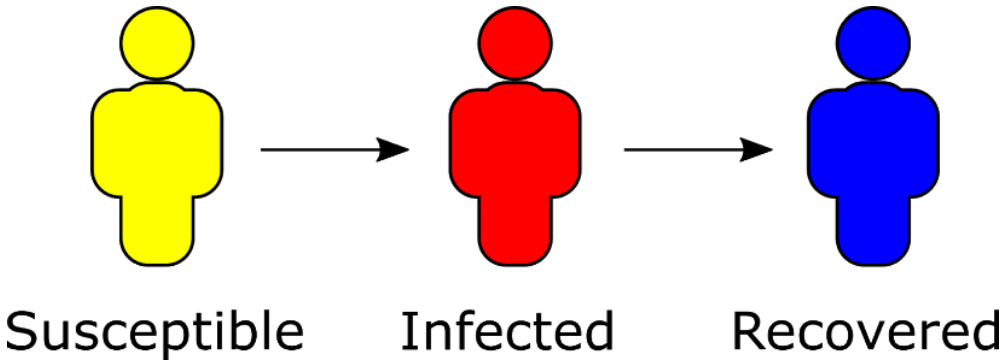
Modeling Epidemics



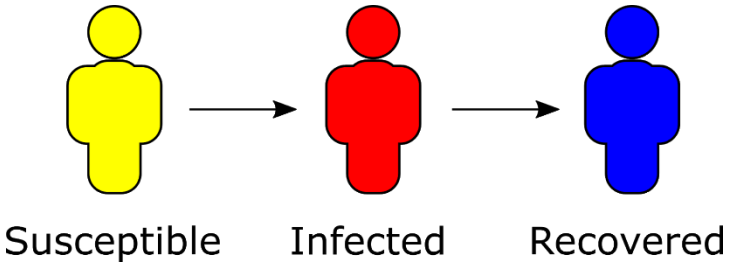
Jeff Saucerman

UNIVERSITY of VIRGINIA
BIOMEDICAL ENGINEERING

THE CARDIOVASCULAR RESEARCH CENTER

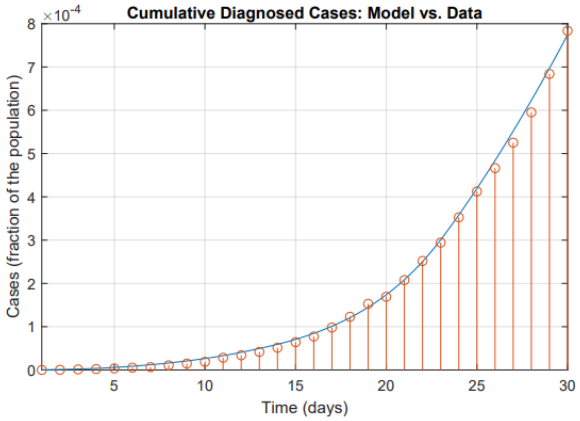
Modeling of Epidemics Overview

1. Schematic
2. Assumptions
3. Equations
4. Parameters
5. Simulation
6. Validation



$$\frac{dI}{dt} = \beta IS - \gamma I$$

β,γ, N

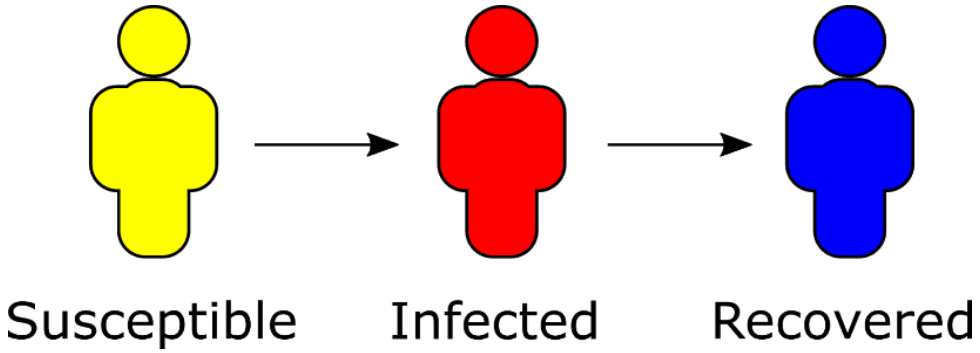


http://arxiv.org/abs/2003.09861

SIR model

This model assumes there are three groups of people:

- (S)usceptible people are not yet Infected, but they may get the disease from Infected people.
- (I)nfected currently have the disease and can spread it to Susceptible people.
- (R)ecovered people were infected but are now immune.



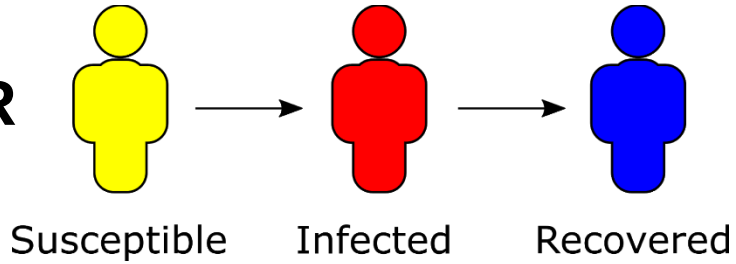
Assumes: lifelong immunity

Ex: measles, mumps, rubella, social contagion

Kermack, W. O., McKendrick, A. G. Contributions to the mathematical theory of epidemics. Proc. Royal Soc. A, 115, 700-721 (1927).

