Sprint Backlog, Iteration #2

Context group: DART-N

Group: PL 4

User Story	Task	Member responsible for task	Member assigned to task	Estimated Effort (hours)	Priority	Actual Effort (hours)	Done (Yes/N)	Notes
	Final version Product Planing	Daphne	Daphne	6	A.1	6	Yes	Done by Niek
	Final version Product Version	Niels	Niels	6	A.1	6	Yes	Done by Niek
	Review Product Planing	Ties	Ties, Arthur	3	A.2	4	Yes	Also done by Daphne
	Review Product Vision	Niek	Niek, Ricardo	3	A.2	4	Yes	Done
When the user opens a DNA sequence, the phylogenetic tree will be shown	Phylogenetic tree Visualize the phylogenetic tree	Niek	Niek, Ties	12	B.1		No	
When the user opens a DNA sequence, he will be able to zoom in and get more details visible	Semantic Zooming	Niels	Daphne, Niels	16	B.2			
	Divide several zooming levels		Niels			20	Yes	
	Visualize the zooming levels		Daphne			22	No	In order to fix this, the whole GUI had to be refactored first
	Create an initial ribbon structure		Niels, Daphne			0	No	Work done related to this is the ability to devide the graph in multiple zooming levels.
When a team member reviews the code, tests will be written and passed	Testing	Arthur	Everyone	16	C.1	12	Yes	New code includes test cases
When a team member reviews the code, there will be no checkstyle/PMD/find bug errors	Error Fixing Resolve checkstyle errors, pmd and findbug errors	Ricardo	Everyone	16	C.2	8	Yes	Horizontal zooming branch contains a large number of fixes which have yet to be merged.
When the user scrolls through the DNA sequence, there will be a box indicating the position in the sequence	ZoomBox Alter the zoombox so that it scrolls with the genome and indicates where we are in the genome	Daphne	Daphne, Ricardo	12	D.1	8	No	Not integrated in master yet
When the user opens the tool, there will be three views: Phylogenetic tree, indication of position and sequence	Window View Integrate the phylogentic tree, graph and zoombox	Ties	Daphne, Ties	12	D.2		No	GUI has been changed significantly and the phylogenetic tree has ye to be visualised.
When the user opens several sequence, he will be able to pick a highlighted genome	Highlighted Genome Give the user the possibility to choos a genome to highlight	Arthur	Ricardo, Ties	12	E	15	Yes	Currently the highlighted genome is still hardcoded but an option to pick any strain will be added once the new GUI is set up properly
When the user opens our tool, he will be able to use the buttons to navigate through several views	Button functionality Give the buttons in the menu funtion such loading a graph, resetting the view or showing the phylogenetic tree	Daphne	Daphne, Niels	8	F	6	No	The GUI is restructed, so that on button clicks we can load a new scene.

Main problems encountered

Problem 1: Semantic zooming and ZoomBox visualization

Description: When trying to get rid of our vertical zooming (which we did by scaling), we found out that we needed to refactor the GUI in order to do so. So, the semantic zooming is not visualized yet and the ZoomBox is integrated in the master yet.

Solution: We will continue to work on this and finish it next week.

Poblem 2: Node display location

Properly aligning every node to give an evenly spaced and uncluttered verview of the genomes continued to be a problem. The z-index does not work as we thought it did.

Problem 3: Phylogenetic tree

Description: We did not manage to visualize the phylogenetic tree this week, since mayor changes in the GUI where made

Solution: We try to do it this weekend.

Problem 4: Executable jar file

Description: It took a lot of time to get an executable jar file. After spending a lot of time working on it, we finally have one. (Arthur)