1. Before Preprocessing

* Aligments.fas: Aligned Sequences of SARS-CoV-2 Spike
* Sequences.csv: Metadata of Sequences
* Sequences.acc: Accession Code of Sequences
* Refseq.fasta: The reference sequence

1. After Preprocessing

* Mutations.csv: Containing Metadata + mutations.
* LocationMutations.csv: Containing Geographical Region + mutations.