Detailed description of these algorithms can be found in Deb [Deb01].

References


Chapter 4

GOSET Data Structures and Algorithm Execution

4.1 Data structures  
4.2 Algorithm execution flow  
4.3 Execution of GOSET
4.1 Data Structures

A large amount of information is involved in the genetic algorithm execution. To facilitate the information in an organized fashion, GOSET categorizes the information into the following three structures:

<table>
<thead>
<tr>
<th>MATLAB structure name</th>
<th>Contents</th>
</tr>
</thead>
<tbody>
<tr>
<td>P</td>
<td>Population information</td>
</tr>
<tr>
<td>GAP</td>
<td>Genetic Algorithm Parameters</td>
</tr>
<tr>
<td>GAS</td>
<td>Genetic Algorithm Statistics</td>
</tr>
</tbody>
</table>

Table 4.1 Data structures

We will begin our description of these with population information structure P.

Structure: P

Structure P contains all the information related to the current population. There are 16 fields associated with this structure. Field names and their descriptions are list in the following table.

<table>
<thead>
<tr>
<th>P.[Field name]</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>P.fithandle</td>
<td>Handle to the fitness function</td>
</tr>
<tr>
<td>P.size</td>
<td>The number of individuals in the population</td>
</tr>
<tr>
<td>P.mfit</td>
<td>Unconditioned fitness function values (P.nobj × P.size)</td>
</tr>
<tr>
<td>P.fit</td>
<td>Fitness function values (1 × P.size)</td>
</tr>
<tr>
<td>P.eval</td>
<td>Fitness evaluation flag (1 × P.size)</td>
</tr>
<tr>
<td></td>
<td>0: fitness is not evaluated</td>
</tr>
<tr>
<td></td>
<td>1: fitness is evaluated</td>
</tr>
<tr>
<td>P.age</td>
<td>Age of each individual of the population in generations</td>
</tr>
<tr>
<td>P.ngenes</td>
<td>Number of genes in all chromosomes of an individual</td>
</tr>
<tr>
<td>P.min</td>
<td>GAP.gd_min</td>
</tr>
<tr>
<td>P.max</td>
<td>GAP.gd_max</td>
</tr>
<tr>
<td>P.type</td>
<td>GAP.gd_type</td>
</tr>
<tr>
<td>P.chrom_id</td>
<td>GAP.gd_cid</td>
</tr>
<tr>
<td>P.normgene</td>
<td>Normalized gene values (P.nobj × P.size)</td>
</tr>
</tbody>
</table>
Table 4.2 Data structure of the population

**Structure: GAP**

Structure GAP has all the parameters about genetic operations. There are 67 fields associated with GAP. They are listed below with their description and default values

<table>
<thead>
<tr>
<th>GAP.[Field name]</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Fundamental parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.fp_nngen</td>
<td>Number of generations to evolve</td>
<td>100</td>
</tr>
<tr>
<td>GAP.fp_ipop</td>
<td>Number of chromosomes in initial population</td>
<td>100</td>
</tr>
<tr>
<td>GAP.fp_npop</td>
<td>Number of chromosome in normal population</td>
<td>100</td>
</tr>
<tr>
<td>GAP.fp_nobj</td>
<td>Number of objectives</td>
<td>Argument for gapdefault</td>
</tr>
<tr>
<td>GAP.fp_obj</td>
<td>Objective to optimize</td>
<td>1: fp_nobj =1 0: fp_nobj &gt;1</td>
</tr>
<tr>
<td><strong>Diversity control parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.dc_act</td>
<td>Diversity control usage flag</td>
<td>1</td>
</tr>
<tr>
<td>GAP.dc_alg</td>
<td>Diversity control algorithm used in selection</td>
<td>4</td>
</tr>
<tr>
<td>GAP.dc_spd</td>
<td>Diversity control space</td>
<td>1</td>
</tr>
<tr>
<td>GAP.dc_mnt</td>
<td>Minimum threshold for algorithm 1</td>
<td>0.02</td>
</tr>
<tr>
<td>GAP.dc_mxt</td>
<td>Maximum threshold for algorithm 1</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP.dc_ntr</td>
<td>Number of trials for algorithm 2</td>
<td>3</td>
</tr>
<tr>
<td>GAP.dc_mnb</td>
<td>Minimum number of bins relative to population size for algorithm 2</td>
<td>0.5</td>
</tr>
<tr>
<td>GAP.dc_mxb</td>
<td>Maximum number of bins relative to population size for algorithm 2</td>
<td>2</td>
</tr>
<tr>
<td>GAP.dc_dc</td>
<td>Diversity control distance constant for algorithm 3 and 4</td>
<td>0.001</td>
</tr>
<tr>
<td>GAP.dc_nt</td>
<td>Diversity control test population size for algorithm 4</td>
<td>50</td>
</tr>
<tr>
<td><strong>Selection algorithm parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Parameter</td>
<td>Description</td>
<td>Value</td>
</tr>
<tr>
<td>-----------</td>
<td>-------------</td>
<td>-------</td>
</tr>
<tr>
<td>GAP.sl_alg</td>
<td>Selection algorithm</td>
<td>1: Roulette wheel 2: Tournament 3: Custom</td>
</tr>
<tr>
<td>GAP.sl_nts</td>
<td>Number of individuals used in a tournament</td>
<td>4</td>
</tr>
<tr>
<td>GAP.sl_cah</td>
<td>Custom algorithm handle</td>
<td>[]</td>
</tr>
<tr>
<td>GAP.dt_alg</td>
<td>Selection algorithm</td>
<td>1: Replace parents 2: Random replacement 3: Tournament on fitness 4: Tournament of age 5: Custom 6: Random among 1-4</td>
</tr>
<tr>
<td>GAP.dt_nts</td>
<td>Number of individuals used in a tournament</td>
<td>4</td>
</tr>
<tr>
<td>GAP.dt_cah</td>
<td>Custom algorithm handle</td>
<td>[]</td>
</tr>
<tr>
<td>GAP.mc_pp</td>
<td>Percentage of population replaced by children</td>
<td>0.6</td>
</tr>
<tr>
<td>GAP.mc_fc</td>
<td>Fraction of chromosomes involved in crossover</td>
<td>1</td>
</tr>
<tr>
<td>GAP.mc_alg</td>
<td>Crossover algorithm</td>
<td>1: Single point crossover 2: Scalar simple blend crossover 3: Vector simple blend crossover 4: Scalar simulated binary crossover 5: Vector simulated binary crossover 6: Randomly apply above algorithms</td>
</tr>
<tr>
<td>GAP.mc_gac</td>
<td>Number of generations between changing algorithms for random crossover algorithm</td>
<td>3</td>
</tr>
<tr>
<td>GAP.mc_ec</td>
<td>Tightness of distribution ($\eta_c$) for algorithms 4 and 5</td>
<td>2</td>
</tr>
<tr>
<td>GAP.mt_ptgm</td>
<td>Probability of a total gene mutation</td>
<td>0.001</td>
</tr>
<tr>
<td>GAP.mt_prgm</td>
<td>Probability of a relative partial gene mutation</td>
<td>0.002</td>
</tr>
<tr>
<td>GAP.mt_srgm</td>
<td>Standard deviation of relative partial gene perturbation</td>
<td>0.3</td>
</tr>
<tr>
<td>GAP.mt_pagm</td>
<td>Probability of an absolute partial gene mutation</td>
<td>0.002</td>
</tr>
<tr>
<td>GAP.mt_sagm</td>
<td>Standard deviation of absolute partial gene mutation</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP.mt_prvm</td>
<td>Probability of a relative vector mutation</td>
<td>0.002</td>
</tr>
<tr>
<td>GAP.mt_srvm</td>
<td>Standard deviation of relative vector mutation</td>
<td>0.3</td>
</tr>
<tr>
<td>GAP.mt_pavm</td>
<td>Probability of an absolute vector mutation</td>
<td>0.002</td>
</tr>
<tr>
<td>GAP.mt_savm</td>
<td>Standard deviation of absolute vector mutation</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP.mt_pigm</td>
<td>Probability of integer gene mutation</td>
<td>0.008</td>
</tr>
<tr>
<td>GAP.mg_nreg</td>
<td>Number of geographic regions the population is distributed</td>
<td>1</td>
</tr>
<tr>
<td>GAP.mg_tmig</td>
<td>Time between migrations in generations</td>
<td>0</td>
</tr>
<tr>
<td>Parameter</td>
<td>Description</td>
<td>Value</td>
</tr>
<tr>
<td>--------------</td>
<td>-----------------------------------------------------------------------------</td>
<td>-------</td>
</tr>
<tr>
<td>GAP.mg_pmig</td>
<td>Probability of an individual to migrate</td>
<td>0</td>
</tr>
<tr>
<td><strong>Evaluation Parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.ev_bev</td>
<td>Block evaluation flag (1 × P.size)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0: evaluate an individual at a time</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1: evaluate all the individual in a population</td>
<td></td>
</tr>
<tr>
<td>GAP.ev_are</td>
<td>Fitness reevaluation option</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0: evaluate the unevaluated chromosomes only</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1: always reevaluate</td>
<td></td>
</tr>
<tr>
<td>GAP.ev_ssd</td>
<td>Supplementary data passing</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0: pass only gene values and optional data if exist</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1: pass also age, region No. and previous fitness value</td>
<td></td>
</tr>
<tr>
<td><strong>Scaling parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.sc_alg</td>
<td>Scaling algorithm</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>0: none</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1: offset so minimum fitness is zero</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2: linear scaling (most fit individual GAP.sc_klin more likely to be selected than average fit)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3: linear scaling (most fit individual GAP.sc_klin more likely to be selected than median fit)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>4: linear scaling (most fit individual GAP.sc_klin more likely to be selected than least fit)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5: sigma truncation</td>
<td></td>
</tr>
<tr>
<td></td>
<td>6: quadratic scaling</td>
<td></td>
</tr>
<tr>
<td>GAP.sc_kln</td>
<td>Scaling factor for linear scaling algorithms</td>
<td>10</td>
</tr>
<tr>
<td>GAP.sc_cst</td>
<td>Scaling constant for sigma truncation</td>
<td>2</td>
</tr>
<tr>
<td>GAP.sc_kmxq</td>
<td>Maximum scaling factor for quadratic scaling (most fit individual GAP.sc_kln more likely to be selected than median fit)</td>
<td>10</td>
</tr>
<tr>
<td>GAP.sc_kmnq</td>
<td>Minimum scaling factor for quadratic scaling (least fit individual GAP.sc_kln more likely to be selected than median fit)</td>
<td>0.01</td>
</tr>
<tr>
<td><strong>Elitism parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.el_act</td>
<td>Elitism activation flag</td>
<td>1</td>
</tr>
<tr>
<td>GAP.el_fgs</td>
<td>Fraction of generations to pass before starting elitism</td>
<td>0</td>
</tr>
<tr>
<td>GAP.el_fpe</td>
<td>Fraction of population protected as elite state for multi-objective optimization</td>
<td>0.5</td>
</tr>
<tr>
<td><strong>Random search parameters</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAP.rs_fgs</td>
<td>Fraction of generations to pass before starting random search</td>
<td>0.5</td>
</tr>
<tr>
<td>GAP.rs_fps</td>
<td>Fraction of total population size used in random search</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP.rs_srp</td>
<td>Standard deviation used in relative perturbation</td>
<td>0.3</td>
</tr>
<tr>
<td>GAP.rs_sap</td>
<td>Standard deviation used in absolute perturbation</td>
<td>0.1</td>
</tr>
<tr>
<td>GAP.rs_frp</td>
<td>Fraction of the time that relative random perturbations are used. Absolute random perturbations are used for the rest of the time.</td>
<td>0.7</td>
</tr>
<tr>
<td>Parameter</td>
<td>Description</td>
<td>Value/Options</td>
</tr>
<tr>
<td>-------------</td>
<td>-----------------------------------------------------------------------------</td>
<td>--------------------------------------------</td>
</tr>
<tr>
<td>GAP.rs_fea</td>
<td>Fraction of generations on which to execute the algorithm</td>
<td>0.2</td>
</tr>
<tr>
<td>GAP.rp_lvl</td>
<td>Reporting level</td>
<td>-1: no reporting</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0: text reporting only</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1: plots and text reporting</td>
</tr>
<tr>
<td>GAP.rp_gbr</td>
<td>Generation between reports</td>
<td>5</td>
</tr>
<tr>
<td>GAP.rp_crh</td>
<td>Custom reporting function handle</td>
<td>[]</td>
</tr>
<tr>
<td>GAP.op_list</td>
<td>List of objectives to make objective plots for</td>
<td>[1]</td>
</tr>
<tr>
<td>GAP.op_style</td>
<td>Style for each objective</td>
<td>0: logarithmic</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1: linear</td>
</tr>
<tr>
<td>GAP.op_sign</td>
<td>Sign of fitness for each objective</td>
<td>-1: negative</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1: positive/mixed</td>
</tr>
<tr>
<td>GAP.pp_list</td>
<td>List of 2 or 3 objectives to be used in Pareto plot</td>
<td>[]</td>
</tr>
<tr>
<td>GAP.pp_xl</td>
<td>x-axis label</td>
<td>'Objective 1'</td>
</tr>
<tr>
<td>GAP.pp_yl</td>
<td>y-axis label</td>
<td>'Objective 2'</td>
</tr>
<tr>
<td>GAP.pp_title</td>
<td>Pareto plot title</td>
<td>'Solution Space'</td>
</tr>
<tr>
<td>GAP.pp_style</td>
<td>Style for each objective</td>
<td>0: logarithmic</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1: linear</td>
</tr>
<tr>
<td>GAP.pp_sign</td>
<td>Sign of fitness for each objective</td>
<td>-1: negative</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1: positive/mixed</td>
</tr>
<tr>
<td>GAP.pp_axis</td>
<td>Axis limits for Pareto plot</td>
<td>[]</td>
</tr>
<tr>
<td>GAP.dp_type</td>
<td>Distribution plot type</td>
<td>1: plot individuals</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2: plot histograms</td>
</tr>
<tr>
<td>GAP.dp_np</td>
<td>Maximum no. of individuals to plot for type 1</td>
<td>100</td>
</tr>
<tr>
<td>GAP.dp_res</td>
<td>Number of bins in distribution plot for type 2</td>
<td>20</td>
</tr>
<tr>
<td>GAP.gd_min</td>
<td>Minimum value of gene ($P.ngenes \times 1$)</td>
<td></td>
</tr>
<tr>
<td>GAP.gd_max</td>
<td>Maximum value of gene ($P.ngenes \times 1$)</td>
<td></td>
</tr>
<tr>
<td>GAP.gd_type</td>
<td>Types of genes ($P.ngenes \times 1$)</td>
<td>1: integer</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2: linear</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3: logarithmic</td>
</tr>
<tr>
<td>GAP.gd_cid</td>
<td>Chromosome ID of gene ($P.ngenes \times 1$)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Used for multiple chromosome case</td>
</tr>
</tbody>
</table>

Table 4.3 Data structure of GAP
Default values for GAP are defined in gapdefault.m. Thus the user can load the gapdefault and then redefine only the required fields, instead of defining all the fields. In the multi-objective optimization problems, default values for GAP can be initialized by using the number of objectives as the argument of GAP. For example, if there are 4 objectives, using gapdefault(4) returns the appropriate GAP.

**Structure: GAS**

The best fitness values, median fitness values, average fitness values, and best chromosomes over the generations are stored in GAS. Current generation number and the number of total objective function evaluations are also stored.

<table>
<thead>
<tr>
<th>GAS.[Field name]</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>GAS.cg</td>
<td>Current generation number</td>
</tr>
<tr>
<td>GAS.medianfit</td>
<td>The median fitness values of each objective (No. of objectives × No. of generations)</td>
</tr>
<tr>
<td>GAS.meanfit</td>
<td>The average fitness values of each objective (No. of objectives × No. of generations)</td>
</tr>
<tr>
<td>GAS.bestfit</td>
<td>The best fitness values of each objective (No. of objectives × No. of generations)</td>
</tr>
<tr>
<td>GAS.bestgenes</td>
<td>The best gene values for each objective over the generations (No. of genes × No. of generations × No. of objectives)</td>
</tr>
<tr>
<td>GAS.ne</td>
<td>The number of the total objective function evaluations</td>
</tr>
</tbody>
</table>

Table 4.4 Data structure of GAS

### 4.2 Algorithm Execution flow

The algorithm execution flow of GOSET is depicted in Figure 4.1. Together with the short description of each step, the related GOSET function names are listed.
Initialization

In this step, the initial population is randomly generated and data structures $P$, $GAP$, and $GAS$ are initialized. When the population does not exist, the initial population of size `GAP.ipop` is randomly generated. Then the fitness value for each individual is evaluated. The other data structures are also initialized accordingly. If the steady-state
population size \texttt{GAP.npop} is smaller than the initial population size \texttt{GAP.ipop}, then the population size is reduced to \texttt{GAP.npop} by discarding inferior chromosomes.

***Genetic operators***

Various genetic operators act on the current population to generate new population. The detailed descriptions on these operators are in Chapter 5.

***Post-processing***

Once the new population has been generated, the best fitness value, the average fitness value, and the gene values of the best individual are stored in the data structure \texttt{GAS}.

***Report plot***

At the completion of the genetic operations, \texttt{GOSET} reports the information on the new population in the gene distribution plot and/or the Pareto plot. In the gene distribution plot, the normalized gene values of the individuals are plotted and also the best fitness value, the average fitness value, the average fitness value, and the worst fitness value over the generations are plotted. In the Pareto plot, the population is plotted in objective function space.

### 4.3 Execution of \texttt{GOSET}

When using \texttt{GOSET} from a MATLAB script, \texttt{GOSET} is initiated by \texttt{gaoptimize.m} that has the following syntax.

\begin{verbatim}
[fP,GAS]=gaoptimize(objhandle,GAP,D,GAS,iP,GUIhdl)
\end{verbatim}

There are 12 arguments for \texttt{gaoptimize.m} which needs to be defined before executing \texttt{GOSET}.

\begin{verbatim}
objhandle
\end{verbatim}

\texttt{objhandle} is the handle of the m-file for the fitness function.
**GAP**  
GAP is the structure of genetic algorithm parameters.

**D**  
D is the optional data for the fitness function.

**GAS**  
GAS is the structure of genetic algorithm statistics. If this does not yet exist, pass an empty matrix ‘[]’

**iP**  
iP is the initial population (a structure). If not used, pass an empty matrix ‘[]’

**GUIhdl**  
GUIhdl is the handle used for GUI. When GUI is not used, pass an empty matrix ‘[]’.

The outputs of *gaoptimize.m* are **Pout** and **GAS**.

