

Computational models of epidemics

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Microquiz 2

- * On Wednesday April 22, the quiz will be available at 3:55pm MIT time and it will be taken down 12 hours later.
- * You may begin the quiz within that time period but will have 30 minutes to complete it once you view the questions.
- * The quiz will cover material from Lectures 1-6.
- * The quiz will be coding questions.
- * You may use an IDE of your choice to write code but you must submit code on the quiz site.
- * We allow you to use materials provided in lectures (slides or posted code). You are not allowed to use the Internet or discuss the quiz with anyone for the 12 hours while the quiz is available.
- * If you have already given me your accommodations letter you'll receive an email today, and your timer will be adjusted accordingly.
- Each question has a separate Submit button, there is no overall Submit or checkout password.
 - * To end the quiz, you can close the page and/or just let the timer run out.
 - * You can submit answers as often as you want, the last submission is the one we grade.
 - * By starting the quiz, you are automatically agreeing to the honor pledge.
 - * Be mindful of the time and submit often -- no exceptions are made if you cannot submit when the timer reaches 0 time left.
 - * If there is something confusing during the quiz, there will be a text box where you can write your confusions/assumptions you made.
 - * During the quiz, may not see any test cases due to the nature of the problem asked. If there are any test cases, they are there to avoid copy/paste errors from your IDE to the submission page. Your score will be based on how it performs on the test cases WE use.

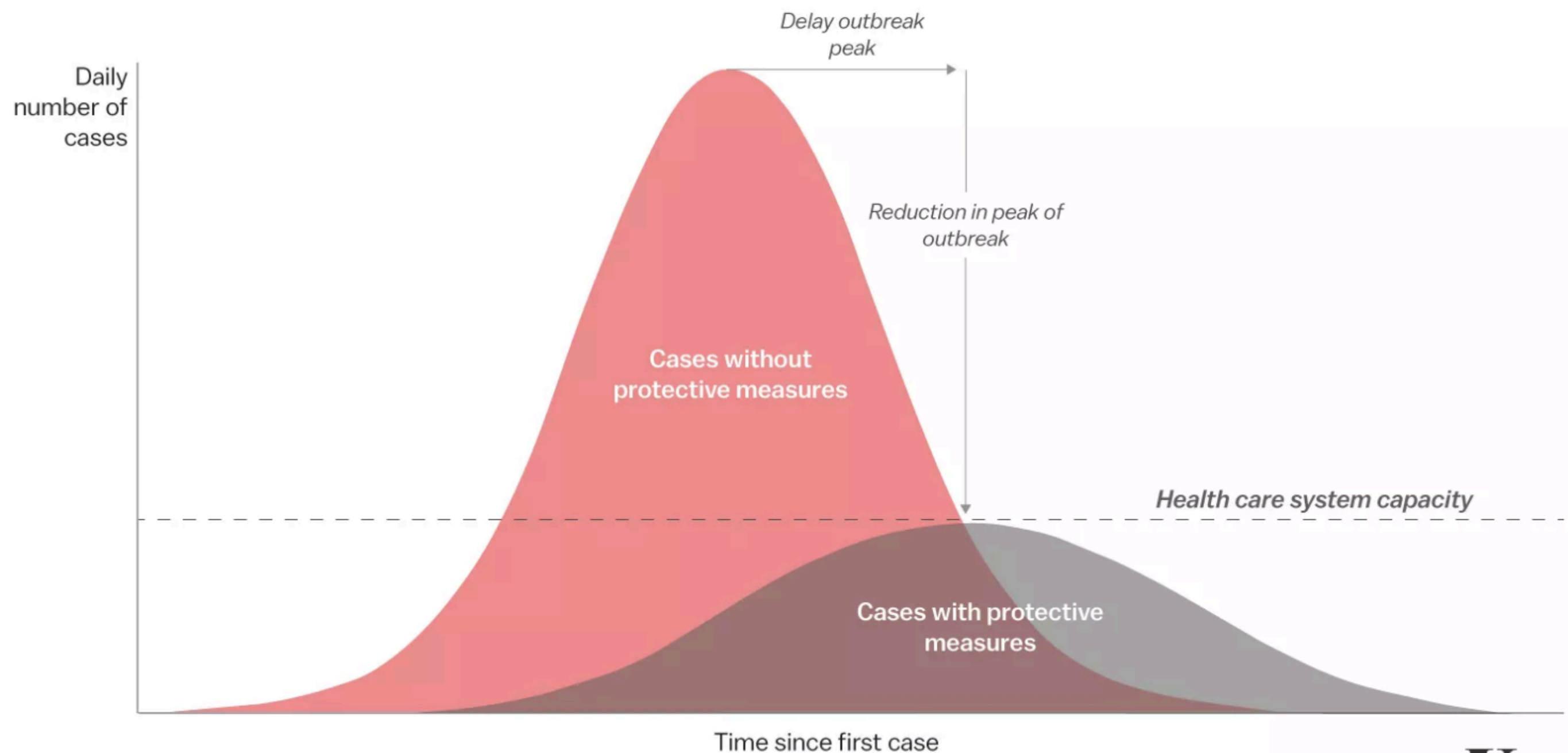
Trigger warning

- This lecture deals with epidemics and COVID-19
- If you'd rather think of something else, you can watch an alternative lecture recorded by Prof. Grimson about stock market simulation (bonus: no French accent)
- I hope you and your family are safe

The world has been different

- Lots of graphs, simulations, R_0 , exponentials, predictions
- We are all trying to flatten the curve

