

**Single and Multiobjective Genetic Algorithm
Toolbox for Matlab in C++**

Kumara Sastry

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Illinois Genetic Algorithms Laboratory
University of Illinois at Urbana-Champaign
117 Transportation Building
104 S. Mathews Avenue Urbana, IL 61801
Office: (217) 333-2346
Fax: (217) 244-5705

Single and Multiobjective Genetic Algorithm Toolbox for Matlab in C++

Kumara Sastry
Illinois Genetic Algorithms Laboratory (IlliGAL),
Materials Computation Center, and
Department of Industrial and Enterprise Systems Engineering
University of Illinois at Urbana-Champaign, Urbana IL 61801

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Abstract

This report provides documentation for the general purpose genetic algorithm toolbox for matlab in C++. The fitness function used in the toolbox is written in matlab. The toolbox provides different selection, recombination, mutation, niching, and constraint-handling operators. Problems with single and multiple objectives can be solved with the toolbox. Moreover, the toolbox is easily extensible and customizable for incorporating other operators and for solving user-defined search problems.

1 Introduction

This document briefly describes how to download, compile, and run the GA toolbox for matlab. The source code is an extension of the GA toolbox implementation in C++ (Sastry, 2007) so that it can be used inside matlab with fitness functions written in matlab. Interested user should refer to the extensive comments in the code for an explanation of the more intricate GA-implementation and the code structure details. This report also explains how to modify the objective function that comes with the distribution of the code. The source is written in C++ but knowledge of matlab and C is sufficient to modify the objective function so that you can try the toolbox for your own problems.

2 How to download the code?

The code is available from `ftp://ftp-illigal.ge.uiuc.edu/pub/src/GA/GAtoolbox_matlab.tgz`. After downloading it, uncompress and untar the file by typing

```
tar zxvf GAtoolbox_matlab.tgz
```

At this point you should have in your directory the following files:

DISCLAIMER	README	chromosome.cpp	chromosome.hpp
crossover.cpp	crossover.hpp	ga.cpp	ga.hpp
globalSetup.cpp	globalSetup.hpp	individual.cpp	individual.hpp
localsearch.cpp	localsearch.hpp	nsgapopulation.cpp	population.cpp
population.hpp	random.cpp	random.hpp	selection.cpp
selection.hpp	userDefinables.cpp	sgaFitnessFunction.m	mogaFitnessFunction.m
plotFunction.m			

3 How to compile the code?

To compile the code, a C++ compiler needs to be installed on your computer. I also assume that you have Matlab properly installed and that `mex` is fully configured on your system. The code has been compiled using GNU C++ and Matlab with version 6 and above under Linux. For windows, the toolbox has been compiled and tested with Microsoft Visual C++ compiler version 6.0 and Matlab version 6 and above.

In Unix- and Linux-based systems, start matlab by typing `matlab` in the unix/linux command prompt. Compile the source code using `mex` in the Matlab command window as follows:

```
mex -output GAtbxm -f /usr/local/matlab/bin/cxxopts.sh *.cpp
```

The `cxxopts.sh` is a C++ options file needed to let matlab know that you are compiling C/C++ source code. Once the compiling is successfully completed, a Matlab executable file, `GAtbxm.mexglx`, is created.

In Windows-based systems, launch the matlab application and compile the source code using `mex` in the Matlab command window as follows:

```
mex -output GAtbxm *.cpp
```

Note that depending on your Matlab installation, you might need to use a specific C++ options file with the `-f` option. The C++ options file in Windows is a `.bat` file and is typically in the `%Matlab%\bin` or `%Matlab%\bin\mexopts` directory, where `%Matlab%` is the Matlab root directory. For example, `%Matlab%` can be `C:\Program Files\MATLAB704\`. Once the compiling is successfully completed, a Matlab executable file, `GAtbxm.mexw32` or `GAtbxm.dll`, is created.

An alternative way of compiling the source code in Microsoft Visual Studio is given here: <http://www.mathworks.com/support/solutions/data/1-180D4.html?solution=1-180D4>.

4 How to run the code?

The matlab executable `GAtbxm` needs one argument: the name for an input file. The toolbox reads its parameters from the input file and outputs the results onto the screen (`stdout`). Four sample input files—`input_sga_maxSpec`, `input_sga_minSpec`, `input_nsga_maxSpec`, and `input_nsga_minSpec`—are provided as examples with the distribution of this code.