**fP**  
fP is the final population (a structure).

**GAS**  
GAS is the structure of genetic algorithm statistics.

The source code for *gaoptimize.m* is given in Figure 4.2. It is easy to verify that *gaoptimize.m* follows the algorithm execution flow given in Figure 4.1. As the *gaoptimize.m* has a simple modularized structure, it can be modified easily so that the users can experiment with their own routine.
Figure 4.2 gaoptimize.m

For the detailed description about running GOSET, refer to Chapter 7 that contains step-by-step illustrations of using GOSET in the command line mode and the GUI mode for several different optimization problems.
In this section, the genetic operators used in GOSET are explained in detail.

5.1 Objective Weighting
5.2 Diversity control
5.3 Scaling
5.4 Selection
5.5 Death
5.6 Mating and crossover
5.7 Mutation
5.8 Migration
5.9 Fitness evaluation
5.10 Elitism
5.11 Random search
5.1 Objective weighting

In the multi-objective optimization problem, there are more than one fitness values for each individual. objwght.m randomly generates a normalized weighting vector to be used for scalarization of the objective function values.

In the multi-objective optimization problem (P.nobj > 1), it is possible to use only one objective function value for fitness evaluation. If the objective function number to be used is specified in GAP.fp_obj, then the output weight vector owv has all zero values except for the element corresponding to the objective function specified by GAP.fp_obj.

5.2 Diversity control

Four different diversity control algorithms are available to maintain the diversity of the solutions in GOSET. These routines generate a fitness weight value for each individual. These fitness weight values constitute the fitness penalty vector (P.pen) that is used for determining an aggregated fitness P.fit in the scaling process. Individuals with many other individuals close to them are assigned a small fitness weight value (thereby reducing the effective fitness) and those with small number of neighboring individuals are assigned with fitness weight value near unity (thus, penalizing the fitness less).

The diversity control can be applied to either the parameter (or decision) space or the fitness function (or objective) space. For the diversity control in the parameter space, use GAP.dc_spc = 1 and GAP.dc_spc = 2 is for the diversity control in the fitness function space.

a. Diversity control algorithm 1 (GAP.dc_alg = 1)

In this approach, the number of neighboring individuals of each individual is counted. The neighboring individuals are those within the threshold distance which is determined as

Threshold distance = (mean distance between points) × α,

where $\alpha = (\text{GAP.dc_mnt} + \text{rand} \times (\text{GAP.dc_mxt} - \text{GAP.dc_mnt}))$.

Then the fitness weight of an individual is the reciprocal of the counted number of individuals. Figure 5.1 illustrates this method with three examples.
While very systematic, one major drawback of this approach is the necessity of evaluating the distance between all the individuals which requires a computation time proportional to the square of the population.

### b. Diversity control algorithm 2 (GAP.dc_alg = 2)

This approach is based on the idea that individuals with similar gene values have similar weighted sum of their gene values for any weight vector. In this method, first an integer weight vector is generated at random, where the element value come from the integer set \{1, 2, ..., P.ngenes\}. Then the weighted sum of the normalized genes for each individual is evaluated. Individuals with similar weighted sum values are grouped and put into bins based on the weighted sum. The total number of bins are randomly chosen from \{\text{GAP.dc_mnb} \times \text{GAP.fp_npop}, ..., \text{GAP.dc_mx} \times \text{GAP.fp_npop}\}. For the individuals in a specific bin, their fitness penalty weights become the reciprocal of the number of individuals in that bin.

Since it is possible that two individuals with drastically different gene values have similar weighted sum for some weight vector, this procedure is repeated \text{GAP.dc_ntr} times and the largest fitness penalty weight is chosen as the final fitness penalty weight for each individual. This reduces the chance of assigning an individual a smaller fitness penalty weight than appropriate.

Figure 5.2 shows an illustration of the diversity control algorithm mentioned above. For example, if we look at the bin No. 1, there are two individuals. So the penalty value for the individuals in bin No. 1 is \(\frac{1}{2}\), and likewise, the penalty value of the individual in bin No. 5 is \(\frac{1}{4}\).
Random weight
vector

Group individuals according to their weighted sum

Bin No. 1 2 3 4 5

Figure 5.2 Illustration of diversity control method 2.

Although this approach is not as systematic as the first approach, the computation time is proportional to the population size, not the square of the size.

c. Diversity control algorithm 3 (GAP.dc_alg = 3)

The idea of this diversity control algorithm is similar to the diversity algorithm 1. Instead of using the count of solutions in a neighborhood, the sum of infinity norm between a solution and all the other solutions is used to determine the penalty value. The fitness penalty weight for \( k \)’th individual is express as

\[
P_{pen}^k = \frac{1}{\sum_{i=1}^{n} \exp \left( -\frac{d_{i,k}}{d_c} \right)},
\]

where \( d_{i,k} \) is the infinity norm between \( k \)’th and \( i \)’th individual, that is, the maximum absolute gene difference between \( k \)’th and \( i \)’th individual and \( d_c \) is the distance constant (GAP.dc_dc) which controls the size of the neighborhood. If a small \( d_c \) is used, then the effective size of the neighborhood is also small. Thus only the solutions with many neighboring solutions that are very close to them are penalized severely and most of other solutions are not penalized. As the \( d_c \) increases, the effective size of the neighborhood increases and the penalty level also increases.

The fitness penalty weight in the algorithm 3 can take continuous value rather than discrete value as in the algorithm 1. As with the algorithm 1, the distance evaluation
between all the individuals requires a computation time proportional to the square of the population.

d. Diversity control algorithm 4 (GAP.dc_alg = 4)

This approach is identical to the diversity control algorithm 3. However, only GAP.dc_nt individuals among the population are randomly selected for the distance evaluation. The random selection of the individuals is performed for each different individual. This reduces the computational load at the cost of some inaccuracy in the distance measurement. The fitness penalty weight for \( k \)’th individual is express as

\[
P_{pen}^k = \frac{1}{1 + \frac{\text{Number of population in the region}}{\text{GAP.dc_nt}} \sum_{i=1}^{\text{GAP.dc_nt}} \exp \left( -\frac{d_{i,k}}{d_c} \right)},
\]

where \( d_{i,k} \) is the infinity norm between \( k \)’th and \( i \)’th individual, \( d_c \) is the distance constant (GAP.dc_dc).

5.3 Scaling

In the early stage of the evolution, if there are few individuals with very large fitness values, then these strong individuals will dominate the entire population very quickly which can lead to convergence to some local optimum without thorough exploration of the search space. This is called as premature convergence. Towards the end of the evolution, when the population is almost converged with most of the individuals sharing similar fitness values, then the competition among individuals is weak and the evolution process slows down. As a remedy to both these problems, scaling can be employed to maintain the appropriate evolution pressure throughout the evolution process. Scaling is also useful in the multi-objective optimization problems that have different scales in the objective functions.

As the first step in the scaling operation, the fitness values are scaled using one of the six scaling methods. After scaling, all negative fitness values are clipped to zero, and then the objective function weight vector (GAP.owv) is applied to scalarize the fitness values (P.mfit) in the multi-objective optimization. Finally, the penalty vector (P.pen) is applied and the scalarized the fitness values are penalized to yield the aggregated fitness values (P.fit) that are used in the selection operation.
Several different scaling methods are available in GOSET. Options include no-scaling, offset scaling, standard linear scaling, modified linear scaling, mapped linear scaling, sigma truncation, and quadratic scaling. These methods are described below.

**a. No scaling** \( (\text{GAP.sc}_\text{alg} = 0) \)

Scaling is not applied and the actual fitness value is used as shown in Figure 5.3. This option is primarily intended for fitness functions that have been carefully constructed so that no scaling is necessary.

\[
\begin{align*}
    f' &= af + b \\
    f_{\min} &\leq f \leq f_{\max} \\
    f' &= 0 \\
    f_{\max} &= f_{\max} - f_{\min} \\
    a &= 1 \\
    b &= 0
\end{align*}
\]

![Figure 5.3 No scaling](image)

**b. Offset scaling** \( (\text{GAP.sc}_\text{alg} = 1) \)

In this method, fitness values are mapped linearly such that the minimum fitness value is mapped to 0 and the maximum value is mapped to \( f_{\max} - f_{\min} \).

\[
\begin{align*}
    f' &= af + b \\
    f_{\min} &\leq f \leq f_{\max} \\
    f' &= 0 \\
    f_{\max} &= f_{\max} - f_{\min} \\
    a &= 1 \\
    b &= -f_{\min}
\end{align*}
\]

![Figure 5.4 Offset scaling](image)
c. **Standard linear scaling** \( (\text{GAP.sc\_alg} = 2) \)

In this method, a linear scaling is used in such a way that the average fitness is not modified and the maximum fitness is \( \text{GAP.sc\_kln} \) times the average fitness value.

\[
\begin{align*}
    f' &= af + b \\
    k &= \frac{(k - 1)f_{\text{avg}}}{f_{\text{max}} - f_{\text{avg}}} \\
    b &= f_{\text{avg}}(1 - a) \\
    f_{\text{avg}} &= \frac{f_{\text{min}} + f_{\text{max}}}{2}
\end{align*}
\]

\( f_{\text{avg}} \) = original fitness \( \quad \) \( f' \) = scaled fitness

\( k \) = \( \text{GAP.sc\_kln} \)

![Figure 5.5 Standard linear scaling](image)

---

d. **Modified linear scaling** \( (\text{GAP.sc\_alg} = 3) \)

In this method, a linear scaling is applied in such a way that the median fitness is not modified and the maximum fitness is \( \text{GAP.sc\_kln} \) times the median fitness value.

\[
\begin{align*}
    f' &= af + b \\
    k &= \frac{(k - 1)f_{\text{med}}}{f_{\text{max}} - f_{\text{med}}} \\
    b &= f_{\text{med}}(1 - a) \\
    f_{\text{med}} &= \text{median of fitness}
\end{align*}
\]

\( f_{\text{med}} \) = median fitness \( \quad \) \( f' \) = scaled fitness

\( k \) = \( \text{GAP.sc\_kln} \)

![Figure 5.6 Modified scaling](image)

---

e. **Mapped linear scaling** \( (\text{GAP.sc\_alg} = 4) \)

This method is another linear scaling that maps the maximum fitness to \( \text{GAP.sc\_kln} \) and the minimum fitness to 1.
f. **Sigma truncation** (*GAP.sc_alg = 5*)

In the sigma truncation method, all the fitness values smaller than \((f_{\text{avg}} \times GAP.sc\_cst} \times f_{\text{std}})\), where \(f_{\text{avg}}\) is the average fitness value and the \(f_{\text{std}}\) is the standard deviation of the fitness values, are mapped to negative values and therefore disregarded later by clipping to zeros. It is useful when there are a few individuals with very small fitness value and most individuals have large fitness values.

\[
a = \frac{k - 1}{f_{\text{max}} - f_{\text{min}}} \\
b = -f_{\text{min}} \cdot a + 1 \\
k = GAP.sc.kln
\]

\[f' = af + b\]

**Figure 5.8 Sigma truncation scaling**

---

**g. Quadratic scaling** (*GAP.sc_alg = 6*)

This algorithm emphasizes the large fitness value and deemphasizes the small fitness value. The maximum fitness value is mapped to \(GAP.sc.kmxq\), the average fitness value to 1, and the minimum fitness value to \(GAP.sc.kmnq\). The quadratic scaling is the only nonlinear scaling method in GOSET.
5.4 Selection

The selection operators choose individuals from the population to constitute a mating pool for reproduction. When the multiple regions are used, selection operations are confined to each region. For each region, the selection operator picks same number of chromosomes as those in the current region and moves them to the mating pool for that region.

There are two pre-defined selection operators that the user can choose from. They are roulette wheel selection and tournament selection.

**a. Roulette wheel selection**

Each individual is assigned with the selection probability that is proportional to the aggregate fitness value \( P_{fit} \). Then individuals are chosen based on the selection probability. It is more likely that the better individual is chosen and copied to the mating pool which mimics principle of the survival of the fittest.

**b. Tournament selection**

Number of individuals are randomly chosen from the population and their aggregate fitness values \( P_{fit} \) are compared. Then the individual with the best fitness value is selected to be in the mating pool.

Illustrations of these selection operators are in the section 2.2.

---

Figure 5.9 Quadratic scaling
**Custom algorithm**

In the case that the user wants to use his/her own selection algorithm, the custom algorithm handle `GAP.sl_cah` can be defined as long as the algorithm follows certain format. The details regarding the custom algorithm can be found in the Appendix B.

### 5.5 Death

Death operator determines which individual is to die and replaced by the children. The followings are possible options for the death operators.

a. **Replacing parents**

   Parents are replaced by their own children.

b. **Random selection**

   The parents to be replaced are randomly chosen.

c. **Tournament on fitness**

   The parent to be replaces is determined via the tournament based on the aggregate fitness value. `GAP.dt_nts` number of parents are randomly chosen for a tournament and the one with worst aggregate fitness value is marked for death.

d. **Tournament on age**

   The parent to be replaces is determined via the tournament based on the age. Among the randomly chosen `GAP.dt_nts` number of parents, the oldest one is marked for death.

e. **Custom algorithm**

   User defined custom death algorithm is used. The custom function handle is assigned to `GAP.dt_cah`. Refer to the Appendix B for the details on the format of the custom algorithm.

f. **Random algorithm**
If this option is selected, the death algorithm is randomly chosen among the first four death algorithms at each generation.

## 5.6 Mating and crossover

There are three different crossover operators in GOSET. All the crossover operation is performed on the normalized gene values and the actual gene values are updated based on the crossovered normalized gene values.

These crossover operations have correction routine for illegal genes. That is, if a gene value lies outside of the allowed range $[0, 1]$ after the crossover operation, that gene value is automatically fixed using the *ring-mapping*. Ring-mapping maps a value to the modulus after division by 1. For example, if a resultant gene value is 1.2, it is adjusted to 0.2, and if it is -2.1, it is adjusted to 0.9.

### a. Single point crossover

This crossover operator is similar to the crossover operator in binary-coded GAs. In multiple chromosome setting, single point crossover occurs in each chromosome. The following example shows a single point crossover operation on individuals with two chromosomes.

![Crossover points](image)

**Figure 5.10** Single point crossover with two chromosomes

### b. Simple blend crossover

In the simple blend crossover, the children are generated from the weighted sum of their parents. It is implemented so that the gene values of the two children have same distance from the average value of the gene values of the parents. Figure 5.11 illustrates how simple blend crossover works. Filled circles represent the gene values of parents positioned at $p$ and $q$ respectively, and white circles represent those of children. The gene values of children can take any values between $(3p - q)/2$ and $(3q - p)/2$ and they are equally distanced from the center of $p$ and $q$. 
Scalar simple blend crossover

In the scalar simple blend crossover operation, each gene position has different ratio of blending. For example, two parents

\[
\text{Parent 1} = [0 \ 0.8 \ 0.3] \quad \text{and} \quad \text{Parent 2} = [1 \ 0.2 \ 0.5]
\]

can generate

\[
\text{Child 1} = [0.25 \ 0.95 \ 0.4] \quad \text{and} \quad \text{Child 2} = [0.75 \ 0.05 \ 0.4]
\]

via scalar simple blend crossover. The first gene values moved 25% of their distance towards the average value of them. The second gene, -25%. And the third gene, 50%.

Vector simple blend crossover

In the vector simple blend crossover operation, all the genes are blended using same ratio. For example, two parents

\[
\text{Parent 1} = [0 \ 0.8 \ 0.3] \quad \text{and} \quad \text{Parent 2} = [1 \ 0.2 \ 0.5]
\]

can generate

\[
\text{Child 1} = [0.25 \ 0.65 \ 0.35] \quad \text{and} \quad \text{Child 2} = [0.75 \ 0.35 \ 0.45].
\]

For all three genes, the parent gene values are blended in such a way that they moved 25% of the distance between them towards their average values.

c. Simulated binary crossover
As the name suggests, the simulated binary crossover operator mimics the behavior of the single-point crossover operator in binary-coded genetic algorithm. Detailed description of the simulated binary crossover operator is beyond the scope of this manual and only the basic concepts are introduced here. Interested readers are referred to [p109, Deb01]

![Crossover point distribution](image)

Figure 5.12  Single point crossover example

Figure 5.12 illustrates an example of the single point crossover operation on the binary chromosomes. Note that the average values are same before and after the crossover operation. Hence, the amount of increase in one chromosome is same as the decrease in another chromosome and the children are equally distanced from the center point of the parents.

Each point of the chromosome has the same probability to be selected as a crossover point. And the crossover in the lower bit results in children closer to the parents point. Thus the values of children are more like to be near the values of parents. With these investigations, the single point crossover can be simulated in real-coded genetic algorithms by using the probability density for the children as in Figure 5.13.

![Probability density](image)

Figure 5.13  Simulated binary crossover

In Figure 5.13, it is assumed that the parents are positioned at 0.3 and 0.6. The distribution index $\eta_c$ is a non-negative real number that controls the spread of the
children. If the distribution index $\eta_c$ is large, the probability of generating children that are closer to the parents are higher. As the distribution index $\eta_c$ becomes smaller, it is allowed to create solutions that are far from the parents.

As in the simple blend crossover, there are scalar simulated binary crossover and vector simulated binary crossover depending on whether the each gene value is crossovered using same ratio or each gene value is crossovered independently.

**d. Random crossover**

When $\text{GAP.mc_alg}$ is set to 6, GOSET chooses a mating crossover algorithm randomly among the five methods described above. They are

- Single point crossover
- Scalar simple blend crossover
- Vector simple blend crossover
- Scalar simulated binary crossover
- Vector simulated binary crossover.

For every $\text{GAP.mc_gac}$ generation, the crossover algorithm changes randomly.

### 5.7 Mutation

The mutation operators of GOSET can be categorized into three types as described in this section. All the mutation operations are applied to the normalized gene value and the actual gene values are updated based on the mutated normalized gene values.

**a. Total mutation**

With the probability of $\text{GAP.mt_ptgm}$, each gene value can be replaced by a new randomly generated gene value within the prescribed range that is defined by $P_{\text{max}}$ and $P_{\text{min}}$. For the integer type gene, the gene value takes any integer value within the allowed range.

In the following figure, let us assume that the real-typed third gene is mutated. As the mutation is applied to the normalized gene values, each gene has a value between 0 and 1.
Two types of partial mutations are employed. They are the relative partial mutation and the absolute partial mutation. Integer genes are not involved in the partial mutations.

These mutation operations have correction routine for illegal genes. That is, if the mutated gene value lies outside of the allowed range, i.e. $[0, 1]$, the mutated gene value is automatically ring-mapped. Ring-mapping maps a value to the modulus after division by 1. For example, if the resultant gene value is 1.7, it is adjusted to 0.7, and if it is -0.6, it is adjusted to 0.4.

