Using Graph Databases to Explore Genetic Programming Run Dynamics

Nicholas Freitag McPhee, David Donatucci, and Thomas Helmuth and others(?)

Abstract Each chapter should be preceded by an abstract (10–15 lines long) that summarizes the content. The abstract will appear *online* at www.SpringerLink.com and be available with unrestricted access. This allows unregistered users to read the abstract as a teaser for the complete chapter. As a general rule the abstracts will not appear in the printed version of your book unless it is the style of your particular book or that of the series to which your book belongs.

Key words: keywords to your chapter, these words should also be indexed

1 Note to early reviewers

This is definitely still very much a work in progress, and we apologize for its incompleteness. We're still working through small bits of the many, many gigabytes of data that we have access to, looking for good stories to tell. Hopefully, however, this will give a sense of our goals, plan, and some of our early results. We'd certainly love feedback on which of these stories you feel are the most interesting, informative, and ultimately helpful for the community, as well as any suggestions you have regarding the telling of the stories.

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2 Introduction

It would be nice to scrape, say, the GECCO 2014 proceedings and get some numbers to back this up.

It is common practice in most empirical evolutionary computation (EC) research to perform numerous (possibly hundreds) of runs, and then simply report a handful of aggregate statistics at the end that are expected to summarize and represent the (hopefully) complex interactions and dynamics of those many runs. Tables present values such as mean or median best fitnesses at the end of runs, collapsing the complexities of dozens or hundreds of runs into a single number, possibly with a standard deviation or (even better) a confidence interval to give a sense of the distribution. Often more informative are plots, which can, for example, show how these numbers change over time during the runs, possibly giving a sense of the system dynamics. These plots, however, often aggregate runs in a way that obscure important moments that, if explored, might reveal valuable insight into the evolutionary dynamics being reported.

Perhaps include a sample plot and show how it hides things? One of Tom's diversity or cluster plots? A synthetic plot? Maybe that's just not necessary?

While this sort of aggregate reporting is often valuable, allowing for important comparative analysis of, for example, the impact of different genetic operators, it typically fails to provide any sense of the *why*. Yes, Treatment A led to better aggregate performance than Treatment B – but what happened in the runs that led to that result? Any success at the end of a run is ultimately the intricate combination of hundreds or thousands of selections, recombinations and mutations, and if Treatment A is in some sense "better" than Treatment B, it must ultimately be because it affected all those genealogical and genetic events in some significant way, biasing them towards events that made success more likely.

Unfortunately, published research very rarely includes information that might shed light on these *why* events. We rarely see evolved programs, for example, or any kind of post-run analysis of those programs, and there is almost never any data or discussion of the genealogical history that might help us understand how a successful program actually came to be.

Sometimes this isn't included for reasons of space and time; evolved programs, for example, are often extremely large and complex, and a meaningful presentation and discussion of such a program could easily take up more space than authors have available given the typical space limitations in published work. Our suspicion, however, is that this sort of *why* analysis often isn't reported because it isn't even *done*, in no small part because it's hard. As EC researchers we're in the "happy" position of being able to collect anything and everything that happens in a run, but that leaves us with two problems: How to *store* the data, and how to *analyze* the data after it's stored. Decreasing data storage costs have done much to mitigate the first problem. If, however, one collects a very rich data set it's still easy to quickly generate terabytes of data, and even if one has a place to put the data, one still needs reasonable tools to analyze the data.

Databases provide a natural tool for storing and accessing the data, but traditional relational databases are poorly suited for a variety of queries that are important for the genealogical analysis we need for exploring the evolutionary dynamics of our EC runs. If, for example, we have a `ParentChild` table, it's easy enough to find Alice's parents, but finding Alice's grandparents, siblings, or cousins requires multi-

ple joins. Moving further out in Alice's tree of relatives requires complex and computationally expensive recursive joins, making this approach increasingly infeasible. In exploring the dynamics of an EC run, for example, we're going to want to be able to make connections across dozens or even hundreds of generations, which simply isn't feasible with a relational database. (See, for example, Robinson et al (2013) for more on these feasability/efficiency issues.)

In this chapter we illustrate the use of graph databases as an alternative storage and analysis tool for evolutionary computation runs. In Donatucci et al (2014) we have demonstrated that graph databases can be an effective tool for analyzing complex genetic programming (GP) dynamics, which led directly to a proposed change to standard sub-tree crossover in tree-based GP, McPhee et al (2015). Here we will use the open source Neo4J graph database tool[1] to explore data from a collection of PushGP runs on several problems drawn from a benchmark collection of introductory programming problems taken from Helmuth and Spector (2015).

