Epidemic Modeling and Simulations

Madhab Barman
Visiting Researcher
madhabbrmn@gmail.com

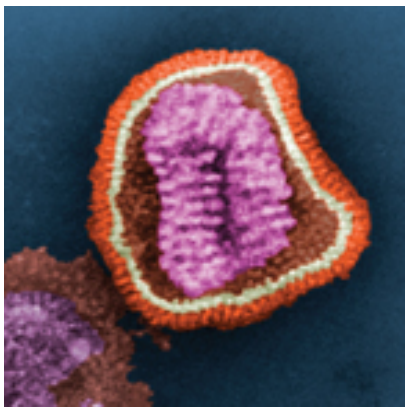
Supervisor: Dr. Tanujit Chakraborty
Sorbonne University
Abu Dhabi

November 26, 2024

SORBONNE UNIVERSITY ABU DHABI

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

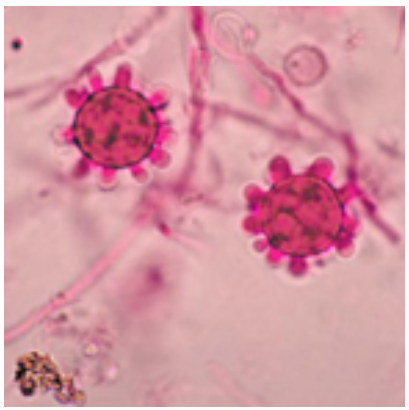
common cold, measles, influenza

Credit: Dr. Cynthia Goldsmidth/CDC

Bacteria

coccus, bacillus, vibrio

Credit: The National Academics



Other Microbes

fungi, protozoa, helminths

Credit: Dr. Libero Ajjelo/CDC

SORBONNE UNIVERSITY ABU DHABI

Types of infectious diseases

Type	Descriptions
Virus	• 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. (Common cold, Flu, COVID-19, Stomach flu, Hepatitis, RSV)
Bacteria	• 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. (Strep throat, Salmonella, Tuberculosis, Whooping cough (pertussis))
Fungal	• 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. (Ringworm (like athlete's foot), Fungal nail infections)
Parasitic	• use the bodies of other organisms to live and reproduce. •include worms (helminths) and some single-celled organisms (protozoa). (Giardiasis, Toxoplasmosis, Hookworms, Pinworms)

SORBONNE UNIVERSITY ABU DHABI

Preventing Spread

- **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.

SORBONNE UNIVERSITY ABU DHABI

Epidemic, Endemic, Pandemic[1]

- **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

Credit: www.shutterstock.com

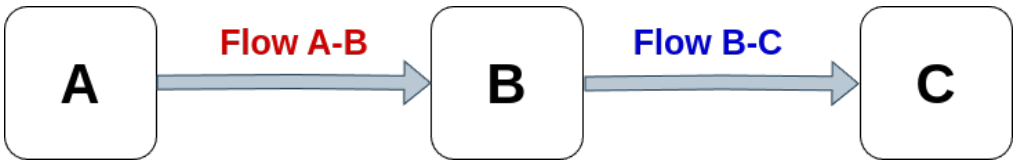
[1] www.publichealth.columbia.edu

Modeling Epidemics: Questions?

- **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?

SORBONNE UNIVERSITY ABU DHABI

Compartmental Model



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

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

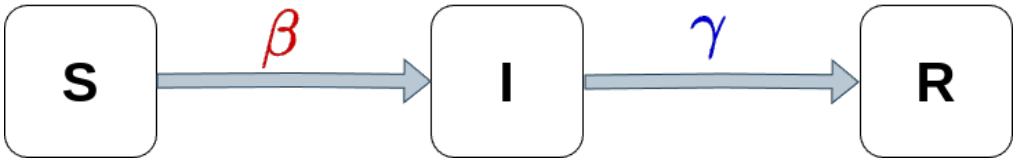
SORBONNE UNIVERSITY ABU DHABI

SIR-model

- Introduced by Kermack and McKendrick in 1927[2]
- 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

[2] Kermack & McKendrick, A Contribution to the Mathematical Theory of Epidemics (1927)

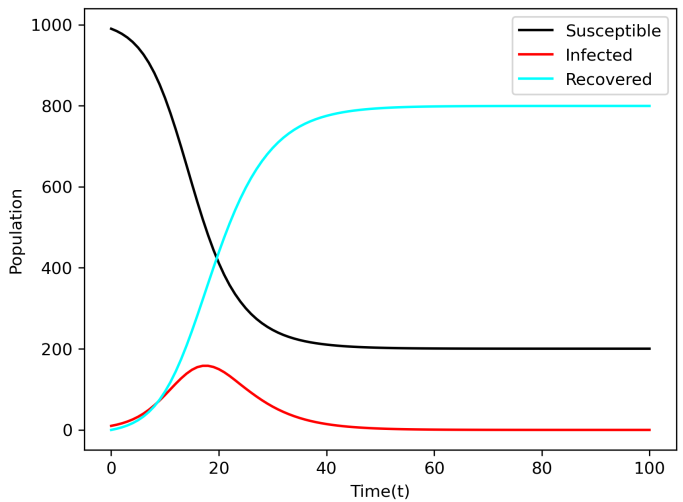
SIR-model



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

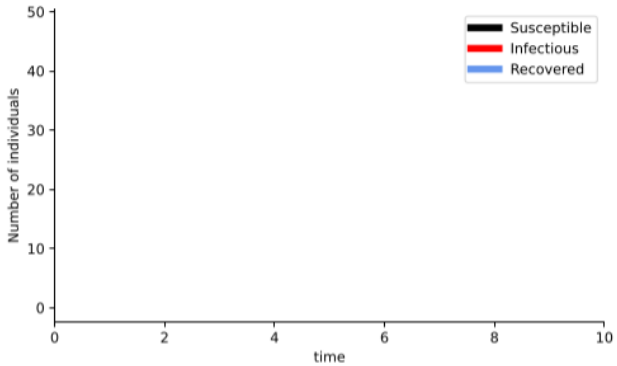
- (rate out): (infectiousness)× P(contact with infectious person) $= \beta \times \frac{I}{N}$
- Assumption: $S + I + R = N$ = constant
- β := infectiousness, γ := recovery rate

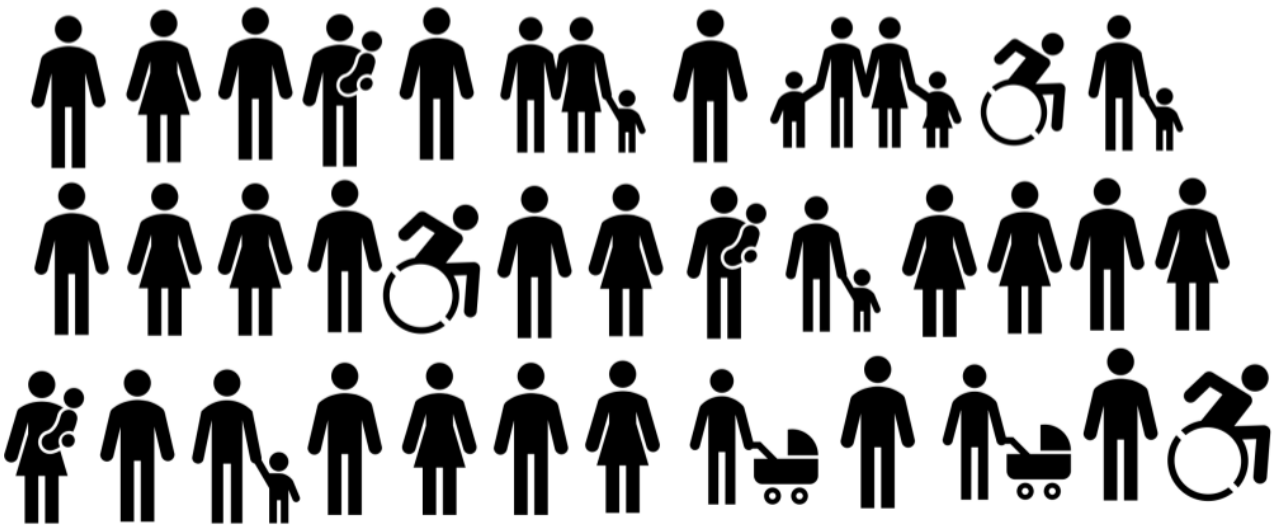
$$\begin{cases} S'(t) = -\beta \frac{I}{N} S \\ I'(t) = \beta \frac{I}{N} S - \gamma I \\ R'(t) = \gamma I \end{cases}$$



