

```
>>gp=runGP(@Y7_config);  
Press a key to continue
```

```
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GPTIPS 2  
Symbolic data mining platform for MATLAB  
Copyright (C) Dominic Searson 2009-2015
```

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Run parameters
```

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Population size:      100  
Number of generations: 100  
Number of runs:      1  
Parallel mode :      off  
Tournament type:      regular  
Tournament size:      15  
Elite fraction:       0.3  
Fitness cache:        enabled  
Lexicographic selection: True  
Max tree depth:       4  
Max nodes per tree:   Inf  
Using function set:    TIMES MINUS PLUS  
Number of inputs:     4  
Max genes:            12  
Constants range:      [-10 10]  
Complexity measure:    expressional  
Fitness function:      regressmulti_fitfun.m
```

```
Generation 0  
Best fitness:      2.0798  
Mean fitness:      9.6122  
Best complexity: 190  
Inputs in best individual: x1 x2 x3 x4
```

```
Generation 20  
Best fitness:      1.924
```

Mean fitness: 2.0312  
Best complexity: 236  
Inputs in best individual: x1 x2 x3 x4

Generation 40  
Best fitness: 1.8928  
Mean fitness: 2.1023  
Best complexity: 262  
Inputs in best individual: x1 x2 x3 x4

Generation 60  
Best fitness: 1.8863  
Mean fitness: 2.0143  
Best complexity: 258  
Inputs in best individual: x1 x2 x3 x4

Generation 80  
Best fitness: 1.8844  
Mean fitness: 2.1755  
Best complexity: 272  
Inputs in best individual: x1 x2 x3 x4

Finalising run.  
GPTIPS run complete in 0.85 min.  
Best fitness acheived: 1.8839

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Evaluate the best individual of  
the runs on the fitness function using:  
>>runtree(gp,'best');  
Press a key to continue

Next, use the the GPPRETTY command on the best individual:  
>>gppretty(gp,'best')  
Press a key to continue

Simplified genes  
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Gene 1 and bias term

10.18 x2 + 0.4484

Gene 2

- 0.0277 x3 - 0.003974 x1 x4

Gene 3

$$0.2426 x_1 (x_2 - 1.0)$$

Gene 4

$$-0.0000902 x_1 x_2 (2.0 x_1 - 1.0 x_3)$$

Gene 5

$$0.0006369 (x_1 - 1.0 x_3 + 1.05) (x_1 + x_2 x_4 - 1.05)$$

Gene 6

$$- 0.02163 x_1 x_2^2$$

Gene 7

$$0.01331 x_2 - 0.01331 x_1 + 0.01331 x_3 + 0.01331 x_4$$

Gene 8

$$(0.000002592 x_1 - 0.000002592 x_3 + 0.000002723) (x_2 + x_3 + x_2 x_4)$$

Gene 9

$$- 0.003866 x_2 x_3 - 0.003866 x_2 x_4 - 0.009637$$

Gene 10

$$0.003774 x_1^2 + 0.003774 x_2 + 0.003774 x_4$$

Gene 11

$$- 0.0005649 x_1^2 - 0.0005649 x_1 + 0.0005649 x_2 x_3 x_4$$

Gene 12

$$- 0.0001198 x_2 x_4^2 + 0.0007154 x_3 x_4$$

Simplified overall GP expression

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$$- 0.0001804 x_1^2 x_2^2 + 0.003846 x_1^2 - 0.02163 x_1 x_2^2 + 0.0000902 x_1 x_2 x_3 + 0.0006395 x_1 x_2 x_4 + 0.2426 x_1 x_2 - 0.0006343 x_1 x_3 - 0.003974 x_1 x_4 - 0.2565 x_1 -$$

$$\begin{aligned} &0.00007464 \, x_2 \, x_3 \, x_4 - 0.003868 \, x_2 \, x_3 - 0.0001198 \, x_2 \, x_4 - 0.003194 \, x_2 \, x_4 + 10.2 \, x_2 - \\ &\quad \quad \quad 2 \\ &0.000002592 \, x_3^2 + 0.0007154 \, x_3 \, x_4 - 0.01372 \, x_3 + 0.01709 \, x_4 + 0.4381 \end{aligned}$$

Next, use the the DRAWTREE command:

```
>>drawtrees(gp,'best')
```

Press a key to continue

Trees drawn to trees.htm

Opening in system browser.

Finally, an HTML report listing the models on the Pareto optimal front of model expressional complexity and performance can be generated using the PARETOREPORT function.

```
>>paretoreport(gp)
```

Press a key to continue

100 models passed R<sup>2</sup> training ( $\geq 0$ ) and expressional complexity ( $\leq \text{Inf}$ ) filter ...

Computing pareto front on training data...

Removing genotype duplicates from 7 remaining models ...

6 models passed the filtering process.

Model report created in pareto.htm

Opening report in system browser.

end

```
>>
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