3 A little background on problems and tools

3.1 PushGP and lexicase selection

Say a little about

- Plush genomes
- Push programs
- Alternation
- The two kinds of mutation

Say enough about lexicase so people have some sense of why it might be interesting and different from, e.g., tournament selection.

3.2 Replace-space-with-newline

Say enough about this problem so that people can understand the error vectors.

4 Lexicase, meet Replace-space-with-newline

We did one hundred runs of the replace-space-with-newline problem using lexicase selection, and found that 55 of these succeeded in the sense that an individual was discovered that had zero error on all 200 of the training cases. Tournament selection

[1] http://neo4j.com/

Query 1 Cypher query to find all the ancestors of "winners" in the last 9 generations of a run. The pattern `(w {total_error: 0})` matches nodes with total error 0, i.e., "winners". The pattern `(c)-[*0..7]->(w)` matches any path from some node `c` to a winning node `w` that has between 0 and 7 edges.

```
MATCH (p)-->(c)-[*0..7]->(w {total_error: 0})
RETURN DISTINCT id(p), id(c);
```

with tournament size 7 only had 13 successes out of 100 runs, and IFS only had 17 successes out of 100 runs, so it seems that lexicase selection provides a significant advantage here.

4.1 Hey, we won! But why*?*

It's interesting the lexicase did so well, but that leaves us with the crucial question of *why*? So we chose one successful run to explore in more detail. It's important to note here that we're making no claims that this is a "representative" run (whatever that would even mean); it's an *interesting* run, though, and our hope is that by understanding its dynamics better we can learn useful things about both the problem and the tools we're applying.

An obvious place to start is at the end when the GP system solved the problem. So we used Neo4J to find all the ancestors of any "winning" individual, i.e., individual with a total error of on all 200 test cases. Using Cypher (Neo4J's query language), we can easily ask for this subset of the population going back to generation 79 using the query in Query 1.[2]

Should all the query details go in an appendix that eventually becomes a tech report or some such? I'm not sure if they aren't just a distraction here.

We need the crazy `p->c->w` thing in Query 2 to extract single edges, but I don't know if we want to talk about that.

Figure 1 shows the ancestry of all of the winners from generation 87 (when we first found a winner in this run) back to generation 79. Each node in the graph represents an individual, and each directed edge indicates a parent-child relationship, with the edge going from the parent to the child. The numbers inside the nodes are Neo4J internal IDs; we'll use these as "names" for the individuals as we tell the stories we uncover. [3] As a happy accident coming from having a population size of 1,000, the first two digits of the Neo4J idea also happens to indicate what generation that individual was from.

Ignoring for the moment the adornments (shape, shading, etc.), there are several things that we can observe right away:

[2] We could certainly have gone back farther in time, but the graph would have become impossible to read as the number of nodes would have ballooned from a few dozen to hundreds or thousands. We went back to generation 79 because that was the most recent generation that had more than 10 distinct ancestors of a winning individual.

[3] We actually assign each individual a UUID so we can combine multiple runs, but the Neo4J IDs are shorter and easier to use in our story telling.

