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Introduction and Purpose

Over the course of the COVID-19 pandemic, tracking virus spread has been crucial for preparing necessary safety guidelines and keeping the public informed. Our goal is to interpret the GISAID phylogenetic data and better understand the mobility of various COVID-19 strain/lineages/variants in the US.

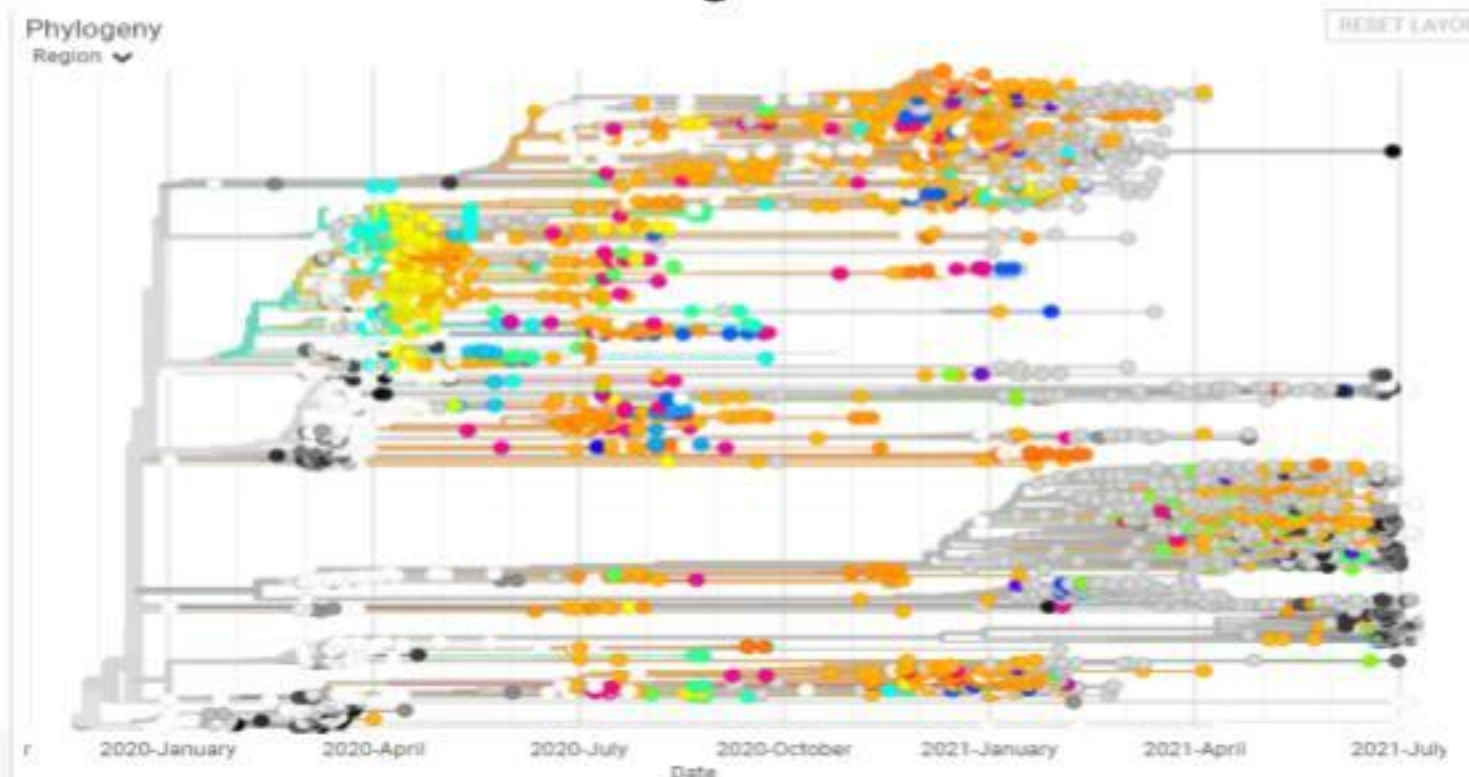


Fig 1: Phylogeny Tree (1/2020 - 4/2020) (GISAID, 2021)

