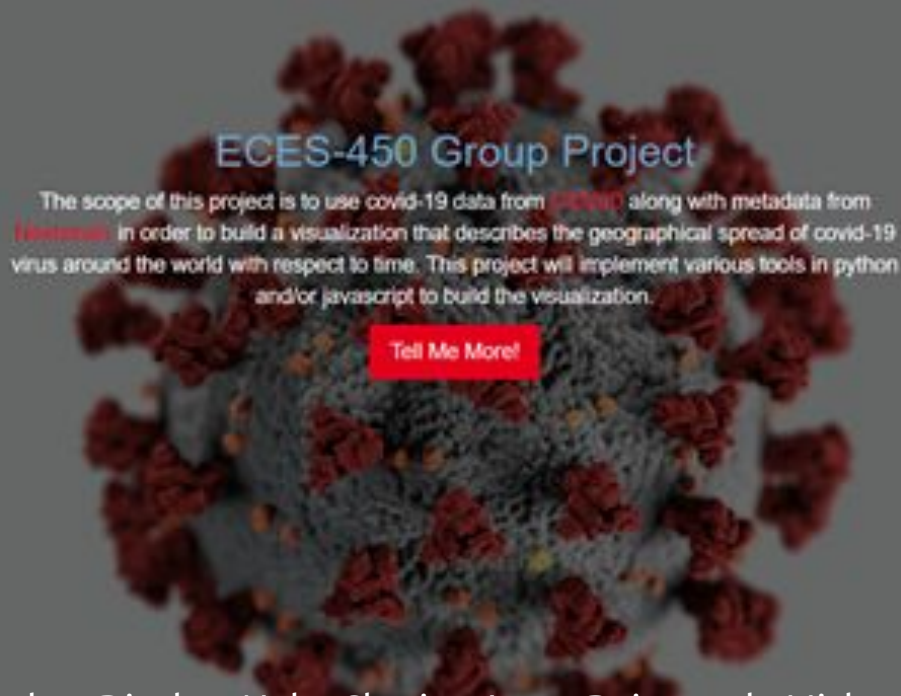


COVID-19 Interactive Interface



ECES-450 Group Project

The scope of this project is to use covid-19 data from [ECDC](#) along with metadata from [Twitter](#) in order to build a visualization that describes the geographical spread of covid-19 virus around the world with respect to time. This project will implement various tools in python and/or javascript to build the visualization.

[Tell Me More!](#)

Presenters: Joshua Shelley, Joshua Divaker, Neha Cherian, Lyssa Buissereth, Michael Russo

ECES 450/650

Dr. Gail Rosen

June 8, 2020

Background: COVID-19

- Disease rooted from the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).
- Novel coronavirus
 - Has not been previously identified
- Oily membrane
 - Basically, a layer of fat protecting the virus from the rest of the world
- To date, worldwide:
 - ~ 7 million confirmed cases
 - ~ 400,00 deaths

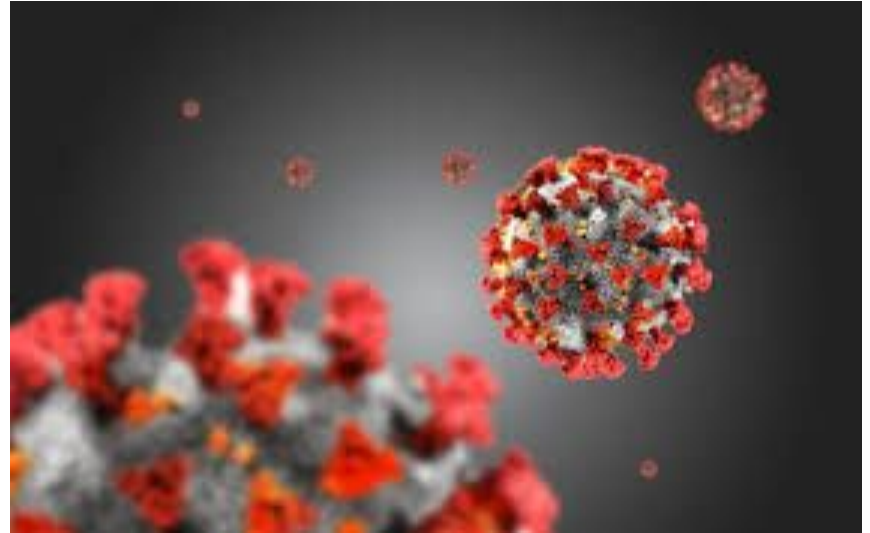


Image cred: elgin.edu

Background: Transmission

- Each virus carries instructions to make a million copies of itself.
- And so each cell infected by the coronavirus is subject to releasing millions of new viruses.
- With each genome replication process arises an opportunity for mutations to occur
 - As it spread from person to person, the more random mutations accumulate
- These accumulated mutations allow scientists to track the virus's evolution around the world.