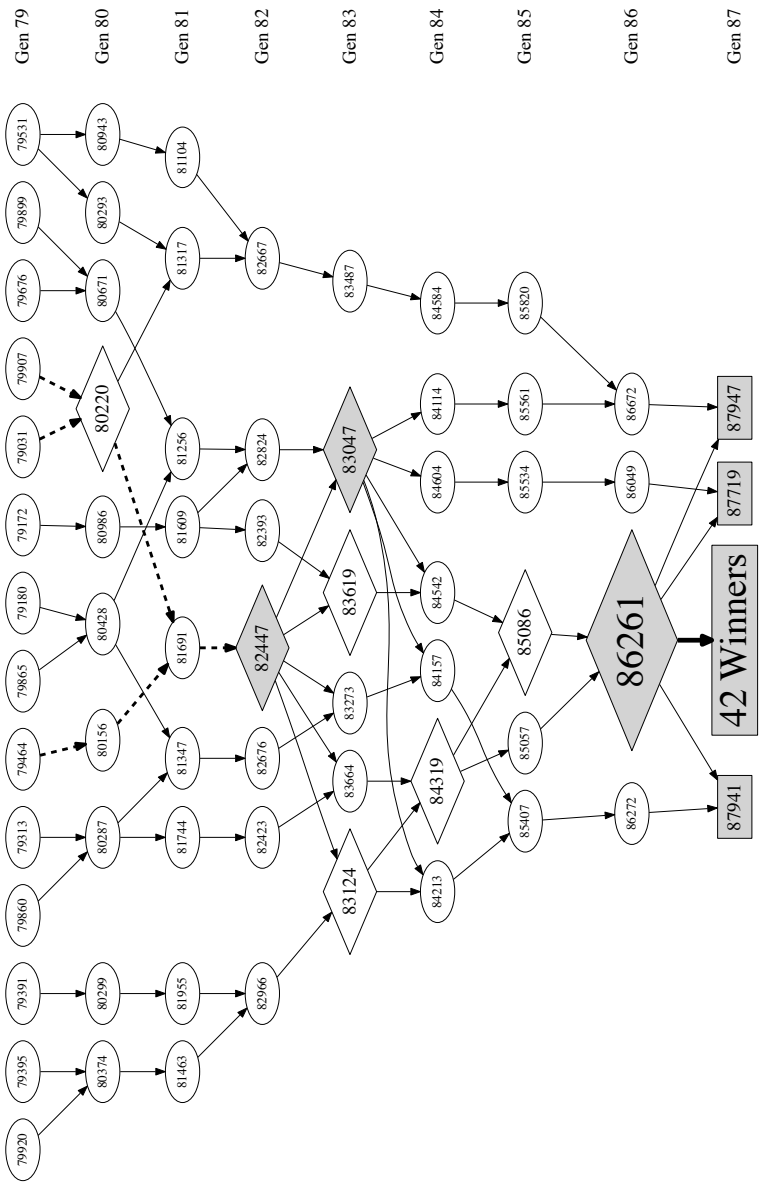

Fig. 1 Ancestry of the 45 "winners" from run 6 of lexicase, replace-space-with-newline. Nodes with diamonds instead of ellipses had an unusually large number of offspring. Shaded nodes had an unusual number of offspring that were ancestors of winners. The dashed lines highlight individuals that had an unusually large number of distinct ancestry paths down to a winner. See the text for more details

- There are 45 distinct winners in the final generation, or 4.5% of the population of 1,000 individual. This tells us that constructing a winner from the individuals in generation 86 wasn't entirely trivial, but it also wasn't a huge challenge and happened multiple times.
- Those 45 winners only had four distinct ancestors in the preceding generation.
- All 45 winners had a single individual (86261, marked with a large shaded diamond near the center bottom) as at least one of their parents, and 42 of them had 86261 as their *only* parent, i.e., they were mutations of 86261, or were the result of self-crosses of 86261. To simplify the graph, we've combined those 42 individuals into a single node labelled "42 Winners".
- The number of ancestors of winners doesn't grow quickly as we move back in time. We have to go back to generation 80 to find 10 individuals (or 1% of the population) that are ancestors of winners, and in generation 79 there are still only 14 ancestors of winners. In fact we have to go back all the way to generation 63 to find a time where over 100 individuals (or over 10% of the population) were ancestors of a winning individual.

Looking at Figure 1 we can also see that a few individuals have more offspring represented than others. As we've already mentioned, individual 86261 has 45 successful offspring, and both individuals 82447 and 83047 have five offspring in the graph, i.e., five offspring that were ancestors of a winning individual in generation 87. Each of these is marked in Figure 1 with a shaded diamond.

Figure 1, however, only tells us home many offspring an individual had that were themselves either a winner or an ancestor of a winner, as no other nodes are displayed. might, however, wonder how many total offspring an individual has regardless of whether they were a winner or not. Query 2 identifies the most fecund ancestors of winners in these last nine generations. That reveals several results that were quite surprising to at least some of the authors, the most remarkable being that individual 86261 was a parent of 934 of the 1,000 individiuals in generation 87! Given that lexicase selection was designed in significant part of spread selection events out across the population, this makes it clear that there are times when lexicase does the opposite, and instead puts nearly all its eggs in a single basket. This level of selection focus would simply be impossible using almost any other common type of selection such as tournament selection; in most uses of tournament selection, for example, no individual can be in more than a relative handful of tournaments, and thus can't be a parent terribly often no matter how fit they are.

While no other node in Figure 1 has nearly as many children as 86261 did, there are several that had very high reproduction rates, putting them well above what would be possible with something like tournament selection. Individual 82447, for example, had 443 offspring, including the 5 illustrated in Figure 1. In fact there were eight individuals in Figure 1 that have more than 100 offspring; each of these is indicated with a diamond shape instead of the standard ellipse. This highlights a particularly interesting ancestry chain from 82447 through 83124, 84319, 85086 to 86261, each of which had more than 100 offspring. Here the test case results for each of these individuals must be quite "special" in the sense that they are be able to solve an large set of test cases that other individuals simply aren't able to solve.

