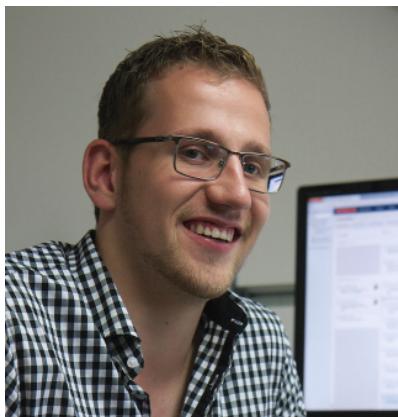


LifeTiles - Product Planning



Jos Winter



Joren Hammudoglu



Rutger van den Berg



Albert Smit



Arjan Langerak

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1. Introduction

We will be building a product capable of displaying, and comparing strains of DNA, called LifeTiles. In this document we will describe what the goal and target group of LifeTiles is, what features must, should and could be implemented, how we will do that and when those features and the product itself are considered done.

2. The goal and target group of our product

2.1. The goal of our product

Our products goal is to make it possible for its user to open a phylogenetic tree file and DNA sequence graph files. LifeTiles is a tool for the interactive visualization of DNA sequence graphs to represent the genome architecture of organisms of interest. LifeTiles lets users compare DNA strands and their mutations. Together with the visualization of the phylogenetics of the strands, users can discover how (mutated) genes express themselves.

2.2. The target group of our product

The target groups can be divided in two subgroups. The first subgroup are researchers at the Broad Institute of MIT and Harvard in Cambridge, MA, USA. A genome sequencing center interested in sequencing large genomics datasets. The second subgroup are researchers and doctors at the KwaZulu Natal Research Institute for Tuberculosis and HIV (KRITH) in Durban, South-Africa. A tuberculosis and HIV research center interested in stopping the tuberculosis and HIV epidemics in South-Africa.

2.3. Unique Selling Points

There are several existing product which provide a visualization of DNA sequences, but there aren't a lot of products which provide interactive visualization of DNA sequence graphs. The following set of products provide visualization of DNA sequences:

- CLC Sequence Viewer provides a large number of bioinformatics analysis tools. It provides visualization, creation and editing of alignments and the visualization of phylogenetic trees. Its unique selling point is that it's specialized in visualization of DNA sequences, phylogenetic trees and editing.
- Artemis: Genome Browser and Annotation Tool is a free genome browser and annotation tool that allows visualisation of sequence features, next generation data and the results of analyses within the context of the sequence, and also its six-frame translation. Its unique selling point is that it allows specialized visualization of DNA sequences, annotations and sequence features.

The following product provides visualization of DNA sequence graphs:

- Cytoscape is an open source software platform for visualizing complex networks and integrating these with any type of attribute data. It's unique selling point is that it can work with a lot of different file types. So it isn't specifically designed for the visualization of DNA sequence graphs which decreases its performance.

3. MoSCoW

3.1. Must haves

- Visualization of the DNA alignment graph (graph view)
- Visualization of the phylogenetic tree (tree view)
- Display strands with their metadata (strand view)
- Filter the strands from either tree view, graph view and strand view interactively
- Semantic zooming of the graph view
- Labelling of mutation types (insertion, deletion and polymorphism)
- Index the graph relative to a selected reference stand

3.2. Should haves

- Consistent visualization of the DNA alignment graph
- Absolute indexing, display the graph without reference

3.3. Could haves

- Semantic scrolling

4. The Roadmap

- Sprint 1
 - As a user I want to load newick files so I can use the phylogenetic tree.
 - As a user I want to use a GUI so that I can use the software
 - As a user I want to load DNA comparison graph files so that I can use them
- Sprint 2
 - As a user I want to navigate using any view panel so that I can filter the displayed strands.
 - As a user I want to view a visualization of the phylogenetic tree
- Sprint 3
 - As a user I want to have an overview of all sequences and see its metadata so that I can view details of sequences.
 - As a user I want to look at a visualization of the DNA strains so that I can compare them
- Sprint 4
 - As a user I want to look at a visualization of the DNA strain edges so that I can observe the structure of the graph.

- As a user I want to be able to load in graph files from the GUI.
 - As a user I want to be able to filter the data by using the graph visualization, the sequence list or the tree.
- Sprint 5
- Sprint 6
- Sprint 7
- Sprint 8

5. Definition of Done

The last part gettings looked at, is the final product that can be considered ‘done’. This is already discussed in previous sections, but we will give a recapitulation based on the previously mentioned points, with a focus on the definition of done for a feature, sprint and a release.

A feature is considered done when it is fully implemented, tested, approved by the other developers and integrated. The testing covers automated testing (e.g. unit tests) and static analysis (e.g. code coverage). When all tests pass, there are no errors, and the feature is approved by other developers, the feature can be merged into the product.

HA sprint is considered to be finished after a week. It is desired that the features from the sprint plan are done, and the product is in a ship-ready state.

For the final product to be considered done, the previously mentioned constraints for all features and sprints need to be fulfilled. Additionally, the product has to be user-tested not only by the developers, but the customer(s) as well. Each of the the must have’s (section 3) need to be implemented in the product.

6. User Stories

1. As a researcher I want to view multiple DNA strands so that I can compare them for mutations.
 1. As a researcher I want to view a single DNA strand so that I know the structure of the DNA strand.
 2. As a researcher I want to be able to select the level of detail of the viewport of DNA so that I can see the relevant parts of DNA that I am interested in.
 3. As a researcher I want to be able to filter certain types of mutations so that I can identify specific types of mutations: SNP, insertion, deletion, inversion, translocation and duplication.

4. As a researcher I want to be able to compare two DNA strands so that I know the structure of mutations between them.
2. As a researcher I want to create a phylogenetic tree based on several DNA strands so that I can compare them and observe the timeline and the common ancestors of several functionalities.
 1. As a researcher I want to be able to compare two DNA strands so that I know the overlapping functionality and the non-overlapping functionality between the DNA strands.
 2. As a researcher I want to be able to compare multiple DNA strands so that I know the overlapping functionalities and the non-overlapping functionalities between the DNA strands.
 3. As a researcher I want to use the overlapping functionalities and the non-overlapping functionalities between the DNA strands to generate a phylogenetic tree which is splitted by functionalities so that I know the relation between DNA strands.