Reaction-diffusion spatial modeling of COVID-19 in Chicago

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Outline

1. The COVID Problem
2. Project Context and Objectives
3. Current Work
4. Future Goals

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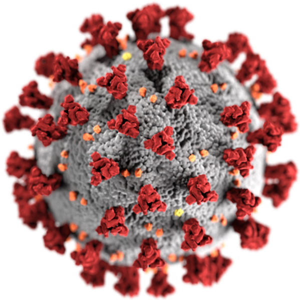
The COVID Problem

Identified in Wuhan, China in December 2019.
Caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

In the United States alone, we currently have

- **37,768,911** total cases
- **626,833** total deaths



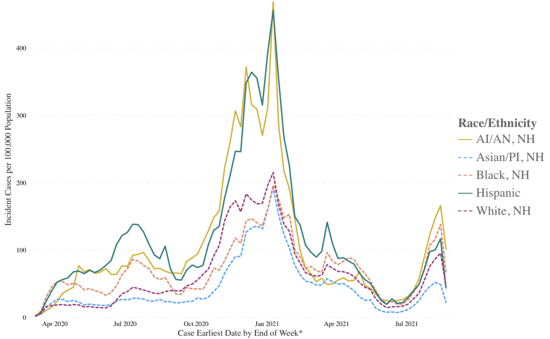
The COVID Problem

Transmission by exposure to infectious respiratory fluids:

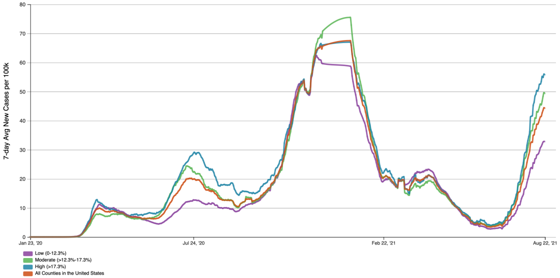
1. Inhalation of virus
2. Deposition of virus on exposed mucus membranes
3. Touching mucous membranes with soiled hands contaminated with virus

The COVID Problem

COVID-19 weekly cases per 100,000 population by race/ethnicity, United States



COVID-19 weekly case rate per 100,000 population by percentage of county population in poverty, United States



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Project Context and Objectives

Why make a mathematical study of COVID-19?

An epidemic model provides ...

- a convenient summary of the data
- insight into the underlying processes of the disease spread
- a testing ground for assessing control procedures

Project Context and Objectives

Models of infectious diseases are usually variations on the **Kermack-McKendrick model** (1927).

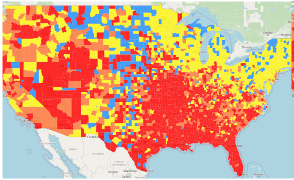
Usual assumptions:

- Population is *homogeneous*
- Transmission is spatially independent

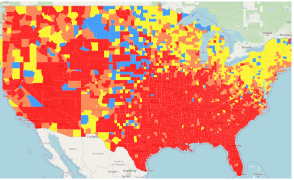
Project Context and Objectives

These assumptions don't match reality!

Level of community transmission by county



(a) 7/22/2021



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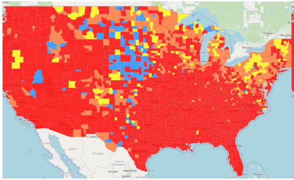
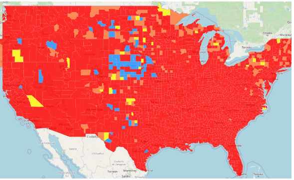
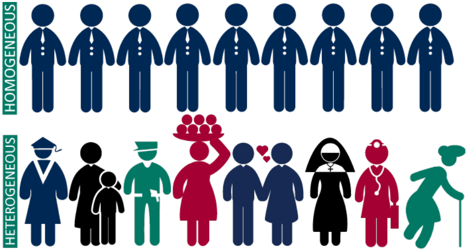