Flattening the curve



Source: CDC

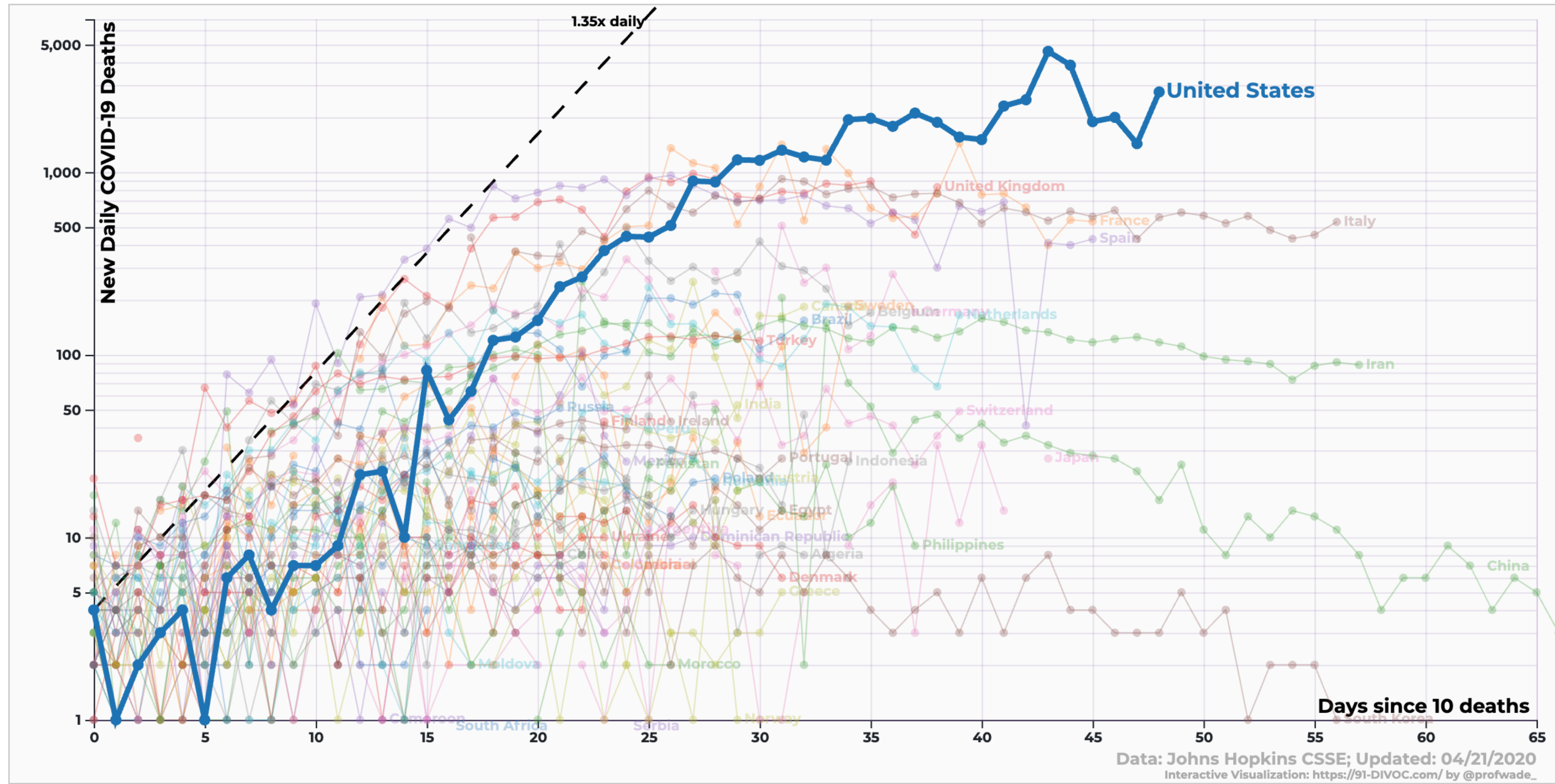
Christina Animashaun/Vox

Vox



Covid-19 epidemic

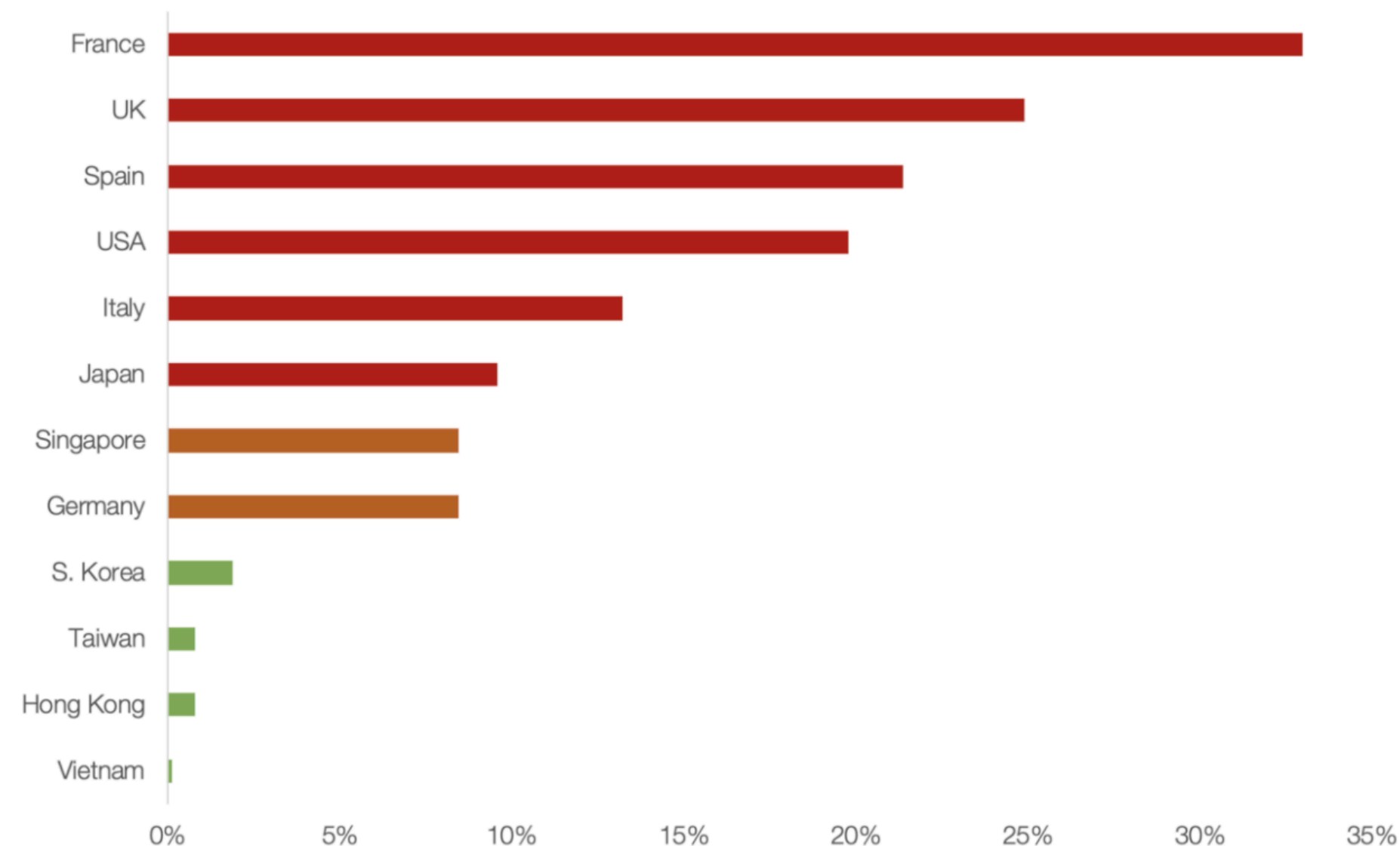
COVID-19 Cases by Country



Enormous flaws in the data

- Number of cases probably wrong by a factor of 2-10
- Not enough tests !
- Number of tests (and quality) varies in time and space

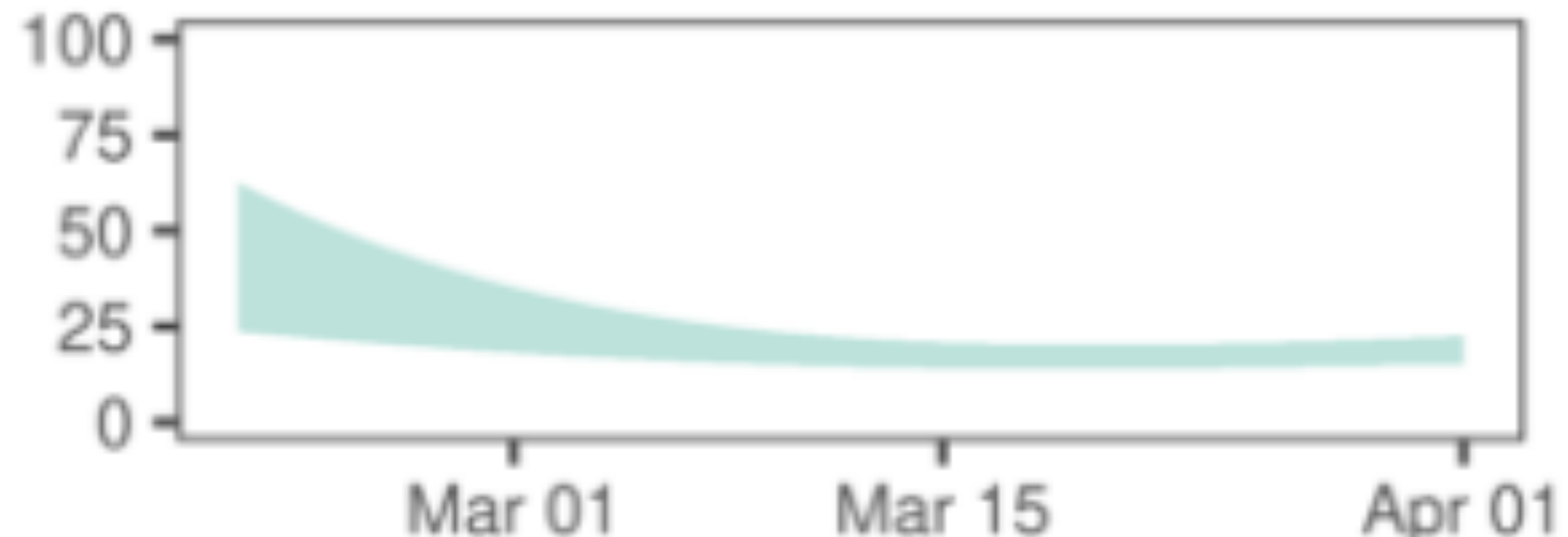
Chart 7: Share of Positive Coronavirus Tests
As of April 20th 2020



