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 variant call analysis of 33 SARS-CoV-2 samples showed that the greatest numbers of high quality, distinct SNPs in the named genes originated in the Amazonian states of Maranhao and Para.

Methods

Tabular data analysis

TODO: tabular parsing walkthrough: trace piping especially.

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

Illumina NGS runs were collected as 33 .fasta files from the NCBI SRA website. Under the project number PRJNA662684, the runs came grouped by region, being specific to the Brazillian Amazon.

\textcolor{red}{TODO: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, if applicable.)}

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

Lastly, single nucleotide polymorphisms (SNPs) were tallied and grouped by region, gene, and quality (Table 1).

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 times the excess mortality of female patients of the same age at 54.8 deaths/1000 (Figure 6).

Genetic data analysis

The variant call analysis resulted in a set of ___ high quality, distinct SNPs. The notable majority of these SNPs in named genes came from Maranhao and Para, as opposed to the other nearby Amazonian states (Table 1).
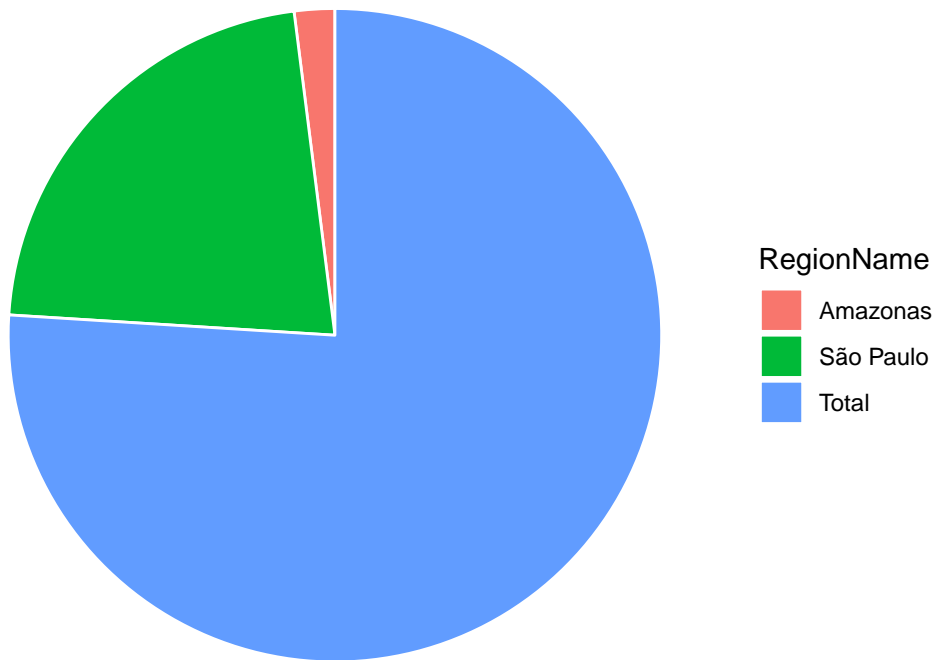
