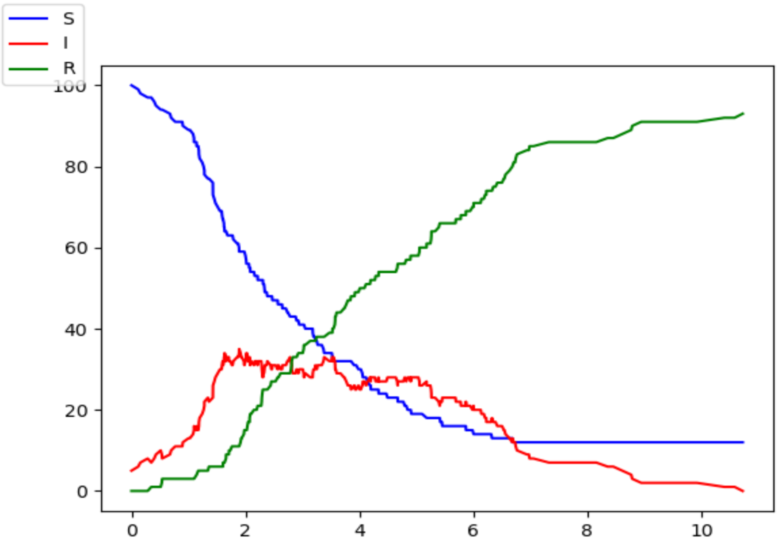
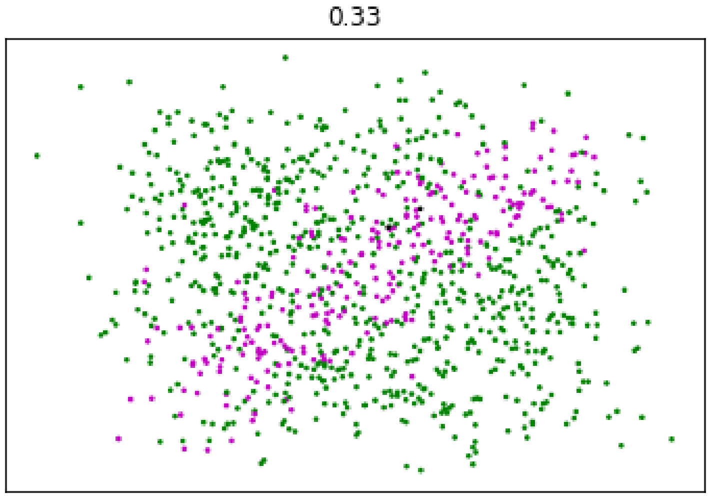
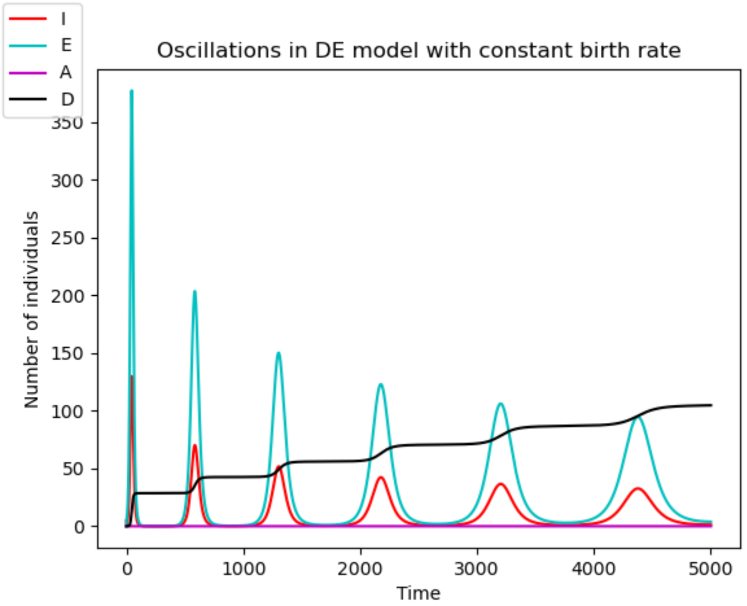


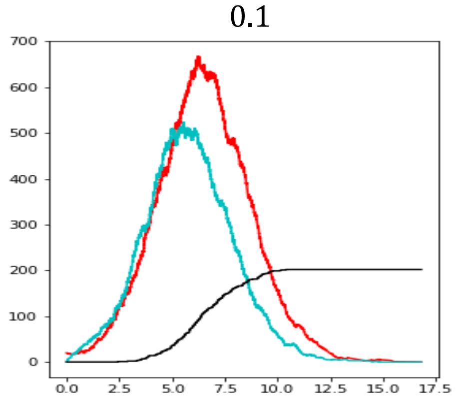


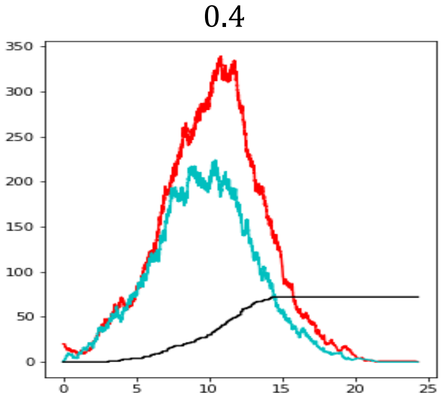


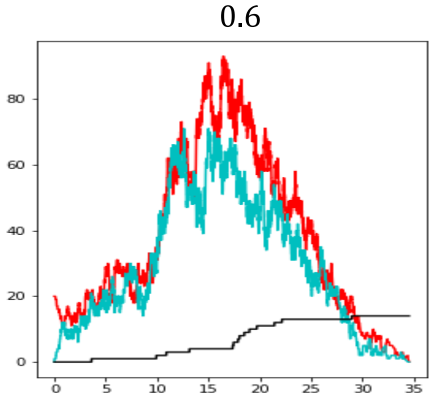
Epidemic Modelling

Henry Nguyen

Mentors: Max Wolf + Yuri Wolf







ZIMIN FOUNDATION

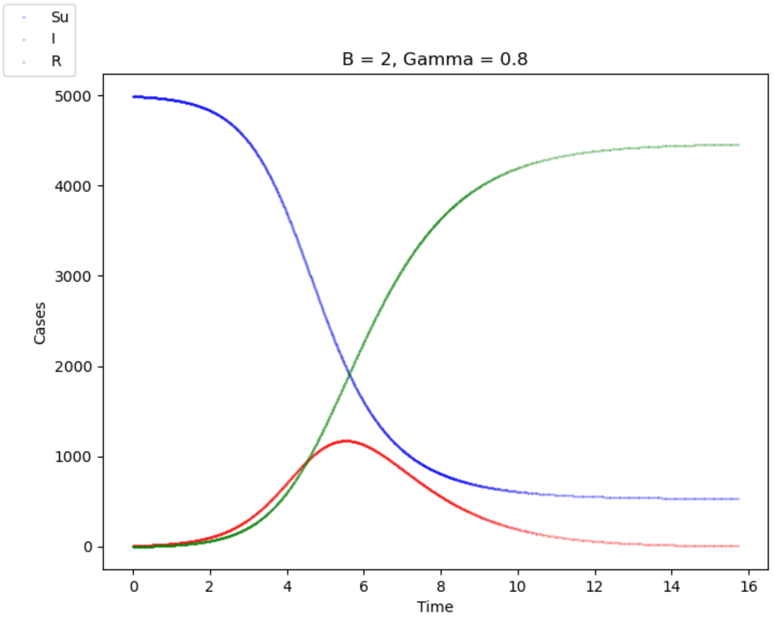
School of molecular and theoretical biology

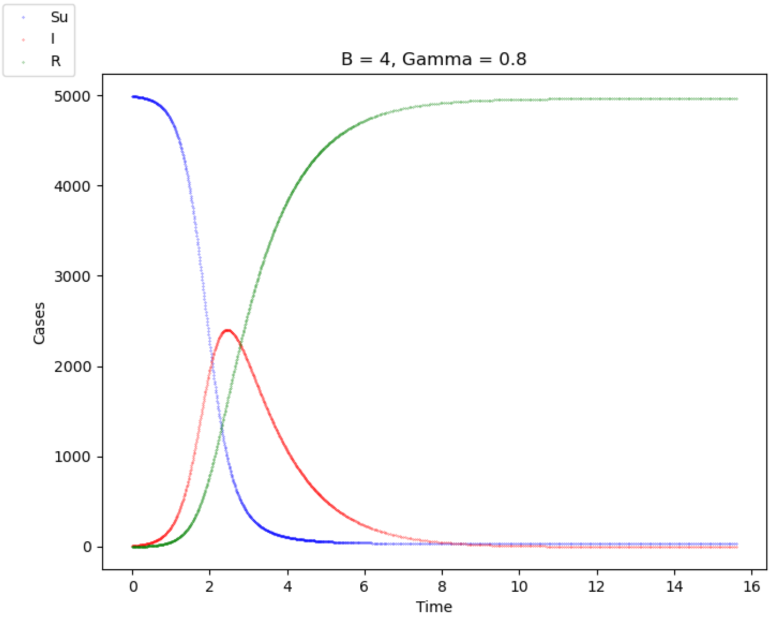
Differential Equations to Model Epidemics

