

Accelerated case rates led to herd immunity but also elderly and male mortality in Amazonas, Brazil during the COVID-19 pandemic

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Background and Overview

What happened in the Amazon and São Paulo during COVID-19?

This exploratory analysis of tabular and genetic data shows that the city of Manaus, and its state, Amazonas, were hit harder per capita than the city and state of São Paulo through the second (Q2) and third quarters (Q3) of 2020 **TODO: additional citations**. Deaths were especially high for elderly patients, as well as male patients in Manaus.

From Q2 into Q3, the intense period of infection correlated with the emergence of an antibody prevalence among Manaus blood donors that was approximately threefold greater than antibody prevalence among São Paulo blood donors (Buss *et al.*, 2020). This is an indication of good news and herd immunity for Manaus, heading into Q4.

Additionally, a genetic analysis of 33 SARS-CoV-2 samples showed that **TODO: sequencing and bash findings**.

Methods

Tabular data analysis

TODO: tabular parsing walkthrough: trace piping especially. pkg citations; See methods section of <https://elifesciences.org/articles/61981> Describe what I did in prose form Data were downloaded from the NCBI SRA archive from project numbers __ on date. Then processed with trimmomatic and run through a bwa variant calling pipeline (CITATION from bwa paper). ... That data was then brought into RStudio to analyze in combination Include steps of modifying datatables, e.g. age ranges

In the final steps of data processing, I temporarily created a column in `Mortality_data.csv` that compared the ratios of mortality figures. I selected the age range 55-60 to show the maximum ratio seen between male and female excess mortality in Manaus this year.

Genetic data analysis

TODO: sequencing and bash walkthrough: trace scripts as sets by format; citations