Query 2 Cypher query to find, for each ancestor `p` of a winner, how many distinct offspring `n` that ancestor `p`, regardless of whether `n` is itself an ancestor of a winner. The query then sorts by that count, and returns the 20 highest results.

```
MATCH (p)-->(c)-[*0..7]->(w {total_error: 0})
MATCH (p)-->(n)
RETURN DISTINCT id(p), count(DISTINCT n)
ORDER BY count(distinct n) DESC
LIMIT 20;
```

The dashed lines indicate individuals with lots of different paths to a winner, i.e., they are the ancestor of a winner in several different ways. we still need to write that up.

How did we get the 45 winners?

- 18 uniform-close-mutation alone
- 17 alternation followed by uniform-mutation
- 6 alternation alone
- 4 uniform-mutation alone

Notes

- Individual 81691 is on a critical path from 80220 to 82447, but didn't actually have a ton of children (17 total, only one of which was an ancestor of a winner).
- 82447 has 396 paths to a winner. 83047 only has 69, even though they both have 5 offspring that are ancestors of winners. Maybe that's not a big deal because 82447 is a generation "older" and gets more paths that way? I'm not sure, though – if there had just been the one path from 82447 to 83047, then their numbers would be the same (e.g., 81691 and 82447).
- There are six distinct paths from 82447 to 86261, more than any other node that isn't an ancestor of 82447.
- Individuals 83124, 83619, and 83047 collectively had 392 offspring of the 1,000 individuals in generation 84.

4.2 Surprising fecundity (especially given that total error)

Lexicase selection (**?**) was designed in significant part with the intent of increasing and maintaining diversity. The key assumption was that it would distribute the selection events across a variety of groups of individuals, as the population separates into sections focusing on different subsets of the test cases. As **?** shows, this is to a significant degree a "true" (or at least reasonable) story, with lexicase generally leading to more diversity than either tournament selection or implicit fitness sharing.

A flip side of that assumption was that individuals probably didn't have disproportionately large numbers of offspring, as the selections are being spread out across these different groups of individuals. In exploring one lexicase run on the Replace

Space With Newlines problem, however, we discovered that while in general this story held true, there were moments in the course of the run where the reality was *wildly* different.

5 Section Heading

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6 Section Heading

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Use the standard `equation` environment to typeset your equations, e.g.

$$a \times b = c\,, \tag{1}$$

however, for multiline equations we recommend to use the `eqnarray` environment.

$$\begin{aligned} a \times b &= c \\ \mathbf{a} \cdot \mathbf{b} &= \mathbf{c} \end{aligned} \tag{2}$$

6.1 Subsection Heading

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1. Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.
   a. Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.
   b. Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.
2. Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.

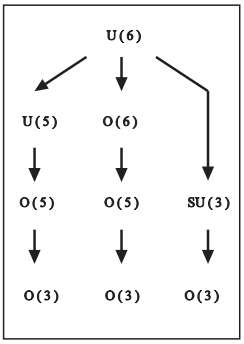
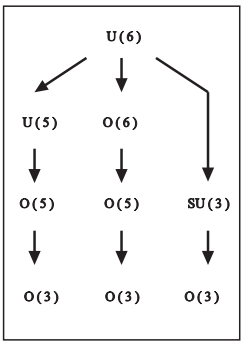


Fig. 2 If the width of the figure is less than 7.8 cm use the `sidecapion` command to flush the caption on the left side of the page. If the figure is positioned at the top of the page, align the sidecaption with the top of the figure – to achieve this you simply need to use the optional argument `[t]` with the `sidecaption` command

[4] Footnotes are easily added with this simple command.



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Subparagraph Heading

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- Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development, cf. Table 1.
  - Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.
  - Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.
- Livelihood and survival mobility are oftentimes coutcomes of uneven socioeconomic development.

Table 1 Please write your table caption here

Classes	Subclass	Length	Action Mechanism
Translation	mRNA[a]	22 (19–25)	Translation repression, mRNA cleavage
Translation	mRNA cleavage	21	mRNA cleavage
Translation	mRNA	21–22	mRNA cleavage
Translation	mRNA	24–26	Histone and DNA Modification

[a] Table foot note (with superscript)

7 Section Heading

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Type 1 That addresses central themes pertainng to migration, health, and disease. In Sect. 5, Wilson discusses the role of human migration in infectious disease distributions and patterns.

Type 2 That addresses central themes pertainng to migration, health, and disease. In Sect. 6.1, Wilson discusses the role of human migration in infectious disease distributions and patterns.

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Theorem 0.1. *Theorem text goes here.*

Definition 0.1. Definition text goes here.

Proof. Proof text goes here. □

Paragraph Heading

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Theorem 0.2. *Theorem text goes here.*

Definition 0.2. Definition text goes here.

Proof. Proof text goes here. □

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