

Visualizing Genetic Programming Ancestries

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VizGEC

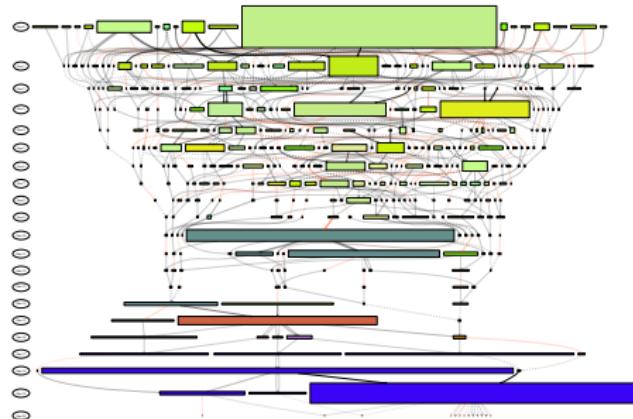
The great waste

- Genetic programming clearly *works*
- But we rarely know *why* or *how*
- Can generate *huge* amounts of data
- We typically throw it away – & paleontologists weep!
- Silico-paleontology can help us understand and improve our tools



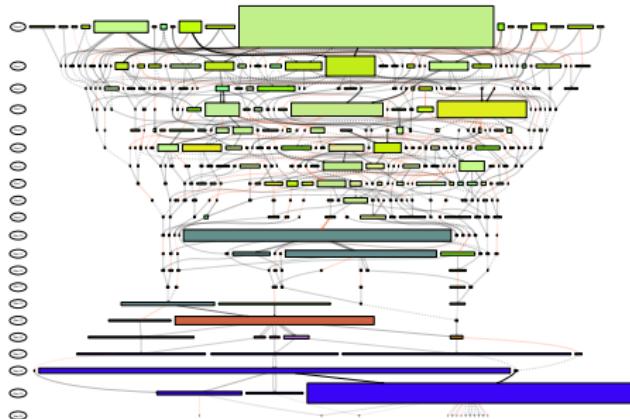
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We have the tools!



- Graph databases allow us to collect and analyze lineages
- Processing and *visualizing* these lineages can help us understand run dynamics

We have the tools!



These visualizations help:

- Turn complex runs into “readable” ancestry trees
- Capture and display key data in nodes and edges
- Find valuable properties and patterns in our runs

Other tools also exist

We're not alone:

- Bogdan Burlacu has done very similar work with HeuristicLab [2, 3]
- Tools like ELICIT (Cruz, et al) [4] and EpochX (Vaseux, et al) [8] also support lineage exploration

All of these are functionality provided by a particular EC system

We use:

- “Off-the-shelf” tools (graph DBs & visualization libraries)
- Could be applied to results from most any EC system

Outline

- 1 Setup
- 2 Graph Structure & Visualization
- 3 What did we learn?
- 4 Conclusions

Outline

1 Setup

- Run Configuration
- Database Configuration

2 Graph Structure & Visualization

3 What did we learn?

4 Conclusions

GP System

GP Tools:

- Clojush implementation of the PushGP system
- Plush (Linear Push) genomes [7]
- Lexicase selection [6]

GP Runs:

- 1,000 individuals per generation
- Up to 300 generations here,
Over 1,000 generations in other cases
100Ks or millions of individuals

Test problem

Replace-Space-With-Newline software synthesis problem:

- Two tasks to solve:
 1. Print input string with all spaces replaced by newlines
 2. Return number of non-space characters in input
- Results in two error values per test case
- Used 100 test cases,
So a total of 200 error values stored in vector

We have hundreds of runs of this problem which we'll use as examples throughout the talk.

Database schema

Used TitanDB graph database to store our data.

Nodes = individuals

- UUID
- Plush genome
- Error vector
- Number of children
- Number of selections

Edges = parent-child relationships

- Genetic operator
- Damerau-Levenshtein distance

Outline

1 Setup

2 Graph Structure & Visualization

- Graphviz and DOT
- Edges
- Nodes

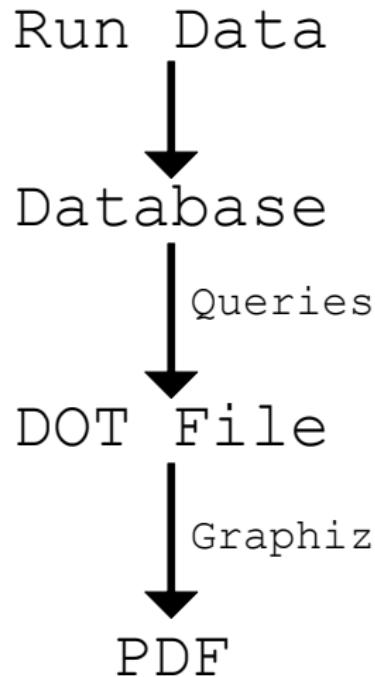
3 What did we learn?

4 Conclusions

Graphviz and DOT for visualization

- Load run data into database for processing & analysis
- Queries extract relevant data
- Scripts generate DOT input
- DOT generates PDF output

PDF output supports arbitrary zooming
– huge amounts of detail in paper



Genetic Operators

Edges represent parent-child relationships

Styled to indicate genetic operators used to create the child

Two classes of operators: Alternation & Mutation

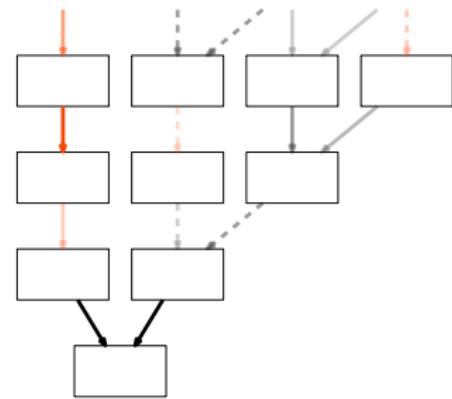
Four different operators:

- Alternation
- Uniform-Mutation
- Alternation & Uniform-Mutation
- Uniform-Close-Mutation

