

Sprint Backlog, Iteration #2

Context group: DART-N

Group: PL 4

ends 09:00,06-05-2016

May 5 and 6 off

User Story	Task	Member responsible for task	Member assigned to task	Estimated Effort (hours)	Priority
	Final version Product Plan	Daphne	Daphne	6	A.1
	Final version Product Version	Niels	Niels	6	A.1
	Review Product Plan	Ties	Ties, Arthur	3	A.2
	Review Product Vision	Niek	Niek, Ricardo	3	A.2
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
When the user opens a DNA sequence, he will be able to zoom in and get more details visible	Semantic Zooming Divide several zooming levels Visualize the zooming levels Create an initial ribbon structure	Niels	Daphne, Niels Niels Daphne Niels, Daphne	16	B.2
When a team member reviews the code, tests will be written and passed	Testing	Arthur	Everyone	16	C.1
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
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
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
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
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