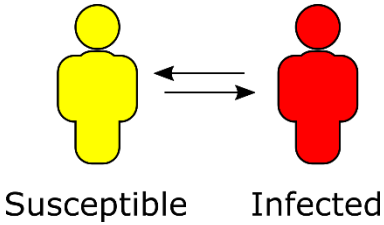
Variants of the SIR model

SIR



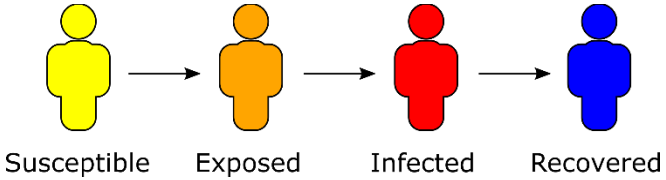
Assumes: lifelong immunity
Ex: measles, mumps, rubella

SIS



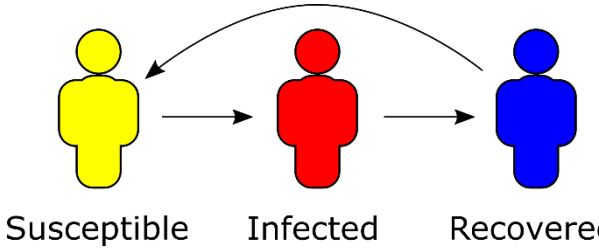
Assumes: no immunity
Ex: common cold

SEIR



Assumes: delay before infective
Ex: HIV, chicken pox, COVID-19

SIRS



Assumes: limited immunity
Ex: seasonal influenza

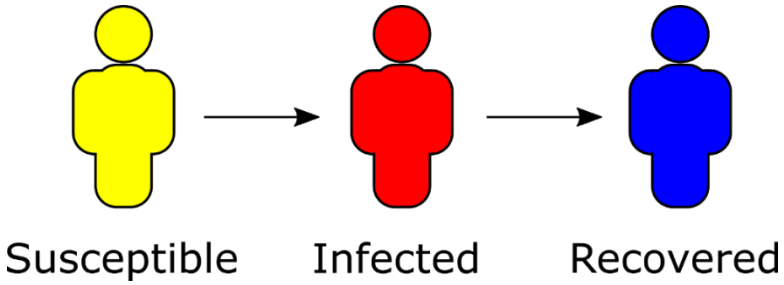
Typical Assumptions when Modeling Epidemics

large numbers → continuum approximations dX/dt…
→deterministic
small numbers → discrete, stochastic/probabilistic

homogeneous, large numbers → ODEs
homogeneous, small numbers → non-spatial stochastic
heterogeneous, discrete space → spatial agent-based model
heterogeneous, continuous space → PDEs

Conservation of “Mass” / “Population”, “Mass Action” kinetics
Other assumptions:
relative populations (initial infected << population)
relative timescales: rapid equilibrium d[X]/dt = 0

SIR model: ordinary differential equations



Population ODEs, no birth or death:

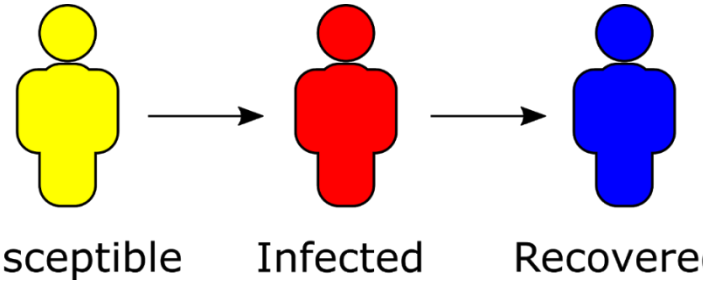
$$\frac{dS}{dt} = -\beta IS \qquad \frac{dI}{dt} = \beta IS - \gamma I \qquad \frac{dR}{dt} = \gamma I$$

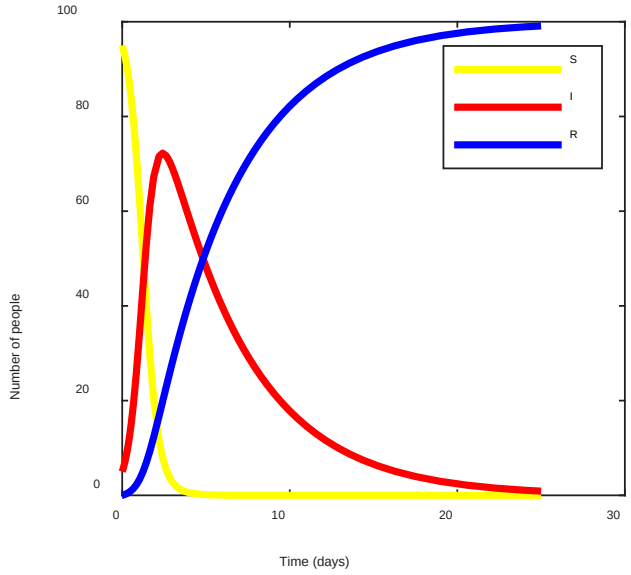
β	transmission rate constant [1/days/people]
γ	recovery rate constant [1/days]
N	size of population [people]

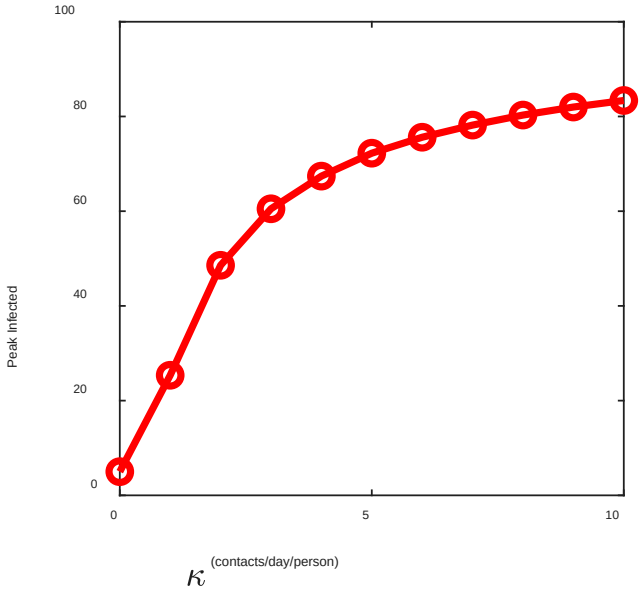
$R_e = S(t=0)\beta/\gamma$ effective reproductive number [people infected per person]
The epidemic will spread if $R_e > 1$. Note: R_e is is unrelated to Recovered.

