

# Analysis of Ancestry in Genetic Programming with a Graph Database

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# The Big Picture

- Genetic programming (GP) demonstrably works.
- Difficult to determine how this process works.
- Databases allow examination of the internal interactions of a run.
- Graph databases more efficient for this task than relational DBs.
- Analysis may allow us to improve GP tools.

# Outline

- 1 Genetic Programming
- 2 Graph Database
- 3 Results
- 4 Conclusions

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  - Transformations and genealogical history
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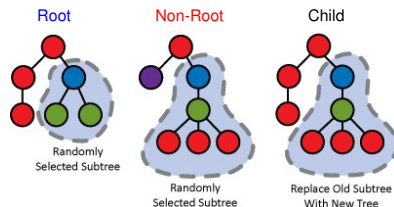
# Transformations and genealogical history

**Crossover** sexual reproduction  
(**root** and **non-root**)

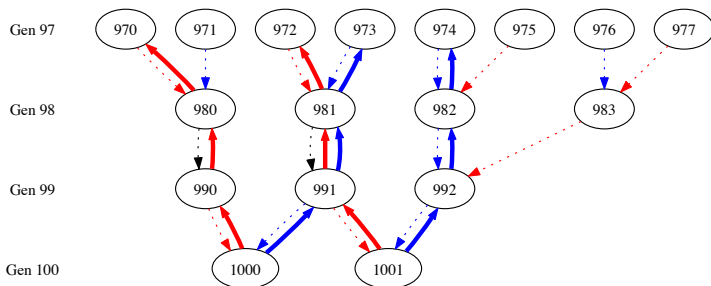
**Mutation** subtrees altered

**Reproduction** asexual reproduction

**Elitism** reproduction based on fitness



geneticprogramming.us



# Outline

## 1 Genetic Programming

## 2 Graph Database

- Neo4j
- Cypher
- DB setup
- Cypher examples

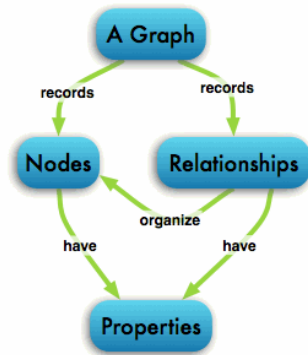
## 3 Results

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# Neo4j

Neo4j is a graph database.

- Relatively new tool
  - Initial release 2007
  - V1.0 in 2010, V2.0 last December
- Information is stored using a graph consisting of nodes and relationships
- Efficient recursive queries compared with traditional databases



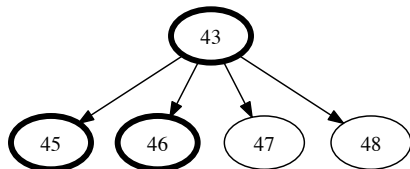
Neo4j <http://goo.gl/nzRWSV>

# Cypher

Neo4j's query language is Cypher.

Fundamental elements of  
Cypher queries:

- START
- MATCH
- WHERE
- RETURN



```
START parent=node(43)  
MATCH (parent)-[:PARENTOF]->(child)  
WHERE id(child) < 47  
RETURN parent, child;
```

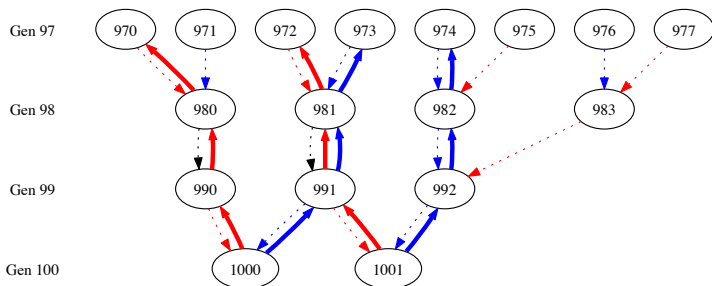


# DB setup

We store:

- Individuals as nodes + data, e.g., program, fitness, generation
- XO, mutation, replication events as edges between nodes

Different edge types indicate relationship types, e.g., *ROOT\_PARENT* edge from 991 to 1000 says 991 is the root-parent of 1000.



# Finding the “winning” fitness and individual

Finding the minimal fitness across all individuals (nodes) in the DB:

```
start n=node(*)
return min(n.penalizedFitness);
```

Finding one (arbitrary) “winning” individual:

```
start n=node(*)
return n
order by n.penalizedFitness
limit 1;
```

These are not unlike queries in relational databases.