**Relative partial mutation**

With the probability of $\text{GAP.mt_prgm}$, each gene value is perturbed by certain fraction of the current gene value. The amount of perturbation is obtained using a Gaussian random variable with standard deviation of $\sigma_{\text{rgm}}(\text{GAP.mt_srgm})$.

The figure 5.15 illustrates a relative partial mutation on the third gene, when the Gaussian random variable $N(0,\sigma_{\text{rgm}})$ has a value -0.055.
**Absolute partial mutation**

With the probability of GAP.mt_pagm, each gene value is added with a Gaussian random variable with zero mean and standard deviation of $\sigma_{agm}(GAP.mt_sagm)$.

![Mutation Point Diagram]

**Figure 5.16 Absolute partial mutation**

The figure 5.16 illustrates a relative partial mutation on the third gene, when the Gaussian random variable $N(0,\sigma_{agm})$ has a value 0.55.

c. **Vector mutation**

Vector mutation is very similar to the partial mutation. However, the vector mutation changes the each and every gene of the individual undergoing mutation. Integer genes do not participate in the vector mutations.

These mutation operations also have ring-map correction routine for illegal genes as in the partial mutation.

**Relative vector mutation**

Each individual undergoes relative vector mutation with the probability of GAP.mt_prvm. Every gene value of the individual is perturbed by certain fraction of the current gene value. The amount of perturbation is obtained using

$$\text{Random vector} = v_{dir} \cdot N(0,\sigma_{rvm})$$

where $v_{dir}$ is a normalized random vector ($P_{genes} \times 1$) specifying the direction of perturbation and $N(0,\sigma_{rvm})$ is a Gaussian random variable with mean 0 and standard deviation GAP.mt_srvm.
The figure 5.17 illustrates a relative vector mutation when the random vector is given as
\[
[0.03, -0.15, -0.08, 0.18, -0.08].
\]

**Absolute vector mutation**

Each individual undergoes absolute vector mutation with the probability of GAP.mt_pavm. If an individual mutates, each and every gene value of the individual is added with a random vector

\[
\text{Random vector} = v_{dir} \cdot N(0, \text{GAP.mt_savm}),
\]

where \(v_{dir}\) is a normalized random vector \((P_{genes} \times 1)\) specifying the direction of perturbation and \(N(0, \sigma_{avm})\) is a Gaussian random variable with mean 0 and standard deviation GAP.mt_savm.

The figure 5.18 illustrates an absolute vector mutation with the random vector
\[
[-0.01, 0.02, 0.01, 0.0, -0.01].
\]

**d. Integer mutation**

Integer mutation is applied only to integer genes. Each gene is mutated to a randomly generated integer within the allowed range with the probability of GAP.mt_igm.
5.8 Migration

Migration is meaningful only when there are multiple regions defined, that is, \( \text{GAP.mg_nreg} > 1 \). This operator selects some individuals in the population and moves them to different regions. Each individual is migrated with the probability of \( \text{GAP.mg_pmig} \). The parameter \( \text{GAP.mg_tmig} \) determines the frequency of applying the migration operator and the migration interval is randomly chosen between \( 0.5 \times \text{GAP.mg_tmig} \) and \( 1.5 \times \text{GAP.mg_tmig} \). For example, if \( \text{GAP.mg_tmig} \) is set to 4, then the possible migration intervals are 2, 3, 4, 5, and 6 generations.

5.9 Fitness evaluation

In this step, the fitness values of all individuals are evaluated. \( \text{GAP.ev_bev} \) determines whether to evaluate the fitness of an individual at a time (\( \text{GAP.ev_bev} = 0 \)) or to evaluate the fitness of the entire population at once (\( \text{GAP.ev_bev} = 1 \)).

When an individual is moved from the previous generation without any change, the fitness value of the individual does not change and there is no need to evaluate the fitness again. In this case, GOSET can evaluate only the unevaluated individuals by setting \( \text{GAP.ev_are} = 0 \). Setting \( \text{GAP.ev_are} = 1 \) will force GOSET evaluate all individuals.

Evaluation of the fitness usually requires only the gene values of the individual (\( \text{P.gene} \)). If the optional data \( \text{D} \) is specified for the \text{gaoptimze} function call, then the optional data is also passed to the fitness function. On top of this, other information like age(\( \text{P.age} \)), previous fitness function values(\( \text{P.mfit} \)), and region(\( \text{P.region} \)) can be send to the fitness function by setting \( \text{GAP.ev_ssd} = 1 \). The order of the information passed to the fitness function is \( \text{P.gene}, \text{P.age}, \text{P.mfit}, \text{P.region}, \) and \( \text{D} \).

There are many different ways to define a valid fitness function for a given optimization problem. One fundamental rule is that the better gene should have more positive fitness function value than those of inferior genes.

As an example, let’s look at the minimization problem of Powell function. The Powell function [CHO96] is described as
\[ f(x_1, x_2, x_3, x_4) = (x_1 + 10x_2)^2 + 5(x_3 - x_4)^2 + (x_2 - 2x_3)^4 + 10(x_1 - x_4)^4. \]

It is the minimization problem and the smaller function value is better. Hence, we can simply take the negative of \(f(x)\) as the fitness function. The following is the fitness evaluation routine in m-file for the problem of minimizing Powell function with \(-f(x)\) as the fitness function.

```matlab
function fv = powell(x)
    x1 = x(1);
    x2 = x(2);
    x3 = x(3);
    x4 = x(4);
    f = (x1 + 10*x2)^2 + 5*(x3 - x4)^2 + (x2 - 2*x3)^4 + 10*(x1-x4)^4;
    fv = -f;
end
```

The Powell function always takes the nonnegative value, and thus the inverse of \(f(x)\) can be another valid fitness function. A small positive value is added to the denominator to avoid the possible singularity at the optimum point. In this case, the last line of above m-file is replaced by the following line.

```matlab
fv = 1/(0.001+f);
```

### 5.10 Elitism

Elitism is a device to insure that the fittest individual in a population is preserved unless a better fit individual is found.

**Single-objective optimization case**

Old population \[\rightarrow\] Genetic operation \[\rightarrow\] New population

1. Pick the best chromosome
2. Put the better chromosome back
Elitism in the single objective optimization is straightforward. The best individual of the population $P_k$ and the best individual of the population after the genetic operations performed are compared. The better of the two becomes a member of the next population. As this operation is confined within a region, the best one of each region is preserved for the multi-region case.

Even in the multi-objective optimization case, there are cases that it is desirable to use only one specific fitness function value for elitism. This can be done by setting $\text{GAP.fp_obj}$ to the number indicating a specific objective function. The elitism, then, performs in the same way as with the single-objective optimization using only one objective function value.

**Multi-objective optimization case**

In the multi-objective optimization case, the objective of elitism is to preserve non-dominated solutions. Thus, it is necessary to retain multiple individuals.

First, the old population and the modified population in the same region are combined, and the non-dominating solutions are found.

As the number of non-dominated solution can increase, the number of non-dominated solutions is limited to

\[
\text{Maximum No. of non-dominated solutions} = \text{GAP.el_fpe} \times (\text{No. of individuals in the region}).
\]

If the reserved space for the non-dominating solutions is enough for the non-dominating solutions just found, then some individuals corresponding to dominated solutions are randomly removed from the population and replaced by non-dominated solutions. If the reserved space cannot accommodate all the non-dominated solutions, then the appropriate number of non-dominated solutions are chosen using a diversity control algorithm and placed in the population for the next generation.
5.11 Random search

Random search operator is specialized for a local search. It can reduce the convergence time significantly near the optimum point. In the initial stage of the evolution when the active exploration is desirable, it is unnecessary to apply random search. The parameter GAP.rs_fgs specifies the point of starting the random search. If GAP.rs_srp = 0.2, then the random search is inactive for the first 20 percent of entire generation. At each generation with the active random search, the random search occurs with the probability given by GAP.rs_fea.

Given the best solution, random search operator generates mutants of the best chromosome. Mutants are generated in the same way as the relative vector mutation based on GAP.rs_srp and the absolute vector mutation with GAP.rs_sap. The relative vector mutation is chosen with the probability of GAP.rs_frp and the absolute vector mutation is chosen with the probability of (1 − GAP.rs_srp). The number of the generated mutants is determined by the parameter GAP.rs_fps that specifies the fraction of the total population size, that is

\[
\text{The number of mutants} = \text{GAP.rs_fps} \times \text{Size of the population}.
\]

Then the best solution among the mutants is found and this solution replaces the existing best only if this solution is better than the existing best solution.
References


Chapter 6

GOSET
Graphical User Interface (GUI)

In this section, the GOSET GUI is introduced. GOSET GUI provides an intuitive and convenient method to use GOSET.

6.1 GOSET GUI
6.2 Main Window
6.3 Menu bar
6.4 Evolution status, output report and start/stop/continue buttons
6.5 Main menu
6.1 GOSET GUI

GOSET has the built-in graphic user interface (GUI) that provides an intuitive interface for the user. With the GOSET GUI, the user has total control over GOSET without having to remember parameter names or consult the documentation.

GOSET GUI also provides extra features that help the user to utilize GOSET more efficiently. Some of them are listed below.

**Stop & Continue:**

GOSET can be stopped at any time of the evolution process. The user may want to change some parameters, check the best chromosome value, or manipulate with the current population. The evolution process also can be resumed from the point it was stopped.

**Project save & load:**

The current population and all the parameters can be saved for later use. When the saved project is loaded, the evolution process can be resumed as if it is continued from the moment the project was saved.

**View & save setting:**

Current parameter settings for GA operators, gene definitions and fitness function information can be viewed. It is also possible to save these information in a text file.

**Best chromosome value display:**

The actual values of the best chromosome together with the gene description can be viewed.

**Mouse-on help:**

For the most GUI objects, mouse-on help is provided for efficient documentation.

*Example*

![Example](image)

**Flexibility in the optional data for the fitness function:**
For the optional fitness function data, a vector with actual numerical elements, a variable name in the workspace or a `.mat` file name containing the appropriate data can be used.

### 6.2 Main window

The GOSET GUI can be initiated by typing `goset` in the MATLAB command window. If the GOSET GUI does not start, refer to Section 1.3 to check if the GOSET is properly installed.

The main window of GOSET GUI is shown in Figure 6.1. There are five sections in the main window:

- Menu bar
- Evolution status display
- Output report option
- Start/Stop/Continue buttons
- Main menu
We will look at each part of the GOSET GUI in the following sections.

6.3 Menu bar

The menu bar, shown below, is located at the top of the main GOSET GUI window.

![Menu bar of the GOSET GUI](image)

The menu bar has the following menus.

- File
- Setting
- Option
- Help

a. File menu

File menu has submenu as in Figure 6.3.

![File menu of GOSET GUI](image)

**Save current project**: Store all the information of current generation including the population information and the parameters of genetic operators.

**Load saved project**: Load a previously saved project.
Recent files: Five most recently accessed fitness function files are listed. They can be loaded directly by clicking them.

Exit GOSET: Close GOSET GUI. The shortcut key is Ctrl+Q.

b. Setting menu

Parameter settings of the current project can be viewed and the default settings can be loaded. Figure 6.4 shows the setting menu.

![Setting menu of GOSET GUI](image)

Figure 6.4 Setting menu of GOSET GUI

View setting: Display the fitness function information, gene parameters, parameters of GA operators as in the following figure.

![Setting Viewer](image)

Figure 6.5 Setting Viewer

Selecting ‘Fitness function’, ‘Gene parameters’, and ‘GA operators’ will display corresponding information.
‘Export to text file’ button on the upper right corner of the setting window saves all these information to a text file.

**Load default setting:** Load default setting for GA operators. The fitness function, gene parameters are unchanged.

c. **Option menu**

Currently, the option menu has only one submenu ‘Extra user routine’ as in Figure 6.6.

![Option menu](image)

Figure 6.6 Option menu

**Extra user routines:** Define M-files to be executed before and after the GA.

![User routine input box](image)

Figure 6.7 User routine input box

d. **Help menu**

There is one submenu ‘About GOSET’ in Help menu as shown in Figure 6.8.

![Help menu](image)

Figure 6.8 Help menu

**About GOSET:** Display information on GOSET.
**Forced Exit:** Forcefully terminate GOSET GUI when the exit does not working.

### 6.4 Evolution status, output report, and start/stop/continue buttons

#### a. Evolution status display section

Evolution status display section shows the current generation number, the best fitness value, and the average fitness value. It also has a progress bar visualizing the evolution process with the completion percentage.

![Evolution status](image)

Figure 6.9 Evolution status

#### b. Output report option

The level of output report, the report interval and the computation time report flag can be set according to the need of the user. The plot of current generation and gene value of the best individual can be displayed.

![Output report](image)

Figure 6.10 Output report option

**Report level:** Define the output report level. There are three options in the report level.

*None:* output report is not given.
**Text only:** Text report of the generation number, the best fitness value, average fitness value, median fitness value, and the number of evaluations in the MATLAB main window.

*Example*

Statistics for generation 46
Best fitness = -0.12645
Mean fitness = -3.0653
Median fitness = -1.6876
Number of evaluations = 2928

**Text and plot:** Together with text report in the MATLAB main window, the plot is displayed and updated every generation as defined by the plotting parameters.

**Report interval:** Set the number of generations between reports.

**Report computation time:** When checked, the time spent on each GA operation is displayed. If the report level is set to ‘None’, the computation time is not reported.

*Example*

Absolute computation times for generation 56
OWV: 0.00e+000 DC: 3.20e-002 SCALE: 0.00e+000
SELECT: 0.00e+000 MC: 3.10e-002 MUT: 0.00e+000
MIGRATE: 0.00e+000 EVAL: 1.50e-002 ELITE: 0.00e+000
RS: 0.00e+000 STAT: 0.00e+000 REPORT: 4.70e-002

Relative computation times for generation 56
OWV: 0.00 DC: 25.60 SCALE: 0.00
SELECT: 0.00 MC: 24.80 MUT: 0.00
MIGRATE: 0.00 EVAL: 12.00 ELITE: 0.00
RS: 0.00 STAT: 0.00 REPORT: 37.60

**Plot current:** Display the plot of current generation as defined in the plotting parameters.

**Display best:** Show the gene number, its description and the actual value of it as in Figure 6.11.

![Gene values of the best individual](image)

**Figure 6.11** Gene values of the best chromosome
c. Start/stop/continue buttons

Start, stop and continue buttons are enabled and disabled depending on the situation, as shown in Figure 6.12.

![Status of buttons](image)

For example, when the GOSET is stopped before reaching the last generation, the start and the continue buttons are enabled. If the continue button is pressed, the evolution process is resumed from where it is stopped. If the start button is pressed, all the evolution result accumulated up to that point will be discarded and the GA starts from the generation number 1.

6.5 Main menu

The fitness function information, the definition of the genes, plotting parameters and all the genetic operator parameters are defined in the main menu.

There are 14 buttons in the main menu section. When each button is pressed, the corresponding parameter input box will appear. In most case, it is clear what to do with these input fields. Therefore, we will look at only a part of the main menu section.

a. Fitness function button

The fitness function button and the fitness function name field are shown in Figure 6.13.
**Fitness function button:** Open the fitness function parameter input box shown below.

![Fitness Function Input Box](image)

**Mode of optimization:** For the single objective optimization problem, ‘S’ is displayed. And ‘M’ is shown for the multi-objective optimization problem.

**Fitness function name:** Display current fitness function file name.

**b. Gene parameters**

The total number of genes and their descriptions, maximum values, minimum values, gene types, and the chromosome number are defined.
When a gene number is selected using the slide bar, its gene description, minimum and maximum values, type and chromosome ID are shown in the following fields. Gene description can be used to specify what each gene is representing.

**c. Fundamental parameters**

The total number of generations for evolution, the initial population size, the regular population size, the number of objective functions and the objective function number to be used in the optimization are defined.

For multi-objective optimization, use value 0 in the objective function to optimize. Even if there are multiple objectives, a specific objective function can be used for the optimization, in which case, it becomes single-objective optimization problem.
**d. Diversity control**

Diversity control has ON/OFF toggle switch and the user can decide whether to use the diversity control operator or not.

![Diversity control ON/OFF button](image)

Figure 6.17 Diversity control ON/OFF button

In the parameter input box, the diversity algorithm and other parameters are defined. The diversity control can be applied to either the parameter space or the fitness function space.

![Diversity Control input box](image)

Figure 6.18 Diversity control input box

**e. Elitism**

Elitism has the ON/OFF toggle switch to activate or deactivate it as in the diversity control.

![Elitism ON/OFF button](image)

Figure 6.19 Elitism ON/OFF button
In this section, some optimization problems are considered with step-by-step guidance to familiarize the users with GOSET. Each problem is solved using both the command line approach and the GUI approach.

7.1 Rosenbrock’s banana function
7.2 Tanaka problem
7.3 Power diode curve fitting
7.4 Transfer function fit
7.1 Rosenbrock’s banana function

Problem description

Rosenbrock’s function [p.55, CHO96] is a real-valued function given in the following:

\[ f(x_1, x_2) = 100(x_2 - x_1^2)^2 + (1 - x_1)^2 \]

We want to find the minimizer of the function \( f(x_1, x_2) \). Rosenbrock’s function and its level sets are depicted in Fig. 7.1. Due to the shape of level sets that resemble bananas, it is also referred to as the banana function. The global optimizer of Rosenbrock’s function is at \((1, 1)\) where the function has its value 0.

![Figure 7.1 Rosenbrock’s function](image1)

![Figure 7.2 Level sets](image2)

Before using GOSET, the fitness function for the given problem needs to be defined as an mfile. There are many different ways to define a valid fitness function. As it is a minimization problem and the Rosenbrock’s function value is non-negative, one simple way is to take the inverse as the fitness function. A small positive value is added to the denominator to prevent the singularity of the fitness function value at the minimizer. The following mfile `banana.m` defines a fitness function for Rosenbrock’s function.
The above mfile is located in the folder 'Rosenbrock' under 'goset 1.0x examples' folder.

a. Command line approach

With the fitness function defined, we are now ready to use GOSET to find the minimizer of the Rosenbrock’s function.

First of all, GAP and other parameters related to the population need to be determined.

```
GAP = gapdefault;
GAP.fp_nngen = 200; % Total generation number
GAP.fp_ipop = 100; % Initial population size
GAP.fp_npop = 100; % Population size
GAP.op_style = 0; % Logarithmic scale for objective plot
```

`gapdefault` is used to define GAP and only some parameters are redefined. For the detailed information regarding the default setting of GAP, refer to `gapdefault.m`.