Two objective functions that comes with the distribution of the code; one is a single objective problem with two constraints (`sgaFitnessFunction.m`) and the other is a multiobjective problem with two objectives (`mogaFitnessFunction`). The single objective test function is the constrained Himmelblau's function (Rekalaitis, Ravindran, & Ragsdell, 1983). Himmelblau's function is a minimization problem with two decision variables. The objective value for this case is:

$$f(x_1, x_2) = (x_1^2 + x_2 - 11)^2 + (x_1 + x_2^2 - 7)^2, \quad (1)$$

with the following two constraints

$$(x_1 - 5)^2 + x_2^2 \leq 26, \quad (2)$$

$$4x_1 + x_2 \leq 20. \quad (3)$$

The multiobjective test function is the Kuroswae test function (Deb, Pratap, Agrawal, & Me-
yarivan, 2002):

$$f_1(x_1, x_2, x_3) = \sum_{i=1}^2 \left[-10 * \exp \left(-0.2 \sqrt{x_i^2 + x_{i+1}^2} \right) \right], \quad (4)$$

$$f_2(x_1, x_2, x_3) = \sum_{i=1}^3 \left[|x_i|^{0.8} + 5 \sin x_i^3 \right]. \quad (5)$$

The steps required to write your own fitness function are described in section 7.
To run the GA toolbox, at the command prompt, type

```
GAtbxm('<input file name>')
```

For example to use `input_sga_maxSpec` as the input file type `GAtbxm('input_sga_maxSpec')`.

Relevant statistics are plotted, depending on the input file specifications, at the end of each gener-
ation. The output plotted is handled by the matlab function `plotFunction.m`. The input to the
function is the decision variable values, objective function values, and constraint violation values
of the individuals in the current population. `plotFunction.m` is called within the C++ in the
function

```
std::ostream &operator<< (std::ostream &out, const Population &pop)
```

implemented in the file `population.cpp`.

5 Description of GA toolbox Capabilities

This section presents an overview of the operators and components implemented in the GA toolbox.
The toolbox can solve both single- and multi-objective problems with or without constraints. The
multiobjective genetic algorithm implemented is the non-dominated sorting GA II (NSGA-II) (Deb,
Pratap, Agrawal, & Meyarivan, 2002).

The decision variables of the problem are encoded as real numbers or as integers within their
specified ranges. This encoding procedure permits the decision variables to be binary, discrete,
 χ -ary alphabet or a real number. The decision variable type needs to be specified in the input file
and the valid options are `double` or `int`.

The following genetic operators are supported by GAtbxm:

Selection The following selection procedures are available in GA toolbox:

1. Tournament selection with replacement (Goldberg, Korb, & Deb, 1989; Sastry & Gold-
berg, 2001)
2. Tournament selection without replacement (Goldberg, Korb, & Deb, 1989; Sastry &
Goldberg, 2001)

3. Truncation selection (Mühlenbein & Schlierkamp-Voosen, 1993)
4. Roulette-Wheel selection (Goldberg, 1989)
5. Stochastic universal selection (SUS) (Baker, 1985; Baker, 1987; Grefenstette & Baker, 1989; Goldberg, 1989)

Recombination/Crossover The recombination procedures implemented in the GA toolbox are:

1. One point crossover (Goldberg, 1989; Sastry, Goldberg, & Kendall, 2005)
2. Two point crossover (Goldberg, 1989; Sastry, Goldberg, & Kendall, 2005)
3. Uniform crossover (Goldberg, 1989; Sastry, Goldberg, & Kendall, 2005)
4. Simulated binary crossover (SBX) (Deb & Agarwal, 1995; Deb & Kumar, 1995)

Mutation Different mutation procedures implemented in the GA toolbox are:

1. Selective mutation, where a randomly selected gene is replaced by a *uniformly distributed* random value in the interval $[x_{i,min}; x_{i,max}]$ with probability p_m .
2. Genewise mutation, where every gene is mutated using Gaussian mutation with probability p_m .
3. Polynomial mutation (Deb & Agarwal, 1995; Deb & Kumar, 1995; Deb, 2001).

Niching Niching methods implemented in the GA toolbox are:

1. Fitness sharing (Goldberg & Richardson, 1987; Goldberg, 1989)
2. Deterministic crowding (Mahfoud, 1992)
3. Restricted tournament selection (Harik, 1995)

Scaling Three scaling procedures are implemented in the GA toolbox:

1. Linear ranking (Baker, 1985; Goldberg, 1989),
2. Sigma scaling (Forrest, 1985; Goldberg, 1989), and
3. Default scaling which is only used if any one of the following conditions hold true: (a) The selection procedure is roulette-wheel or SUS, and the minimum fitness value is negative, or (b) the niching method is fitness sharing and the minimum fitness value is negative.

