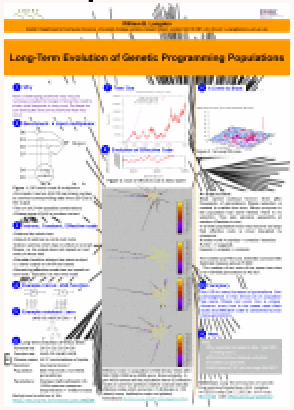
Long-Term Stability of Genetic Programming Landscapes

Workshop on Landscape-Aware Heuristic Search,16 July 2017, Nadarajen Veerapen *et al*.,
GECCO-2017, Berlin, Germany. Room Diamant

W. B. Langdon

Department of Computer Science

Long-Term Evolution of GP Populations
Poster Monday 17:50-20:00
GECCO companion p235-236



Technical report RN/17/05
https://arxiv.org/abs/1703.08481

Video1
Video2

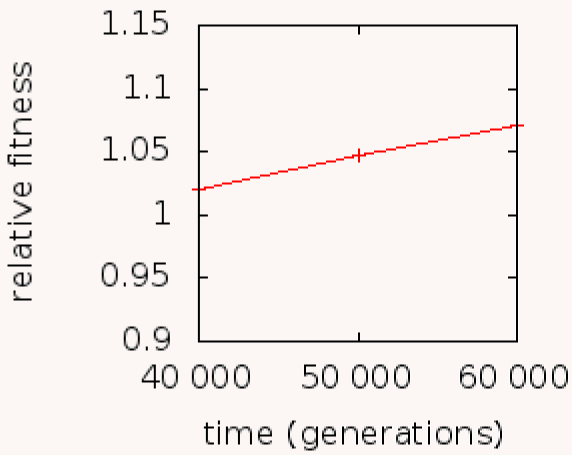
Genetic Programming and Long-Term Evolution Experiments

- Why we care about LTEE
- Evolving Bacteria 60,000 generations v. evolving programs 100,000 generations
- LTEE continuous innovation v convergence
- Existing results on landscape of large trees
- New results
  - Increase in code (bloat), end of bloat
  - Theory some true, some less so
  - Evolution has smoothed large tree landscape although fitness distribution remains rugged.

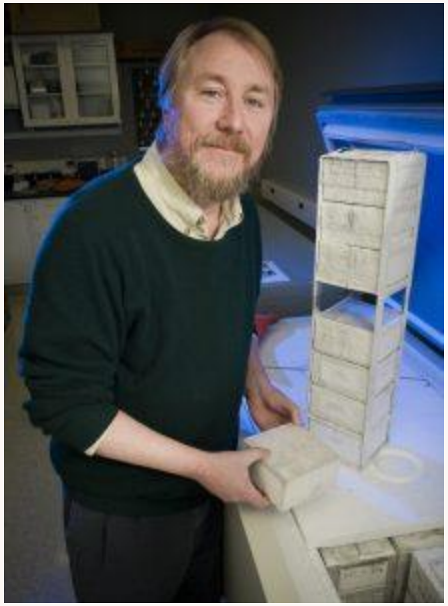
Why Long Term Evolution Matters

- More challenging problems may require running evolution for longer.
- Hence the need to study what happens in long runs.
- By mapping landscape far from origin, perhaps we can anticipate and solve problems that may occur.

Long-Term Evolution Experiment



Mean fitness of nine E. coli populations from the LTEE



Richard Lenski pulls frozen bacteria cultures out of a freezer 15 Oct 2009

Evolving Bacteria 60,000 generations

Even after 60000 gens fitness still improving

R. E. Lenski *et al*. 2015. Sustained fitness gains and variability in fitness trajectories in the long-term evolution experiment with Escherichia coli. Proc. Royal Soc.

Convergence of Fitness Distribution

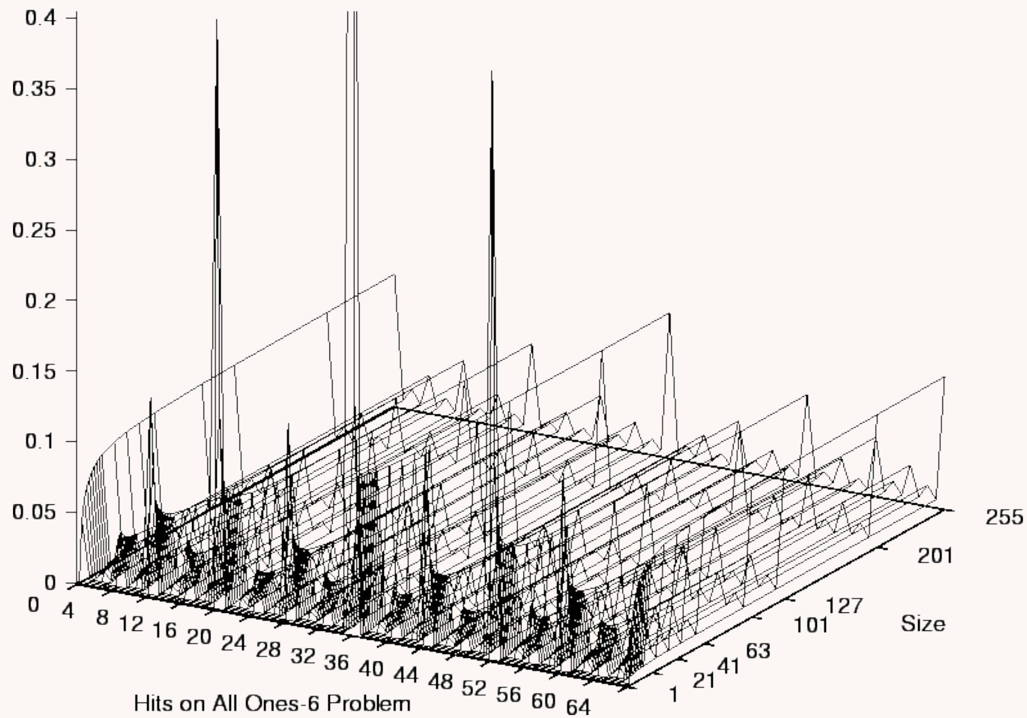


Fig. 7.7 Foundations of Genetic Programming

Large tree fitness distribution remains rugged like small trees but as we will see GP population maintains smooth landscape

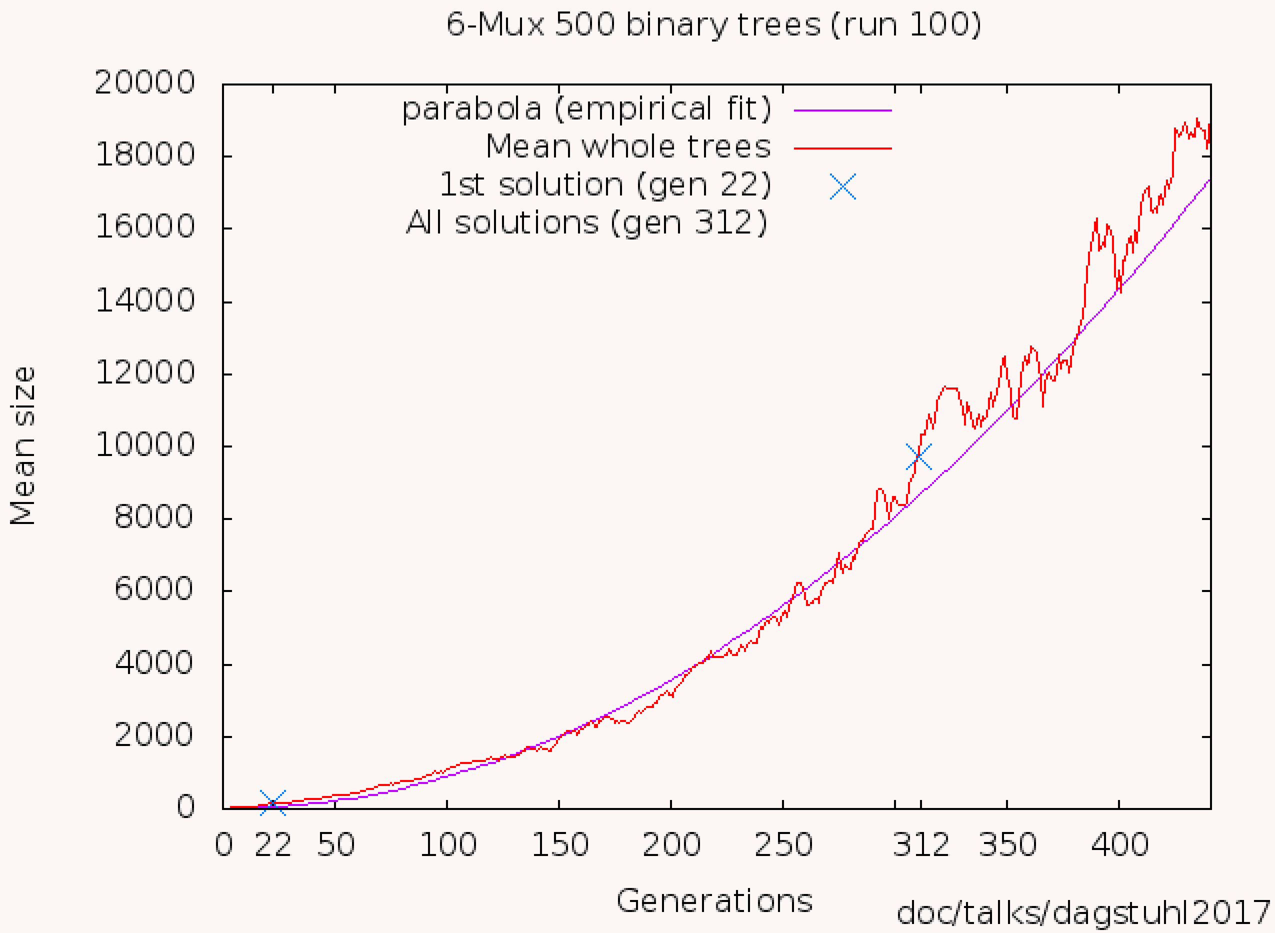
Genetic Programming and Long-Term Evolution Experiments

