Pantzerfaust

ProgrammingLife 2016 - Technical Customer Reflection

Overview

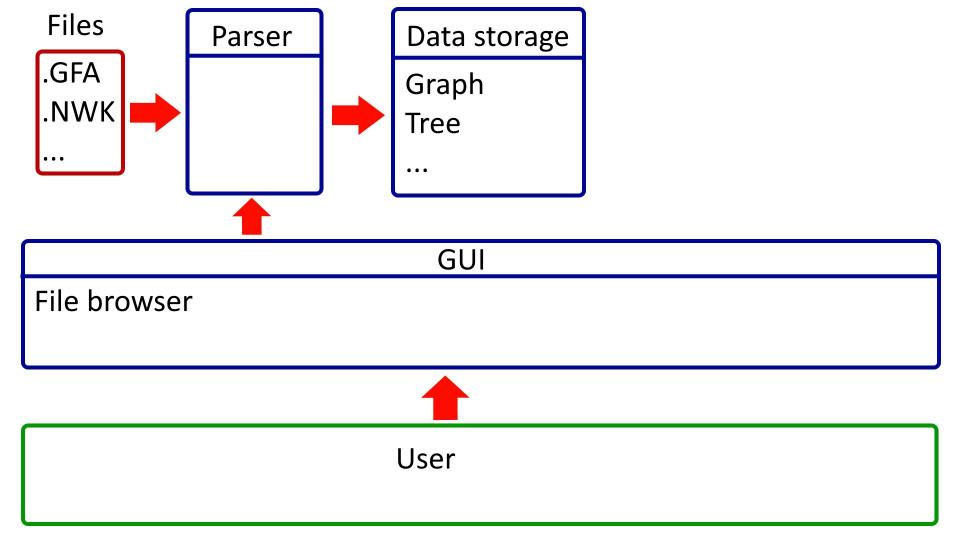
- Application architecture
- Internal data representation
- Visual components and scalability
- Semantic zoom strategy
- Technology stack
- General recommendations

