Sprint Retrospective 8

User Story	Task	Task Assigned To	Estimated Effort per Task *(in hours)*	Actual effort *(in hours)*	Done	Comment
As a user, I want to have mutations visualized	Calculate mutations on the fly	Jeffrey	16	16	Yes	
	Make mutations visible	Matthijs, Jeffrey	6	4	Yes	The visualization of different mutations in the frontend turned out to be one server request, meaning time was saved on programming multiple icons.

	Make sure mutation visibility is based on zoom level	Matthijs, Jeffrey	2	2	Yes	
As a user I want to make sure the program is responsive	Make zooming view draggable	Thomas	8	2	Yes	Both the dragging and zooming provided less complications, as the jittery behaviour of the view turned out to be a rounding error. However, in hindsight, the zooming still needs some improvement (perhaps we did not invest enough time).
	Smooth zooming	Thomas	6	4	Yes	
	Create zoom button as alternative for scroll wheel	Thomas	1	1	Yes	This was trivial.

As a user, I want to be able to search on annotations	Create a search bar for genome features	Thomas	6	6	Yes	
As a user I want to be able to see which ribbon belongs to which genome	Make legend on y coordinates	Matthijs	6	1	different	On monday it was decided that both the Meta- data and legend would be designed differently, and would be implemented using a combination of labels, edge coloring and phylotree annotations. The time invested in this remained about the same as the time planned for the old tasks.
	Show meta-data on mouse over legend	Matthijs	6	0	different	
As a user, I want to have a intuitive way	Change heat map phylogenetic tree	Thomas	3	1	Different	Since we opted to not use a heatmap but

of selecting the genomes from the phylogenetic tree.						instead just change the coloring of the metadata annotations, time was saved on having to implement a heatmap algorithm.
	Create a list view of the selected genomes	Thomas	2	4	Yes	Library used for the phylogenetic tree caused difficulties saving the list data.
As a user, I want to have a clear view of the genome	Make sure x-coordinates are accurate	Matthijs	10	2	Yes	Turned out the existing code was already sufficient and the only change to be made was a recalculation when selecting new genomes had to be made instead of a new algorithm. Extra

					time was spent on improving y-coordinates
	Make minimap clearer	Matthijs	5	5	Yes	
As a user I want the program to be fast, even with large datasets	Finish coupling to database	Youp	12	16	Yes/no (see comment down)	
	Refactor certain classes to better suit the database structure	Youp	15	20	Partially	Several problems came up with the fields of the classes, mainly related to unnormalized data kept in them

	Implement caching algorithm	Youp	8	0	No	Eventually, it turned out that integrating the database caused too much trouble and resulted in a degrading of the performance, meaning the database was abandoned
As a user I want to be able to query the graph to derive useful information.	Come up with a good algorithm to detect convergent evolution.	Kasper	15	15	Yes	
	Implement the algorithm to detect convergent evolution.	Kasper	15	15	Yes	
	Convergent evolution viewing in the GUI.	Kasper	5	0	No	This was deferred in favor of improving our existing product, which

						had a higher priority for our project.

Problem 1

Description: The database proved difficult to integrate in the program, mostly due to the fact that all data is stored in a tree which has to be loaded in its entirety. Moreover, the current largest dataset can be loaded into memory in its entirety without issues, whereas the DB only negatively influenced performance.

Reaction: The database was abandoned, with the responsible team member spending his time on implementing the metadata.

Problem 2

Description: We made design choice changes at the beginning of the sprint.

Reaction: Since most of these decisions not only made the UI better, but also implementation easier, the extra time available was spent on implementing more (and improving existing) functionality (see comments).

Adjustments for the next Sprint

N/A