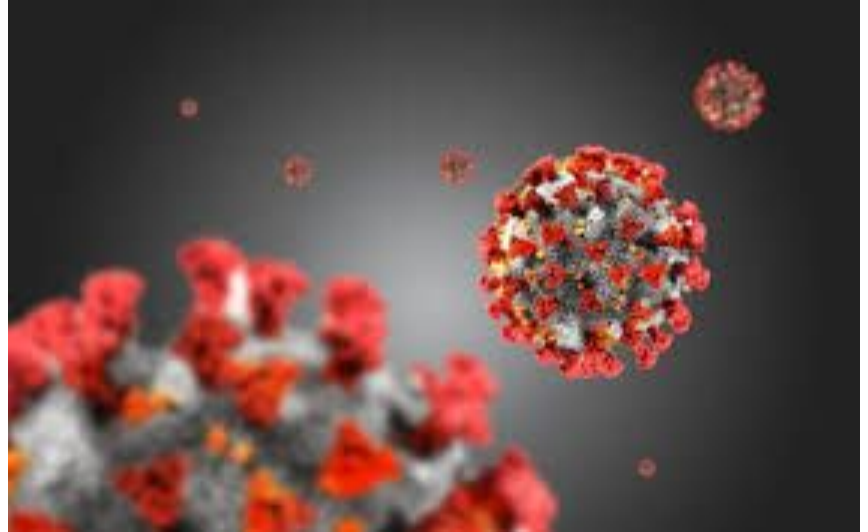


Image cred: elgin.edu

Background: Genetic Variation in COVID-19

Silent mutation

If the codon **acu** mutates to **aca** or **acc** or **acg**
the amino acid **T** won't change:
(Threonine)

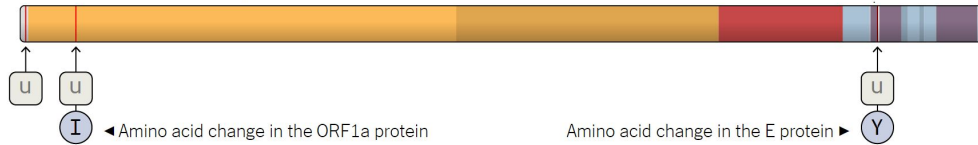
Non-silent mutation

But if **acu** mutates to **auu**
then **T** will change to **I**
(Isoleucine)

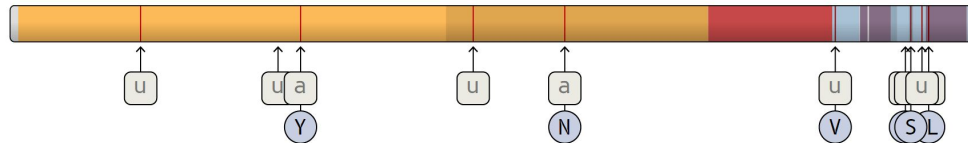
Genome **WH-09**, collected on Jan. 8 from another patient in Wuhan



ORF1a protein



Genome **VIC995**, collected on March 31 from a woman in Victoria, Australia



Aim

- Create a site that will allow visitors to easily visualize the locations, relative sizes of breakouts, and spread of different SARS-CoV-2 strains around the world.
- The site's user interface will consist of a interactive geojson map accompanied by visualizations of outbreak data.
- When a user clicks one geographical representation, the site will display the different SARS-CoV-2 sequences in both a pie and time series charts