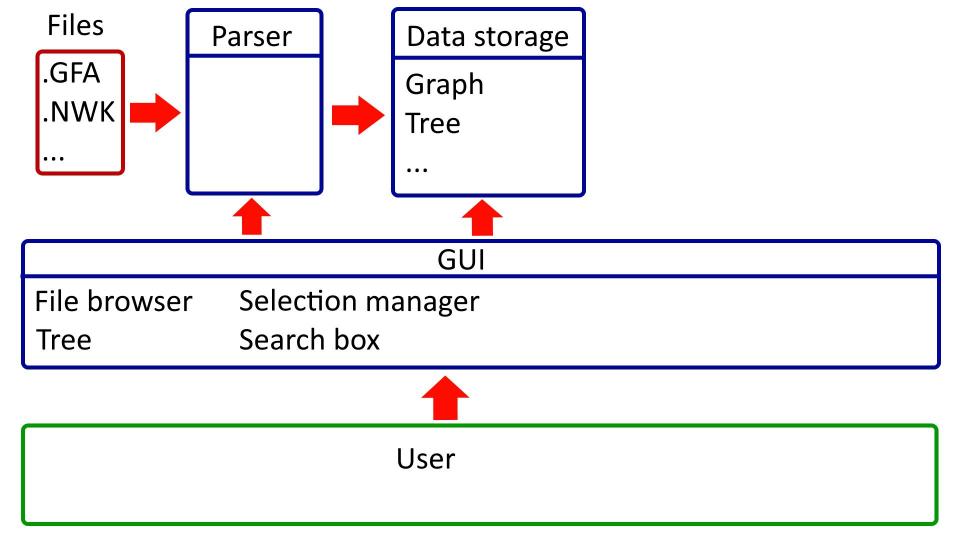
Application architecture

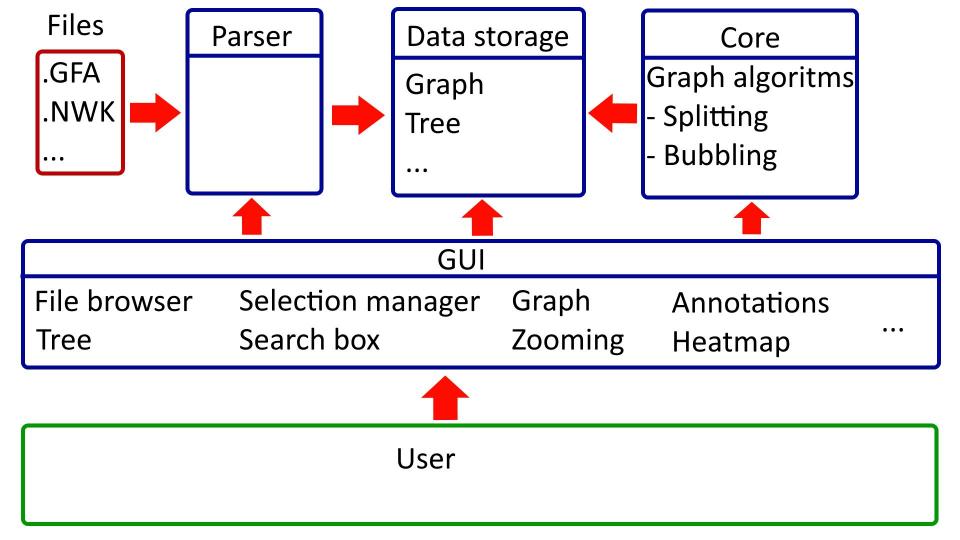
- GUI
- Parser
- Data storage
- Core

GUI File browser

User







Application architecture

Good

- Simplicity
- Loosely coupled modules

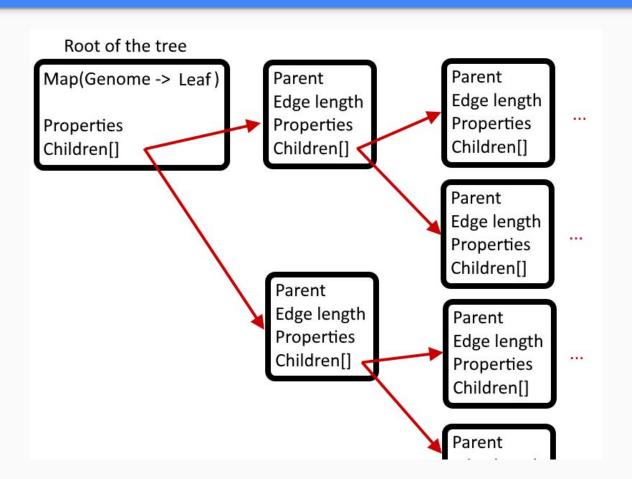
Could be improved

 Some of our GUI files have a high complexity. It would've been better to make them smaller

