

User story	Task	Groupmember responsible	Assignee	Estimated effort (hours)	Priority (1 low - 5 high)
As a user, I must be able to see the whole graph in the upper-most view.	Show the amount of difference between bubbles in graphs	Cas	Cas	8.0	4
	Create 'random' bubbles to be able to show top level overview	Cas	Cas & Casper	10	3
	Modify the data containers of the current graph comparison algorithm, so further calculates can be done on the graph	Faris	Faris	2.0	5
As a user, I want to load my data in an instantaneous manner	Design persistent database structure to store the 'default' representation of the graph	Justin	Justin & Wouter	8.0	5
	Setup Streaming Framework to support streamed parsing	Justin	Justin	4.0	5
	Design API and queries to provide to the GUI	Wouter	Wouter	8.0	3
	Profiling and Performance Improvement	Justin	Justin & Wouter	12.0	3
As a user, I must be able to zoom in into the bubbles	Finish zooming algorithm for bubbles	Casper	Casper	8.0	5
	Refactor code relate to filtering/zooming bubbles	Casper	Casper	8.0	3
As a user, I want to be able to see the phylogenetic tree next to the graph so I know which genomes I am comparing.	Create a better transition from the tree to the graph. The tree should still be visible when viewing the graph, so the user can see what is being compared in the graph.	Faris	Faris	4.0	2
As a user, I want to be able to easily distinguish edges containing many genomes from edges containing few genomes	Make the thickness of the edges containing many genome paths thicker than the edges containing few genome paths.	Faris	Faris	1.5	4
As a user ,I want to be able to distinguish nodes containing many bases (ATGCs) from nodes containing few bases	Make the nodes containing many bases bigger than the nodes which contain few bases.	Faris	Faris	1.5	4
As a user, I want to be able to compare any pair (or set) of random genomes which I can select in the graph	Make it possible to select an arbitrary set of nodes to compare	Faris	Faris	3.0	3
As a user, I want to be able to see the evolutionary distance between different children in the phylogenetic tree	Use the edge length of the phylogenetic tree in the user interface.	Faris	Faris	4.0	3
As a developer, I want to get an accurate analysis of my code	Exclude 3rd party code from analysis tools	Wouter	Wouter	1.0	1