SORBONNE UNIVERSITY ABU DHABI

SIR-model

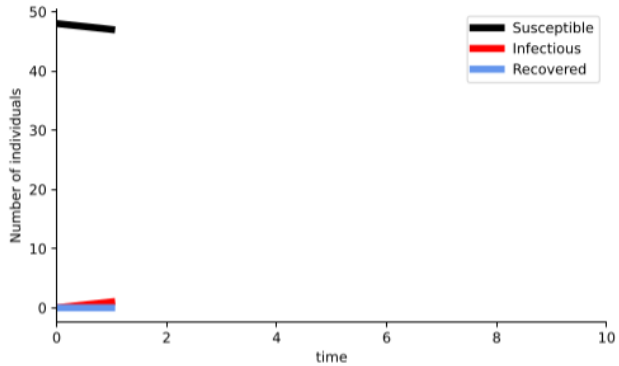


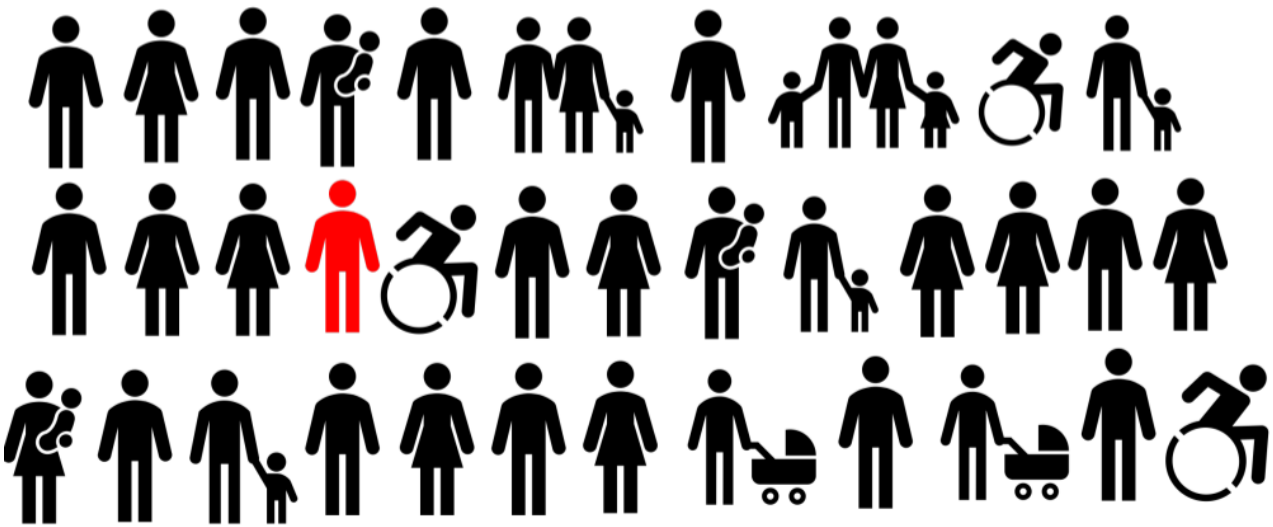


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

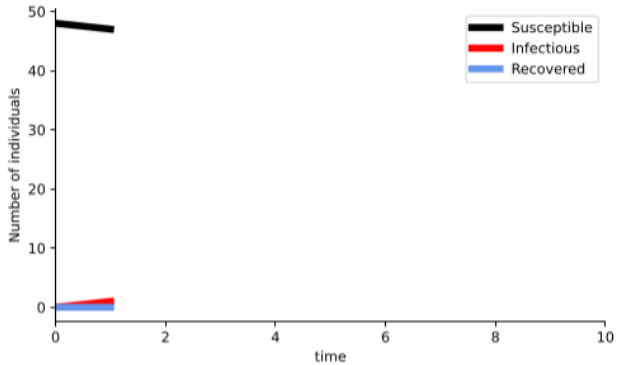


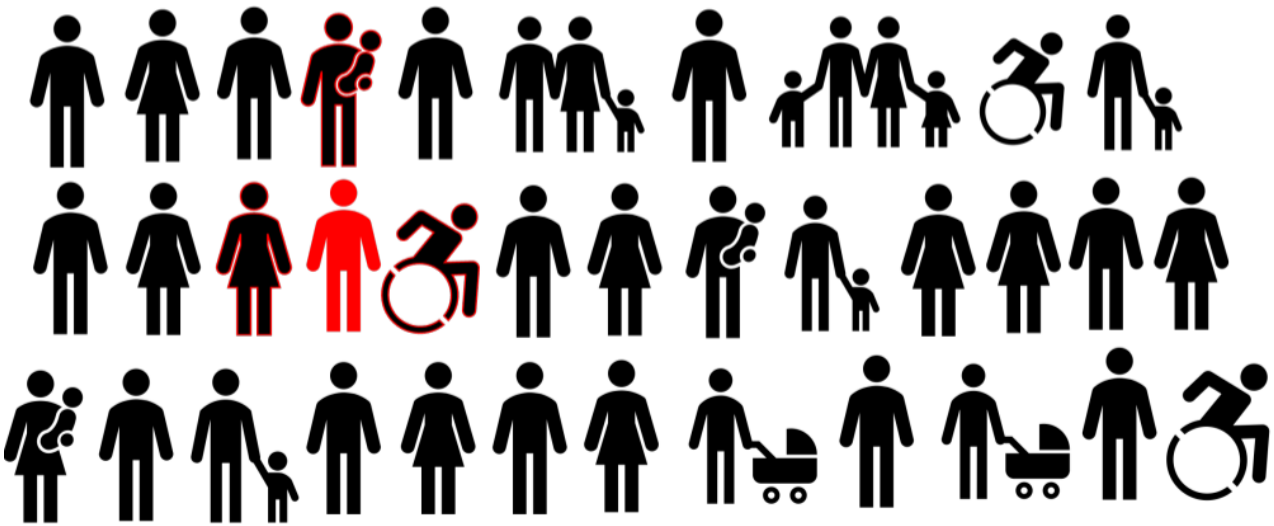


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

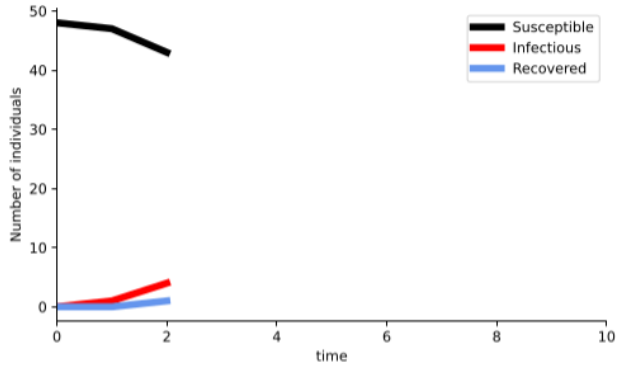


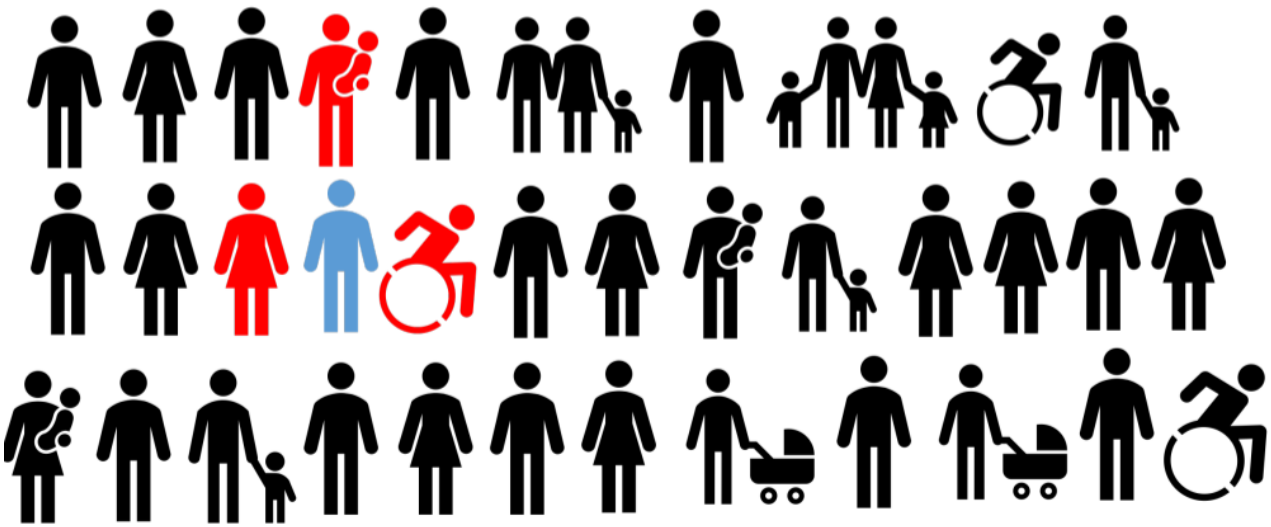


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

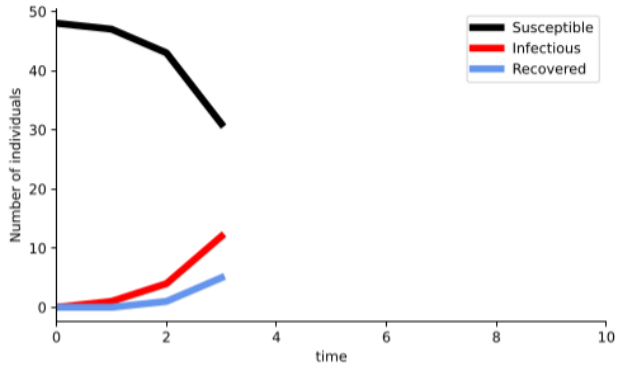


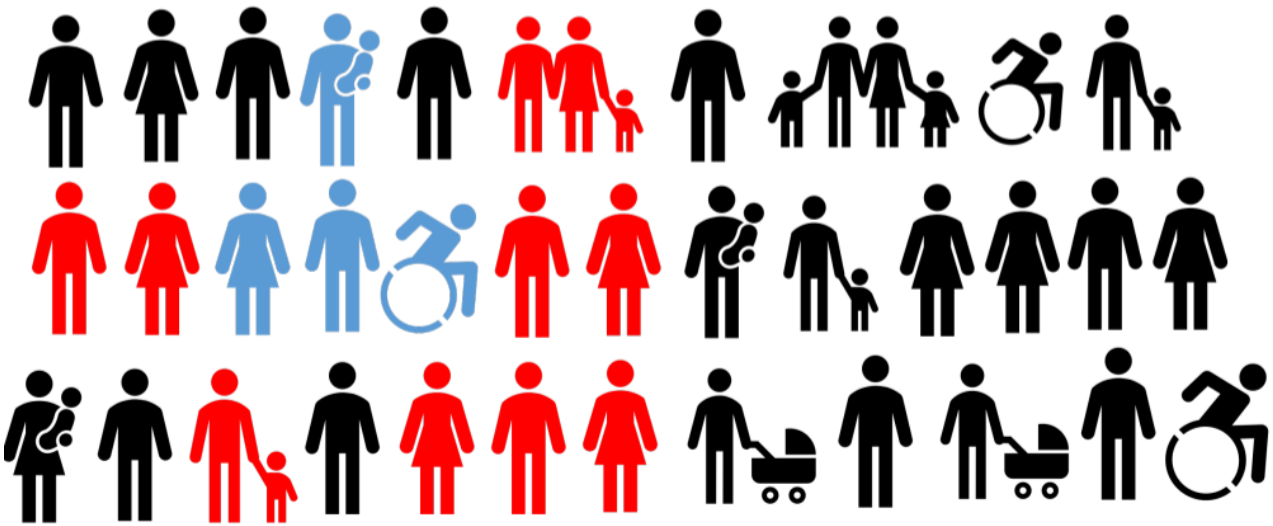


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

