

Epidemic Modeling and Simulations

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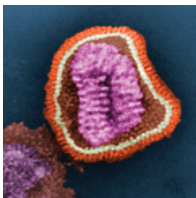
Sorbonne University

Abu Dhabi

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What are infectious diseases?

- ▶ **Caused by:** harmful agents (pathogens) that get into your body.
- ▶ **Most common causes:** viruses, bacteria and other microorganisms.
- ▶ **Usually spread** from person to person, through contaminated food or water and through bug bites.
- ▶ Some infectious diseases are **minor** and some are **very serious**.



Viruses

common cold, measles, influenza

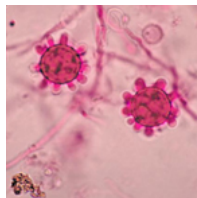
Credit: Dr. Cynthia Goldsmith/CDC



Bacteria

coccus, bacillus, vibrio

Credit: The National Academics



Other Microbes

fungi, protozoa, helminths

Credit: Dr. Libero Ajello/CDC

Types of infectious diseases

Type	Descriptions
Virus	<ul style="list-style-type: none">• a piece of information (DNA or RNA).• no way to reproduce on their own.• get inside our cells and use our cells' machinery to make copies of themselves. <p>(Common cold, Flu, COVID-19, Stomach flu, Hepatitis, RSV)</p>
Bacteria	<ul style="list-style-type: none">• single-celled organisms.• all around us, including inside of our body and on our skin.• Many bacteria are harmless or even helpful, but certain bacteria release toxins that can make you sick. <p>(Strep throat, Salmonella, Tuberculosis, Whooping cough (pertussis))</p>
Fungal	<ul style="list-style-type: none">• like bacteria, there are many different fungi.• live on and in your body.• when your fungi get overgrown or when harmful fungi get into your body through your mouth, your nose or a cut in your skin, you can get sick. <p>(Ringworm (like athlete's foot), Fungal nail infections)</p>
Parasitic	<ul style="list-style-type: none">• use the bodies of other organisms to live and reproduce.• include worms (helminths) and some single-celled organisms (protozoa). <p>(Giardiasis, Toxoplasmosis, Hookworms, Pinworms)</p>

- ▶ **Vaccination Programs, Antiviral and Antibiotic Treatments, Public Health Campaigns, Isolation and Quarantine, etc..**
- ▶ While these interventions are **effective** in controlling outbreaks, they can become **costly** during widespread epidemics
- ▶ However, **leveraging mathematical modeling** allows us to:
 - ▶ understand the dynamics
 - ▶ early prediction
 - ▶ scenario simulations
 - ▶ optimizing resources
 - ▶ global spread analysis, etc.

Epidemic, Endemic, Pandemic¹

▶ **Epidemic:**

- ▶ an unexpected increase in the number of disease cases in a specific geographical area.

- ▶ Yellow fever, smallpox, measles, and polio

▶ **Pandemic:**

- ▶ a disease's growth is exponential. This means the growth rate skyrockets, and each day cases grow more than the day prior.

- ▶ covers a wide area, affecting several countries and populations.

▶ **Endemic:**

- ▶ consistently present but limited to a particular region.

- ▶ **Malaria** is infectious disease that is endemic to Africa.

- ▶ **Caribbean Dengue** is still present due to a failure to eradicate the *Aedes aegypti* mosquito



- ▶ **What is the risk** of an epidemic to occur?
- ▶ **How long** will it last?
- ▶ Are **all individuals** at risk of **becoming infected**?
- ▶ **How far** will it spread?
- ▶ What **impact** does a particular **intervention** have on the risk and duration of the epidemic?



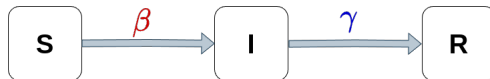
Difference Equations

$$\begin{cases} A(t+1) = A(t) - \text{Flow A-B} \\ B(t+1) = B(t) + \text{Flow A-B} - \text{Flow B-C} \\ C(t+1) = C(t) + \text{Flow B-C} \end{cases}$$

