

Backlog v0.1 Programming Life

User stories

1 Starting the program

1.1 Starting the program

As a user, I want a GUI, so that I can use it like a “normal” application

When I start the program

Then a new window is opened for the program

And there is a simple instruction on how to open files in the main area*

* something like: “choose “file → open” in the top left corner to open a file”.

1.2 Opening files: user initiates opening

As a user, I want to open a .gfa file, so that I can use the program

When I open a file with file → open

Then a “loading” dialog box appears* while the file is being parsed and processed

And the file starts being parsed and processed

And opened in the main view

* with a message about what is loading (“opening [filename].[extension]”), possibly with “cancel” button

1.3 Opening files: correct file

As a user, I want opened files to open, so that I can use the program

When opening a file (see 1.2)

And the file is formatted correctly

When the file is done parsing and processing

Then the “loading” dialog box is closed

And the graph is displayed in the “top-level” view*

* as zoomed out as possible.

1.4 Opening files: Incorrect file

As a user, I want an error message when opening incorrect files, so that I know why it won’t open

When opening a file (see 1.2)

And the file is not formatted correctly

Then a dialog box describing the error is shown (with line number if it is a text file, and possibly suggested fixes)

2 Using the program

Note: priorities are not yet decided as we don't have a good idea which of these is most important.

Zooming in

As a user, I want to be able to zoom in on part of the graph, so I can see the details.
When zooming in the separate nodes should become bigger
and the nodes should move away from each other to still keep the correct distance

Zooming out

As a user I want to be able to zoom out to get better overview of the graph
When zooming out nodes should become smaller
and get closer together to fit more nodes in the screen

Add a bookmark

As a user, I want to make bookmarks on the graph, so that I can easily find a place I was working on
When I have opened a graph (see 1.3)
And I <do the thing (to be decided)>
Then a bookmark is created (which is visualized how?)

Going to a bookmark

As a user, I want to go a bookmark someone made previously, so that I can easily find that place.

- mark a gene (begin, end, genome(s), name, description)
- Find mutations (with mutation type)
- select a genome
- Edit a graph?
- Searching: show a list that can be filtered
 - for bookmarks
 - for genes
 - for (sub)sequences

3 saving information

- export bookmarks / genes / mutations

- create cache (so that less processing needs to be done when opening later)
- save subset of graph (to load faster)

4 closing the program

- dialog box when unsaved changes