The values of $x_1$ and $x_2$ become the gene values, and their minimum, maximum values are defined as

```
GAP.gd_min = [-2 -1 ];
GAP.gd_max = [ 2 3 ];
```

The types of the genes are given in the vector,

```
GAP.gd_type = [ 2 2 ];
```

And employing only one chromosome for all the genes results in the following chromosome ID vector

```
GAP.gd_cid = [ 1 1 ];
```
All the parameters are defined in the MATLAB workspace, and thus we can execute GOSET by

\[
[P,GAS] = \text{gaoptimize(@banana,GAP,[],[],[],[]);}
\]

All the above commands are in the script file ‘runme.m’ located in the same folder as ‘banana.m’, so type ‘runme’ in the main window to start GOSET.

Observe that the fitness function handle name is ‘@banana.’

As the default value for the report level is set to \( \text{GAP.rlp}_\text{lvl} = 1 \), a plot will appear to show the normalized objective function values and the fitness function values as the GOSET evolves over the generations. Figure 7.3 is the report plot after 200 generations.

![Figure 7.3 Report plot for Rosenbrock’s function](image)

There is also the text report displayed in the MATLAB main window. For this example the text report is:

Statistics for generation 1
Best fitness = 16.3028
Mean fitness = 0.19982
Median fitness = 0.0074076
Number of evaluations = 100
.
.
.
Statistics for generation 200
Best fitness = 999.9466
Mean fitness = 304.7056
Median fitness = 199.2891
Number of evaluations = 12687

The generation number and the best, mean, and median fitness values together with the
number of evaluations are reported.

The best gene values can be found by checking the last element of GAS.bestgenes.

>> GAS.bestgenes(:,200)

ans =
1.0003
1.0005

The resultant minimizer found by GOSET turned out to be very close to the actual
minimizer (1, 1).

b. GUI approach

The procedure for GUI approach is very similar to that of command line approach. The
main difference is that the parameters are defined in the GUI window, not in the
MATLAB command window or a script M-file.

To start the GOSET GUI, type ‘goset’ in the MATLAB command window.

Then the GOSET GUI window will appear.
Fitness function selection

The first step is choosing the fitness function. Click ‘Fitness function’ button in the main menu.

Then, click browse button.

After locating the fitness function ‘banana.m’, select it and click ‘open.’
Click ‘Apply’ button to finish selecting the fitness function.

Parameter input

Once the fitness function is chosen, we are ready to define gene parameters. Select gene parameters button.

The default value for the gene number is 3. There are 2 gene values in this problem, so change the gene number to 2.

Then, for each gene, the minimum, maximum, gene type, and chromosome ID number need to be defined. Gene description can also be assigned if necessary. For the first gene, move the slider bar to so the number at the right of ‘Parameters of the gene #’ is 1 and type information as in the following figure.
For the second gene, use the slider bar again to select 2\textsuperscript{nd} gene and enter the appropriate information as in the following figure and click apply.

Then select fundamental parameters button in the main menu.

In the input fields, insert parameter values as in the following and click apply.
The last parameters to be adjusted are the plotting parameters, so click it.

Set the plot scale for the objective plot to 0 (logarithmic scale), select ‘Gene value’ for the distribution plot type and click apply.

For the plotting and text report, select the report level to ‘Text and plot.’
Starting GOSET

Now, we are ready to start the GOSET and click the start button.

![Start button]

As in the command line approach, the report plot and text will be shown and refreshed in every GAP.rp_gbr generation. The evolution status section in the GUI window also shows the current generation number, best fitness value, average fitness value and the progress bar.

<table>
<thead>
<tr>
<th>EVOLUTION STATUS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Generation No.</td>
</tr>
<tr>
<td>Best fitness</td>
</tr>
<tr>
<td>Mean fitness</td>
</tr>
</tbody>
</table>

GOSET can be stopped at any time by clicking stop button. Try it.

![Stop button]

The simulation is now stopped and the user can do all kinds of things with the data structures generated in the Matlab workspace. You can change parameters for genetic operators, or check the actual value of the best gene in the current generation by clicking ‘Display best’ button in the output report section.

Let’s try and click ‘Display best’ button.

![Output report]

Then the following window will pop up to list the gene numbers, gene descriptions and their actual values.
GOSET can resume the optimization process using the continue button.

The following is the final report plot after 200 generations.

The best chromosome at the last generation has the gene values that are very close to the actual optimum point (1, 1).
7.2 Tanaka Problem

Problem description

One of the most important features of GOSET is the capability to handle multi-objective optimization problems. As a multi-objective optimization problem, Tanaka problem [TAN95] is considered in this section. The Tanaka problem is a constrained optimization problem with two objectives to be minimized:

\[
\begin{align*}
\min f_1(x_1, x_2) &= x_1 \\
\min f_2(x_1, x_2) &= x_2 \\
\text{subject to } C_1(x_1, x_2) &= x_1^2 + x_2^2 - 1 - 0.1 \cos \left( 16 \arctan \frac{x_1}{x_2} \right) \geq 0, \\
C_2(x_1, x_2) &= (x_1 - 0.5)^2 + (x_2 - 0.5)^2 \leq 0.5, \\
0 &\leq x_1 \leq \pi, \\
0 &\leq x_1 \leq \pi.
\end{align*}
\]

Figure 7.4 The feasible objective space and the Pareto-optimal fronts of Tanaka problem.

In this problem, the variable space is also the objective space. The feasible objective space and the Pareto-optimal front are shown in Figure 7.4.

In the first step, the fitness function for the given problem needs to be defined in a m-file. There are two objectives to be minimized and they all have positive values. And the fitness function values are defined to be the negative of the objective function values. Infeasible
solutions are assigned with the value -10 to reduce the chance of surviving in the population. The following mfile `tanaka.m` defines a fitness function for Tanaka problem.

```matlab
% Tanaka problem (1995)
function [f] = tanaka(x)

C1 = x(1)^2+x(2)^2-1-0.1*cos(16*atan(x(1)/x(2))) >= 0;
C2 = (x(1)-0.5)^2+(x(2)-0.5)^2 <= 0.5;

if C1 & C2
    f(1,1) = -x(1);
    f(2,1) = -x(2);
else
    f(1,1) = -10;
    f(2,1) = -10;
end
```

### a. Command line approach

First of all, GAP and other parameters related to the population need to be defined as in the following,

```matlab
GAP = gapdefault(2); % default setting for two objectives
GAP.fp_ngen = 200; % Total generation number
GAP.fp_ipop = 200; % Initial population size
GAP.fp_npop = 200; % Population size
GAP.fp_obj = 0;  % Multi-objective problem
GAP.sc_alg = 6;  % Quadratic scaling
GAP.op_list = []; % Do not show distribution plot
GAP.pp_list = [1, 2]; % List of parameters for Pareto plot
GAP.pp_sign = [-1,-1]; % Sign of fitness for each objective
GAP.pp_axis = [0 1.25 0 1.25] % axis limits for Pareto plot
GAP.dp_np = 200; % Max no. of population to plot for type 1
GAP.gd_min = [ 0 0 ];
GAP.gd_max = [ pi pi ];
GAP.gd_type = [ 2 2 ];
GAP.gd_cid = [ 1 1 ];
```
where the `gapdefault(2)` is used to define default GAP for the problem with two objectives and the maximum number of population for plotting `GAP.dp_np` is set to 200 to display all the individuals in the population.

Then `gaoptimize` is called to perform optimization:

```matlab
[P,GAS] = gaoptimize(@tanaka,GAP,[],[],[],[]);
```

The fitness function handle is `@tanaka`.

The script file `runme.m` in the folder `Tanaka` has all the above commands and executing `runme` will start the evolution to solve Tanaka problem.

![Figure 7.5 Pareto plot for Tanaka problem](image)

The distribution plot is turned off by using null matrix `[]` for `GAP.op_list`, and only the Pareto plot is displayed as in Figure 7.5.
The final population after 200 generation is plotted on the feasible objective space with the non-dominated solutions in black circles in Figure 7.6. Comparison of this figure with Figure 7.4 demonstrates the performance of GOSET with respect to multi-objective optimization problems.

b. GUI approach

As in the previous example, the beginning of GUI approach starts with choosing the fitness function.

Fitness function selection

In the GOSET GUI window, go to fitness function browse menu and locate the fitness function `tanaka.m` and select it.
Parameter input

Gene parameters are needed to be typed as in the following illustrations.

Fundamental parameters are set as in the following. There are two fitness functions, so the number of objective function is set to 2 and the objective function to optimize is set to 0 for multi-objective optimization.

For the scaling algorithm, Quadratic scaling is used with the default scaling parameters.
Plotting parameters are set to display only the Pareto plot as in the following. Axis limits are also given to fix the range of plotting and the maximum number of individuals for plotting is set to 200.

For plotting the Pareto plot, check the output level setting if it has been set to ‘Text and plot.’

User routines

GOSET GUI allows the user to execute user routines before and after the GA optimization process. In the menu bar, select ‘Option’ and then click ‘Extra user routines’.
Then the following user routine menu pops up.

![User routines](image1)

Click ‘Browse’ button to choose the mfiles executed before and after GA. In this example, ‘tanaka_pre.m’ and ‘tanaka_post.m’ are chosen respectively.

![User routines](image2)

‘tanaka_pre.m’ plots the feasible objective space and the Pareto optimal front of Tanaka problem and ‘tanaka_post.m’ plots the final population with the non-dominated solutions in black circles.

**Starting GOSET**

When the GOSET is started, the mfile ‘tanaka_pre.m’ is first executed to display the Pareto optimal front of Tanaka problem in Figure 7.6. Observe the Pareto plot to see how the solutions are distributed throughout the Pareto front over the generations. At the end of the GOSET run, ‘tanaka_post.m’ is executed and a figure with final solutions will be shown as in Figure 7.7.
7.3 Power diode curve fitting

Problem description

In this section, GOSET is applied to power diode curve fitting. The diode of interest is a part of Fuji Electric 6MBI 30L-060 which is commonly used for an inverter for motor drivers and AC-DC servo drive amplifiers. The configuration of Fuji 6MBI 30L-060 is shown in Figure 7.7 and its characteristics are listed in Table 7.1.

![Figure 7.7 Circuit schematic of the IGBT module](image)

<table>
<thead>
<tr>
<th>Description</th>
<th>Rating</th>
</tr>
</thead>
<tbody>
<tr>
<td>Collector-Emitter Voltage</td>
<td>600V</td>
</tr>
<tr>
<td>Gate-Emitter Voltage</td>
<td>±20V</td>
</tr>
<tr>
<td>Collector Current – Continuous</td>
<td>30A</td>
</tr>
<tr>
<td>Collector Current – 1ms Pulse</td>
<td>60A</td>
</tr>
<tr>
<td>Maximum Power Dissipation</td>
<td>120W</td>
</tr>
<tr>
<td>Operating Junction Temperature</td>
<td>150°C</td>
</tr>
<tr>
<td>Thermal Resistance – IGBT Junction to Case</td>
<td>1.04°C/W (Max)</td>
</tr>
<tr>
<td>Thermal Resistance – Diode Junction to Case</td>
<td>2.01°C/W (Max)</td>
</tr>
</tbody>
</table>

Table 7.1 IGBT Module device characteristics
The voltage versus current (V-I) curve of the Power diode is measured using the hardware configuration shown in Figure 7.8

![Figure 7.8 Hardware Test Configuration for Diode V-I characteristic](image)

<table>
<thead>
<tr>
<th>Voltage (V)</th>
<th>Current (A)</th>
<th>Voltage (V)</th>
<th>Current (A)</th>
<th>Voltage (V)</th>
<th>Current (A)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.3130</td>
<td>0</td>
<td>1.2178</td>
<td>6.0040</td>
<td>1.5160</td>
<td>18.0660</td>
</tr>
<tr>
<td>0.4145</td>
<td>0</td>
<td>1.2548</td>
<td>7.0870</td>
<td>1.5358</td>
<td>19.0300</td>
</tr>
<tr>
<td>0.5154</td>
<td>0</td>
<td>1.2844</td>
<td>8.0360</td>
<td>1.5527</td>
<td>19.9480</td>
</tr>
<tr>
<td>0.6140</td>
<td>0.0400</td>
<td>1.3122</td>
<td>9.0000</td>
<td>1.5716</td>
<td>21.0100</td>
</tr>
<tr>
<td>0.7120</td>
<td>0.1495</td>
<td>1.3412</td>
<td>10.0520</td>
<td>1.5885</td>
<td>22.0200</td>
</tr>
<tr>
<td>0.8056</td>
<td>0.3915</td>
<td>1.3654</td>
<td>11.0290</td>
<td>1.6065</td>
<td>23.0800</td>
</tr>
<tr>
<td>0.8942</td>
<td>0.8345</td>
<td>1.3888</td>
<td>11.9900</td>
<td>1.6229</td>
<td>24.0400</td>
</tr>
<tr>
<td>0.9649</td>
<td>1.4103</td>
<td>1.4134</td>
<td>13.0640</td>
<td>1.6389</td>
<td>25.0000</td>
</tr>
<tr>
<td>1.0405</td>
<td>2.3180</td>
<td>1.4345</td>
<td>14.0280</td>
<td>1.6565</td>
<td>26.0500</td>
</tr>
<tr>
<td>1.1092</td>
<td>3.4680</td>
<td>1.4570</td>
<td>15.0860</td>
<td>1.6720</td>
<td>27.0000</td>
</tr>
<tr>
<td>1.1722</td>
<td>4.8340</td>
<td>1.4768</td>
<td>16.0510</td>
<td>1.6880</td>
<td>27.9700</td>
</tr>
</tbody>
</table>

Table 7.2 Measured voltage and current of the power diode
The V-I data set measured at 36 points is listed in Table 7.2 and it is depicted in Figure 7.9. Using the measured V-I date set $(v_k, i_k), k = 1, \ldots , n$, a model of the power diode is going to be developed. It is assumed that the voltage is expressed as the function of the current in the following way

$$v = ai + (bi)^c$$

where the parameter $a$, $b$, and $c$ are to be identified using GA.

A fitness function candidate is

$$f(a, b, c) = \frac{1}{\sum_{k=1}^{n} \left| \frac{1}{v_k} - \frac{ai_i + (bi_i)^c}{v_k} \right| + 10^{-3}}$$

where $v_k$ and $i_k$ are measured voltage and current in $k^{th}$ point. This fitness function is coded to mfile diode.m as in the following.

```matlab
% DIODE.M
% IGBT diode V-I curve fitting fitness function
function f = diode(parameters,data)
% assign genes to parameters
a = parameters(1);
b = parameters(2);
c = parameters(3);
v = a*data.i + (b*data.i).^c;
error = abs(1-v./data.v);
f = 1.0/(1.0e-3 + mean(error));
end
```

**a. Command line approach**

In the first step, the voltage and current measurement data is defined and saved for later use.

```matlab
data.v = [.313,.4145,.5154,.614,.712,.8056,.8942,.9649,1.0405,1.1092,1.1722,...
1.1811,1.2178,1.2548,1.2844,1.3122,1.3412,1.3654,1.3888,1.4134,1.4345,...
1.4570,1.4768,1.4955,1.5160,1.5358,1.5527,1.5716,1.5885,1.6065,1.6229,1.6389,...
1.6565,1.6720,1.6880,1.7054];
data.i=[0,0,0,.040,.1495,.3915,.8345,1.4103,2.318,3.468,4.834,5.032,6.004,7.087, ...
8.036,9,10.052,11.029,11.990,13.064,14.028,15.086,16.051,17.007,18.066,19.030, ...
19.948,21.01,22.02,23.08,24.04,25,26.05,27,27.97,29.02];
save 'data.mat' data
```
To save some chores, you can load the stored ‘data.mat’ from the directory ‘…/GOSET/goset 1.05 examples/power diode curve fit/’.

load data

The default values are used for GAP except for the mating crossover algorithm and the total generation number for evolution.

```matlab
GAP = gapdefault;  % load the default values for GAP
GAP.mc_alg = 2;  % Scalar simple blend crossover
GAP.fp_nngen = 200;  % Total number of generation to evolve
```

The range, type and chromosome ID vectors are defined as

```matlab
GAP.gd_min  = [ 1e-6 1e-6 1e-6 ];
GAP.gd_max  = [ 1e+3 1e+3 1e+3 ];
GAP.gd_type = [ 3 3 3 ];
GAP.gd_cid  = [ 1 1 1 ];.
```

The range of each gene is from $10^{-5}$ to $10^3$ and the logarithmic gene type is used. As the necessary parameters are all defined, execute the GOSET.

```matlab
[P,GAS]= gaoptimize(@diode,GAP,[],[],[],[]);
```

Execute the script ‘runme.m’ to start GOSET. After 200 generations, the best individual (GAS.bestgenes(:,200)) has the following parameter values.

```matlab
a = 0.0091
b = 0.5066
c = 0.1363
```

These parameters yield the best fitting V-I curve expressed as

$$v = (0.0091)i + (0.5066)^{0.1363}i.$$ 

The plots of measured data and the estimated curve are shown in Figure 7.10. The estimated curve fits very closely to the measured data.
B. GUI approach

With an assumption that the previous two examples gave enough chance to learn how to start GOSET GUI, how to enter parameter values, etc., only the parts where changes need to be made will be described.

In the fitness function window, browse and select the fitness function ‘diode.m.’ The optional data for fitness function is set to ‘data.mat’ which is located in the same folder as ‘diode.m’.

The gene parameters are defined next. As there are three parameters to be identified, the total number of gene is set to 3. For each gene, the minimum gene value is set to 1e-5, the
maximum gene value to 1000, gene type to logarithmic and the chromosome ID to 1. Gene description can be specified, if desired. The first gene is names as ‘a’ in the following figure.

In the fundamental parameter input window, the total generation number for evolution is set to 200.

For the comparison between the measured data and the estimated curve, an m-file named ‘plotcurve.m’ is provided in the ‘power diode curve fitting’ folder. To execute this m-file, go to the extra user routine menu

and set ‘Mfile to execute after GA’ to ‘plotcurve.m’
Now the GOSET can be started. When the evolution process is over, ‘plotcurve.m’ is executed and a comparison plot similar to the Figure 7.10 will be shown.

7.4 Transfer function fitting

Problem description

In this section, GOSET is employed to estimate the transfer function given the transfer function values. The transfer function values are admittances looking into the d-axis of brushless DC motor.