Optional: $\beta = \frac{\kappa\tau}{N}$ κ: # contacts/time [1/days]
τ: transmissibility (fraction contacts→infection)

SIR model: ordinary differential equations



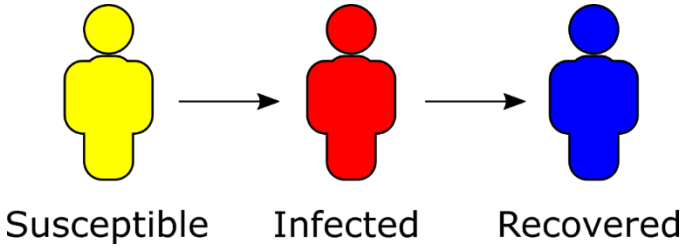




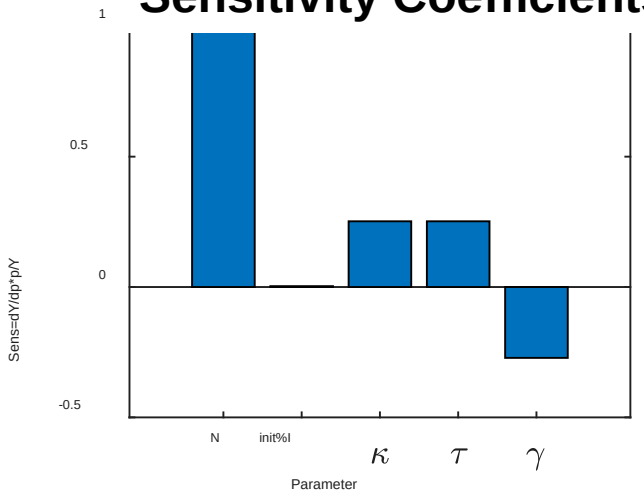
N = 100 [people], κ = 5 [contacts/day/person],
τ = 0.5, γ = 1/5 [1/days],