- GP system able to run thousands of generations. (Do not stop when solved)
  - Expect bloat (tree growth)
  - Compact representation of trees
  - Fast fitness evaluation
    - GPquick C++, written by Andy Singleton

    ≈ two bytes per tree node
- Submachine code genetic programming

CREST

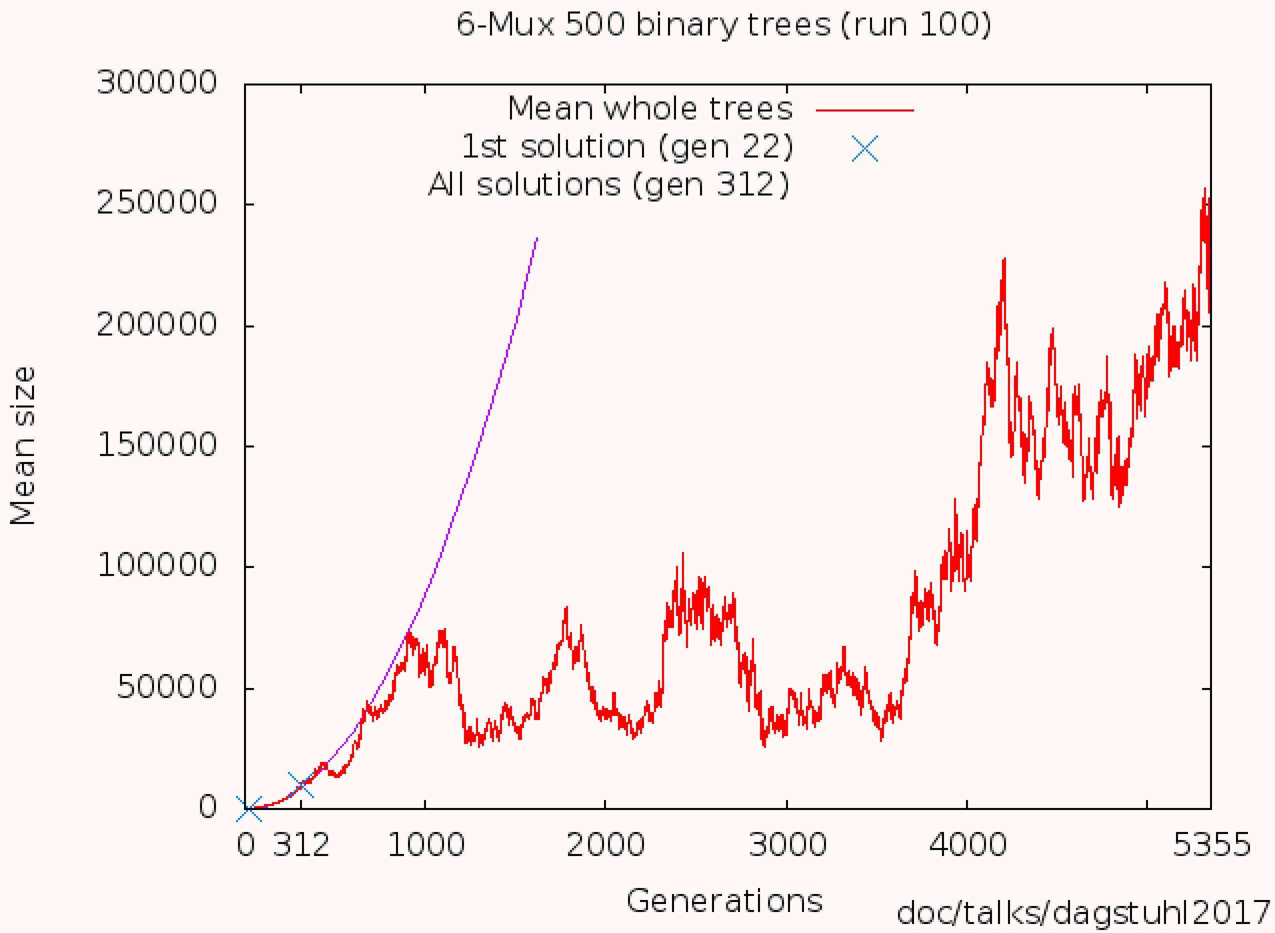
Evolution of Program Size



Note evolution continues after 1st solution found in generation 22 and even after 1st population when everyone has maximum fitness (generation 312).