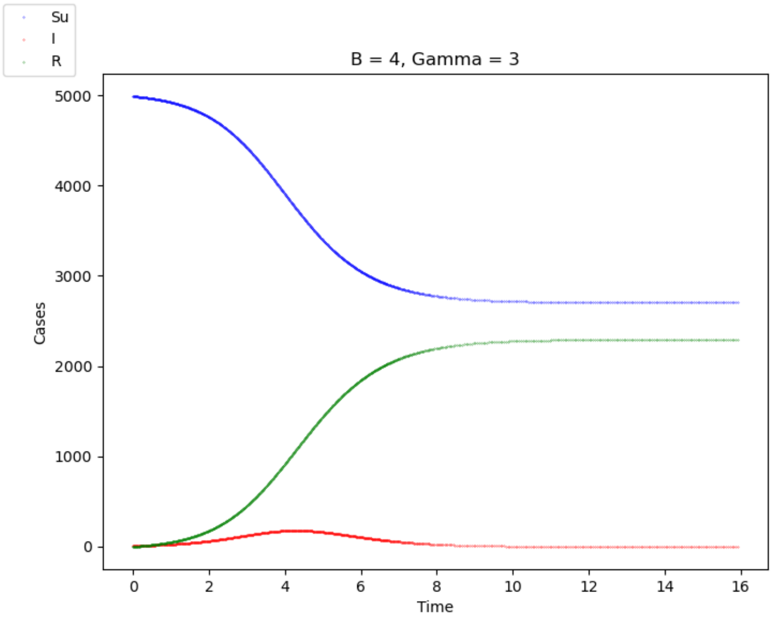
S – Susceptible
I – Infectious
R – Recovered

$$S \xrightarrow{\beta} I \xrightarrow{\gamma} R$$

$$\frac{dS}{dt} = -\beta I \left(\frac{S}{N}\right) \qquad \frac{dI}{dt} = \beta I \left(\frac{S}{N}\right) - \gamma I \qquad \frac{dR}{dt} = \gamma I$$



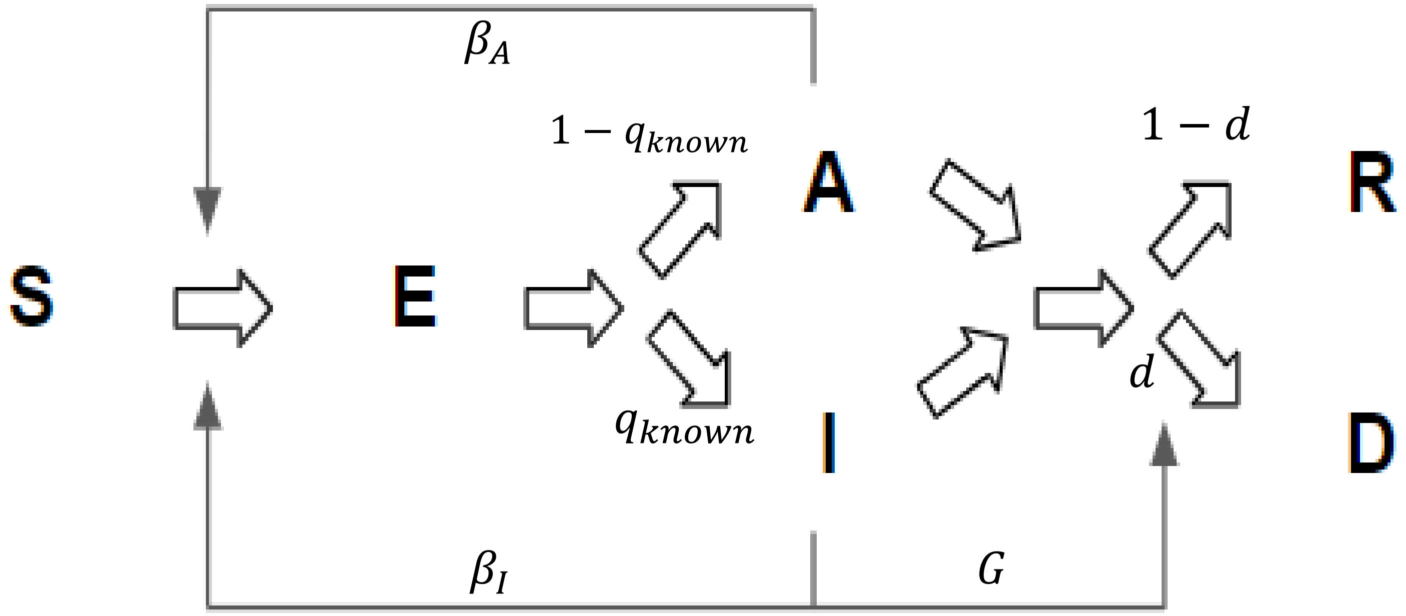




Assumptions of DE model

- Continuously, uniformly mixed
- Natural birth and death rates are negligible (small epidemic timeframe)
- Sufficiently large population (imagine chemical systems)
- All individuals have the same infectivity
- Incubation/infectious period is small

- S = Susceptible
- E = Exposed (Incubation period, does not spread)
- A = Asymptomatic (or Unknown)
- I = Infected
- R = Recovered
- D = Dead



d is calculated by $d = \min\left(d_0 + m\left(\frac{I}{total}\right), d_1\right)$