SIRcompute.m
SIRode.m

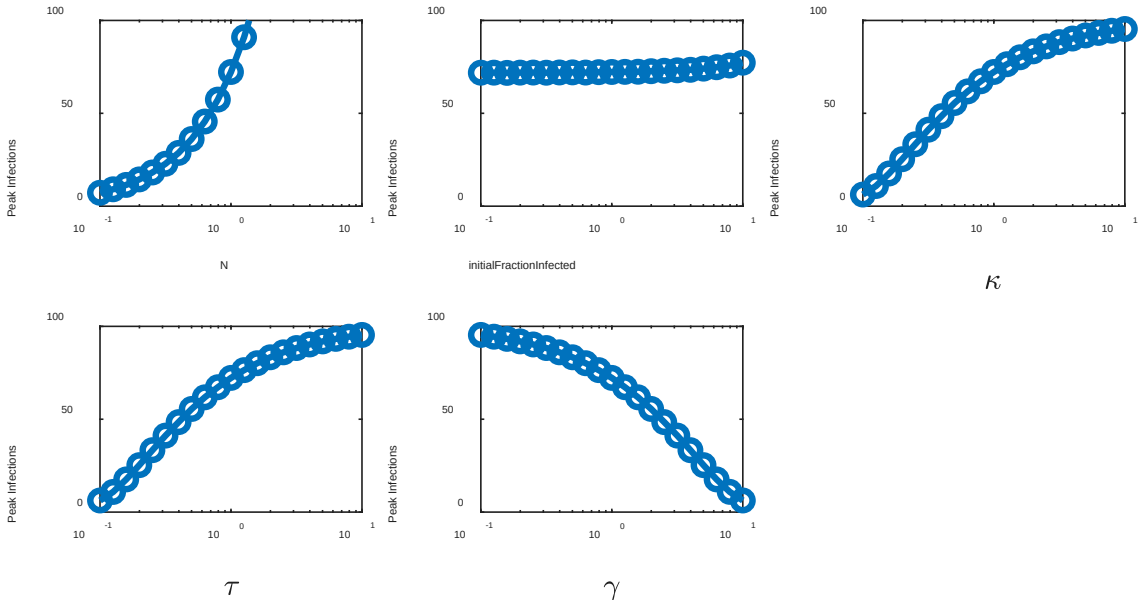
SIR model (ODE): sensitivity analyses



Sensitivity Coefficients

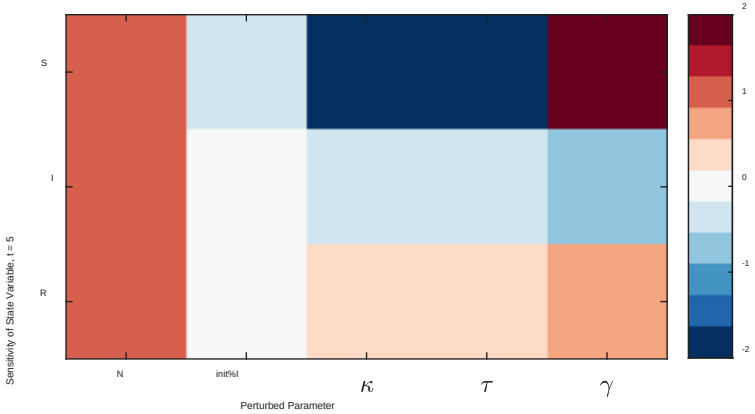


Response Curves



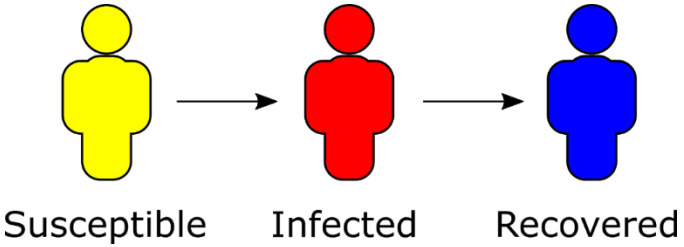
relative parameter values

Sensitivity Matrix



SIRsensitivity.m

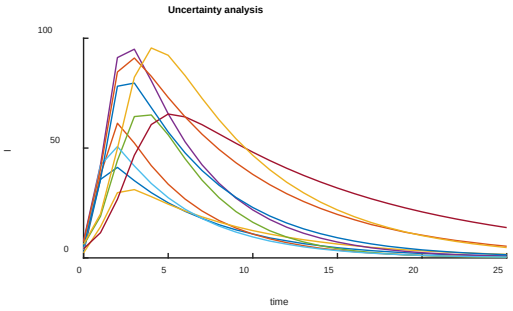
SIR model (ODE): uncertainty analysis

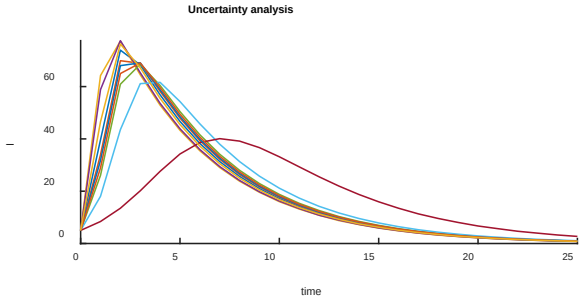


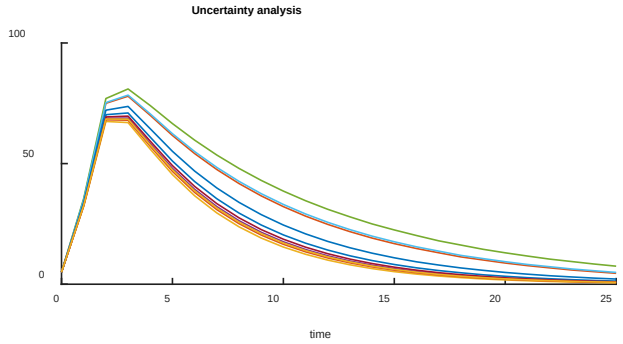
Vary all parameters
CV = 30%

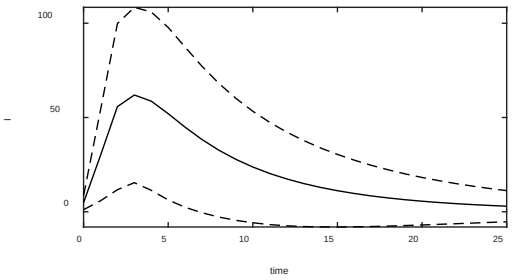
Vary contacts/day
κ CV = 30%

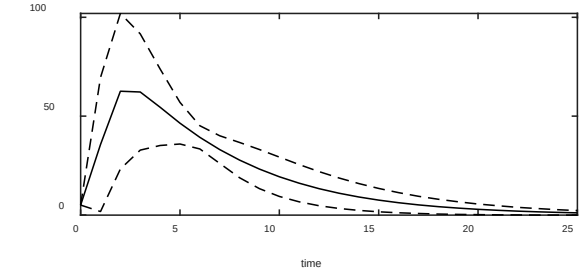
Vary recovery rate
γ CV = 30%

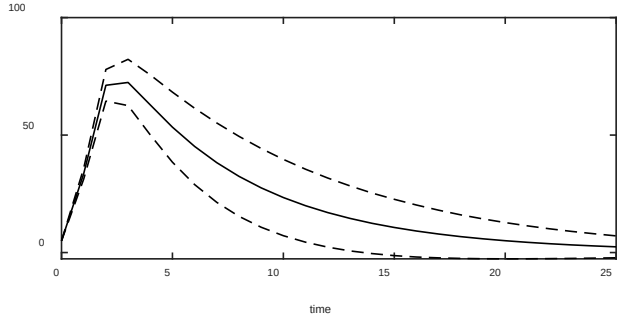








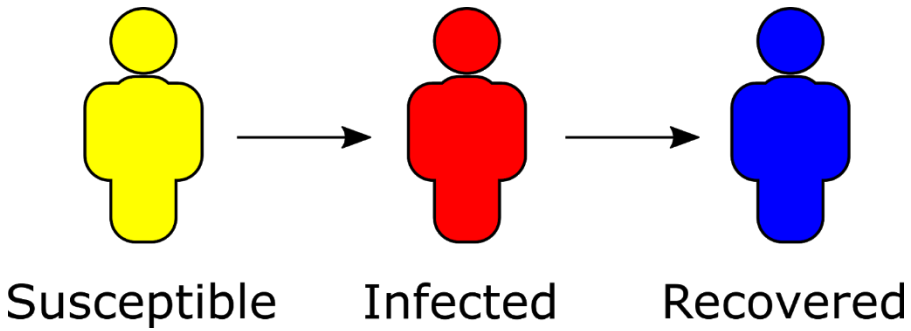




SIRsensitivity.m

SIR model: probabilistic, continuous time

$$E[S] = NP(S)$$
$$E[I] = NP(I)$$
$$E[R] = NP(R)$$



substitute

Population ODEs → continuous-time Markov chain

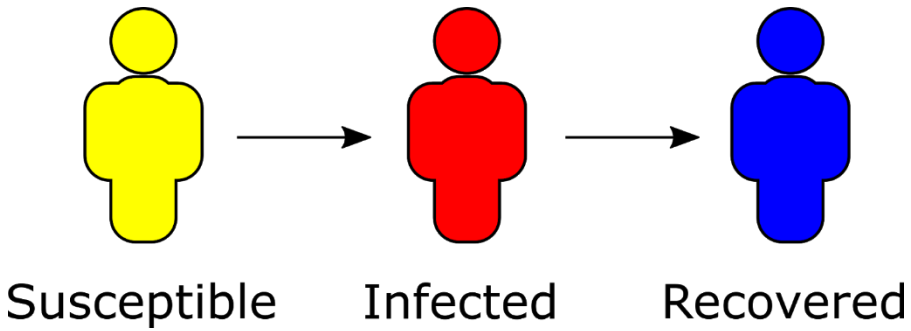
$$\frac{dP(S_t)}{dt} = -\beta NP(I_t)P(S_t)$$

