

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

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-medrxiv-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")`

Subsections are ok too

Results and Discussion

```
## Error in parse_tidy_and_stack_vcfs(vcf_dir_path = params$vcf_dir_path): could not find function "par
## Error in read_gff(gff_file_path = params$gff_file_path): could not find function "read_gff"
## Error in extract_genes_from_gff(annotation_object = gff): could not find function "extract_genes_fro
## Error in add_genes_metadata_to_vcfstack(sra_runnable_path = params$sra_runnable_path, : could not fi
```

Figures

```
## Error in eval(lhs, parent, parent): object 'vcf_with_metadata' not found
```

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

```
## Error in ox - plot <- bra_epi_tab %>% group_by(date) %>% ggplot(aes(x = date, : object 'ox' not found
## Error: Unknown graphics device ''
```

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

```
## Error in eval(lhs, parent, parent): object 'prevalence_path' not found
## Error in grid.draw(plot): object 'prevalence' not found
```

```
## Error in eval(expr, envir, enclos): object 'prevalence' not found
```

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

Tables

```
## Error in eval(lhs, parent, parent): object 'gene_table' not found
```

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*.