TODO: fastqc screenshot: evidence that it's reasonable Quality, length, WATCH a few weeks ago on fastqc examples with one goofy one , citations.
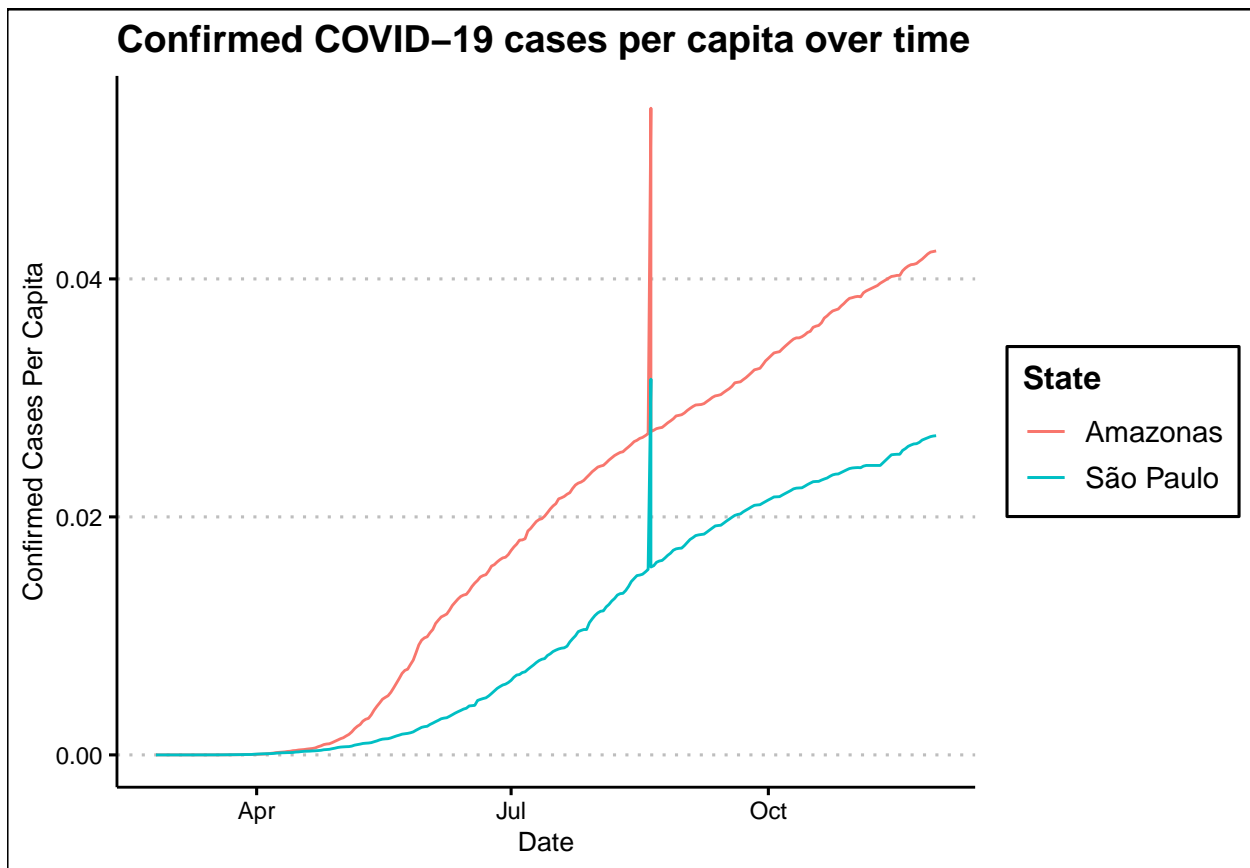
Figures
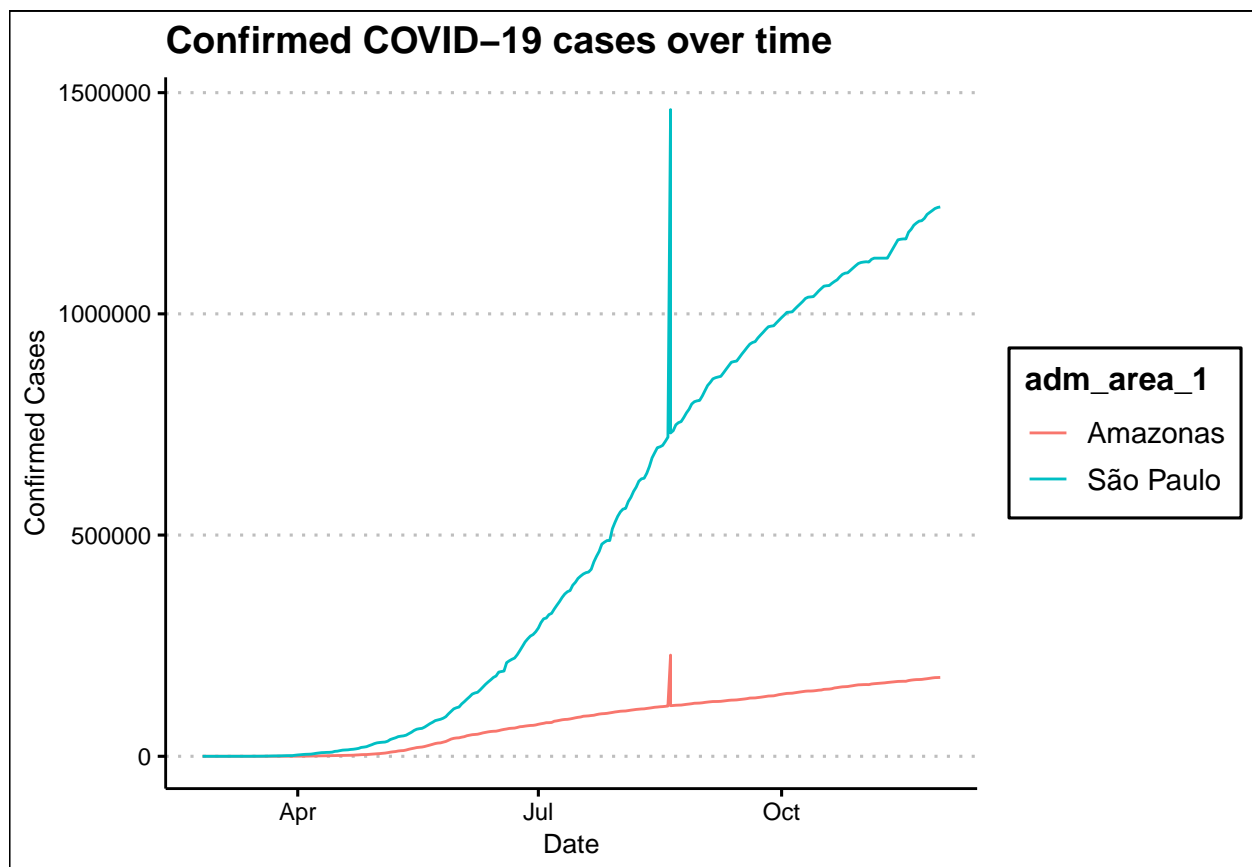
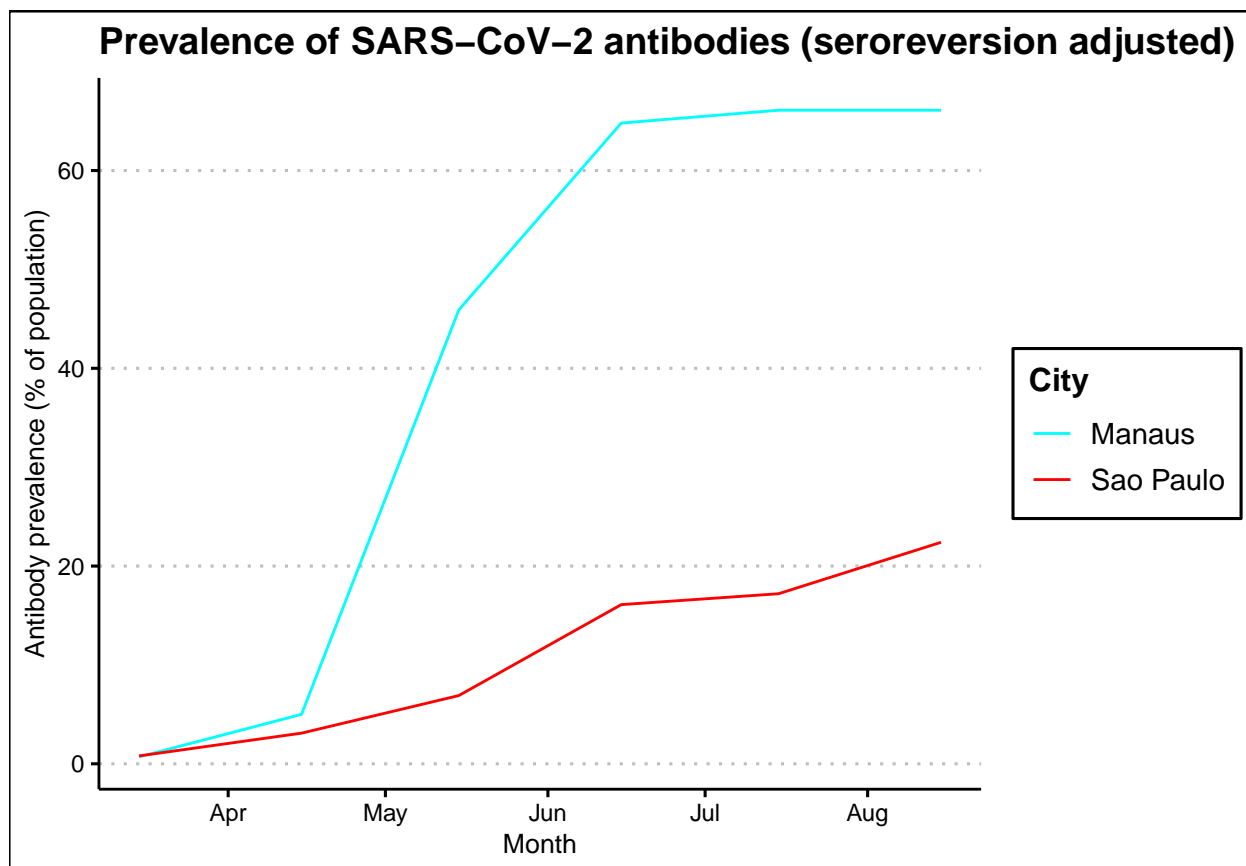**Figure 1**: The state of São Paulo saw more total confirmed cases than the state of Amazonas.
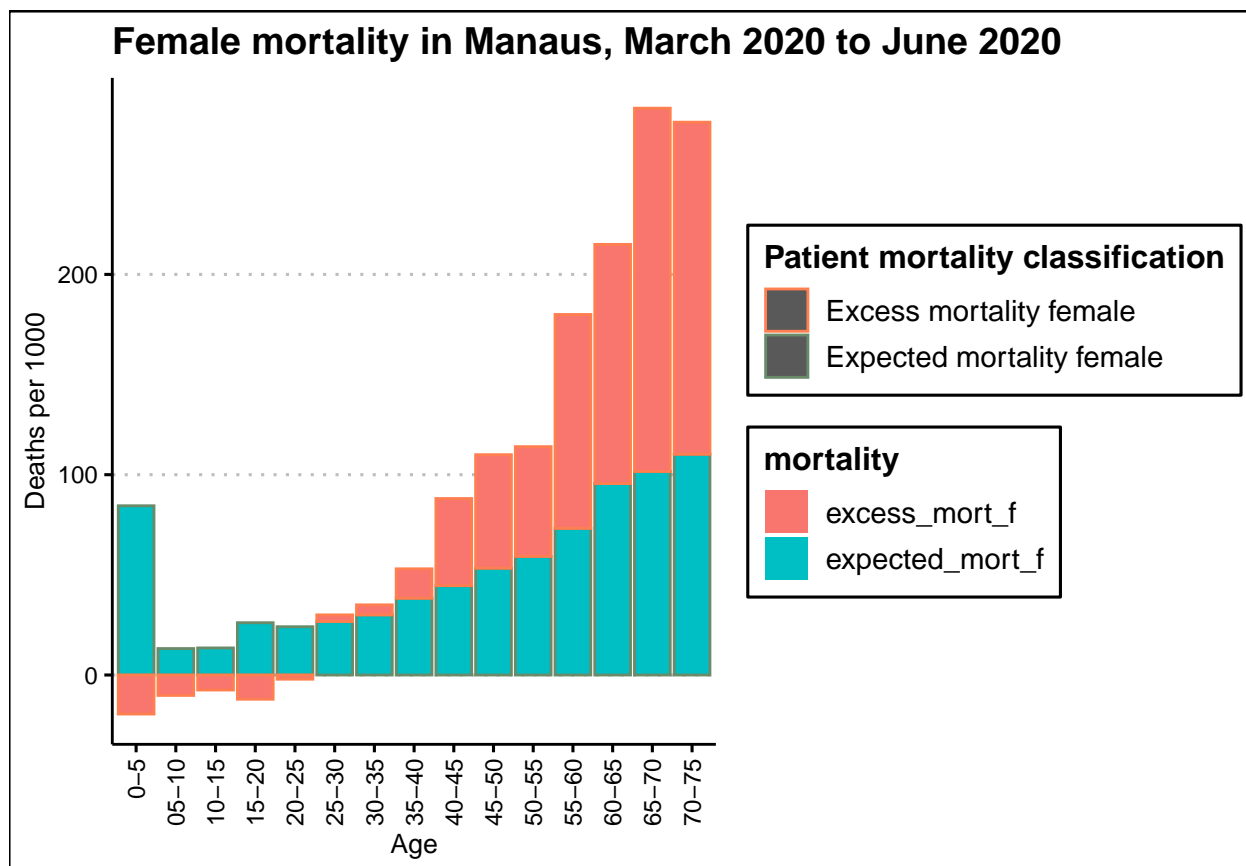
Population of Brazil