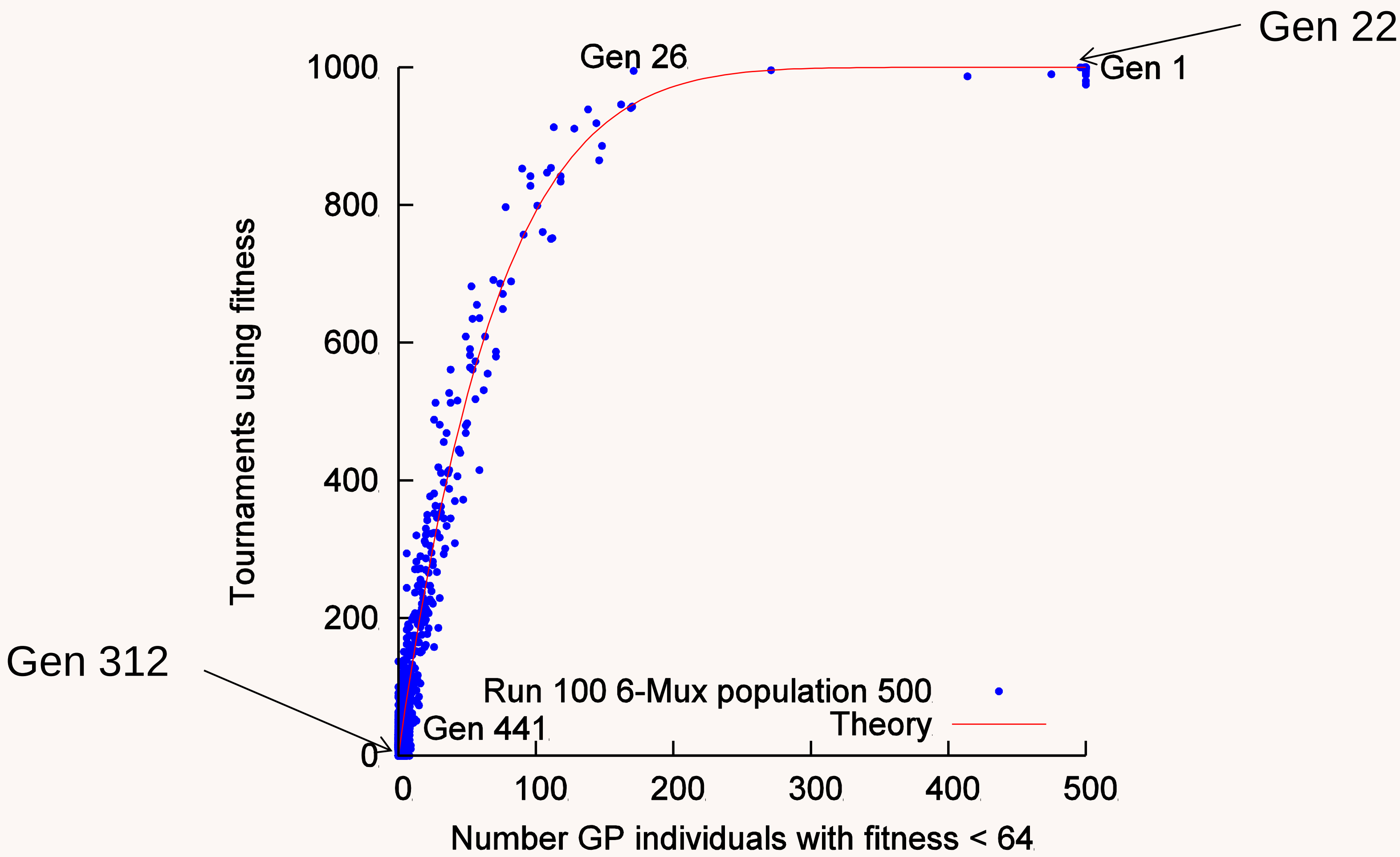
GP+EM (1)1 pp95-119

Evolution of Program Size



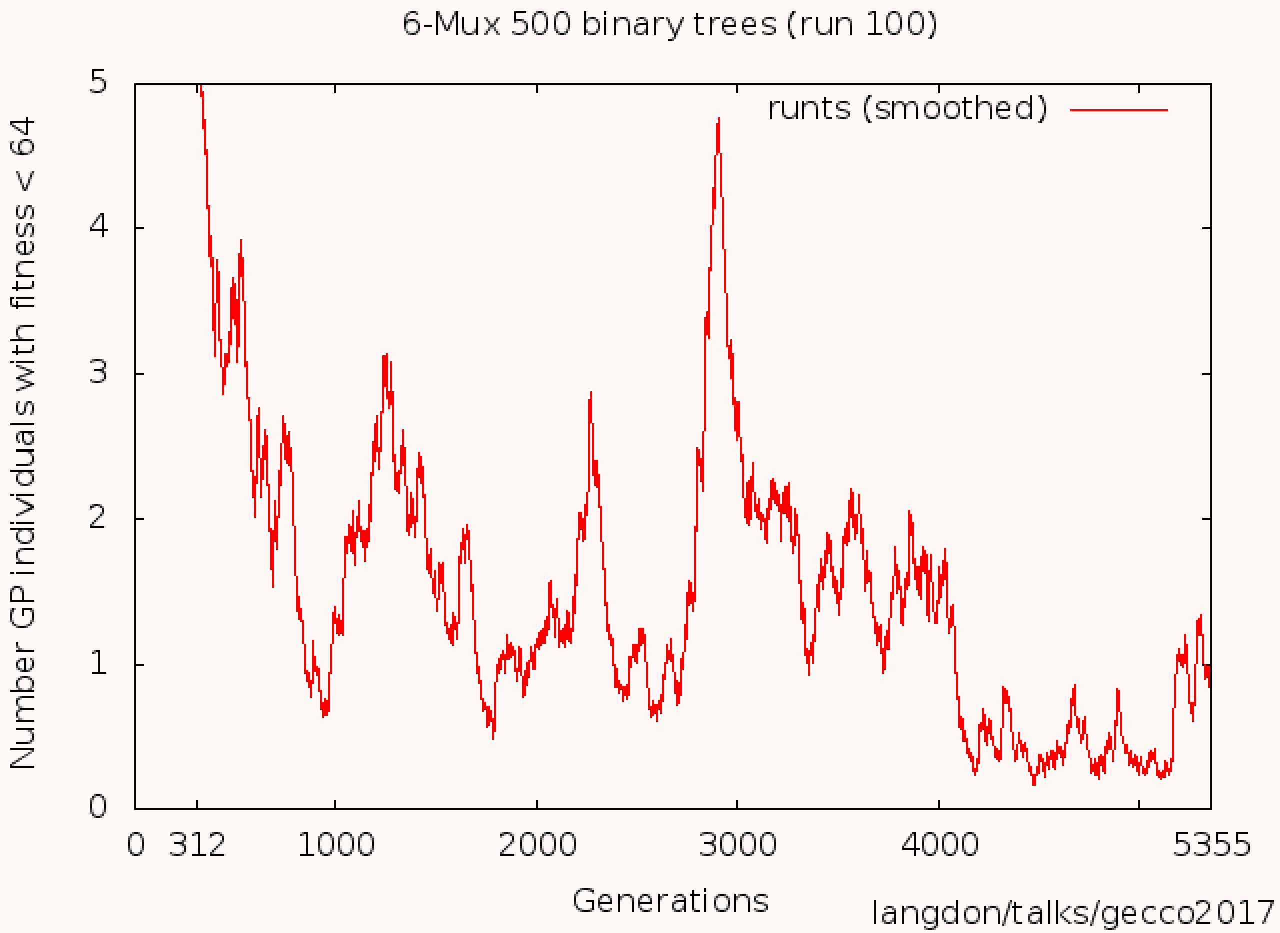
Note evolution continues even after 1st population when everyone has maximum fitness (generation 312) but tree size falls as well as rises.

6-Mux Fitness Convergence



Theory $y = 2\text{popsize}(1-(1-x/\text{popsize})^7)$ matches experiment

6-Mux Fitness Convergence



Plot smoothed by taking running average over 30 generations

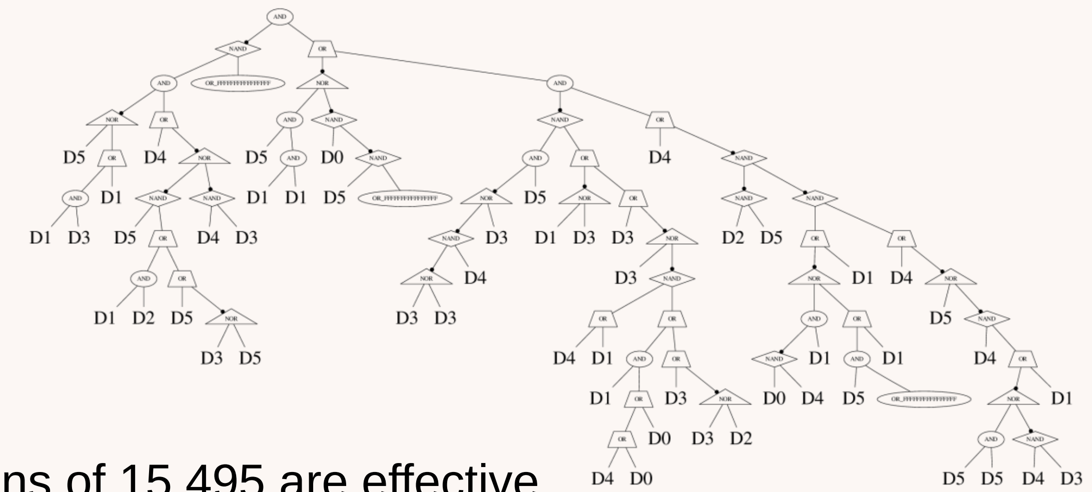
Convergence in Genetic Programming

- GP genotypes do not converge. Even after many generations every tree in the population is different, BUT…
- Every (or almost all) trees give the same answers (phenotypic convergence)
- Effective code, i.e. code to solve problem, does converge.

