The Brazillian Amazon & COVID-19

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Background and Overview

This is a report on SARS-CoV-2 genetic data, as well as some COVID-19 prevalence data for Manaus and Sao Paulo. (Buss *et al.*, 2020).

Methods

Suggested Sources

- vcfR package website.
- 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")`
- https://rt.live/
  - `readr::read_csv("https://d14wlfuexuxgcm.cloudfront.net/covid/rt.csv")`

Results and Discussion

Figures

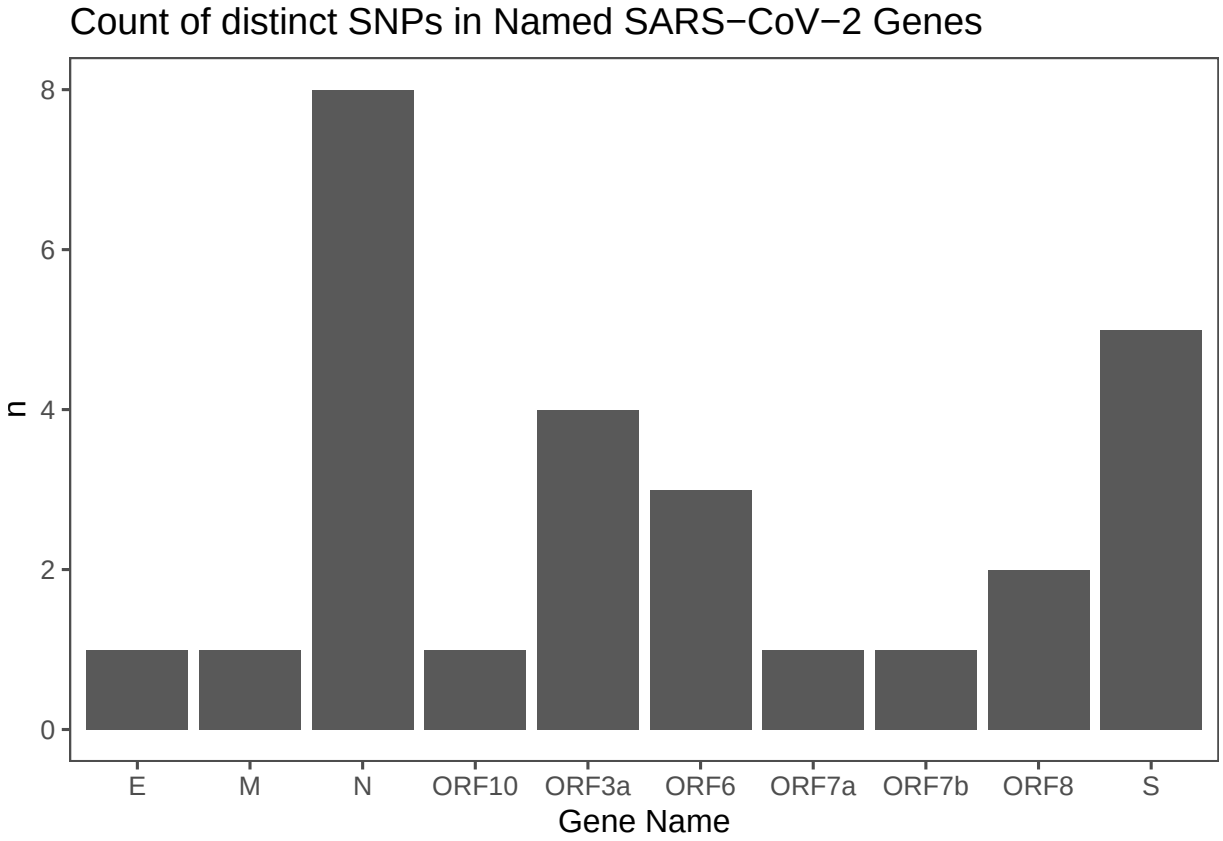

Figure 1: N and S genes have more unique SNPs in the set of samples analyzed.