Constraint handling Three constraint handling methods are implemented in the GA toolbox:

1. Tournament method (Deb, 2001)
2. Linear penalty method, where a weighted sum of the constraint violations of an individual is added to or subtracted from its objective value depending on whether we are minimizing or maximizing the objective function.
3. Quadratic penalty method, which is similar to linear penalty, except that the penalty value is computed as a weighted sum of the square of constraint violation values of a candidate solution.

It is important to note that the constraint handling methods use the constraint violation value and not constraint function value. For example, if the constraint is

$$10x_1 + x_2 \leq 20,$$

$x_1 = 2$, and $x_2 = 2$, the constraint violation value is 2. However, if $x_1 = 1$, $x_2 = 7$, then the constraint violation value is 0.

Local search The local search method implemented in the GA toolbox is the *Nelder-Mead* algorithm (Nelder & Mead, 1965; Press, Flannery, Teukolsky, & Vettering, 1989). Local search is applied to an individual with probability p_{ls} . The solution obtained through the local search is incorporated using the *Baldwinian strategy*—where the local search solution replaces the individual, but the fitness of the individual is not modified—with probability, p_b , and *Lamarckian strategy*—where both the fitness and the individual are replaced with local search solution and its fitness—with probability, $1 - p_b$.

Elitist Replacement In GA toolbox, both the old and new population is sorted according to their fitness and constraint violation. A user specified proportion, p_e , of top individuals are retained and the rest, $n(1 - p_e)$ individuals are replaced by the top individuals in the new population. Here n is the population size.

5.1 Statistics

Various statistics are collected from the population every generation. These not only aid the user with the progress of genetic search, but are also used in many operators and functionalities. Statistics are also used to determine if the genetic search should be terminated or not. The statistics collected are the mean, minimum, and maximum fitness and objective values. Other statistics include, fitness variance and objective variance in the population. For the multiobjective case, the statistics are collected separately for each objective.

5.2 Stopping Criteria

GA toolbox provides the following stopping criteria for the GA runs

1. **Number of Function Evaluations:** This option terminates the run after certain number of function evaluations have been performed by the GA.
2. **Fitness Variance:** This option stops the once the fitness variance of the population reaches below a specified value.
3. **Best Fitness:** This criterion terminates the run once the fitness of the best individual in the population exceeds a specified value.
4. **Average Fitness:** This option stops the run once the average fitness of the population exceeds a specified value.
5. **Average Objective:** This option stops the run once the average objective function value of the population exceeds a specified value.
6. **Change in Best Fitness:** This option terminates the run once the change in fitness of the best individual in the population over the previous generation is below a specified value.

7. **Change in Average Fitness:** This option terminates the run once the change in average fitness of the population over the previous generation is below a specified value.
8. **Change in Fitness Variance:** This option terminates the run once the change in fitness variance of the population over the previous generation is below a specified value.
9. **Change in Best Objective:** This option terminates the run once the change in change in objective value of the best individual in the population over the previous generation is below a specified value.
10. **Change in Average Objective:** This option terminates the run once the change in change in average objective value the population over the previous generation is below a specified value.
11. **Number of Fronts:** This option is available only for NSGA. It terminates the run after the number of non-dominated fronts in the population goes below a specified value.
12. **Number of guys in first front:** This option terminates the run when the number of individuals in the first exceeds a specified value. It is only available only for NSGA.
13. **Change in number of fronts:** This options stops the run when the change in the number of fronts over the previous generating is below a specified value.

6 Input File Format

The input file `input_sga_maxSpec` is shown (along with line numbers) below. As mentioned earlier, the `GAtbxm` skips all empty lines and those that start with `#`. Then it starts reading the parameters in a predefined order. The program doesn't do any fancy parsing on the input file. This means that **you should not change the order of the lines in the input file** and therefore the choice of operators and parameters will be incorrectly read. The input file is self explanatory and straightforward to understand.

```

1  #
2  # GA type: SGA or NSGA
3  #
4  SGA
5
6  #
7  # Number of decision variables
8  #
9  2
10
11 #
12 # For each decision variable, enter:
13 #   decision variable type, Lower bound, Upper bound
14 # Decision variable type can be double or int
15 #
16 double 0.0 6.0
17 double 0.0 6.0