Effective code other runs converges differently

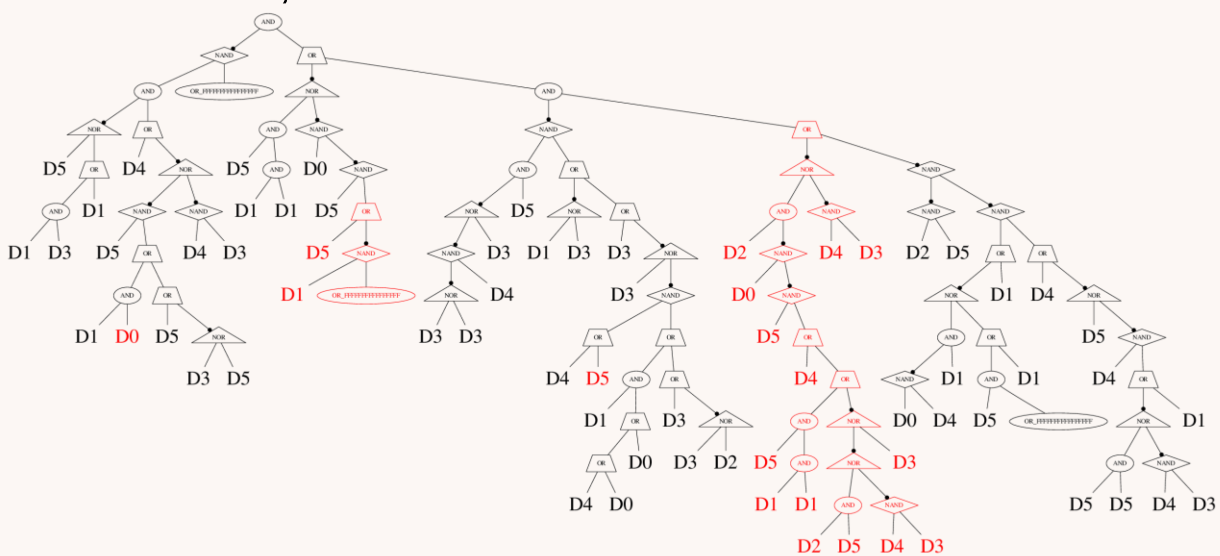
CREST

Convergence of typical Effective Code



Gen 400

Only 111 instructions of 15,495 are effective

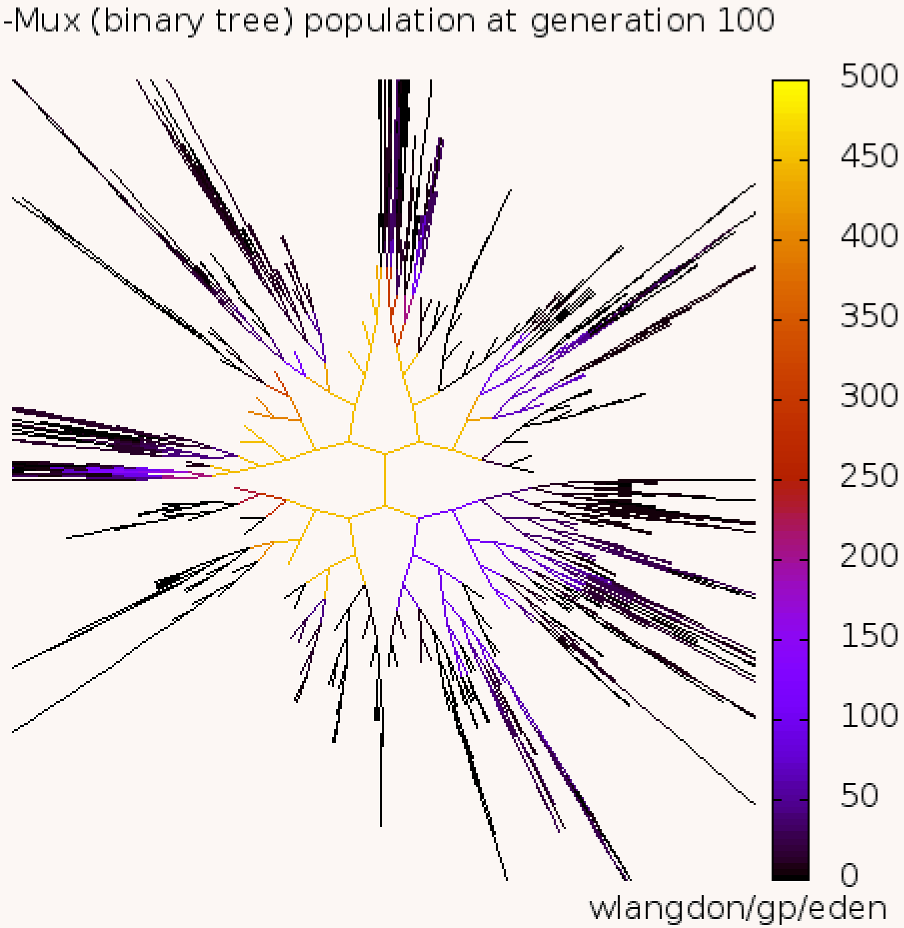


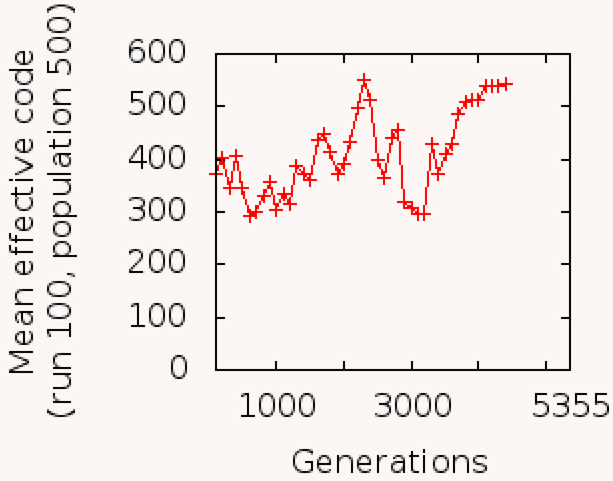
Gen 500

Only 141 instructions of 16,831 are effective

Tree drawing code [lisp2dot.awk]

Convergence of Effective Code



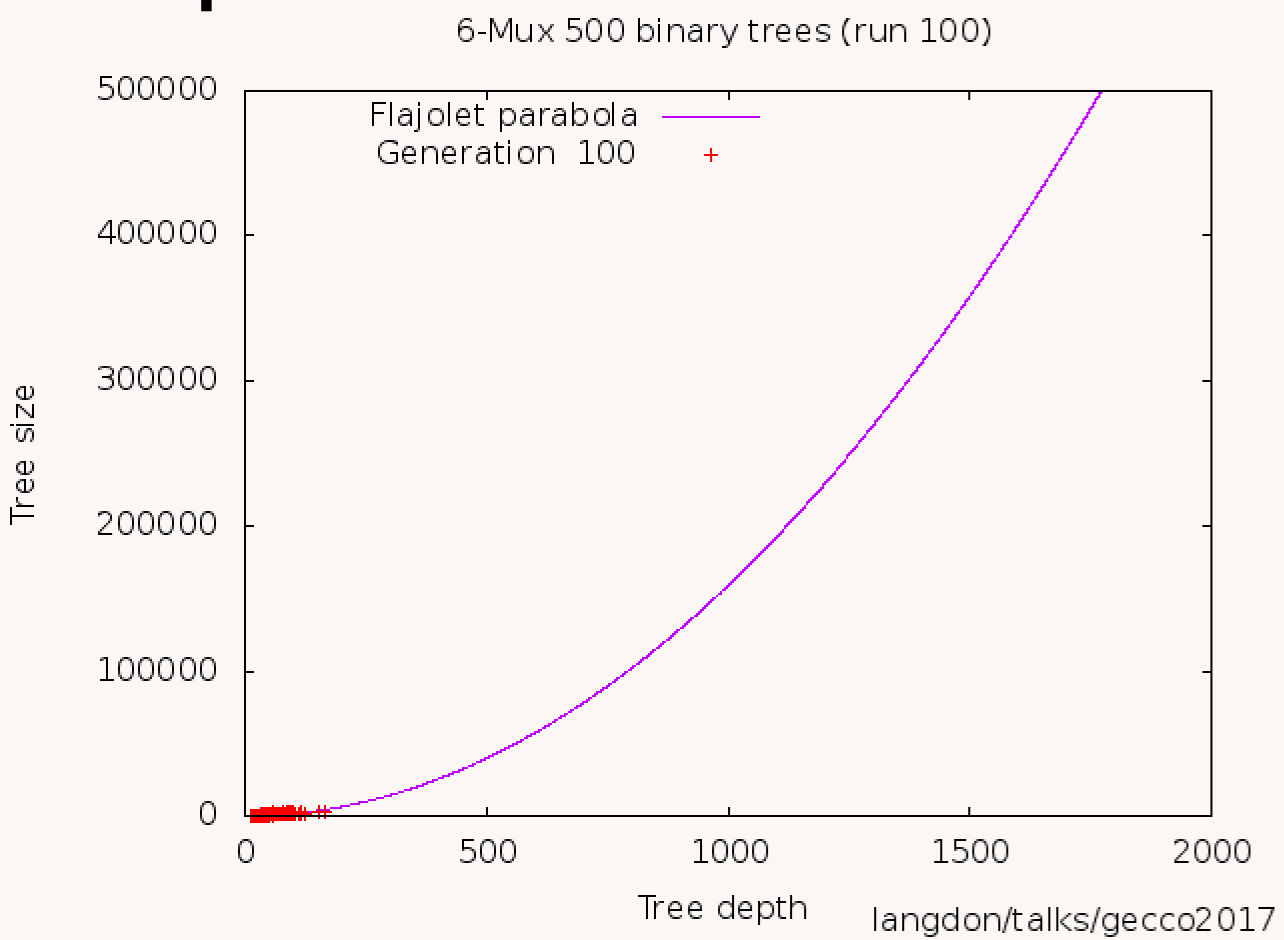


Video

Effective code only. Yellow highly converged.
Black unique code

Circular lattice code gp2lattice.awk

Shapes of Evolved Trees



Video

Both whole trees + and subtrees lie near Flajolet $\text{Depth} \approx 2\left(\frac{\pi\, size}{2}\right)^{1/2}$ limit[1] for random trees