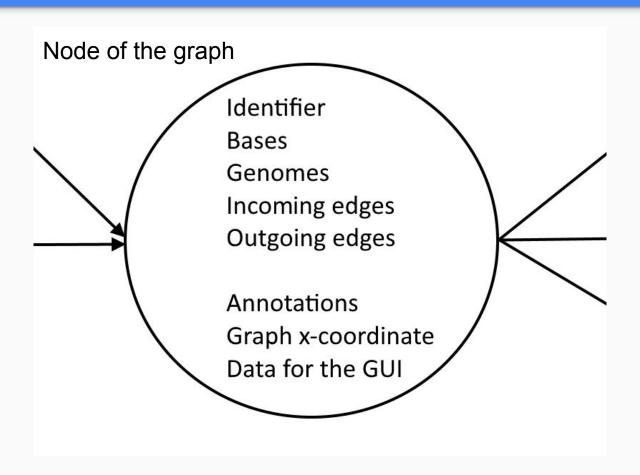
Internal data representation

- Metadata
- Annotations
- Phylogenetic tree
- Genome graph

Phylogenetic tree

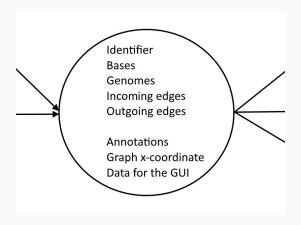


Graph - Node Object



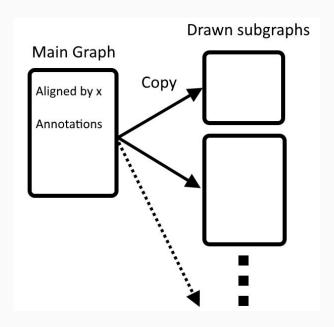
Graph

List of nodes (sorted)
List of genomes
List of root nodes



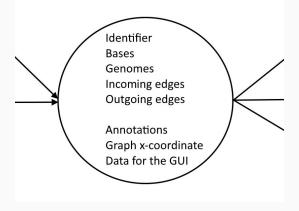
Graph - Main Graph

- Sorted by x-coordinate
- Annotations



Graph

List of nodes (sorted) List of genomes List of root nodes



Graph - Optimizations

- Memory
 - Genomes id instead of string
 - Bases 3 bits encoding*
- Performance
 - Use hashmaps/hashsets
 - Sort lists which will be compared often
- Main tradeoff: HashMap (36 bytes/value***) VS ArrayList (4 bytes/value**)

• https://github.com/ProgrammingLife2016/PL2-2016/blob/dev/PL2/PL2-shared/src/main/java/nl/tudelft/pl2016gr2/model/graph/data/BaseSequence.java

^{**} http://java-performance.info/memory-consumption-of-java-data-types-1/

^{***} http://java-performance.info/memory-consumption-of-java-data-types-2/

Internal data representation

Good

- Don't create objects for each edge storing edges is very expensive
- Do most computations on the main graph and copy the computed values when drawing a subgraph
- Store genomes as efficiently as possible for each node
- Store bases as efficiently as possible
- Use a profiler to check the memory consumption
- Use HashSets/HashMaps if the memory increase isn't too high
- Sort lists which will often be checked for equality. Comparing two sorted lists takes O(n) time while comparing unsorted lists takes O(n2) time.

Could be improved

- Genomes could have been stored for each edge in a node instead of for the node itself. This doesn't cost much more memory and calculating which genomes travel over which edges is expensive.
- Data could be written to a database, so less RAM is needed. This is however pretty complex to implement efficiently and should only be needed for very large datasets. Simply using a powerfull desktop with 128GBs of RAM should be enough to load around 40K-100K genomes (performance would have to be improved though).

Visual components and scalability

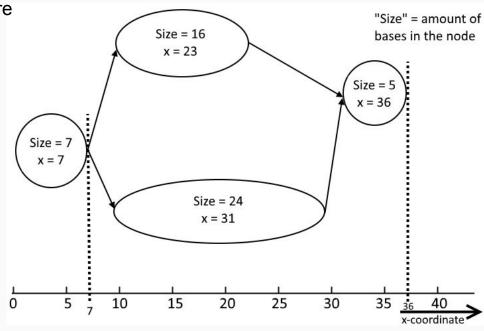
- Our performance (328 graph):
 - O Nodes drawn: around 50 600
 - Edges drawn: around 2,000 16,000
 - FPS: 20 60 while zooming*
 - CPU: below 20% while zooming*
 - Memory: around 500MB

Drawing - Scalability

- Only draw nodes which you can see
- Redraw instead of moving
- Precompute complex computations
- Edges -> canvas

Drawing - horizontal position

- Linear scale
- Custom coordinate system, see picture
- Easy to precompute



Visual components and scalability

Good

- Draw non-interactive components in a canvas (edges)
- Only create JavaFX object for elements which can be seen
- Don't use complex visual elements (such as gaussian blurs)
- A linear coordinate system makes things easier (in our case)