Methods

- Used python libraries ('networkx', 'geopandas', 'matplotlib') and Gephi to create visualizations with data extracted from GISAID database
- gathered human mobility data from Kang et al. (2020)
- processed data to find US disease mobility links that matched human mobility links

Results

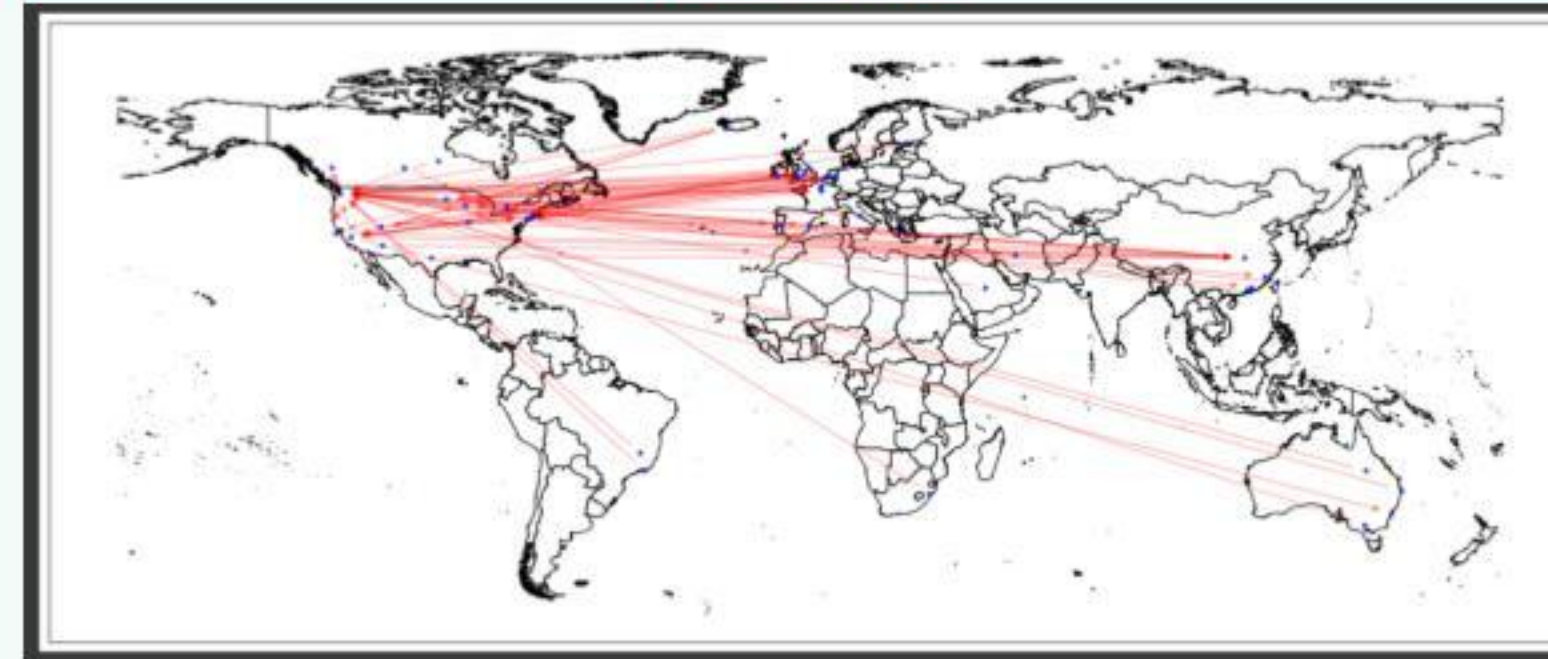


Fig. 2: US Network (1/2020-4/2020)