Bloat limited by Gambler's ruin

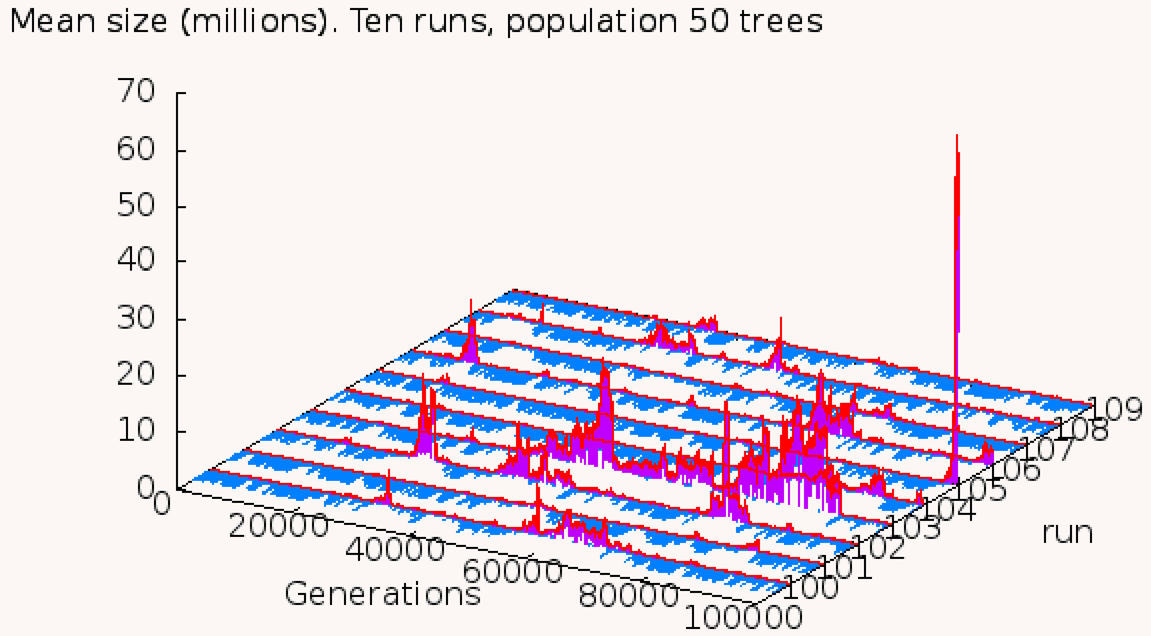
- Tiny fraction of disrupted (low fitness) children sufficient to drive evolution towards ever bigger trees.
- As trees get bigger chance of hitting protected effective code near root node falls.
- In a finite population eventually no child will be disrupted.
- Size, without fitness, wanders at random.
- But wondering towards lower limit will re-establish the conditions for bloat.

  cf. Gambler's ruin.
- Very approximate limit on tree size:

  tree size ≈ number of trees × core code size

CREST

Bloat limited by Gambler's ruin

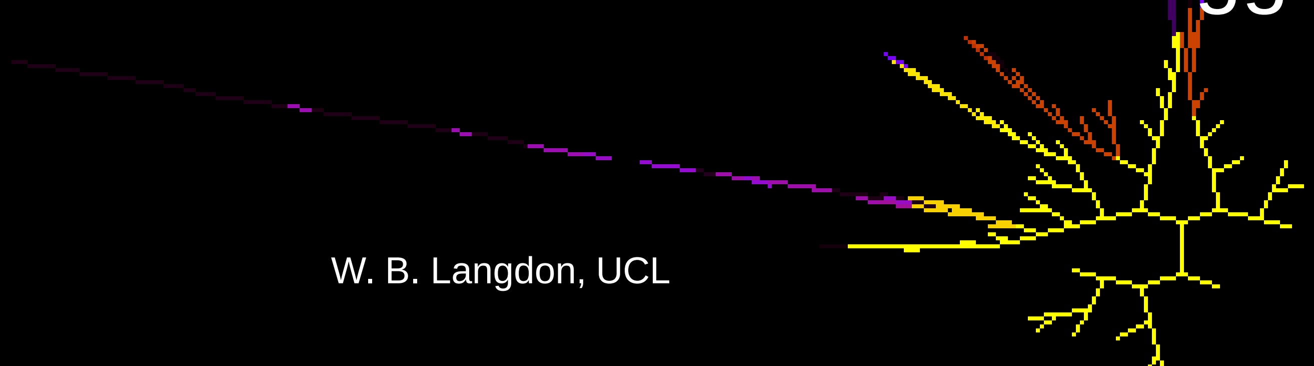


- tree size ≈ number of trees × core code size
- tree size ≈ 50 × 497 ≈ 25 000
- Across ten runs and 100,000 generation, median mean size 42 507 (smallest tree in pop size=10 513)

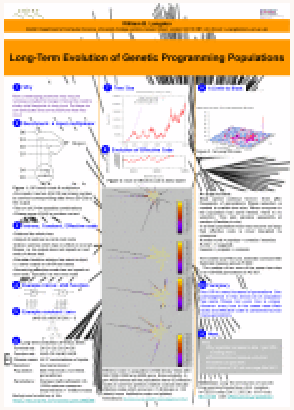
In all ten runs the whole population repeatedly collapses towards smaller trees

Conclusions

- Studied long term evolution (>>any other GP)
- 100s gens where everyone has same fitness
- No selection to drive size increase
- Gambler's ruin with size falling as well as rising
- Evolved effective code surrounded by ring of sacrificial constants and introns
- Trees and subtrees resemble random trees
- Landscape looks smooth but fitness is rugged



Poster Monday 17:50-20:00
GECCO companion p235-236



Technical report RN/17/05
https://arxiv.org/abs/1703.08481

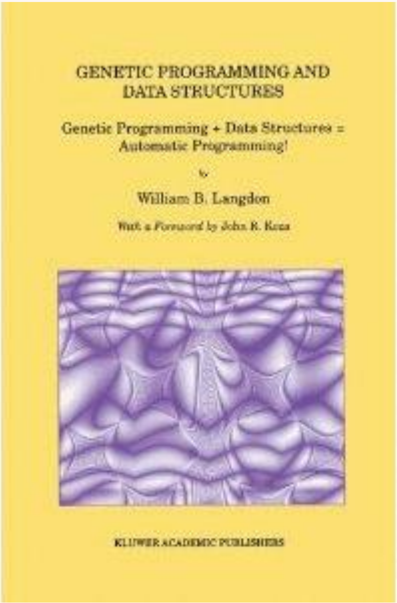
END

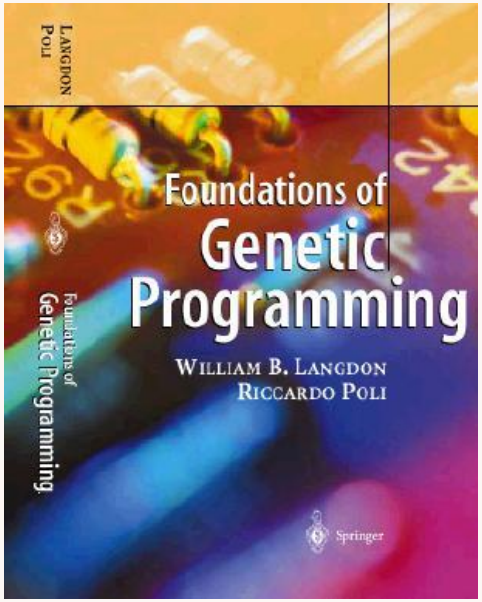
http://www.cs.ucl.ac.uk/staff/W.Langdon/ http://www.epsrc.ac.uk/