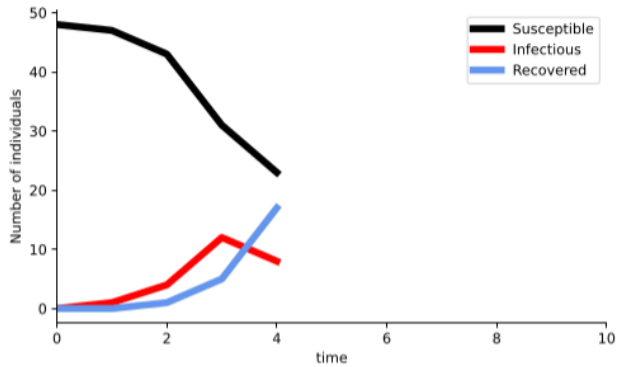


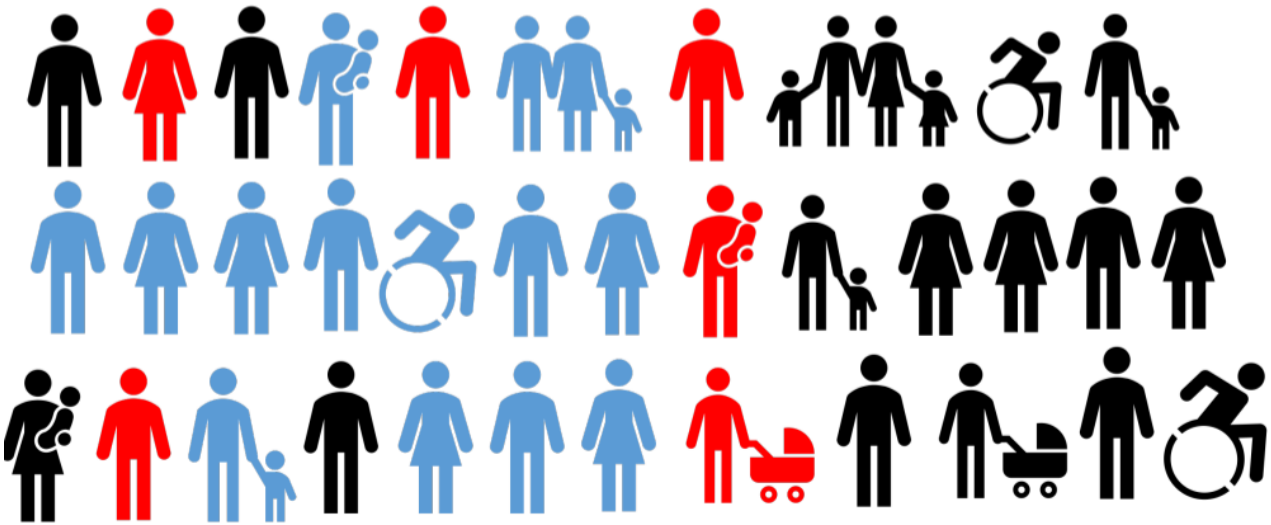


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

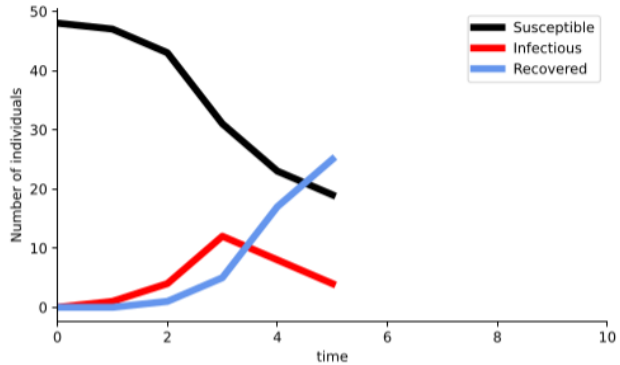


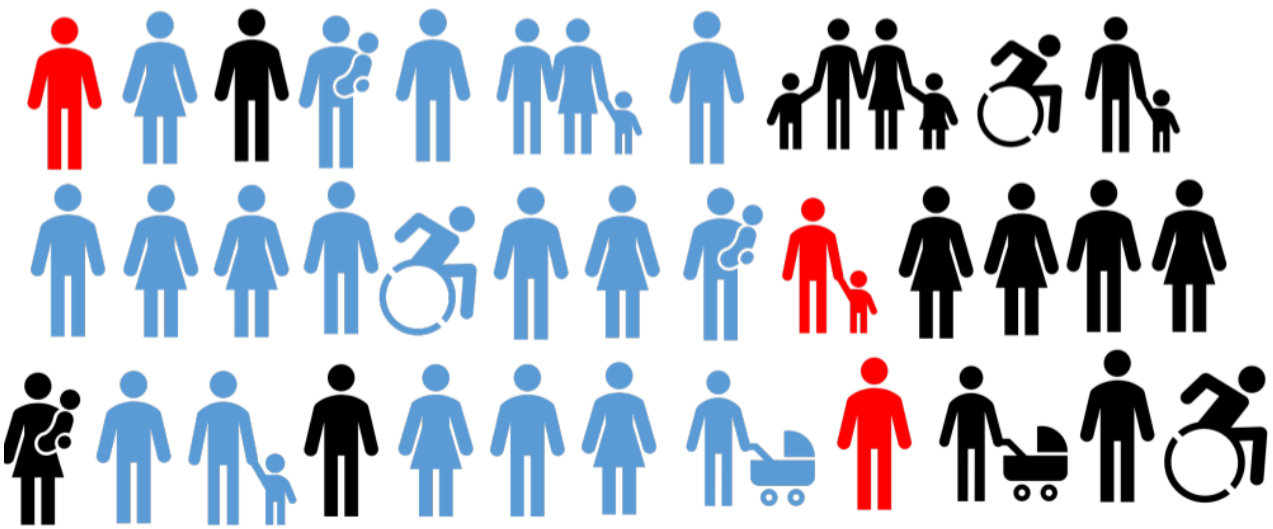


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

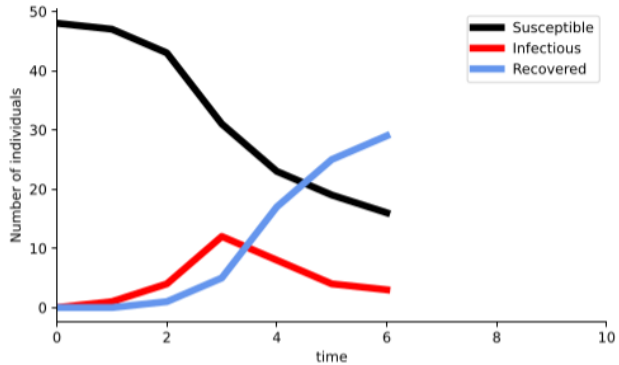


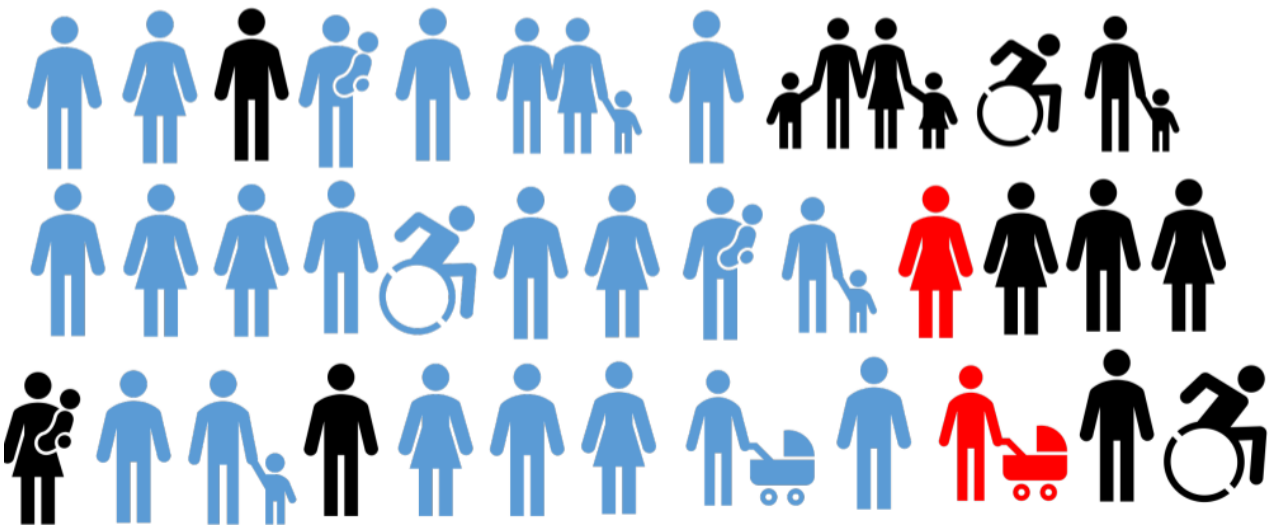


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

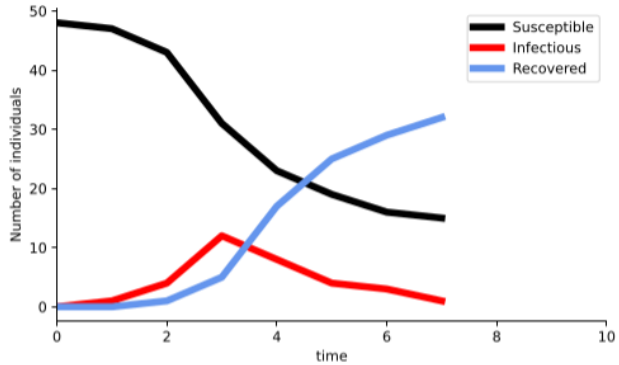


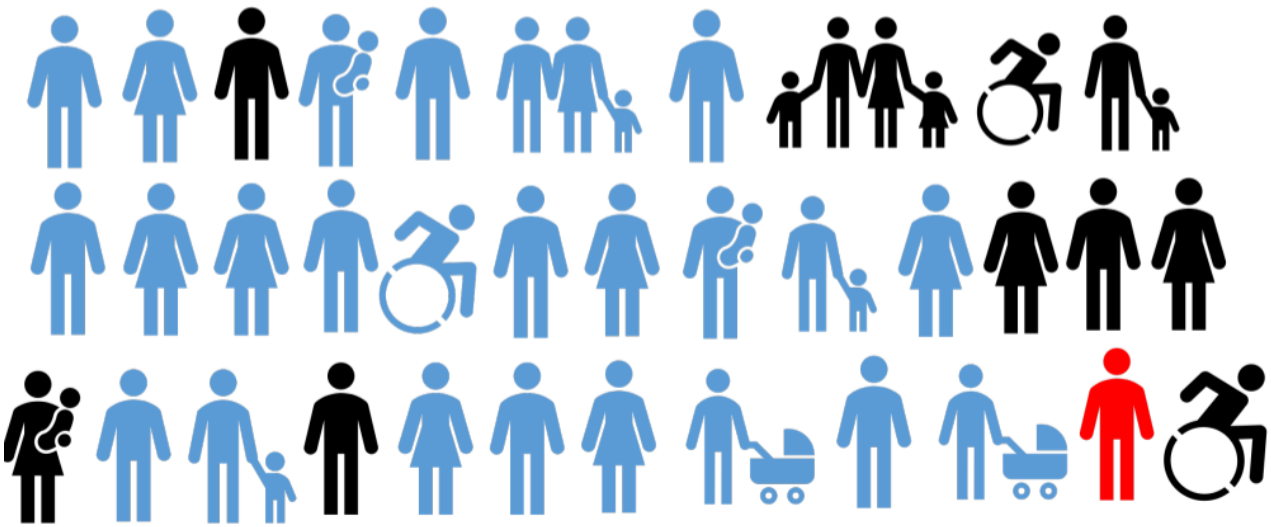


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

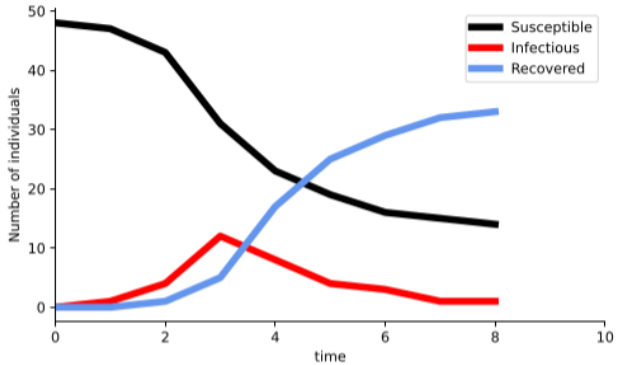


