Sprint Backlog, Iteration #3		ends 09:00,13-05-2016	Ricardo, Niek, Arthur, Daphne absent from 10-05-2016 till 14-05-2016			
Context group: DART-N						
Group: PL 4						
User Story	**Task**	**Member responsible for task**	**Member assig**	**Estimated Effo**	**Priority**	
When the user opens a DNA sequence, the phylogenetic tree will be shown	Phylogenetic tree Visualize the phylogenetic tree	Niek	Niek, Ties	12	A.2	
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	A.1	
	Visualize the zooming levels		Daphne			
	Create an initial ribbon structure		Niels, Daphne			
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, Ricard	12	B.1	
When the user opens the tool, there will be three views: Phylogenetic tree, indication of position and sequen	Window View Integrate the phylogentic tree, graph and zoombox	Ties	Ties, Niels	12	B.2	
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 funtionality, such loading a graph, resetting the view or showing the phylogenetic tree	Daphne	Daphne, Niels	8	C.1	
As a software engineer, I want to the code to look clean, to be readable, properly packages and free of any checkstyle or findbugs errors.	Code cleanup All unrelated code is in different packages There are no checkstyle or findbug errors	Ricardo	Ricardo, Arthur	12	C.2	
When a team member reviews the code, tests will be written and passed	Testing	Arthur	Everyone	12	C.2	
As a user, I want to wait as little time as possible while using the application.	Code enhancement Rendering enhancement	Arthur	Arthur	10	D.1	