User Story	Task	Assigned To	Estimated effort (1-5) 5 = highest	Priority (1-5) 1 = highest
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.	Compute the set of genomes in edges	Boris	2	2
	Change the edge width, accordingly to the number of genomes in the edge.	Boris	1	4
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.	Compute the interestingness of each part of the graph.	Sam	3	2
	Reduce the interestingness of nodes with a high percentage of 'N' data.	Sam	2	5
	Increase the interestingness which nodes contain genes, with an amount depending on the interestingness of the gene.	Tom	2	5
	Compute the interestingness of each node with the currently implemented methods.	Sam	1	2
	Display the interestingness of parts on the scroll bar.	Boris	3	2
As an user, I want to get information about the system, so I can use the system in full extend.	Add a help button to the top toolbar which gives a popdown menu with a hotkey and info/help button.	Kasper	1	4
	Add functionality to the hotkey button, showing all hotkeys available for this application.	Kasper	2	4
	Add functionality to the info/help button, displaying info about the product.	Kasper	2	4
As a developer, I want to ensure maintainability, so I can continue working on the project without changing/fixing existing code.	Write tests for the GUI	Kasper	5	5
	Add the project its hierarchy to the pom file.	Tom	3	5
	Refractor package names from tudelft.* to nl.tudelft.*	Sam	1	4

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.	Locate the currently selected node by a mouseover.	Mathieu	2	1
	Colour edges which contain a genome of the node which is currently selected by a mouseover.	Mathieu	2	5
As an user, I want to load a chosen graph, so I can view the chosen graph.	Combine the edge, node and nwk tree file selection into a single file selection.	Tom	2	5
	Display last x opened files as a quick load option.	Kapser	3	5
As a stakeholder, I want to run the current stable build of the project, so I can review the progress on the product.	Automatically generate jar files when a pull request is pulled/merged to the master.	Tom	3	3
Fix	Check if double edges are filtered correctly	Sam	1	1
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
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
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
	Move the graph with dragging the screen to the left and right with the mouse	Sam	3	5
	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
	Limit the view center within the domain of the graph.	Boris	2	4
	Add a hotkey for the reset button.	Kasper	1	3

	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
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
	Display information about the node in the mouse-over-window.	Mathieu	2	2
	Display information about which genes are located on the selected node in the mouse-over-window.	Mathieu	2	2
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
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	5
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
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