Source: Tomas Pueyo Analysis based on data from Worldometers, <https://www.worldometers.info/coronavirus/#countries>

Estimate of % of cases reported over time

United States of America



https://cmmid.github.io/topics/covid19/severity/global_cfr_estimates.html

<https://medium.com/@tomaspuoyo/coronavirus-learning-how-to-dance-b8420170203e>

We need good data

- Randomize/systematic virus and serology tests

Other online visualizations

- <https://www.youtube.com/watch?v=54XLXg4fYsc> minute physics explains log-log <https://aatishb.com/covidtrends/>
- <http://www.91-divoc.com/pages/covid-visualization/>
- <https://valis.pub/>
- <https://www.ft.com/coronavirus-latest>
- <https://epiforecasts.io/covid/posts/global/>
- <https://robjhyndman.com/hyndsight/logratios-covid19/> shows rate
- <https://blog.datawrapper.de/coronaviruscharts/>
- <https://ourworldindata.org/>
- <https://covidtracking.com/>
- <https://www.economist.com/graphic-detail/2020/04/16/tracking-covid-19-excess-deaths-across-countries>
- <https://www.nytimes.com/interactive/2020/04/02/us/coronavirus-social-distancing.html>
- <https://www.ft.com/content/d184fa0a-6904-11ea-800d-da70cff6e4d3>
- <https://medium.com/nightingale/ten-considerations-before-you-create-another-chart-about-covid-19-27d3bd691be8>
- <https://www.tableau.com/covid-19-coronavirus-data-resources>

Lecture goals

- Simulation and successive model refinement
- Epidemic modeling

Mathematical Modelling of Zombies



Robert Smith?
University of Ottawa Press

Warning

- I am not an expert (beware of Dunning-Kruger effect)
 - Especially not about biology and medicine
- Things are moving really fast
- Available data is terrible. Awful. Appalling. Abysmal. Not good at all
- Be wary of anyone with certainty (I am certain of that)
- Be wary of anyone who takes confirmed case numbers too seriously
- Wash hands, wear mask, social distance

Reminder about simulations

- Only an approximation to reality
- “All models are wrong, but some are useful,” said George Box
- What insights ?
 - Understand basic behavior
 - Understand influence of various factors
 - (Sometimes) Compare clinical and policy options
 - (More rarely) Predict the future

Warning by Chris Whitty

- The tendency of some modelers to present them as scientific predictions of the future rather than models does not help. Models are widely used in government, and some models arguably have too much influence. They are generally most useful when they identify impacts of policy decisions which are not predictable by commonsense; the key is usually not that they are ‘right’, but that they provide an unpredicted insight.
- <https://bmcmmedicine.biomedcentral.com/articles/10.1186/s12916-015-0544-8> What makes an academic paper useful for health policy?

How would one simulate an epidemic?

How would one simulate an epidemic?

- Simulate individuals
 - But that's a lot of people
- Aggregate simulation, statistical
 - Simplified but easier to compute and easier to analyze

Statistical approach

- Only keep track of aggregate numbers
 - For example, total number of infected people
- Model probability of getting infected given current situation
- Similar to statistical physics and chemical kinetics

Basic simulation of infection

- Keep track of number of infectious $I(t)$
- Each infected person infects β per unit time

Basic simulation of infection

- Keep track of number of infectious $I(t)$
- Each infected person infects β per unit time
 - $\text{new_infected}(t) = \beta I(t)$
 - Assumes random homogenous mixing

Code simulation 1

```
def simulation_1(beta, initial_I=100, duration = 60):  
  
    I = [initial_I]  
  
    for t in range(duration):  
        new_infected = beta*I[-1]  
        I.append(I[-1] + new_infected)  
  
    return I
```

