

Reflection on Iteration #4

Context project: Programming life

Group: 2

User Story #	Task #	Task Assigned To	Estimated Effort	Actual Effort	Done (y/n)	Notes
As a programmer I want our documentation to be up to date so I can see the large lines of the project.	1. Update UML diagrams.	1. Oolbekkink	1. 2	1. 3	1. y	
As a team we want to deliver our deliverables.	1. Deliver Sprintplan5.pdf. 2. Deliver Sprintreflection4.pdf.	1. Nieuwdorp 2. Nieuwdorp	1. 1 2. 1	1. 1 2. 1	1. y 2. y	
As a user I want to see which mutations are present.	1. Display mutations in the graph.	1. Hommes	1. 5	1. 5	1. n	1. No existing solutions found. Has to be done ourselves.
As a user I want to see the genome annotated with information from current sources.	1. Select available sources to use. 2. Transform our current coordinate system into other available coordinate systems so we can find the correct available resources.	1. Nieuwdorp 2. Nieuwdorp	1. 2 2. 3	1. 3 2. 3	1. y 2. n	2. No answer on an email with questions about this topic.
As a user I want to be able to reduce the amount of	1. Select information that needs to be reduced.	1. All	1. 3	1.2	1. y	

information (semantic zooming).						
As a user I want see what genomes I'm currently looking at without losing my current view.	1. Make it possible to switch back to the phylogenetic tree and see your old selection (see user story below). 2. Remember old views until you make a view at the same level. 3. Make it possible to go back to the old views.	1. Vennik 2. Vennik 3. Vennik	1. 2 2. 2 3. 2	1. 2 2. 2 3. 2	1. y 2. y 3. y	Will be an overlay with the tree.
As a user I want to be able to select combine different parts of the phylogenetic tree to view in the graph.	1. Make it possible to select parts from the phylogenetic tree. 2. Make it possible to see your selection (in old control panel space). 3. Create a button to load your selection (in old control panel space).	1. Boot 2. Boot 3. Boot	1. 3 2. 2 3. 2	1. 2 2. 3 3. 2	1. y 2. y 3. y	
As a user I want to learn how to make optimally use the program.	1. Select keys and options (shortcuts) that the user should learn. 2. Count the number of times the user used it. 3. Inform the user after a certain amount of times (with don't show again checkbox checked). 4. Make it possible to revert all don't show again boxes, help the user to start his learning journey again.	1. All 2. Oolbekkink 3. Oolbekkink 4. Oolbekkink	1. 2 2. 3 3. 4 4. 2	1. 2 2. 3 3. 4 4. 2	1. y 2. n 3. n 4. n	2., 3. and 4. Replaced by overview of shortcuts accessible for every point in the program. Efford: 4
As a programmer I want clean code.	1. Refactor the load method in Workspace (long method). 2. Refactor the class GraphController (god class).	1. Oolbekkink 2. Vennik	1. 1 2. 1	1. 1 2. 1	1. y 2. y	

As a user I want to see a good looking message (no dialog) when something goes wrong.	1. Display a message when loading the graph goes wrong (wrong files or files missing).	1. Hommes	1. 3	1. 3	1. y	
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Main Problems Encountered

Problem 1 : Waited on a reply to an email with questions concerning annotations.

We got started on the annotations and we found out that the annotations were not very well documented. (We even found a mistake in the suggested UCSC Table Browser) To get started with this we had to make assumptions that we wanted to have checked by T. Abeel. We send him an email but he hasn't responded yet. We feel that we could use more guidance on the biology aspect of the project to make sure that our program is as valuable as it could be for research environments.

Problem 2 : Mutations couldn't be done this Iteration

We got started on the mutations but we couldn't find any existing solutions for detecting all kinds of mutations so we will have to write those algorithms ourselves. We also couldn't find any papers exactly on that. This is very complex (to do efficient) and this also comes back to problem 1, we feel like more guidance on the biology aspect would be beneficial.

Relection:

We started this iteration with a good sprintplan and a lot of features. Features now become more and more complex and we feel like more guidance on the biology aspect would be helpful. We also haven't received any feedback on our deliverables yet so we aren't really sure if our software engineering approach is compliant to the grading rubrics. We also feel that the draft documents that we made aren't going to help us with our project since we didn't receive any feedback. Still we got to do a lot of work, and during the TA meetings we feel that our project is heading in the right direction.