Because testing the GUI turned out to be a very time-consuming and tough task we defined the following method to test the GUI elements of our software. Before releasing GUI-related branches we will create user stories to test the feature added.

Main

Pass/Fail	User story
Pass	As a user, When I start the application, And I have not yet done anything, I should be able to choose a gfa file to load into the application.
Pass	As a user, When I am viewing the graph, I should be able to pan through the graph.
Pass	As a user, When I am viewing the graph, The graph should not cover the toolbar.
Pass	As a user, When I am viewing the graph, I should be able to zoom in and out of the graph.
Pass	As a user, When I am zooming in or out of the graph, SNPs should be semantically put together..
Pass	As a user, When I am zooming in or out of the graph, The application should zoom in or out of the centre of what is on screen right now, Or where my mouse is.
Pass	As a user, When I am fully zoomed into the genome, I should be able to zoom out again.
Pass	As a user, When I am viewing the graph, I should be able to gain more information on nodes by clicking them.
Pass	As a user, When viewing a graph, I want visual feedback on the name of the graph

Pass	As a user, When viewing the title of a graph, And opening a new graph, I do not want the name of the old graph in the new title.
Pass	As a user, When opening the application, I do not want to be able to press buttons that cause exceptions.
Pass	As a user, When viewing the graph, And the nodes in it, There should be visual feedback on the length of the sequence in the node.
Pass	As a user, When zooming through the graph, The edge thickness should be updated accordingly.
Pass	As a user, When viewing the graph, The thickness of the edge should represent the amount of genomes going through it.
Pass	As a user, When loading the graph, I want visual feedback on if the application hasn't crashed.
Pass	As a user, When using the application, I want database corruption, And other database exceptions, To be handled in a user-friendly manner.
Fail	As a user, When running the application, I want it to consistently not crash when loading a new file.

Centre Node and radius

Pass	As a user, When I load a gfa file into the application, I should be able to choose a centre node and radius to be displayed.
Pass	As a user, When I am viewing the graph, I should be able to dynamically change the centre node and radius.
Pass	As a user, When I am zooming in the graph, I want the radius to update dynamically.
Pass	As a user, When I am zooming in the graph, I want the centre node to update dynamically.
Pass	As a user, When a graph has been loaded, I should always be able to use the Go-To Node function.

Bookmarks

Pass/Fail	User Stories
Pass	As a user, When I create a bookmark I want all other bookmarks to make room for the new one.
Pass	As a user, When I create a bookmark, I want to press the bookmark to go to that position.
Pass	As a user, When I create a bookmark, And I close and reopen the application I want my bookmark to still be present.
Pass	As a user, When I create a bookmark for a genome And I open a different genome after that, I do not want to see that bookmark And I should see the bookmarks of that genome.
Pass	As a user, When I use bookmarks, I want it to be functional
Pass	As a user, When I use bookmarks, I want it to look good
Pass	As a user, When viewing a file with bookmarks, And choosing a new file to view And that file has no bookmarks I want to not see the old bookmarks.

File Explorer

Pass/Fail	User Stories
Pass	As a user, When I want to choose a file, I want to only see gfa/gff files.
Pass	As a user, When I want to choose a file, I want the file explorer to open at a logical place.
Pass	As a user, When I want to choose a file for the second time, I want the file explorer to open in the parent directory of the first file.

Recent files

Pass/Fail	User Stories
Pass	As a user, When I open a gfa file, And I open a different gfa file, I want to have quick access to the first file.
Pass	As a user, When I open a new gfa file, I want it to be dynamically added to my recent files.
Pass	As a user, When I open a gfa file using the recent menu, All bookmarks should be shown correctly, And all information should be updated.
Pass	As a user, When I press on a undefined file in the recent menu, I want it to handle the exception in a user-friendly way.
Pass	As a user, When I press on a gfa file using the recent menu, I should be able to view the graph as normal.
Pass	As a user, When I choose a file from the recent list, It should be added to the top of the list.
Pass	As a user, When using recent files a lot, And also opening files normally I do not want duplicate files in my recent files
Pass	As a user, When pressing on a recent file, And when opening a file already in recent files, I want the most recently opened file at the top of the list With no duplicates in the list.

Genomes

Pass/Fail	User Stories
Pass	As a user, When viewing the graph, I want to be able to choose genomes to view in different colours.
Pass	As a user, When viewing the graph with chosen genomes, I want the genomes to be different colours from one and other.
Pass	As a user, When viewing the graph with chosen genomes, I want to be able to have a different option than rainbow view.
Fail	As a user, When viewing the graph with chosen genomes, I want to see the same colours going over edges, Even if those edges are 'dummy nodes'.
Pass	As a user, When viewing the graph with chosen genomes, I want to see the same colours going over edges.
Pass	As a user, When choosing genomes to view, I want to text search through the genomes.
Pass	As a user, When choosing genomes to view, I want to be able to quickly select all genomes.
Pass	As a user, When choosing genomes to view, When I save my genome view, I want to be able to quickly acces it later.
Pass	As a user, When choosing genomes to view, I want to be able to cancel changing my selection.
Fail	As a user, When choosing genomes to view, When I save an empty genome view, It should not be added to my genome bookmarks

Annotations

Pass/Fail	User Stories
Pass	As a user, When viewing annotations, I want the annotations to have different colours.
Pass	As a user, When viewing annotations, I want annotations to be clickable, To see their information.
Pass	As a user, When viewing annotations, I want annotations to have as few overlappings as possible.
Pass	As a user, When viewing annotations I want the graph to be as quick and smooth as before.