$$\frac{dP(I_t)}{dt} = \beta NP(I_t)P(S_t) - \gamma P(I_t)$$

$$\frac{dP(R_t)}{dt} = \gamma P(I_t)$$

β	transmission rate constant
γ	recovery rate constant
N	size of population

SIR model: probabilistic, discrete time



continuous-time Markov chain → discrete-time Markov chain

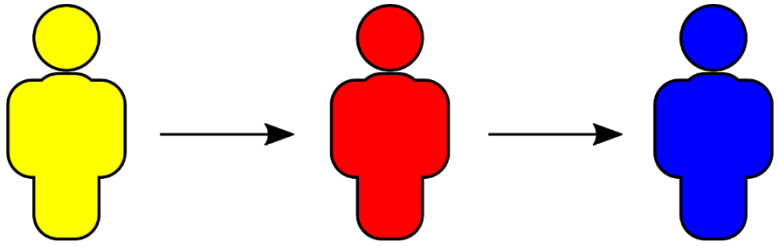
Euler Method

$$\frac{dP(S_t)}{dt} = -\beta N P(I_t) P(S_t) \Rightarrow P(S_{t+1}) = -\beta N P(I_t) P(S_t) \Delta t + P(S_t)$$

$$\frac{dP(I_t)}{dt} = \beta N P(I_t) P(S_t) - \gamma P(I_t) \Rightarrow P(I_{t+1}) = \beta N P(I_t) P(S_t) \Delta t - \gamma P(I_t)\,\Delta t + P(I_t)$$

$$\frac{dP(R_t)}{dt} = \gamma P(I_t) \Rightarrow P(R_{t+1}) = \gamma P(I_t) \Delta t + P(R_t)$$

SIR model: individual-based stochastic



Susceptible Infected Recovered

discrete-time Markov chain → simulate individuals

$$P(I_{t+1}) = \beta N P(I_t) P(S_t) \Delta t - \gamma P(I_t)\, \Delta t + P(I_t)$$

Discrete-time transition probabilities:

S → I $\quad P(I_{t+1}, |S_t) = \beta N P(I_t)\, \Delta t = \beta I \Delta t$

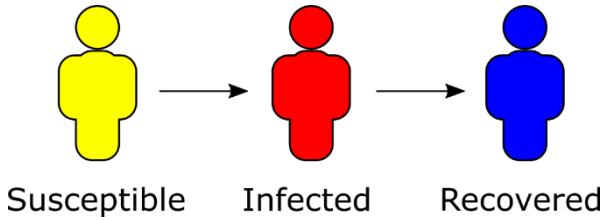
I → R $\quad P(R_{t+1}|I_t) = \gamma \Delta t$

These discrete-time transition probabilities let us simulate stochastic transitions of individuals:

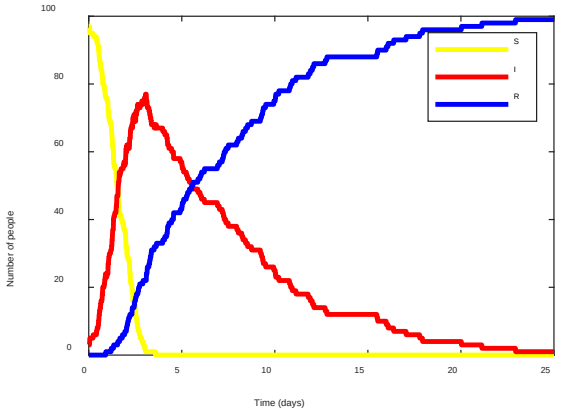
If S: **If rand $\sim$U$[0, 1] < \beta I \Delta t$, then I**