q_{known} is the proportion of infected individuals that go to I

d_0 is death rate with best possible medical care

d_1 is death rate without any medical care

m shows dependence of medical care quality on proportion of infected

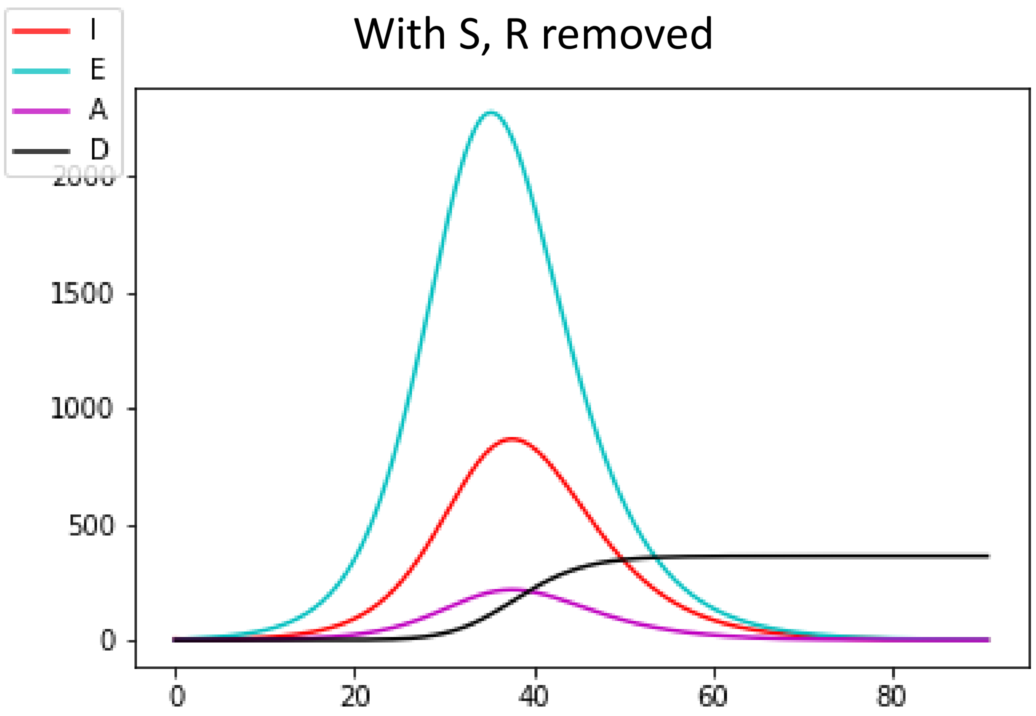
$$d_0 = 0.001; d_1 = 0.1; m = 0.5$$

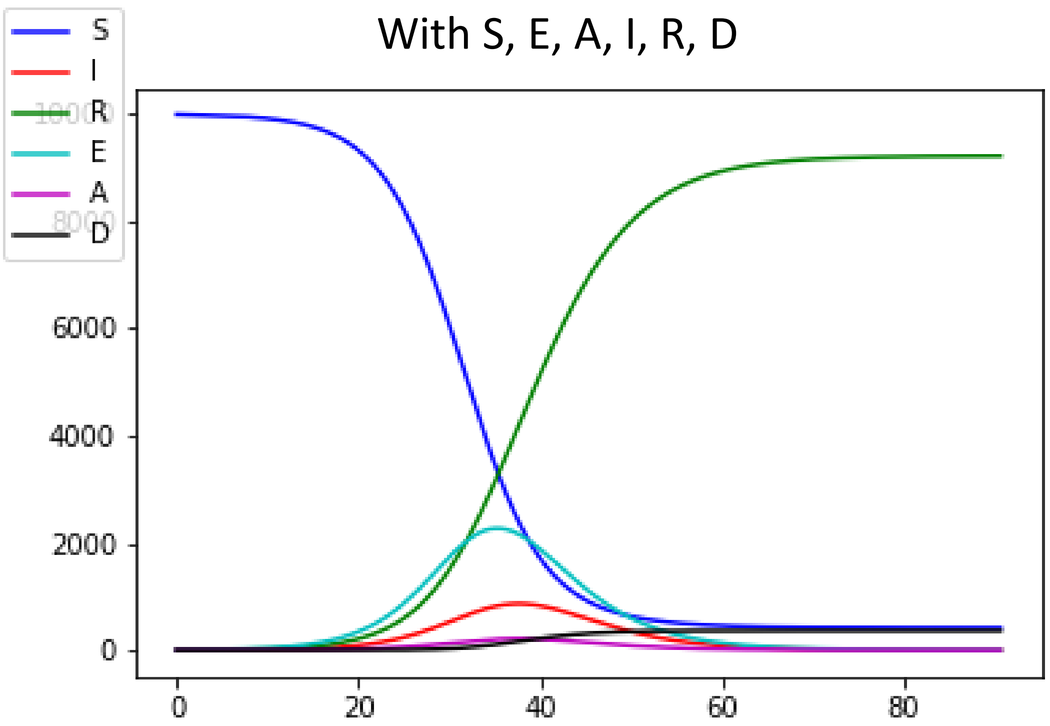
Example Curve

With no birth/death, E, I, A have a single peak.

A and I have the same shape
D and R have the same shape

$$G = 0.4$$
$$q_{known} = 0.4$$
$$B_A = 2.5$$
$$B_I = 1$$

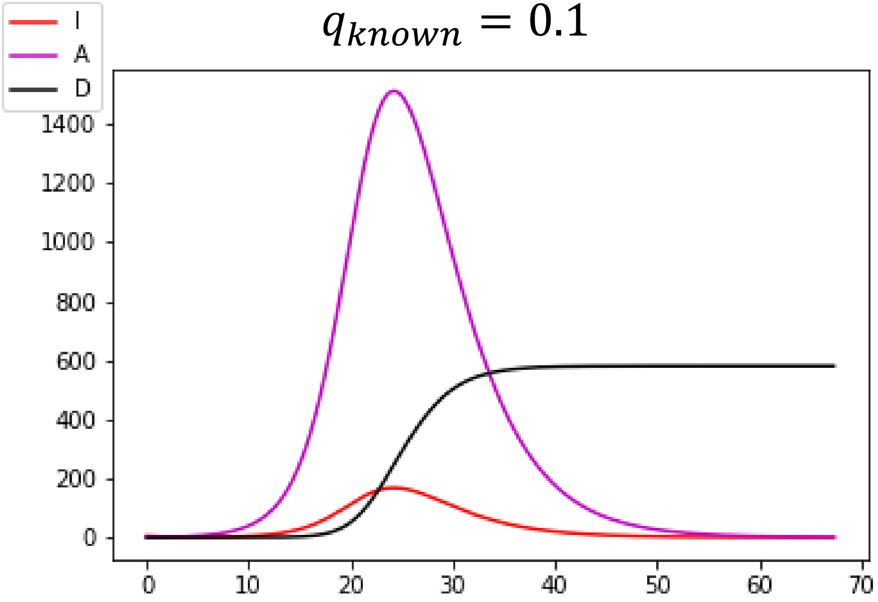




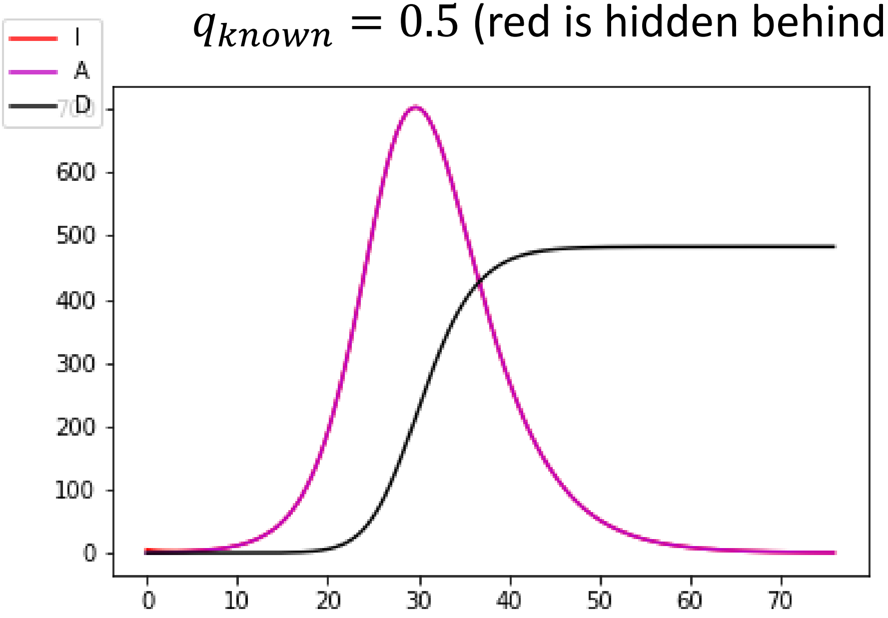
The effect of q_{known}

Example I and A graphs for $\frac{B_A}{B_I} = 2.5$

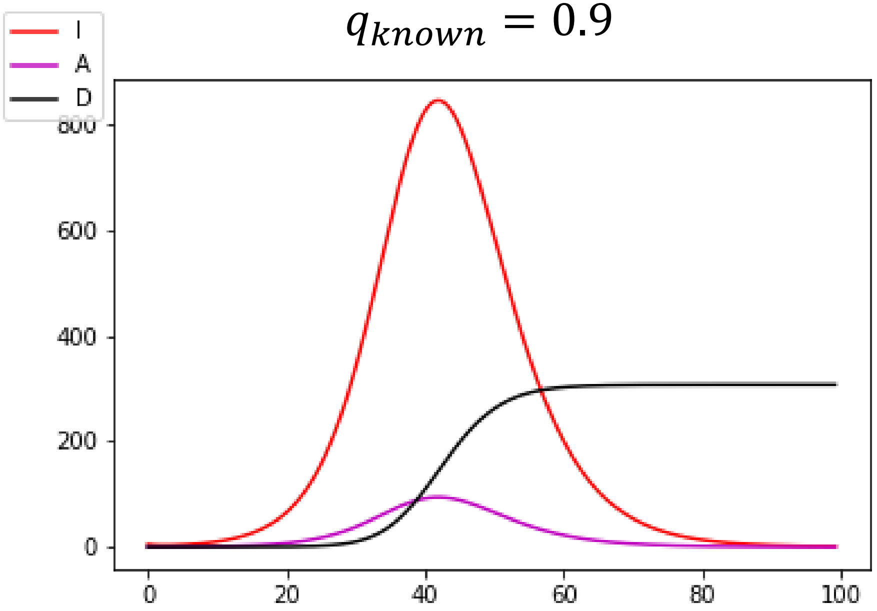
$q_{known} = 0.1$



$q_{known} = 0.5$ (red is hidden behind purple)



