```
>>gp=rungp(@Y10_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
--------------
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:        5
Max genes:               12
Constants range:         [-10  10]
Complexity measure:      expressional
Fitness function:        regressmulti_fitfun.m

Generation 0
Best fitness:    0.41112
Mean fitness:    1.1599
Best complexity: 200
Inputs in best individual: x1 x2 x3 x4 x5

Generation 20
Best fitness:    0.35641
```

```
Mean fitness:    0.38313
Best complexity: 232
Inputs in best individual: x1 x2 x3 x4 x5

Generation 40
Best fitness:    0.35402
Mean fitness:    0.37427
Best complexity: 258
Inputs in best individual: x1 x2 x3 x4 x5

Generation 60
Best fitness:    0.35375
Mean fitness:    0.36701
Best complexity: 264
Inputs in best individual: x1 x2 x3 x4 x5

Generation 80
Best fitness:    0.35366
Mean fitness:    0.37926
Best complexity: 264
Inputs in best individual: x1 x2 x3 x4 x5

Finalising run.
GPTIPS run complete in 0.75 min.
Best fitness acheived: 0.35337
------------------------------------------------------------

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
----------------

Gene 1 and bias term

  1.334 x4 + 10.8

Gene 2

                                          2
  - 0.00001491 (x3 - 1.0 x4) (x4 - 2.929) (x4  - 3.004)

Gene 3
```

```
  -0.01273 x5 (x1 + x3 - 1.0 x4)

Gene 4

  0.03695 x1 - 0.03695 x2 - 0.03695 x3 + 0.03695 x4 - 0.03695 x5 (x4 - 1.0 x5)

Gene 5

  1.978 x1

Gene 6

  0.01294 x1 + x2 (0.01294 x3 + 0.1199)

Gene 7

  -0.000701 x2 x3 (x3 + x4)

Gene 8

  -0.000000000000000001084 x2 (x3 - 1.0 x4) (2757700000000000.0 x3 +↙
25533000000000000.0)

Gene 9

  0.1527 x1 x3 - 0.01855 x2 - 0.01855 x1 - 0.1527 x1 x5 + 0.01855 x3 x5

Gene 10

  0.8165 x3 - 1.633 x4 - 0.8165 x5

Gene 11

  0.001528 x1 x2 x3

Gene 12

  -1.0 (x2 + x3) (0.004934 x1 - 0.004934 x4 + 0.004934 x5 + 0.03121)

Simplified overall GP expression
--------------------------------

  2.009 x1 + 0.03323 x2 + 0.7483 x3 - 0.2624 x4 - 0.8165 x5 - 0.004934 x1 x2 + 0.1478 x1↙
x3 +

     0.01017 x2 x3 - 0.1654 x1 x5 + 0.007701 x2 x4 - 0.004934 x2 x5 + 0.004979 x3 x4 +

                                                    2                    2
     0.0008902 x3 x5 - 0.02423 x4 x5 - 0.0009996 x2 x3  + 0.00004368 x3 x4  -
```

```
                    3               2                 3             2                 4
     0.00001491 x3 x4  - 0.0000448 x4  - 0.00004368 x4  + 0.03695 x5  + 0.00001491 x4  +

     0.001528 x1 x2 x3 - 0.0004023 x2 x3 x4 + 10.8

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^2 training (>= 0) and expressional complexity (<= Inf) filter ...
Computing pareto front on training data...
Removing genotype duplicates from 8 remaining models ...
5 models passed the filtering process.
Model report created in pareto.htm
Opening report in system browser.
end
>>
```