Figure 2: The state of São Paulo is much larger than Amazonas by population at 46 million versus 4 million.

Figure 3: Amazonas saw greater confirmed cases per capita than São Paulo.

Figure 4: Manaus saw more widespread prevalence of SARS-CoV-2 antibodies vs. São Paulo, up to 66% vs. 22% of the population respectively.

Figure 5: Excess mortality, unexpected deaths of any cause, reached a maximum of 2.49 times the expected mortality in female patients.
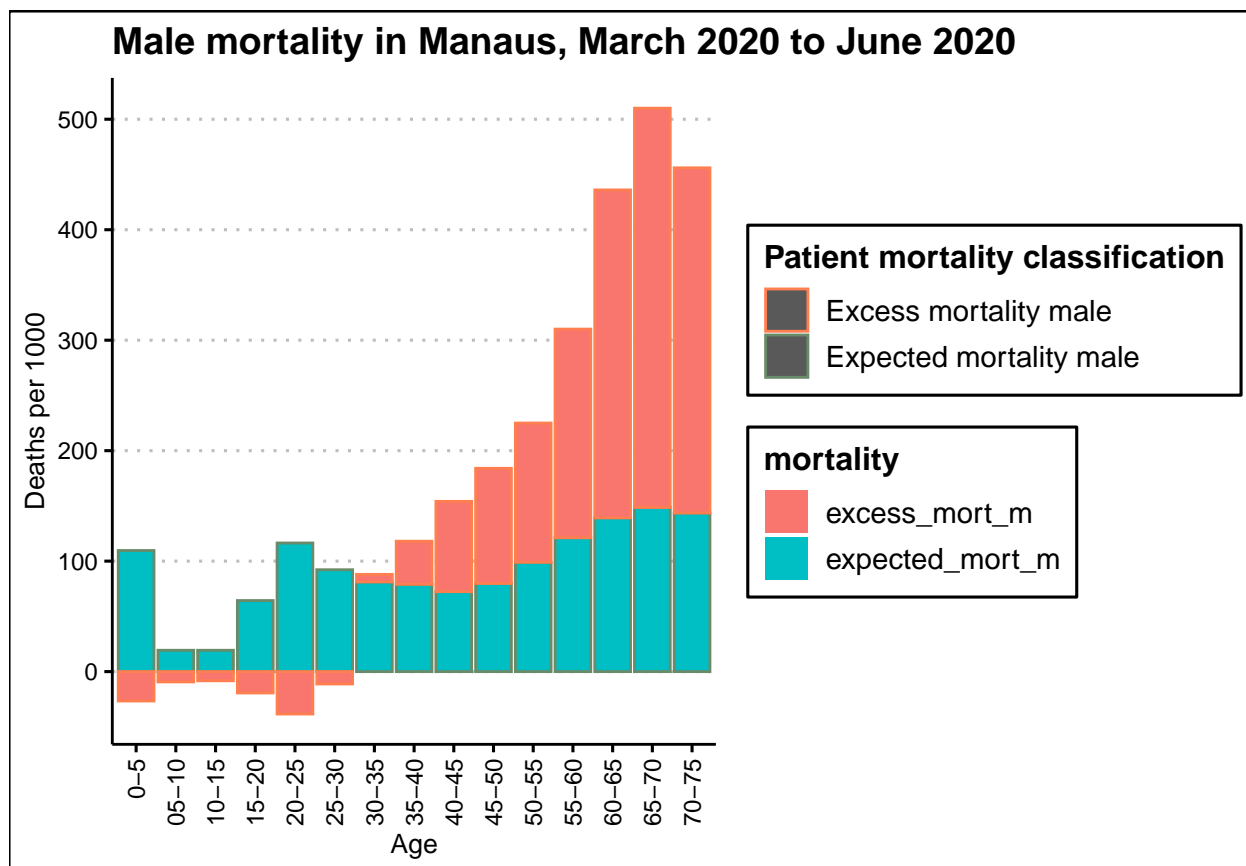
Figure 6: Excess mortality in male patients reached a maximum of more than double their expected mortality, as well as double the excess mortality of female patients.