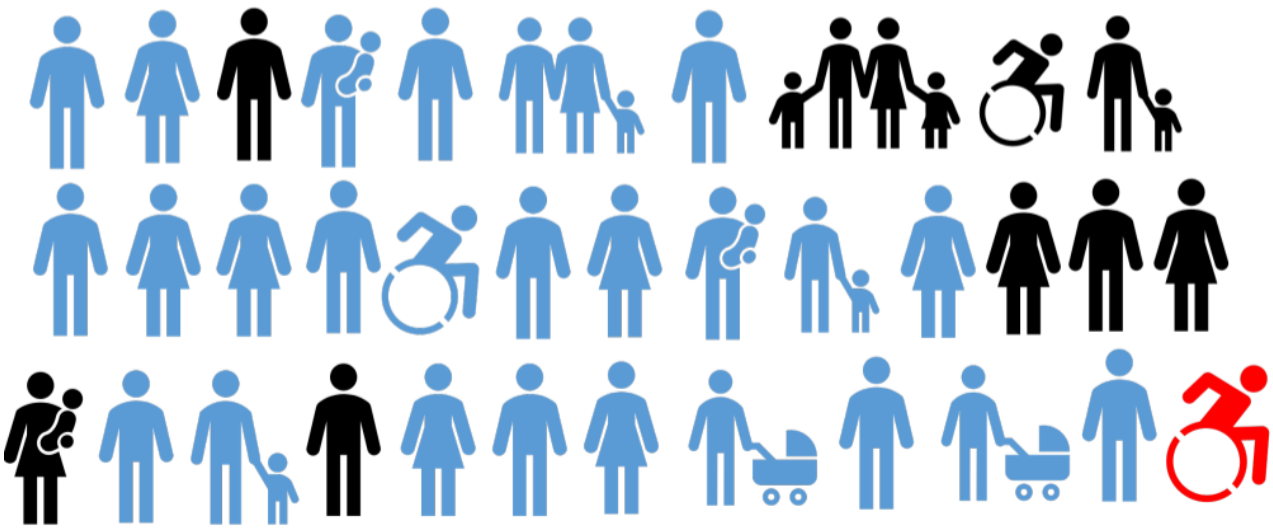


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model

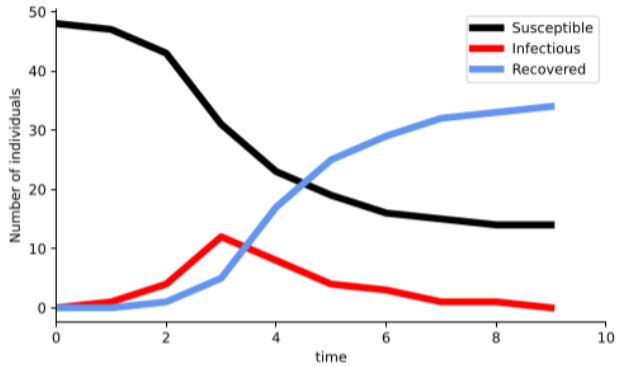


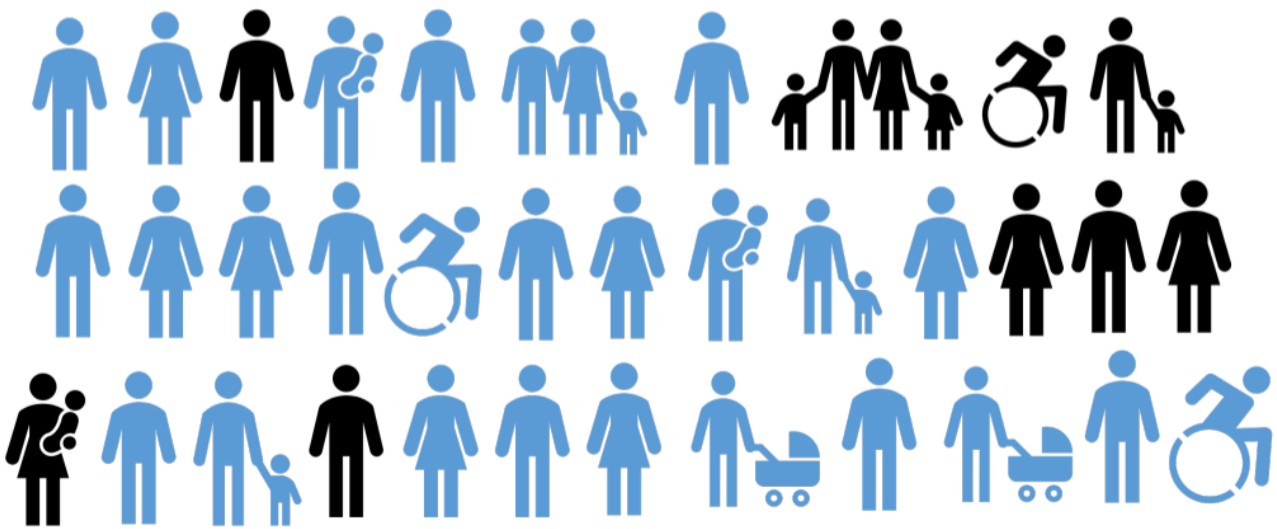


Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

SIR-model





Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

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: $\mathcal{R}_0 > 1$.

SORBONNE UNIVERSITY ABU DHABI

Basic reproduction number

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

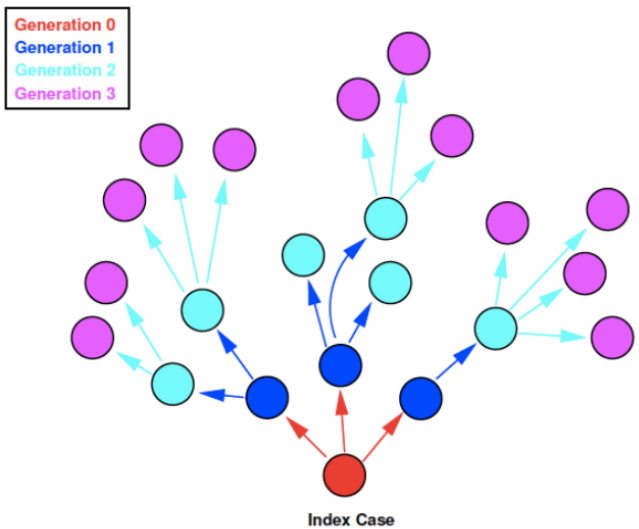
SORBONNE UNIVERSITY ABU DHABI