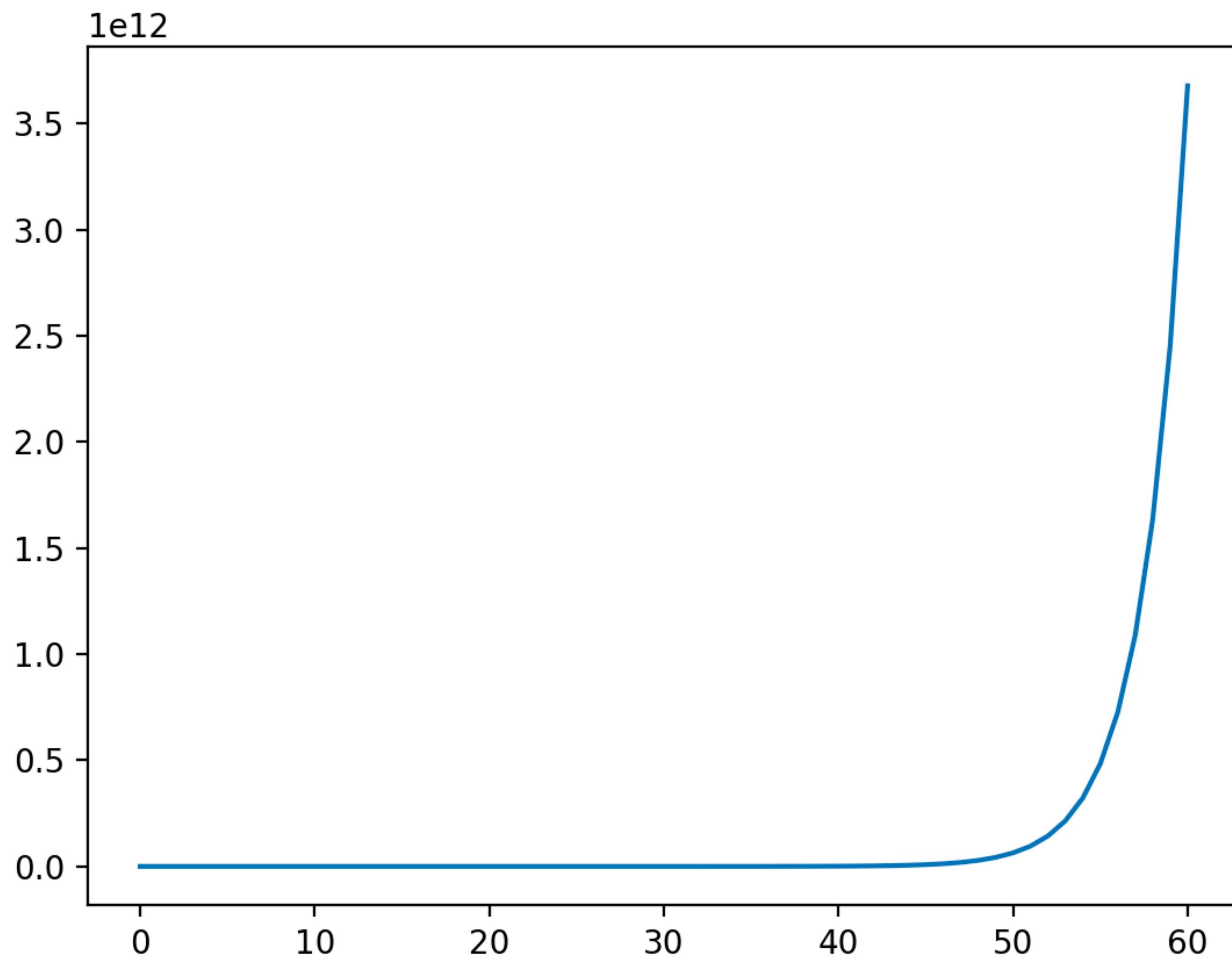
In file SIR-2.py

Code simulation 1

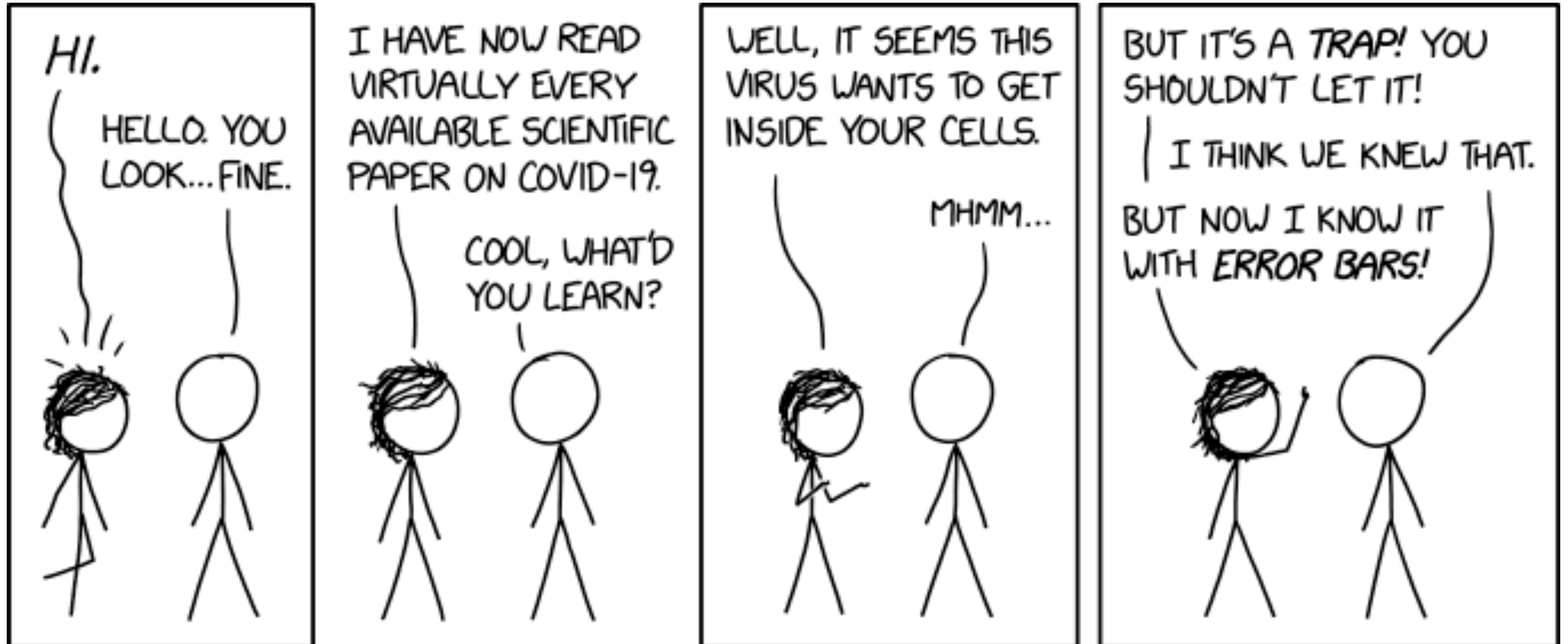
```
def simulation_1(beta, initial_I=100, duration = 60):  
    I = [initial_I]  
  
    for t in range(duration):  
        new_infected = beta*I[-1]  
        I.append(I[-1] + new_infected)  
  
    return I
```

- I use a list to keep track of history and be able to plot
- Looks a lot like compounding in 6.0001

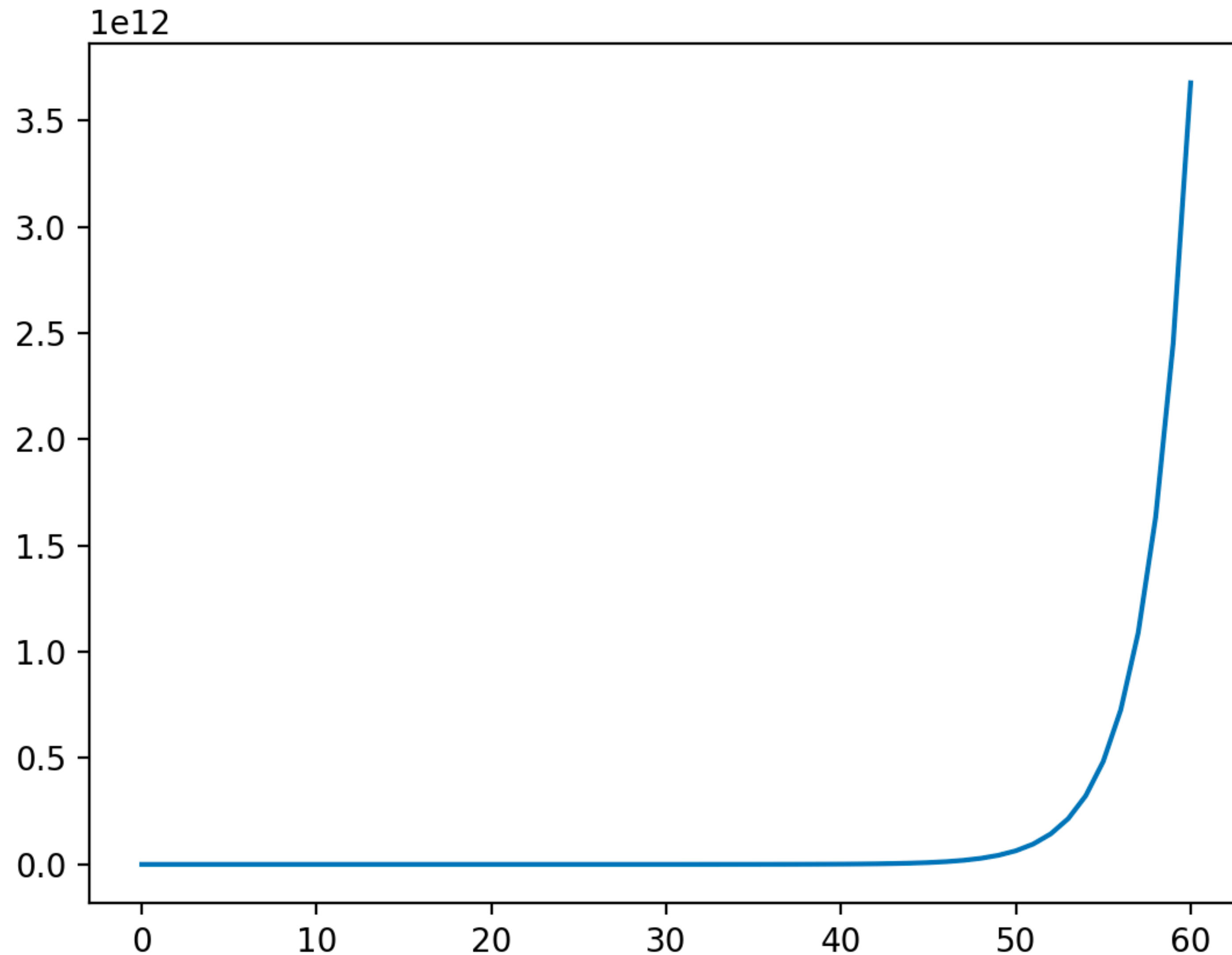
Plot



Questions?