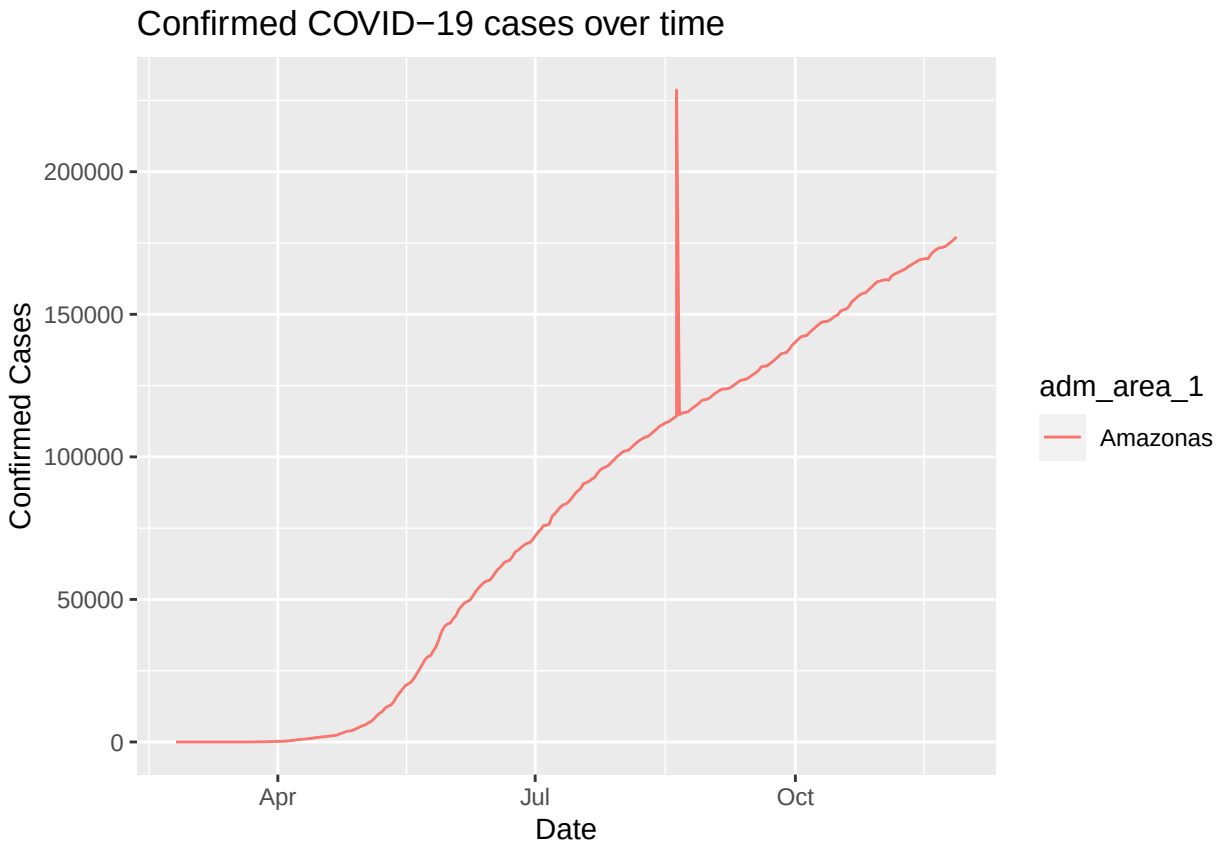

**Figure 2: Manaus saw more severe confirmed cases of COVID-19 than Sao Paulo.

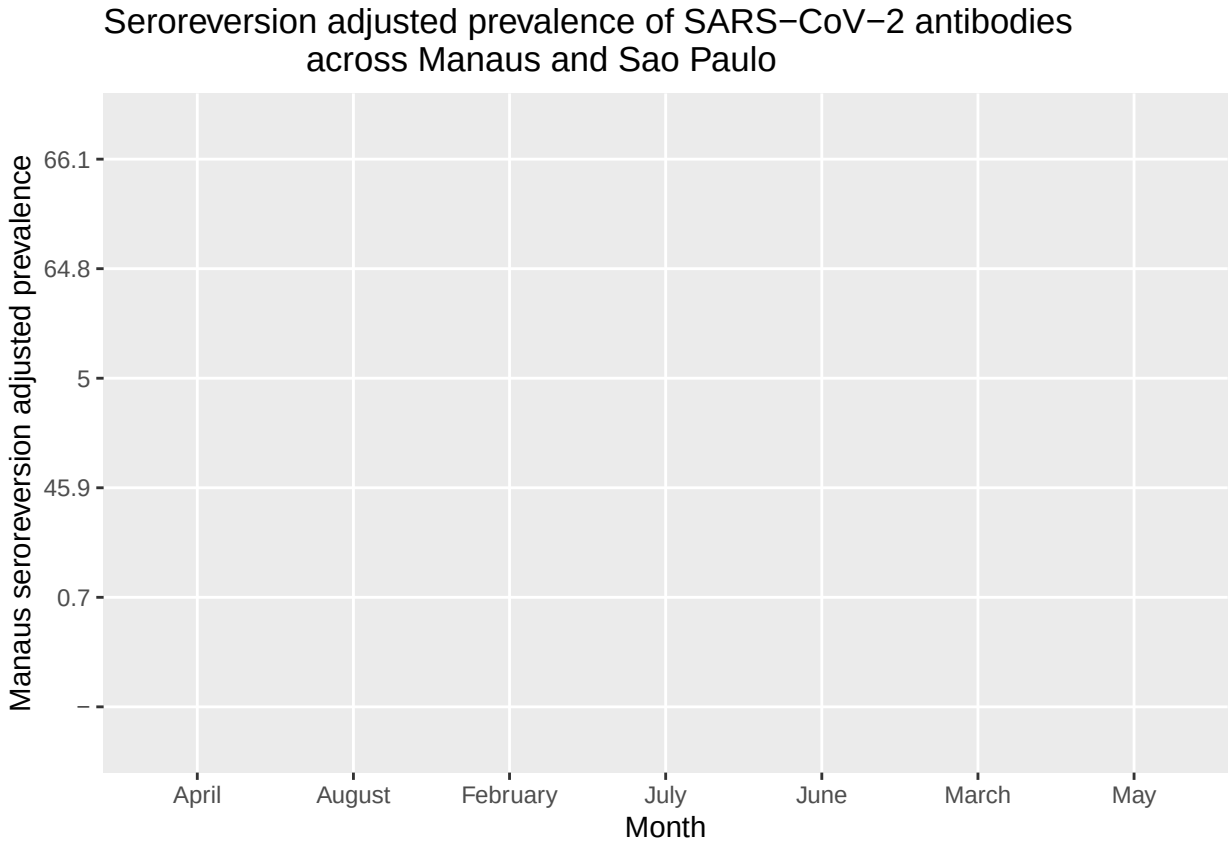

**Figure 3: Manaus saw more antibody prevalence of SARS-CoV-2 than Sao Paulo.

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

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

Sources Cited

Buss,L.F. *et al.* (2020) COVID-19 herd immunity in the brazilian amazon. *medRxiv*.