TI2806 Contextproject

EWI/EEMCS
Sprint plan 6

Programming Life Group 4

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Sprint Plan #6					
Programming Life 4					
User story	**Task**	**Task assigned t**	**Estimated number of hours**	**Priority (scale 1-5; low to high)**	**Notes**
As a user, I want to be able to navigate the phylogenetic tree.	Rewrite the phylogenetic tree	Jente & Piet	20	5	Rewrite is necessary to allow zooming, panning and collapsing of subtrees.
	Implement zooming on the phylogenetic tree	Jente & Piet	5	5	
	Implement panning on the phylogenetic tree	Jente & Piet	5	5	
	Implement collapsing of subtrees	Skip & Owen	15	3	
	Implement subtree highlighting	Skip & Owen	15	3	
As a user, I want to be able to put the graph in context of evolutionary relationships through phylogeny, so I can see more of the phylogeny of my DNA samples.	Implement dynamic freeing of memory space for ModelItem	Skip & Piet & Gerlof	10	4	This is necessary to increase performance
	Implement additional clustering and filtering constraints for ModelItem	Owen & Piet & Gerlof	20	4	
	Identify source strains in the strain view	Jente & Gerlof	15	5	
	Highlight and filter identified strains, bidirectional (strain view <-> pylogenetic view)	Jente & Gerlof	20	5	
As a user, I want to know to which annotations a sequence belongs.	Parse and store annotation data	Piet & Skip	15	4	
	Research how to operate on the annotation data	Owen & Skip	10	4	Ensure we have a clear vision on how we are going to implement this. UML required.
As a user, I want to have annotations and other metadata visible as a second map into the strain view	Update and extend the property pane	Owen	8	3	
	Make the animations generic	Owen	6	1	
Justification of priorities					
It is important to start adding new features and extend existing ones in this sprint. The customer indicated that they do not find the application to be very usable or useful at the moment. The customer mentioned that the representation of the strain data lacks the necessary visualized information to be regarded as something useful that may be used in actual research. Therefore this sprint we will be focusing primarily on improving interactiveness, usability and furthermore lay down the foundation for visualizing gene annotations.					