Poll: What's wrong with our model?



Finite population, compartments

- Only finite number of people can get infected
 - The ones not yet infected.

Finite population, compartments

- Only finite number of people can get infected
 - The ones not yet infected, aka “Susceptible”
 - keep track of them too: $S(t)$
- Only $S/\text{population}$ fraction contacted by infectious can become infected
- $\text{new_infected} = \text{beta} * I(t) * S(t) / \text{population}$

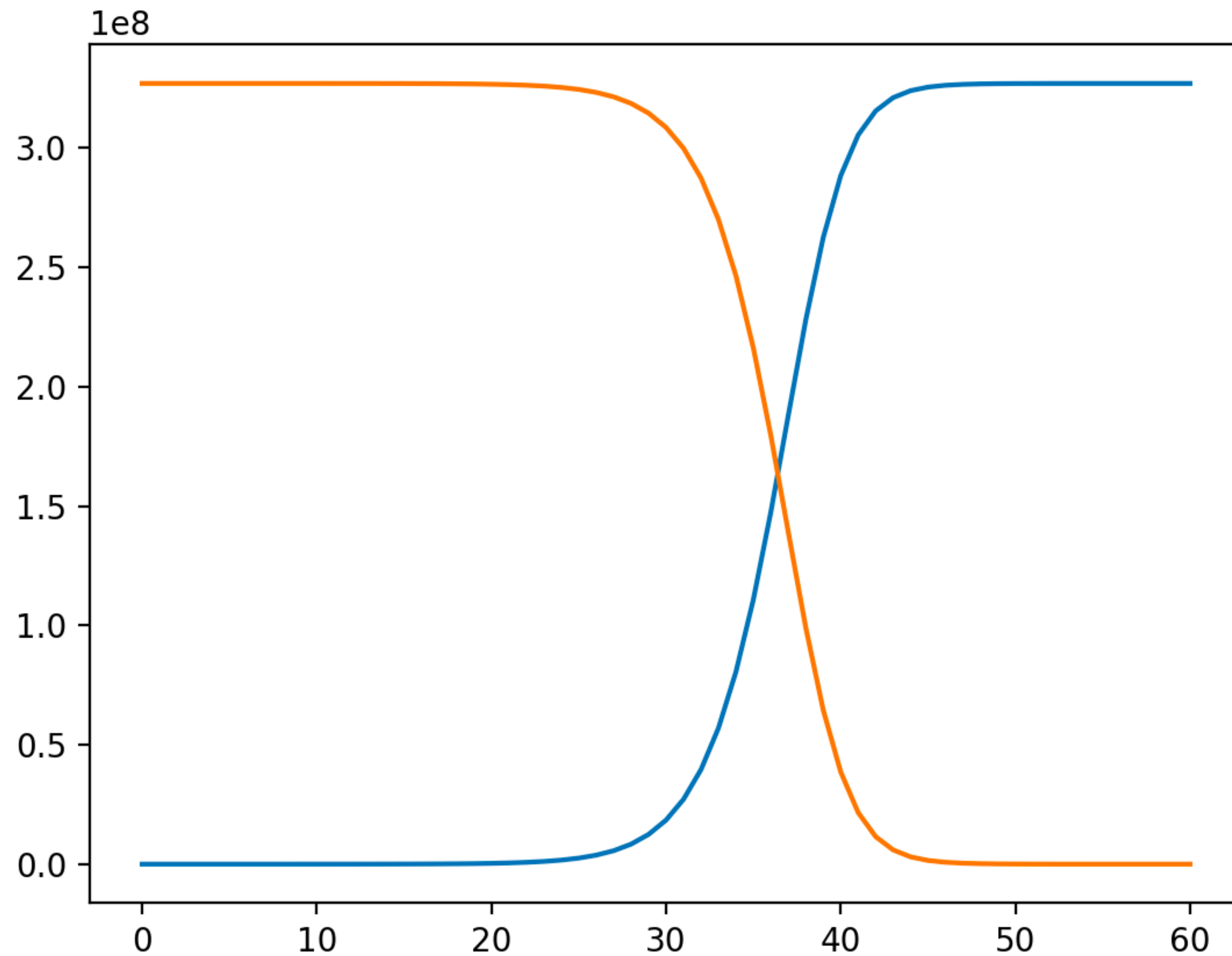
Starting from previous code

```
def simulation_1(beta, initial_I=100, duration = 60):  
  
    I = [initial_I]  
  
    for t in range(duration):  
        new_infected = beta*I[-1]  
        I.append(I[-1] + new_infected)  
  
    return I
```

Simulation 2: compartmental, SI

```
def simulation_2(beta, initial_I=100, population = 327e6, duration = 60):  
  
    I = [initial_I]  
    S = [population-initial_I]  
    for t in range(duration):  
        new_infected = beta*I[-1]*S[-1]/population  
        I.append(I[-1] + new_infected)  
        S.append(S[-1]- new_infected)  
    return S, I
```

