

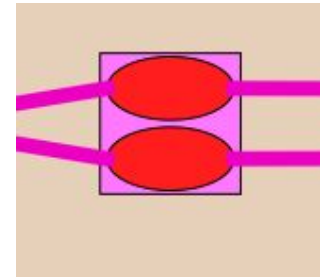
Programming life 2016 - Pantzerfaust

Overview

- Features (1 – 9)
- Strengths
- Outlook
- Demo

Features – part 1

- Interactively explore a sequence graph
 - Highest level – nucleotide level
 - Legend
 - Search functionalities
 - 328 genomes easy



Features – part 2

- Semantic zooming
 - Intuitive
 - Meaningful sizing of nodes and edges
 - Meaningful nodes in context
 - Clickable nodes

Phylogenetic bubble
In this bubble:
Indels: 0
Point mutations: 1
Genomes in this bubble (328):

Features – part 3

- Evolutionary relationship
 - Full integration with phylogenetic tree
 - Selection device
 - Highlighting
 - Zoom-in on phylogenetic tree
 - Phylogeny-based bubbles
 - Group mutations based on evolutionary closeness

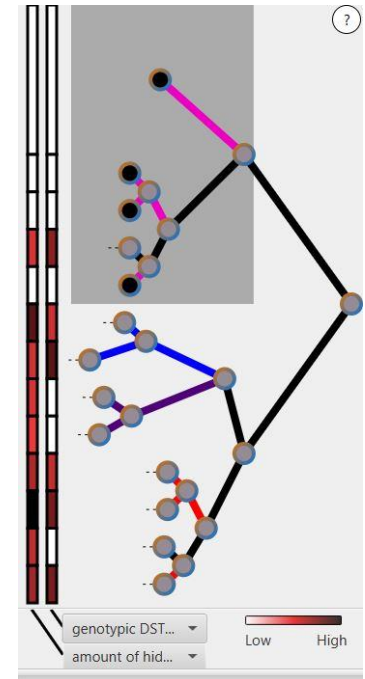
Features – part 4

- Mutations in the context of gene annotations
 - Annotations present for reference genome
 - Searching functionalities



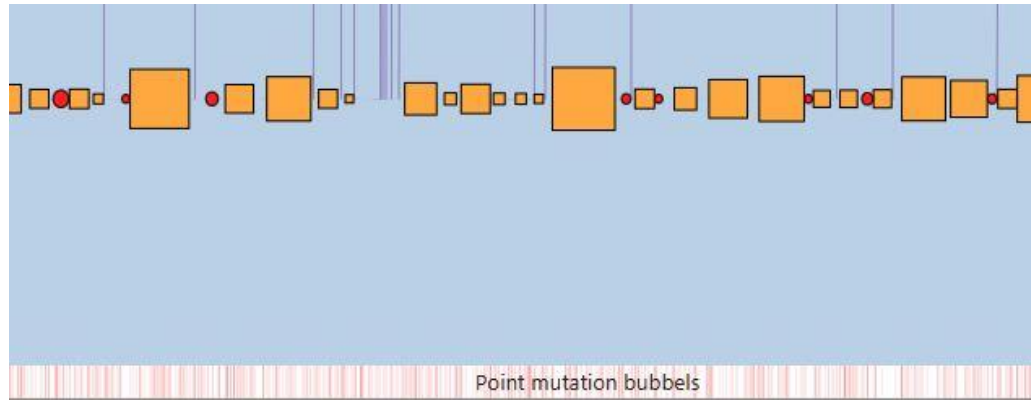
Features – part 5

- Visual representation of metadata
 - Filter & search options
 - Heatmap for phylogeny



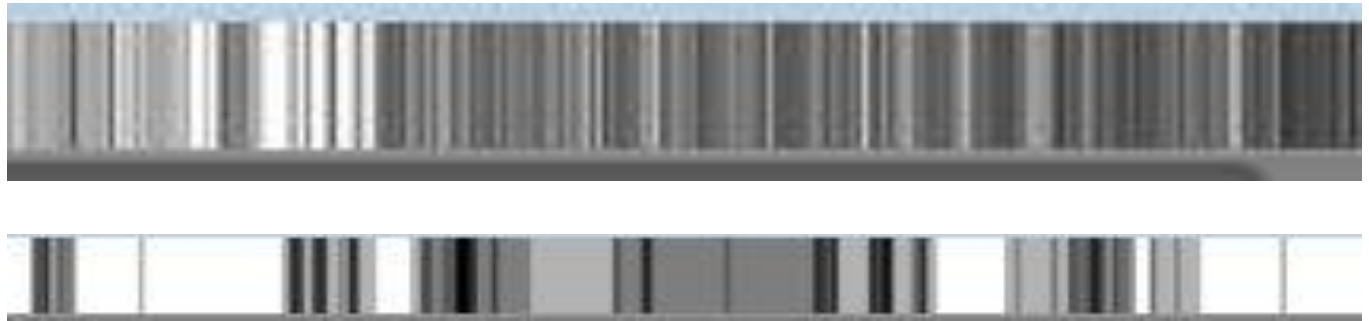
Features – part 6

- Visual encodings for classes of mutations
 - In/del, point mutation, (straight sequence – only point and indel mutations)
 - Heatmap under graph



Features – part 7

- Identify mutations
 - Together with the visuals
 - Heatmaps



Features – part 8

- Convergent evolution
 - Smart selection of graphs
 - Making use of the highlighting
 - Possible, but difficult to find by eye

Features – part 9

- Linking external resources
 - Loose coupling of modules – easy to add

Strengths

- Comparing two graphs
- Integration with phylogeny
- Performance
 - Fast loading, smooth zooming
- Innovative visualization
 - Realistic data presentation
- Ready for the big datasets?

Outlook

- Better integration with the needs of the end user
- Convergent evolution
- Automatically recognizing interesting parts of the data
- Vertical-scaling

Questions?

Demonstration of the final product

- Thanks for listening
- Demonstration next, demo video is more or less the same