

Sprint Backlog, Iteration #8

| User Story | Task | Member responsible for the task | Task Assigned To | Estimated Effort per Task (in hours) | Actual Effort per Task (in hours) | Priority (A—E) (A is highest) | Done (yes/no) | Notes |
|--|---|---------------------------------|------------------|--------------------------------------|-----------------------------------|-------------------------------|---------------|---|
| As a user I want to be able to load and examine the 328 genomes set | Improve performance of application so that it loads the 328 genomes dataset. | Björn | Björn, Hugo | 13 | 15 | B | no | See problem #1 |
| As a user, I want to have visual encodings for different classes of mutations and the ability to filter on mutation class | Implement the ability to highlight snips in the gui. Snips should be colored according to their normal colouring, whereas the rest of the graph should be colored black/grey. | Daniel | Daniel, Björn | 10 | 12 | A | yes | Referenced in problem #5 |
| | Implement the ability to filter on indels in the gui. Indels should be colored according to their normal colouring, whereas the rest of the graph should be colored black/grey. | Evan | Evan | 6 | 6 | B | yes | |
| As a user, I want the application to load smoothly without it appearing to freeze. | Include the graph loading into the loading bar so that the loading progress can be fully followed. Also verify what values of the progressbar should be used for which part of the loading. | Björn | Björn | 10 | 11 | A | yes | |
| As a user, I want the graph nodes to be correctly displayed when zooming in | Fix the horizontal lines bug so that the graph is correctly displayed when fully zoomed in (like in release 7.0.2) | Rob | Rob | 12 | 13 | A | yes | |
| As a developer, I want to have clear and understandable code in the ribbon view/controller | Remove the GraphController and graph tab and place the ribbon view and graph view in separate files. | Daniël | Daniël | 8 | 8 | A | no | This task was almost finished but could not be completed due to some problems working concurrently on the exact same parts of the code. |
| As a user I want to select certain genomes based on certain criteria found in the metadata.xlsx file | Implement filtering on metadata in the phylogenetic tree. | Hugo | Hugo | 16 | 6 | B | no | |
| As a user, I want to be able to search on annotation and go to the location of the found annotation. | Implement search box in the gui for the annotations. | Hugo | Björn, Hugo | 9 | 1 | C | no | |
| As a user, I want to at which node of the graph an annotation starts and at which node it ends. This should be visible using edges to the start and end, when the annotation is clicked. | Implement edges between the annotations and nodes when the annotations are clicked. | Daniël | Daniël | 15 | 1 | B | no | See Problem #5 |
| As a user, I want to have a correct and clear annotation view | Fix the inreadability of the annotations when zooming out and make sure the annotations match the alignment of the graph. | Rob | Rob | 11 | 0 | B | no | See Problem #2 |
| As a user, I want the ribbon view to have the right colours | Determine graph lineage colour by majority vote, instead of top genome | Evan | Evan | 7 | 8 | B | yes | |
| As a user, I don't want to have any bugs while executing the program | Fix the bug that the nodes were unreadable in the TB328 file | Rob | Rob | 5 | 6 | A | yes | |
| | Fix the bug that the graph view isn't using the full vertical distance | Rob | Rob | 6 | 5 | A | yes | |
| As the client i want to see a presentation and demo every week to keep me up to date with how the project is progressing. | Create, practice, and present the client meeting presentation. | Evan | Evan | 3 | 2 | C | yes | |
| As the client I want to be able to view the Architecture design document and understand the design of the project | Update the Architecture Design Document to be current with the projects architecture | Evan | Evan | 4 | 2 | D | yes | |
| As the coordinator, I want to have a good understanding what the programmers did | Write the draft for the final report | Evan | Evan | 6 | 6 | C | yes | |

Problems

Problem #1: Optimization

Description: Improving the performance for the 328 genomes data set turned out to be very difficult. We tried all methods we could think of and have researched different approaches. In the end, nothing seemed to improve the performance.

Solution: We did not improve the performance but we managed to run the TB328 by pre processing the TB328 on a computer and ran it for 12 hour

Problem #2: Annotation inreadability

Description: There was no time left to fix the annotation inreadability, because the bugs that were discovered (which had greater priority) were fixed first

Solution: We should have reserved time for fixing existing bugs in the sprint plan, that can have a higher priority than the feature

Problem #3: Metadata selection

Description: There was no time for selecting certain genomes based on the criteria found in the metadata.xlsx file. More important things had to be done, such as detecting mutations, fixing the NewickTree, being able to show the 328 genomes, writing the Interaction Design document and writing the final draft document.

Solution: The time planned for this was instead spent on the more important issues named the problem description. The task itself is of lesser importance, but it will be finished if there is time before wednesday.

Problem #4: Annotation search

Description: There was no time to look at this feature.

Solution: See solution of #3

Problem #5: Annotation edges

Description: After researching the possibilities to implement edges from the annotations to the corresponding start and end nodes, it became clear that this would not be possible without refactoring large parts of the annotations.

Solution Given the available time, we decided to drop this task. The person assigned to it, Daniël, replaced this task with work on the indel/snp highlighting and on creating information popups. To prevent this sort of problem in the future, we will research the possibilities before creating a task.