

## Sprint plan # 3

Contextproject: Programming life

Group: 2

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

As a team we want to have a current list of resources we have used	1. Create a Bibliography.	1. Nieuwdorp	1. 2
As a user I want to be able to navigate between the phylogenetic tree and the genome graph.	1. Create a link from the phylogenetic tree to the genome graph 2. Create a link from the genome graph to the phylogenetic tree	1. Boot 2. Boot	1. 2 2. 2
As a user I want to simply load all relevant files in a certain directory.	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	1. Oolbekkink 2. Oolbekkink 3. Oolbekkink	1. 3 2. 3 3. 3