Contextproject Programming Life Group 2 - GEVATT

Sprint Reflection 3, week 7

TU Delft



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Task	Effort	Assignment	Actual effort	Done	Notes
Show CADD score in patient overview visualization	4	Mathijs	6 hours	Yes	Was a challenge to distill the right information from a function someone else made. QueryProcessor.java and Mutation.java needed refactoring
Show relevant information per chromosome in patient overview visualization	4	Mathijs	1 hour	No	Have not yet found a good way to divide the mutations
Sort mutations per column in patient overview visualization	က	Mathijs	4 hours	Yes	Quite easy one the right third-party library was found
Show a starting point of a mutation in the mutation view	က	Willem Jan	4 hours	No	Need to find external information first
Look if other genes are near the location of a mutation	က	Willem Jan	3 hours	No	Have only made a start, again, external information is needed
Implement database testing	ro	Willem Jan & Ruben	7 hours	o N	Mostly done by Ruben. Have tried using PowerMock, but had trouble with queries returning a ResultSet. Then tried using PowerMock in combination with MockRunner to make a mocked ResultSet, but due to mismatching types this failed. We have decided to create a test database instead of mocking
Make information in the query processor clear (gen vs. protein etc.)	က	Ruben	2 hours	Yes	Changed a few names to match whether a protein or gene was mentioned
Add annotations in the mutation view	8	Ruben	2 hours	Yes	None

Write query to find all interactions in- cluding strengths in a set of proteins Make highlights work in the patient overview page General visualization of protein interac- tion Visualize protein information per node in the mutation view Show strength of relations in the muta- tion view Make a vision about the color usage in the mutation view Look for a way to save retrieved data Even Ruben 3 hours Yes 1 hour No 1 hour No Look for a way to save retrieved data from string database Yes Robbert Yes Tesper Shours Yes Thour No Thour No Thour No Thour No Thour No Thour Thour No Thour Thour No Thour Thour No Thour Thour No Though database	None	Easy once I found out how to use on() in jQuery in combination with hover (or mouseenter and mouseleave in this case)	The basics are done, but after our meeting with the client we discovered they wanted the possibility to click on a protein and inspect the interactions of that protein. This will be done the rest of this sprint as well as next week.	Have put more time in other visualizations to make them more solid	Had to extend the library we use to support different line widths	Have given it some thought, but need to change the query parser to supply the first node	Decided to make separate classes proteine, proteineconnection and proteinegraph to store the data in a way that is easy to use in the visualization.
re query to find all interactions in- ing strengths in a set of proteins e highlights work in the patient view page aral visualization of protein interac- re mutation view view view e a vision about the color usage in to a vision about the color usage in to a vision view to a vision about the color usage in to a vision about the vision abo	Yes	Yes	Yes	No	Yes	No	Yes
ing strengths in a set of proteins e highlights work in the patient view page alize protein information per node e mutation view v strength of relations in the muta- view e a vision about the color usage in mutation view for a way to save retrieved data t string database	3 hours	3 hours	25 hours	2 hours	3 hours	1 hour	3 hours
e query to find all interactions ining strengths in a set of proteins e highlights work in the patient view page alize protein information per node le mutation view view e a vision about the color usage in mutation view for a way to save retrieved data string database	Ruben	Ruben	Jasper	Jasper	Jasper	Jasper	Robbert
Write query to find all interactions including strengths in a set of proteins Make highlights work in the patient overview page General visualization of protein interaction Visualize protein information per node in the mutation view Show strength of relations in the mutation view Make a vision about the color usage in the mutation view Look for a way to save retrieved data from string database	ಣ	ಣ	10	ಬ	က	2	2
	Write query to find all interactions including strengths in a set of proteins	Make highlights work in the patient overview page	General visualization of protein interaction	Visualize protein information per node in the mutation view	Show strength of relations in the mutation view	Make a vision about the color usage in the mutation view	Look for a way to save retrieved data from string database

Repair the Jenkins server	6	Robbert	4 hours	Yes	Used google to search for solutions, but found out an error had occurred in the workspace on the server. This could be restored by wiping out the repository once. Also used the time to add the surefire plug in to the project and put the test result trend on the project page.
Re-factor parsing protein relation data	4	Robbert	6 hours	Yes	Rewritten the parser for protein data from the database and written some new classes for proteins.
Extend parser for protein graph (connections with other connections)	က	Robbert	3 hours	No	Started to extend, but has yet to be finished.

General Reflection

After comments we received about not using Git the way it was supposed to be used, e.g. with branches, we decided to make a couple of branches so we could develop in parallel. However, prior to our meeting with the client on Wednesday we merged our branches in order to have the full functionality. These merges broke our application in several places, and Willem Jan spent most of his time fixing these. At the moment, everything has been repaired and we are fully functional again. Besides the merging slowing us down, we (and the other Programming Life group with the same project) had a lot of trouble logging in to STRING, CADD and dbSNP because of too many open connections. It turns out we were somehow causing these, resulting in a whopping 750 open connections, basically making it near impossible to access the databases with our credentials. Again, mainly Willem Jan has been working to fix this. We are still unsure how this happened as we are using try-with-resources, but at least it is back to normal.

We have also realized this week that the visualizations take more time than expected. This is mostly because we either have to make them ourselves, or need to find libraries which may or may not have to be extended.