

Context Project TI2806

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Context: Programming Life

Group 2

Product Planning [draft]

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//TO DO Add pictures

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1. Introduction

This document should reflect the goal of our product and the possible shape it will take. This document should be read with the product vision in mind. The contrast with the product vision is that this document is more based on the current process of our project team.

2. Product

The product should give an interactive visualisation of multiple genome strands. It is essential that the product can visualise large numbers (less than a thousand) strands of DNA with relevant information. This information can be divided into two main groups, namely present information (information that can be deduced directly from the data) and augmented information (information that is available in different sources and can be linked to the data). The focus lays on the first type of information since the second type can be added later. The product will be used in a diverse but clinical environment and should provide valuable information on every level of detail.

2.1. High-level product backlog

As a user I want to simply load all relevant files in a certain directory.

As a user I want to be able to read the graph files.

As a user I want to be able to see a phylogenetic tree from the genomes.

As a user I want to be able to see the genome graph with edges between the nodes.

As a user I want to have a clear & efficient view of the genome graph

As a user I want to see the DNA-sequence that belongs to each node.

As a user I want to see a detailed view of the phylogenetic tree.

As a user I want to be able to navigate between the phylogenetic tree and the genome graph.

As a user I want the graph to be annotated with information that can be found in the data itself

As a user I want the graph to be annotated with information available from external sources

As a user I want to have a clear view of relevant information on all levels (semantic zooming)

As a user I want a program that is easy to learn and efficient in my work.

2.2. Roadmap

We have 10 weeks. Every week there is an iteration. At the end of every iteration we will deliver: The sprint plan for the coming iteration, the sprint reflection of the previous iteration, a working product and if applicable other documentation.

Week 1: Getting known with the project

Week 2: Setting up a basic implementation and basis

Week 3: Extending the basic implementation and inquiring about needs

Week 4: Extend implementation

Week 5: Adapt the implementation to the target audience

Week 6: Extend implementation and add features

Week 7: Add features and analyze release environment.

Week 8: Adding features, improving previous work

Week 9: Finalize product

Week 10: Make last changes

3. Product Backlog

Sprint plan # 1

| User Story | Task | Est. Effort per Task (1-5) |
|---|---|--|
| As the scrummaster I want to have a contract describing the rules obeyed by the team members. | 1. Write a collaboration contract 2. Agree to collaboration contract | 1. 3 2. 2 |
| As a user I want to be able to see a phylogenetic tree from the genomes. | 1. Parse the tree file into JGraphT 2. Display the simple version of the tree graph | 1. 2 2. 4 |
| As a user I want to be able to read the graph files. | 1. Parse graph files into JGraphT 2. Display a simple version of the graph | 1. 2 2. 5 |
| As a programmer I want to set up a specific programming environment with all the desired tools. | 1. Set up Travis 2. Set up Octopull 3. Set up Checkstyle 4. Set up Maven 5. Set up Cobertura 6. Set up PMD 7. Define a document flow | 1. 2 2. 3 3. 1 4. 1 5. 1 6. 1 7. 2 |
| As a product owner I want to have a backlog with all potential features for the application. | 1. Add features to the issue tracker on GitHub 2. Judge and prioritize issues from GitHub | 1. 3 2. 2 |
| As a team we want to deliver our deliverables. | 1. Deliver Sprintplan1.pdf | 1. 1 |
| As a programmer I want to know what direction the project is heading and have knowledge about the context I'm working in. | 1. Have a brainstorm session for ideas 2. Determine the direction the project and make decisions. 3. Select relevant papers/information 4. Discuss what libraries to use | 1. 2 2. 2 3. 4 4. 2 |

Sprint plan # 2

| User Story | Task | Est. Effort per Task (1-5) |
|---|--|--|
| As a team we want to deliver our deliverables. | <ol style="list-style-type: none"> 1. deliver sprintplan3.pdf 2. deliver sprintreflection2.pdf 3. deliver productplanning.pdf 4. deliver final productvision.pdf | <ol style="list-style-type: none"> 1. 1 2. 1 3. 1 4. 1 |
| As a team we want to create and maintain our documents. | <ol style="list-style-type: none"> 1. Review and redact the product vision based on received feedback. 2. Review and redact the arch. design based on received feedback. 3. Create a product planning | <ol style="list-style-type: none"> 1. 4 2. 3 3. 3 |
| As a user I want to be able to see the genome graph with edges between the nodes. | <ol style="list-style-type: none"> 1. Draw edges between the nodes. | <ol style="list-style-type: none"> 1. 3 |
| As a user I want to have a clear & efficient view of the genome graph | <ol style="list-style-type: none"> 1. Use an algorithm to filter out the crossed lines. 2. Show % of ATCG per node on high-level view 3. Enlarge the scrollbar for bigger graphs 4. Research if a dropdownmenu is better than the menu used for nodes and edges loading 5. If so, implement a dropdown menu | <ol style="list-style-type: none"> 1. 5 2. 4 3. 3 4. 2 5. 3 |
| As a user I want to see the DNA-sequence that belongs to each node. | <ol style="list-style-type: none"> 1. Display DNA-sequence on node. | <ol style="list-style-type: none"> 1. 3 |
| As a user I want to see a detailed view of the phylogenetic tree. | <ol style="list-style-type: none"> 1. Show the names as nodes 2. Add edges between nodes | <ol style="list-style-type: none"> 1. 2 2. 2 |
| As a user I want to be able to navigate between the phylogenetic tree and the genome graph. | <ol style="list-style-type: none"> 1. Create a link from the phylogenetic tree to the genome graph 2. Create a link from the genome graph to the phylogenetic tree | <ol style="list-style-type: none"> 1. 2 2. 2 |
| As a user I want to simply load all relevant files in a certain directory. | <ol style="list-style-type: none"> 1. Create a workspace for data files 2. Create a scanner for the files in the workspace 3. Create a select menu for selecting which node, edge and nwk files to use for displaying | <ol style="list-style-type: none"> 1. 3 2. 3 3. 3 |

