### The Palestinian Covid Conflict

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## Background and Overview

The outbreak of the SARS-CoV-2 infection was catastrophic for the people in Palestine. Palestinians were in amidst a cloudy political climate with the people of Israel. The Israeli-Palestinian conflict not only became the reason for the increased cases per day, this conflict expanded the Coronavirus geographically exponentially. The objective of this analysis was to assess the number of cases and their locations in correlation with the Israeli-Plaestinan conflict. This was done by ....... My findings concluded that ... This is a report on SARS-CoV-2, including some variant analysis (Koyama et al., 2020).

#### Methods

See the set of tutorials on the vcfR package website.

You may also want to use any of a range of different COVID data packages and data sources:

- https://kjhealy.github.io/covdata/
- https://github.com/como-ph/oxcovid19
- https://ropensci.org/blog/2020/10/20/searching-medrxivr-and-biorxiv-preprint-data/
- https://covidtracking.com/data/api
  - readr::read\_csv("https://api.covidtracking.com/v1/states/daily.csv")

#### Subsections are ok too

### Results and Discussion

# Figures

# Count of distinct SNPs in Named SARS-CoV-2 Genes

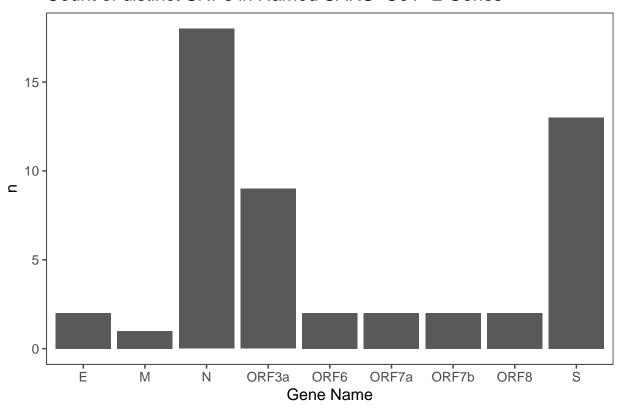


Figure 1: N and S genes have more unique SNPs in the set of samples analyzed.

### **Tables**

Gene Name	Start	End	Length
S	21563	25384	3821
ORF3a	25393	26220	827
E	26245	26472	227
M	26523	27191	668
ORF6	27202	27387	185
ORF7a	27394	27759	365
ORF7b	27756	27887	131
ORF8	27894	28259	365
N	28274	29533	1259
ORF10	29558	29674	116

 $\textbf{Table 1:} \ \ \textbf{Gene names, locations, and lengths in the SARS-CoV-2 genome.} \ \ \textbf{Higher SNP counts in the S and N genes may be related to the larger size of these genes.}$ 

### **Sources Cited**

Koyama, T. et al. (2020) Variant analysis of sars-cov-2 genomes. Bulletin of the World Health Organization, 98, 495.