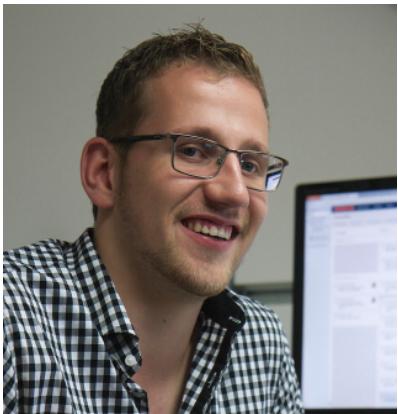


LifeTiles - Sprint Reflection 2



Jos Winter



Joren Hammudoglu



Rutger van den Berg



Albert Smit



Arjan Langerak

Sprint backlog

User Story	Task	Assigned to	Estimated effort	Actual effort	Done	Notes
As a user I want to navigate using any view panel so that I can filter the displayed strains.	Build the controllers the filter the strains in the views.	Rutger	8h	2h	Yes	After giving some thought to how to implement this it turned out to be much simpler than expected.
As a user I want to have an overview of all sequences and see its metadata so that I can view details of sequences.	Build the data view	Joren	8h	4h	No	Because of the dependency of strain models and it wasn't possible until late in the sprint to finish this.
	Build the models for the sequence metadata	Rutger	4h	2h	Yes	Wasn't much work.
	Implement filtering	Joren	4h		no	Dependent on the (unfinished) tree view, graph view and data view.
As a user I want to view a visualization of the phylogenetic tree	Fix the SunburstJ library and use it.	Albert	4h	6h	no	sunburst library is working again, not yet in GUI, short on time because last weeks parser and model had to be fixed first
	Make navigation possible in the tree	Albert	4h			dependent on above
	Implement filtering	Albert	2h			same as above
As a user I want to look at a visualization of the DNA strains so that I can compare them	Display multiple DNA sequences in TileMap with basic vertical alignment of boxes.	Arjan	2h	3.5h	yes	there was an issue with deciding how to display sequences correctly
	Display multiple DNA sequences in TileMap with	Arjan	8h	13h	yes	same as above

	horizontal alignment of boxes					
	Indicate mutation types based on empty tiles and relative coordinates (insertion, deletion and SNP)	Jos	2h	6h	yes	It was hard to determine the difference between polymorphism and insertion. finally found the solution using absolute coordinates by mapping to the reference coordinates.
	Draw the visualization axis	Jos	2h	1h	no	Dependency on graph visualization, will be implemented next sprint
	Insert empty nodes (insertion / deletion) in DNA sequence graph	Jos	2h	4h	yes	Works, took more time than expected to communicate with team about the details of the empty node implementation.
	Implement filtering	Arjan, Jos	4h	0h	no	Could not be implemented because of large dependency on the graph visualization and the tree visualization
	Create multiple DNA strains navigation in TileMap (non-semantic)	Arjan, Jos	2h	1h	yes	Was easy to implement just using the standard UI functionality