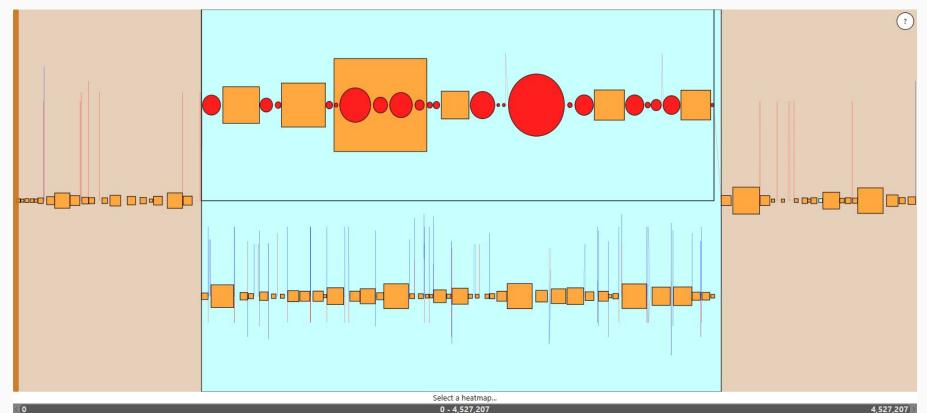
Could be improved

 Better memory management of JavaFX objects: remembering and reusing old JavaFX objects will make the life of the garbage collector a lot easier.

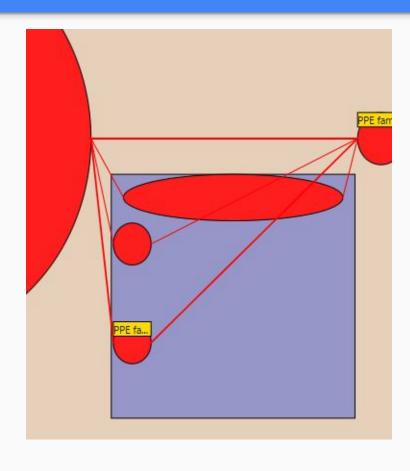
Semantic zoom strategy

- Semantic -> Bubbles
 - Phylogenetic
 - Graph (source sink pairs)
 - Point mutation
 - Indel
- Non-Semantic -> change x-coordinates

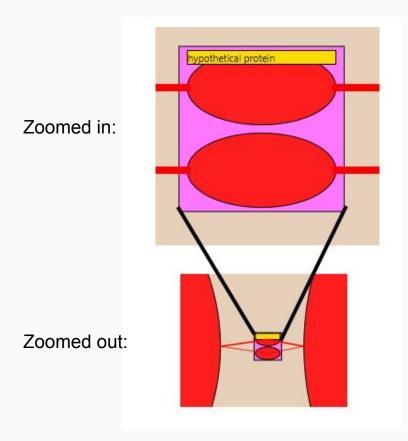
Bubble - Phylogenetic



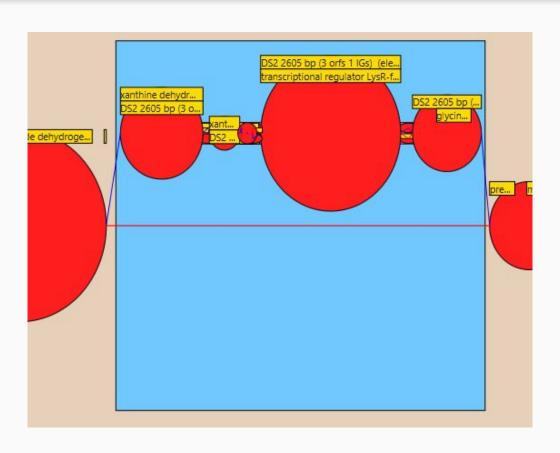
Bubble - Graph (source-sink pairs)