- `vcfR` package website.
- <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")
```

Results and Discussion

Tabular data analysis

This analysis indicates that living in Manaus, being elderly, and being male were risk factors for Brazillians facing COVID-19 in Q2 and Q3 of 2020. It surprised me to see that male patients in Manaus were at such markedly higher risk of death than female patients, to the order of **TODO: insert ratio**.

TODO: tabular parsing; refer to figures; 66Fix fill for col.

Excess mortality in 50-55 year old male patients reached a maximum of 126 deaths/1000, 1.30 times their expected mortality of 99 deaths/1000, as well as 2.49 the excess mortality of female patients of the same age at 54.8 deaths/1000 (**TODO: Figure number;**)

Genetic data analysis

TODO: fastqc screenshot: evidence that it's reasonable Quality, length, WATCH a few weeks ago on fastqc examples with one goofy one , citations.

Figures

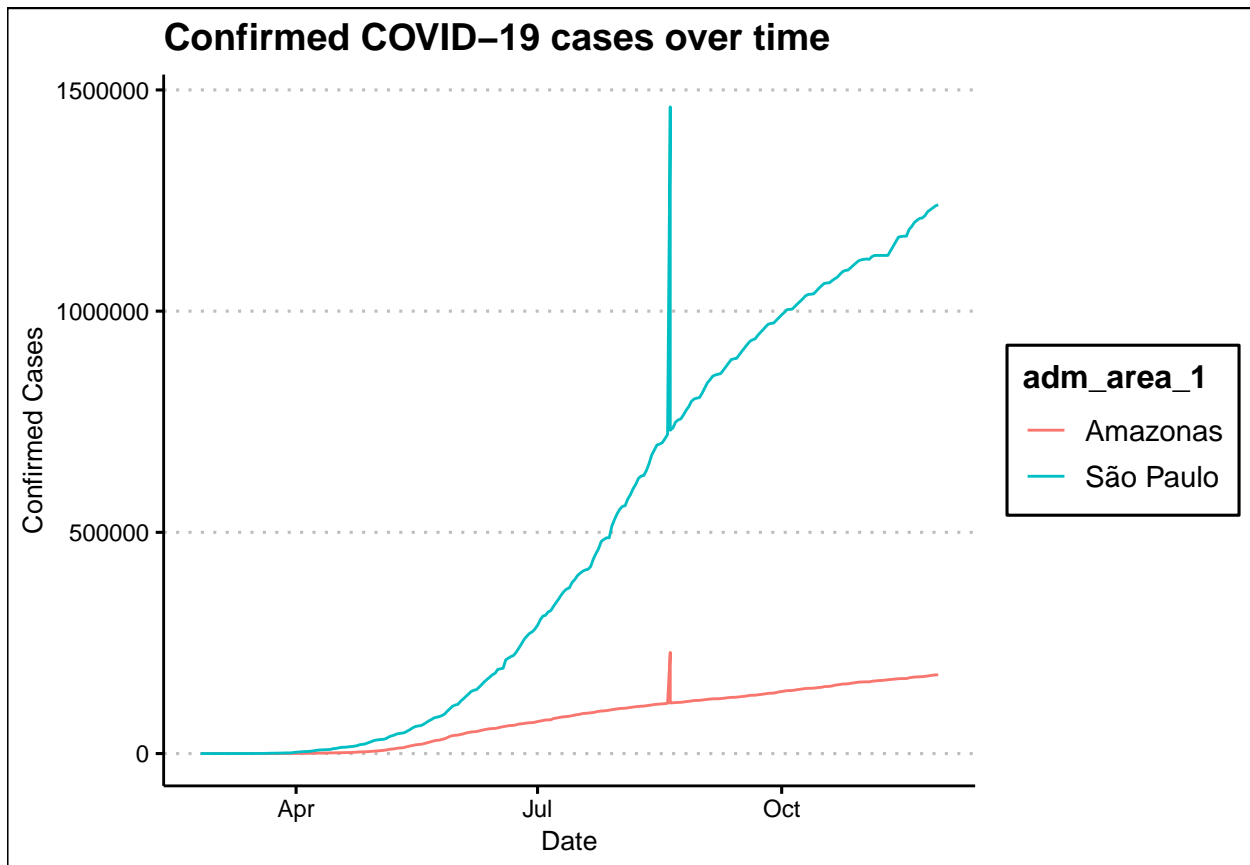