If I: **If rand $\sim$U$[0, 1] < \gamma \Delta t$, then R**

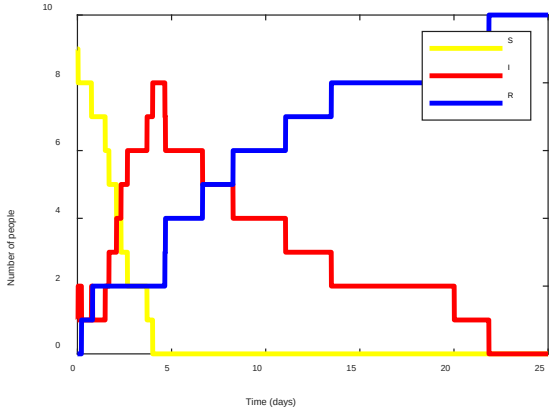
SIR model: individual-based stochastic



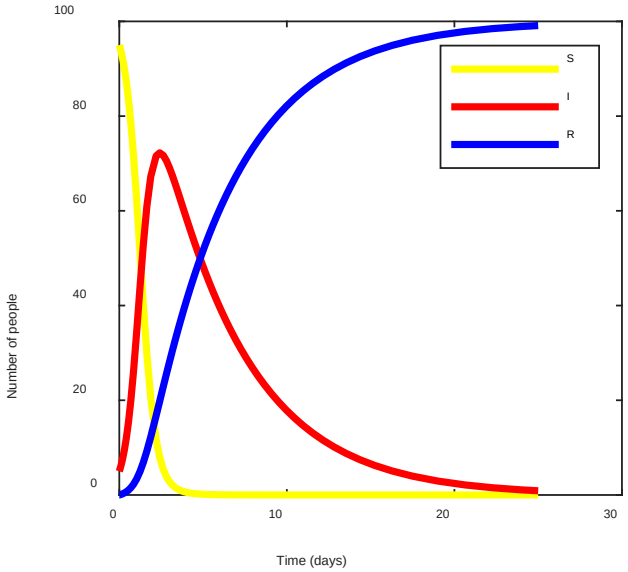
N = 100, run 1



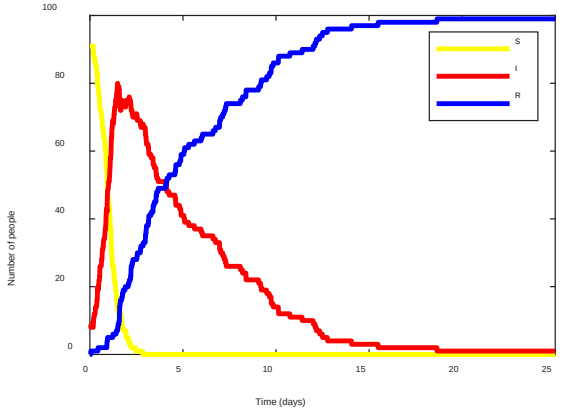
N = 10, run 1



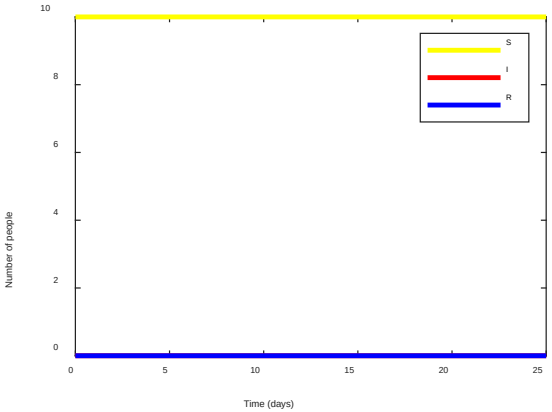
N = 100, ODEs



N = 100, run 2

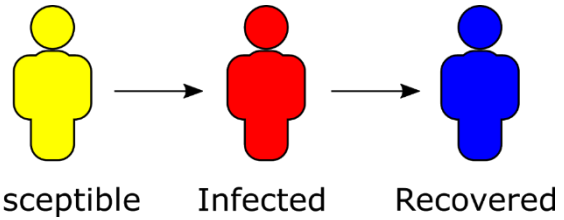


N = 10, run 2

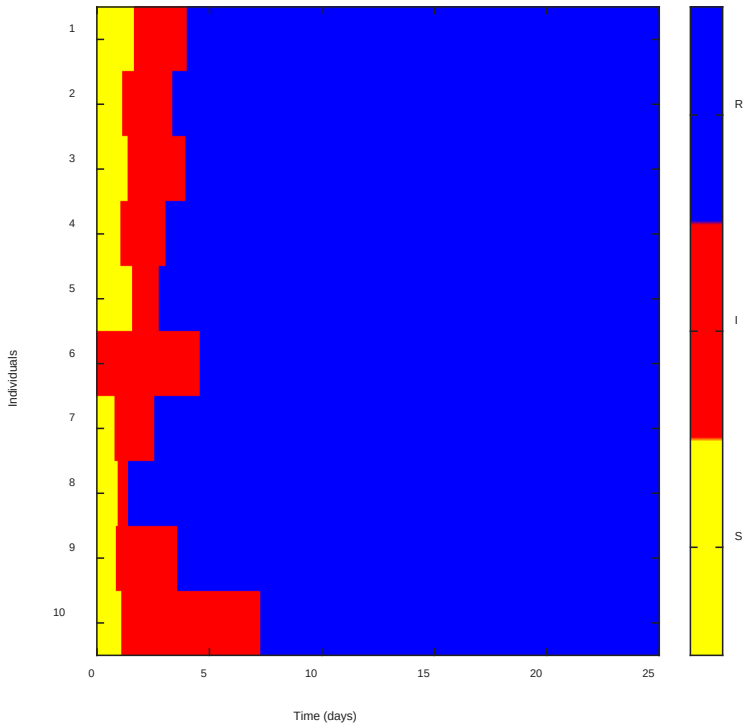


SIRabm.m

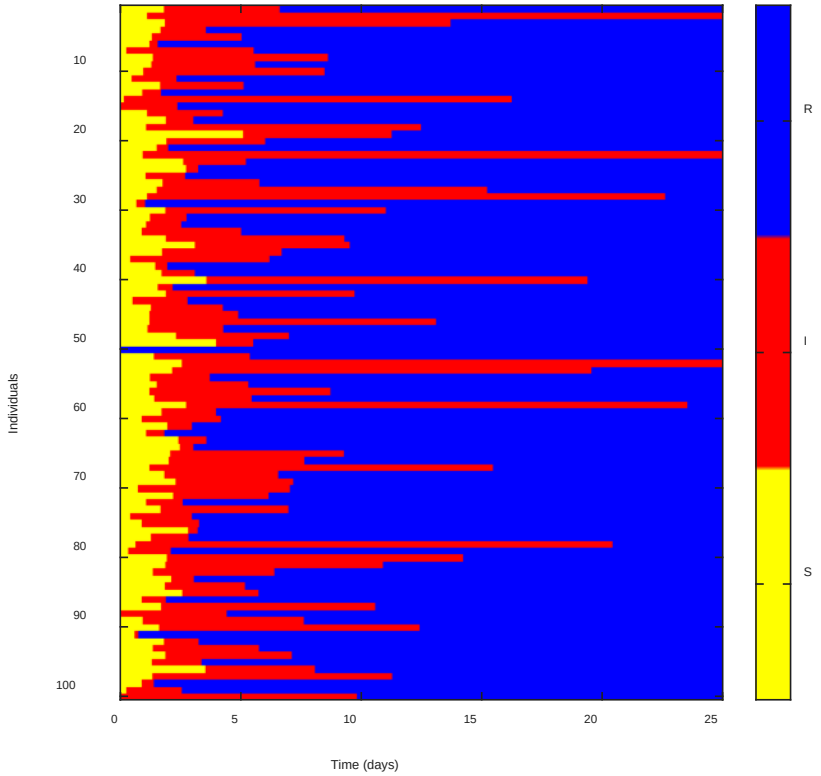
SIR model: individual-based stochastic



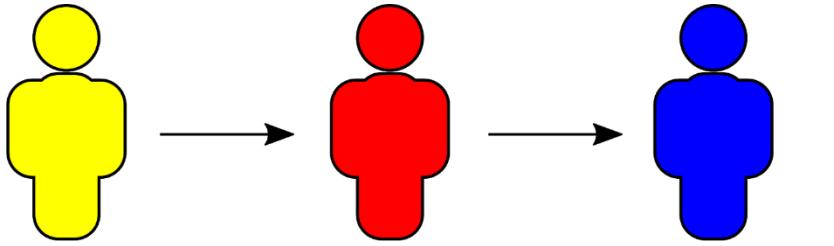