(c) 8/8/2021



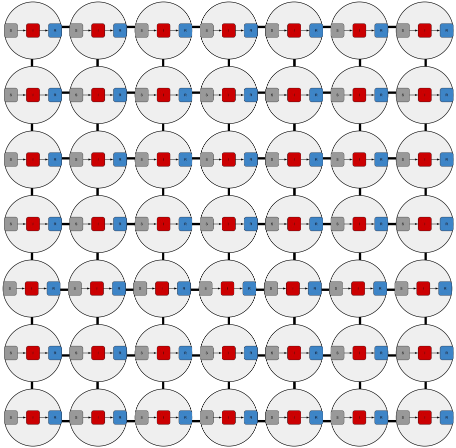
(d) 8/21/2021



Project Context and Objectives

Idea: Use reaction-diffusion to build a spatially explicit model.

- The data clearly shows a diffusive pattern
- Spatial dependence can approximate demographic differences
- Spatially dependent data exists for many scales and regions



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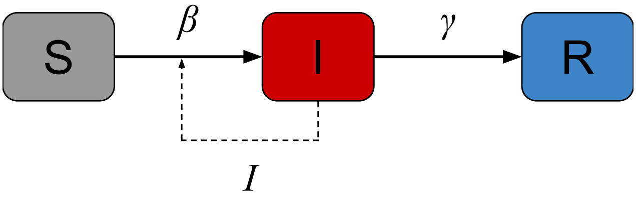
Current Work

Original motivation from Summer 2020 IPRO with Prof. Robert Ellis and Mr. David Eads (NPR).
Expanded over Summer 2021 with Prof. Chun Liu and Prof. Yiwei Wang.

Start by defining the zero-dimension (ODE) model:

1. Start with a population of *susceptibles* (S)
2. Some of the population may become *infected* (I) upon emergence of the virus
3. Infected individuals interact with susceptibles at rate β to draw new members into I
4. A fraction of I recover or die at a rate γ moving to the *removed* (R) population



This represents processes that occur in a "well mixed" situation.

Current Work

The population model at the PDE level is an autonomous diffusion with a source:

$$\begin{aligned} S_t &= \nabla(\mathfrak{D}_s \nabla S) - \beta S I, \\ I_t &= \nabla(\mathfrak{D}_I \nabla I) + \beta S I - \gamma I, \\ R_t &= \gamma I. \end{aligned}$$

Assumptions:

- The R population has immunity.
- Diffusion performs all relevant spreading.
- Arriving infected individuals form local hotspots.

Current Work

Next we identify the parameters β and γ at the ODE level:

Idea: Minimize the distance between the model time series and the observed time series.

$$\mathcal{N} = \sum_{i}^{t_{\text{fit}}^{\text{end}}} \left(\left| C_{\text{num}}(t_i) - C_{\text{obs}}(t_i) \right|^2 + \left| D_{\text{num}}(t_i) - D_{\text{obs}}(t_i) \right|^2 \right)$$

where the index i identifies a point in the time series.

Optimize the parameters to reproduce:

- the reported *total* number of infected cases $C(t) = I(t) + R(t)$
- the *total* number of deceased $D(t) = R(t)$.

Current Work

Table: ODE parameters for Chicago: optimal (best-fitting), median and interquartile range, and variation range used in the optimization algorithm. Initial parameter guesses were uniformly sampled within these ranges.

		Median (interquartile range)	Initial value
Population	N	2,695,598	
Initial population	(I_0, R_0)	(127, 2)	
Transmission rate, $S \to I$ [per day]	β[1]	0.38206(0.38204-0.38209)	$c \in U[0, 1]$
Transition rate, $I \to R$ [per day]	γ	0.39656(0.39654-0.39659)	$c \in U[0.25, 0.75]$

[1] The transmission rate β must be divided by N when used in the ODE model.

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