Plot



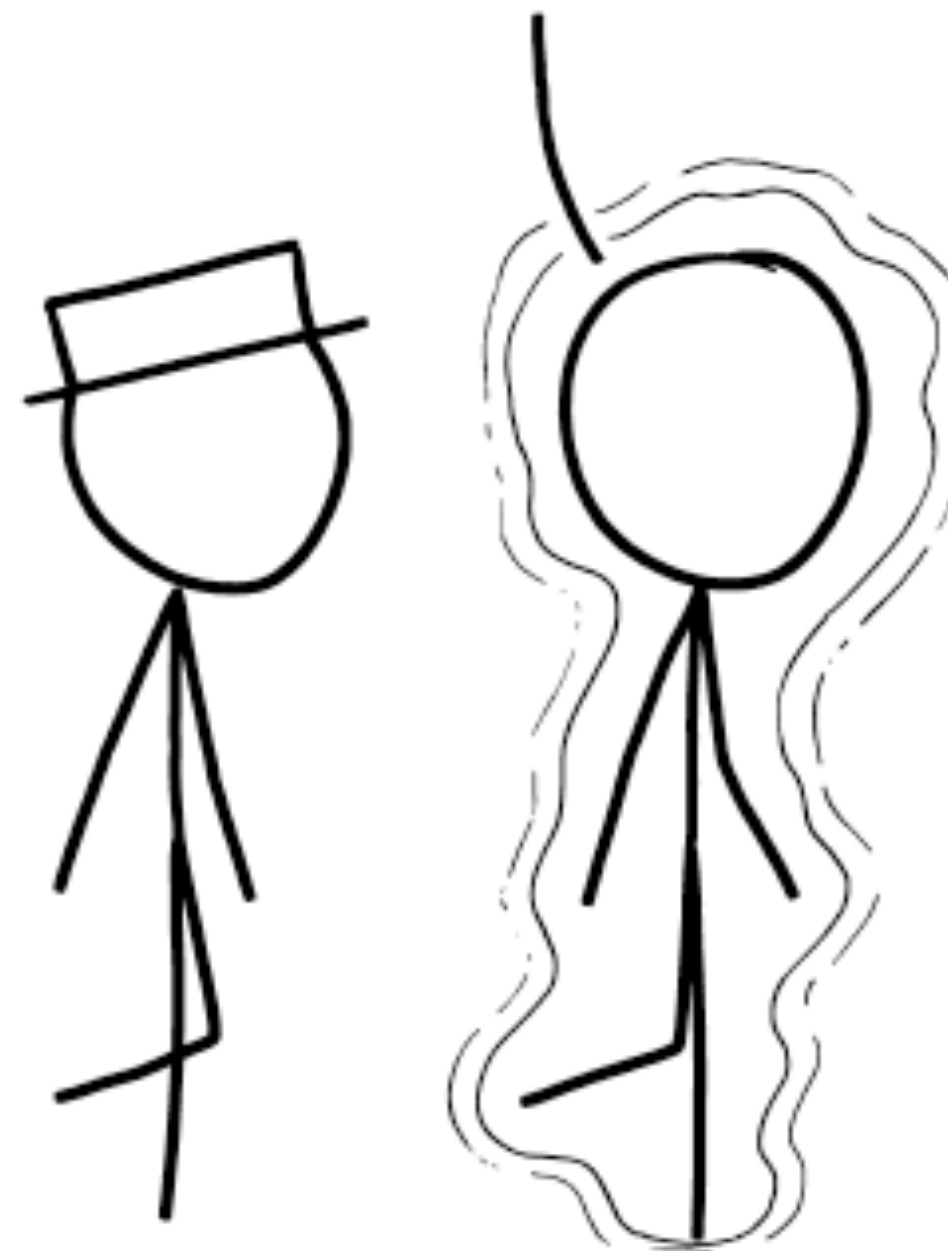
Similar to chemical kinetics

Questions?

WHAT ARE THINGS LIKE TEN YEARS FROM NOW IN 2020?
WE HAVE THIS NEW "BITCOIN" THING—DOES IT EVER CATCH ON AND BECOME NORMAL?



IT'S STILL AROUND.
I JUST BOUGHT
A BOTTLE OF
HAND SANITIZER
FOR ONE BITCOIN.

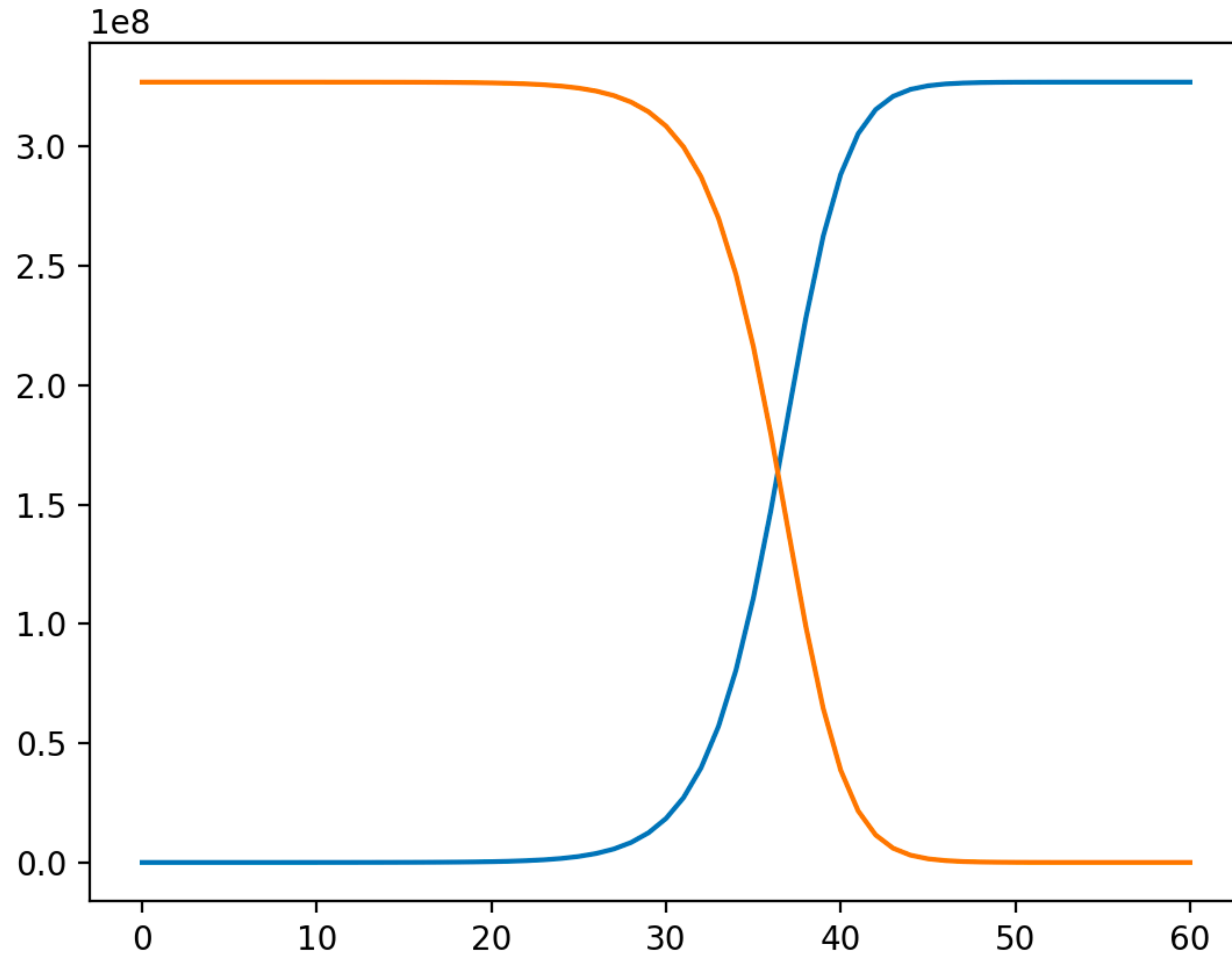


COOL, THAT SOUNDS
PRETTY NORMAL.

WELL, HERE'S
THE THING...



Poll: Now that was pessimistic too. Why?



Finally add recovery

- Infection only lasts D days on average
 - People recover at rate $\gamma = 1/D$
- Add compartment for Recovered aka Removed : $R(t)$
 - $\text{new_recovered} = \gamma * I(t)$
 - Assume long-lasting immunity for now

