Sprint backlog, Iteration #6   ends 09:00, 3-06-2016

Context group: DART-N

Group: PL 4

User Story	Task	Member responsible for task	Member assigned to task	Estimated Effort (hours)	Priority
When the user opens a DNA sequence, he will be able to zoom in and get more details visible	Semantic zooming	Niek	Niek, Arthur	30	A.1
	- Node collapsing	Niek	Niek	10	A.4
	- Arrow Edge	Arthur	Arthur	6	B.3
As a user, I want to wait as little time as possible while using the application.	Rendering enhancement: divide the graph in tiles and draw only relevant tiles	Ties	Ties, Daphne	25/8	A.3
	Refactor	Arthur	Ties	8	A.2
As a user, I want the nodes of the graph to be placed in a logical and space-efficient manner.	Node placement	Ricardo	Ricardo	8	A.2
	- Deal with inversion in graph		Ricardo, Niek	8	A.2.1
As user, the zoomBox will show which part of the graph is visible	ZoomBox	Daphne	Daphne	**14**	B.1
	- Let box indicate which part of graph is shown		Daphne	8	B.1.1
	- Only refresh box when indicating new highlight strain		Daphne	6	B.1.2
As user, the GUI will be self explanatory and it will look good	GUI	Daphne	Daphne	**21**	B.2
	- CSS styling		Daphne	4	B.2.1
	- Add zooming buttons on screen/ make scrollable, this means refactoring several classes		Daphne, Ties	8	B.2.2
	- Fix legenda		Daphne	4	B.2.3
	- Give user possibility to select own gfa-file		Daphne	1	C
	- give user possibility to select own nwk-file		Daphne	1	C
	- Loading indication		Daphne	1	B.2.4
	- Fix small bug in interaction list		Daphne	1	
As a user, I want to see all the available data for a genome	Elaborate the metadata-parser	Arthur	Arthur	2	B.3
	Write the annotations parser	Niels	Niels	1	B.4
	- Make information available for user		Niels	8	B.4.1
	Controller testing	Niels	Niels	15	C
	GUI testing	Ricardo	Ricardo	15	C