```

```

18
19 #
20 # Objectives:
21 #   Number of objectives
22 #   For each objective enter the optimization type: Max or Min
23 #
24 1
25 Min
26
27 #
28 # Constraints:
29 #   Number of constraints
30 #   For each constraint enter a penalty weight
31 #
32 2
33 1.0
34 1.0
35 #
36 # General parameters: If these parameters are not entered default
37 #                       values will be chosen. However you must enter
38 #                       "default" in the place of the parameter.
39 #
40 #   [population size]
41 #   [maximum generations]
42 #   [replace proportion]
43 #
44 100
45 100
46 0.9
47
48 #
49 # Niching (for maintaining multiple solutions)
50 # To use default setting type "default"
51 # Usage: Niching type, [parameter(s)...]
52 # Valid Niching types and optional parameters are:
53 #   NoNiching
54 #   Sharing [niching radius] [scaling factor]
55 #   RTS [Window size]
56 #   DeterministicCrowding
57 #
58 # When using NSGA, it must be NoNiching (OFF).
59 #
60 NoNiching
61
62 #
63 # Selection
64 # Usage: Selection type, [parameter(s)...]
65 # To use the default setting type "default"
66 #

```

```

67 # Valid selection types and optional parameters are:
68 #   RouletteWheel
69 #   SUS
70 #   TournamentWOR [tournament size]
71 #   TournamentWR [tournament size]
72 #   Truncation [# copies]
73 #
74 # When using NSGA, it can be neither SUS nor RouletteWheel.
75 #
76 TournamentWOR 2
77
78 #
79 # Crossover
80 # Crossover probability
81 # To use the default setting type "default"
82 #
83 # Usage: Crossover type, [parameter(s)...]
84 # To use the default crossover method type "default"
85 # Valid crossover types and optional parameters are
86 #   OnePoint
87 #   TwoPoint
88 #   Uniform [genewise swap probability]
89 #   SBX [genewise swap probability][order of the polynomial]
90 #
91 0.9
92 SBX 0.5 10
93
94 #
95 # Mutation
96 # Mutation probability
97 # To use the default setting type "default"
98 #
99 # Usage: Mutation type, [parameter(s)...]
100 # Valid mutation types and the optional parameters are:
101 #   Selective
102 #   Polynomial [order of the polynomial]
103 #   Genewise [sigma for gene #1][sigma for gene #2]...[sigma for gene #ell]
104 #
105 0.1
106 Polynomial 20
107
108 #
109 # Scaling method
110 # To use the default setting type "default"
111 #
112 # Usage: Scaling method, [parameter(s)...]
113 # Valid scaling methods and optional parameters are:
114 #   NoScaling

```

```

115 #           Ranking
116 #           SigmaScaling [scaling parameter]
117 #
118 NoScaling
119
120 #
121 # Constraint-handling method
122 # To use the default setting type "default"
123 #
124 # Usage: Constraint handling method, [parameters(s)...]
125 # Valid constraint handling methods and optional parameters are
126 #           NoConstraints
127 #           Tournament
128 #           Penalty [Linear|Quadratic]
129 #
130 Tournament
131
132 #
133 # Local search method
134 # To use the default setting type "default"
135 #
136 # Usage: localSearchMethod, [maxLocalTolerance], [maxLocalEvaluations],
137 #           [initialLocalPenaltyParameter], [localUpdateParameter],
138 #           [lamarckianProbability], [localSearchProbability]
139 #
140 # Valid local search methods are: NoLocalSearch and SimplexSearch
141 #
142 # For example, SimplexSearch 0.001000 20 0.500000 2.000000 0.000000 0.000000
143 NoLocalSearch
144
145 #
146 # Stopping criteria
147 # To use the default setting type "default"
148 #
149 # Number of stopping criterias
150 #
151 # If the number is greater than zero
152 #   Number of generation window
153 #   Stopping criterion, Criterion parameter
154 #
155 # Valid stopping criterias and the associated parameters are
156 #   NoOfEvaluations, Maximum number of function evaluations
157 #   FitnessVariance, Minimum fitness variance
158 #   AverageFitness, Maximum value
159 #   AverageObjective, Max/Min value
160 #   ChangeInBestFitness, Minimum change
161 #   ChangeInAvgFitness, Minimum change
162 #   ChangeInFitnessVar, Minimum change