Tables

Gene Name	Brazillian State	Quality
N	Brazil: Acre	225
ORF6	Brazil: Acre	225
S	Brazil: Acre	225
NA	Brazil: Acre	225
N	Brazil: Acre	228
NA	Brazil: Acre	228
NA	Brazil: Acre	38.782
N	Brazil: Amapa	194
M	Brazil: Amapa	225
N	Brazil: Amapa	225
ORF3a	Brazil: Amapa	225
ORF6	Brazil: Amapa	225
S	Brazil: Amapa	225
NA	Brazil: Amapa	225
N	Brazil: Amapa	228
S	Brazil: Amapa	228
NA	Brazil: Amapa	228
NA	Brazil: Maranhao	101
ORF7a	Brazil: Maranhao	136
NA	Brazil: Maranhao	137
ORF6	Brazil: Maranhao	142
N	Brazil: Maranhao	20.4535
N	Brazil: Maranhao	225
ORF3a	Brazil: Maranhao	225
ORF6	Brazil: Maranhao	225
S	Brazil: Maranhao	225
NA	Brazil: Maranhao	225
N	Brazil: Maranhao	228
ORF6	Brazil: Maranhao	228
NA	Brazil: Maranhao	228
S	Brazil: Maranhao	32.4168
N	Brazil: Maranhao	38.415
S	Brazil: Maranhao	4.5236
N	Brazil: Maranhao	42.4147
ORF3a	Brazil: Para	120
ORF8	Brazil: Para	163
NA	Brazil: Para	173
S	Brazil: Para	223
N	Brazil: Para	225
ORF10	Brazil: Para	225
ORF3a	Brazil: Para	225
ORF6	Brazil: Para	225
ORF7b	Brazil: Para	225
ORF8	Brazil: Para	225
S	Brazil: Para	225
NA	Brazil: Para	225
E	Brazil: Para	228
N	Brazil: Para	228
ORF3a	Brazil: Para	228
NA	Brazil: Para	228

Gene Name	Brazillian State	Quality
ORF6	Brazil: Para	44.7802
S	Brazil: Paraiba	225
NA	Brazil: Paraiba	225
N	Brazil: Rio_Grande_do_Norte	225
ORF6	Brazil: Rio_Grande_do_Norte	225
S	Brazil: Rio_Grande_do_Norte	225
NA	Brazil: Rio_Grande_do_Norte	225

Table 1: The greatest numbers of high quality, distinct SNPs in the named genes came from Maranhao and Para, Brazil.

Sources Cited

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