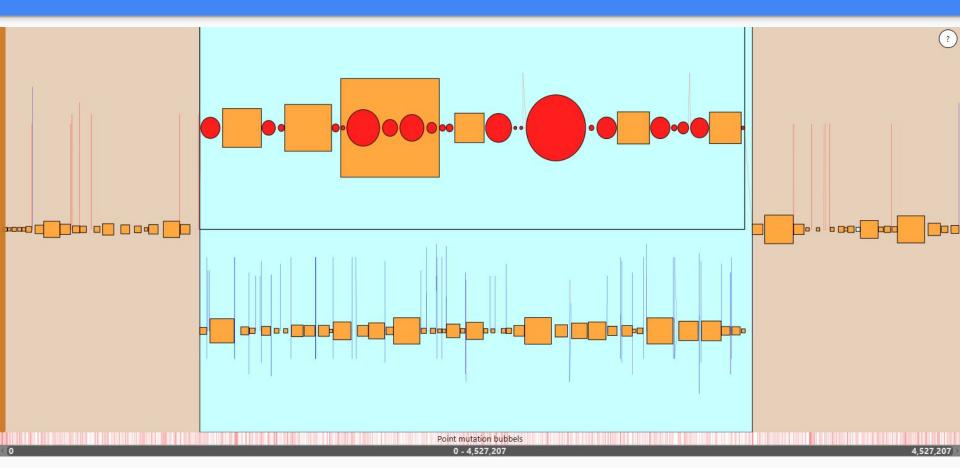
Bubble - Point mutation



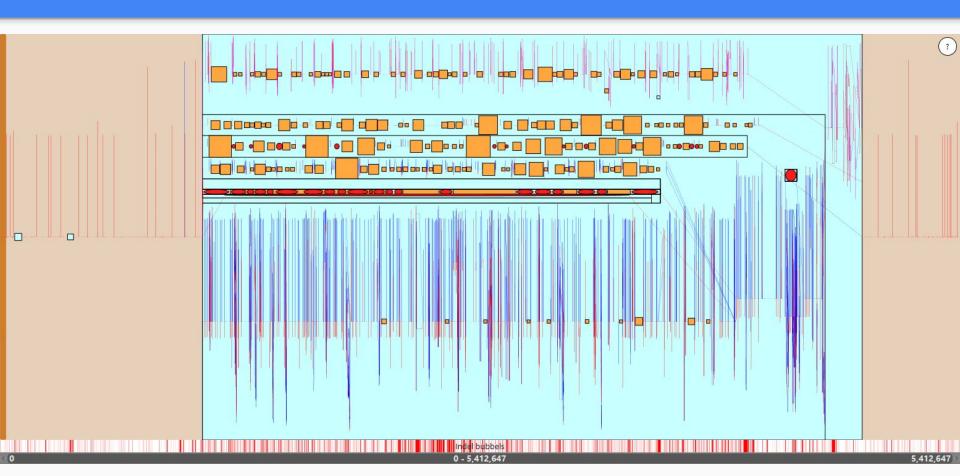
Bubble - Indel



Point mutation heatmap

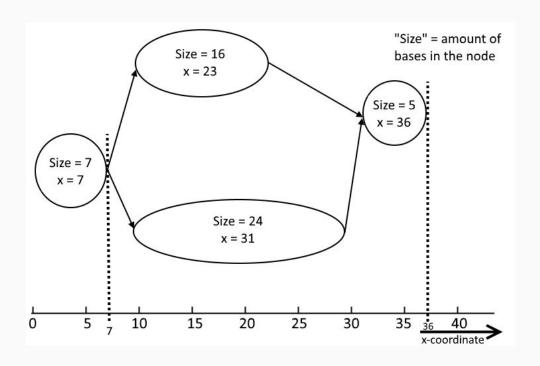


328 graph with indel heatmap



Non-Semantic Zoom

Change range of drawn x coordinates



Semantic zoom strategy

Good

- Smooth zooming
- Smooth semantic zooming
- Easy to identify mutations
- Nice graph heatmap integration

Could be improved

- Very small nodes (with fewer than 150 bases) are drawn larger, thus they overlap.
- When zoomed in a logarithmic scale might be more useful. This could be done by implementing a way to toggle between linear and logarithmic scaling.