Basic reproduction number

Definition

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

Here, $\mathcal{R}_0 = 3$.



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

- Mostly used: Next-generation Matrix Method[3]

[3] Diekmann et al, The construction of next-generation matrices for compartmental epidemic models (2009)

Can we prevent the outbreak?

- **IDEA! Vaccination!!!**
- What proportion, p, should we vaccinate such that $I'(t) < 0$

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

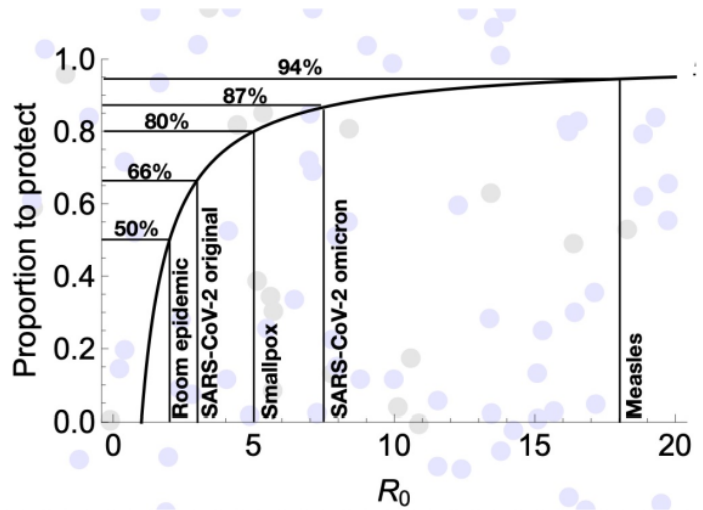
- At initially, p portion vaccination of N is pN, thus

