

Sprint Plan

Programming Life Team 1

Sprint 8

Week 4.9

Requirement/Story	Task	Task assigned to <i>name(s)</i>	Estimated effort per task <i>hours</i>	Notes
Provide semantic zooming to enable useful visual interpretation at various zoom levels from whole-genome to individual	Adjust the horizontal placements after collapsing nodes.	Justin	5	
	Extend the pointsystem to make the semantic zooming more dynamic.	Chak Shun, Marissa	7	
Put this graph in the context of the evolutionary relationship between bacteria.	Detect whether a mutation is phylogenetically inheritted. [1]	Mark	8	
	Combine evolutionary inherittance with the mutation score.	Marissa	4	
Identify mutations and determine the type of variant (insertion, deletion, SNP) uniformly across the samples.	Identify and collapse complex mutations.	Justin, Maarten	10	
Put bubbles (mutations) in the graph in the context of well-known references genomes with their gene annotations and integrate with other reference databases.	Create the ability to navigate to a certain gene.	Chak Shun	5	
	Show well known mutations in a minimap.	Maarten	5	
User interface improvements.	Improve the vertical placement of the nodes.	Maarten	2	Get rid of the inconsistency between different graphs.
	Write Help content.	Marissa	2	
	Create a Help dialog.	Maarten	3	Based on structure of help content. Add visual elements.
	Enable configuring thresholds and weights.	Maarten	5	
	Add keyboard control of main functions.	Mark	3	

[1] NSY SNP/indel that is phylogenetically inherited, i.e. only present in strains that come from the same ancestor