

Sprint Retrospective, Iteration 7						
Context Project: Programming Life						
Group: PL-2 (Pantzerfaust)						
User story	Task	Assignee	Estimated effort (hours)	Actual effort (hours)	Done (Yes/No/Partly)	Notes
As a client, I want an organized and maintainable codebase, so that future changes require less hours	Refactor Semantic Zoom GUI	Faris	10.0	8.0	Yes	This was easier than expected
	Test Semantic Zoom GUI components	Faris	10.0	8.0	Partly	Some gui components are unreasonably hard to test, so these aren't tested
	Refactor Semantic Zoom Bubbles	Casper	10.0	10.0	Yes	
	Test Semantic Zoom Bubble components	Casper	10.0	5.0	Partly	Only the shared classes are untested, the core is tested
As a user, I want explicit highlight of mutational structures to better understand the data	Highlight convergent evolution	Wouter	10.0	10.0	No	This proved too complex to calculate, so another approach has to be taken.
	Implement/Integrate more mutation bubbles (indel, point mutation)	Wouter & Cas	15.0	Cas - 3.0 Wouter - 10.0	Yes	
	Finish indel/point mutation bubble algorithm	Cas	5.0	10.0	Yes	Took more time than expected
	Create formal algorithm definition for bubble algorithms	Wouter	5.0	5.0	Yes	
	Implement bubble comparison	Casper	5.0	0	No	We decided not to implement this, because it doesn't have added value
	Port phylogenetic algorithm to normal grouping algorithm (with toggle feature)	Casper	15.0	8.0	Partly	It's not done yet, but there is progress.
	Enable GUI to draw bubble with comparison	Faris	5.0	5.0	Yes	
As a user, I want an intuitive and finished GUI, so that I can clearly navigate and reach all functionality of the application	Refine search functionality and improve interface	Justin	10.0	12.0	yes	
	Implement 'Jump to Base position' as specified by customers	Justin	7.0	2(faris) 1 (justin)	Partly	Jump to base now jumps to a numeral offset. The customer would like to be able to jump by means of giving a name of a (genome) annotation.
	Make bubbles fade fully when zoomed in far enough	Faris	1.0	0.5	Yes	
	Add Sequences to nodes so they can be viewed	Justin	2.0	2.0	yes	
	Parse and test gene annotation file and potentially extend gfa parser	Cas	3.0	3.5	Yes	

	Implement gene annotations in highlighting	Cas	10.0	6.0	Yes	This was done by Faris
As a customer, I require documentation to monitor the development process	Update Architecture Design	Wouter	4.0	0.0	No	Miscommunication in the team caused a delay
As a user, I want to see metadata when I select a node in the graph	implement metadata on nodes	Justin	7.0	4.0	partly	Changes have been made that prevented original plan for this task. Further changes have been made that make this task easier but is not finished for this sprint.
	Implement metadata on Bubbles	Justin	4.0	4.0	partly	See above, same problem.
As a user, I want a bug-free application when I buy something	Fix split-graphs bug for edge pruning	Wouter	3.0	5.0	Yes	Bug was deeper than originally expected
	Fix graph comparison and node selection in phylo tree	Faris	6.0	4.0	Yes	
	Fix phylo subtree generation	Casper	3.0	3.0	Yes	
As a customer, I want an application that is easy to use	Setup User test experiment	Cas	10.0	10.0	Yes	
As a customer, I want to have a weekly demo to see the progress of my product	Prepare a presentation	Cas	2.0	2.0	Yes	
		Motivate any adjustments that will be made for the next Sprint.				
Communication was not always good						
Description: some things like the annotation parser have been implemented twice	Integrating phylo bubbles with other bubble types (straight sequence/point mutations/indels)					
Reaction: We discussed this with the people responsible such that this will not happen again	Integrating the phylo bubbles with the other bubble types caused problems, which took quite some time to resolve. Because of this, other tasks that were scheduled weren't finished.					
Problem ...						
Description:						
Reaction:						