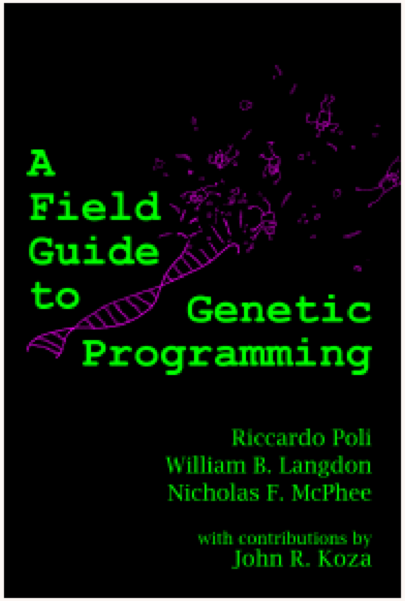
Genetic Programming

W. B. Langdon

CREST
Department of Computer Science



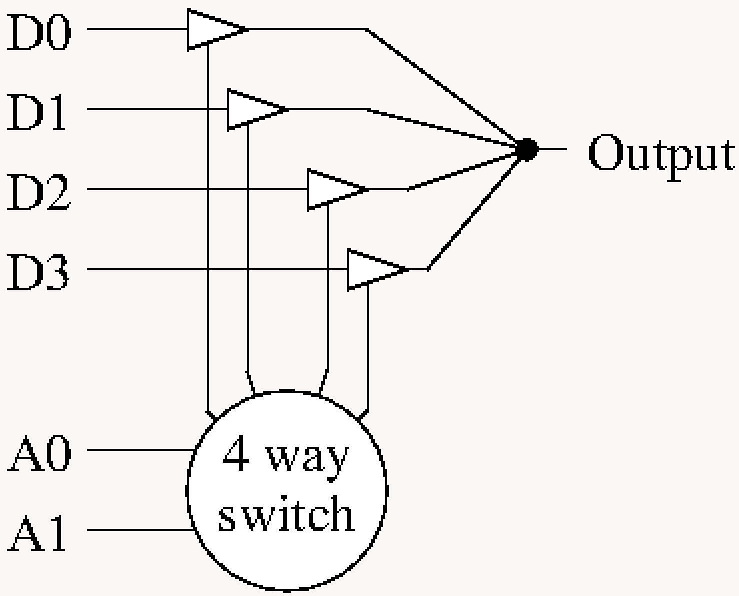




GPquick

- GPquick C++, written by Andy Singleton
  ≈ two bytes per tree node
- Submachine code GP
  – Boolean (bit) problems.
  – AND, NAND, OR, NOR operate simultaneously in parallel on bits in word (e.g. 32 or 64 bits)
  – 64 bit computer can do 64 test cases in parallel

6 Multiplexor



- GP bench mark.
- Six inputs:
  - Use two (D4 D5) as binary number to connect corresponding data lines (D0-D3) to the output
- Test on all 2^6=64 possible combinations
- Fitness score (0-64) is number correct

Genetic Programming to solve 6-Mux

- Terminals (tree leafs)
  - D0,D1,D2,D3 D4,D5
- Function set: 2 input gates→ binary trees
  - AND, NAND, OR, NOR. No side effects
- Generational population of 500 trees
- Tournament selection: choose best of 7
- 100% subtree crossover
- Initially hard limit on tree size (10^6)

Impact of Subtrees

- Subtree like whole tree.
- Output of subtree is via its root node
- **Intron**: subtree which has no effect on overall fitness. I.e. its output does not impact on root node of whole tree.
- **Constant** subtree always has same output, i.e. same output on all 64 test cases.
- Remaining **effective code** has an impact on root node. Typically it is next root node

Example Intron: AND Function

A	B	Out
0	0	0
0	1	0
1	0	0
1	1	1

A	B	Out
0	0	0
~~0~~	~~1~~	~~0~~
1	0	0
~~1~~	~~1~~	~~1~~

Left: two input AND node.

Right: same but input B is always 0.

So output always 0. Input A has no effect.

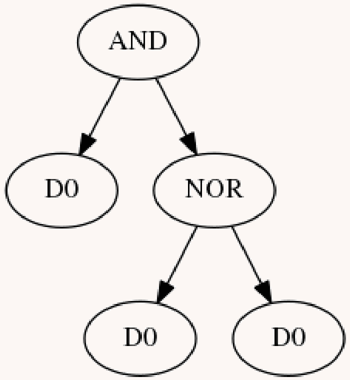
Subtree A is always ignored, even in child.

(NB no side effects)

Constants

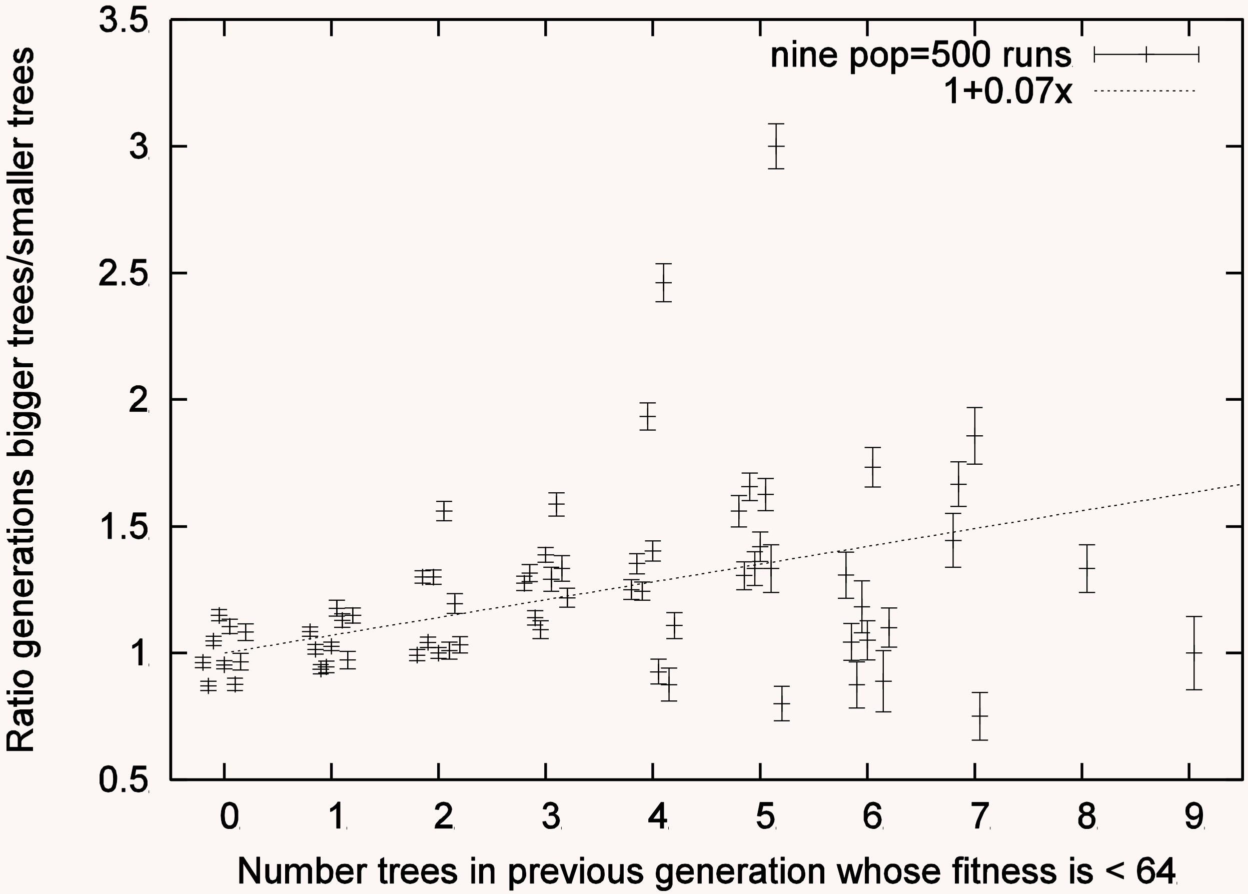
- Two constants: always 0 and always 1 (FFFFFFFFFFFFFFFF).
- E.g. evolve by negating input and ANDing with same input

  (AND D0 (NOR D0 D0)) = 0



- Constants help form introns but may be disrupted by crossover.
- However large subtrees which always output either 0 or 1 tend to be resilient to crossover