$q_{known} = 0.9$



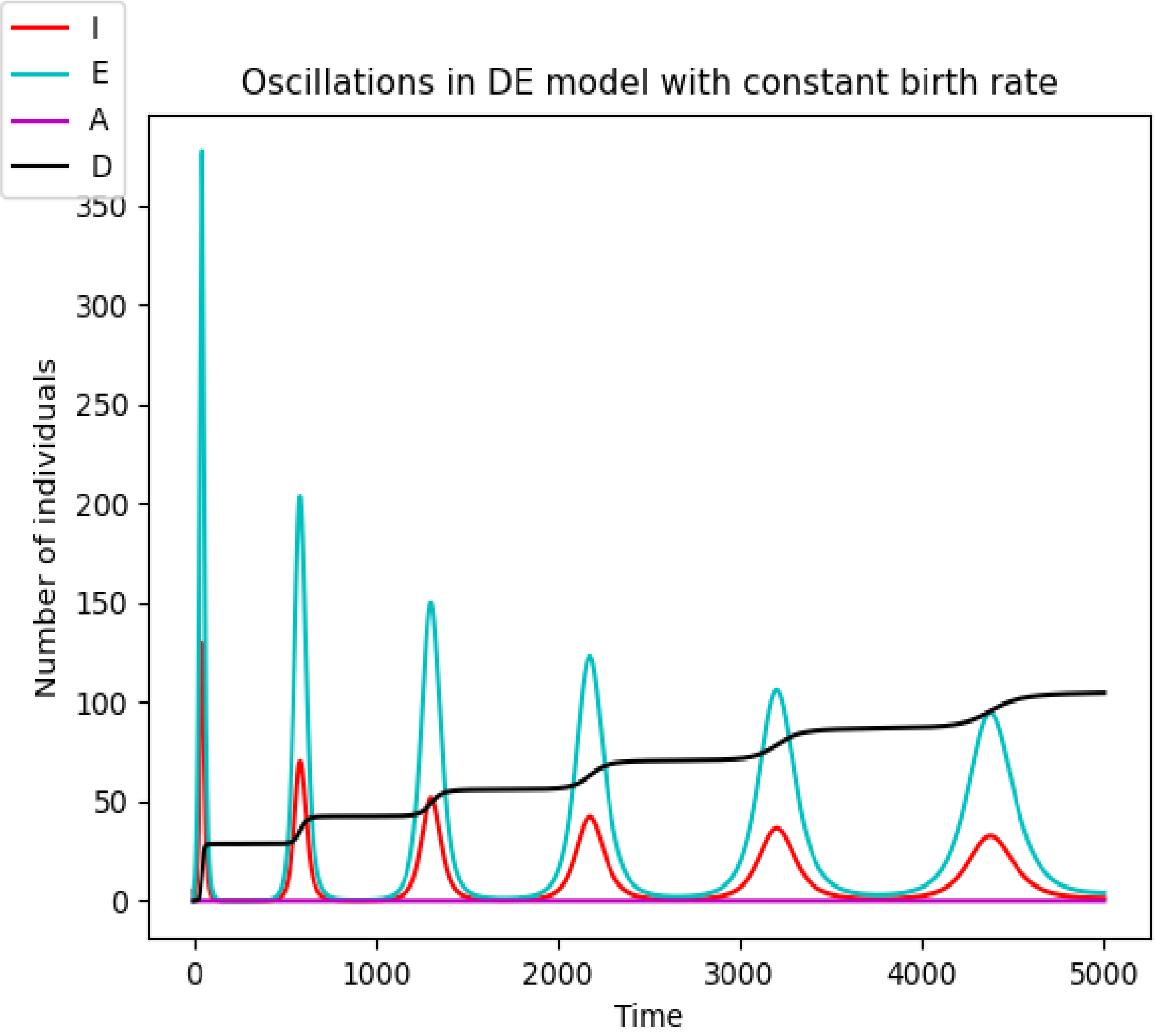
Population Flux, Oscillations

All populations die at a constant rate

$$\frac{dx}{dt} = -\mu x$$

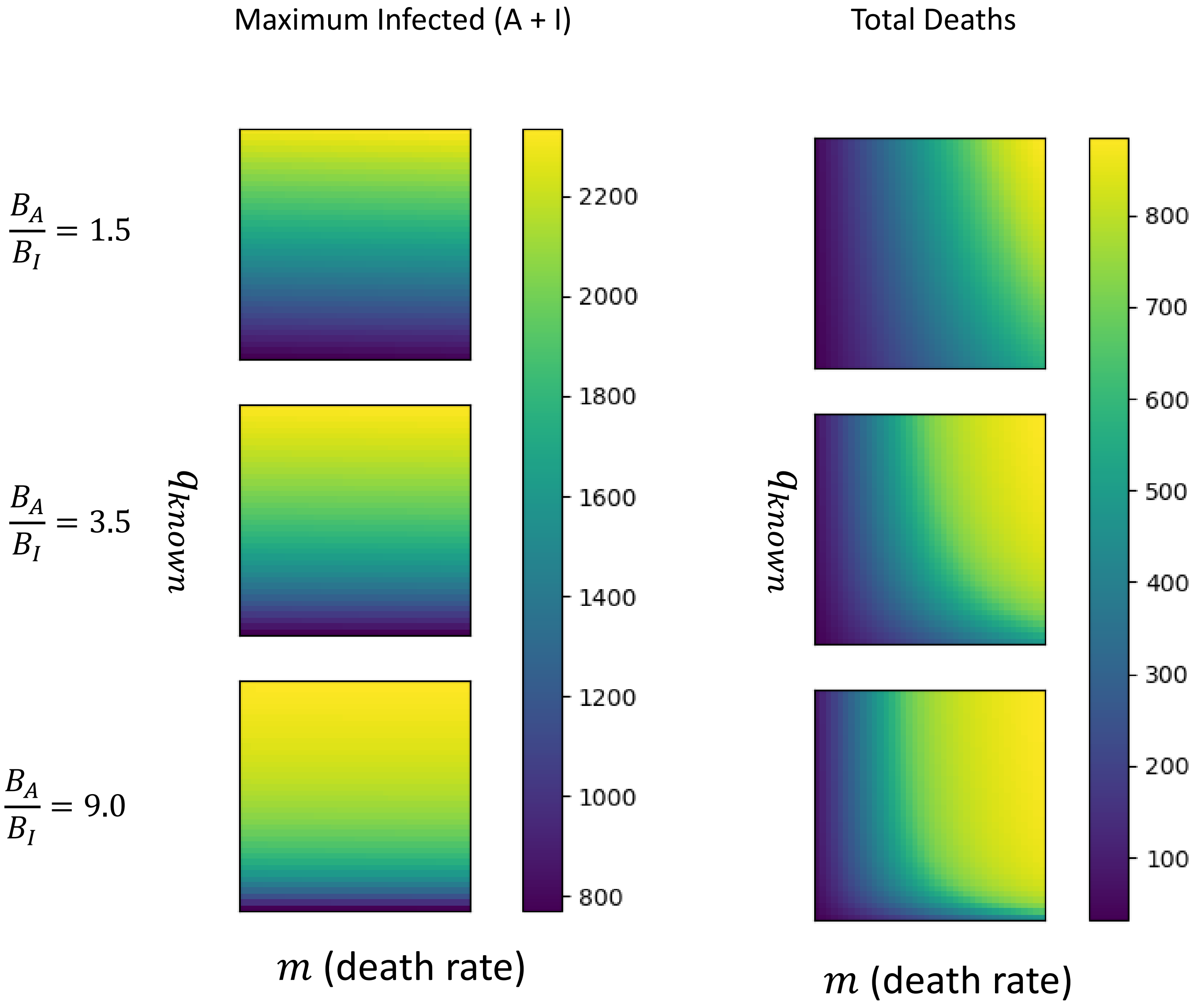
New births into S population balanced to match natural deaths

$$\frac{dS}{dt} = \mu N$$



S and R are hidden

Deaths and Time to Completion based on q_{known} and m



B_A is infectivity of asymptomatic (unknown)

B_I is infectivity of symptomatic (known)

q_{known} is proportion of unknown cases

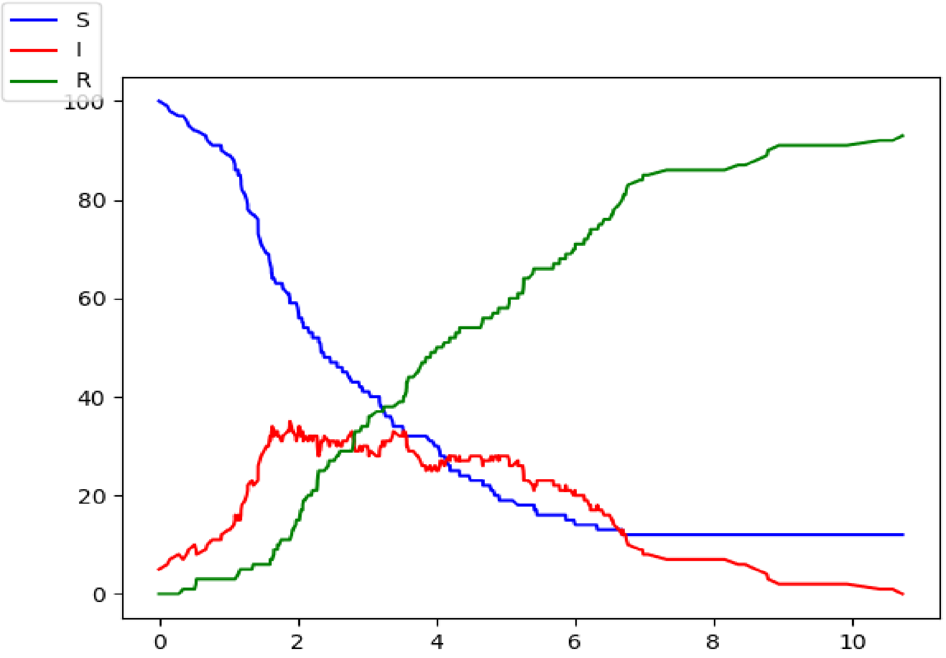
m is the linear burdening of the healthcare system

Heatmaps from different rows are not directly comparable due to different B_{avg}.