The admittances measured at 60 different frequencies are listed in Table 7.3 and plotted in Figure 7.11.
Table 7.3  Admittances of the brushless DC motor in the d-axis

<table>
<thead>
<tr>
<th>96</th>
<th>0.0401 + 0.1108i</th>
<th>1079</th>
<th>0.0026 + 0.0130i</th>
<th>12106</th>
<th>0.0004 + 0.0016i</th>
</tr>
</thead>
<tbody>
<tr>
<td>109</td>
<td>0.0333 + 0.0999i</td>
<td>1218</td>
<td>0.0023 + 0.0117i</td>
<td>13661</td>
<td>0.0004 + 0.0014i</td>
</tr>
<tr>
<td>123</td>
<td>0.0280 + 0.0903i</td>
<td>1375</td>
<td>0.0021 + 0.0105i</td>
<td>15416</td>
<td>0.0003 + 0.0012i</td>
</tr>
<tr>
<td>138</td>
<td>0.0238 + 0.0818i</td>
<td>1551</td>
<td>0.0019 + 0.0095i</td>
<td>17397</td>
<td>0.0003 + 0.0011i</td>
</tr>
<tr>
<td>156</td>
<td>0.0201 + 0.0735i</td>
<td>1750</td>
<td>0.0017 + 0.0085i</td>
<td>19632</td>
<td>0.0003 + 0.0010i</td>
</tr>
<tr>
<td>176</td>
<td>0.0171 + 0.0661i</td>
<td>1975</td>
<td>0.0016 + 0.0076i</td>
<td>22154</td>
<td>0.0003 + 0.0009i</td>
</tr>
<tr>
<td>199</td>
<td>0.0146 + 0.0593i</td>
<td>2229</td>
<td>0.0014 + 0.0069i</td>
<td>25000</td>
<td>0.0002 + 0.0008i</td>
</tr>
</tbody>
</table>

It is assumed that the transfer function of the admittance has the form

\[
Y(s) = \frac{a_1}{\tau_1 s + 1} + \frac{a_2}{\tau_2 s + 1} + \cdots + \frac{a_n}{\tau_n s + 1},
\]

where \( n \) is the order of the transfer function, \( a \)-s and \( \tau \)-s are the parameters to be identified.

The fitness function \( F \) is defined as
\[ F(a_1, \ldots, a_n, \tau_1, \ldots, \tau_n) = \frac{1}{\sum_{k=1}^{m} |Y_k - Y(s_k)| + 10^{-12}}, \]

where \( m \) is the number of admittance data set and \( s_k = j2\pi f_k \).

In the example, the order of the transfer function to be estimated is assumed to be \( n = 6 \). The following is the fitness function m-file.

```matlab
% TFFIT.M
% Transfer function fitting fitness function
function f = tffit(parameters, data)
   a = parameters(1:6);
   tau = parameters(7:12);
   tpred = zeros(size(data.s));
   for i = 1:6,
      tpred = tpred + a(i)./(tau(i)*data.s + 1);
   end
   terror = data.t - tpred;
   error = norm(terror./abs(data.t))/length(tpred);
   f = 1.0/(1.0e-12 + error);
```

a. Command line approach

The transfer function values at 60 different frequencies are defined first in the workspace.

\[
f = [20 \ 23 \ 25 \ 29 \ 32 \ 37 \ 41 \ 47 \ 53 \ 59 \ 67 \ 76 \ 85 \ 96 \ 109 \ 123 \ 138 \ 156 \ 176 \ 199 \ \ldots
\]
\[
224 \ 253 \ 286 \ 322 \ 364 \ 410 \ 463 \ 523 \ 590 \ 666 \ 751 \ 848 \ 957 \ 1079 \ 1218 \ 1375 \ \ldots
\]
\[
1551 \ 1750 \ 1975 \ 2229 \ 2516 \ 286 \ 322 \ 364 \ 410 \ 463 \ 523 \ 590 \ 666 \ 751 \ 848 \ 957 \ 1079 \ 1218 \ 1375 \ \ldots
\]
\[
7465 \ 8424 \ 9506 \ 10728 \ 12106 \ 13661 \ 15416 \ 17397 \ 19632 \ 22154 \ 25000];
\]

% frequency vector in s-domain
\[
data.s = \{20 \ 23 \ 25 \ 29 \ 32 \ 37 \ 41 \ 47 \ 53 \ 59 \ 67 \ 76 \ 85 \ 96 \ 109 \ 123 \ 138 \ 156 \ 176 \ 199 \ \ldots
\]
\[
224 \ 253 \ 286 \ 322 \ 364 \ 410 \ 463 \ 523 \ 590 \ 666 \ 751 \ 848 \ 957 \ 1079 \ 1218 \ 1375 \ \ldots
\]
\[
1551 \ 1750 \ 1975 \ 2229 \ 2516 \ 286 \ 322 \ 364 \ 410 \ 463 \ 523 \ 590 \ 666 \ 751 \ 848 \ 957 \ 1079 \ 1218 \ 1375 \ \ldots
\]
\[
7465 \ 8424 \ 9506 \ 10728 \ 12106 \ 13661 \ 15416 \ 17397 \ 19632 \ 22154 \ 25000\};
\]

% frequency vector in s-domain
\[
data.t = \{0.2754+0.2059i \ 0.2470+0.2106i \ 0.2299+0.2116i \ 0.1992+0.2100i \ \ldots
\]
\[
0.1794+0.2066i \ 0.1517+0.1987i \ 0.1336+0.1914i \ 0.1117+0.1987i \ \ldots
\]
\[
0.0948+0.1685i \ 0.0815+0.1579i \ 0.0679+0.1452i \ 0.0565+0.1326i \ \ldots
\]
\[
0.0480+0.1219i \ 0.0401+0.1108i \ 0.0333+0.0999i \ 0.0280+0.0903i \ \ldots
\]
\[
0.0238+0.0818i \ 0.0201+0.0735i \ 0.0171+0.0661i \ 0.0146+0.0593i \ \ldots
\]
\[
0.0126+0.0531i \ 0.0108+0.0478i \ 0.0094+0.0428i \ 0.0082+0.0385i \ \ldots
\]
\[
0.0072+0.0345i \ 0.0063+0.0310i \ 0.0056+0.0278i \ 0.0049+0.0249i \ \ldots
\]
\[
0.0044+0.0223i \ 0.0040+0.0201i \ 0.0035+0.0180i \ 0.0032+0.0162i \ \ldots
\]
\[
0.0029+0.0145i \ 0.0026+0.0130i \ 0.0023+0.0117i \ 0.0021+0.0105i \ \ldots
\]
Then data.s and data.t are saved in ‘data.mat’ for later use.

save 'data.mat' data

The ‘data.mat’ also can be directly loaded from ‘…/GOSET/goset 1.05 examples/Transfer function fit/’.

load data

The default values are used for GAP and the total generation number for evolution is set to 1000.

GAP = gapdefault;  % load the default values for GAP
GAP.fp_nngen = 1000;  % Total number of generation to evolve

The parameter range, type and chromosome ID vectors are defined as

GAP.gd_min  =  [ 1.0e-8 1.0e-8 1.0e-8 1.0e-8 1.0e-8 1.0e-8... 1.0e-8 1.0e-8 1.0e-8 1.0e-8 1.0e-8 ];
GAP.gd_max  =  [ 1.0e+1 1.0e+1 1.0e+1 1.0e+1 1.0e+1 1.0e+1 ... 1.0e+0 1.0e+0 1.0e+0 1.0e+0 1.0e+0 ];
GAP.gd_type =  [ 3 3 3 3 3 3 3 3 3 3 3 3 ];
GAP.gd_cid  =  [ 1 1 1 1 1 1 1 1 1 1 1 1 ];

The first six elements correspond to the parameter a, and the rest are for \( \tau \). GOSET is ready to go.

[P,GAS] = gaoptimize(@tffit,GAP,[],[],[],[]);

To start GOSET, execute the script ‘runme.m’ with all the commands described above.

After 1000 generations, the best individual (GAS.bestgenes(:,1000)) has the following parameter values.

a = [ 0.00074282873079 0.00020824030313 0.00000009385065 ... 0.00079650808510 0.42038798793770 0.00597311661588 ]
These parameters yield the transfer function

\[ Y(s) = \frac{0.0007428}{0.0002657s + 1} + \frac{0.0002082}{0.0000001815s + 1} + \frac{0.0058660}{0.000001141s + 1} + \frac{0.0008665}{0.00000001815s + 1} + \frac{0.4204}{0.00008666s + 1} + \frac{0.0038902}{0.00008666s + 1} + \frac{0.0002657}{0.00000001815s + 1} + \frac{0.00000001815}{0.00000001815s + 1} + \frac{0.00000001815}{0.00000001815s + 1} + \frac{0.00000001815}{0.00000001815s + 1} \]

Figure 7.12: Plot of the magnitude and phase of the measured transfer function data and the transfer function obtained using GOSET

The magnitude and phase plot of the data set and the estimated transfer function are shown in Figure 7.12. The solid red line is for the transfer function estimated using GOSET and the blue x’s are the measured transfer function values. The estimated transfer function fits the measured data very closely.

**B. GUI approach**

In the first step, select the fitness function file and the optional data file.
Then, the gene parameters are defined as in the following figures. Total number of gene is 12. First six genes correspond to the parameters $a_1,\ldots,a_6$ and their maximum and minimum values are set to 10 and $10^{-8}$, respectively. Rest of the genes are for parameter $\tau_1,\ldots,\tau_6$ and the maximum and minimum values are set to 1 and $10^{-8}$. The gene type is logarithmic for all genes.

The fundamental parameters are set as in the following...
Setting the plot scale to 0 makes the fitness function axis logarithmic.

For the comparison plot after the evolution, ‘plotcurve.m’ is selected in the ‘Mfile to execute after GA’.

The gene distribution at 1000 generation and the fitness values throughout the evolution are shown in Figure 7.13
Figure 7.13  Gene distribution and the fitness history

At the end of the evolution, a comparison plot similar to Figure 7.12 will appear.

References


A. GOSET function list
B. GOSET function reference
C. GOSET parameter list
## Appendix A. GOSET Function List

<table>
<thead>
<tr>
<th><strong>Initialization</strong></th>
<th>** GAPdefault**</th>
<th>contains default parameter values for GAP</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>downsize</strong></td>
<td>reduce the population size to a desired number</td>
</tr>
<tr>
<td></td>
<td><strong>gainit</strong></td>
<td>initialize the genetic algorithm</td>
</tr>
<tr>
<td></td>
<td><strong>unrndinit</strong></td>
<td>initialize a population randomly</td>
</tr>
<tr>
<td></td>
<td><strong>gasetup</strong></td>
<td>sets up a population of chromosomes</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Genetic operators</strong></th>
<th><strong>gaoptimize</strong></th>
<th>GOSET main routine</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>objwght</strong></td>
<td>generate weight vector for multi-objective functions</td>
</tr>
<tr>
<td></td>
<td><strong>divcon</strong></td>
<td>prevent crowding of the chromosomes</td>
</tr>
<tr>
<td></td>
<td><strong>scale</strong></td>
<td>determine the scaled fitness</td>
</tr>
<tr>
<td></td>
<td><strong>select</strong></td>
<td>select chromosomes for reproduction</td>
</tr>
<tr>
<td></td>
<td><strong>death</strong></td>
<td>determine parents to be replaced by children</td>
</tr>
<tr>
<td></td>
<td><strong>matingcrossover</strong></td>
<td>exchanges genes between chromosomes</td>
</tr>
<tr>
<td></td>
<td><strong>mutate</strong></td>
<td>randomly change some gene values</td>
</tr>
<tr>
<td></td>
<td><strong>migrate</strong></td>
<td>move chromosomes from one region to another</td>
</tr>
<tr>
<td></td>
<td><strong>updateage</strong></td>
<td>update the age of all individuals</td>
</tr>
<tr>
<td></td>
<td><strong>evaluate</strong></td>
<td>evaluate the fitness values of chromosomes</td>
</tr>
<tr>
<td></td>
<td><strong>elitism</strong></td>
<td>preserve best chromosomes</td>
</tr>
<tr>
<td></td>
<td><strong>randsearch</strong></td>
<td>search the vicinity of the best chromosomes</td>
</tr>
<tr>
<td></td>
<td><strong>updatenstat</strong></td>
<td>update the statistic information of GAS structure</td>
</tr>
<tr>
<td></td>
<td><strong>normgene</strong></td>
<td>updates the normalized genes based on raw genes</td>
</tr>
<tr>
<td></td>
<td><strong>rawgene</strong></td>
<td>updates the raw genes based on normalized genes</td>
</tr>
<tr>
<td></td>
<td><strong>nondom</strong></td>
<td>find the non-dominated solutions</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Plotting</strong></th>
<th><strong>reportplot</strong></th>
<th>plots current population</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>distplot</strong></td>
<td>plots the distribution of the genes</td>
</tr>
<tr>
<td></td>
<td><strong>paretoplot</strong></td>
<td>plots the population in the objective space</td>
</tr>
</tbody>
</table>

| **GUI related** | **goset** | GOSET GUI |

<table>
<thead>
<tr>
<th><strong>Misc.</strong></th>
<th><strong>contents</strong></th>
<th>contains general information of GOSET</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>gasyschck</strong></td>
<td>license checking</td>
</tr>
</tbody>
</table>
Appendix B. GOSF function reference
<table>
<thead>
<tr>
<th><strong>Purpose</strong></th>
<th>Contain general information regarding GOSET</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Syntax</strong></td>
<td>contents</td>
</tr>
<tr>
<td><strong>Arguments</strong></td>
<td>None</td>
</tr>
<tr>
<td><strong>Value</strong></td>
<td>None</td>
</tr>
<tr>
<td><strong>Description</strong></td>
<td>contents.m has descriptions on data structures P, GAS and functions of GOSET and upgrade information</td>
</tr>
<tr>
<td><strong>See Also</strong></td>
<td>gapdefault</td>
</tr>
</tbody>
</table>
### Purpose
Determine parents that are replaced by the children.

### Syntax
\[ \text{Dlist} = \text{select}(\text{Pin}, \text{Plist}, \text{GAP}) \]

### Arguments
- **Pin**: structure of current population
- **Plist**: parent list generated from select algorithm
- **GAP**: structure of genetic algorithm parameters

### Value
- **Dlist**: death list

### Description
Death operator determines which individual is to die and replaced by the children. The followings are possible options for the death operators.

**Replacing parents** \((\text{GAP}.dt_{\text{alg}} = 1)\)
Parents are replaced by their own children.

**Random selection** \((\text{GAP}.dt_{\text{alg}} = 2)\)
The parents to be replaced are randomly chosen.

**Tournament on fitness** \((\text{GAP}.dt_{\text{alg}} = 3)\)
The parent to be replaces is determined via the tournament based on the aggregate fitness value. \(\text{GAP}.dt_{\text{nts}}\) number of parents are randomly chosen for a tournament and the one with worst aggregate fitness value is marked for death.

**Tournament on age** \((\text{GAP}.dt_{\text{alg}} = 4)\)
The parent to be replaces is determined via the tournament based on the age. Among the randomly chosen \(\text{GAP}.dt_{\text{nts}}\) number of parents, the oldest one is selected and marked for death.

**Custom algorithm** \((\text{GAP}.dt_{\text{alg}} = 5)\)
User defined custom death algorithm is used. The handle of the custom function is assigned to \(\text{GAP}.dt_{\text{cah}}\). The custom function must have the following format:

\[ \text{D_list} = \text{f}(\text{region}, \text{size}, \text{age}, \text{mfit}, \text{fit}) \]

- **D_list**: indices of the individuals to be replaced by children
- **region**: the region number
- **size**: number of individuals for the death list
As an example of a custom algorithm, the random death algorithm is written as an mfile called ‘customdeath.m’ which is shown below.

```matlab
% Custom death algorithm example - random death algorithm
function dlist = customdeath(region,size,region_age,region_mfit,region_fit)

% Randomly select death list
regionsize=length(region_age);
randinlist = randperm(regionsize);

dlist = randinlist(1:size);
```

This mfile must exist in the same folder as the fitness function file or in the GOSET folder. Then the custom file handle GAP.dt_cah is set to @customdeath.

Random algorithm (GAP.dt_alg = 6)

If this option is selected, the death algorithm is randomly chosen among the first four death algorithms at each generation.
**distplot**

**Purpose**  
Plot the distribution of the genes in the individuals

**Syntax**  
distplot(fignum, P, objective, GAP, [region])

**Arguments**  
- fignum: figure number  
- P: structure of current population  
- objective: objective function number to show in the plot  
- GAP: structure of genetic algorithm parameters  
- region: plot only the individuals in this specified region (optional)

**Value**  
None

**Description**  
distplot shows the distribution of the genes of the individuals. It is called within the reportplot and plotted together with the fitness history.

There are two types of distribution plot. Setting GAP.dp_type to 1 will show the first type of distribution plot which displays the normalized gene values as in Figure B.1. In this case, there are four genes in each individual. The top 25 percent of the individuals are marked by blue cross (+), the next 25
percentiles are plotted as green X (x), then the next 25 percentiles are in yellow square (□), and the last 25 percentiles are drawn as the red diamonds(◇). The gene values of the best individual of each region are connected by the blue solid line. For multi-region scheme, there are multiple blue solid lines which represent the best individuals in multiple regions.

The second type (GAP.dp_type = 2) of distribution plot shows the histogram of the normalized gene values as in Figure B.2. The number of bars for the histogram can be set using GAP.dp_res. In Figure B.2, the number of bars is set to 5 (GAP.dp_res = 5). The gene values of the best individual of each region are indicated by green horizontal lines. For each gene values, there are as many green lines as the number of regions.

For both of the distribution plot, only a part of the population can be displayed by setting the parameter GAP.dp_np that determines the maximum number of individuals to plot. Only GAP.dp_np individuals are randomly chosen from the population and displayed. The positions of green lines represent the normalized gene values of the best individual.

See also reportplot, paretoplot
divcon

Purpose
Compute penalty function values for maintaining diversities of the population

Syntax
Ppen = divcon(Pin,GAP)

Arguments
Pin structure of current population
GAP structure of genetic algorithm parameters

Value
Ppen penalty function vector

Description
Maintaining genetic diversity in the population is important especially in the multi-objective optimization problem. Diversity control algorithms are employed so that the under represented individuals are emphasized and similar individuals are penalized by degrading their fitness values.

Diversity control can be applied to either the parameter (solution) space or the fitness function space. Setting GAP.dc_spc = 1 causes the diversity control in the parameter space and setting GAP.dc_spc = 2 causes the diversity control in the fitness function space.

Presently, four different diversity control algorithms are used in GOSET.

Diversity control algorithm 1

This algorithm is chosen by setting GAP.dc_alg = 1. For each individual, the distances with all other individuals are evaluated. Then the number of individuals, whose distance from the individual of interest is smaller than the threshold distance, is counted. The threshold distance is randomly determined as a value between the minimum threshold (GAP.dc_mnt) and the maximum threshold (GAP.dc_mxt). That is,

Threshold distance = average distance among the individual H α

where α = (GAP.dc_mnt + randH(GAP.dc_mxt - GAP.dc_mnt)). Then the penalty function value of an individual is defined as the reciprocal of the counted number of individuals.