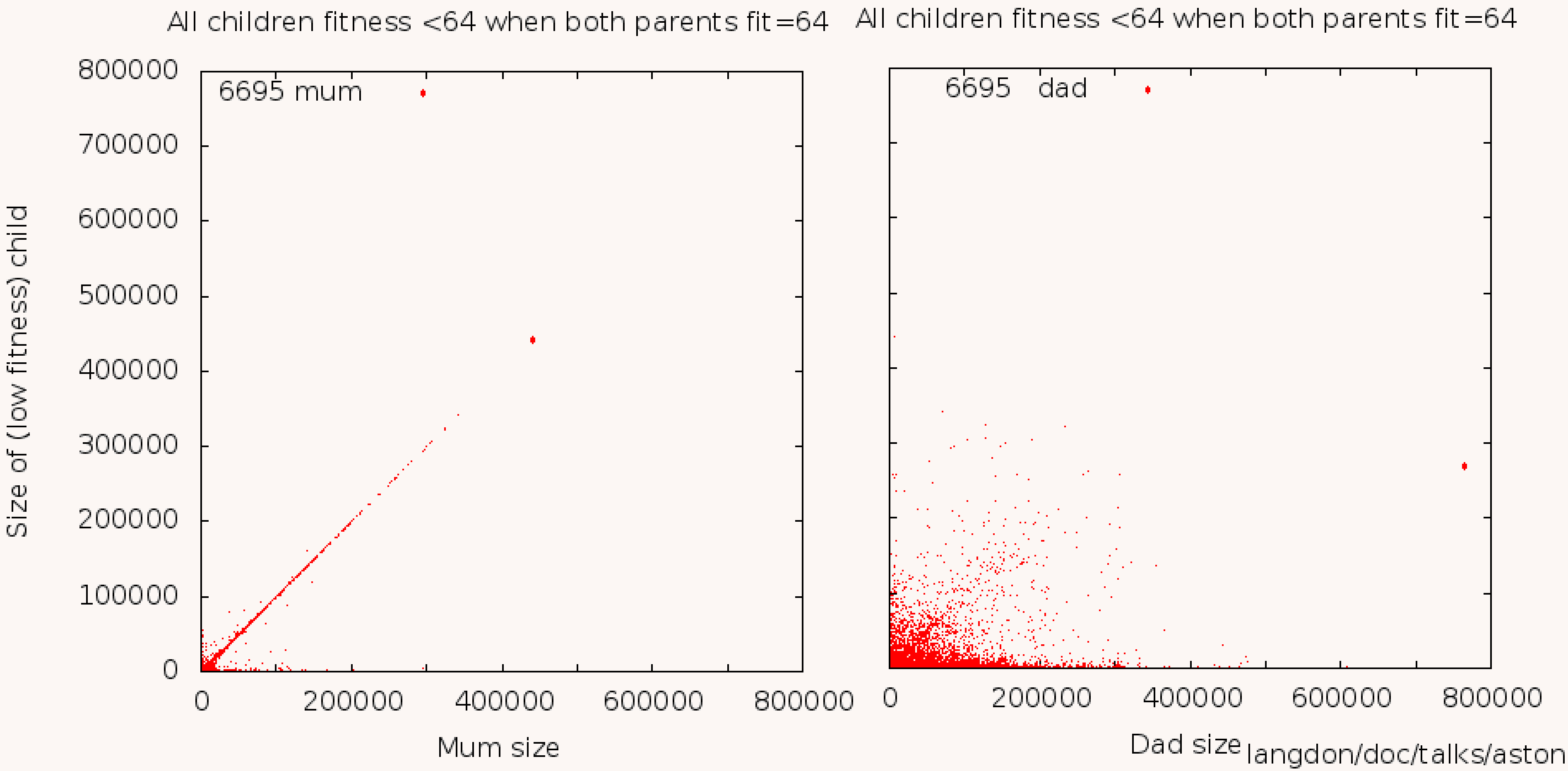
Runts Drive Evolution



Don’t plot ratio if less than 5 data

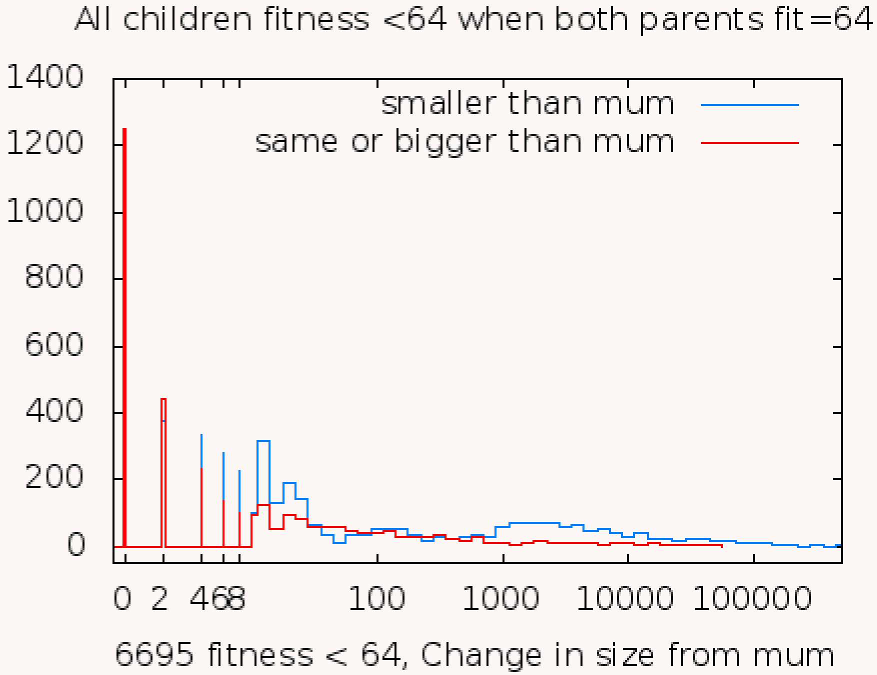
CREST

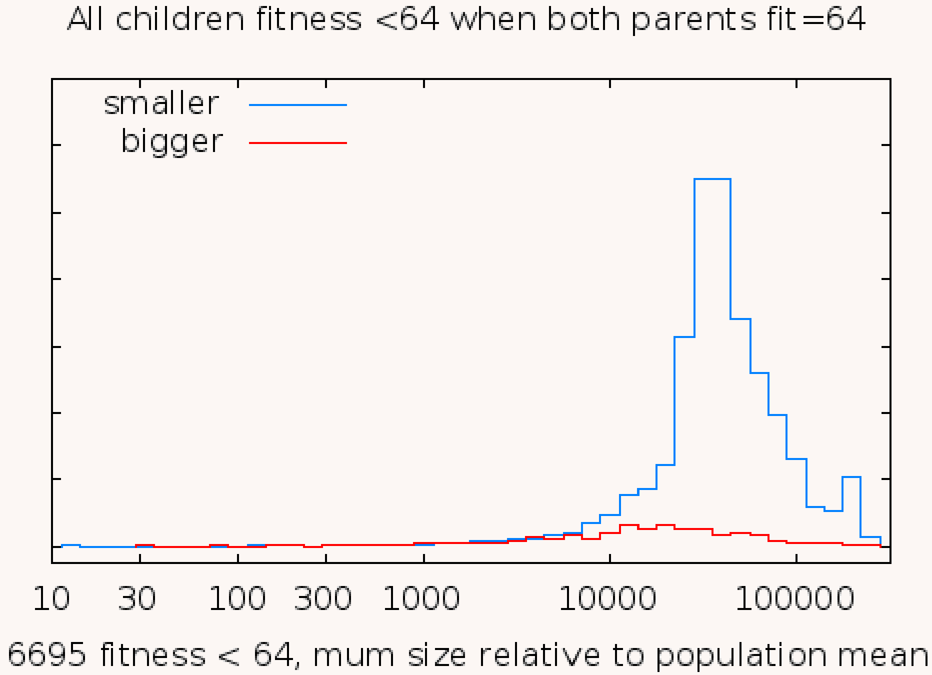
Importance of Mothers



Size of poor fitness children closely related to parent who they inherit root from (mum).

