**Using Phylogenetic trees and substitutions to Capture Relationship of** **SARS-Cov-2 Variants and SARS-like Genomes**

Names: Liz Wyman Z1884762

Kleo Bano Z1940978

Chris Troyer Z1945059

Roberto Rivas Z1906735

Emails: Z1884762@students.niu.edu

Z1940978@students.niu.edu

Z1945059@students.niu.edu

Z1906735@students.niu.edu

Main Question: How do variants of SARS-COV-2 (Omicron, Alpha, etc.) and other SARS-like genomes compare to each other?

Background & Significance:

The COVID19 pandemic created a newfound necessity for research in SARS-COV-2 viruses and variants. Since the start of the pandemic more and more variants have been discovered and sequenced. We will use different algorithms to create multiple phylogenetic trees. This will illustrate the different evolutionary relationships between variants and SARS-like genomes. Using multiple algorithms will allow us to create a clear picture of the evolutionary relationship and compare algorithm outputs. Most people do not understand the difference between any of the SARS genomes enough to care about getting an updated shot, so this should help people understand the differences between them to get them thinking about updated covid shots.

Data:

We will use SARS-Cov-2, variants, and SARS-like genomes that can be downloaded from the NCBI website (data files are prepared by Dr. Hou). We will also use the multi-alignment and pairwise alignment data files provided. Each genome has around 30K DNA bases. We will first conduct all vs. all genome comparison and obtain the similarity measurement between every pair of genomes. The similarity is a numeric value between 0 and 1.

The study:

A comparison of phylogenetic trees will be used to show differences and similarities between SARS-COV-2, variants, and SARS-like genomes. This will help show why the different genomes and given different names and why SARS-COV-2 variants are variants instead of a different SARS-like genome. We will calculate branch lengths for each algorithm and compare trees. We will map indels, substitutions, and log gap rates to compare how those values change or modify the output on a specific phylogenetic tree. In the case of low substitution rate, we expect the branches to be close together. In the case of high substitution rates, we expect the branches to be far apart from one another. We will first start with the SARS-COV-2 and variants, then move onto SARS-like genomes. Graphs will be constructed and provided as a visual aid to view the data that is found and collected.

Programming language & system: Java, Linux

Library packages: BioJava

Work environment: GitHub will be used for collaboration on all files and research.

Contribution: Liz – report writing 25 %

Kleo - design of the program, implementation/debugging/documentation 25 %

Chris - design of the program, implementation/debugging/documentation 25 %

Roberto - report writing 25 %

Timeline:

1-2 weeks – Code phylogenetic trees and branch lengths

1-2 weeks after coding complete – Analyze data

Initial data:

A screenshot of a computer screen

Description automatically generated

A screenshot of a computer screen

Description automatically generated

Initial analysis:

Comparing the wildtype SARS-COV-2 genome to SARS-COV-2 variants and SARS-like genome sars, shows how the substitution rate is substantially greater for sars than any of the variants. Also, the substitution rates comparing sars to variants are within a ~0.002 margin to the substitution rate of sars to SARS-COV-2 of 0.194913. This shows how closely related the variants are compared to one another and the wildtype SARS-COV-2 genome, which is why they are not considered variants of SARS-like genome sars.