Stochastic Models

- Instead of continuous changes (e.g. it is possible for $I = 0.5$ to start an epidemic), stochastic predicts based on discrete changes.
  - More realistic for smaller populations

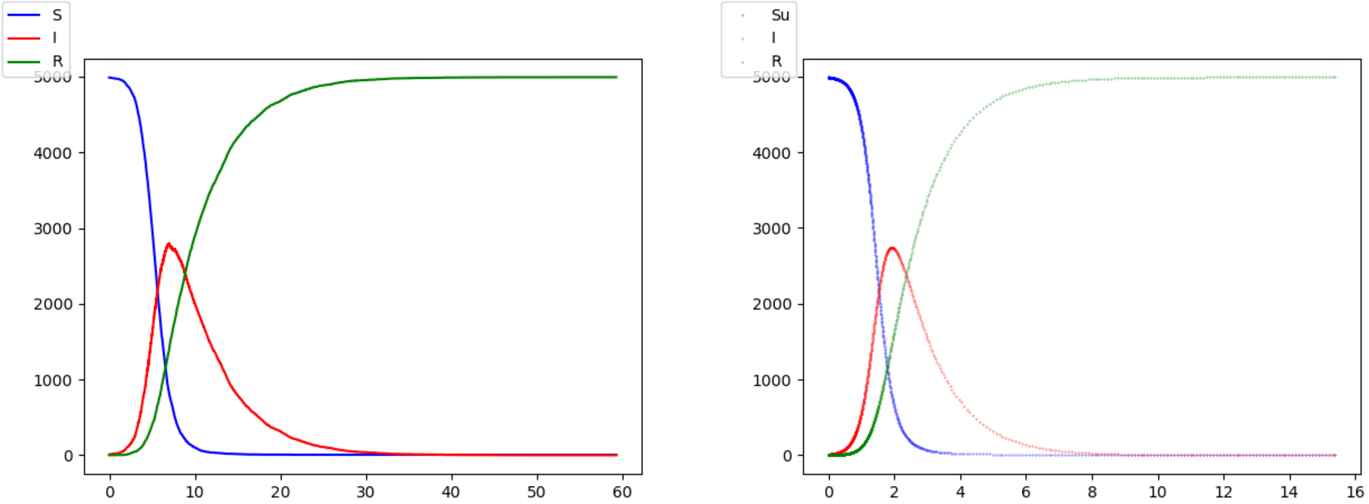
- Uses random number generator, so simulations with same parameters might produce different results (false for large populations)



SIR model with discrete changes, simulated using Gillespie algorithm

Advantages:

- Can model individuals with different characteristics
  - **Mask-wearing**
  - **Geographic location**
    - Closely connected hubs, small communities, …
  - Different individual Betas (infectivity)
  - Communities with occasional contact
  - Age, socioeconomic status, infectivity, death rate, travel, …



Left: Stochastic, Right: DE; same rate constants, SIR model
At sufficiently large populations, stochastic models have the same result as DE

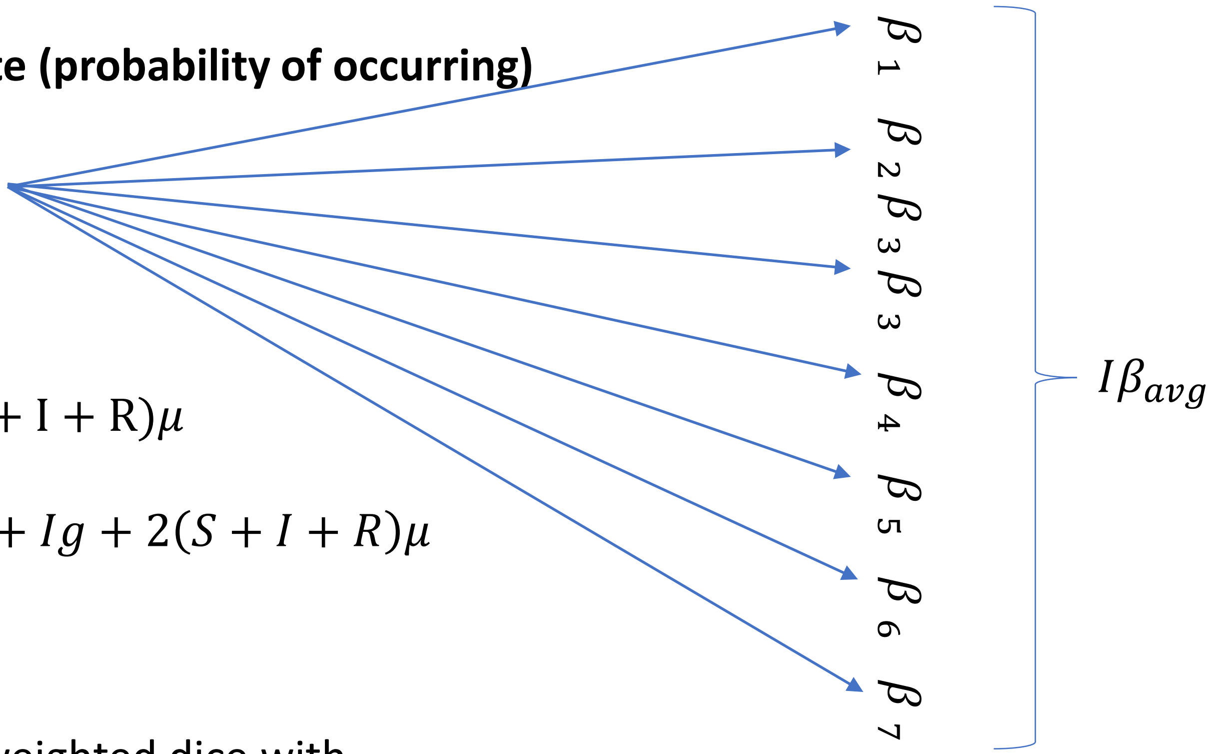
Implementation based on discrete events
SIR

Event	**Rate (probability of occurring)**	**Action**
I interacts with any alive individual	$I\beta$	• If I interacts with S, then that S turns to I, else nothing
I turns to R	Ig	• I turns to R
Death of x (S, I, R)	$x\mu$	• Individual turns to D
Births	$(\mathrm{S}+\mathrm{I}+\mathrm{R})\mu$	• One individual is added to S collection
All events rate	$\boldsymbol{I\beta + Ig + 2(S + I + R)\mu = r}$	

For total event rate r, the times between events is given by distribution $t = -\frac{\ln(1-x)}{r}$, x is random in $[0 \ldots 1)$

Implementation based on discrete events, with individual beta
SIR

Event	**Rate (probability of occurring)**
I interacts with any alive individual	$I\beta$
I turns to R	Ig
Death of x (S, I, R)	$x\mu$
Births	$(\mathrm{S}+\mathrm{I}+\mathrm{R})\mu$
All events rate	$I\beta + Ig + 2(S + I + R)\mu$

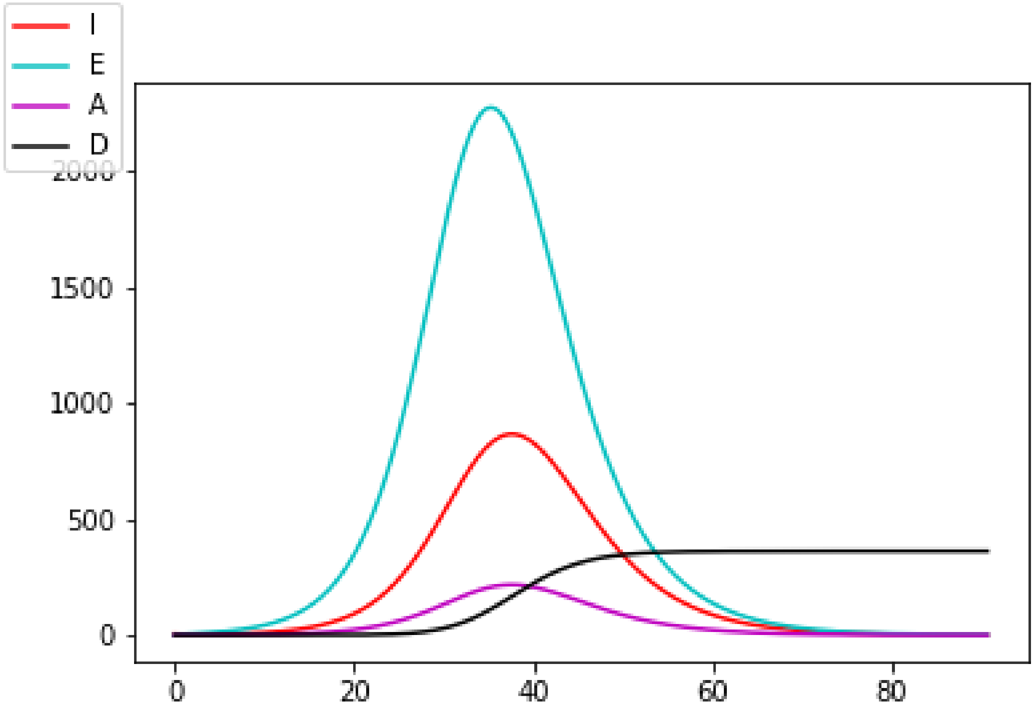


Choose which events by rolling n-sided weighted dice with probabilities for each side equal to specific rate