Figure : The state of São Paulo saw more total confirmed cases than the state of Amazonas.

Population of Brazil

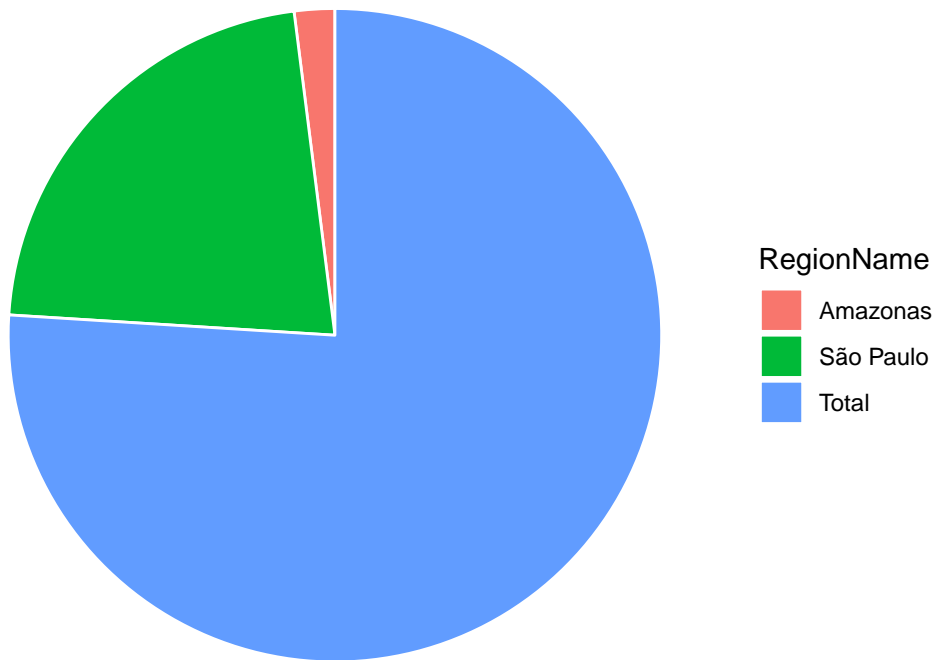


Figure: The state of São Paulo is much larger than Amazonas by population at 46 million versus 4 million.

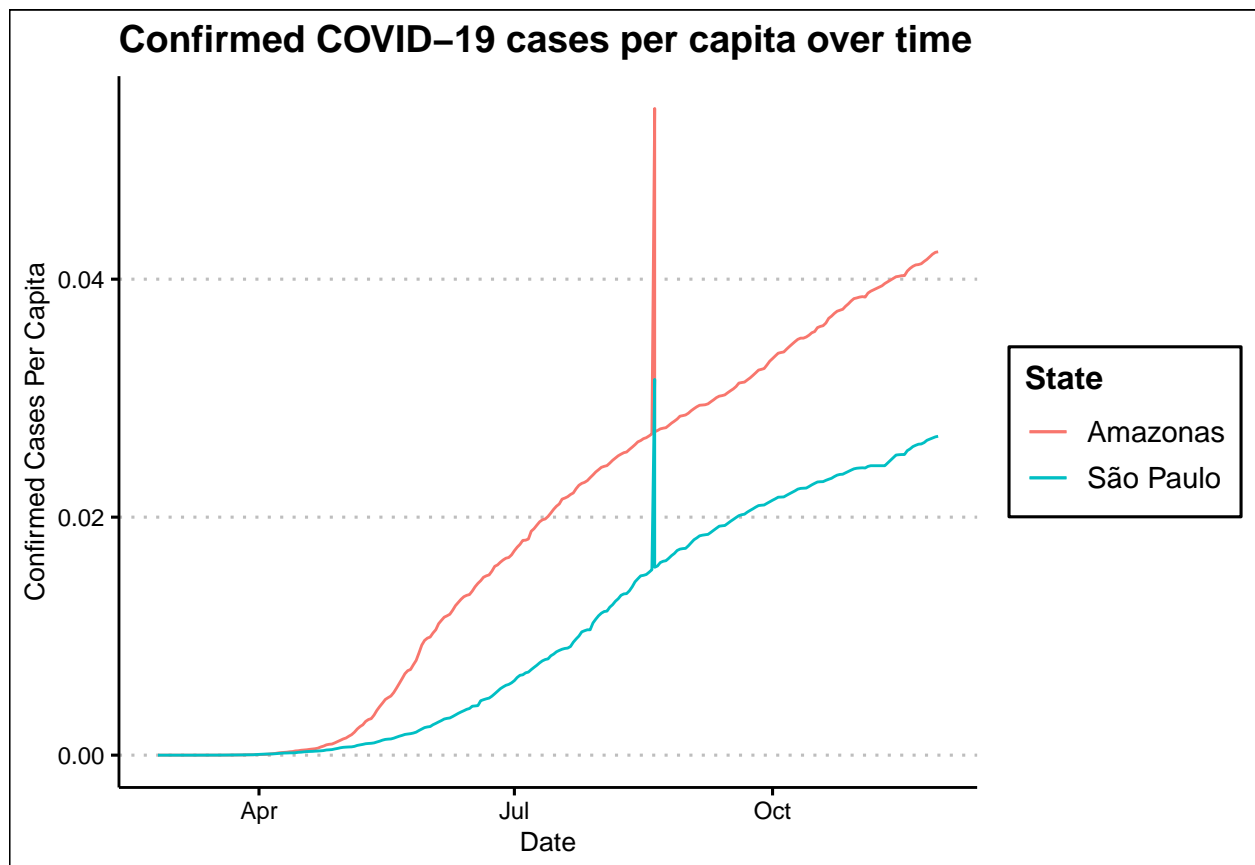


Figure: Amazonas saw greater confirmed cases per capita than São Paulo.

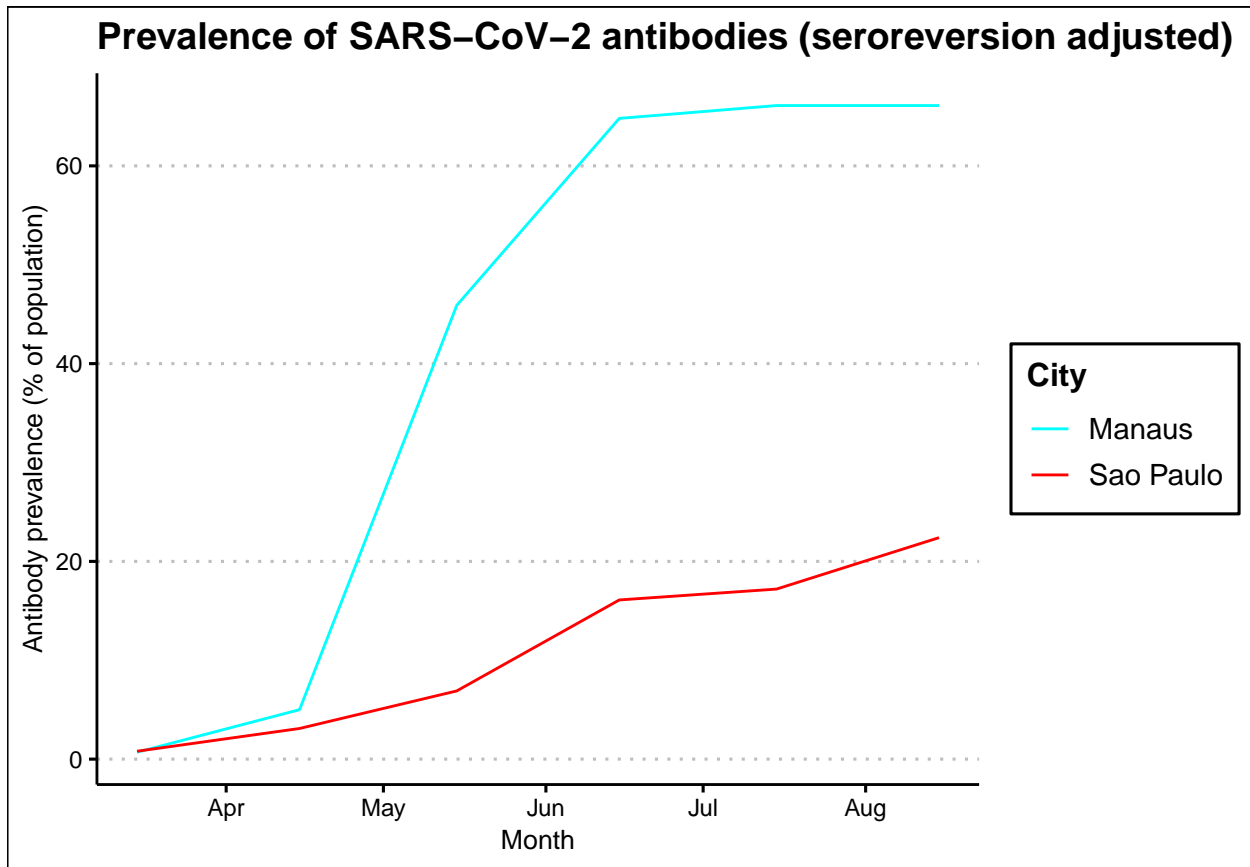


Figure: Manaus saw more widespread prevalence of SARS-CoV-2 antibodies vs. São Paulo, up to 66% vs. 22% of the population respectively.

