**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.

**Main components**

1. Install and test available vcf parsers (what kind of data do they output?)
2. Work on Taxonium for display of tree topology and "condensed MSA" (SNPs only)

**Reasons for taking this approach**

* Time is limited, re-use existing software as much as possible
* Prepare for open source project

**Issues**

* Labels for MSA positions
* NA vs AA