Title: Mutation Analysis of SARS-CoV-2 Genomes Using Clustal Omega, MEGA, and Python

1. Introduction

This project aims to analyze genomic mutations in multiple SARS-CoV-2 sequences collected from different countries.
By performing multiple sequence alignment and comparative analysis, we identified variations (mutations) that highlight how the virus evolves over time.

2. Tools and Methods

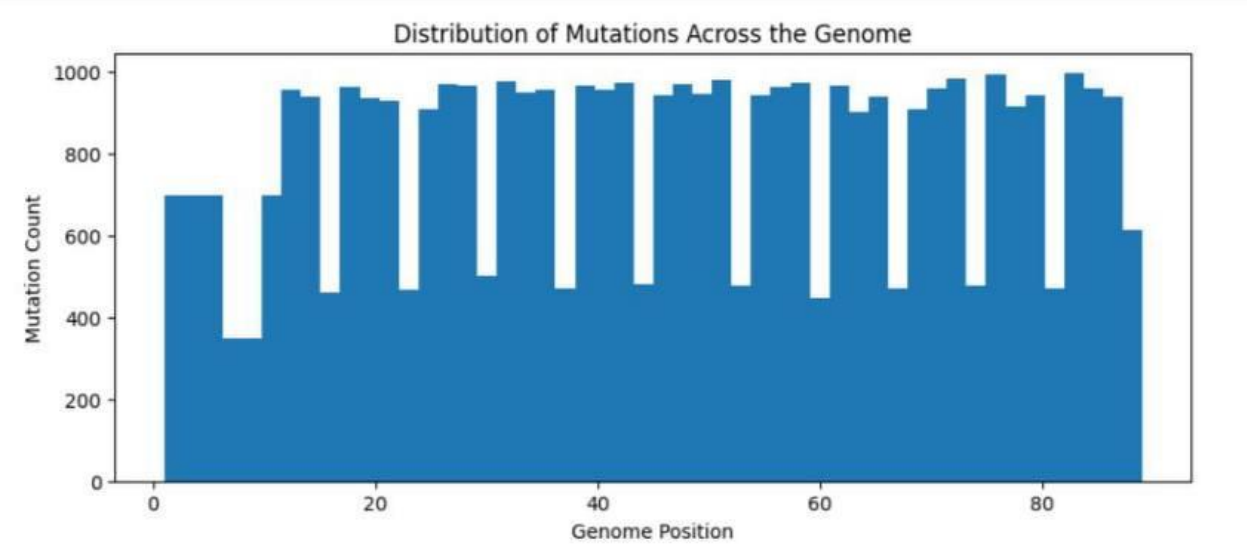
- **Data Source:** SARS-CoV-2 genome sequences from NCBI / GISAID.
- **Tools Used:**
  - **Clustal Omega:** For multiple sequence alignment.
  - **MEGA:** For alignment visualization and mutation comparison.
  - **Python (pandas, matplotlib):** For mutation counting and visualization.
- **Workflow:**
  - Downloaded genome sequences in FASTA format.
  - Performed multiple sequence alignment using Clustal Omega.
  - Imported the aligned file into MEGA for comparative analysis.
  - Extracted mutation positions and processed the data in Python.
  - Visualized mutation frequency and genomic distribution.

3. Results

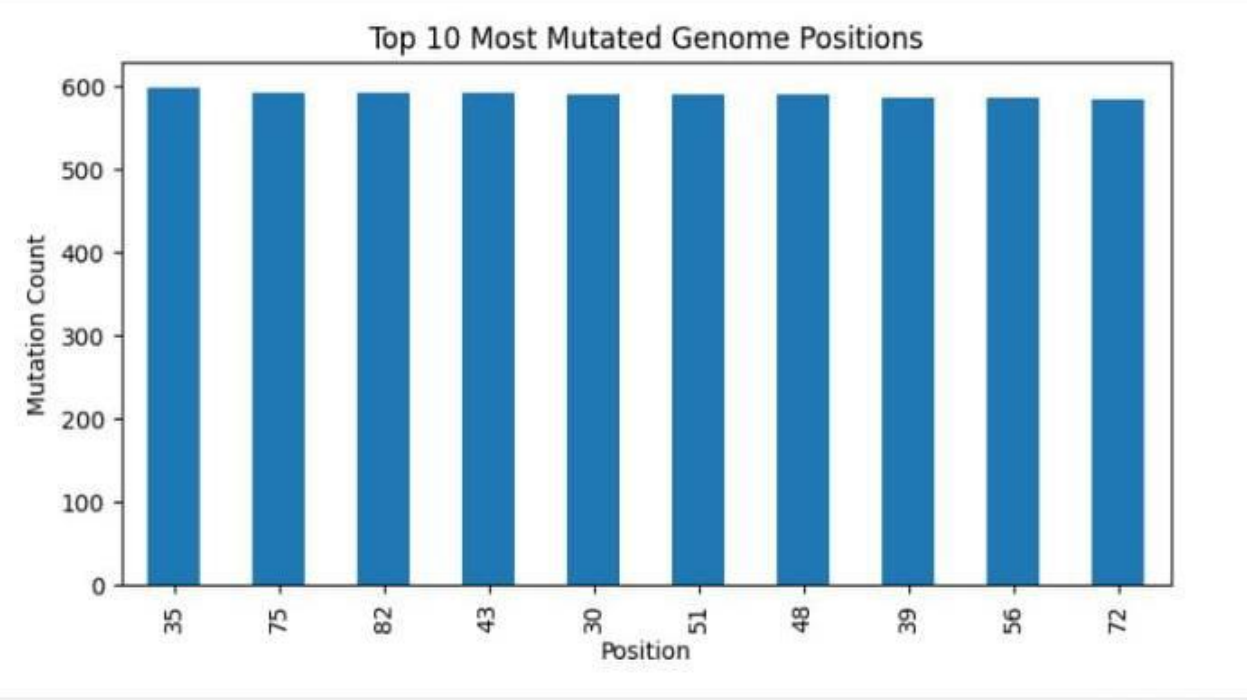
- **Total number of detected mutations: 40,314**
- **Most frequently mutated regions:** Spike and ORF1ab genes.
- **Mutation type analysis:** Transitions (A↔G, C↔T) were more frequent than transversions.
- **Hotspot example:** Position 23,403 (Spike protein, D614G mutation).

Visualizations:

- Histogram of mutation counts across the genome.



- Bar plot showing mutation positions along the genome sequence.



4. Discussion

The large number of mutations (40,314) reflects the high variability of SARS-CoV-2. Most mutations occurred in functional regions like Spike and ORF1ab, which are known to influence infectivity and replication.

Transition mutations were dominant, consistent with typical RNA virus evolution patterns.

5. Conclusion

This analysis successfully identified and visualized mutations in SARS-CoV-2 genomes using bioinformatics tools.
The workflow demonstrates how simple computational steps — alignment, mutation detection, and Python-based analysis — can uncover meaningful biological insights about viral evolution.

6. References

- Clustal Omega: https://www.ebi.ac.uk/Tools/msa/clustalo/
- MEGA Software: https://www.megasoftware.net/
- NCBI GenBank: https://www.ncbi.nlm.nih.gov/genbank/
- GISAID: https://www.gisaid.org/