

TI2806 Contextproject

EWI/EEMCS

Sprint plan 5

Programming Life Group 4

May 22, 2015



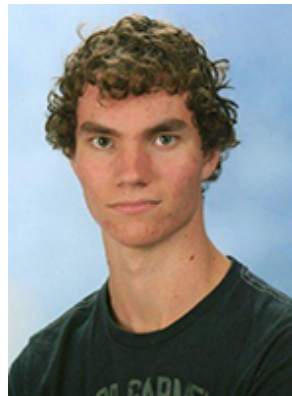
Owen Huang
ohuang 4317459



Gerlof Fokkema
gfokkema 4257286



Jente Hidskes
jhidskes 4335732



Piet van Agtmaal
pvanagtmaal 4321278



Skip Lentz
smlentz 4334051

Sprint Plan #5

Programming Life 4

| User story | Task | Task assigned to | Estimated number of hours | Priority (scale 1-5; low to high) | Notes |
|--|--|----------------------------|---------------------------|-----------------------------------|-----------------------------------|
| As a user, I want to be able to put the graph in context of evolutionary relationships through phylogeny, so I can see more of the phylogeny of my DNA samples. | Highlight strains in DNA view, based on clicks on leaf nodes in the phylogenetic tree. | Jente & Piet | 15 | 5 | |
| | Filter strains in DNA view, based on clicks on internal nodes in the phylogenetic tree. | Jente & Piet | 15 | 4 | |
| | If requested by a click in the phylogenetic tree, automatically choose and apply a color on the nodes. | Owen & Skip | 8 | 4 | Moved on from last week |
| As a user, I want to be able to cluster nodes. | Partially redesign model for cluster -> cluster edges. | Skip & Gerlof | 6 | 4 | |
| | Implement clustering of nodes. | Skip & Gerlof | 10 | 4 | |
| As a user, I want to know to which annotations a sequence belongs. | Explore and document possibilities for parsing, visualizing and using annotations. | Skip & Owen | 10 | 4 | |
| | Make sure you completely understand annotations and our graph model. | Owen & Skip & Jente & Piet | 5 | 5 | Make sure you do this. Mandatory. |
| As a user, I want to be able to interact with nodes. | Make group selection on nodes. | Jente & Gerlof | 10 | 5 | Moved on from last week |
| | Prepare for SIG | Everyone | 6 | 4 | Code will be submitted on Friday. |
| | | | | | |
| Justification of priorities | | | | | |
| <p>Top priority this sprint is making sure everyone is on the same page of the application's internal structure. This is the result of overhauling the model which the application maintains. Furthermore, researching our possibilities on the visualization and parsing of annotations will be important. This allows us getting early feedback from the customer. Highlighting of strains in the graph was moved from last week and will be done alongside highlighting in the phylogenetic tree. These tasks will have a fairly high priority. The remaining tasks are mostly just as important as the previously mentioned. Finally, at the end of this sprint there is the deadline for submission to SIG. Running final checks on aspects of the application such as quality of code will acquire some attention.</p> | | | | | |
| | | | | | |
| | | | | | |