

Stuart Kettler

Bioinformatics

Assignment 5

muscle -in bats_ace2.fasta -out bats_ace2_aligned.fasta

raxmlHPC-HYBRID_AVX -T 4 -N result -s infile.txt -c 25 -p 12345 -m PROTCATDAYHOFF -f a -N 100 -x 12345 --

4) *Dobsonia_viridis*, *Empomophorus_wahlbergi*, *Rousettus_leschenaultii*,
cynopterus_sphinx, *syconycteris_australis*

5. useful for knowing spread of new diseases like covid. Looking at similar species to one that is a source of a new zoonotic disease. Phylogenetics helps us understand transmission of new diseases.