```
>>gp=rungp(@Y9_config);
Press a key to continue
```

```
--------------------------------------------------------------------------
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:    0.1452
Mean fitness:    0.33075
Best complexity: 216
Inputs in best individual: x1 x2 x3 x4 x5

Generation 20
Best fitness:    0.13422
```

```
Mean fitness:     0.14287
Best complexity: 237
Inputs in best individual: x1 x2 x3 x4 x5


Generation 40
Best fitness:     0.13369
Mean fitness:     0.14128
Best complexity: 293
Inputs in best individual: x1 x2 x3 x4 x5


Generation 60
Best fitness:     0.13364
Mean fitness:     0.14174
Best complexity: 293
Inputs in best individual: x1 x2 x3 x4 x5


Generation 80
Best fitness:     0.13362
Mean fitness:     0.13914
Best complexity: 279
Inputs in best individual: x1 x2 x3 x4 x5


Finalising run.
GPTIPS run complete in 0.65 min.
Best fitness acheived: 0.13361
------------------------------------------------------------

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

  0.09565 x1 + 0.09565 x2 - 0.09565 x4 + 6.988

Gene 2

  - 0.02072 x3 - 0.05531 x4 x5

Gene 3
```

- 0.005295 x3 - 0.01413 x1 x4

Gene 4

  -0.1784 x4

Gene 5

  0.0008008 x4 - 0.0008008 x2 - 0.0008008 x2 (x2 - 1.0 x5) - 0.0008008 x3 x4

Gene 6

  0.06228 x4 - 0.06228 (x1 + x3) (x1 - 1.0 x3) + 0.06228 x4 x5

Gene 7

  -0.2889 x5

Gene 8

  0.001951 x4 + 0.001951 x1 x3 (x2 - 1.0 x4)

Gene 9

  $- 0.0001016 (x2 - 1.0 x4) (x3 - 1.0 x5) - 0.0001016\ x2\ x3^{2}$

Gene 10

  -0.000006581 (x3 + x5) (x4 - 1.0 x5) (x3 x5 - 1.0 x5 + 9.434)

Gene 11

  0.0171 x1 + 0.0171 x5 - 0.0171 x3 x5

Simplified overall GP expression

  $0.1128\ x1 + 0.09485\ x2 - 0.02602\ x3 - 0.209\ x4 - 0.2718\ x5 + 0.000006581\ x3^{2}\ x5^{2}\ -$

     0.01413 x1 x4 - 0.0001016 x2 x3 + 0.0009025 x2 x5 - 0.0007613 x3 x4 - 0.01704 x3 x5 ↙
  +

     $0.006804\ x4\ x5 - 0.0001016\ x2\ x3^{2} - 0.000006581\ x3\ x5^{2} + 0.000006581\ x3\ x5^{3}\ +$

     $0.000006581\ x4\ x5^{2} - 0.06228\ x1^{2} - 0.0008008\ x2^{2} + 0.06228\ x3^{2} + 0.00006209\ x5^{2}\ -$

$$0.000006581\ x5^{3}\ -\ 0.000006581\ x3\ x4\ x5^{2}\ -\ 0.000006581\ x3^{2}\ x4\ x5 + 0.001951\ x1\ x2\ x3 ↙$$
$$-$$

$$0.001951\ x1\ x3\ x4 + 0.000006581\ x3\ x4\ x5 + 6.988$$

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 3 remaining models ...
3 models passed the filtering process.
Model report created in pareto.htm
Opening report in system browser.
end
>>