

| Sprint Retrospective, Iteration 6   |  |              |                          |                           |                      |   |
|---|--|--------------|--------------------------|---------------------------|----------------------|---|
| Context Project: Programming Life   |  |              |                          |                           |                      |   |
| Group: PL-2 (Pantzerfaust)  |  |              |                          |                           |                      |   |
|   |  |              |                          |                           |                      |   |
| User story  | Task   | Assignee     | Estimated effort (hours) | Actual effort (hours)     | Done (Yes/No/Partly) | Notes   |
| As a user I want to be able to zoom in and out, to choose the level of detail that I see                          | Add (semantic) zooming through scrolling   | Faris        | 8.0                      | 20.0                      | yes                  | The amount of hours spent should be self-explanatory.   |
|   | Modify Bubbles to work in alignment algorithm  | Faris        | 12.0                     | 30.0                      | yes                  | There were a lot more bugs in the bubbling algorithms than expected   |
|   | Refactor and Test PhyloBubbles   | Casper       | 8.0                      | 8.0                       | partly               | There is still some refactoring to be done  |
|   | Modify Bubble data types to accomodate for new bubbles and their needs   | Casper       | 12.0                     | 10.0                      | yes                  | -   |
|   | Create custom phylo trees that show only nodes currently in the graph, so the bubbling algorithm can use the a correct phylogenetic tree for any set of selected genomes | Casper       | 7.0                      | 5.0                       | yes                  | -   |
|   | Create bubble for distinct genome paths through the graph, because sleeping more than a few hours per week is not appreciated by Thomas                                  | Wouter       | 10.0                     | 0.0                       | no                   | This ended up unnecessary when less 'random' bubbles were implemented.  |
|   | Highlight convergent evolution somehow   | Wouter       | 10.0                     | 1.0                       | no                   | This could not be done because debugging and trying to integrate the Mutation Bubbles took much more time   |
| As a user, I want to be able to distinguish elements in the graph, such as mutations                              | Integrate Mutation Bubbles   | Wouter & Cas | 10.0                     | Wouter - 20.0, Cas - 10.0 | yes                  | Required more time than expected. Contrary to the expectation, the code for this was nowhere near ready. Additionally, bugs in the GUI caused false positives for bugs in this code, costing extra hours of debugging |
| As a user I want to be able to run the program with minimal resources   | Integrate Genome Mapping   | Wouter       | 2.0                      | 3.0                       | yes                  | A few more complex tests had to be rewritten, which caused slight delay   |
| As a user I want to query the data to easily navigate   | Add an option to search for genomes  | Justin       | 8.0                      | 12.0                      | yes                  | More complex than expected, but provides strong basis for other things (i.e. info about genomes, highlighting)  |
| As a User I want to be able to look up genomes with a certain property in their metadata to easily group genomes. | Highlight genomes according to metadata  | Justin       | 8.0                      | 1.0 Faris, 8.0 Justin     | yes                  | Highlight is possible with search   |

|   |  |              |      |                         |     |  |
|---|--|--------------|------|-------------------------|-----|--|
| As a User I want to be able to see stats about genomes by selecting them in the graph to better understand what is on the screen. | Show annotations in more versatile ways, including a way to see difference between two nodes / genomes / elements                                      | Justin       | 8.0  | 1                       | no  | There was no basis for properly selecting multiple genomes. Other tasks had higher priority and took more time.  |
| As a user I need a well-designed GUI to know what I am doing  | Implement a minimap of the graph (and tree) to distinguish where you are in the data   | Cas          | 12.0 | 0.0                     | no  | This ended up unnecessary because the overview is already good   |
|   | Implement a legend/popup to explain color coding and other annotations   | Justin       | 12.0 | 6.0                     | yes | Legend is implemented, but doesn't include all info. This was not stable until very late. This can now be easily added.                                |
|   | Adjust the vertical position of nodes in the graph to better fit the customer needs (as was explained in the meeting with the Programming Life group). | Faris        | 4.0  | 8.0                     | yes | Contained more complexity than initially expected  |
| As a developer, I need good documentation   | #62 Let PMD errors be equally generated by the build and the site  | Wouter       | 1.0  | 1.0                     | yes | The cause of this was finally found after 3+ weeks   |
|   | Update the Architecture Design   | Wouter & Cas | 3.0  | Wouter - 3.0, Cas - 1.0 | yes | Lack of time resulted in a version that lacks finishing. The concepts are laid out, but no layout and prettifying has been done yet (such as diagrams) |
| As a customer, I want to have a weekly demo to see the progress of my product   | Prepare a presentation   | Wouter & Cas | 2.0  | Wouter - 2.0, Cas - 1.0 | yes | -  |

|                           |  |   |  |  |  |  |
|---------------------------|--|---|--|--|--|--|
| Main Problems Encountered |  | Adjustments for the next Sprint   |  |  |  |  |
|                           |  | 1. Features will be smaller and more controlled.  |  |  |  |  |
| Problem 1                 | Absence of Team Member   | 2. Generally, no other problems were encountered and no further adjustments need be made.   |  |  |  |  |
| Description:              | Due to absence of one team member, more work had to be done by the other members   |   |  |  |  |  |
| Reaction:                 | The rest slept (even) less   |   |  |  |  |  |
|                           |  | Motivate any adjustments that will be made for the next Sprint.   |  |  |  |  |
| Problem 2                 | Complex feature became detached from the main application  | 1. This adjustment will prevent repetition of problem 2. This is important to remain efficient and spend hours on development rather than trying to empty the ocean with a thimble. |  |  |  |  |
| Description:              | The phylogenetic bubbling algorithm required a lot of work and contained an enormous amount of changes. This caused integration problems at the end of the sprint, losing many hours | 2. All in all, the sprint was completed rather successfully.  |  |  |  |  |
| Reaction:                 | Setting limits in future cases and merging the code in temporary branches.   |   |  |  |  |  |