Sprint Reflection   *Programming Life Team 1*   Week 4.6   Sprint 5

Requirement/Story	Task	Actual time spent					Estimated time	Done	Notes
		Chak Shun	Justin	Mark	Marissa	Maarten	hours	y/n	
Enable us to interactively explore a sequence graph representing the genome architecture of multiple strains.	Visualize genome filtering.			1,5			10,0	no	
	Enable user to switch between semantic zoom levels.				4,0	0,0	3,0	no	Interactive image zooming enabled.
	Fix the graph view dimensions.				4,0	2,0	3,0	yes	Works for placer, needs work for gui
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.		10,0				4,0	yes	we will look at a graph database which makes things much easier
	Setup the extendable class structure for DNodes.	10,0					5,0	yes	Overall structure should be done, specific DNodes we need are already there.
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.	0,0					3,0	no	
	Visualize the location of the genes.	0,0					7,0	no	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		2,0		2,0		4,0	yes	
Put this graph in the context of the evolutionary relationship between bacteria.	Visualize the phylogenetic tree in a horizontal tree layout.		12,0			12,0	10,0	yes	Tree visualization finished. Collapsing possible. Ready for interaction with graph.

Main Problems and Adjustments

Problem 1 - Lack of scalability

Description	We did not take into account the scalability of the problem early enough.
Effect	Be will run into big problems if we don't save the graph in a suitable structured file on disk.
Improvement	Implement a graph database system.