Edge Coloring & Style

Edge Coloring:

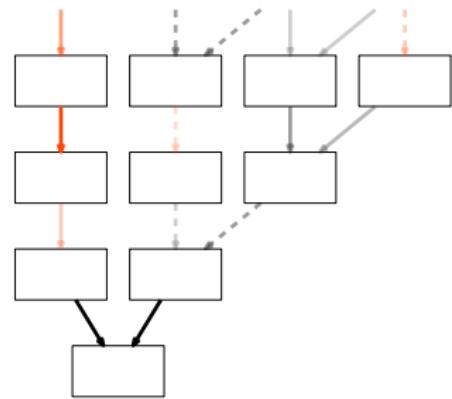
- Alternation is black and solid
- Uniform-Mutation is orange and solid
- Alternation & Uniform-Mutation black and dashed
- Uniform-Close-Mutation is orange and dashed



Edge Coloring & Style

Edge Opacity: Based on number of children of the child.

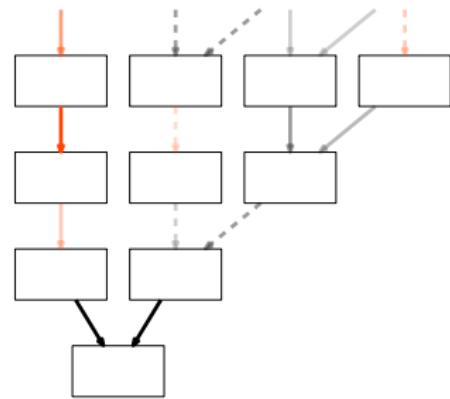
- Transparent: Few Children
- Opaque: Many Children



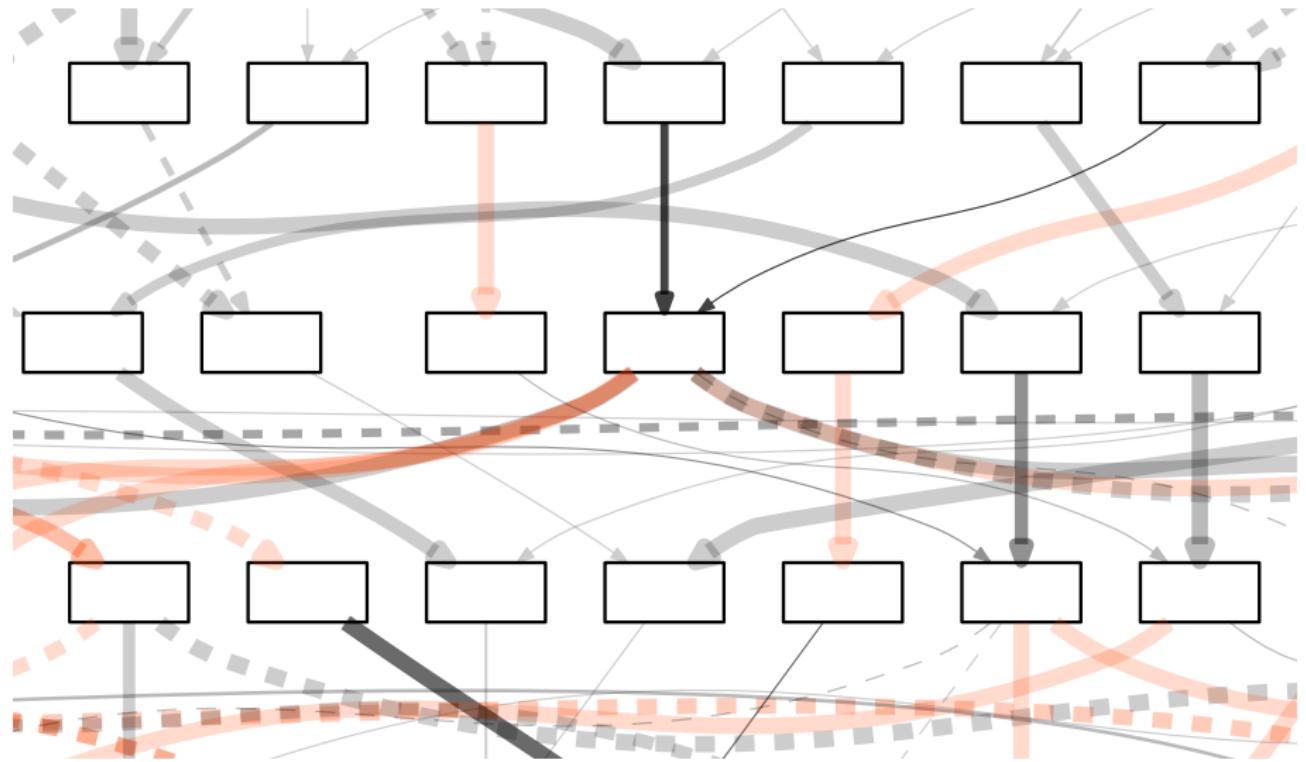
Edge Coloring & Style

Edge Thickness: Based on Damerau-Levenshtein distance, (measure of genome difference)

- Thin: Very Different Genome – High DL-Distance
- Wide: Very Similar Genome – Low DL-Distance



Edge Coloring & Style Example



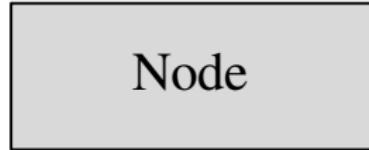
Node Basics

Nodes represent an individual or program:

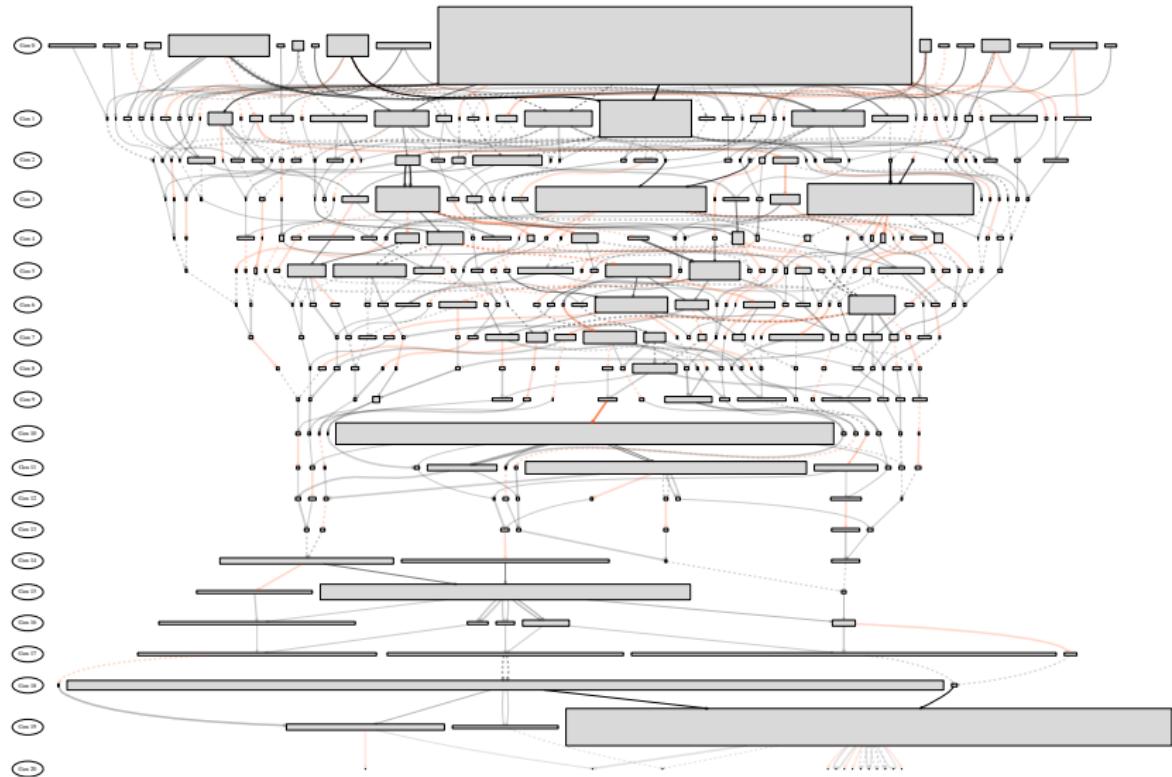
- Number of selections: Width
- Number of children: Height