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

Therefore,

$$\beta \frac{I}{N}(1-p)N < \gamma I \implies \beta(1-p)I < \gamma I$$
$$\implies 1 - p < \frac{\gamma}{\beta}$$
$$\implies 1 - p < \frac{1}{\mathcal{R}_0}$$
$$\implies p > 1 - \frac{1}{\mathcal{R}_0}$$

(Critical vaccination threshold)



Credit: S. Kissler, UCB

SORBONNE UNIVERSITY ABU DHABI

Extensions of the SIR model

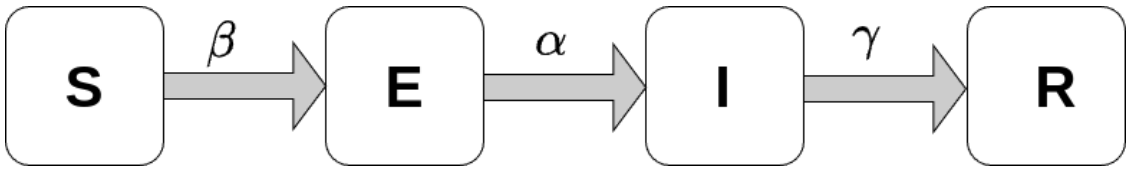
We can increase model complexity and realism by:

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

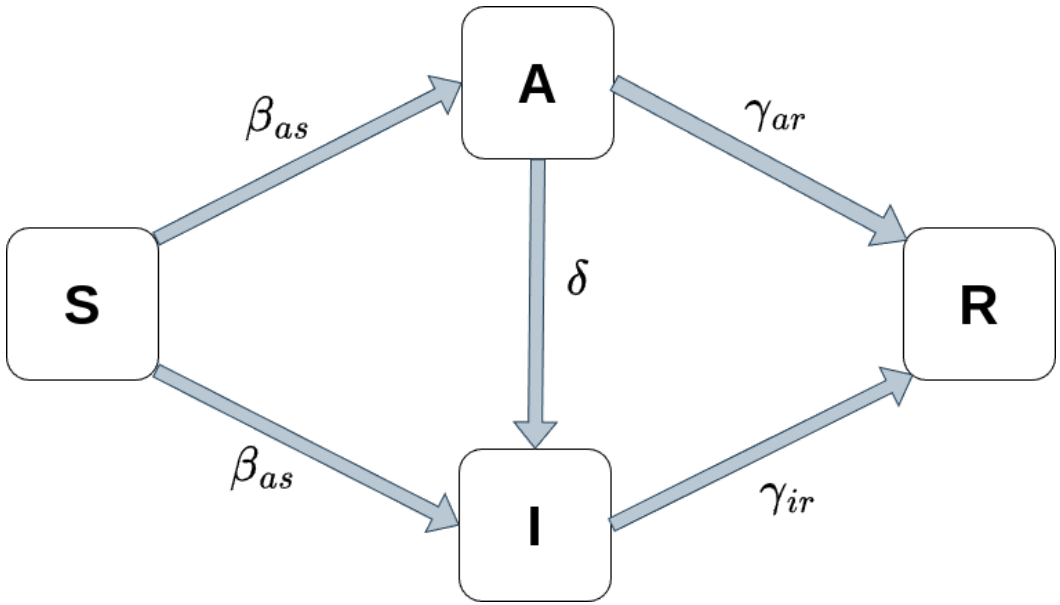
SORBONNE UNIVERSITY ABU DHABI

With more compartments

- Adding Exposed compartment (E)



- Adding Symptomatic (I) and Asymptomatic (A)

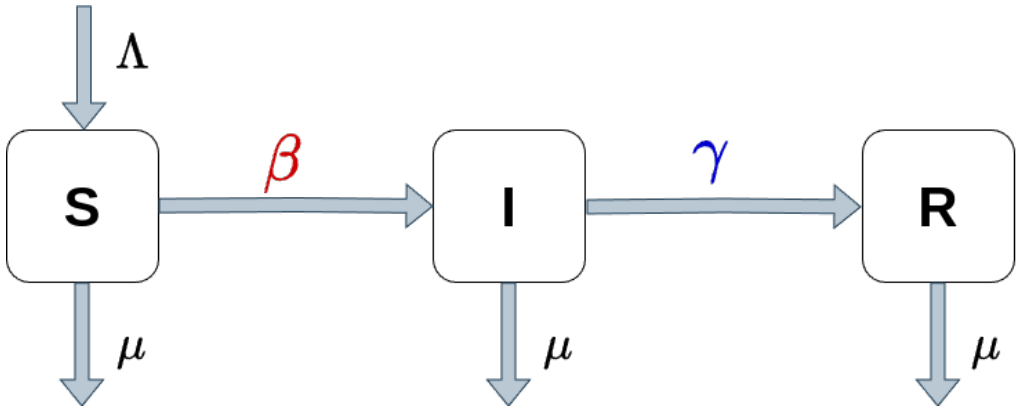


- Othres: Quarantine (Q), Disease-related death (D), Hospitalization (H), Vaccination (V), etc.