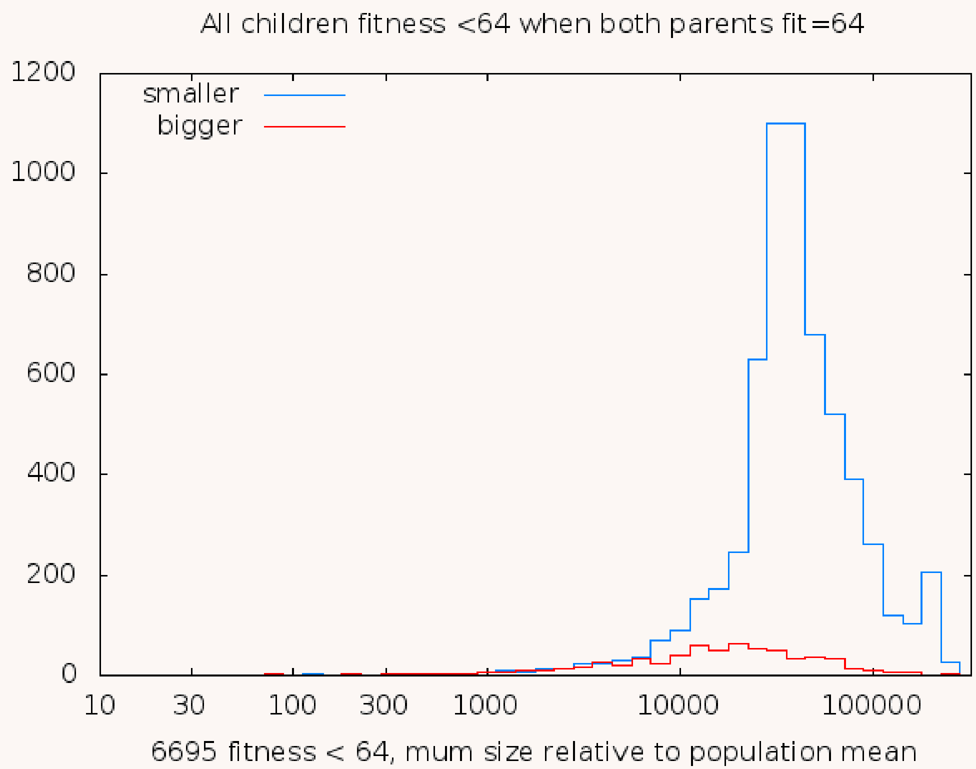
Importance of Mothers





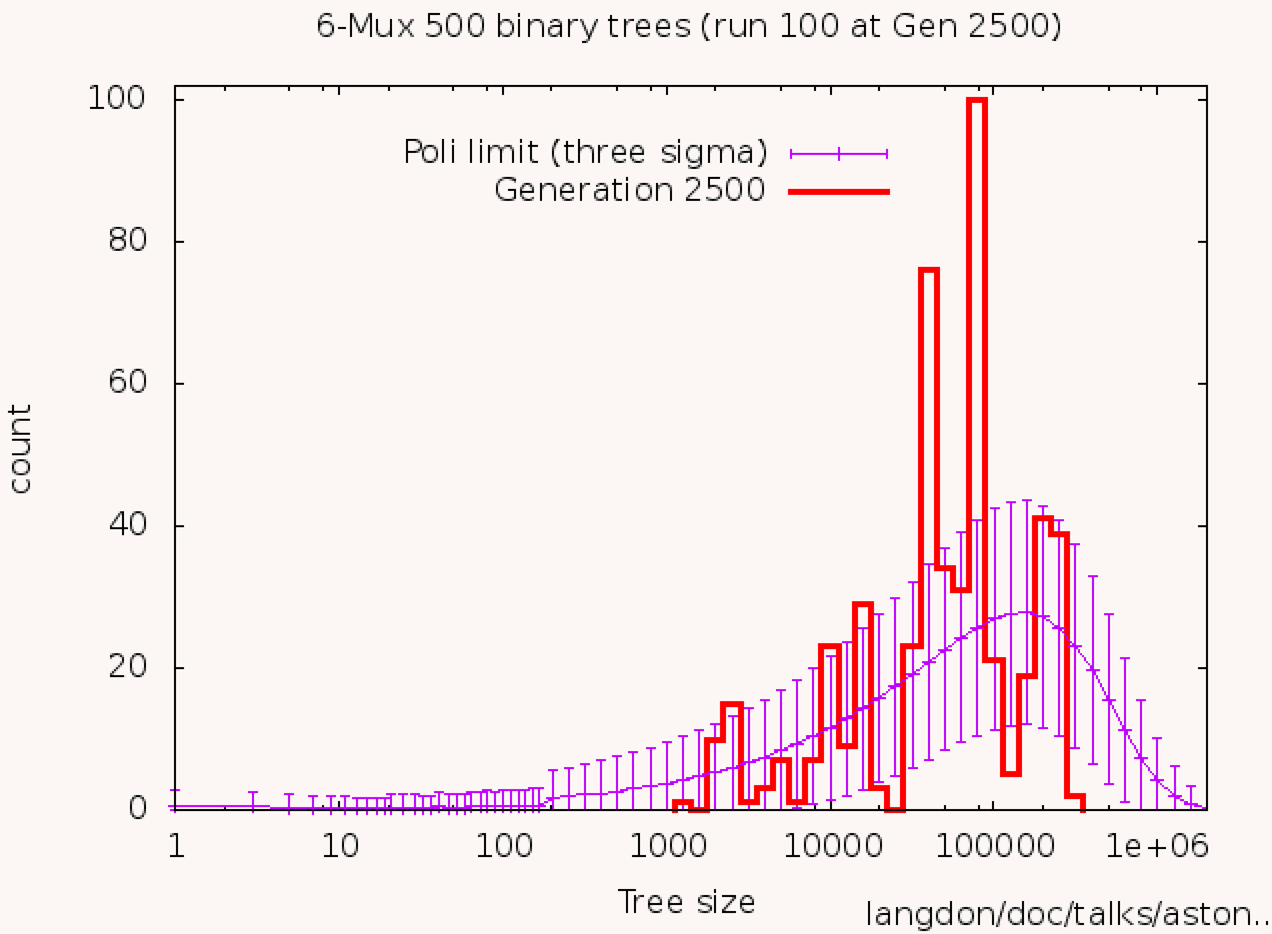
- Although many runts are smaller than their mum,
- many mothers of runs are smaller than average.
- Selection removes all low fitness children,
- Since these are smaller than average, the average size increases

A few runts drive size increase



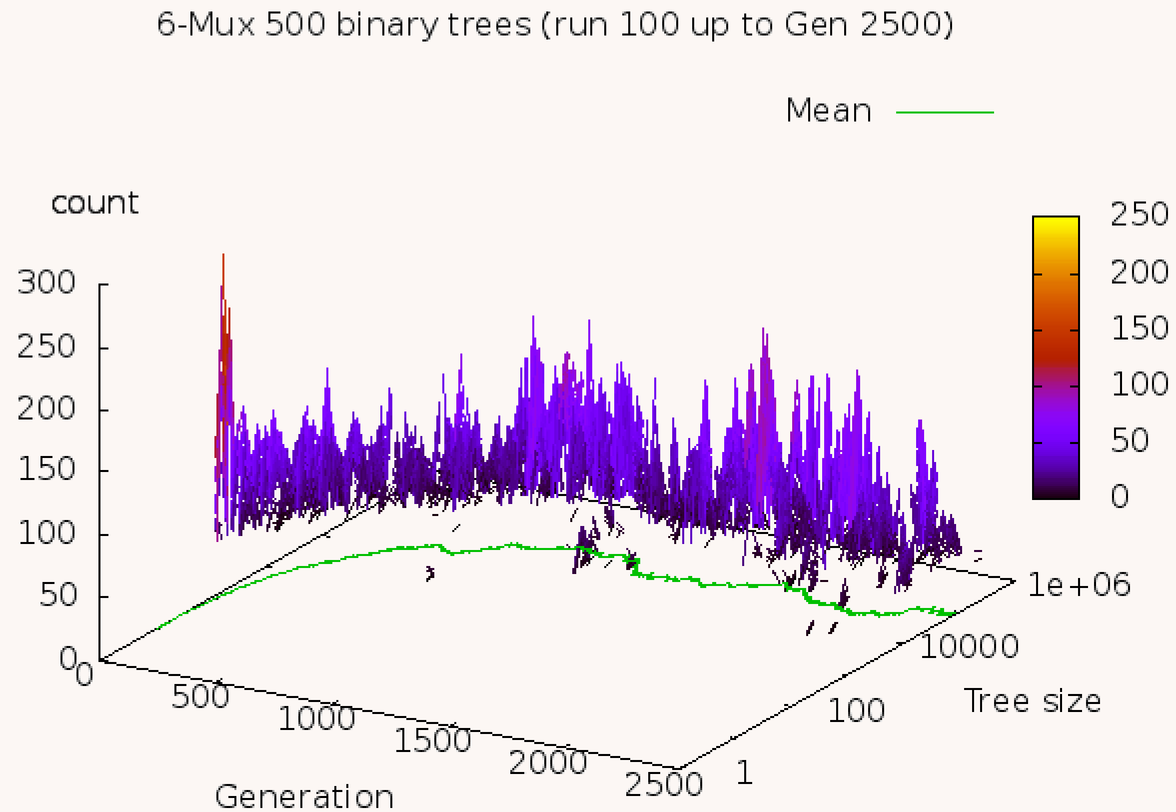
- Many mothers of runts are smaller than average (blue)
- Selection removes all low fitness children (runts)
- Since these are smaller than average
- Although there is noise, on average size increases

Testing Theory



- Theory assumes crossover only (no selection). In earlier work distribution of sizes converged to limit rapidly.
- Selection caused by a few runts modifies size distribution

Testing Theory



- Same as testing theory plot but do every generation
- Colour only part of histogram ≥ 3σ
- Small tree and large tree tails ok (not coloured)

The Genetic Programming Bibliography

http://www.cs.bham.ac.uk/~wbl/biblio/

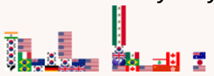
11628 references, 10000 authors

Make sure it has all of your papers!

E.g. email W.Langdon@cs.ucl.ac.uk or use | Add to It | web link

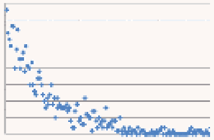

Co-authorships

RSS Support available through the Collection of CS Bibliographies.

Downloads by day


Co-authorship community.
Downloads

A personalised list of every author's GP publications.


Your papers

blog

Search the GP Bibliography at
http://liinwww.ira.uka.de/bibliography/Ai/genetic.programming.html