# Ancestry of an individual (hard for relational DBs)

Find all the root ancestors of individual 99,000:

```
start n=node(99000)
match ps =
  (n) <- [r:ELITISM|PARENTOF|ROOT_XOOF|MUTANTOF*] - (p)
return distinct ps;
```

Find the fitness of all the root ancestors of individual 99,000:

```
start n=node(99000)
match ps =
  (n) <- [:ELITISM|PARENTOF|ROOT_XOOF|MUTANTOF*] - (p)
where p.generation=1
return extract(x in nodes(ps) | x.fitness);
```

# Outline

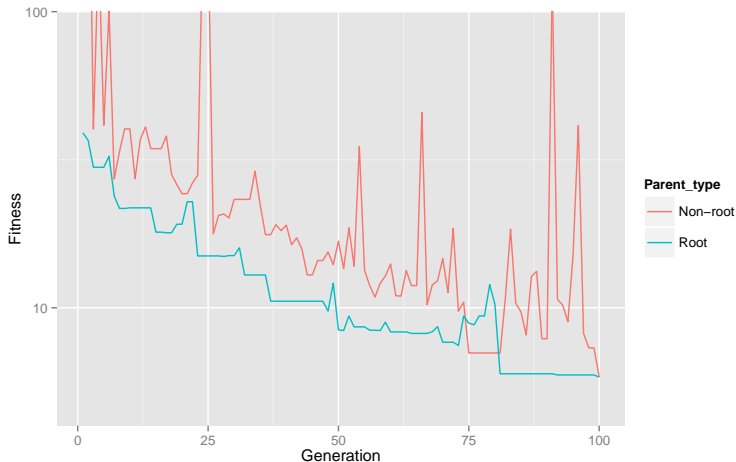
- 1 Genetic Programming
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- 3 Results**
  - A few questions
  - Fitness Over Time
  - Improved Transformations
  - Common Ancestor(s)
- 4 Conclusions

# A few questions

- 1 What does the fitness of the “winning” individual’s ancestry line look like over time?
- 2 How often does mutation improve fitness? Also, how often does crossover improve fitness, where the root parent is more fit than the non-root parent, and vice versa?
- 3 Does a group of individuals have a common root parent ancestor and what is the latest generation where such an ancestor occurs?
- 4 How many individuals in the initial generation have any root parent descendants in the final generation?

# Fitness Over Time

*What does the fitness of the “winning” individual’s ancestry line look like over time?*



# Percentage of Improved Transformations

*How often do mutation and crossover improve fitness?*

Results for one 10,000 individual run and three 1,000 individual runs

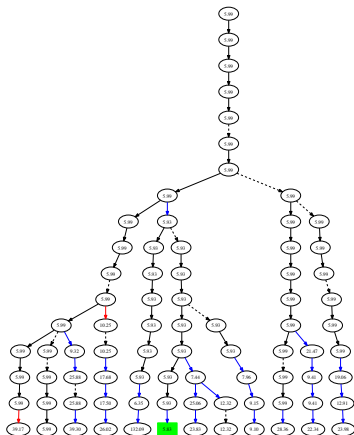


# Common Ancestor

*How far back to a common root parent ancestor? How many initial generation individuals have descendants in the final generation?*

In run w/ 10K individuals for 100 gens:

- Final pop consists of 2 clades
- One clade *strongly* dominates (only 24 left in small clade)
- Each clade root-descends from single individual in initial population





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# Conclusions

## Conclusions

- We can collect & extract useful data about evolutionary dynamics
- More detailed analysis that moves beyond statistical summaries
- Suggests interesting avenues to explore
  - Importance of having root parent be more fit
  - Changing role of mutation over the life of a run
  - Potential for clades/quasi-species and their impact

## Future Work

- Enforcing the root parent to have better fitness in XO
- Exploring equivalents in other EC systems (e.g., Push)

# Thanks!

Thank you for your time and attention!

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- Twitter **@NicMcPhee**
- Paper: `https://github.com/NicMcPhee/MICS-2014-GraphDB-EC`

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## Questions?

# References



LUKE, S.

*Essentials of Metaheuristics*, second ed.

Lulu, 2013.

Available for free at <http://cs.gmu.edu/~sean/book/metaheuristics/>.



MCPHEE, N. F., AND HOPPER, N. J.

Analysis of genetic diversity through population history.

In *Proceedings of the Genetic and Evolutionary Computation Conference* (1999), vol. 2, Citeseer, pp. 1112–1120.



POLI, R., LANGDON, W. B., AND MCPHEE, N. F.

*A Field Guide to Genetic Programming*.

Published via <http://lulu.com> and freely available at <http://www.gp-field-guide.org.uk>, 2008.

(With contributions by J. R. Koza).



ROBINSON, I., WEBBER, J., AND EIFREM, E.

*Graph Databases*.

O'Reilly Media, Inc., 2013.

# Run Configurations

Target Function  $\sin(x)$

Variables  $x$  (range 0.0 to 6.2, incremented by steps of 0.1)

Constants range between -5.0 and 5.0

Operations addition (+), subtraction (-), multiplication (\*),  
protected division (/)

Generation Number 100

Population Size Per Gen 1,000 (3 runs) and 10,000 (1 run)

Transform Percentages crossover (90%), mutation (1%), reproduction (9%)

Elitism best 1%

Fitness absolute error between target function and  
individual function