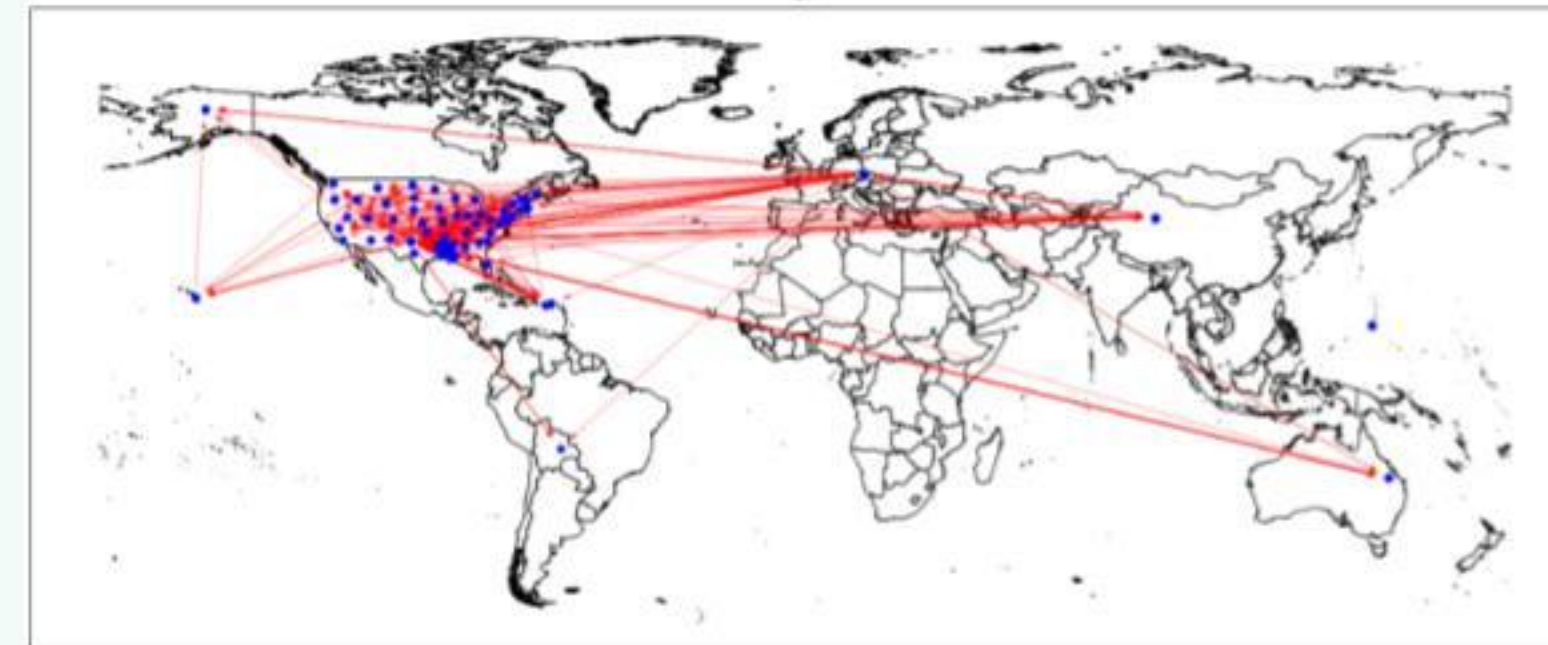


Fig. 3: Louisiana Network (2019-2021)