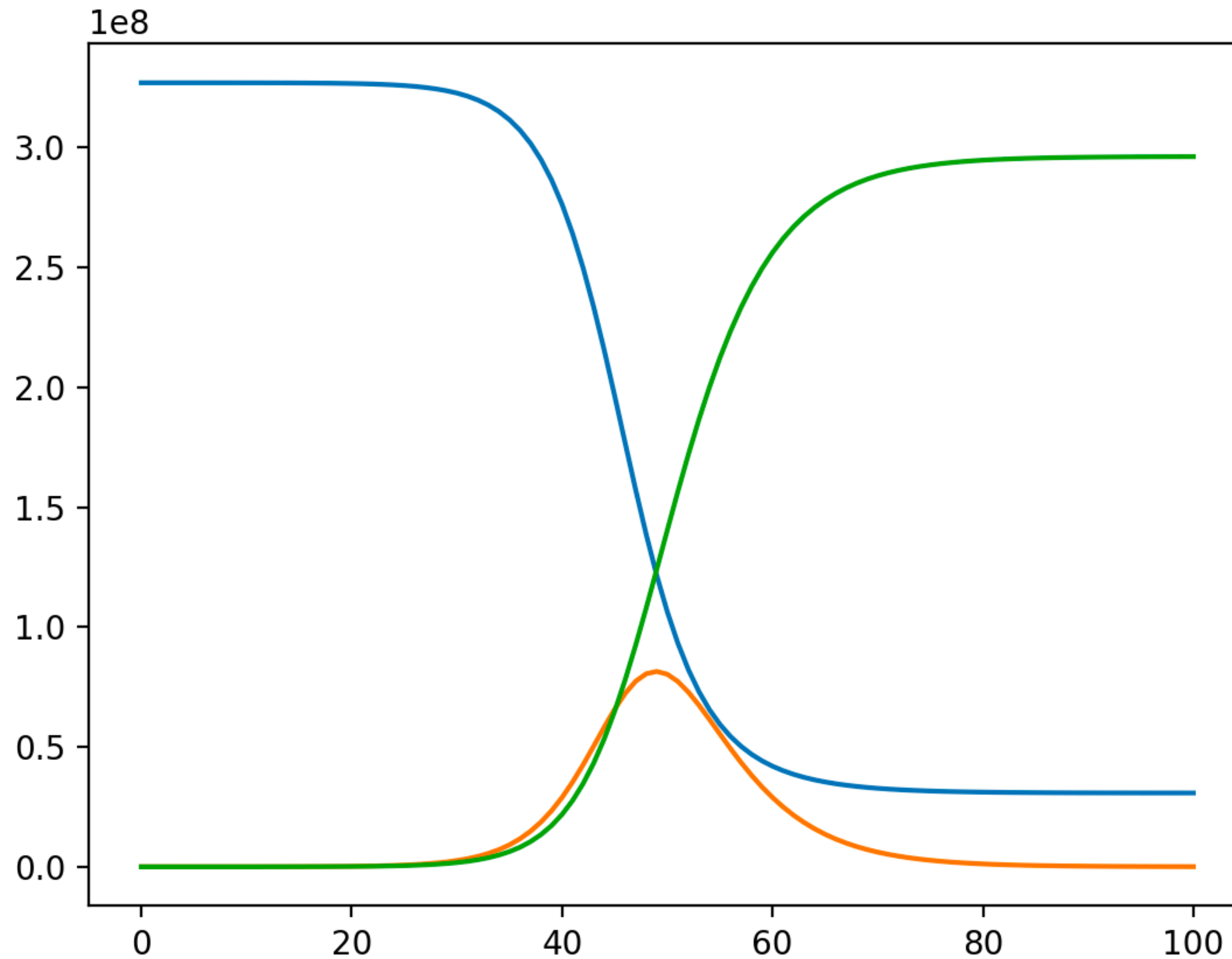
Starting from previous code

```
def simulation_2(beta, initial_I=100, population = 327e6, duration = 60):  
  
    I = [initial_I]  
    S = [population-initial_I]  
  
    for t in range(duration):  
        new_infected = beta*I[-1]*S[-1]/population  
        I.append(I[-1] + new_infected)  
        S.append(S[-1]- new_infected)  
  
    return S, I
```

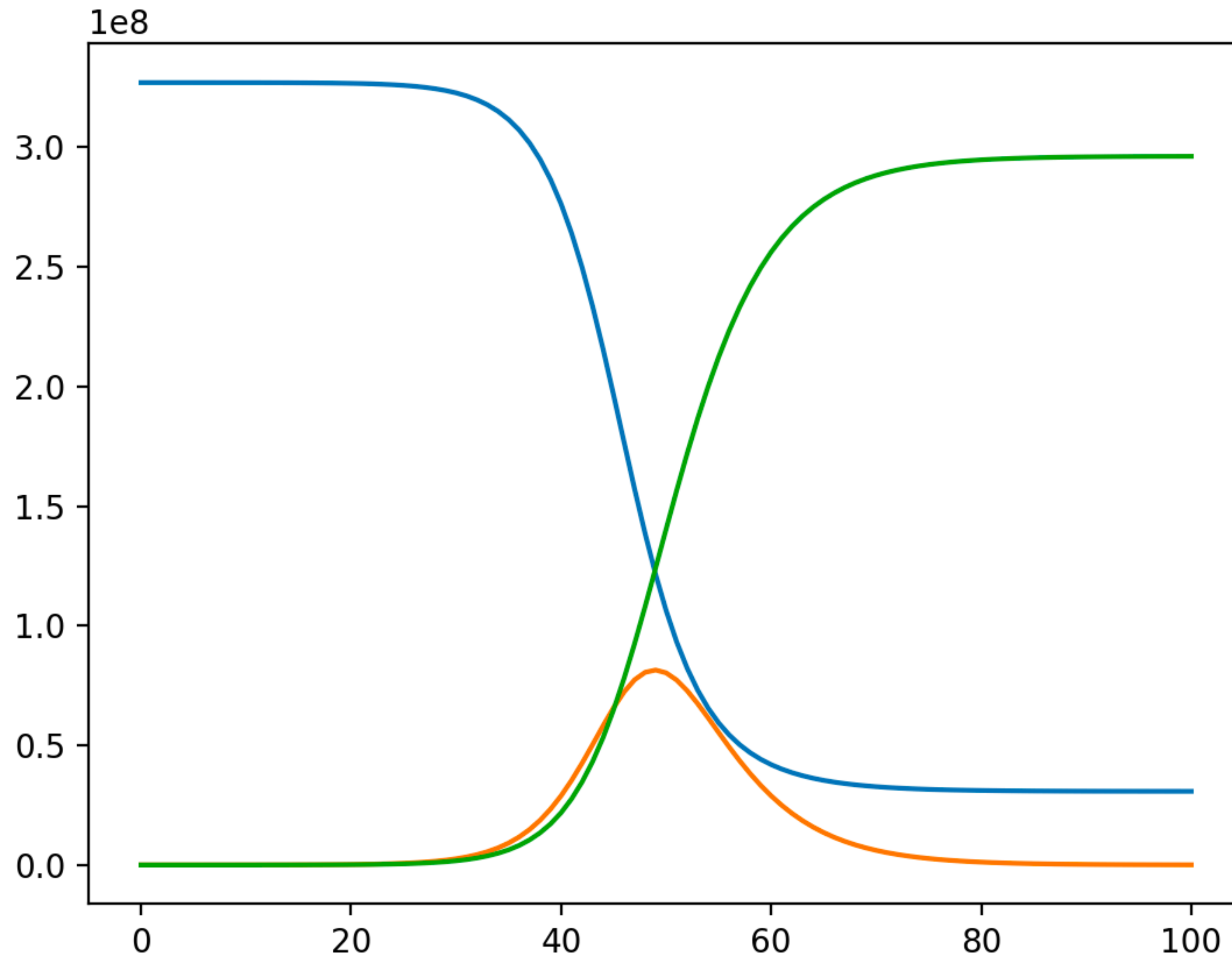
Compartmental SIR model

```
def simulation_sir(beta, gamma, initial_I=100, population = 327e6, duration = 365):  
  
    I = [initial_I]  
    S = [population - initial_I]  
    R = [0]  
  
    for t in range(duration):  
        new_infected = beta*I[-1]*S[-1] / population  
        new_recovered = gamma * I[-1]  
        I.append(I[-1] + new_infected - new_recovered)  
        S.append(S[-1] - new_infected)  
        R.append(R[-1] + new_recovered)  
  
    return S, I, R
```

