

<b>Sprint Backlog, Iteration #8</b>					
User Story	Task	Member responsible for the task	Task Assigned To	Estimated Effort per Task (in hours)	Priority (A—E) (A is highest)
As a user I want to be able to load and examine the 328 genomes set	Improve performance of application so that it loads the 328 genomes dataset.	Björn	Björn, Hugo	13	A
As a user, I want to have visual encodings for different classes of mutations and the ability to filter on mutation class	Implement the ability to highlight snips in the gui. Snips should be colored according to their normal colouring, whereas the rest of the graph should be colored black/grey.	Evan	Evan	10	B
	Implement the ability to filter on indels in the gui. Indels should be colored according to their normal colouring, whereas the rest of the graph should be colored black/grey.	Evan	Evan	6	B
As a user, I want the application to load smoothly without it appearing to freeze.	Include the graph loading into the loading bar so that the loading progress can be fully followed. Also verify what values of the progressbar should be used for which part of the loading.	Björn	Björn	10	C
As a user, I want the graph nodes to be correctly displayed when zooming in	Fix the horizontal lines bug so that the graph is correctly displayed when fully zoomed in (like in release 7.0.2)	Rob	Rob	12	B
As a developer, I want to have clear and understandable code in the ribbon view/controller	Remove the GraphController and graph tab and place the ribbon view and graph view in seperate files.	Daniël	Daniël	8	C
As a user I want to select certain genomes based on certain criteria found in the metadata.xlsx file	Implement filtering on metadata in the phylogenetic tree.	Hugo	Hugo	16	B
As a user, I want to be able to search on annotation and go to the location of the found annotation.	Implement search box in the gui for the annotations.	Hugo	Björn, Hugo	9	C
As a user, I want to at which node of the graph an annotation starts and at which node it ends. This should be visible using edges to the start and end, when the annotation is clicked.	Implement edges between the annotations and nodes when the annotations are clicked.	Daniël	Daniël	15	B
As a user, I want to have a correct and clear annotation view	Fix the inreadability of the annotations when zooming out and make sure the annotations match the alignment of the graph.	Rob	Rob	11	B
As a user, I want the ribbon view to have the right colours	Determine graph lineage colour by majority vote, instead of top genome	Evan	Evan	7	B
As the client i want to see a presentation and demo every week to keep me up to date with how the project is progressing.	Create, practice, and present the client meeting presentation.	Evan	Evan	3	C
As the client I want to be able to view the Architecture design document and understand the design of the project	Update the Architecture Design Document to be current with the projects architecture	Evan	Evan	4	D
<b>Context Project: Programming Life</b>					
<b>Group: PL3</b>					