

```
>>gp=runGP(@Y3_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:     3  
Max genes:            12  
Constants range:      [-10 10]  
Complexity measure:   expressional  
Fitness function:     regressmulti_fitfun.m
```

Generation 0

Best fitness: 0.36557  
Mean fitness: 0.71296  
Best complexity: 149  
Inputs in best individual: x1 x2 x3

Generation 20

Best fitness: 0.34545

Mean fitness: 0.36053  
 Best complexity: 207  
 Inputs in best individual: x1 x2 x3

Generation 40  
 Best fitness: 0.34082  
 Mean fitness: 0.36921  
 Best complexity: 294  
 Inputs in best individual: x1 x2 x3

Generation 60  
 Best fitness: 0.33395  
 Mean fitness: 0.36657  
 Best complexity: 296  
 Inputs in best individual: x1 x2 x3

Generation 80  
 Best fitness: 0.33151  
 Mean fitness: 0.34458  
 Best complexity: 320  
 Inputs in best individual: x1 x2 x3

Finalising run.  
 GPTIPS run complete in 0.64 min.  
 Best fitness acheived: 0.32919

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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

$$- 29.69 x_1^2 x_3 - 29.69 x_1 x_3^2 + 249.4 x_1 x_3 + 0.4373$$

Gene 2

$$- 1.0 x_3^2 (10.4 x_1 - 46.97)$$

Gene 3

$$204.9 \, x_1^2$$

Gene 4

$$0.01279 \, x_1^3 \, x_2$$

Gene 5

$$- 0.0009345 \, x_3^2 \, x_2^2 + 0.0009345 \, x_1$$

Gene 6

$$3.795 \, x_2^2 - 3.795 \, x_1^2 - 3.795 \, x_3^2 - 25.98 \, x_1 \, x_3$$

Gene 7

$$- 1.0 \, x_2^2 \, x_3^2 (0.5726 \, x_1 - 0.3806)$$

Gene 8

$$-0.0002235 \, x_2^2 (x_3^2 - 1.0 \, x_2^2 + x_1 \, x_2)$$

Gene 9

$$- 206.0 \, x_1^2 - 206.0 \, x_3^2 \, x_1 + 206.0 \, x_2^2$$

Gene 10

$$7.087 \, x_1^2 - 6.333 \, x_2^2$$

Gene 11

$$x_2^2 (0.001308 \, x_1 \, x_2 \, x_3^2 - 0.001308 \, x_3^2 + 0.006925)$$

Gene 12

$$85.63 \, x_1^2 \, x_3^2 - 203.5 \, x_2^2$$

Simplified overall GP expression

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$$0.01279 \, x_1^3 \, x_2^2 + 85.63 \, x_1^2 \, x_3^2 - 29.69 \, x_1^2 \, x_3^2 - 1.179 \, x_1^2 + 0.001308 \, x_1 \, x_2^2 \, x_3^2 -$$

$$\begin{aligned} & 0.0002235 x_1^2 x_2^2 - 0.5726 x_1^2 x_2 x_3^2 - 40.09 x_1^2 x_3^2 + 17.34 x_1 x_3^2 + 3.293 x_1^2 - \\ & 0.0009345 x_2^2 x_3^2 + 0.0002235 x_2^2 + 0.3806 x_2^2 x_3^2 - 0.001532 x_2 x_3^2 - 0.02367 x_2^2 + \\ & 46.97 x_3^2 - 3.795 x_3^2 + 0.4373 \end{aligned}$$

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.

```
>>pareto report(gp)
```

Press a key to continue

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

Computing pareto front on training data...

Removing genotype duplicates from 9 remaining models ...

6 models passed the filtering process.

Model report created in pareto.htm

Opening report in system browser.

end

```
>>
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