Why?
Allows us to model every individual

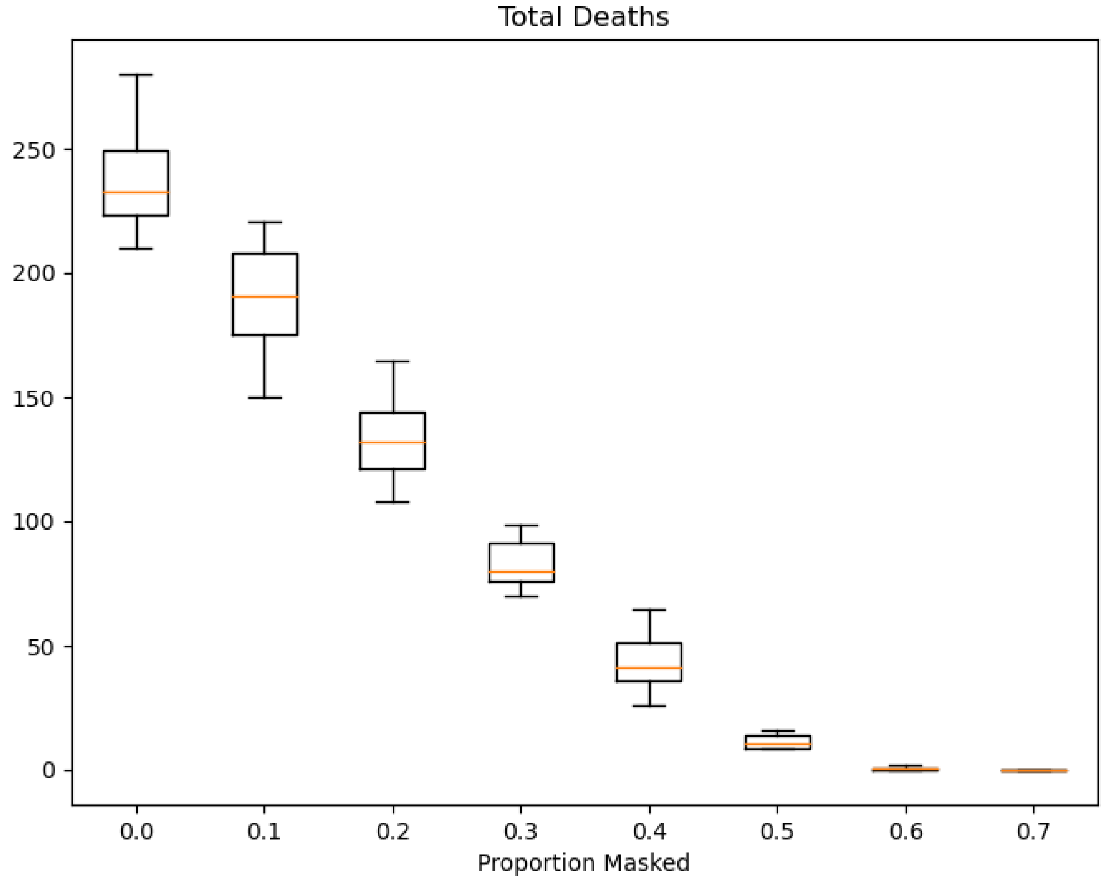
Measurements

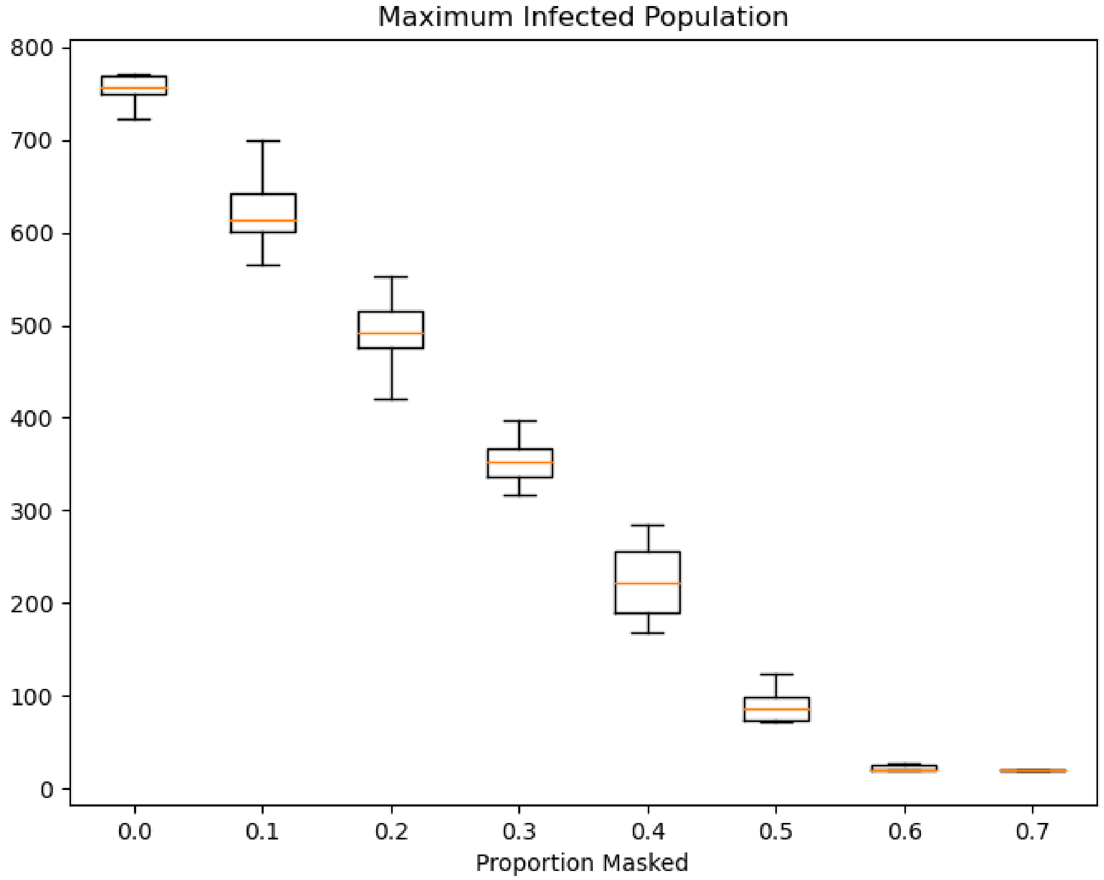
- Total deaths
- Length of epidemic (when the population of Infected is 0)
- Peak of infected population
- Time to peak of infected population



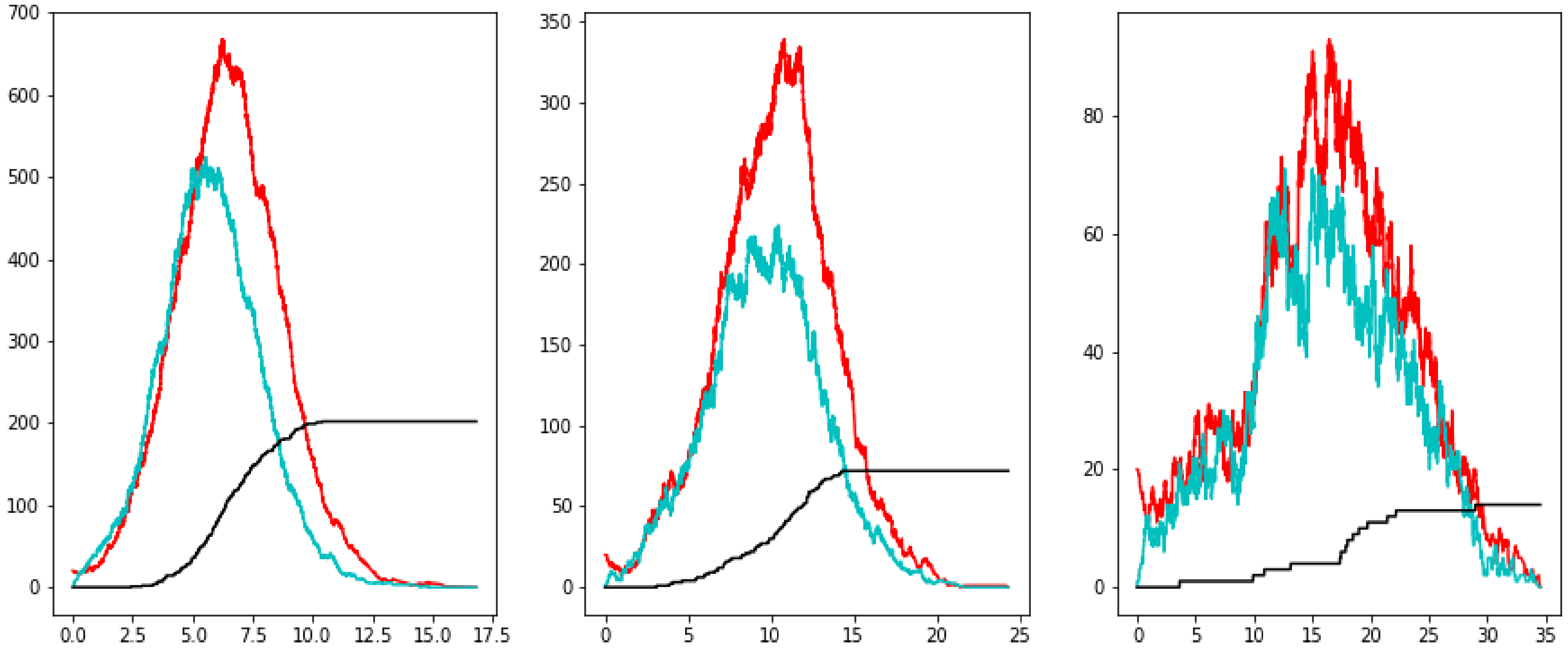
Simulating mask wearing (5000 individuals)