Diversity control algorithm 2

This algorithm is chosen by setting GAP.dc_alg = 2. To overcome the problem of the computational load in the first method, this algorithm uses a weighted sum of gene values for diversity control. For an arbitrary weight
vector whose element number is same as gene number in an individual, the weighted sum of each individual is evaluated. Then the modulus after dividing the weighted sum by 1 is taken. If the gene values of individuals are very similar, then the modulus of the weighted sum must be also similar. Then the individuals are grouped according to the modulus values and put into a corresponding bin. The number of bins, that is the number of groups, is randomly determined as the following

\[
\text{No. of bins} = \text{round} \left( \alpha \cdot \text{Number of individual} \right),
\]

where \( \alpha = \text{GAP.dc_mnb} + \text{rand}(\text{GAP.dc_mxnb-GAP.dc_mnb}) \). Then the interval [0,1] is divided into (No. of bins) equally distanced subintervals. The penalty value of an individual is the reciprocal of the total number of individuals in the same bin.

However, even with different gene values, individuals may have similar modulus for some weight vectors. In such cases, the penalty value does not reflect the actual proximity of gene values. Hence, the procedure is repeated \( \text{GAP.dc_ntr} \) times and the largest penalty function value is chosen as the final penalty function value for each individual.

**Diversity control algorithm 3**

This algorithm is chosen by setting \( \text{GAP.dc_alg} = 3 \). The idea of this diversity control algorithm is similar to the diversity algorithm 1. The sum of infinity norm between the solutions is used to determine the penalty value as shown in the following formula

\[
p_{\text{pen}}^k = \frac{1}{\sum_{i=1}^{\text{NT}} \exp \left( -\frac{d_{i,k}}{d_c} \right)},
\]

where \( d_{i,k} \) is the infinity norm between \( k \)'th and \( i \)'th individual and \( d_c \) is the distance constant (\( \text{GAP.dc_dc} \)) which controls the size of the neighborhood. As the distance constant \( d_c \) increases, the effective size of the neighborhood increases and the penalty level also increases.

**Diversity control algorithm 4**

This algorithm is chosen by setting \( \text{GAP.dc_alg} = 4 \). It is identical to the diversity control algorithm 3 except the fact that only a part of the population, that is, for each individual, \( \text{GAP.dc_nt} \) individuals are randomly chosen and
used in the distance evaluation. The following formula is used to calculate the fitness penalty weight for $k$’th individual.

$$
P^k_{\text{pen}} = \frac{1}{1 + \text{Number of population in the region GAP.dc_nt} \sum_{j=1}^{GAP.dc_nt} \exp \left( -\frac{d_{i,k}}{d_c} \right)}
$$

where $d_{i,k}$ is the infinity norm between $k$’th and $i$’th individual, $d_c$ is the distance constant (GAP.dc_dc)
**downsize**

**Purpose**
Reduce the population to a desired size

**Syntax**
\[ Pout = \text{downsize}(Pin, \text{Newsize}) \]

**Arguments**
- **Pin**: structure of current population
- **Newsize**: the size of the new population

**Value**
- **Pout**: structure of downsized population

**Description**
This function reduces the size of the population to a desired number based on the (cumulative) rank of the individual.

In the multiple region (multi-population) case, the number of individuals in a region is determined such that the ratio of individuals among regions is maintained. For example, suppose a population with 100 individuals that are distributed in 3 different regions as in the following table. If we want the new population to have only 50 individuals, then the number of individuals in the new populations becomes the half of the number of individuals in the original population as shown in Table B.1.

<table>
<thead>
<tr>
<th>Region</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>total</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of individuals in Pin</td>
<td>30</td>
<td>50</td>
<td>20</td>
<td>100</td>
</tr>
<tr>
<td>No. of individuals in Pout</td>
<td>15</td>
<td>25</td>
<td>10</td>
<td>50</td>
</tr>
</tbody>
</table>

Table B.1

The selection of the individuals is based on the rank in single objective case. In the multi-objective case, cumulative rank is used to pick the individuals for the new population. Consider a 3-objective optimization problem in Table B.2. If we have four individuals and need to reduce the size to two, then individual **A** and **D** are selected according to the cumulative rank.

<table>
<thead>
<tr>
<th>Individual</th>
<th>Rank in each objective</th>
<th>Cumulative Rank</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>3 1 1</td>
<td>5</td>
</tr>
<tr>
<td>B</td>
<td>4 4 2</td>
<td>10</td>
</tr>
<tr>
<td>C</td>
<td>2 3 4</td>
<td>9</td>
</tr>
<tr>
<td>D</td>
<td>1 2 3</td>
<td>6</td>
</tr>
</tbody>
</table>

Table B.2
elitism

**Purpose**  
Preserve the best individuals

**Syntax**  
Pout = elitism(Pin,Porg,GAP,GAS)

**Arguments**  
- Pin  
  structure of current manipulated population
- Porg  
  structure of original population
- GAP  
  structure of genetic algorithm parameters
- GAS  
  structure of genetic algorithm statistics

**Value**  
Pout  
structure of output population

**Description**  
Elitism is activated by setting GAP.el_act = 1. The starting point of elitism can be using the parameter GAP.el_fgs that specifies the fraction of the population. For example, if GAP.el_fgs = 0.25 with the total generation number of 100, then the elitism is effective starting from 25th generation.

In single objective optimization problems, the best individual in each region of the processed population and the best one in the original population are compared. If the best individual of the processed population is worse than that of the original population, then the best one in the processed population is replaced by the best one in the old population. In multi-objective optimization problem, it is guaranteed that a limited number of non-dominated individuals of the population are preserved up to certain number. The maximum number of preserved non-dominated individuals is determined by (population size H GAP.el_fpe).
**Purpose**
Evaluate the fitness of chromosomes

**Syntax**
\[ [\text{mfit, es, une}] = \text{evaluate}(\text{Pin, GAP, cne, D}) \]

**Arguments**
- **Pin** structure of current population
- **GAP** structure of genetic algorithm parameters
- **cne** current number of evaluations performed
- **D** an optional data structure used for fitness evaluation

**Value**
- **mfit** multi-objective fitness
- **es** evaluation status of each member of population
- **une** updated number of evaluations

**Description**
evaluate assigns individuals with fitness values obtained from the fitness function defined by \text{P.fithandle}.

When \text{GAP.ev_are} is set to 0, this function only updates the individuals whose fitness values have not been evaluated. When \text{GAP.ev_are} = 1, the fitness value of all the individuals are evaluated.

Also \text{GAP.ev_bev} determines whether to pass all the individuals to the fitness evaluation function at the same time (when set to 1) or to evaluate one individual at a time (when set to 0). The fitness function must be written to handle the vector evaluation.

Normally, the only gene values are passed to the fitness function. If the supplementary data flag \text{GAP.ev_ssd} = 1, then the age(\text{P.age}), previous fitness values(\text{P.mfit}) and the region(\text{P.region}) are also sent to the fitness function.

\text{D} is the optional data structure that is required for evaluating the fitness function and it is passed to the fitness function if it is defined when the \text{gaoptimize} is called.

The passed data and its order are listed in the following table.

<table>
<thead>
<tr>
<th>Optional data D</th>
<th>\text{GAP.ev_ssd}</th>
<th>Data and its order passed to the fitness function</th>
</tr>
</thead>
<tbody>
<tr>
<td>exists</td>
<td>0</td>
<td>\text{P.gene, D}</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>\text{P.gene, P.age, P.mfit, P.region, D}</td>
</tr>
<tr>
<td>does not exist</td>
<td>0</td>
<td>\text{P.gene}</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>\text{P.gene, P.age, P.mfit, P.region}</td>
</tr>
</tbody>
</table>
**gainit**

**Purpose**
Initialize the genetic algorithm

**Syntax**
\[
\text{[GAP,GAS,Pout]=gainit(numargin,@fitfun,D,GAP, GAS,iP,GUIhdl)}
\]

**Arguments**
- `numargin` number of argument of the GAOPTIMIZE
- `@fitfun` name of the m-file that evaluates the fitness
- `D` optional data needed by fitness function
- `GAP` structure of genetic algorithm parameters
- `GAS` structure of genetic algorithm statistics
- `iP` optional initial population
- `GUIhdl` handle used for GUI (Pass empty matrix ‘[]’ when not in use)

**Value**
- `GAP` structure of genetic algorithm parameters
- `GAS` structure of genetic algorithm statistics
- `Pout` structure of the population

**Description**
gainit initializes the genetic algorithm by setting up the population. If the optional initial population is passed, gainit only evaluates the fitness of the population. Otherwise gasetup is called to generate initial population, and the fitness is evaluated. If the size of the initial population (`GAP.fp_ipop`) is larger than the steady state population (`GAP.fp_ipop`), the population size is reduced. In the last step, gainit generates a report on initial evaluation.

**See Also**
gasetup
gaoptimize

Purpose
Perform function optimization using GOSET

Syntax
[Pout,GAS]=gaoptimize(@fitfun,GAP,D,GAS,iP,GUIhdl)

Arguments
@fitfun name of the m-file that evaluates the fitness
GAP structure of genetic algorithm parameters
D optional data required by fitness function
GAS structure of genetic algorithm statistics
iP optional variable with initial population
GUIhdl handle used for GUI (Use empty matrix when not in use)

Value
Pout structure of final population
GAS structure of genetic algorithm statistics

Description
As the main function of GOSET, it performs the function optimization using GOSET. The structure of gaoptimize.m is modularized. Thus users who want to experiment their own operator, can easily modify this function.
Purpose  Assigns default values to the genetic algorithm parameters used in GAP

Syntax  \( \text{GAP} = \text{gapdefault}(\text{nobj}) \)

Arguments  \( \text{nobj} \) number of objectives

Value  GAP  structure of genetic algorithm parameters

Description  This function returns the structure of genetic algorithm parameters GAP with their default values. The user can load the \text{gapdefault} and then redefine only the required fields, instead of defining all the fields.

The following Table B.3 shows the default values defined in \text{gapdefault}.

<table>
<thead>
<tr>
<th>Fundamental parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.fp_ngen = 100</td>
<td>GAP.fp_ipop = 100</td>
</tr>
<tr>
<td>GAP.fp_npop = 100</td>
<td>GAP.fp_nobj = 1</td>
</tr>
<tr>
<td>GAP.fp_obj = 1</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Diversity control parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.dc_act = 1</td>
<td>GAP.dc_alg = 4</td>
</tr>
<tr>
<td>GAP.dc_sp = 1</td>
<td>GAP.dc_mnt = 0.02</td>
</tr>
<tr>
<td>GAP.dc_mxt = 0.1</td>
<td>GAP.ntr = 3</td>
</tr>
<tr>
<td>GAP.dc_mnb = 0.5</td>
<td>GAP.dc_mxb = 2.0</td>
</tr>
<tr>
<td>GAP.dc_dc = 0.001</td>
<td>GAP.dc_nt = 50</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Selection algorithm parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.sl_alg = 2</td>
<td>GAP.sl_nts = 4</td>
</tr>
<tr>
<td>GAP.sl_cah = []</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Death algorithm parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.dt_alg = 2</td>
<td>GAP.dt_nts = 4</td>
</tr>
<tr>
<td>GAP.dt_cah = []</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Mating and crossover parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.mc_pp = 0.6</td>
<td>GAP.mc_fc = 1.0</td>
</tr>
<tr>
<td>GAP.mc_alg = 4</td>
<td>GAP.mc_gac = 3</td>
</tr>
<tr>
<td>GAP.mc_ec = 2</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Mutation parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.mt_ptgm = 0.001</td>
<td>GAP.mt_prgm = 0.002</td>
</tr>
<tr>
<td>GAP.mt_srgm = 0.3</td>
<td>GAP.mt_pagm = 0.002</td>
</tr>
<tr>
<td>GAP.mt_sagm = 0.1</td>
<td>GAP.mt_prvm = 0.002</td>
</tr>
<tr>
<td>GAP.mt_srvm = 0.3</td>
<td>GAP.mt_pavm = 0.002</td>
</tr>
<tr>
<td>GAP.mt_savm = 0.1</td>
<td>GAP.mt_pigm = 0.008</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Migration parameters</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.mg_nreg = 1</td>
<td>GAP.mg_tmig = 0</td>
</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP.mg_pmig</td>
<td>0</td>
</tr>
</tbody>
</table>

**Evaluation Parameters**

| GAP.ev_bev  | 0       |
| GAP.ev_ssd  | 0       |

**Scaling parameters**

| GAP.sc_alg   | 1       |
| GAP.sc_cst   | 2       |
| GAP.sc_klin  | 10      |
| GAP.sc_kmxq  | 10      |
| GAP.sc_kmnq  | 0.01    |

**Elitism parameters**

| GAP.el_act   | 1       |
| GAP.el_fpe   | 0.5     |

**Random search parameters**

| GAP.rs_fgs   | 0.25    |
| GAP.rs_fps   | 0.1     |
| GAP.rs_srp   | 0.3     |
| GAP.rs_sap   | 0.1     |
| GAP.rs_frp   | 0.7     |
| GAP.rs_fea   | 0.2     |

**Reporting parameters**

| GAP,rp_lvl   | 1       |
| GAP,rp_gbr   | 5       |

**Objective plot parameters**

| GAP.op_list  | [1]     |
| GAP.op_style | 1       |

**Pareto plot parameters**

| GAP.pp_list  | []      |
| GAP.pp_style | 1       |
| GAP.pp_sign  | 1       |

**Distribution plot parameters**

| GAP.dp_type  | 2       |
| GAP.dp_np    | 100     |
| GAP.dp_res   | 20      |

**Gene description parameters**

| GAP.gd_min    | user defined |
| GAP.gd_max    | user defined |
| GAP.gd_type   | user defined |

Table B.3  Default values of GAP defined in gapdefault.m

For the full description regarding these parameters, refer to first section of GOSET data structures and algorithm execution or gapdefault.m. The m-file gapdefault.m also has default values of the GAP listed in Table B.3.
**gasetup**

**Purpose**
Set up a population of chromosomes

**Syntax**

```
[P,GAS] = gasetup(popsize,GAP,@fitfun,[D])
```

**Arguments**
- `popsize` number of individuals in the population
- `GAP` structure of genetic algorithm parameters
- `@fitfun` name of the m-file that evaluates the fitness
- `D` optional data needed by fitness function

**Value**
- `P` structure of the population
- `GAS` structure of genetic algorithm statistics

**Description**
gasetup is called within gainit when the initial population does not exist. It sets up the population data structure P based on the assigned maximum value, minimum value, type, and the chromosome ID of each gene and by defining initial values using unrndinit.

The initial evaluation of the fitness function is also included and the statistic structure GAS is returned together with the population data structure P.

**See Also**
gainit, unrndinit
**gasyschck**

**Purpose**
Check the license information

**Description**
Each version of GOSET is subject to the license control. The license of GOSET expires after certain period of time from the date of release. This is to prevent the unlawful distribution of GOSET and also to mandate the users to update their GOSET to the latest version.

gasyschck checks the license information and if the license is expired, GOSET is terminated.

When there is less than a week left in the GOSET license, you will get the following message:

There are only $n$ days left in GOSET 2.X License.
goset

**Purpose**  Start GOSET GUI (Graphic User Interface)

**Syntax**  goset

**Arguments**  none

**Value**  none

**Description**  goset initiates the GOSET GUI window as in the Figure B.3.

![GOSET GUI main window](image)

**Figure B.3**  GOSET GUI main window

For the detailed description of GOSET GUI, refer to Chapter 6.
matingcrossover

**Purpose**
Perform mating and genetic crossover on a population

**Syntax**
```
Pout = matingcrossover(Pin, Plist, PLsize, Dlist, GAP, GAS)
```

**Arguments**
- **Pin**: structure of current population
- **Plist**: parent list from selection operator
- **PLsize**: size of the parent list
- **Dlist**: death list from death operator
- **GAP**: structure of genetic algorithm parameters
- **GAS**: structure of genetic algorithm statistics

**Value**
- **Pout**: structure of the population after crossover

**Description**
Perform crossover operations on a population. Three different types of crossover methods are used in GOSET; single point crossover, simple blend crossover, and simulated binary crossover.

The parameter `GAP.mc_pp` specifies the mating crossover probability, that is, the fraction of the population replaced by children. The fraction of the chromosome undergoes crossover is determined by `GAP.mc_fc`.

All crossover operation is region specific and parents that are selected from one region reproduce children into the same region. Also all the crossover operations are chromosome-ID specific. Hence genes of different chromosome ID are treated separately and the crossover operators are applied independently.

The mating crossover methods are determined by `GAP.mc_alg` as in the following table.

<table>
<thead>
<tr>
<th>GAP.mc_alg</th>
<th>Mating Crossover method</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Single point crossover</td>
</tr>
<tr>
<td>2</td>
<td>Scalar simple blend crossover</td>
</tr>
<tr>
<td>3</td>
<td>Vector simple blend crossover</td>
</tr>
<tr>
<td>4</td>
<td>Scalar simulated binary crossover</td>
</tr>
<tr>
<td>5</td>
<td>Vector simulated binary crossover</td>
</tr>
<tr>
<td>6</td>
<td>Random algorithm</td>
</tr>
</tbody>
</table>

Let’s discuss the mating crossover methods one by one.

**Single point crossover**
This crossover operator is similar to the crossover operator in binary-coded GAs. A crossover point is randomly selected and the gene values after that point are swapped between two parent chromosomes.

If \( P_1 \) and \( P_2 \) are the parent chromosomes with \( n \) genes and \( c \) is the crossover point, then the children chromosomes are

\[
C_1 = [P_{1(1:c-1)} \ P_{2(c:n)}] \quad \text{and} \quad C_2 = [P_{2(1:c-1)} \ P_{1(c:n)}]
\]

where \( P_{1(a:b)} \) is a vector whose elements are gene values from \( a \)'th to \( b \)'th positions of \( P_1 \).

**Scalar simple blend crossover**

Scalar simple blend crossover generates the children from the weighted sum of their parents by the following steps;

STEP 1 : For \( i \)'th gene, choose a random number \( u_i \in [-1, 1] \)

STEP 2 : Calculate the average of the parents

\[
m_i = \frac{P_{1,i} + P_{2,i}}{2}
\]

STEP 3 : Calculate the amount of change

\[
\delta_i = u_i \cdot |P_{1,i} - P_{2,i}|
\]

STEP 4 : Compute the offspring

\[
C_{1,i} = m_i + \delta_i \quad \text{and} \quad C_{2,i} = m_i - \delta_i
\]

Note that each gene in the same chromosome is crossovered with the different amount of change.