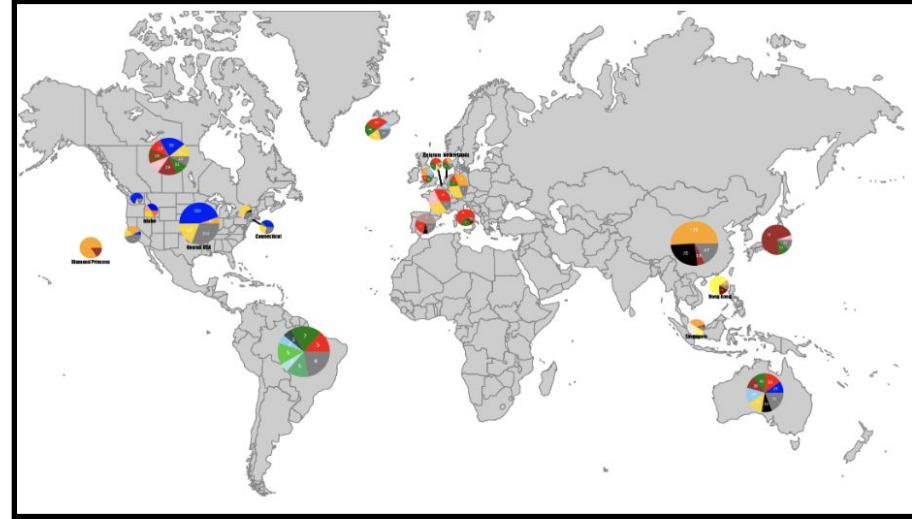


Fig.1 Conceptual overview of our proposed interactive map with corresponding pie charts. [2]

Comparison of Previous Methods (Lit. Review)

Open access epidemiologic data & interactive dashboard to monitor the COVID-19 outbreak in Canada (Berry, et al)

- Interactive COVID-19 data visualization is a fundamental tool
 - Public health
 - Research
 - Wider audience
- Reported cases are documented per each providence
- More information for each province is supplemented within the website. (location, report date, travel history, exposure source, time series deaths, and recoveries)
- Comparison
 - Berry, et al: visualization of infectious rates
 - Our team: visualization of variability of COVID-19 strains

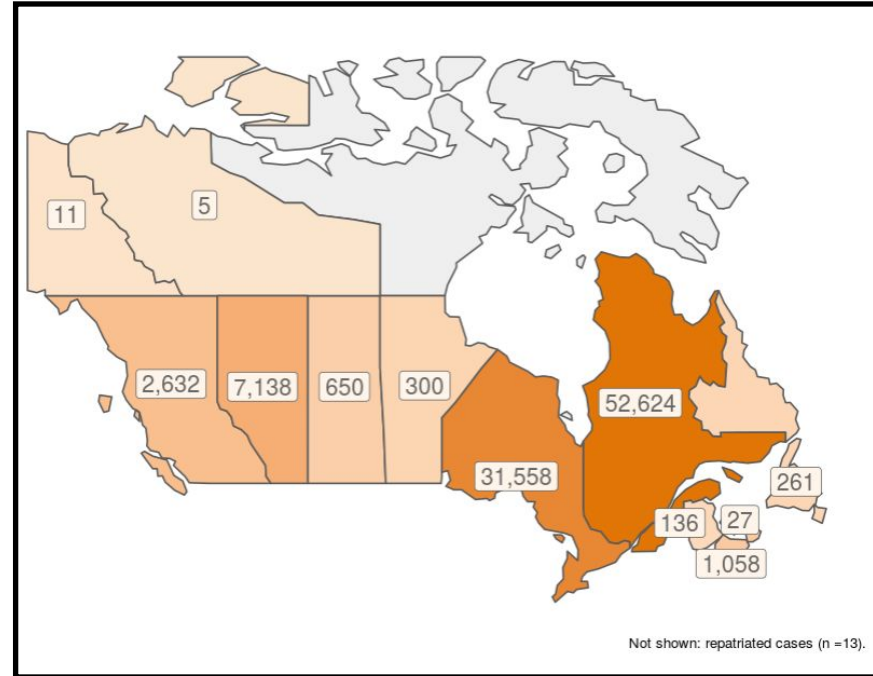
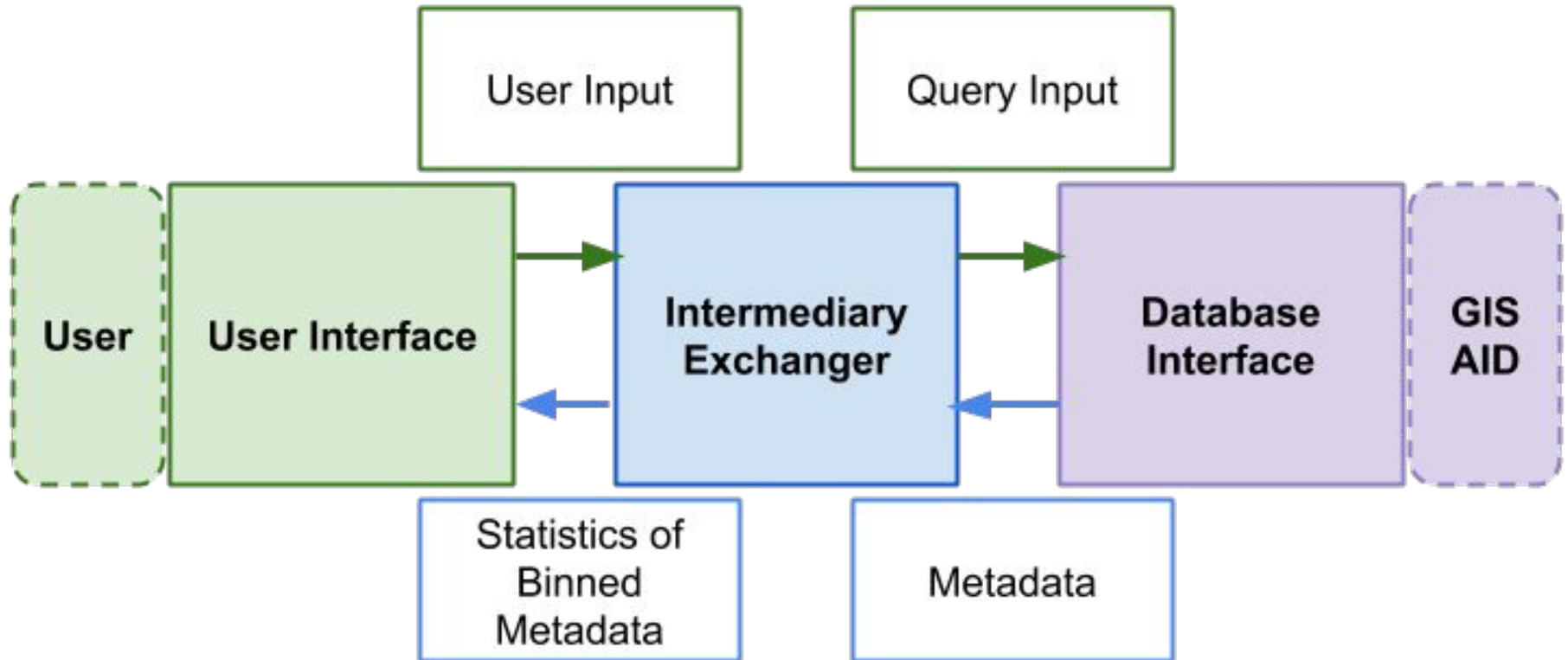