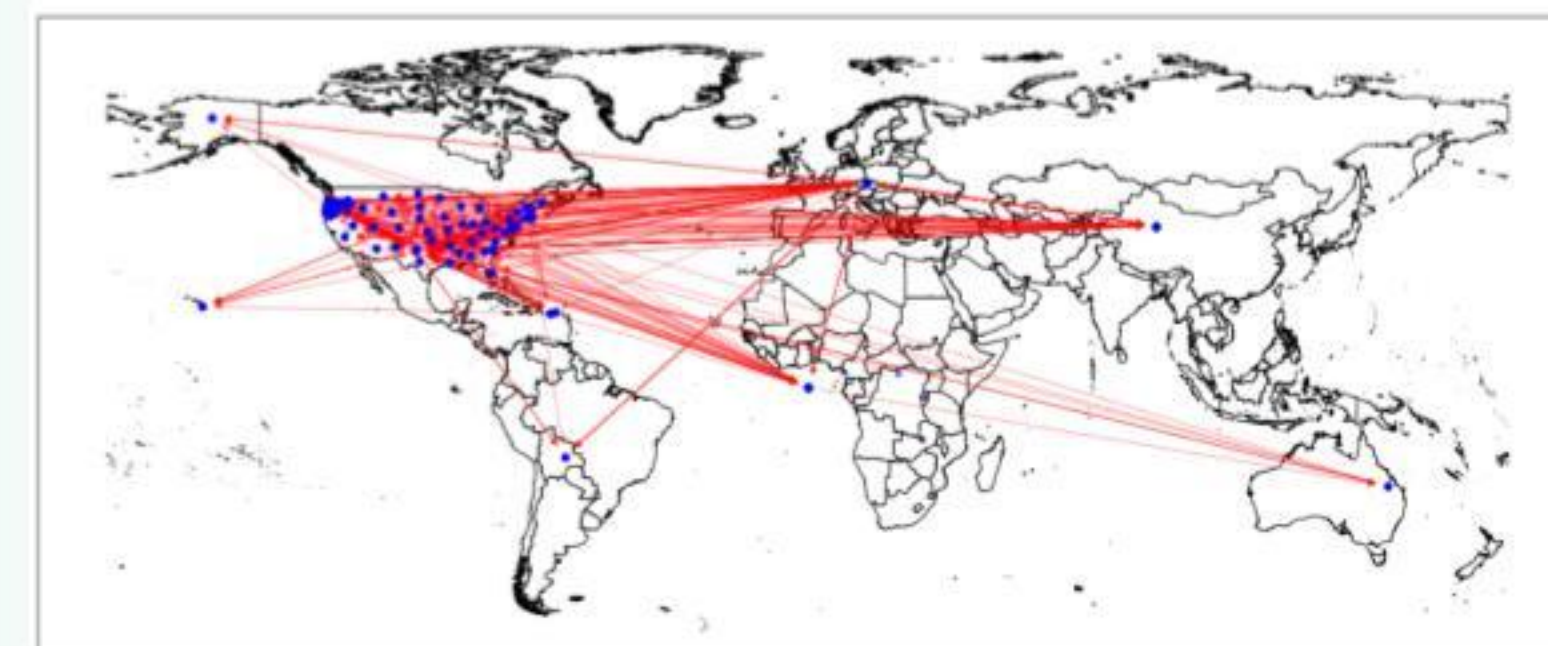


Fig. 4: Oregon Network (2019-2021)

Discussion and Conclusions

Currently working on:

- finding socioeconomic and geographic similarities between origin points to identify risk factors of developing/spreading new strains
- finding a quantitative correlation between disease and human mobility pre- and post- pandemic
- enriching our visualizations to show the time frame

Conclusions:

- visualizations will aid in communicating the flow of COVID-19 geographically
- hope that as a result of our research, better policies/protocols can be implemented by officials (WHO, CDC)

Major Citations

- GISAID. (2021, August 9). *Phylogeny*. GISAID. <https://www.gisaid.org/phylogenetics/global/nextstrain/>
- Kang, Y., Gao, S., Liang, Y. et al. Multiscale dynamic human mobility flow dataset in the U.S. during the COVID-19 epidemic. *Sci Data* 12 7, 390 (2020). <https://doi.org/10.1038/s41597-020-00734-5>

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