**Vector simple blend crossover**

Vector simple blend crossover is similar to the scalar simple blend crossover. The only difference is that all genes in the same chromosome are crossovered with the same amount of change as in the following steps

STEP 1 : Choose a random number \( u \in [-1, 1] \)

STEP 2 : Calculate the average of the parents
STEP 3: Calculate the amount of change

\[ \delta_i = u \left| P_{1,i} - P_{2,i} \right| \]

STEP 4: Compute the offspring

\[ C_{1,i} = m_i + \delta_i \quad \text{and} \quad C_{2,i} = m_i - \delta_i \]

Note that all genes in the same chromosome are crossovered with the same amount of change.

**Scalar simulated binary crossover**

Scalar simulated binary crossover generates the children by the following steps;

STEP 1: For \( i \)'th gene, choose a random number \( u_i \in [0, 1] \)

STEP 2: Calculate the spread factor

\[ \beta_i = \begin{cases} 
(2u_i)^{\frac{1}{\eta_c}}, & \text{if } u_i \leq 0.5; \\
\left( \frac{1}{2(1-u_i)} \right)^{\frac{1}{\eta_c}}, & \text{otherwise.} 
\end{cases} \]

where \( \eta_c \) is the distribution tightness parameter \( \text{GAP.mc}_ec \).

STEP 3: Compute the offspring

\[
C_{1,i} = 0.5[(1+\beta_i)C_{1,i} + (1-\beta_i)C_{2,i}], \\
C_{2,i} = 0.5[(1-\beta_i)C_{1,i} + (1+\beta_i)C_{2,i}].
\]

Note that each gene in the same chromosome can be recombined with different spread factor.

**Vector simulated binary crossover**

Vector simulated binary crossover is identical as scalar simulated binary crossover except that the spread factor is same for all the genes in the same chromosome.
The following describes the vector simulated crossover;

**STEP 1**: Choose a random number $u \in [0,1]$

**STEP 2**: Calculate the spread factor beta

$$
\beta = \begin{cases} 
2u, & \text{if } u \leq 0.5; \\
\left(\frac{1}{2(1-u)}\right)^{\frac{1}{u}}, & \text{otherwise.}
\end{cases}
$$

**STEP 3**: Compute the offspring

$$
C_1 = 0.5[(1 + \beta)C_1 + (1 - \beta)C_2], \\
C_2 = 0.5[(1 - \beta)C_1 + (1 + \beta)C_2].
$$

**Random crossover**

For every GAP.mc_gac generation, a mating crossover methods are randomly selected from the five mating crossover methods described above.

migrate

**Purpose**  
Change the region of individuals

**Syntax**  
\[ P_{\text{out}} = \text{migrate}(P_{\text{in}}, \text{GAP}, cg) \]

**Arguments**  
- \( P_{\text{in}} \): structure of population before migration  
- \( \text{GAP} \): structure of genetic algorithm parameters  
- \( cg \): current generation number

**Value**  
\( P_{\text{out}} \): structure of population after migration

**Description**  
This function works only when there are multiple regions. If the migration occurs, some individuals are selected and moved to other regions. The migration interval is randomly chosen from the integer values between \( 0.5 \times \text{GAP}.tmig \) and \( 1.5 \times \text{GAP}.tmig \). For example, if \( \text{GAP}.tmig = 6 \) then, the migration interval can be any integer from 3 to 9. Each individual is selected and migrated with the probability of \( \text{GAP}.pmig \). The target region is chosen randomly among \( \text{GAP}.nreg \) number of regions.
**mutate**

**Purpose**
Perform mutation on a population of chromosomes

**Syntax**

\[ \text{Pout} = \text{mutate}(\text{Pin}, \text{GAP}) \]

**Arguments**
- **Pin** structure of population before mutation
- **GAP** structure of genetic algorithm parameters

**Value**
- **Pout** structure of the population after mutation

**Description**
This function applies genetic mutation on the population. Four different mutation algorithms are applied sequentially in the order of total mutation, partial mutation, vector mutation, and integer mutation.

These mutation operations are performed on the normalized gene values. When a gene value lies outside of the allowed range after mutation, then its value is corrected using the ring-mapping, that is, its modulus after division by 1 is used instead.

**Total mutation**

Each gene can be mutated to any value within the predetermined range with the probability of \( \text{GAP.mt.ptgm} \). Thus, the mutated genes have no relationship to their previous value.

**Partial mutation**

Each gene can be perturbed with respect to its current value by using a random value generated using a Gaussian random variable. The mutated gene value is related to the original gene value.

**Relative gene mutation**

In the relative gene perturbation, with the probability of \( \text{GAP.mt.prgm} \), each gene value is perturbed by certain fraction of the current gene value. The amount of perturbation is determined using a Gaussian random variable with standard deviation of \( \text{GAP.mt.srgm} \).

The relative gene mutation on \( j \)’th gene in \( k \)’th individual can be expressed as

\[ P_{ng;j,k} = P_{ng;j,k} \cdot (1 + N(0, \sigma_{rvm})) \]
where $N(0, \sigma_{rvm})$ is a Gaussian random variable with mean 0 and standard deviation $\sigma_{rvm}(\text{GAP.mt_srgm})$.

**Absolute gene mutation**

In the absolute gene perturbation, each gene value is added with a Gaussian random variable with standard deviation of $\text{GAP.mt_sagm}$. The probability of absolute gene perturbation is defined in $\text{GAP.mt_pagm}$.

The absolute gene mutation on $j$’th gene in $k$’th individual can be expressed as

$$P_{ng;j,k} = P_{ng;j,k} \cdot (1 + N(0, \sigma_{rvm}))$$

where $N(0, \sigma_{rvm})$ is a Gaussian random variable with mean 0 and standard deviation $\sigma_{rvm}(\text{GAP.mt_srgm})$.

**Vector mutation**

This function is similar to partial mutation except the fact that all the genes of an individual are involved.

**Relative vector mutation**

Each individual undergoes the relative vector mutation with the probability of $\text{GAP.mt_prvm}$. Every gene value of the individual is perturbed by certain fraction of the current gene value. The relative vector mutation on the $k$’th individual can be expressed as

$$P_{ng;k} = P_{ng;k} \cdot (1 + v_{dir} \cdot N(0, \sigma_{rvm}))$$

where $v_{dir}$ is a normalized random vector ($P_{genes} \times 1$) specifying the direction of perturbation and $N(0, \sigma_{rvm})$ is a Gaussian random variable with mean 0 and standard deviation $\sigma_{rvm}(\text{GAP.mt_srvm})$.

**Absolute vector mutation**

Each individual undergoes absolute vector mutation with the probability of $\text{GAP.mt_pavm}$. The absolute vector mutation on the $k$’th individual can be expressed as
\[
P_{ng;k} = P_{ng;k} + \nu_{dir} \cdot N(0, \sigma_{avm})
\]

where \( \nu_{dir} \) is a normalized random vector \((P_{genes} \times 1)\) specifying the direction of perturbation and \( N(0, \sigma_{avm}) \) is a Gaussian random variable with mean 0 and standard deviation \( \sigma_{avm}(\text{GAP.mt_savm}) \).

**Integer mutation**

Each integer gene can be mutated to any integer value within the predetermined range with the probability of \( \text{GAP.mt_pigm} \).
**nondom**

**Purpose**
Find the set of non-dominated solutions for multi-objective optimization

**Syntax**

\[ \text{Nd} = \text{nondom}(O, \text{flag}) \]

**Arguments**

- **O**  
  a matrix of objective function values whose dimension is 
  (Number of objective functions) by (Number of solutions)

- **flag**  
  1 indicates that the larger objective value is better 
  0 indicates that the smaller objective value is better

**Value**

**Nd**  
 a row vector with dimension equal to the number of solutions whose 
 elements are 1 if the solutions are non-dominated and 0 if they are 
 dominated

**Description**

nondom is used to identify the non-dominated solutions among the solutions 
using the objective function value matrix. The method proposed by Kung et al. 
is employed.

---

**Kung et al.’s method of identifying the non-dominated solution set**

| Step 1 | Sort the population according to the descending order of importance in the first 
|        | objective function and name the population as \( P \) |
|        | |

**Step 2** \( \text{Front}(P) \)

- \( |P| = 1 \), 
  Return \( P \) as the output of \( \text{Front}(P) \)
- \( |P| > 1 \), 
  \[ \text{T} = \text{Front} \left( P(1: \lfloor |P|/2 \rfloor) \right) \]
  \[ \text{B} = \text{Front} \left( P(\lfloor |P|/2 - 1 \rfloor : |P|) \right) \]
  
  - IF \( \) the \( i \)-th non-dominated solution of \( B \) is not dominated by 
    any non-nominated solution of \( T \), 
    \[ \text{M} = T \cup \{i\} \]
    Return \( M \) as the output of \( \text{Front}(P) \)

**Note**

1. \( \lfloor \cdot \rfloor \) is the number of the elements
2. \( P(a : b) \) means all the elements of \( P \) from index \( a \) to \( b \),
3. \( \lfloor \cdot \rfloor \) is an operator gives the nearest smaller integer value.

It is a recursive algorithm, and it may not be easy to visualize. However, it is 
the most computationally efficient method known at the time this manual is 
written.
**Examples**  Suppose we have the following objective function value matrix with two objectives and five solutions,

\[
O = \begin{bmatrix}
4 & 6 & 9 & 8 & 2 \\
5 & 1 & 6 & 7 & 4
\end{bmatrix}.
\]

Then \(Nd = \text{nondom}(O,1)\) returns

\[Nd = [0 \ 0 \ 1 \ 1 \ 0].\]

normgene

**Purpose**  
Update the normalized gene values based on the raw gene values

**Syntax**  
\[
P_{\text{out}} = \text{normgene}(P_{\text{in}})
\]

**Arguments**  
\(P_{\text{in}}\) structure of population before updating the normalized gene values

**Value**  
\(P_{\text{out}}\) structure of population after updating the normalized gene values

**Description**  
normgene updates the normalized gene values \((P_{\text{normgene}})\) based on the actual gene values \((P_{\text{gene}})\). The raw gene value is mapped to a value between 0 and 1 according to the type of the gene \((P_{\text{type}})\). Note that only the population members who have not been evaluated are updated.

The following table shows how `normgene` maps the raw gene value to the normalized gene values on \(j\)’th gene of the \(m\)’th chromosome for different types of gene.

<table>
<thead>
<tr>
<th>Gene type</th>
<th>(P_{\text{type}})</th>
<th>Operation</th>
</tr>
</thead>
</table>
| Integer & linear| 1, 2                | \[
\begin{align*}
P_{\text{ng};j,k} &= \frac{(P_{\text{g};j,k} - P_{\text{min};j})}{(P_{\text{max};j} - P_{\text{min};j})}
\end{align*}
\] |
| Logarithmic     | 3                   | \[
\begin{align*}
P_{\text{ng};j,k} &= \frac{\ln(P_{\text{g};j,k}) - \ln(P_{\text{min};j})}{\ln(P_{\text{max};j}) - \ln(P_{\text{min};j})}
\end{align*}
\] |

| Table B.4 |

**Examples**  
With the following parameters

\[
P_{\text{min}} = [0 \ 1 \ 10], \quad P_{\text{max}} = [10 \ 2 \ 1000], \quad \text{and} \quad P_{\text{type}} = [1 \ 2 \ 3],
\]

if a chromosome with normalized gene values is

\[
P_{\text{g};k} = [5 \ 1.5 \ 500],
\]

then the corresponding chromosome with actual gene values is

\[
P_{\text{ng};k} = [0.5 \ 0.5 \ 0.8495].
\]

**See Also**  
`rawgene`
**objwght**

**Purpose**
Create an objective weight vector for use in multi-objective optimization

**Syntax**
\[ \text{owv} = \text{objwght}(\text{GAP}) \]

**Arguments**
\text{GAP} \quad \text{structure of genetic algorithm parameters}

**Value**
\text{owv} \quad \text{normalized weight vector for scalarization of the multi-objective function values}

**Description**
\text{objwght} generates a normalized weight vector to be used for scalarization of the fitness function values in the multi-objective optimization problem.

In the single-objective optimization problem where \( \text{GAP.fp_nobj} = 1 \), there is only one objective function. Thus \text{objwght} returns \( \text{owv} = 1 \)

Even in the multi-objective optimization problem (\( \text{GAP.fp_nobj} > 1 \)), it is possible to use one objective function value for fitness evaluation. The objective function number to be used is specified in \( \text{GAP.fp_obj} \). Then the output weight vector \( \text{owv} \) has all zero values except for the element corresponding to the objective function specified by \( \text{GAP.fp_obj} \).

**Example**
Consider a multi-objective optimization with three objectives \( f_1, f_2 \) and \( f_3 \). A possible weight vector is
\[ \text{owv} = [0.2 \ 0.7 \ 0.1]. \]

Then the fitness value is calculated as
\[ \text{Fitness} = 0.2 f_1 + 0.7 f_2 + 0.1 f_3. \]

If \( \text{GAP.fp_obj} = 2 \), then \text{objwght} generates
\[ \text{owv} = [0 \ 1 \ 0]. \]

Hence the fitness value is calculated as
\[ \text{Fitness} = f_2. \]
**paretoplot**

**Purpose**
 Plot two objective functions in 2D objective space

**Syntax**
 `paretoplot(fignum, P, GAP, [region])`

**Arguments**
- `fignum`: figure number
- `P`: structure of current population
- `GAP`: structure of genetic algorithm parameters
- `region`: an optional integer argument specifies the region of which the chromosomes are plotted

**Description**
 `paretoplot` generates 2D plot of 2 objective functions as in Figure B.4. It is called within `reportplot`.

![Figure B.4 Pareto plot for Tanaka problem](image)

**See also**
 `reportplot`, `distplot`
**Purpose**
Perform a random search in the vicinity of the best individual in each region for better individual

**Syntax**
\[ Pout = \text{randsearch}(Pin, \text{GAP}, \text{GAS}, D) \]

**Arguments**
- **Pin**: structure of current population
- **GAP**: structure of genetic algorithm parameters
- **GAS**: structure of genetic algorithm statistics
- **D**: an optional data structure if needed for fitness evaluation

**Value**
- **Pout**: structure of the population after the random search

**Description**
randsearch explores the neighborhood of the best individual for better solution by random mutation of the best individual. By extensively exploring the vicinity of the best individual, it helps the GA to converge to the optimal solution faster.

There are two different random search operations. They are the relative random search that uses the relative vector mutation and the absolute random search that employs the absolute vector mutation. At each generation, only one of the two random search operations is active.

Random search starts at \((\text{GAP.rs_fgs} \times \text{GAP.fp_nngen})\)'th generation and \((\text{GAP.rs_fps} \times \text{GAP.fp_npop})\) individuals are randomly generated using relative vector mutation with the standard deviation of \(\text{GAP.rs_srp}\) or absolute vector mutation with the standard deviation of \(\text{GAP.rs_sap}\). The choice between the two random mutations is dependant on the value \(\text{GAP.rs_frp}\). \(\text{GAP.rs_frp}\) is the probability that the absolute mutation is used and thus the probability that the relative mutation is utilized is \((1-\text{GAP.rs_frp})\).

After generating the mutants, the fitness values of the mutants are evaluated. If there exists an individual whose fitness is better than that of the current best individual, then the current best is replaced by the new individual.
rawgene

**Purpose**  Update the raw gene values based on the normalized gene values

**Syntax**  
\[ P_{\text{out}} = \text{rawgene}(P_{\text{in}}) \]

**Arguments**  
- **Pin**: structure of population before updating raw gene values
- **Pout**: structure of population after updating raw gene values

**Description**  
`rawgene` updates the actual gene values \( (P.gene) \) based on the normalized gene values \( (P.normgene) \). The normalized gene value is mapped to a value in the predefined range according to the type of the gene \( (P.type) \). Note that only the population members who have not been evaluated are updated.

The following table shows how `rawgene` maps the normalized gene value to the actual gene values on \( j \)’th gene of the \( k \)’th chromosome for different types of gene.

<table>
<thead>
<tr>
<th>Gene type</th>
<th>( P_{\text{type}} )</th>
<th>Operation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Integer</td>
<td>1</td>
<td>[ P_{g,j,k} = [(P_{\text{max},j} - P_{\text{min},j}) \cdot P_{\text{ng},j,k} + P_{\text{min},j}] ] where [ ] is the round-up operator</td>
</tr>
<tr>
<td>Real</td>
<td>2</td>
<td>[ P_{g,j,k} = (P_{\text{max},j} - P_{\text{min},j}) \cdot P_{\text{ng},j,k} + P_{\text{min},j} ]</td>
</tr>
<tr>
<td>Logarithmic</td>
<td>3</td>
<td>[ P_{g,j,k} = \exp\left((\ln(P_{\text{max},j}) - \ln(P_{\text{min},j})) \cdot P_{\text{ng},j,k} + \ln(P_{\text{min},j})\right) ]</td>
</tr>
</tbody>
</table>

**Examples**  
With the following parameters  
\[ P_{\text{min}} = [0 1 10], \ P_{\text{max}} = [10 2 1000], \ \text{and} \ P_{\text{type}} = [1 2 3], \]

if a chromosome with normalized gene values is  
\[ P_{ng,k} = [0.5 0.5 0.5], \]

then the corresponding chromosome with actual gene values is  
\[ P_{g,k} = [5 1.5 100]. \]

**See Also**  
normgene
**Purpose**  
Plot the distribution of the genes of the chromosomes, the fitness history and Pareto plot

**Syntax**  
`reportplot(GAP,GAS,Pk,GUIhdl)`

**Arguments**  
- **GAP**: structure of genetic algorithm parameters  
- **GAS**: structure of genetic algorithm statistics  
- **P**: structure of the current population  
- **GUIhdl**: handle for GOSET GUI

**Value**  
None

**Description**  
Plots the distribution of the genes of the chromosomes with the fitness history as in Figure B.5 or the Pareto plot as in Figure B.6

![Figure B.5 Gene distribution plot](image1)  
![Figure B.6 2D Pareto plot](image2)

It is also possible to use a custom plotting routine on top of the distribution/fitness history plot and the Pareto plot by defining custom report plot handle `GAP.rp_crh`. The custom report plotting routine must have the following format without output return value.

```
f(P,GAP)
```

- **P**: structure of current population  
- **GAP**: structure of genetic algorithm parameters

**See also**  
distplot, paretoplot
scale

**Purpose**
Update scaling parameters and computes the scaled and aggregated fitness

**Syntax**
\[ F = \text{scale}(\text{Pin}, \text{GAP}) \]

**Arguments**
- \( \text{Pin} \)  structure of the input population
- \( \text{GAP} \)  structure of genetic algorithm parameters

**Value**
\( F \)  scaled and aggregated fitness

**Description**
scale generate the scaled and aggregated fitness value (\( \text{P.fit} \)) based on the current \( \text{GAP} \) and the current population. Scaling operator is applied independently to each region in the multiple region case.

