Sprint Retrospective, Iteration #6

Context Project: Programming Life

Group: Byzantine Generals (PL1)

User Story	Task	Task Assigned To	Esmitated Effort per Task *(in man-hours)*	Actual Effort per Task *(in man-hours)*	Done *(yes/no)*	Notes
As a DNA researcher, I want to highlight specific genomes and lineages So that the subjects I'm interested are distinct	Implement genome highlighting	Adam el Khalki	6	7	yes	
	Implement lineage highlighting	Adam el Khalki	12	12	yes	
As a DNA researcher, I want to have a fast application So that even larger datasets can be analyzed	Increase the performance of the web app	Ali Smesseim	16	15	yes	
	Decrease the memory usage of the server	Ali Smesseim	8	8	yes	
	(Add bubble information to the database)	(Ravi Shivam Autar)	n/a	8	yes	Since the bubbles were implemented this week, it turned out that our previous database was not suited for the bubbles (i.e. only for the individual segments). Hence, this task arised.
As a DNA researcher, I want to be able to quickly navigate to interesting positions So that these positions can easily be found and researched	Implement jumping to specific base	Kamran Tadzjibov	8	3	no	See problem 1
	Implement navigation based on metadata	Ravi Shivam Autar	16	8	no	See problem 1
As a DNA researcher, I want to have semantic zooming So that the information displayed is always relevant	Classify the level of the bubbles	Kamran & Ali	20 + 4	23 + 4	yes	
	Integrate the bubbles into the web app	Adam el Khalki	10	10	yes	
As a DNA researcher, I don't want to see graphical quirks and noises in the graph So that the graph is easier to understand	Remove simple bubbles from the graph	Ravi Shivam Autar	6	7	yes	
	Only zoom horizontally (opt. by selection from minimap)	Ravi Shivam Autar	6	4	yes	
	Base the horizontal distances on segment size	Samuel D. Sital	10	6	partly	The horizontal distances have been altered since last week, but they are not clearly visible. Basing the horizontal distances on the segment size requires a drastic change in positioning, which has been accounted for in the sprint backlog. See problem 2
As a DNA researcher, I want to see the phylogenetic tree and interact with it So that the graph can be interacted with using phylogeny	Integrate the phylogenetic tree into the web app	Samuel D. Sital	6	8	yes	
	Trigger actions (e.g. highlighting) upon proper interactions	Samuel D. Sital	12	14	yes	

Main Problems Encountered

Problem 1

Description:

We didn't fully understand all of the metadata and auxiliary information. That made it hard to implement navigation. Instead of asking the context instructors for clarity, we have decided to put our time into the newly arisen tasks.

Reaction:

We should ask the context instructors questions about the data in the meeting. If any additional questions arise during the sprint, we shouldn't hesitate to send them an email.

Problem 2

Description:

The horizontal distances should be based on the size of the segments, not on the size of the nodes. This was noted in the meeting. We thought the problem could simply be fixed by changing the size of the segments, but this approach resulted in a hardly noticeable change.

Reaction:

We should ask the context instructors questions about the data in the meeting. If any additional questions arise during the sprint, we shouldn't hesitate to send them an email.

Problem 3

Description:

The bubble collapsing algorithm was worked on for three weeks. Since it was not finished until this week, no pull requests were opened for the bubbles, therefore there was no code review. The consequence is that the code quality of the bubble collapser algorithm is not up to standard.

Reaction:

First of all, the problem was that the bubble collapsing took three sprints. Since we have a good base we can work on, we predict that there are no such big tasks any more. Furthermore, if there is such a big task, then it should be split up into multiple tasks, so that at least a part of it can be integrated into the application. Also, the current bubble collapser has to be refactored to improve the code quality.