

| User story | Task | Groupmember responsible | Assignee | Estimated effort (hours) | Priority (1 low - 5 high) |
|---|--|-------------------------|-----------------|--------------------------|---------------------------|
| As a developer, I want to get an accurate analysis of my code | #65 Exclude 3rd party code from analysis tools | Wouter | Wouter | 1.0 | 1 |
| | #62 Let PMD errors be equally generated by the build and the site | Wouter | Wouter | 3.0 | 3 |
| | #53 All Site reports should be both aggregate and per-module | Wouter | Wouter | 3.0 | 4 |
| As a developer, I want to work with maintainable code | #83 Refactor Model Class structure to correct inheritance and loosely coupled design patterns | Wouter | Wouter | 9.0 | 5 |
| As a user, I want to zoom intuitively | Add (semantic) zooming through scrolling | Faris | Casper en Faris | 6.0 | 5 |
| As a user I want to have semantically grouped data for easy grouping | Create an algorithm to filter straight sequences into a bubble | Cas | Cas | 4.0 | 4 |
| | Create an algorithm to filter snips into a bubble | Cas | Cas | 6.0 | 3 |
| | Create an algorithm to filter indels into a bubble | Cas | Cas | 6.0 | 3 |
| | #109 Finish the algorithm to make bubbles based on the phylogenetic tree | Casper | Casper | 8.0 | 5 |
| As a user I want to have more metadata attached to the phylogenetic tree and graph to derive the types of genomes from. | Use the lineage color to represent the types of genomes in the phylogenetic tree. | Faris | Faris | 3.0 | 3 |
| | Create multiple heatmaps using the metadata file | Casper | Casper | 8.0 | 2 |
| | #110 Parse annotations for phylo tree | Justin | Justin | 6.0 | 5 |
| | Add annotations to the nodes in the phylo tree | Justin | Justin | 4.0 | 3 |
| | Make clear what the user is seeing in the phylo tree by adding a legend (or something else) | Justin | Justin | 6.0 | 4 |
| As a user I want to be able to select any node in the phylogenetic tree and draw it in a graph. | Add drag and drop to the phylogenetic tree nodes. If a tree node is dragged on top of a graph, the user should get a list of possible actions: | Faris | Faris | 3.0 | 4 |
| | add to drawn graph | Faris | Faris | 2.5 | 4 |
| | clear old graph and draw in graph | Faris | Faris | 2.0 | 4 |
| | create and add to new graph | Faris | Faris | 2.5 | 4 |
| | Create a layout (visual representation) for the points mentioned above | Faris | Faris | 2.0 | 4 |

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|---|--|--------|-----------------|-----|---|
| As a user I want to have elaborate statistical data to use while browsing the genomes. | Add heatmaps/annotations on Bubbles with relevant information about the bubbled structure | Casper | Casper | 3.0 | 2 |
| | Add legend in the graph view to explain the annotations on the bubbles | Faris | Casper en Faris | 2.0 | 2 |
| As a user I want to see a top level overview of the graph | Create top level overview with only edges (no nodes). When zoomed out, if the bubbles/nodes have a size below a certain treshold, show only the edges. | Faris | Faris | 2.0 | 2 |
| | Create a minimap indicating where in the graph you are | Faris | Wouter | 7.0 | 1 |
| As a user I want to be able to open any gfa and nwk file | Create option to load file | Justin | Justin | 6.0 | 3 |
| As a user I want to be able to compare two graphs | Work on the comparison between two bubbled graphs | Cas | Cas | 7.0 | 3 |
| As a client, I want a good presentation and demo to bring me up to date on the progress | Create a presentation | Wouter | Wouter | 2.0 | 5 |