
MATERIALS

The following materials were used to gather sequences, align said sequences, and create and manipulate phylogenetic trees:

1. Modern computer with proper software downloaded and access to internet
2. A Nucleotide Database: ncbi.nlm.nih.gov OR hiv.lanl.gov
3. Version Control
 - a. Required in order to recover old files
 - b. Used *Git*Hub
4. Software
 - a. Sequence Manipulation
 - i. *Komodo Edit*, *SeaView*, *Mafft*, *Mesquite*, *Linsi*
 - b. Phylogenetic Analysis Using Parsimony
 - i. *PAUP**
 - c. Bayesian Analysis / BEAST Suite
 - i. *BEAST*, *BEAUTi*, *Tree Annotator*, *Tracer*
 - d. Tree Viewing
 - i. *FigTree*