

Sprint Plan

Programming Life Team 1

Sprint 5

Week 4.6

Requirement/Story	Task	Task assigned to <i>name(s)</i>	Estimated effort per task <i>hours</i>	Notes
Enable us to interactively explore a sequence graph representing the genome architecture of multiple strains.	Visualize genome filtering.	Mark	10	Find solution for the 'hiding nodes' problem.
	Enable user to switch between semantic zoom levels.	Maarten	3	
	Fix the graph view dimensions.	Marissa	3	
Provide semantic zooming to enable useful visual interpretation at various zoom levels from whole-genome to individual mutations.	Implement writer and reader for the new graph data model.	Mark	4	
	Setup the extenable class structure for DNodes.	Chak Shun	5	Implementation is dependent on genome filtering, probably won't have time to actually implement it.
Put bubbles (mutations) in the graph in the context of well-known references genomes with their gene annotations and integrate with other reference databases.	Locate the genes in the reference genome.	Chak Shun	3	
	Visualize the location of the genes.	Chak Shun	7	Mark the location.
Have visual encodings for different classes of mutations and the ability to filter on mutation class.	Collapse nodes horizontally based on content size	Marissa, Justin	4	
Put this graph in the context of the evolutionary relationship between bacteria.	Visualize the phylogenetic tree in a horizontal tree layout.	Maarten, Justin	10	Keep the interactiveness of the tree in mind.