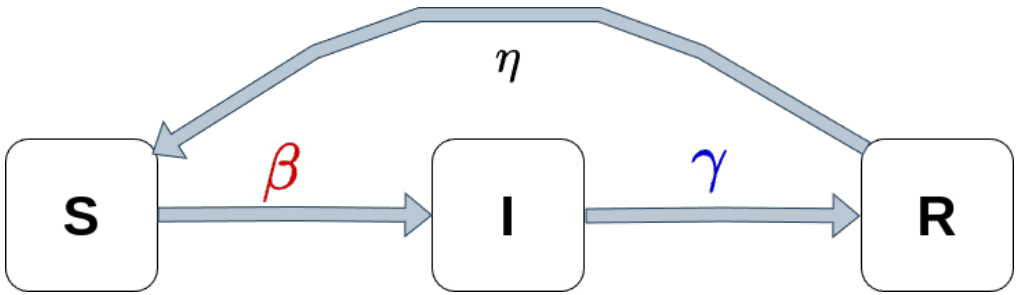
SORBONNE UNIVERSITY ABU DHABI

With vital dynamics and loss of immunity

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

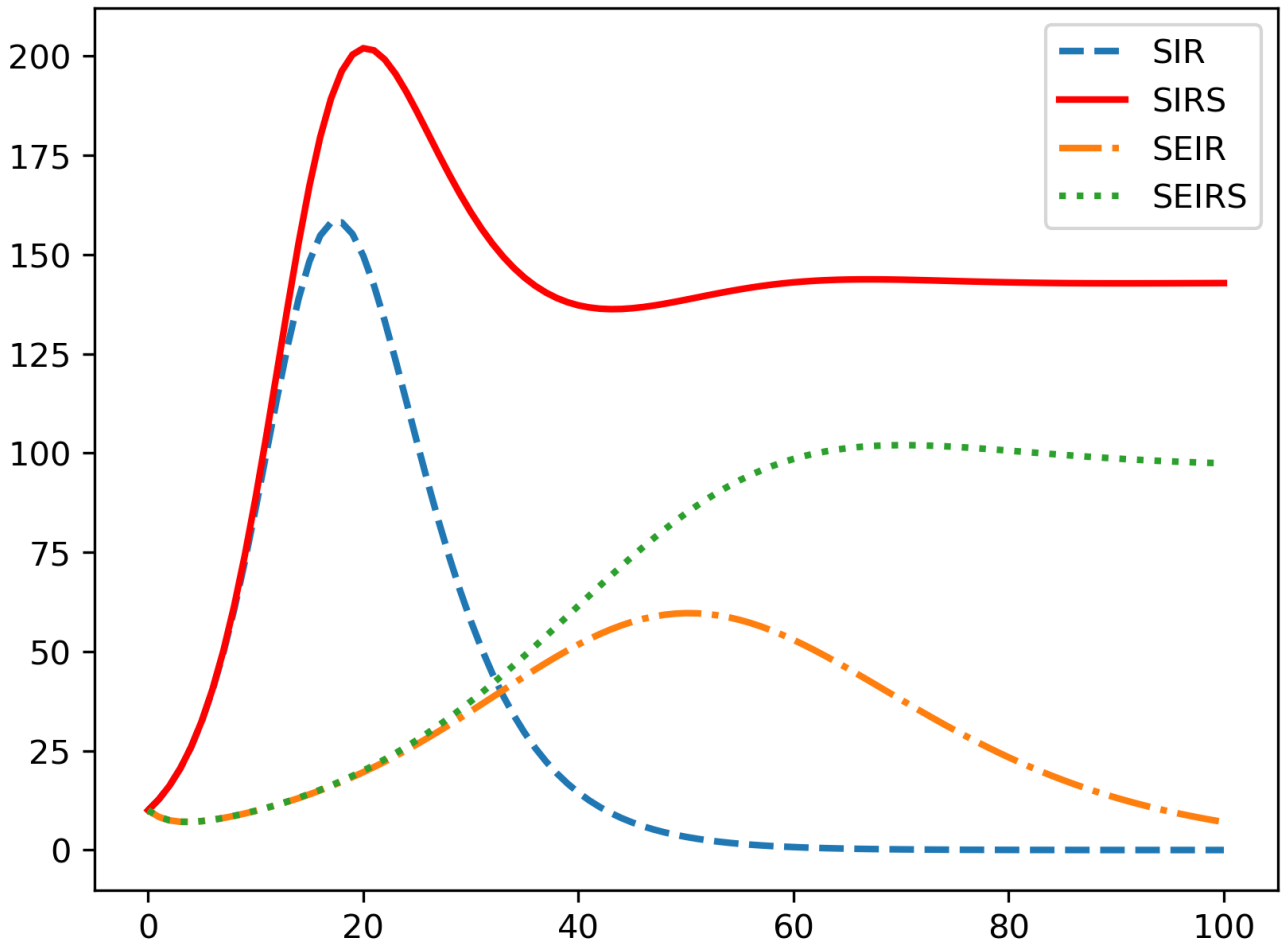


- η := rate of loss of immunity (SIRS model)



SORBONNE UNIVERSITY ABU DHABI

Comparison:



SORBONNE UNIVERSITY ABU DHABI

With transitions

- 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:

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

where B describes a Brownian motion, etc.

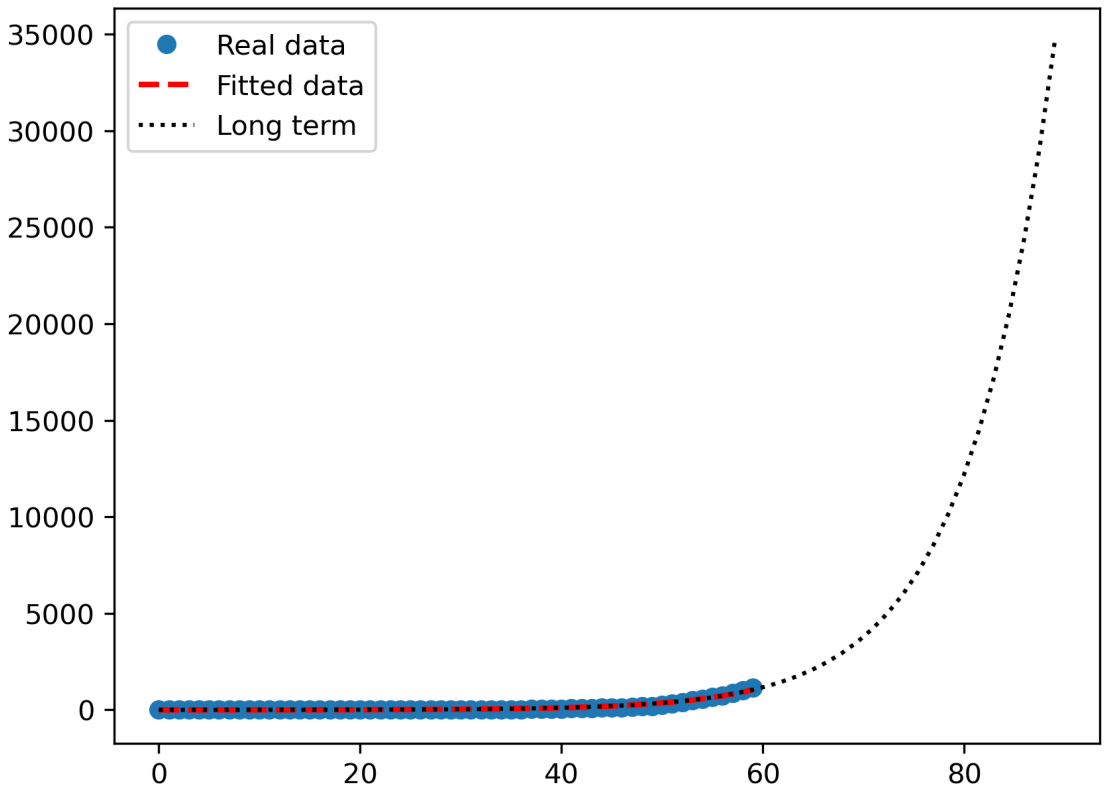
- Introducing Nonlinear Incidence Rates: Replace simple standard bilinear incidence with saturation functions:

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

SORBONNE UNIVERSITY ABU DHABI

Parameter Estimation

- With confirmed cases of COVID19-India data[4] 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)`



Estimated parameters: $\beta \approx 1.177 \times 10^{-1}$ and $\gamma \approx 1.975 \times 10^{-5}$

[4] covid19dashboard.mohfw.gov.in

Spatial disease spread

- 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

$$\begin{cases} \dfrac{\partial S}{\partial t} = -\beta \dfrac{I}{N} S + \dfrac{\partial^2 S}{\partial x^2} \\ \dfrac{\partial I}{\partial t} = \beta \dfrac{I}{N} S - \gamma I + \dfrac{\partial^2 I}{\partial x^2} \\ \dfrac{\partial R}{\partial t} = \gamma I + \dfrac{\partial^2 R}{\partial x^2} \end{cases}$$

Network-based Method

$$\begin{cases} \dfrac{\partial S}{\partial t} = -\beta \dfrac{I}{N} S + \Delta S \\ \dfrac{\partial I}{\partial t} = \beta \dfrac{I}{N} S - \gamma I + \Delta I \\ \dfrac{\partial R}{\partial t} = \gamma I + \Delta R \\ \Delta F(x) = \displaystyle\sum_{y \sim x, y \in \mathbf{V}} \big[F(y) - F(x)\big] \end{cases}$$

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

SORBONNE UNIVERSITY ABU DHABI

Reform of the network model

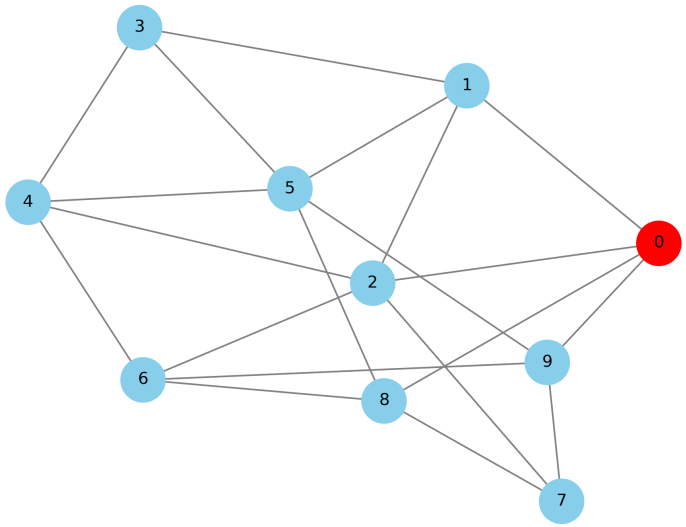
- Let S_i, I_i, R_i at node i and time t
- Let N_i is constant population of node i
- The Laplacian matrix associated with G: $L = A - D$, where A, D are adjacent matrix and degree matrix, respectively.
- Then, we can reform the network model[5] as follows:

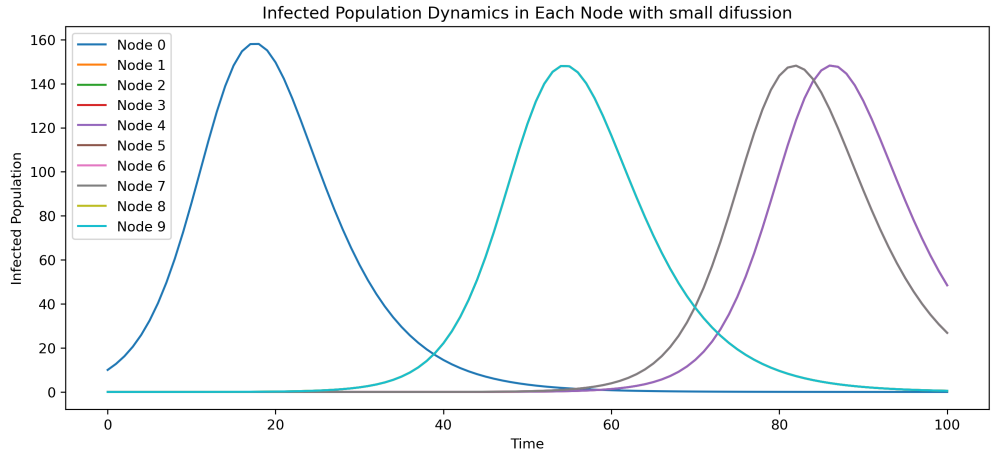
$$\begin{cases} \dfrac{dS_i}{dt} = -\beta \dfrac{I_i}{N_i} S_i + \sigma \displaystyle\sum_{j=1}^{n} L_{ij} S_j, \quad S_i(0) = S_{i0} \\ \dfrac{dI_i}{dt} = \beta \dfrac{I_i}{N_i} S_i - \gamma I_i + \sigma \displaystyle\sum_{j=1}^{n} L_{ij} I_j, \quad I_i(0) = I_{i0} \\ \dfrac{dR_i}{dt} = \gamma I_i +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

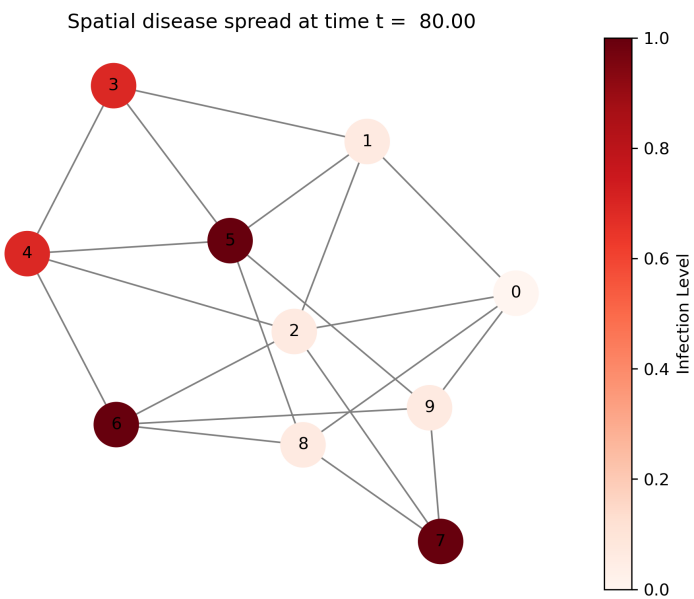
where $i = 1, 2, \ldots, n$.

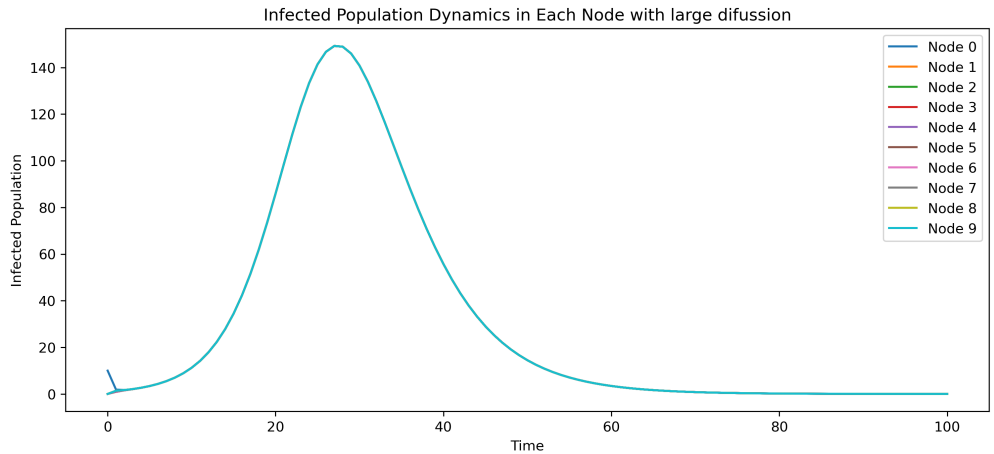
SORBONNE UNIVERSITY ABU DHABI

[5] Barman & Mishra, SIR Epidemic Model On Network: A Migration Flow Study (2022)

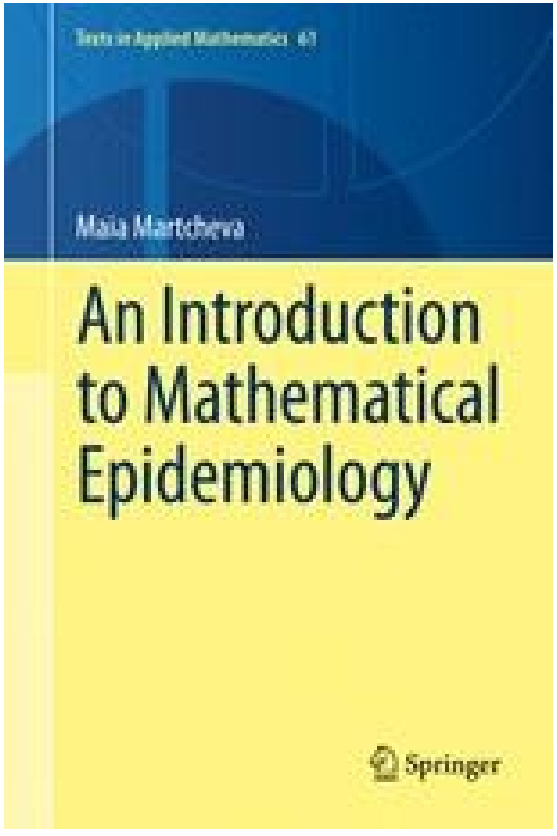

3
1
4
5
0
2
9
6
8
7

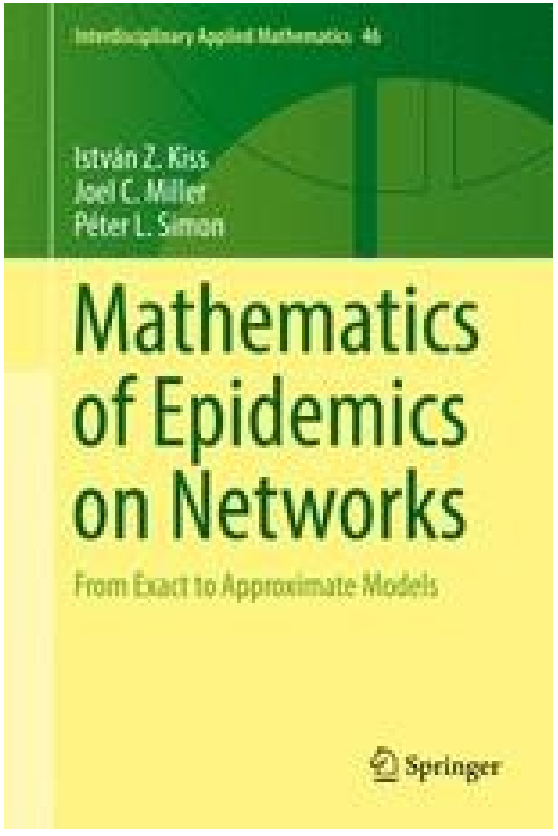

Infected Population Dynamics in Each Node with small difussion
Node 0
Node 1
Node 2
Node 3
Node 4
Node 5
Node 6
Node 7
Node 8
Node 9
Infected Population
Time
0
20
40
60
80
100
120
140
160


Spatial disease spread at time t = 80.00
Infection Level
1.0
0.8
0.6
0.4
0.2
0.0


Infected Population Dynamics in Each Node with large difussion
Node 0
Node 1
Node 2
Node 3
Node 4
Node 5
Node 6
Node 7
Node 8
Node 9
Infected Population
Time
0
20
40
60
80
100
120
140

References





SORBONNE UNIVERSITY ABU DHABI

SORBONNE UNIVERSITY ABU DHABI