Differential Equations

$$\begin{cases} A'(t) = -aA \\ B'(t) = aA - bB \\ C'(t) = bB \end{cases}$$

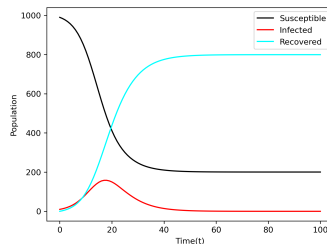
- ▶ Introduced by Kermack and McKendrick in 1927²
- ▶ Divides the population into three compartments: S , I and R
- ▶ $S(t) :=$ the number of susceptibles at time t
 - ▶ those individuals who are healthy and can be infected
- ▶ $I(t) :=$ the number of infectives at time t
 - ▶ those individuals who are infected and are able to transmit the disease
- ▶ $R(t) :=$ the number of immune at time t
 - ▶ those individuals who are immune because have been infected and now have recovered



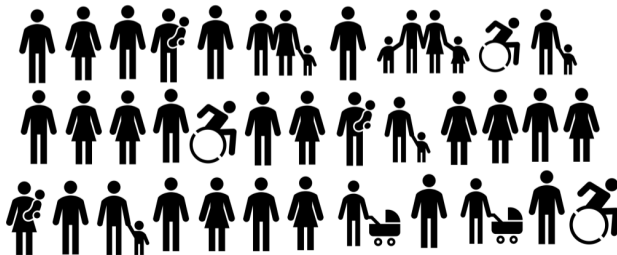
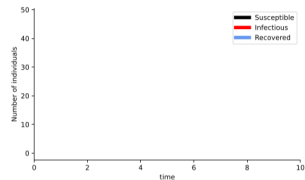
$$\begin{cases} S'(t) = -(\text{rate out})S \\ I'(t) = (\text{rate in})S - (\text{rate out})I \\ R'(t) = (\text{rate in})I \end{cases}$$

- **(rate out)**: (infectiousness) \times P(contact with infectious person) $= \beta \times \frac{I}{N}$
- Assumption: $S + I + R = N = \text{constant}$
- $\beta :=$ infectiousness, $\gamma :=$ recovery rate

$$\begin{cases} S'(t) = -\beta \frac{I}{N} S \\ I'(t) = \beta \frac{I}{N} S - \gamma I \\ R'(t) = \gamma I \end{cases}$$

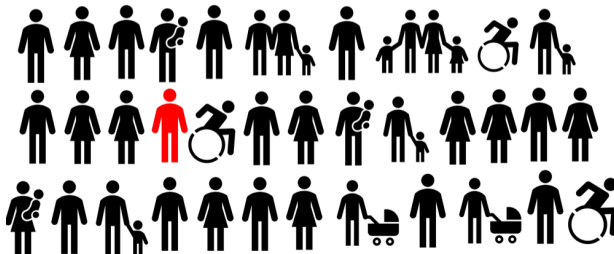
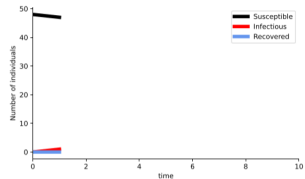


SIR-model



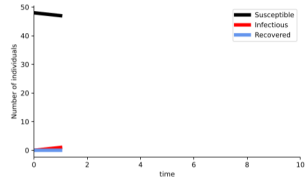
Credit: S. Kissler, UCB

SIR-model



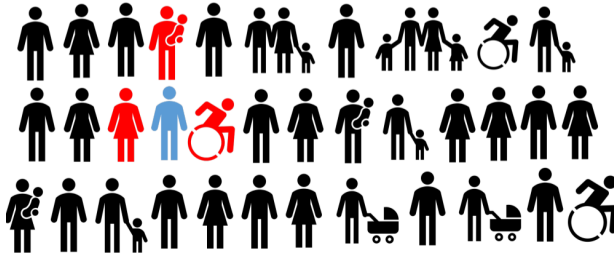
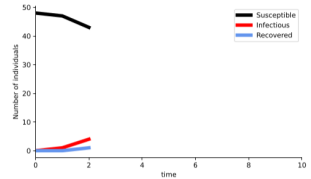
Credit: S. Kissler, UCB

SIR-model



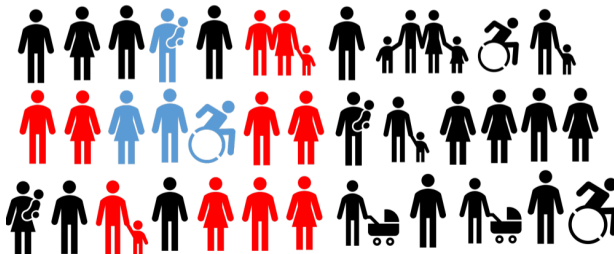
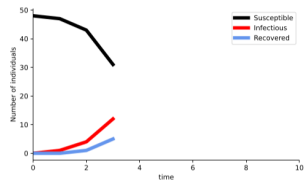
Credit: S. Kissler, UCB