Infectious Mask status	Susceptible Mask status	Chance of infection in interaction
0	0	1
1	0	0.1
0	1	0.6
1	1	0.05





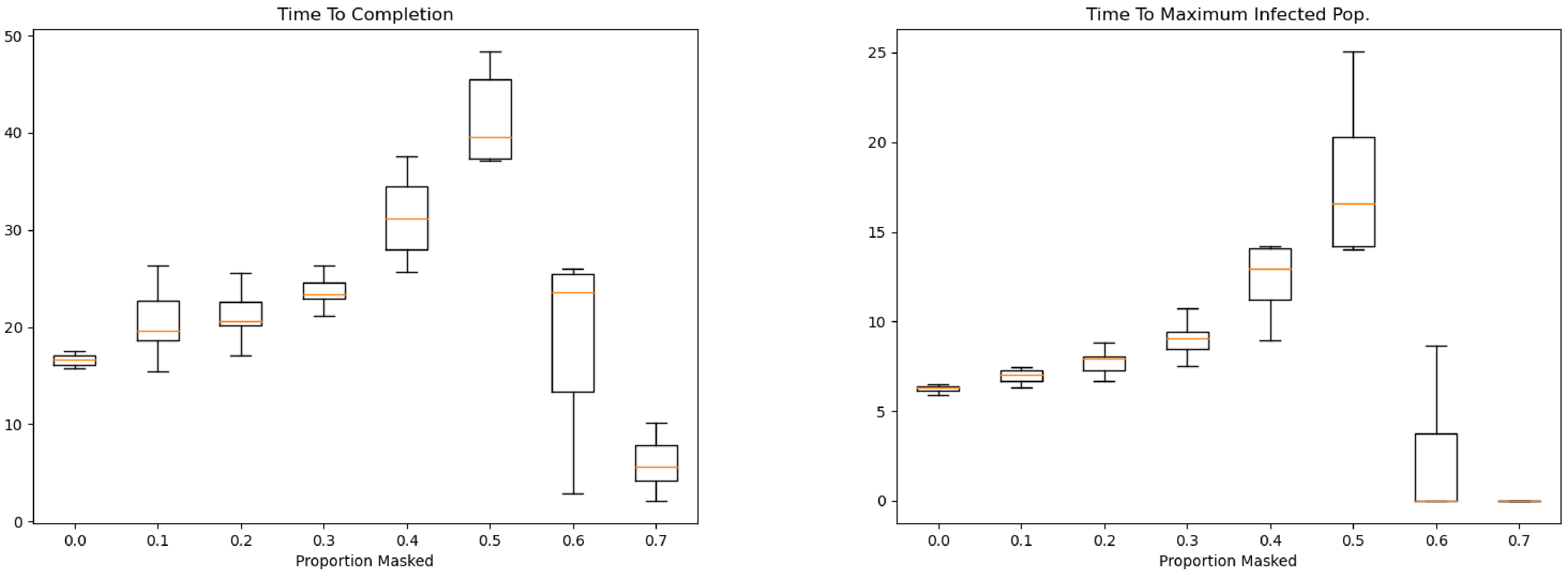
Proportion masked: 0.1 0.4 0.6



Masks:

- Increase length of epidemic (17 to 25 to 35)
- Increase time to peak of infection
- Decrease peak of infection

Red: Infected
Cyan: Exposed
Black: Dead



Time To Completion
50
40
30
20
10
0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Proportion Masked
Time To Maximum Infected Pop.
25
20
15
10
5
0
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Proportion Masked

Aside: implementing masks with DE?

Infectious Mask status	Susceptible Mask status	Chance of infection in interaction	
0	0	1	k_1
1	0	0.1	k_2
0	1	0.6	k_3
1	1	0.05	k_4

Reason:
Masked and unmasked populations don't interchange

$$S_m \to I_m \to R$$
$$S_{um} \to I_{um} \to R$$

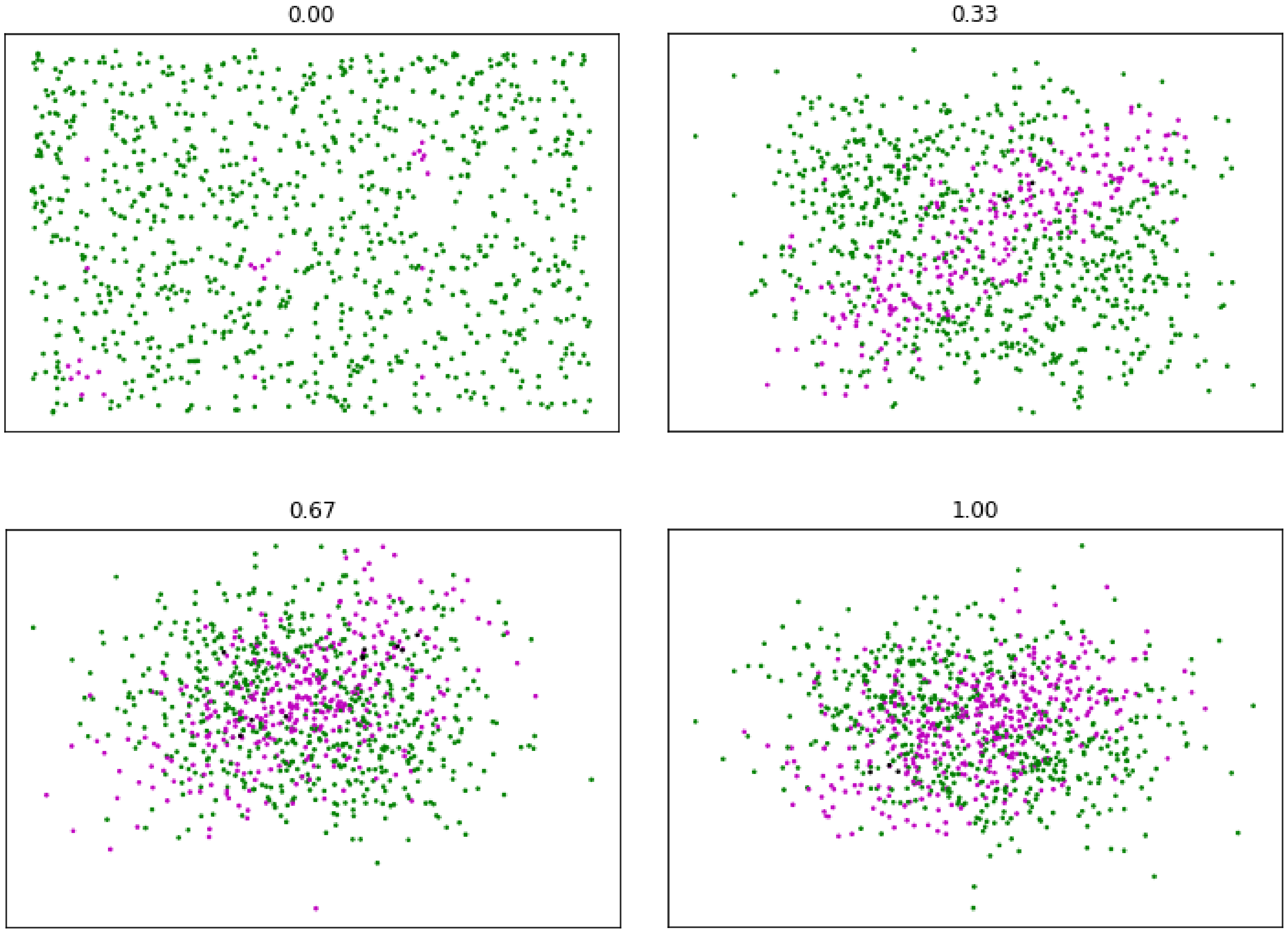
Sample equations for $\boldsymbol{I_m}$ and $\boldsymbol{S_m}$

