**Members**

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**Proposed Goal**

Develop a drag and drop interface where the user provides (1) a vcf file and (2) a tree file and render a visualization focusing on SNV’s.

**JavaScript resources**

https://developer.mozilla.org/en-US/docs/Web/JavaScript/Guide/Introduction

**D3 resources**

https://observablehq.com/@d3/gallery

**VCF format resources**

* <https://github.com/moonso/vcf_parser>
* <https://github.com/GMOD/vcf-js>
* <https://www.ebi.ac.uk/training/online/courses/human-genetic-variation-introduction/variant-identification-and-analysis/understanding-vcf-format/>
* <https://samtools.github.io/hts-specs/VCFv4.2.pdf>
* Parsing with Pandas: <https://www.biostars.org/p/416324/>
* Usher: <https://usher-wiki.readthedocs.io/en/latest/UShER.html>
  + Uses protobuf format which stores a mutation annotated tree object

**Misc.**

Possibly write the backend in Python, the frontend in JS, and tie it together in a flask app?

**References/Previous art/examples**

* Taxonium:
  + See Theo Sanderson post on Slack channel
  + Description: JS library for displaying large phylogenetic trees and associated metadata.
  + Pros:
    - Support for large trees
    - Protein alignment in-line with phylogeny
    - Gene browser
  + Cons:
    - Can’t collapse to variable positions
    - Unclear whether you can visualize nucleotide information
* Geneious:
  + [Link to screenshot](https://ibb.co/kJBS8BY)
  + Description: GUI for performing a large number of sequencing data analyses.
  + Pros:
    - Alignment in-line with phylogeny
    - Custom annotations
  + Cons:
    - Can only display trees constructed with Geneious. I.e. can’t visualize imported newick tree.
    - Can’t collapse to variable positions
    - Paid program
* ETE toolkit:
  + [link](http://etetoolkit.org/treeview/)
* Phylotree.JS:
  + [link](https://github.com/veg/phylotree.js)
* Snipit:
  + [Link to repository](https://github.com/aineniamh/snipit)
  + Description: Small program which plots snps relative to a reference sequence. Included here as a nice example of how to plot collapsed alignment.

**Task Distribution**

1. Install and test available vcf parsers (what kind of data do they output?) (**Chrissy, Grace**)
2. Work on Taxonium (**Nate, Christian**)
3. As a team we could do a beginners' training on JavaScript
4. Details on python flask- **Chrissy**
   1. Simple python framework to put a website up such that you can write the backend in python and the frontend in JS: <https://flask.palletsprojects.com/en/2.1.x/>
5. Download everything and test (**Diana**)
6. Put together readme and general documentation (**Diana, Grace**)