SIR-model



Credit: S. Kissler, UCB

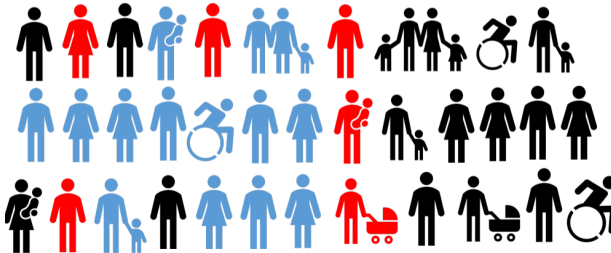
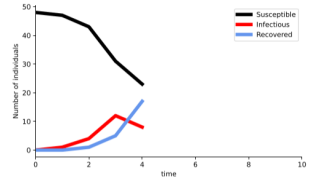
SIR-model



Credit: S. Kissler, UCB

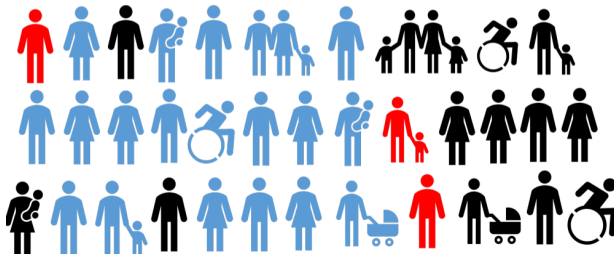
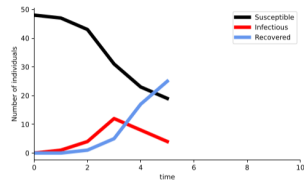
SIR-model

Susceptible Infectious Recovered



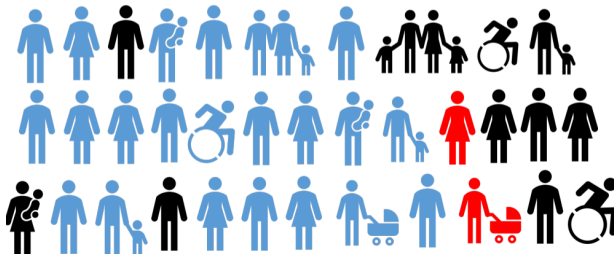
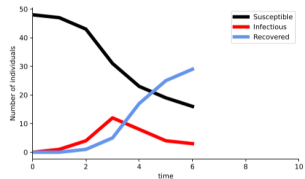
Credit: S. Kissler, UCB

SIR-model



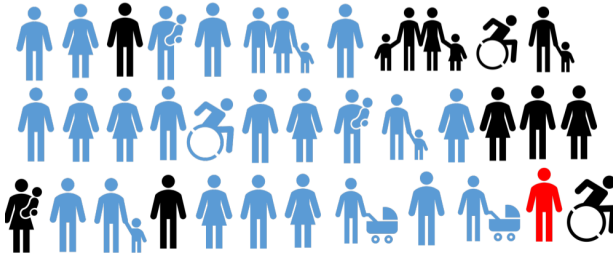
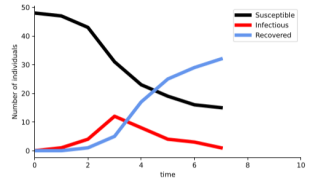
Credit: S. Kissler, UCB

SIR-model



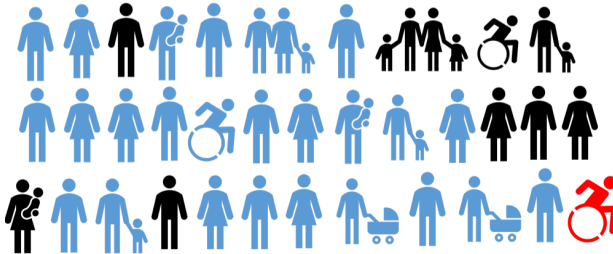
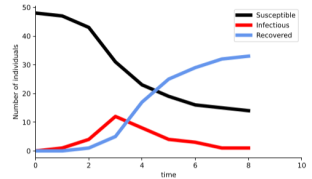
Credit: S. Kissler, UCB

