

User Story	Task	Assigned To	Estimated effort (1-5) 5 = highest	Priority (1-5) 1 = highest	Actual effort (in hours)	Done	Done by	Actual outcome
<i>As an user, I want to be informed about how many genomes follow a certain path in the graph, so I can estimate the interestingness of the edge and the connected nodes.</i>	Compute the set of genomes in edges	Boris	2	2	5	Y	Boris	
	Change the edge width, accordingly to the number of genomes in the edge.	Boris	1	4	5	Y	Boris	
<i>As an user, I want to see what parts of the graph are interesting, so I can zoom in on these parts which are most interesting to me.</i>	Compute the interestingness of each part of the graph.	Sam	3	2	3	Y	Sam	
	Reduce the interestingness of nodes with a high percentage of 'N' data.	Sam	2	5	1	Y	Sam	
	Increase the interestingness which nodes contain genes, with an amount depending on the interestingness of the gene.	Tom	2	5	3	Y	Tom	
	Compute the interestingness of each node with the currently implemented methods.	Sam	1	2	3	Y	Sam	
	Display the interestingness of parts on the scroll bar.	Boris	3	2	5	Y	Boris	
<i>As an user, I want to get information about the system, so I can use the system in full extend.</i>	Add a help button to the top toolbar which gives a popdown menu with a hotkey and info/help button.	Kasper	1	4	6	Y	Kasper	
	Add functionality to the hotkey button, showing all hotkeys available for this application.	Kasper	2	4	2	Y	Kasper	
	Add functionality to the info/help button, displaying info about the product.	Kasper	2	4	2	Y	Kasper	
<i>As a developer, I want to ensure maintainability, so I can continue working on the project without changing/fixing existing code.</i>	Write tests for the GUI	Kasper	5	5	6	Y	Kasper	Some GUI elements were skipped because of the planned MVC fix.
	Add the project its hierarchy to the pom file.	Tom	3	5	0	N		Decided not to do this as it doesn't make sense, our app isn't modular
	Refractor package names from tudelft.* to nl.tudelft.*	Sam	1	4		N		This will be delayed to a more quiet moment, because this will cause a lot of merge conflicts.
<i>As an user, I want to have visual information of how the genomes are connected, so I can visually understand how the graph is constructed.</i>	Locate the currently selected node by a mouseover.	Mathieu	2	1	6	Y	Mathieu	
	Colour edges which contain a genome of the node which is currently selected by a mouseover.	Mathieu	2	5	0	N		This is forwarded to the next sprint.
<i>As an user, I want to load a chosen graph, so I can view the chosen graph.</i>	Combine the edge, node and nwk tree file selection into a single file selection.	Tom	2	5	5	Y	Tom	
	Display last x opened files as a quick load option.	Kasper	3	5	5	Y		
<i>As a stakeholder, I want to run the current stable build of the project, so I can review the progress on the product.</i>	Automatically generate jar files when a pull request is pulled/merged to the master.	Tom	3	3	5	Y	Tom	
<i>Fix</i>	Check if double edges are filtered correctly	Sam	1	1	1	Y		

As an user, I want to refer to the software with a professional name, so that people understand where I'm talking about.	Choose a project name and apply it in the pom file, readme, window title, project title, etc.	Tom (all)	1	1	2	Y	Tom	
As a user, I want to filter my data on certain subset of genomes, so that I can filter out irrelevant information.	Combine horizontal wrap-able nodes on the lowest layer into DataNode Wrappers, so that they can't be unfolded.	Sam	2	2	2	Y	Sam	
As a user, I want to navigate through the graph, so I can search for interesting positions.	Add buttons in the top toolbar for moving left and right, as if you are using the left and right arrow keys.	Kasper	1	5	1	Y	Kasper	
	Move the graph with dragging the screen to the left and right with the mouse	Sam	3	5	0	N		We decided that we didn't want this. The scroll bar and arrow keys will be sufficient.
	Make the reset button center your view to the center of the graph, and use the same position when you just loaded the screen	Mathieu	3	4	1	Y	Boris	
	Limit the view center within the domain of the graph.	Boris	2	5	1	Y	Boris	
	Add a hotkey for the reset button.	Kasper	1	3	1	Y	Kasper	R now resets the view
	Fix: Always have a node present at the beginning and the end of the graph, to solve the GraphStream issue where zooming changes the size of the graph.	Boris	2	1	1	Y	Mathieu, Sam	
As an user, I want to view information of individual displayed nodes in the graph, because I want to see what data is contained in a node.	Display a window on mouseover, which is able to display information.	Mathieu	3	2	8	Y	Mathieu	
	Display information about the node in the mouse-over-window.	Mathieu	2	2	6	Y	Mathieu	
	Display information about which genes are located on the selected node in the mouse-over-window.	Mathieu	2	2	2	Y	Mathieu	
As an user, I want to use this program with different screen sizes, so that I can use this program on any monitor.	Fix: Screen & graph rescale when the screen size changes. Ensure that the graph fits on the screen.	Tom	2	3	4	Y	Tom	
As an user, I want to have a visual representation of genes on the graph, so I can visually understand where genes are located.	Display where genes are located, with lines displaying the domains of genes.	Boris	3	2	0	N		
As an user, I want to have a clear semantic zoom, so I have only valuable information on the screen.	Optimising spacing nodes	Sam	3	2	5	Y	Sam	It is optimised as planned, but the planned optimisations were not sufficient to make the graph more readable, and will be continued next sprint
As a user, I want to be able to load large graphs, so that I can research on many genomes.	Fix/search for - problem with 671+ strains	Boris (Tom)	2	2	1	N	Tom	Some problems have been found, but are not yet fixed.