$$\frac{dS_m}{dt} = -\frac{\beta S_m}{N}(k_3 I_{um} + k_4 I_m)$$

$$\frac{dI_m}{dt} = \frac{\beta I_m}{N}(k_2 S_{um} + k_4 S_m) - \gamma I_m$$

$$\frac{dR}{dt} = \gamma(I_m + I_{um})$$

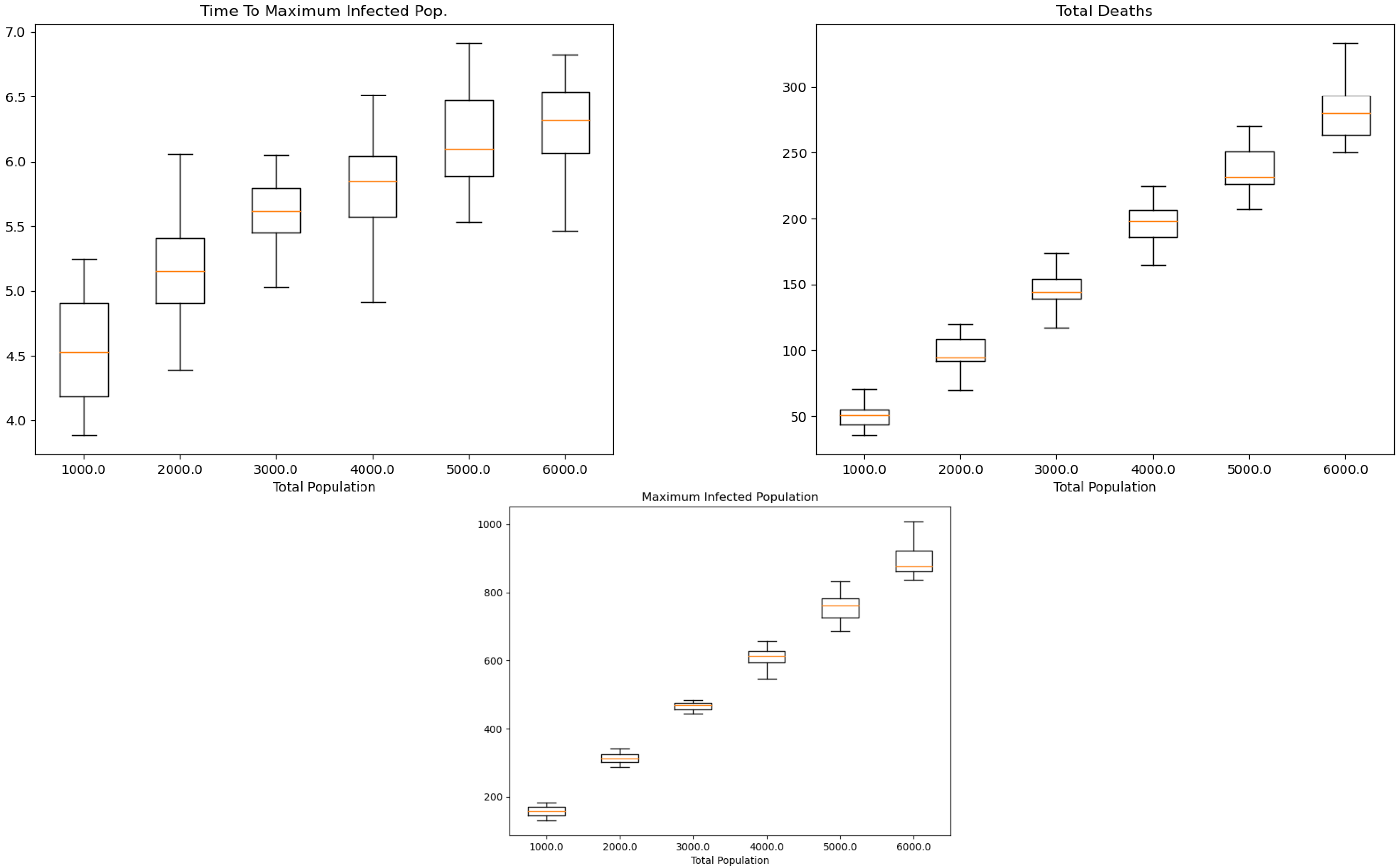
Non-uniform mixing



Green – Susceptible
Purple – Recovered
Black – Dead

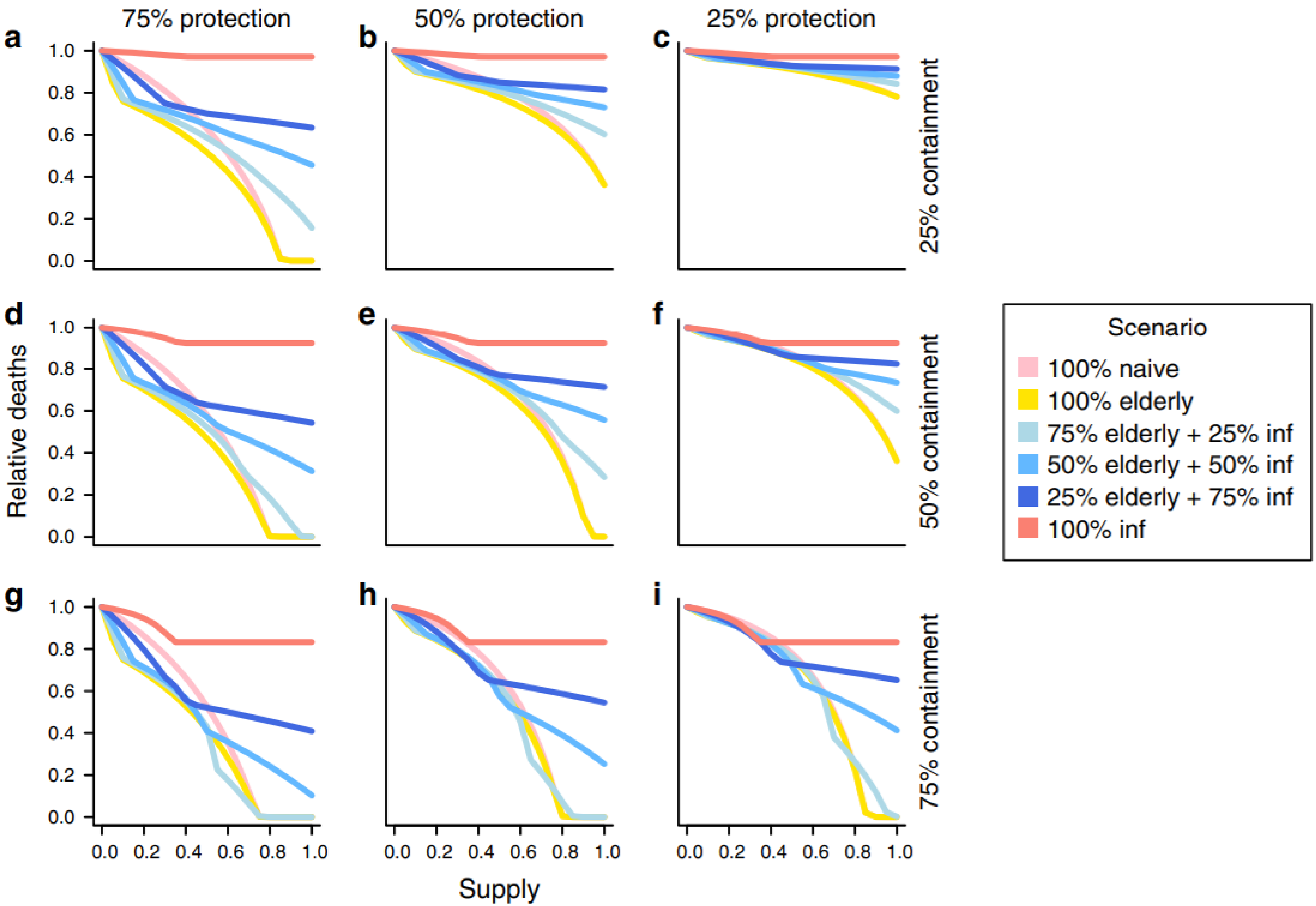
Infectious individuals infect all within a certain radius.

Plot Title - Proportion of population moving per iteration
Simulates travel restrictions, stay at home


Time To Maximum Infected Pop.
7.0
6.5
6.0
5.5
5.0
4.5
4.0
1000.0
2000.0
3000.0
4000.0
5000.0
6000.0
Total Population
Total Deaths
300
250
200
150
100
50
1000.0
2000.0
3000.0
4000.0
5000.0
6000.0
Total Population
Maximum Infected Population
1000
800
600
400
200
1000.0
2000.0
3000.0
4000.0
5000.0
6000.0
Total Population

Protection – chance of being infected

Containment – chance of spreading infection



Worby, C.J., Chang, H. Face mask use in the general population and optimal resource allocation during the COVID-19 pandemic. *Nat Commun* **11,** 4049 (2020). https://doi.org/10.1038/s41467-020-17922-x