SIR-model



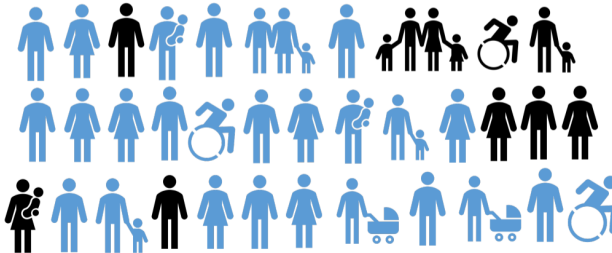
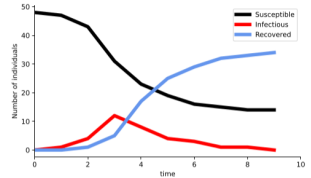
Credit: S. Kissler, UCB

SIR-model



Credit: S. Kissler, UCB

SIR-model



Credit: S. Kissler, UCB

Will there be an outbreak?

$$I'(t) = \beta \frac{I}{N} S - \gamma I$$

- ▶ An epidemic starts if the number of infected individuals increases.

$$I'(t) > 0$$

$$\beta \frac{I}{N} S - \gamma I > 0$$

- ▶ at the beginning of an epidemic $S(t) \approx N$,

$$\beta I - \gamma I > 0$$

$$\left(\frac{\beta}{\gamma} - 1\right) \gamma I > 0$$

$$(\mathcal{R}_0 - 1) \gamma I > 0$$

- ▶ Where $\mathcal{R}_0 = \frac{\beta}{\gamma}$ is called **basic reproduction number**.

For an epidemic to start: $\mathcal{R}_0 > 1$.

Basic reproduction number

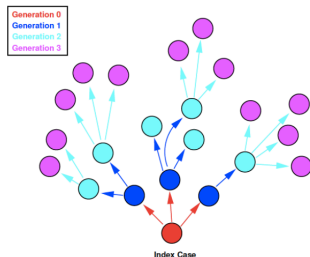


Dr. Erin Mears (Kate Winslet) explains \mathcal{R}_0

Definition

The average number of secondary cases that would be generated by a primary case in a totally susceptible population.

Here, $R_0 = 3$.



Credit: www.mat.uab.cat/matmat

Values of R_0 of well-known diseases

Disease	R_0
Measles	12–18 ^{[1][2]}
Chickenpox	10–12 ^[3]
COVID-19 (Delta variant)	5–9.5 ^[4]
Polio	5–7 ^[a]
Whooping cough	5.5 ^[9]
Smallpox	3.5–6.0 ^[10]
HIV/AIDS	2–5 ^[11]
COVID-19 (ancestral strain)	2–3 ^[12]
Common cold	2–3 ^[13]
Flu (2009 pandemic strain)	1.6 (1.3–2.0) ^[14]
Seasonal flu	1.3 (1.2–1.4) ^[15]

Credit: www.wikipedia.org

Can we prevent the outbreak?

► **IDEA! Vaccination!!!**

► What proportion, p , should we vaccinate such that $I'(t) < 0$

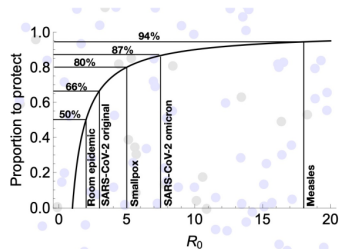
$$\begin{aligned}I'(t) < 0 &\implies \beta \frac{I}{N} S - \gamma I < 0 \\&\implies \beta \frac{I}{N} S < \gamma I\end{aligned}$$

► At initially, p portion vaccination of N is pN , thus

$$S_0 \approx N - pN = (1 - p)N$$

Therefore,

$$\begin{aligned}\beta \frac{I}{N} (1 - p)N &< \gamma I \implies \beta(1 - p)I < \gamma I \\&\implies 1 - p < \frac{\gamma}{\beta} \\&\implies 1 - p < \frac{1}{R_0} \\&\implies p > 1 - \frac{1}{R_0}\end{aligned}$$



Credit: S. Kissler, UCB

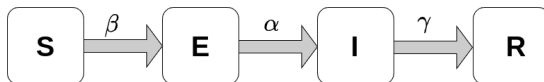
(Critical vaccination threshold)

We can increase model complexity and realism by:

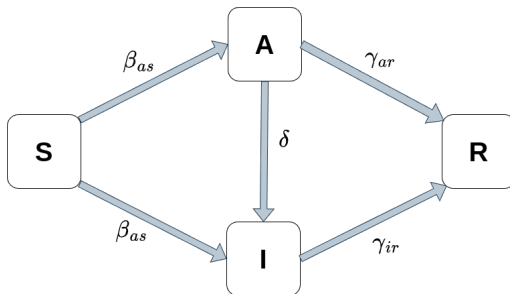
- ▶ adding **vital dynamics** (birth rate and death rate)
- ▶ adding **disease states (compartments)**
- ▶ changing **transitions** (flows), or
- ▶ splitting compartments to account for **population heterogeneity**

With more compartments

- ▶ Adding **Exposed compartment (E)**



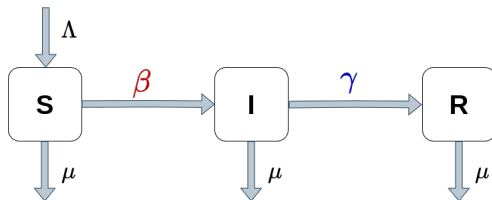
- ▶ Adding **Symptomatic (I)** and **Asymptomatic (A)**



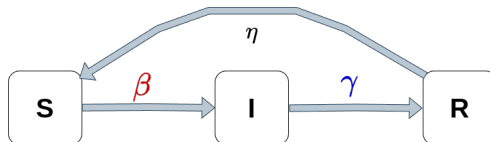
- ▶ **Othres:** Quarantine (Q), Disease-related death (D), Hospitalization (H), Vaccination (V), etc.

With vital dynamics and loss of immunity

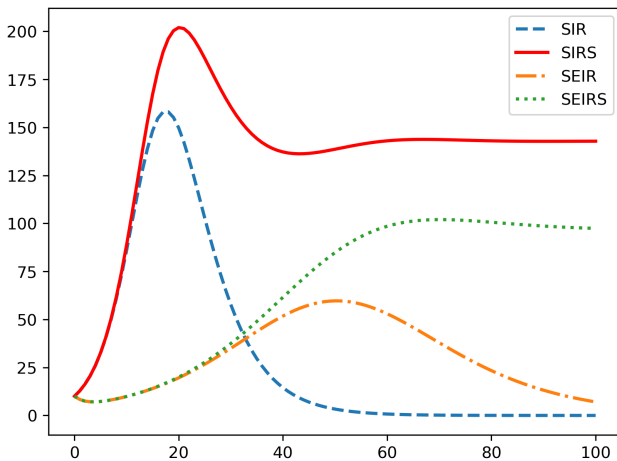
- ▶ λ := natural birth rate
- ▶ μ := natural death rate



- ▶ η := rate of loss of immunity (SIRS model)



Comparison:



- ▶ **Incorporating Delays:** Introduce time delays to represent incubation periods or delayed recovery
- ▶ **Dynamic or Time-Dependent Transition Rates:** Allow parameters like β or γ rates to change over time, reflecting interventions (e.g., lockdowns, vaccination campaigns) or seasonal effects.
- ▶ **Probabilistic or Stochastic Flows:** Introduce randomness into to model variability in real-world dynamics:

$$\beta \rightarrow \beta + \sigma B'(t),$$

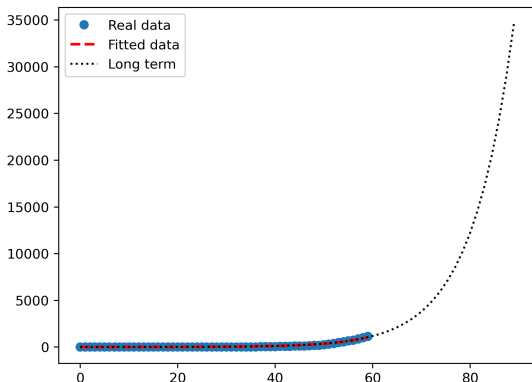
where B describes a Brownian motion, etc.