Technology stack

- Java
- JavaFX

Technology stack

Good

- Everyone was familiar with the used technologies
- Very few different components: easy to test/debug
- No communication overhead between different technologies

Could be improved

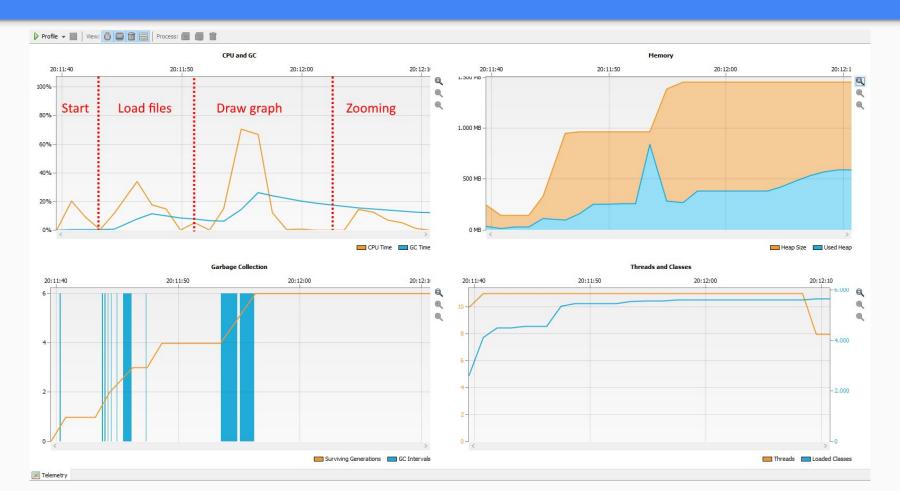
- A database could be used to store parts of the memory which aren't required at the moment. This would reduce the used RAM.
- Some computations could be executed in lower level languages, or even on the GPU, to improve performance.

General recommendations

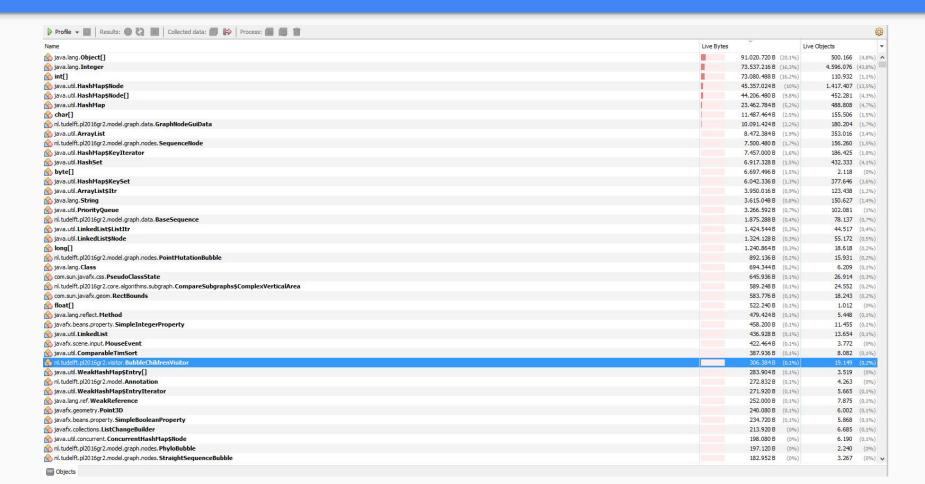
- First focus on the horizontal alignment (topological)
- Don't start too late with the vertical alignment of the graph
- Smooth zooming + popping requires a linear x-scale (?)
- Start with the phylogenetic tree
 - Select based on tree
 - Use tree to search
- Learn how to use a profiler to profile CPU and memory usage (see resources)

Resources

Profiler - CPU usage when loading and drawing the 328 graph (netbeans profiler)



Profiler - memory usage with 328 graph loaded & drawn (default netbeans profiler)



Profiler - time spent in each method (default netbeans profiler)