N = 10



N = 100



SIR model: individual-based stochastic, spatial



Non-spatial ABM → spatial ABM

Discrete-time transition probabilities:

S → I $P(I_{t+1}, |S_t) = \beta I \Delta t$ ➡ **If rand** $\sim \mathbf{U}[0,1] < \boldsymbol{\beta I \Delta t}$**, then I**

Where: $\beta = \frac{\kappa\tau}{N}$

N: # of people

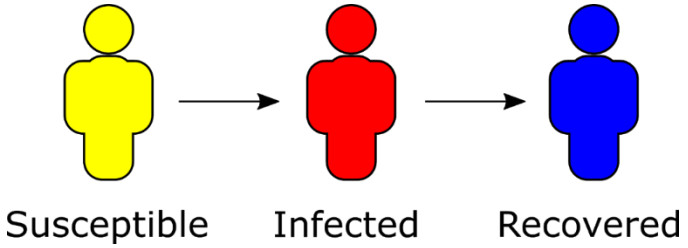
κ: # contacts/time/person [1/days]

τ: transmissibility (fraction contacts→infection)

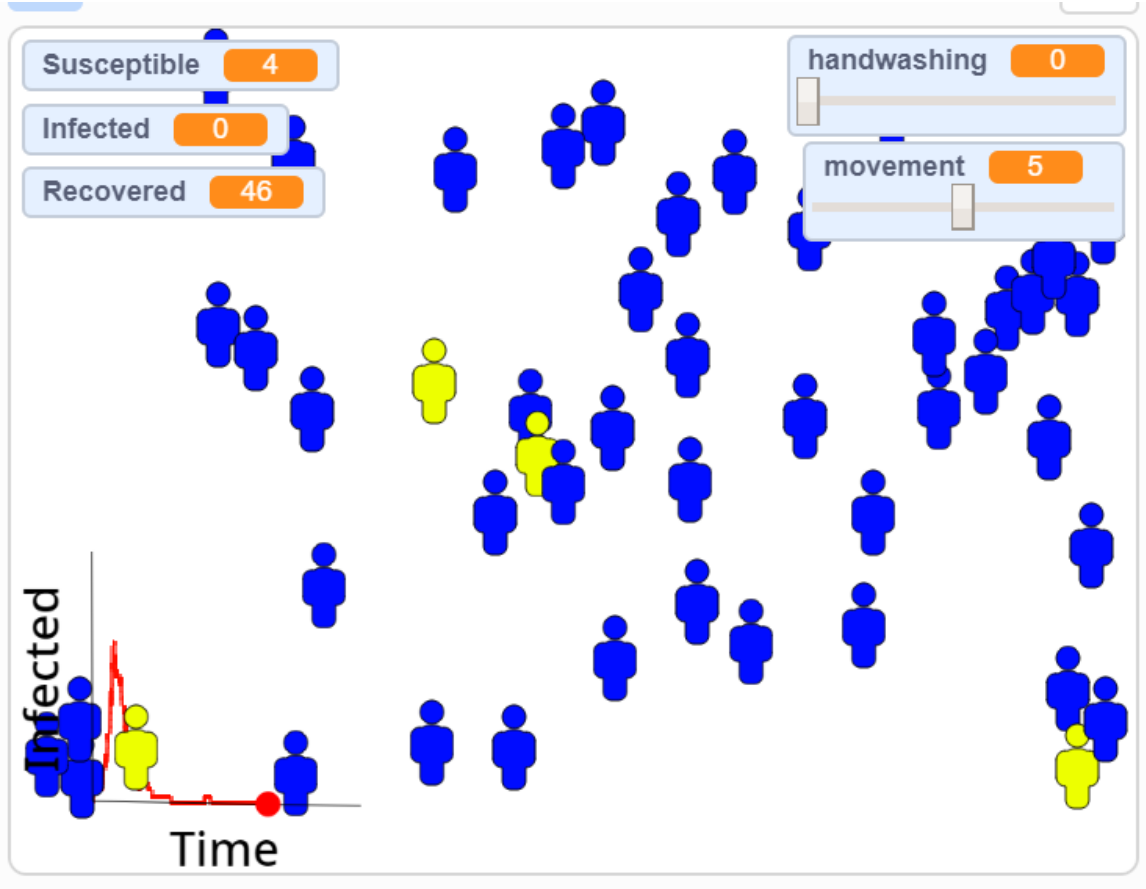
$$\beta I = \frac{\kappa\tau I}{N} = \kappa\tau P_{contact-Inf}$$