← Number of Selections →

↑ Number of Children ↓

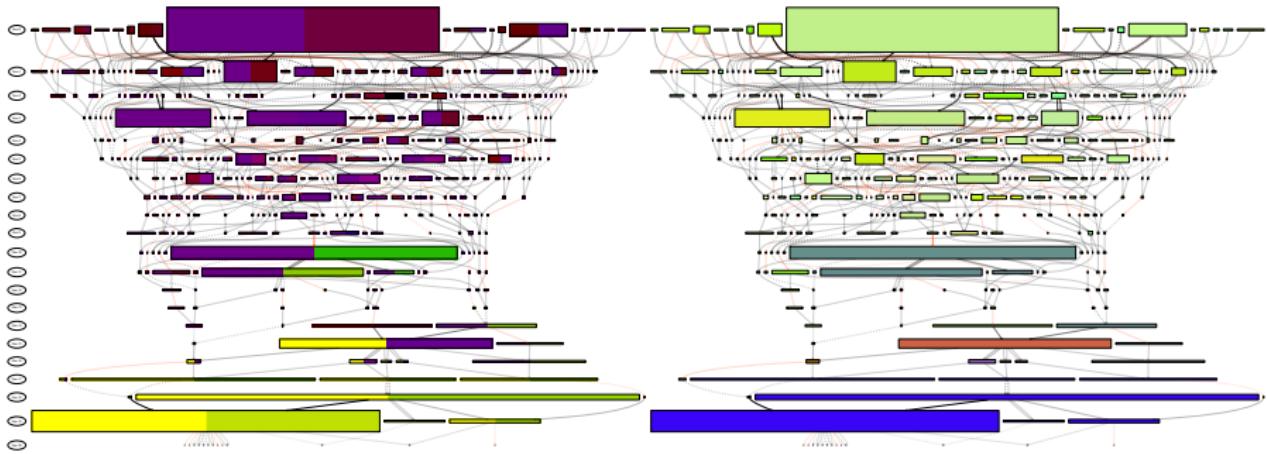


Run 0: No Node Color

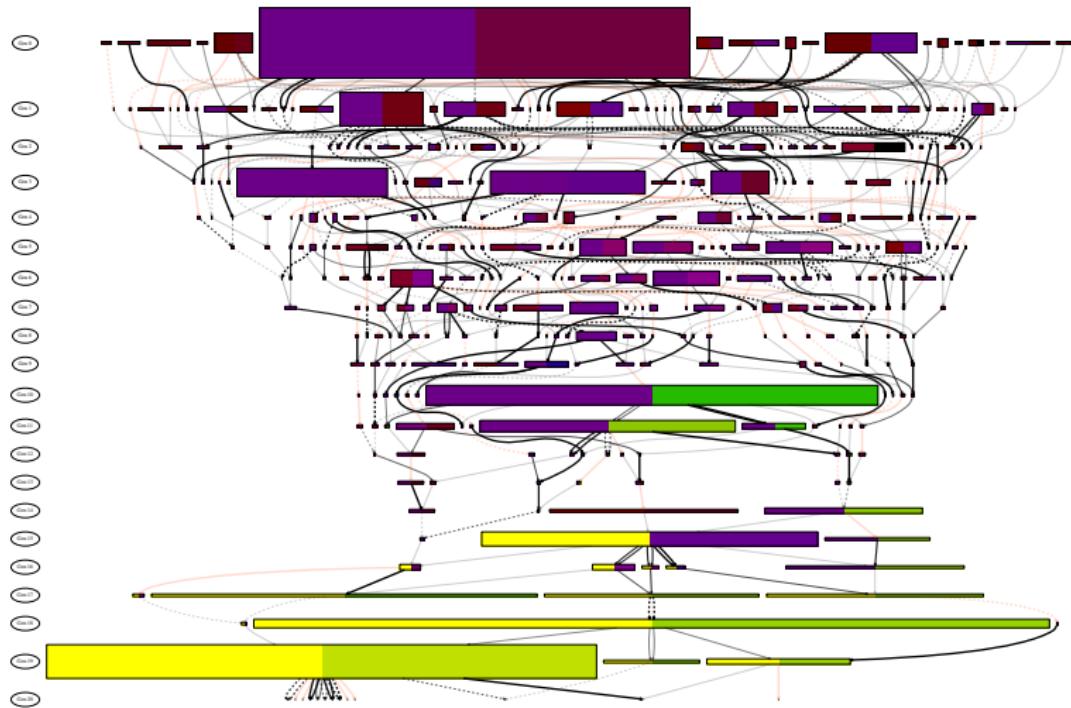


Node Coloring

There are two different techniques we use:
Error Based & RBM

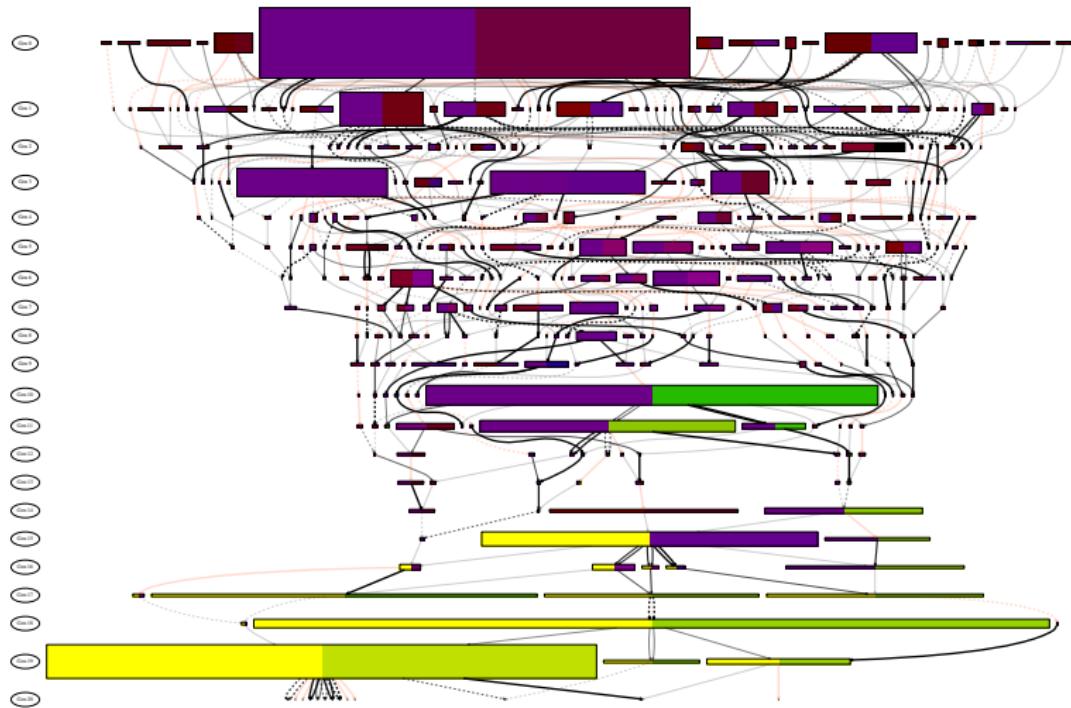


Error Based Node Coloring



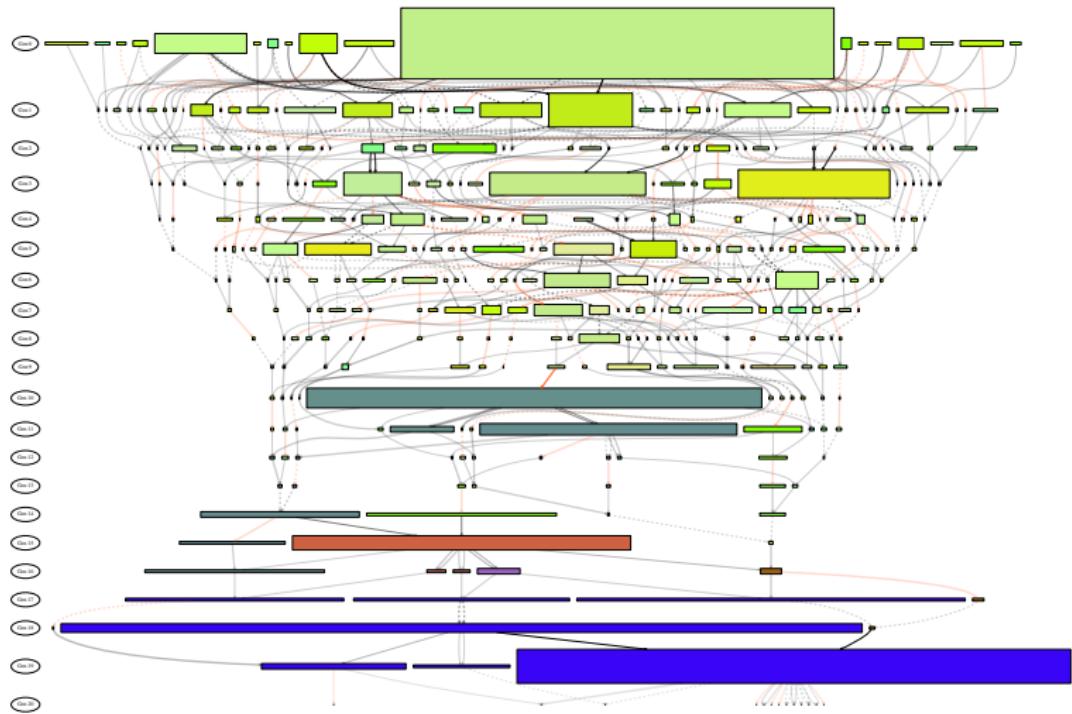
Two colors based on the percent of solved test cases for each task