Sprint plan # 3

| User Story | Task | Est. Effort per Task (1-5) |
|---|---|--|
| As a user I want to see a phylogenetic tree minimap of the active genomes in the graph. | <ol style="list-style-type: none"> 1. Create a view. 2. Display relative tree with lowest common ancestor as root. 3. Highlight the path between all active genomes in the tree. | <ol style="list-style-type: none"> 1. 1 2. 3 3. 2 |
| As a team we want to deliver our deliverables. | <ol style="list-style-type: none"> 1. Deliver Sprintplan4.pdf. 2. Deliver Sprintreflection3.pdf. 3. Deliver Productplanning.pdf (final). | <ol style="list-style-type: none"> 1. 1 2. 2 3. 2 |
| As a user I want to be able to see the difference between 2 paths in the graph. | <ol style="list-style-type: none"> 1. Create selector for 2 paths. 2. Create a difference view. | <ol style="list-style-type: none"> 1. 3 2. 3 |
| As a user I want to have a clear & efficient view of the genome graph. | <ol style="list-style-type: none"> 1. Show % of ATCG per node on the node. 2. Use an algorithm to filter out the crossed lines (from #2). | <ol style="list-style-type: none"> 1. 4 2. 5 |
| As a user I want to see what parts of the genome are important. | <ol style="list-style-type: none"> 1. Detect important parts (clarification during meeting) 2. Display important parts in the view. | <ol style="list-style-type: none"> 1. 4 2. 4 |
| As a user I want to see which mutations are present | <ol style="list-style-type: none"> 1. Explore how to identify different mutations. 2. Display mutations in the graph. | <ol style="list-style-type: none"> 1. 2. |
| As a user I want our documentation to be up to date | <ol style="list-style-type: none"> 1. Maintain ArchDesign.pdf 2. Finalize Productplanning.pdf based on feedback 3. Update UML diagrams | <ol style="list-style-type: none"> 1. 3 2. 3. |
| As a team we want to have a current list of resources we have used | <ol style="list-style-type: none"> 1. Create a Bibliography. | <ol style="list-style-type: none"> 1. 2 |

3.1. User stories of features

As a user I want to simply load all relevant files in a certain directory.
As a user I want to be able to read the graph files.
As a user I want to be able to see a phylogenetic tree from the genomes.
As a user I want to be able to see the genome graph with edges between the nodes.
As a user I want to have a clear & efficient view of the genome graph
As a user I want to see the DNA-sequence that belongs to each node.
As a user I want to see a detailed view of the phylogenetic tree.
As a user I want the graph to be annotated with information that can be found in the data itself
As a user I want to be able to export the visualisation I see
As a user I want to see mutations in the genome marked.
As a user I want to see percentages of each base.
As a user want to have a visible link between the phylogenetic tree and the genome graph.
As a user I want the graph to be annotated with information available from external sources
As a user I want to have a clear view of relevant information on all levels (semantic zooming)
As a user I want a program that is easy to learn and efficient in my work.

3.2. User stories of technical improvements

As a programmer I want to make the product as efficient as reasonably possible to ensure usability on a large scale.
As a programmer I want to make the program run on a lot of different platforms
Aa

3.3. User stories of know-how acquisition

As a team we should follow all lectures and read all given material
As a developer I want to understand the area that I work in and read information about this.
As a programmer I have the duty to read papers about what I'm working in.
As a designer I have to know who my target audience is and what it's needs are.

3.4. Initial release plan

We use milestone oriented planning. At the end of every iteration is a milestone and we want to be done with all tasks that were planned for this milestone. If something changes we will evaluate why this changed (more complex than expected, not as valuable as expected, not reachable) and update the planning accordingly. It is important to have a working version at all times and to constantly prioritize the backlog to ensure an efficient continuation.

4. Definition of done

1. Done implementing means:
 - Test coverage > 75%
 - Implements desired feature
 - Maven builds without errors
 - No severe issues reported by: FindBugs, CheckStyle, PMD, CPD and Travis
 - Code is commented
2. When you believe to be done with a task, commit and create a pull request.
3. After 2 other persons reviewed your code and agreed to it, the last person of the 2 merges the branch.
4. The owner of the tasks is responsible for deleting the branch from Github & Closing the issue.
5. Before the end of each iteration there should be UML supporting the code

A sprint reflection is done when all points from the previous sprint plane are reviewed, assigned an actual effort and notes of applicable. Every team member will get a chance to add problems that he encountered during the iteration and there will be a story looking back on the sprint and providing context that all team members will agree on.

A sprint plan is done when all team members feel they have a fair amount of work that they feel adequate to do and when there is no more reasonable room for more tasks.

5. Glossary

Genome: the haploid set of chromosomes in an organism

Strands: a reading of the genome expressed as a list of A, G, C and T's.

Mutation: an alteration of the DNA, this can be deletion, insertion, translocation & inversion

Phylogenetic tree: diagram showing the inferred evolutionary relationships among species.