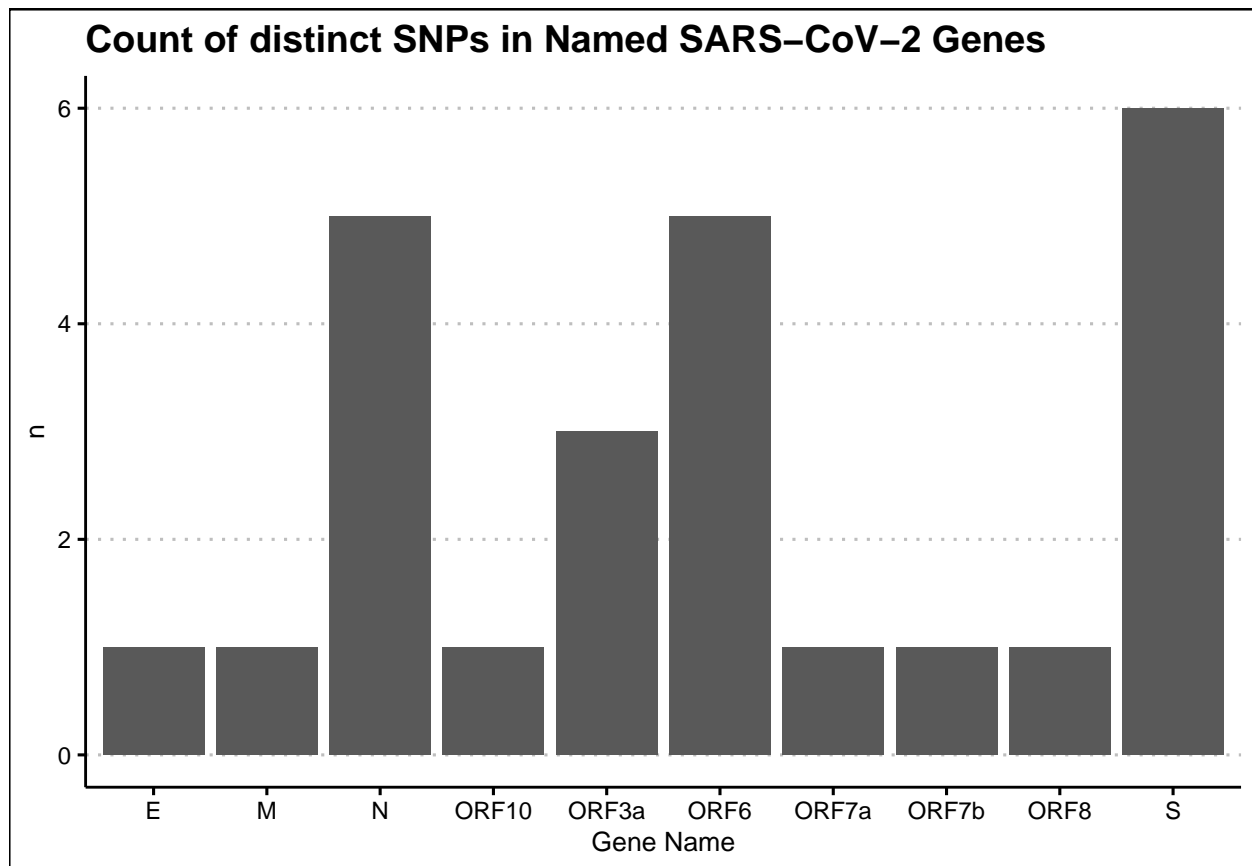


Figure: N and S genes have more unique SNPs in the set of samples analyzed.

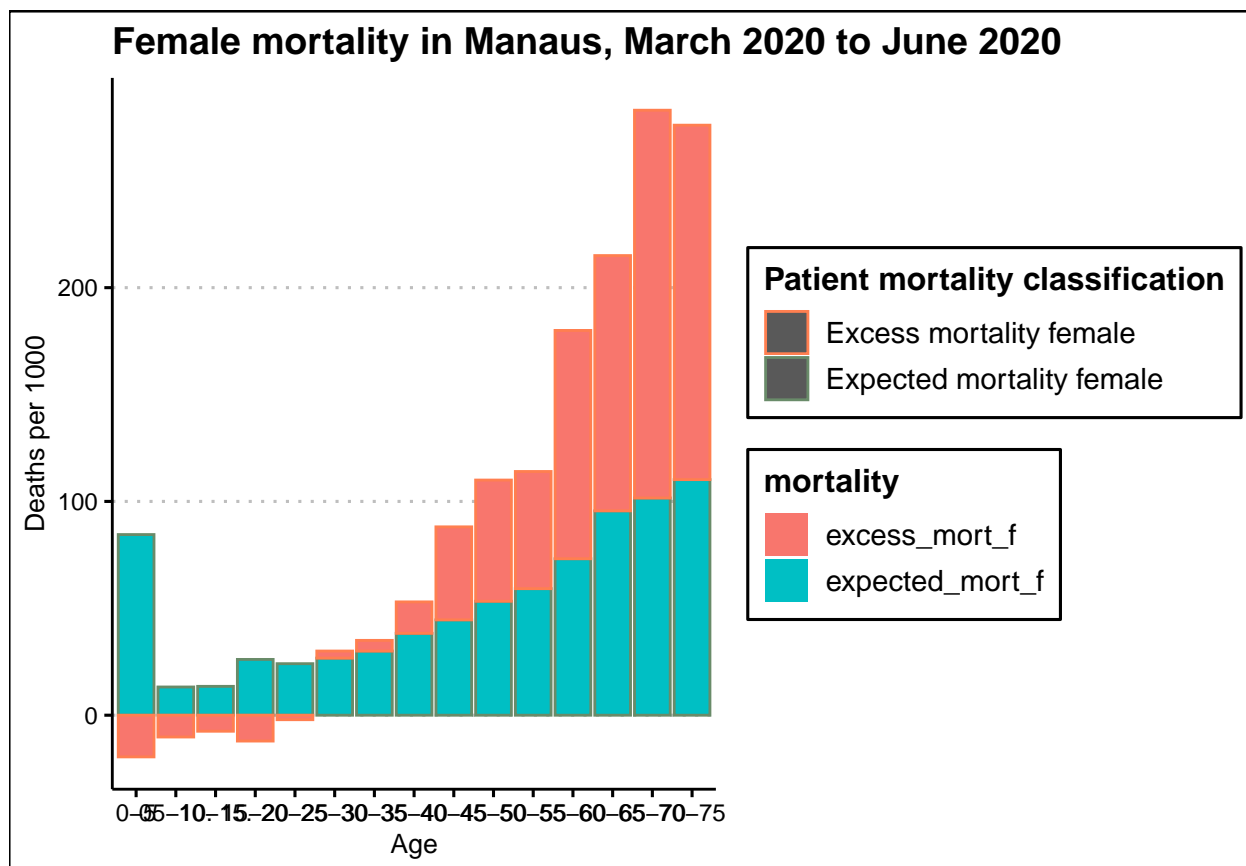


Figure: Excess mortality, unexpected deaths of any cause, reached a maximum of 2.49 times the expected mortality in female patients.

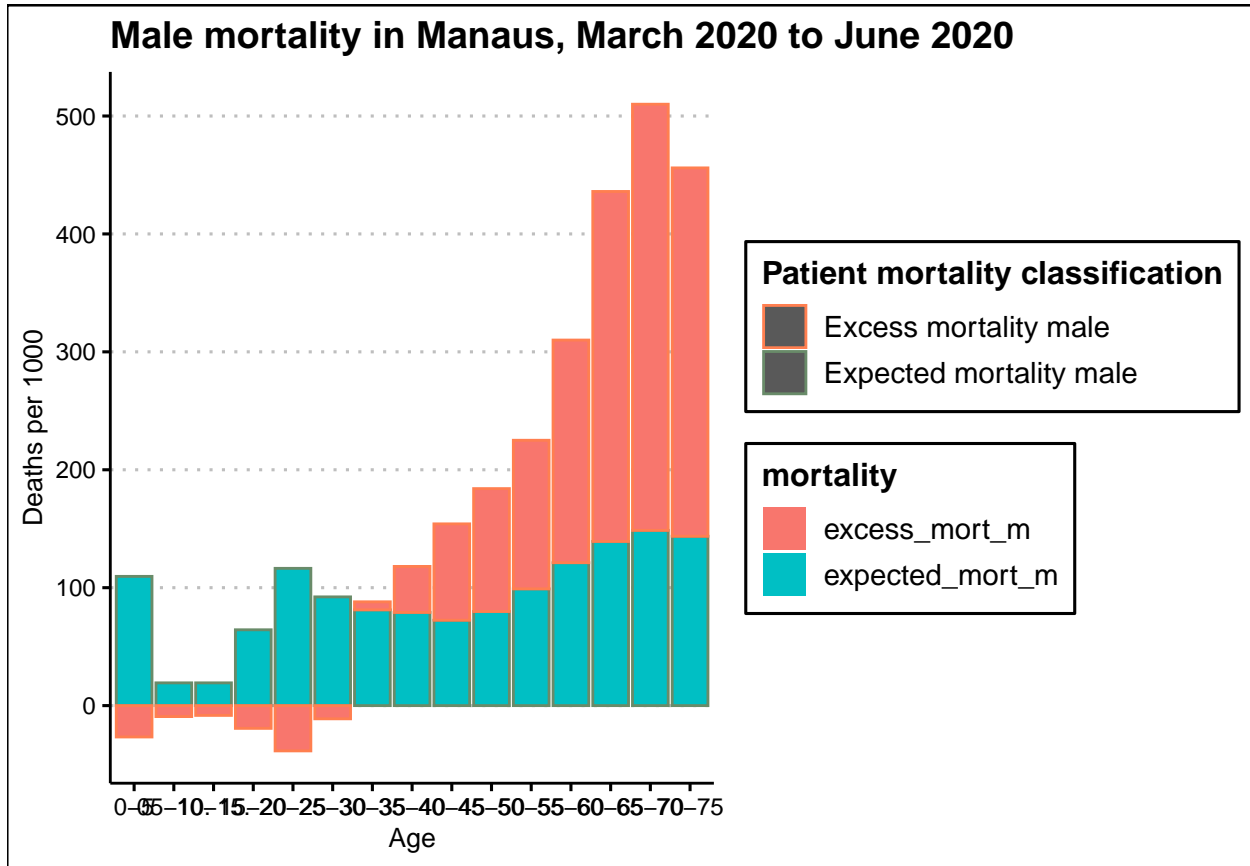


Figure: Excess mortality in male patients reached a maximum of more than double their expected mortality, as well as double the excess mortality of female patients.

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

TODO: say scripts provided by Naupaka Zimmerman “and based on an approach from data carpentry CC” sentence in methods section. In template README steps of this were based on data carpentry, include this in methods Webpage URLs should be in code, not cited. If complicated. “Figured it out based on approach here” Packages in bibtex? Diff schools of thought. Objection that it pollutes biblio Dr. Z leans toward code side Definitely cite oxford19 but not base r packages Can use this for wiggle room. Prefers at least a few peer reviewed articles Adding bibtex and citing Demonstrate skills to use both in Rmd. If you want to mention a webpage or article, how formal: peer reviewed yes, r pkg, have citation function that will give it to you; markdown link is ok for webpage; or create BibTex for website

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