- ▶ **Introducing Nonlinear Incidence Rates:** Replace simple standard bilinear incidence with saturation functions:

$$\frac{\beta SI}{N} \rightarrow \frac{\beta SI}{1 + \alpha I}.$$

Parameter Estimation

- ▶ With confirmed cases of COVID19-India data⁴ from 31-Jan to 29-March
- ▶ Fit with SIR model and estimate the parameters: β and γ
- ▶ python: `optimize.curve_fit(fit_odeint, Time, I_data, p0=p0)`



- ▶ Consider: $S(x, t) :=$ susceptible individuals at time t and space x
- ▶ Consider: $I(x, t) :=$ infected individuals at time t and space x
- ▶ Consider: $R(x, t) :=$ recovered individuals at time t and space x

Classical Method

$$\left\{ \begin{array}{l} \frac{\partial S}{\partial t} = -\beta \frac{I}{N} S + \frac{\partial^2 S}{\partial x^2} \\ \frac{\partial I}{\partial t} = \beta \frac{I}{N} S - \gamma I + \frac{\partial^2 I}{\partial x^2} \\ \frac{\partial R}{\partial t} = \gamma I + \frac{\partial^2 R}{\partial x^2} \end{array} \right.$$

Network-based Method

$$\left\{ \begin{array}{l} \frac{\partial S}{\partial t} = -\beta \frac{I}{N} S + \Delta S \\ \frac{\partial I}{\partial t} = \beta \frac{I}{N} S - \gamma I + \Delta I \\ \frac{\partial R}{\partial t} = \gamma I + \Delta R \\ \Delta F(x) = \sum_{y \sim x, y \in V} [F(y) - F(x)] \end{array} \right.$$

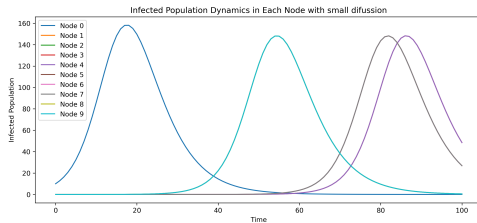
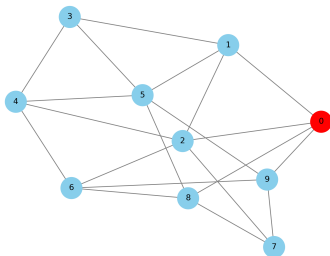
- ▶ In network model, consider $G := \langle \mathbf{V}, \mathbf{E} \rangle$ be a standard connected undirected finite graph with $|\mathbf{V}| = n$

Reform of the network model

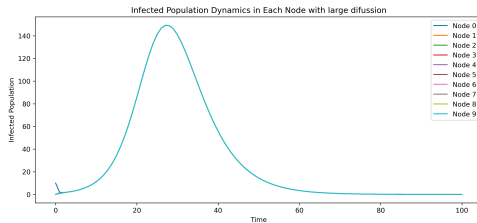
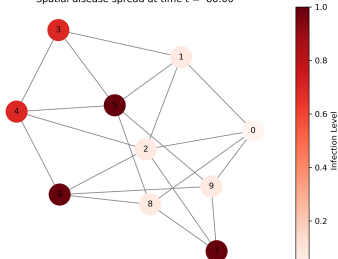
- ▶ Let S_i, I_i, R_i at node i and time t
- ▶ Let N_i is constant population of node i
- ▶ The Laplacian matrix associated with G : $L = A - D$, where A, D are adjacent matrix and degree matrix, respectively.
- ▶ Then, we can reform the network model⁵ as follows:

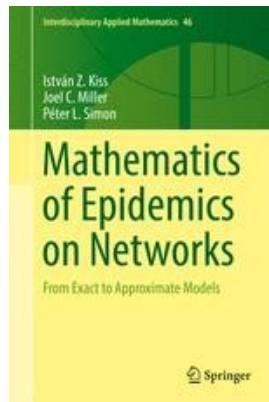
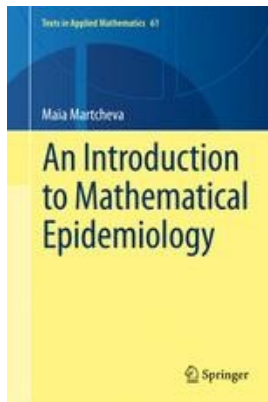
$$\begin{cases} \frac{dS_i}{dt} = -\beta \frac{I_i}{N_i} S_i + \sigma \sum_{j=1}^n L_{ij} S_j, & S_i(0) = S_{i0} \\ \frac{dI_i}{dt} = \beta \frac{I_i}{N_i} S_i - \gamma I_i + \sigma \sum_{j=1}^n L_{ij} I_j, & I_i(0) = I_{i0} \\ \frac{dR_i}{dt} = \gamma I_i + \sigma \sum_{j=1}^n L_{ij} R_j, & R_i(0) = R_{i0} \end{cases}$$

where $i = 1, 2, \dots, n$.



Spatial disease spread at time $t = 80.00$





Thank You!



Scan for Slide, Python Code, and Data.