

GOSET 2.3

The following is a list of updates from GOSET 2.2 to GOSET 2.3. First, it should be noted that GOSET 2.3 should be entirely downward compatible with GOSET 2.2. That is to say that all GOSET 2.2 code will run under GOSET 2.3 without modification. However, GOSET 2.3 contains several new capabilities, has some changes to make it easier to use, and in addition contains a correction.

New Capabilities

- 1.) *TRIMGA*. A new routine titled *TRIMGA* has been added to the GOSET 2.3 toolbox. This routine takes the best solution found from a GA run, and runs a deterministic optimization with the GA solution as a starting point. The goal is that the deterministic optimization takes the GA solution taken by searching the entire search space and finds a more exact solution in the vicinity of the GA solution. Gene range constraints are enforced by subtracting infinity from the fitness function if a gene value fits outside of the allowed range. A sample call is

```
[x,f] = trimga(GAP,P,D)
```

or

```
[x,f] = trimga(GAP,P)
```

where the inputs are the genetic algorithm parameter structure `GAP` the population structure `P` and optional data structure `D`, and where the outputs are `x` the revised solution, and `f` the revised fitness function value.

- 2.) *PARETOPLOT*. The pareto-plot routine has been enhanced in two ways. First, the dominated and non-dominated solutions are now differentiated in these plots. In particular, non-dominated points are shown as o's, while the dominated points as x's. A second enhancement of this routine is that 3-D Pareto Plots are now supported, in addition to the 2-D Pareto Plots that were previously available. This is convenient for the three objective case.
- 3.) *GENEREPAIR*. The gene repair algorithm has been isolated from the crossover and mutation operators, so that the gene repair algorithm can be readily controlled. Previously, only ring-mapping could be utilized for gene repair. Now hard-limiting is also available. The parameter `GAP.gr_alg` controls the algorithm. Setting this parameter to 1 results in hard limiting while setting it to 2 results in the use of ring mapping. The default gene repair algorithm has been set to hard-limiting. This results in significantly better performance in situations where the limit of a variable is a physical limit which also happens to be the location of the optimum solution.

Changes Effecting Ease of Use

- 5.) *Licensing.* The license is no longer required.
- 6.) *GAPDEFAULT.* This routine, which initializes the GA parameters, now supports several call syntaxes. In particular, in addition to

```
[GAP] = gapdefault  
[GAP] = gapdefault(nobj)
```

the syntax

```
[GAP] = gapdefault(nobj,obj,npop,ngen)
```

may also be used, allowing all the fundamental parameters of the GA (the number of objectives *nobj*, objective to optimize *obj*, nominal population size *npop*, and number of generations *ngen* to be set in the call to *gapdefault*.

- 7.) *GAOPTIMIZE.* This routine now supports several new call syntaxes. Supported syntaxes include

```
[fP,GAS]      = gaoptimize(@fitfun,GAP,D,GAS,iP,GUIhd1)  
[fP,GAS]      = gaoptimize(@fitfun,GAP,D,GAS,iP)  
[fP,GAS]      = gaoptimize(@fitfun,GAP,D)  
[fP,GAS]      = gaoptimize(@fitfun,GAP)  
[fP,GAS,bI]   = gaoptimize(@fitfun,GAP,D,GAS,iP,GUIhd1)  
[fP,GAS,bI]   = gaoptimize(@fitfun,GAP,D,GAS,iP)  
[fP,GAS,bI]   = gaoptimize(@fitfun,GAP,D)  
[fP,GAS,bI]   = gaoptimize(@fitfun,GAP)
```

where all arguments are defined as in GOSET 2.2, except for *bI*, which, for the single objective case, is a vector whose elements contain the gene values of the best individual, or, in the multi-objective case is an array wherein each column corresponds to the genes of a non-dominated individual. This saves the user the step of identifying the best individual or set of non-dominated individuals. In addition, because of the new syntaxes which are supported, it is no longer necessary to pass empty arguments into *gaoptimize*.

Corrections

- 8.) *DISTPLOT.* The gene distribution plotting routine contained an error which caused the distribution of the uppermost range to be underreported if the population included genes which were equal to the limit. This was most noticeable in the case where the gene was an integer. While the results were correct, the plot was not. The error has been corrected.

- 9.) *Age.* Some errors effecting calculation of individual age were corrected. In particular, in the random search routine failed to assign age to the population which could cause errors if it was needed. The mating and crossover routine was modified so that children are initialized with an age of zero rather than one.

ISSUE ON AGE: MIGRATION. CURRENTLY RESET TO ZERO. DO WE WANT TO DO THIS ???