Error Based Node Coloring



Additional shading (i.e., darker) for exceptionally high total errors

Restricted Boltzmann Machine Node Coloring



Dimensionality Reduction Problem: 200 test cases → 24 bit RGB color

Restricted Boltzmann Machine Technique

Train an RBM to be a simple autoencoder:
200 inputs to 24 bits to 3 RGB color values

200 test case vector, each case is assigned 1 or 0
(1 for has error or 0 for no error)



New vector made into binary string for machine input



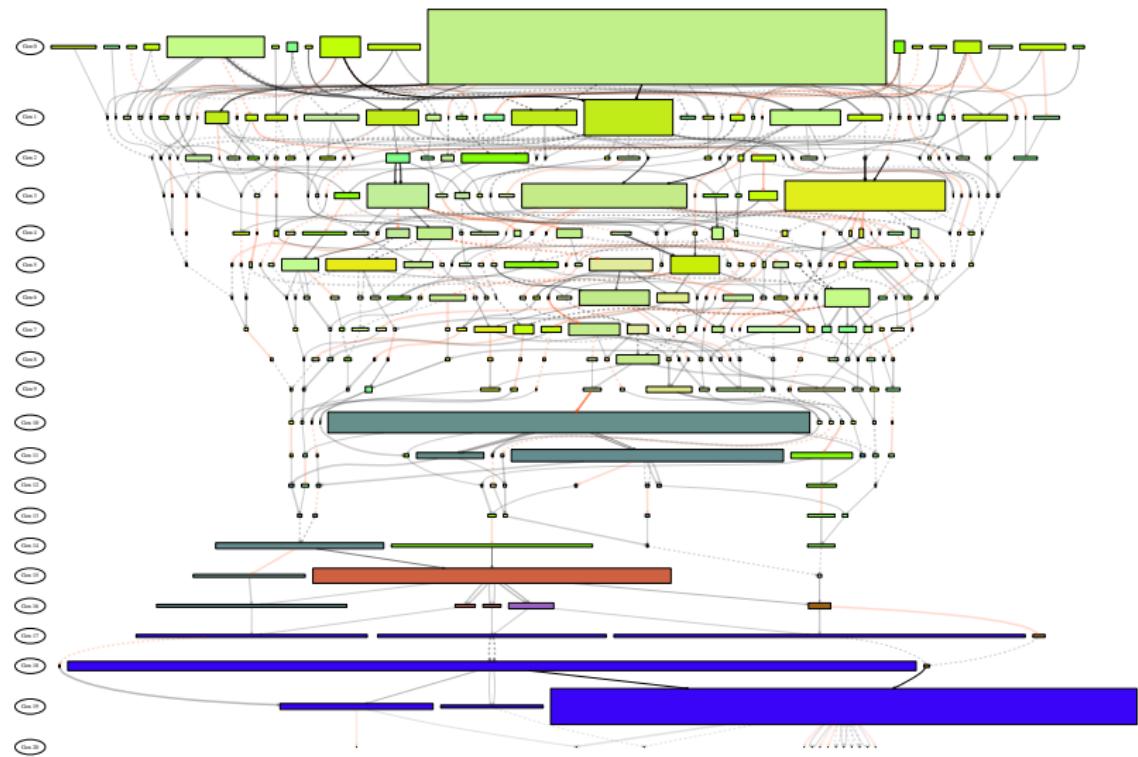
Training RBM analyzes and discovers patterns



Returns RBG values

Similarly colored individuals indicate similar patterns in test cases

Restricted Boltzmann Machine Node Coloring



Outline

1 Setup

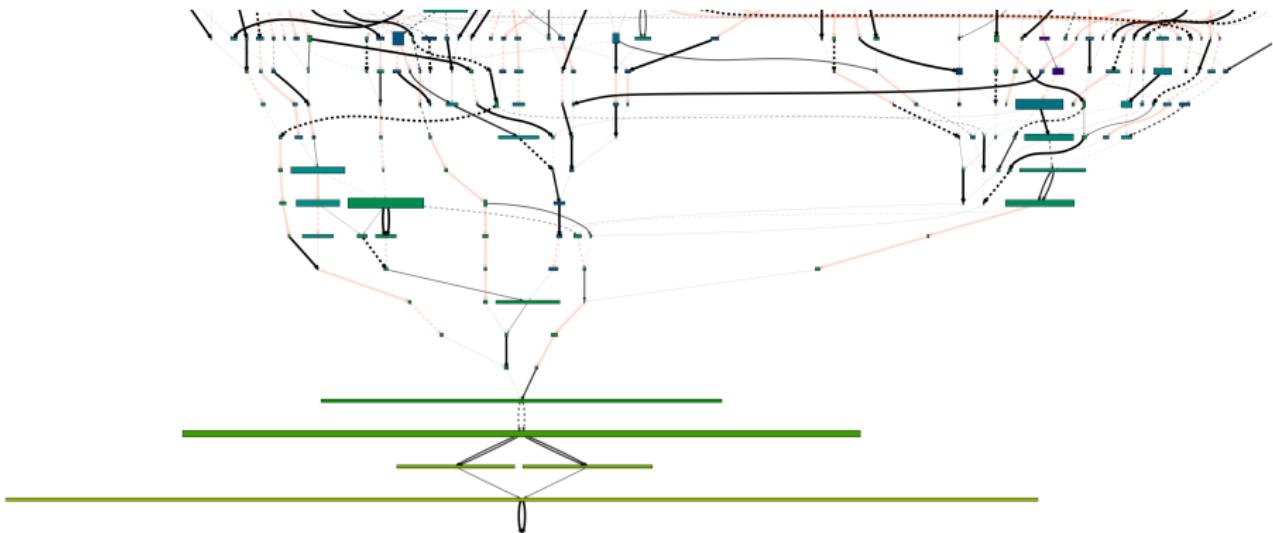
2 Graph Structure & Visualization

3 What did we learn?

- Hyperselection is common – is it important?
- Filtering ancestry trees
- Long (nearly) linear chains
- Ability to compare runs