Fig. 2 Reported cases for both confirmed and presumptive positive cases. [1]

Materials

- Server
- VPN (*pro tempore*)
- GISAID Data
- ISM data analysis
- Multiple languages
 - HTML
 - CSS
 - JS
 - Python

Methods - Schematic



Methods

	Purpose	Inputs	Outputs	Code
User Interface	Chart COVID-19 cases based on user's ROI	Mouse clicks	Coordinates	<ul style="list-style-type: none"> •HTML •CSS •JS •Python •Django ORM •MapBox & geojson
		Statistics	Visualization	
Intermediary Exchanger	Translate user input, bin GISAID query's metadata, and compute stats	Coordinates	Geojson	<ul style="list-style-type: none"> •JS •Python
		GISAID metadata	Summary statistics	

Methods

	Purpose	Inputs	Outputs	Code
Database Interface	Use translated user input to query local database. Gather the json metadata from query results to create pie & time series charts	Latitude / Longitude / Date	Query	<ul style="list-style-type: none"> •Python •Mafft •Sequence data from GISAID website •Run pipeline_0_filter.sh, pipeline_1_mafft.sh, pipeline_2_run_ISM.py. •Json tables
		GISAID metadata	Json tables	

Results/Demo

VPN:

- Connect with cisco anyconnect to drexel vpn

Website:

- <http://10.248.19.125/>

Summary

- An interactive, animated map for the COVID-19 outbreak was created.
- Helps users identify mutational signatures of the virus using ISM (an entropy-based analysis)
- The map is based on GISAID data and Nextstrain for the sequence data and metadata and the ISM data analysis by Dr. Gail Rosen and Zhengqiao Zhao
- The map utilizes Python, Gunicorn, Nginx, Postgresql for developing the environment and Geojson and MapboxJS for visualization.
- Everything is built on open-source, readily available, and easy to manipulate software/code.

Future Directions

- GISAID provides API for access to their data for daily updation
- Display momentum of spread
- Display testing facilities and containment score
- Display details about the patient

Sources

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2	Lyssa
3	
4	
5	Josh Divaker
6	
7	Michael
8	
9	Josh Shelley
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11	
12	Neha
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Sources

Paper must additionally include References Cited of at least **8 references**. Proper citations (10%) (Must cite at least **8 articles from the primary research literature**).

Use Chicago style author-date variety

(http://www.chicagomanualofstyle.org/tools_citationguide.html) **for in-text citations and your list of references (i.e. bibliography which includes all references cited in your paper)**. Remember, you must cite all ideas that are not your own. And your placement of in-text citations should make it clear which statements are yours and which ideas come from your research on previous work.