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 and future work

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1 Genetic Programming

2 Graph Database

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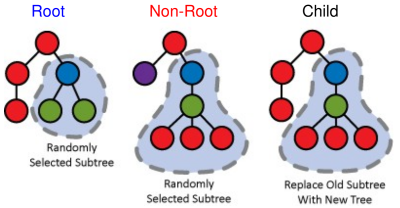
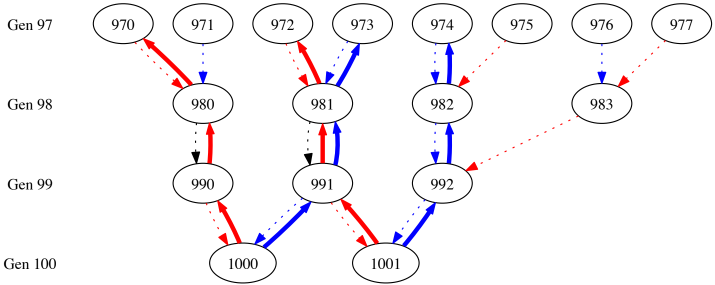
Transformations and genealogical history

Crossover	sexual reproduction (root and non-root)
Mutation	subtrees altered
Reproduction	asexual reproduction
Elitism	reproduction based on fitness



geneticprogramming.us



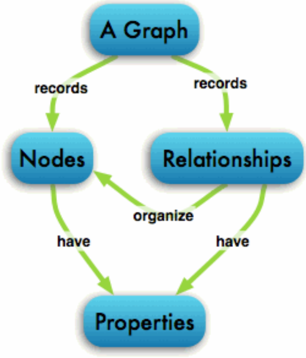
Outline

1. Genetic Programming
2. Graph Database
   - Neo4j
   - Cypher
   - DB setup
   - Cypher examples
3. Results
4. Conclusions and future work

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



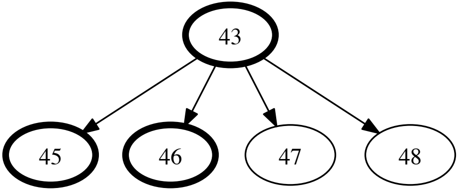
Neo4j `http://goo.gl/nzRWSV`

Cypher

Neo4j's query language is Cypher.

Fundamental elements of Cypher queries:

- START
- MATCH
- WHERE
- RETURN



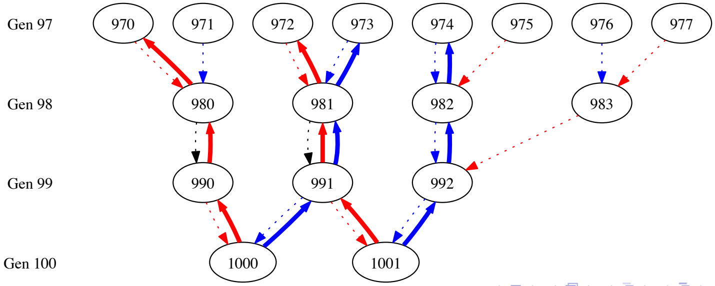

```
START parent=node(43)
MATCH (parent)-[:PARENTOF]->(child)
WHERE id(child) < 47
RETURN parent, child;
```

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.fitness);
```

Finding one (arbitrary) “winning” individual:

```
start n=node(*)
return n
order by n.fitness
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|REPRO|MUTANT|ROOT_PARENT*]-(p)
return distinct ps;
```

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

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

Outline

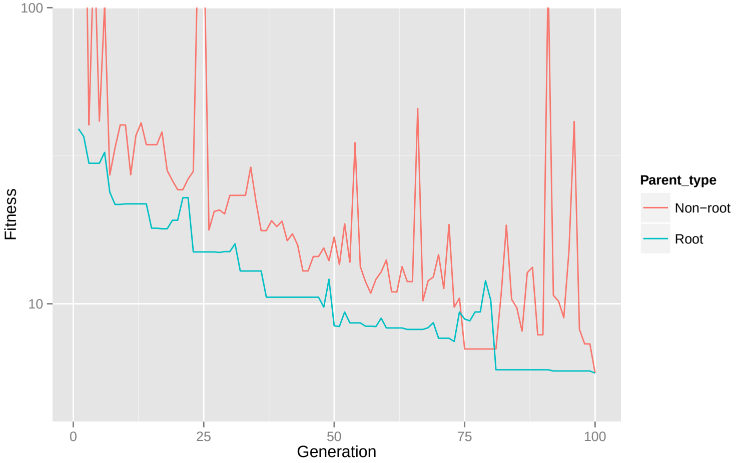
1. Genetic Programming
2. Graph Database
3. Results
   - A few questions
   - Fitness over time
   - Improved transformations
   - Common ancestor(s)
4. Conclusions and future work

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, both when 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

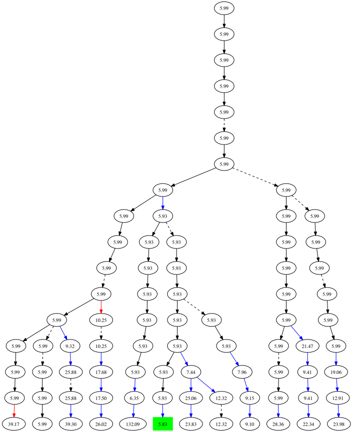
How often do mutation and crossover improve fitness?

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

- 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

Concerns about scaling

- Can we do lots of runs in parallel pouring data into a central DB?
- Can runs be distributed across the network and still perform well?
- How much memory is needed to work with large datasets?

Future work

Requiring the root parent to have better fitness in XO

- Explore its impact across a variety of problems
- Explore equivalents in other EC systems
  - What's the "equivalent" (if any) in Push?
  - Ensure parent that contributes the tail is more fit?

Dynamically set parameters

- This has been done a lot, but usually in an ad hoc way.
- Can we use data collected from runs to do this in a more principled way?

Thanks!

Thank you for your time and attention!

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- 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