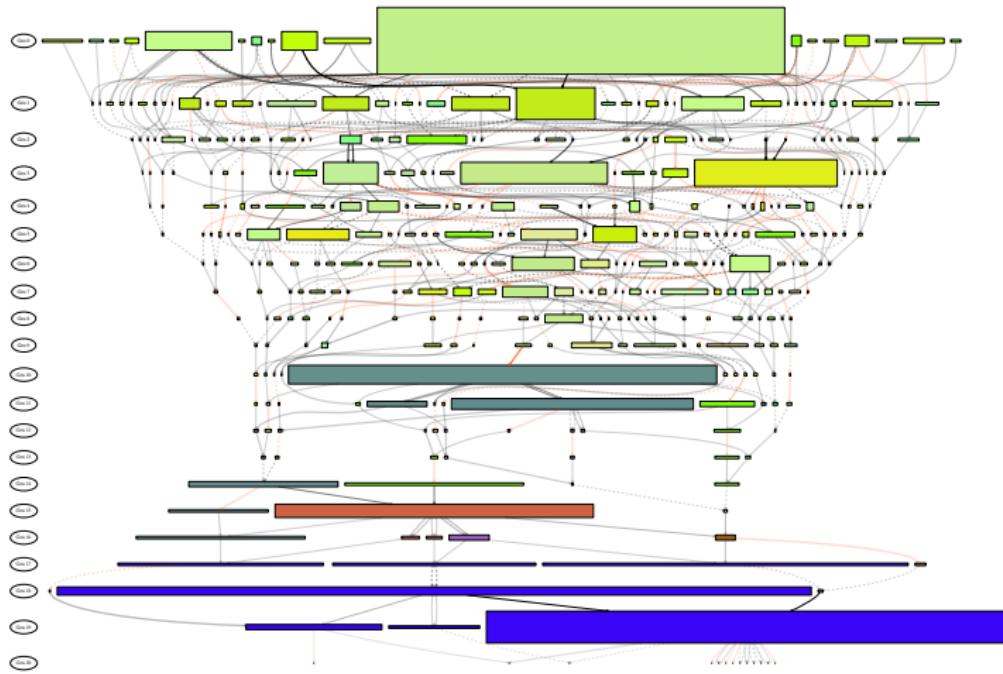
4 Conclusions

Hyperselected nodes are highly visible



In our graphs, we can easily see hyperselection as very wide nodes.

Hyperselection is very common



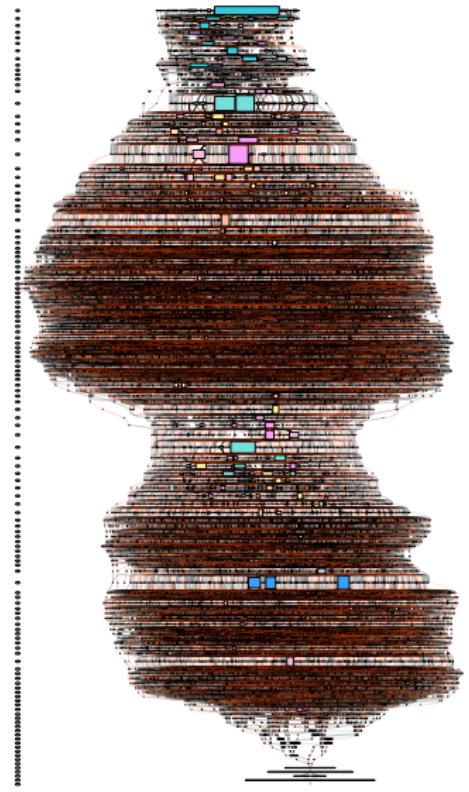
Lots of hyperselection – how important is it to the success of runs? [5]

Filtering ancestry trees

We only graph ancestors of “winning” individuals.

But still a lot of data!

- 22,435 individuals
- 35,403 edges
- (Avg. branching factor of 1.5)

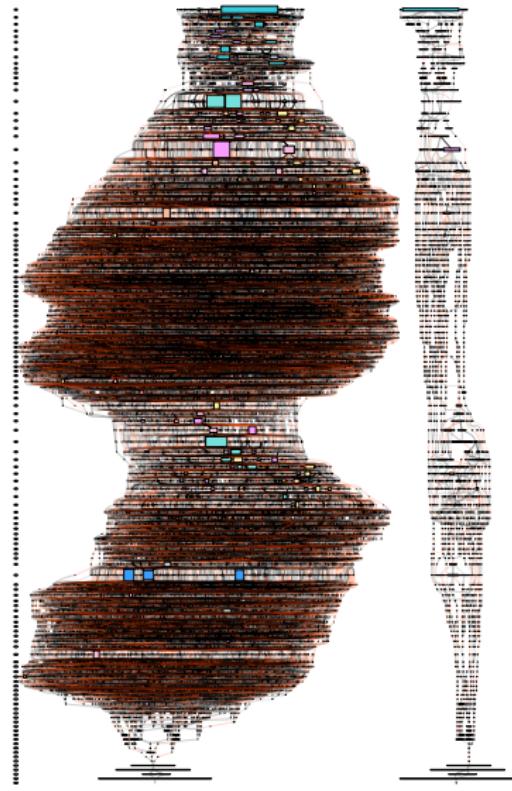


Filtering ancestry trees

So we filter out parents who did not contribute much genetic information.

