

## Sprint Reflection

## Programming Life Team 1

Week 4.5

Sprint 4.1

Requirement/Story	Task	Actual time spent					Estimated time hours	Done y/n	Notes
		Chak Shun	Justin	Mark	Marissa	Maarten			
Enable us to interactively explore a sequence graph representing the genome architecture of multiple strains.	Implement the visual aspects.	5,0					3	yes	There is still a problem concerning hiding the nodes.
	Implement interaction via the user interface.					15,0	8	yes	Still a bug in keeping responsiveness during import.
Provide semantic zooming to enable useful visual interpretation at various zoom levels from whole-genome to individual mutations.	Implement semantic zoom level for joining small point mutations.		8,0		8,0		6	yes	
	Extend the data model.			13,0			5	yes	
Have visual encodings for different classes of mutations and the ability to filter on mutation class.	Identify and visualize point mutations		-		-		5	yes	Overlapped with the zoom level for point mutations.

## Main Problems and Adjustments

### Problem 1 - Inappropriate data model

<b>Description</b>	The data model of the graph library turned out to be insufficient for our needs.
<b>Effect</b>	Halfway down the project we had to refactor the core structure of the data model.
<b>Improvement</b>	Next time, improve the design process using this experience.

### Problem 2 - Task dependencies

<b>Description</b>	In this sprint, multiple tasks depended on each other.
<b>Effect</b>	At the end of the sprint, we had to refactor code dependent on the changed data model.
<b>Improvement</b>	In the future, plan independent tasks.