```

```
163 # ChangeInBestObjective, Minimum change
164 # ChangeInAvgObjective, Minimum change
165 # NoOfFronts (NSGA only), Minimum number
166 # NoOfGuysInFirstFront (NSGA only), Minimum number
167 # ChangeInNoOfFronts (NSGA only), Minimum change
168 # BestFitness (SGA with NoNичing only), Maximum value
169 #
170 0
171
172 #
173 # Load the initial population from a file or not
174 # To use the default setting type "default"
175 #
176 # Usage: Load population (0|1)
177 #
178 # For example, if you want random initialization type 0
179 # On the other and if you want to load the initial population from a
180 # file, type
181 #     1 <population file name> [0|1]
182 #
183 # Valid options for "Load population" are 0/1
184 # If you type "1" you must specify the name of the file to load the
185 # population from. The second optional parameter which indicates
186 # whether to evaluate the individuals of the loaded population or not.
187 0
188
189 # Save the evaluated individuals to a file
190 #
191 # To use default setting type "default".
192 #
193 # Here by default all evaluated individuals are stored and you will be
194 # asked for a file name later when you run the executable.
195 #
196 # Usage: Save population (0|1)
197 # For example, if you don't want to save the evaluated solutions type 0
198 # On the other and if you want to save the evaluated solutions
199 #     1 <save file name>
200 #
201 # Note that the evaluated solutions will be appended to the file.
202 #
203 # Valid options for "Save population" are 0/1
204 # If you type "1" you must specify the name of the file to save the
205 # population to.
206 1 evaluatedSolutions.txt
207
208 #END
```

7 How to plug-in your own objective function?

The code for the objective function is in the matlab function `sgaFitnessFunction.m` (for single-objective) and `mogaFitnessFunction.m` (for multiobjective) and it is called within C++ library in the file `userDefinables.cpp`. These are the only files that you need to rewrite in order to try your own fitness function. The function header which calls the matlab fitness function is as follows:

```
void globalEvaluate(double *x, double *objArray, double *constraintViolation,
                  double *penalty, int *noOfViolations)
```

`globalEvaluate` takes as argument an array `x`, whose ℓ elements contains the decision variables of a candidate solution whose fitness is being evaluated. Here, ℓ is the problem length (# of genes).

The decision variables are then passed on to the matlab function `sgaFitnessFunction.m` (or `mogaFitnessFunction.m`) which evaluates the objective and constraint violation values of the given candidate solution. The function header is as follows:

```
function objConst = sgaFitnessFunction(decVars)
```

`sgaFitnessFunction` (alternatively `mogaFitnessFunction`) takes as argument an array, `decVars`, containing decision variables of the candidate solution. `sgaFitnessFunction` (alternatively `mogaFitnessFunction`) returns objective function value(s) and constraint violation value(s) in the array `objConst`.

8 About the C++ code for Matlab

The implementation of the GA toolbox doesn't use advanced features of the C++ language such as templates and inheritance. This means that you don't need to be a C++ expert in order to modify the code. In fact, you can modify the code and plug-in your own objective function using the C programming language alone. Next, we give brief description of the source files. Each `.cpp` file has a corresponding `.hpp` file, except `nsgapopulation.cpp` and `userDefinables.cpp`. The `.hpp` files are the header files and contain the definitions of the various classes. The `.cpp` files contain the actual implementation.

`chromosome.cpp` contains the implementation of the class `chromosome`. A chromosome is an array of genes. It also contains implementation of mutation operators.

`individual.cpp` contains the implementation of the class `individual`. An individual is a candidate solution for a given search and optimization problem.

`population.cpp` contains the implementation of the class `population`. A population is an array of chromosomes. Objective to fitness mappings and statistics computations are implemented here.

`nsgapopulation.cpp` contains the implementation of the class `nsgapopulation`. It builds on the class `population` and implements nondominated sorting and crowding distance computation required for NSGA-II.

`crossover.cpp` contains the implementation of the class `crossover`. Different crossover operators are implemented here.

`selection.cpp` contains the implementation of the class `selection`. Different selection operators are implemented here.

`localsearch.cpp` contains the implementation of the class `localsearch`. A local search operator is implemented here.

`ga.cpp` contains the implementation of the class `ga`. Different GA architectures (GA and NSGA-II) are implemented here.

`random.cpp` contains subroutines related to the pseudo random number generator.

`globalSetup.cpp` contains the implementation of the class `globalSetup`. Global data needed across different classes are implemented here.

`userDefinables.cpp` contains the code for the objective function. If you want to try the GAtbxm on your own problem, you might have to modify the function `globalEvaluate()` contained in this file.

`sgaFitnessFunction.m` contains an example implementation of a single objective optimization problem with two constraints

`mogaFitnessFunction.m` contains an example implementation of a multiobjective optimization problem.

`plotFunction.m` contains the implementation of graphical display of results obtained through the GA toolbox.

9 Disclaimer

This code is distributed for academic purposes only. It has no warranty implied or given, and the authors assume no liability for damage resulting from its use or misuse. If you have any comments or find any bugs, please send an email to kumara@illigal.ge.uiuc.edu.

10 Commercial use

For the commercial use of this code please contact Prof. David E. Goldberg at deg@uiuc.edu

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