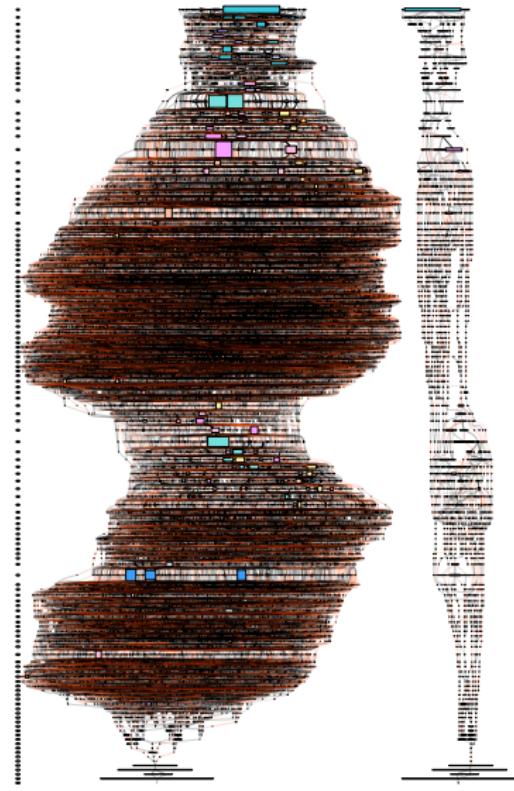
Much more “readable”:

- 1,597 individuals (vs 22,435)
- 1,795 edges (vs 35,403)
- Avg. branching factor of 1.1

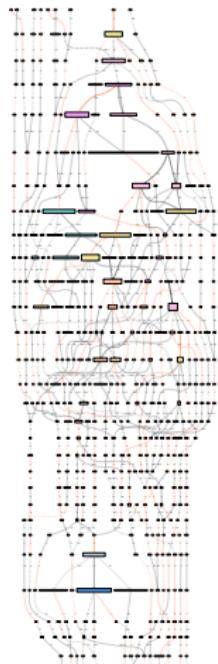
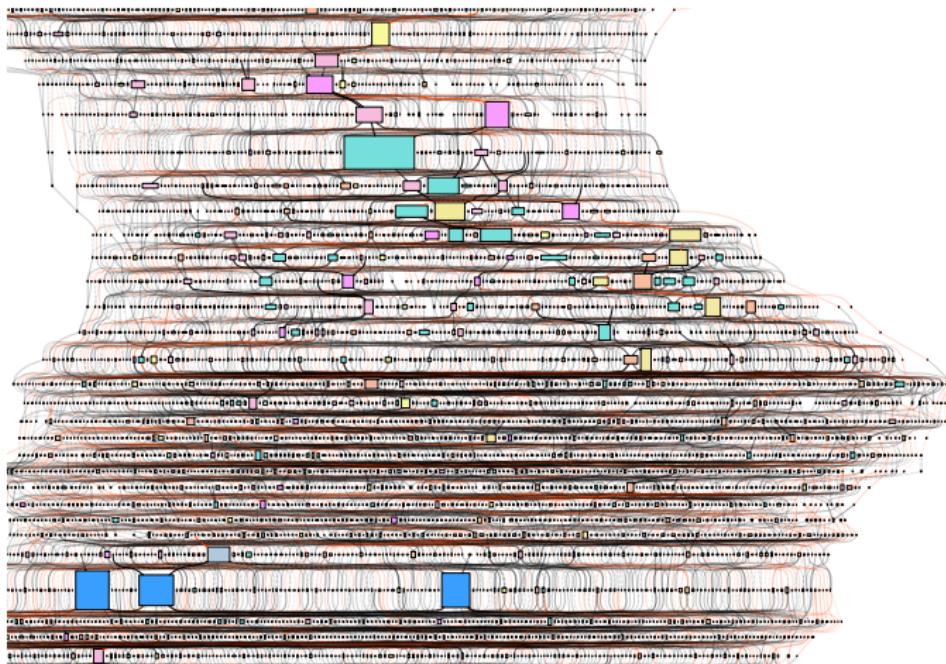


Filtering ancestry trees

- Filtering in paper is a bit of a hack
- Currently (last few weeks) working on tracking every gene (instruction) as it passes from parent to child
- Allows us to visualize *exactly* the parents that contributed genetic material