Given the current fitness values, each fitness values (\( \text{P.fit} \)) is penalized by multiplying the penalty function value (\( \text{P.pen} \)) generated from the diversity control routine. Then the maximum (\( f_{\text{max}} \)), minimum (\( f_{\text{min}} \)), average (\( f_{\text{avg}} \)), media (\( f_{\text{med}} \)) and standard deviation (\( f_{\text{std}} \)) of the penalized fitness value of the population in each region are found.

Depending on the value of scaling algorithm parameter \( \text{GAP.sc_alg} \), different scaling method is used as in Table B.6.

<table>
<thead>
<tr>
<th>Scaling algorithm number</th>
<th>Scaling method</th>
<th>Operation</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{GAP.sc_alg} )</td>
<td></td>
<td>( f = ) original fitness ( f' = ) scaled fitness</td>
</tr>
<tr>
<td>0</td>
<td>None</td>
<td>( a = 1 ) ( b = 0 )</td>
</tr>
<tr>
<td>1</td>
<td>Offset scaling</td>
<td>( a = 1 ) ( b = -f_{\text{min}} )</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>Standard linear scaling</td>
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<tr>
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<td>---</td>
<td>-------------------------</td>
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<tr>
<td></td>
<td><img src="image" alt="Graph" /></td>
<td>$f' = af + b$</td>
</tr>
<tr>
<td></td>
<td>$f_{\text{avg}}$</td>
<td>$f_{\text{min}}$</td>
</tr>
<tr>
<td></td>
<td>$a = \frac{(k - 1) f_{\text{avg}}}{f_{\text{max}} - f_{\text{avg}}}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$b = f_{\text{avg}} (1 - a)$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$k = \text{GAP.sc.kln}$</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
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<th>3</th>
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<tbody>
<tr>
<td></td>
<td><img src="image" alt="Graph" /></td>
<td>$f' = af + b$</td>
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<tr>
<td></td>
<td>$f_{\text{med}}$</td>
<td>$f_{\text{min}}$</td>
</tr>
<tr>
<td></td>
<td>$a = \frac{(k - 1) f_{\text{med}}}{f_{\text{max}} - f_{\text{med}}}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$b = f_{\text{med}} (1 - a)$</td>
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<tr>
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<td>$k = \text{GAP.sc.kln}$</td>
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<table>
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<th>Mapped linear scaling</th>
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<td><img src="image" alt="Graph" /></td>
<td>$f' = af + b$</td>
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<tr>
<td></td>
<td>$f_{\text{std}}$</td>
<td>$f_{\text{min}}$</td>
</tr>
<tr>
<td></td>
<td>$a = k - 1$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$b = -f_{\text{min}} \cdot a + 1$</td>
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</tr>
<tr>
<td></td>
<td>$k = \text{GAP.sc.kln}$</td>
<td></td>
</tr>
</tbody>
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<table>
<thead>
<tr>
<th></th>
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<th>Sigma truncation</th>
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<td><img src="image" alt="Graph" /></td>
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</tr>
<tr>
<td></td>
<td>$f_{\text{std}}$</td>
<td>$f_{\text{min}}$</td>
</tr>
<tr>
<td></td>
<td>$a = 1$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$b = -(f_{\text{avg}} - k \cdot f_{\text{std}})$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$k = \text{GAP.sc.cst}$</td>
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</table>

<table>
<thead>
<tr>
<th></th>
<th>6</th>
<th>Quadratic scaling</th>
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<tr>
<td></td>
<td><img src="image" alt="Graph" /></td>
<td>$f' = af^2 + bf + c$</td>
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<tr>
<td></td>
<td>$f_{\text{max}}$</td>
<td>$f_{\text{min}}$</td>
</tr>
<tr>
<td></td>
<td>$a = \begin{bmatrix} f_{\text{max}} &amp; f_{\text{max}}^2 &amp; 1 \end{bmatrix}^{-1} k_{\text{max}}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$b = \begin{bmatrix} f_{\text{avg}}^2 &amp; f_{\text{avg}} &amp; 1 \end{bmatrix}^{-1} k_{\text{min}}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$c = \begin{bmatrix} f_{\text{min}}^2 &amp; f_{\text{min}} &amp; 1 \end{bmatrix}^{-1} k_{\text{min}}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$k_{\text{max}} = \text{GAP.sc.kmks}$</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$k_{\text{min}} = \text{GAP.sc.kmns}$</td>
<td></td>
</tr>
</tbody>
</table>

**Table B.6 Scaling algorithms**

If $\text{GAP.sc.alg} = 0$, scaling is not used.

If $\text{GAP.sc.alg} = 1$, offset scaling is used and $f_{\text{min}}$ is mapped to 0 and $f_{\text{max}}$ is mapped to $|f_{\text{max}} - f_{\text{min}}|$. 

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When GAP.sc_alg = 2, the fitness values are mapped so that the scaled fitness values also have same average fitness value as the original fitness value and the maximum fitness value is GAP.sc_kln times larger than \( f_{\text{avg}} \).

The case of GAP.sc_alg = 3 is similar to the case of GAP.sc_alg = 2, except that median fitness value is used instead of average fitness value.

With GAP.sc_alg = 4, fitness values are linearly scaled such that \( f_{\text{min}} \) is mapped to 1 and \( f_{\text{max}} \) is mapped to GAP.sc_kln.

Sigma truncation is applied when GAP.sc_alg = 5. All the fitness values smaller than \( (f_{\text{avg}} \cdot \text{GAP.sc_cst} \cdot f_{\text{std}}) \), where \( f_{\text{avg}} \) is the average fitness value and \( f_{\text{std}} \) is the standard deviation of the fitness values, are mapped to negative values and therefore disregarded later by clipping to zeros. It is useful when there are few individuals with very small fitness value and most individuals have large fitness value.

If GAP.sc_alg = 6, quadratic scaling is used. This algorithm emphasizes the large fitness value and deemphasizes the small fitness value. The parameters of a quadratic function is found such that \( f_{\text{max}} \) is mapped to GAP.sc_kmns, \( f_{\text{avg}} \) to 1 and \( f_{\text{min}} \) to GAP.sc_kmns. Then other fitness function values are mapped according to this quadratic function. GAP.sc_kmns is set to less than 1.

After applying the above scaling, all the negative fitness values are set to zeros, the fitness values are divided by the sum of all the fitness values. These final fitness values become the scaled fitness values that represent selection probabilities.

As the last step, the aggregate fitness values \( P.\text{fit} \) for chromosomes are obtained by summing all the objective functions using the objective function weight vector GAP.owv.

**Examples**

Given the fitness function vector \( P.mfit \) with three objective functions and five chromosomes as the following,

\[
P.mfit = \begin{bmatrix} 4 & 5 & 10 & 10 & 11.1111 \\ 14 & -7.5 & 20 & 6.25 & 3.3333 \end{bmatrix}
\]

If the penalty vector is

\[
P.pen = [0.5, 0.8, 0.6, 0.8, 0.9],
\]

then the penalized fitness becomes...
If we apply standard linear scaling with the scaling factor (\texttt{GAP.sc\_klin}) of 2, we have \(a = 1.5, b = -3\) for the first objective and \(a = 0.5385, b = 1.9385\) for the second objective to yield

\[
\begin{bmatrix}
  0 & 3 & 6 & 9 & 12 \\
 5.7077 & -1.2923 & 8.4000 & 4.6308 & 3.5538
\end{bmatrix}.
\]

To make the fitness values non-negative, any negative fitness values are set to zero, that is,

\[
\begin{bmatrix}
  0 & 3 & 6 & 9 & 12 \\
 5.7077 & 0 & 8.4000 & 4.6308 & 3.5538
\end{bmatrix}.
\]

Then the fitness values are normalized by dividing the fitness value by the sum of the fitness value of the corresponding objective.

\[
\begin{bmatrix}
  0 & 0.1 & 0.2 & 0.3 & 0.4 \\
 0.2560 & 0 & 0.3768 & 0.2077 & 0.1594
\end{bmatrix}
\]

With the objective function weight \([0.4 \ 0.6]\), the aggregate fitness values are found to be

\[
P.\text{fit} = [0.1536 \ 0.0400 \ 0.3061 \ 0.2446 \ 0.2557]
\]

Purpose
Select chromosomes from the population and form a mating pool

Syntax
Pout = select(Pin,GAP)

Arguments
Pin  structure of current population
GAP  structure of genetic algorithm parameters

Value
Pout  structure of the population

Description
Selection operator picks chromosomes from the current population to construct a mating pool for reproduction. When multiple regions are used, selection is applied within each region. That is, if there are $m$ chromosomes in a region, the selection operator picks the chromosome only from that region until $m$ spaces of the mating pool are filled. There are two different selection methods in GOSET that one can choose from. They are roulette wheel selection and tournament selection.

In the selection operation, the aggregate fitness values ($P.fit$) are divided by the sum of the aggregate fitness value to yield the normalized aggregate fitness values.

Roulette wheel selection
Setting GAP.sl_alg = 1 will activate roulette wheel selection. In the roulette wheel selection, the probability of an individual to be selected to the mating pool is proportional to the aggregate fitness ($P.fit$).

Tournament selection
Tournament selection is used if GAP.sl_alg is set to 2. In the tournament selection, GAP.sl_nts individuals are randomly chosen, and their aggregate fitness values ($P.fit$) are compared and the individual with best fitness value is selected to the mating pool. This procedure is repeated until the mating pool is occupied.

Illustrations of these selection operators are in Chapter 2.

Custom selection
Custom selection routine can be used instead of the two existing selection algorithms. This is specified by setting GAP.sl_alg to 3 and setting
GAP.dt_cah with the handle of the custom function. The custom function must have the following format

\[ \text{P_list} = f(\text{region}, \text{size}, \text{age}, \text{mfit}, \text{fit}) \]

- **P_list**: indices of the individuals to become parents
- **region**: the region number
- **size**: number of individuals for the death list
- **age**: vector describing ages of the individuals in population
- **mfit**: array with raw fitness values of the individuals in the region
- **fit**: vector of aggregate fitness values of individuals in the region

As an example of a custom algorithm, the Roulette wheel selection algorithm is written as an mfile called ‘customselect.m’ which is shown below.

```matlab
% Custom select algorithm example – Roulette wheel selection algorithm
function plist = customselect(region,size,region_age,region_mfit,region_fit)
% determine the mating probability
Matprob = region_fit/sum(region_fit);
% create a mapping function for selection
map=cumsum(matprob);
% now do the selection
for i=1:size,
    choice=rand;
    j=1;
    while (choice > map(j))
        j=j+1;
    end
    plist(i)=j;
end
```

This mfile must be in the same folder as the fitness function file or in the GOSET folder. Then the custom file handle GAP.sl_cah is set to @customselect.
Purpose
Randomly initialize the gene values and the regions of the individuals

Syntax
Pout = unrndinit(Pin, GAP)

Arguments
Pin structure of current population
GAP structure of genetic algorithm parameters

Value
Pout structure of the population

Description
unrndinit randomly generates chromosomes of the initial population.

First, the normalized gene values are randomly assigned as in the following,

\[ P_{ng;j,k} = \text{rand} \]

where \( P_{ng;j,k} \) represents the normalized gene value of \( j \)'th gene in the \( k \)'th individual and \( \text{rand} \) is MATLAB function that generates a random number between 0 and 1.

For the integer type gene, the normalized gene values are assigned with a discretized value between 0 and 1 such that they can represent correct integer values when mapped to actual gene values, that is,

\[ P_{ng;j,k} = \frac{\text{fix}(\text{rand} \times \text{levels})}{\text{levels} - 1} \]

where \( \text{levels} = P_{\text{max};j} - P_{\text{min};j} + 1 \), and \( \text{fix} \) is a MATLAB function that rounds a number towards zero.

After this step, the actual gene values are determined according to their types by using rawgene.

If multi-regions are used, the chromosomes are distributed into regions by

\[ P_{\text{reg}} = \text{ceil}(\text{rand} \times \text{GAP}.nreg) \]

where \( \text{ceil} \) is a MATLAB function that rounds a number towards positive direction.
**updateage**

**Purpose**
Update the age of each individual in the population

**Syntax**
Newage = updateage(P)

**Arguments**
P  
structure of current population

**Value**
Newage  
vector of new ages

**Description**
The age of each individual in the population is updated. The age of the individual survived from the previous generation increase by one, and the age of the new individual is set to one.
**updatestat**

**Purpose**
Update the statistic information of GAS

**Syntax**
\[ \text{GAS} = \text{updatestat}(\text{GAS}, \text{Pin}) \]

**Arguments**
- **Pin**  structure of current population
- **GAS**  structure of genetic algorithm statistics

**Value**
**GAS**  structure of genetic algorithm statistics

**Description**
The current average fitness value, the median fitness value, the best fitness value, and the gene values of the best individual are added to GAS.meanfit, GAS.medianfit, GAS.bestfit, and GAS.bestgenes respectively. The number of total evaluation is updated to GAS.ne.
### Appendix C. GOSET parameter list

<table>
<thead>
<tr>
<th>GAP[ * ]</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>GAP_dp_seqp</td>
<td>No. of chromosomes in initial population</td>
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</tr>
<tr>
<td>GAP_dp_seqm</td>
<td>No. of chromosomes in the population</td>
<td>100</td>
</tr>
<tr>
<td>GAP_dp_seq</td>
<td>No. of objective functions</td>
<td>1</td>
</tr>
<tr>
<td>GAP_dp_seq_obj</td>
<td>Objective to optimize (1 for Single-objective optimization)</td>
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</tr>
<tr>
<td>GAP_dp_seq_div</td>
<td>Diversity control flag</td>
<td>0</td>
</tr>
<tr>
<td>GAP_dp_seq_alg</td>
<td>Diversity control algorithm</td>
<td>4</td>
</tr>
<tr>
<td>GAP_dp_seq</td>
<td>Diversity control space</td>
<td>1 : Parameter space 2 : Fitness function space</td>
</tr>
<tr>
<td>GAP_dp_min</td>
<td>Minimum threshold for algorithm 1</td>
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</tr>
<tr>
<td>GAP_dp_ntr</td>
<td>No. of trials for algorithm 2</td>
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</tr>
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<td>GAP_dp_min</td>
<td>Min. no. of bins relative to pop. size for algorithm 2</td>
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</tr>
<tr>
<td>GAP_dp_max</td>
<td>Max. no. of bins relative to pop. size for algorithm 2</td>
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<td>GAP_dp_seq_div</td>
<td>Diversity control distance const (Algorithm 1 &amp; 4)</td>
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<tr>
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<td>Diversity control test pop. size (Algorithm 4)</td>
<td>50</td>
</tr>
<tr>
<td>GAP_dp_seq_div</td>
<td>Selection algorithm</td>
<td>1 : Roulette wheel 2 : Tournament</td>
</tr>
<tr>
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<td>Function handle for the custom selection algorithm</td>
<td></td>
</tr>
<tr>
<td>GAP_dp_seq_div</td>
<td>No. of individuals used in tournament</td>
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</tr>
<tr>
<td>GAP_dp_seq_div</td>
<td>Function handle for the custom depth algorithm</td>
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<tr>
<td>GAP_dp_seq_div</td>
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<td>GAP_dp_seq_div</td>
<td>Function handle for the custom depth algorithm</td>
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</tr>
<tr>
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<td>No. of generations used in crossover</td>
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</tr>
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<td>GAP_dp_seq_div</td>
<td>Crossover algorithm</td>
<td>1 : Single point crossover 2 : Scalar simple blend crossover 3 : Vector simple blend crossover 4 : Scalar simulated binary crossover 5 : Vector simulated binary crossover</td>
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<td>No. of generations used in crossover</td>
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</tr>
<tr>
<td>GAP_dp_seq_div</td>
<td>Tightness of distribution (x) for crossover algorithms 4 and 5</td>
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#### GAS[ * ]

<table>
<thead>
<tr>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>GAS_mb_xave</td>
<td>Standard deviation of absolute vector mutation</td>
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<tr>
<td>GAS_mb_gpa</td>
<td>Probability of a relative gene mutation</td>
</tr>
<tr>
<td>GAS_mb_pmea</td>
<td>Standard deviation of relative gene mutation</td>
</tr>
<tr>
<td>GAS_mb_rmea</td>
<td>Probability of a relative gene mutation</td>
</tr>
<tr>
<td>GAS_mb_pmea</td>
<td>Standard deviation of absolute gene mutation</td>
</tr>
<tr>
<td>GAS_mb_rmea</td>
<td>Probability of a relative gene mutation</td>
</tr>
<tr>
<td>GAS_mb_rmea</td>
<td>Probability of a relative gene mutation</td>
</tr>
</tbody>
</table>

#### GOSET parameter list

<table>
<thead>
<tr>
<th>P[ * ]</th>
<th>Description</th>
<th>Default</th>
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</thead>
<tbody>
<tr>
<td>P.t_fitness</td>
<td>Fitness to the fitness function</td>
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</tr>
<tr>
<td>P.t_nreps</td>
<td>The number of individuals in the population</td>
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</tr>
<tr>
<td>P.t_fitness</td>
<td>Unconstrained fitness function values</td>
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</tr>
<tr>
<td>P.t_nreps</td>
<td>Fitness evaluation flag</td>
<td>0 : Fitness is not evaluated 1 : Fitness is evaluated</td>
</tr>
<tr>
<td>P.g</td>
<td>Age of the individuals in generation number</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Number of genes in all chromosomal or an individual</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Minimum gene</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Maximum value of gene</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Mating and crossover parameters</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Fitness evaluation flag</td>
<td>0 : Fitness is not evaluated 1 : Fitness is evaluated</td>
</tr>
<tr>
<td>P.g</td>
<td>Chromosome ID of gene (used for multiple chromosome case)</td>
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</tr>
<tr>
<td>P.g</td>
<td>Normalized gene values</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Fitness evaluation flag</td>
<td>0 : Fitness is not evaluated 1 : Fitness is evaluated</td>
</tr>
<tr>
<td>P.g</td>
<td>Geographic region of an individual</td>
<td></td>
</tr>
<tr>
<td>P.g</td>
<td>Penalty factor which is used for diversity control</td>
<td></td>
</tr>
</tbody>
</table>

### Abbreviation list

- **No.**: Number
- **Min**: Minimum
- **Max**: Maximum
- **Pop.**: population
- **Gen.**: Generation
- **Alg**: Algorithm
- **Neg**: Negative
- **Pos**: Positive

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