Efficient simulation and graphical modeling of Covid-19 spread

Group 13

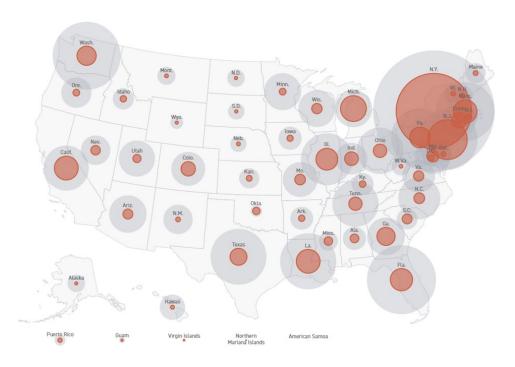
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Project Goals

Efficient simulation and graphical modeling of the spread of Covid-19 in a local community, using real Covid-19 incidents data and human interaction network data online.

We want to apply our simulation model to:

- evaluate the impact of preventative measures on public health outcomes;
- → study the progression of Covid-19 in a new demographic context.



Coronavirus by state map. "Live tracker: How many coronavirus cases have been reported in each U.S. state?" Politico. March, 16, 2020.

Models/Data Sources: (1) Population Network

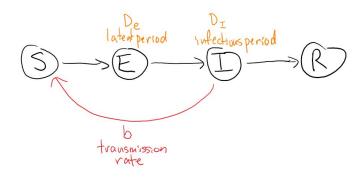
- ★ Obtained population network (list of edges) from an HIV survey done in the 1990s across eight different North American cities
- ★ Eight disjoint sub-networks which can be modelled parallely
- ★ Overall: 49,355 nodes and 64,276 unique edges
- ★ Aim to augment this graph by adding random edges and nodes

HIV Transmission Network Metastudy Project: An Archive of Data From Eight Network Studies, 1988--2001 (ICPSR 22140)

```
ID1
                     ID2 TIETYPE
                                    SEX1
                                           SEX2 AGE1 AGE2 STUDYNUM
                   106_1 sexual
                                  female female
                                                        37
    1:
            1_1
                   236 1 social
                                  female female
                                                        27
                                                        28
                   266 1
                          social
                                  female female
                                                   26
                   283 1
                          social
                                  female female
                                                   26
                                                        20
    5:
                   337 1
                          social female female
                                                   25
                                                        29
64272: 143798_8 36441_8
                                  female.
                                           male
                          sexual
                                                   21
                          sexual
                                           male.
64273: 143798 8
                 36442 8
                                  female
                                                   21
                                                        -9
64274: 143811_8
                 36429_8
                          sexual unknown
                                           male
64275: 143829 8 36447 8
                                    male female
                          sexual
64276: 143829_8 143774_8 sexual
                                    male female
                                                        14
                                                                  8
```

Models/Data Sources: (2) Epidemic Model

SEIR model characterizing disease states and transmission





States:

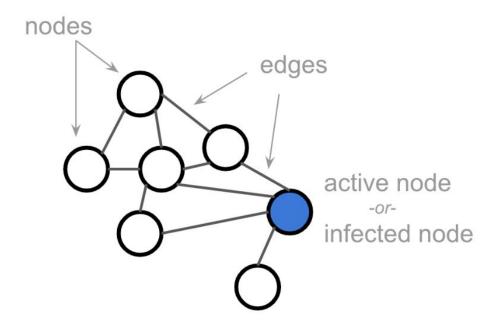
- ★ Susceptible
- **★** Exposed
- **★** Infectious
- ★ Removed (recovered or deceased)

Parameters to estimate:

- ★ Transmission rate, b
- ★ Latent period, D_e
- ★ Infectious period, D

A need for big compute & big data parallel processing

- ★ Big compute will enable us to jointly model disease propagation in our network
- ★ Big data parallel processing will allow us to conduct multiple Monte Carlo simulations simultaneously, while doing probabilistic sensitivity analyses.



Source: https://www.meltingasphalt.com/interactive/going-critical/

Infrastructure

- The project will be written in Python and run using AWS instances
- Networks will be supported by Spark-integrated GraphFrames on Hadoop
- To handle big data requirements, MPI will be used for parallelization
- OpenMP will be used to handle big compute requirements