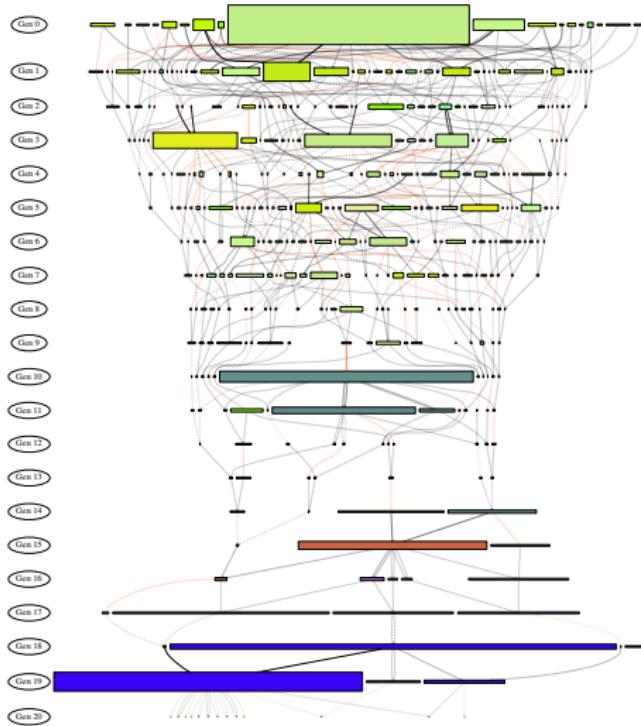


Close-up of filtering

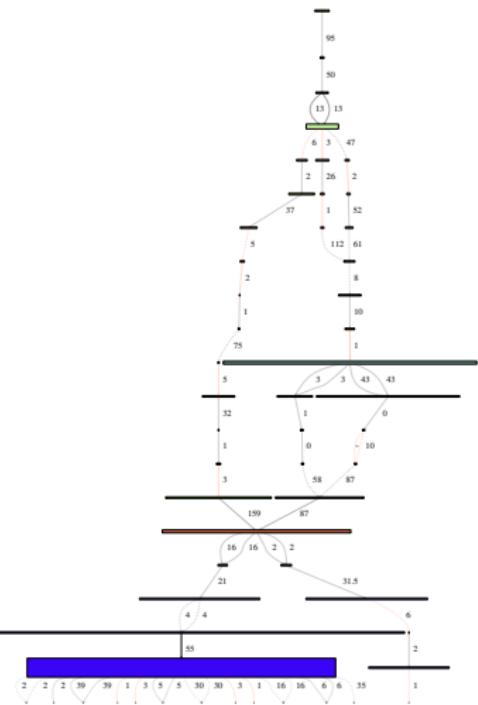


Another filtering example

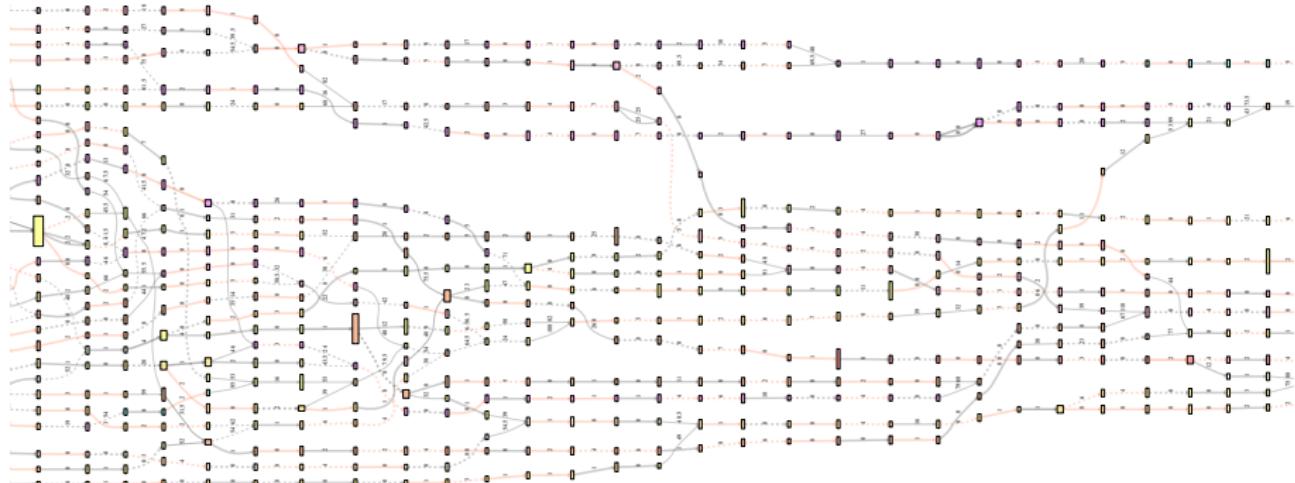
394 Individuals



54 Individuals

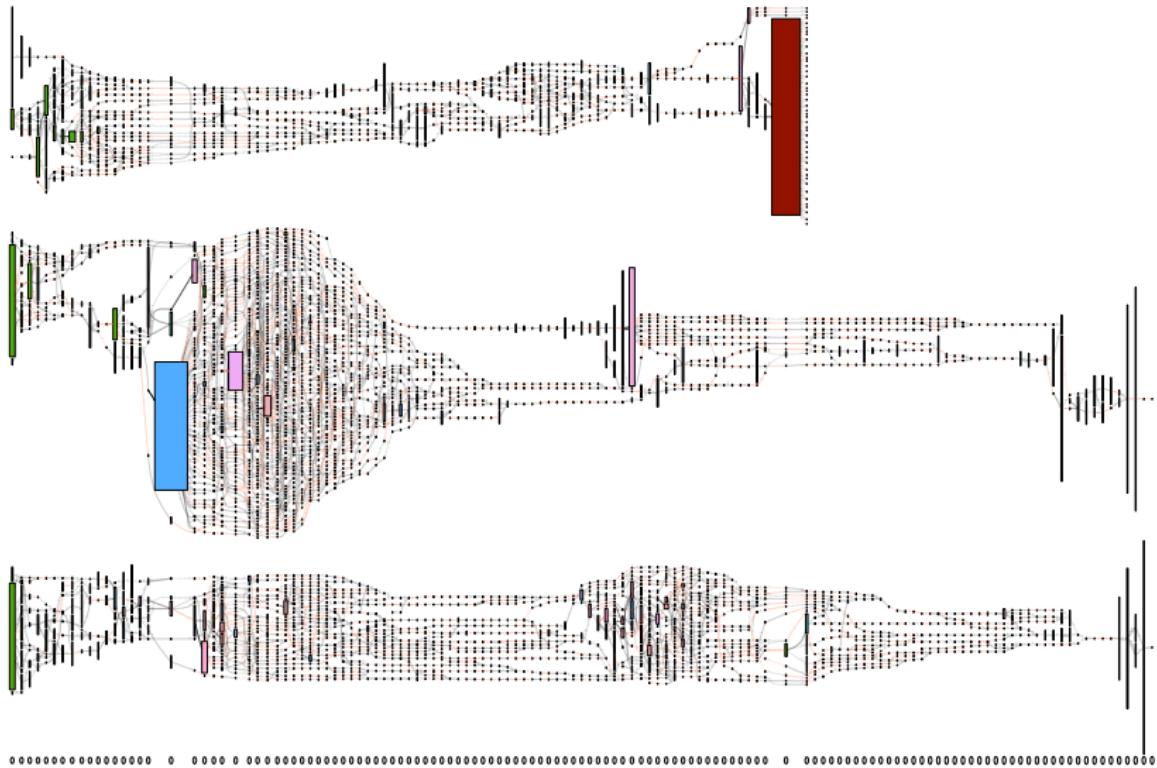


Long (nearly) linear chains



Filtering reveals long nearly linear sequences of pseudo-mutations

Ability to compare runs



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Conclusions

These visualizations have:

- Helped turn complex runs into “readable” ancestry trees
- Modified aspects of both nodes and edges to capture key information from the run dynamics
- Explored ways to filter ancestry trees
- Highlighted prevalence of hyperselection in lexicase selection runs
- Highlighted long chains of pseudo-mutations
- Suggested numerous research directions

Future work

- Improve the filtering
 - Currently working to track at the level of genomes (instructions)
 - Allows more precise tracking of genetic contributions
- Enable more dynamic visualizations
 - Deep Tree exhibit [1]
 - Burlacu's work [3]
- Enable more “on-line” visualization during runs

Thanks!

Thank you for your time & attention!

:-)

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