For spatial: If S is contact with I, $P_{contact-Inf} = 1, so\ P(I_{t+1}|S_t) = \tau\Delta t$

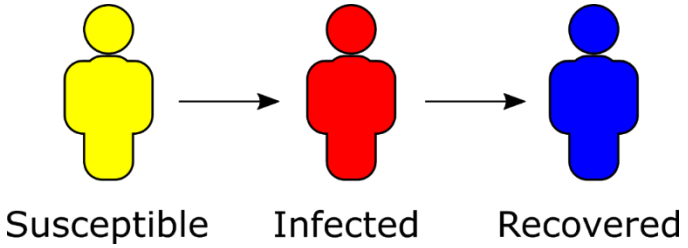
SIR model (ABM): stochastic, spatial



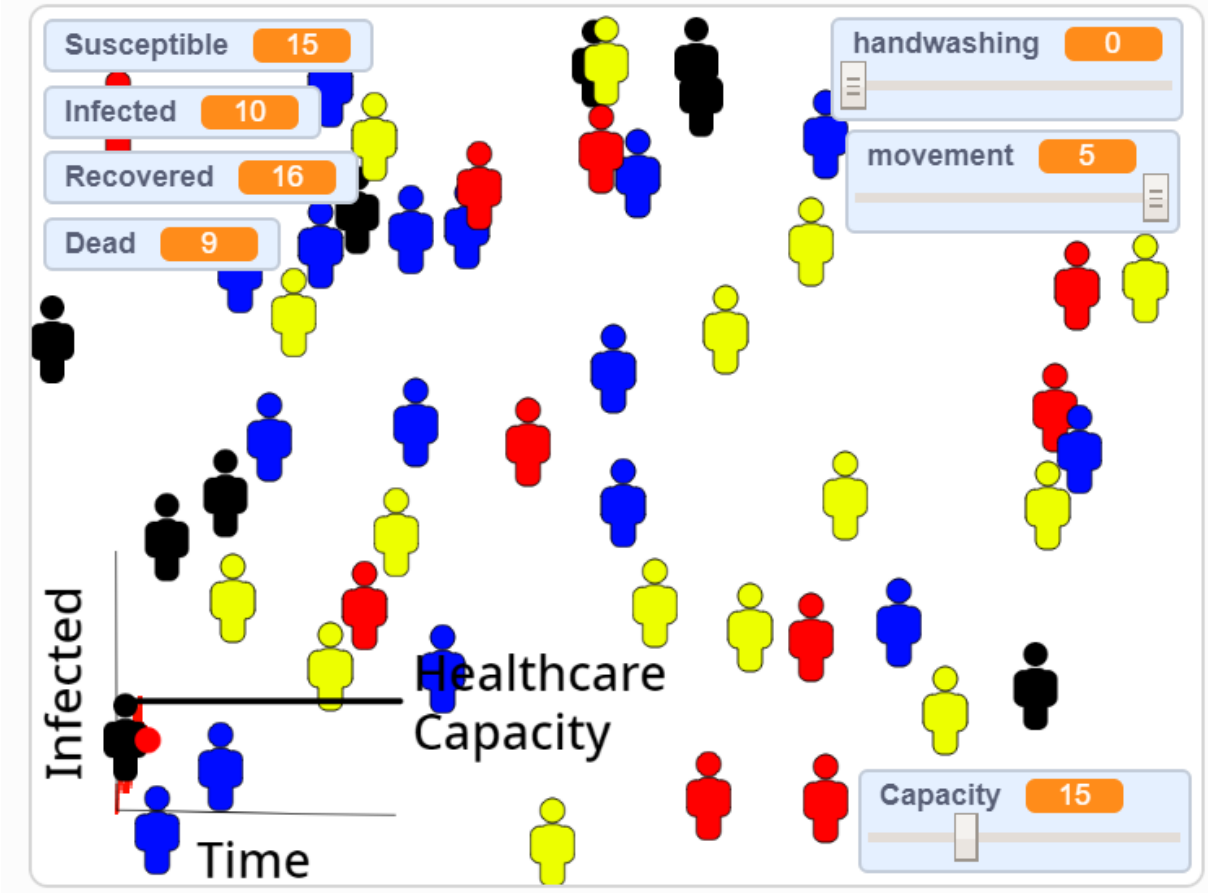
Infectious disease simulator
https://scratch.mit.edu/projects/375763600/



SIR model (ABM): stochastic, spatial



Infectious disease simulator with limited healthcare system capacity
https://scratch.mit.edu/projects/375925004/



References

- Kermack, W. O., McKendrick, A. G. Contributions to the mathematical theory of epidemics. Proc. Royal Soc. A, 115, 700-721 (1927).
- **Excellent article:** Weiss, Howard Howie. “The SIR Model and the Foundations of Public Health.” *Materials Matematics*, 2013, 0001–17. http://mat.uab.cat/matmat/PDFv2013/v2013n03.pdf
- https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology

- Nice table of SEIR COVID-19 parameters from various sources: http://gabgoh.github.io/COVID/index.html
- Imperial College COVID-19 Response Team. Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand https://doi.org/10.25561/77482
- Giordano, Giulia, Franco Blanchini, Raffaele Bruno, Patrizio Colaneri, Alessandro Di Filippo, Angela Di Matteo, Marta Colaneri, and the COVID19 IRCCS San Matteo Pavia Task Force. “A SIDARTHE Model of COVID-19 Epidemic in Italy.” *ArXiv:2003.09861 [Cs, Eess, Math, q-Bio]*, March 22, 2020. http://arxiv.org/abs/2003.09861.