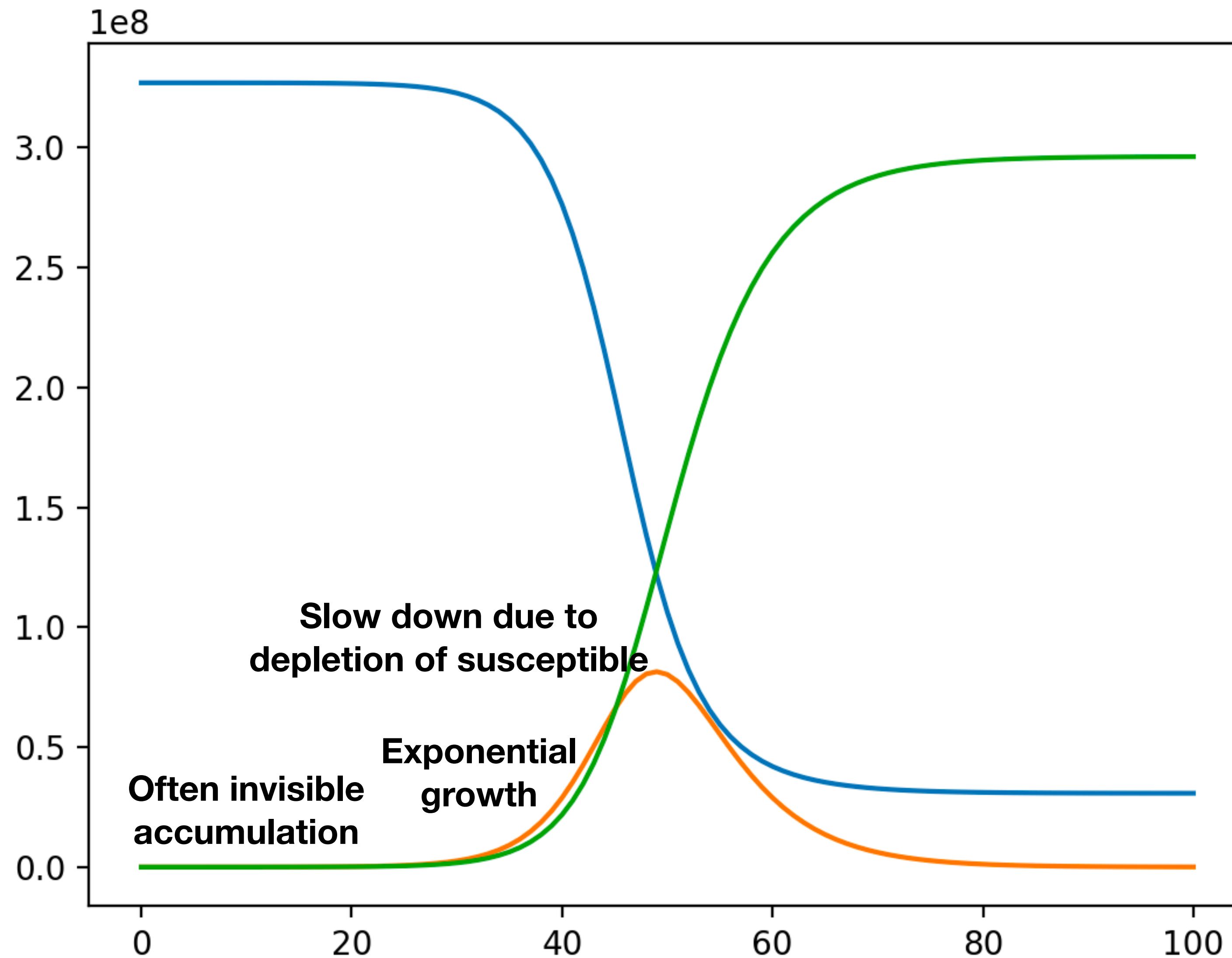

Plot, full SIR simulation



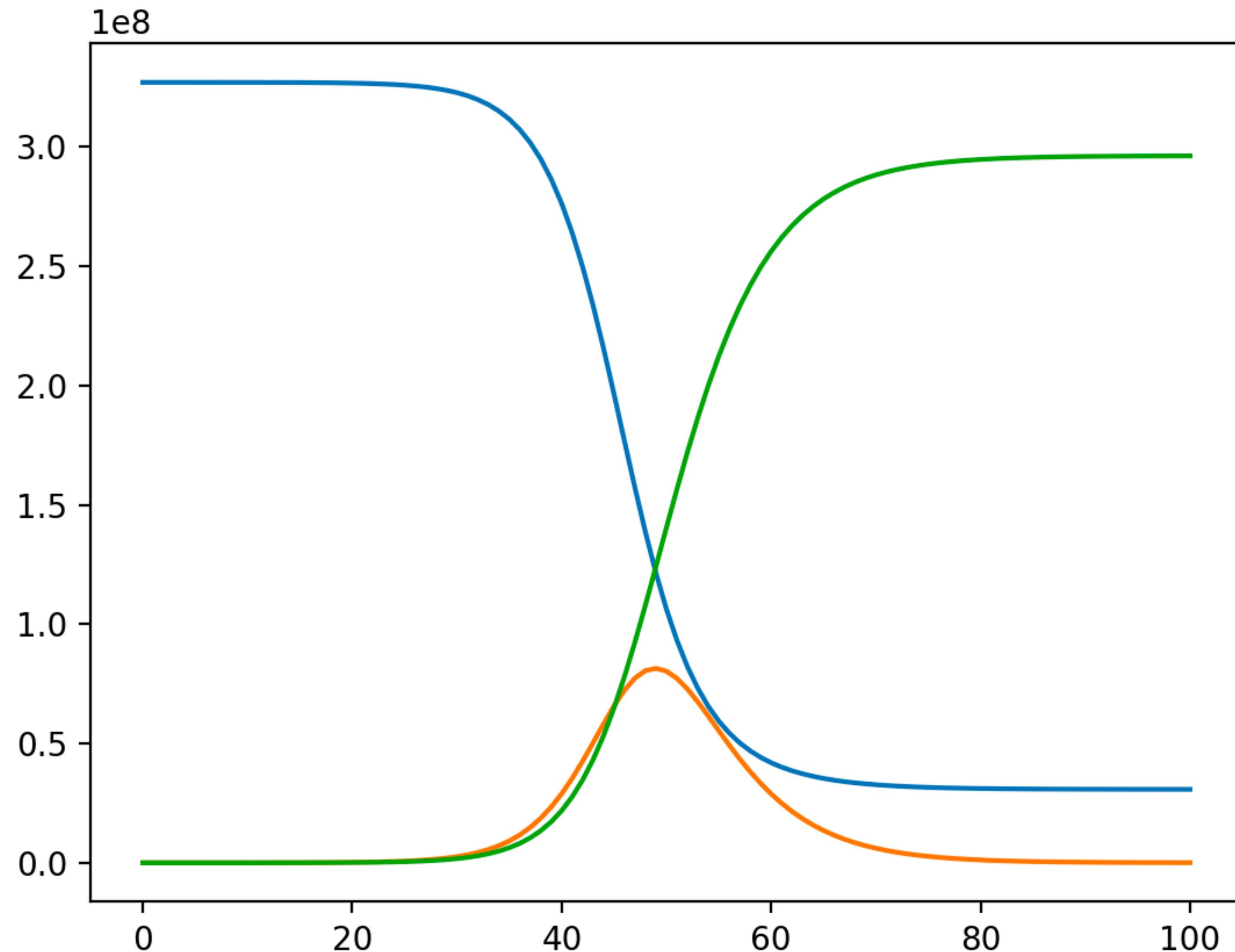
Observed phases



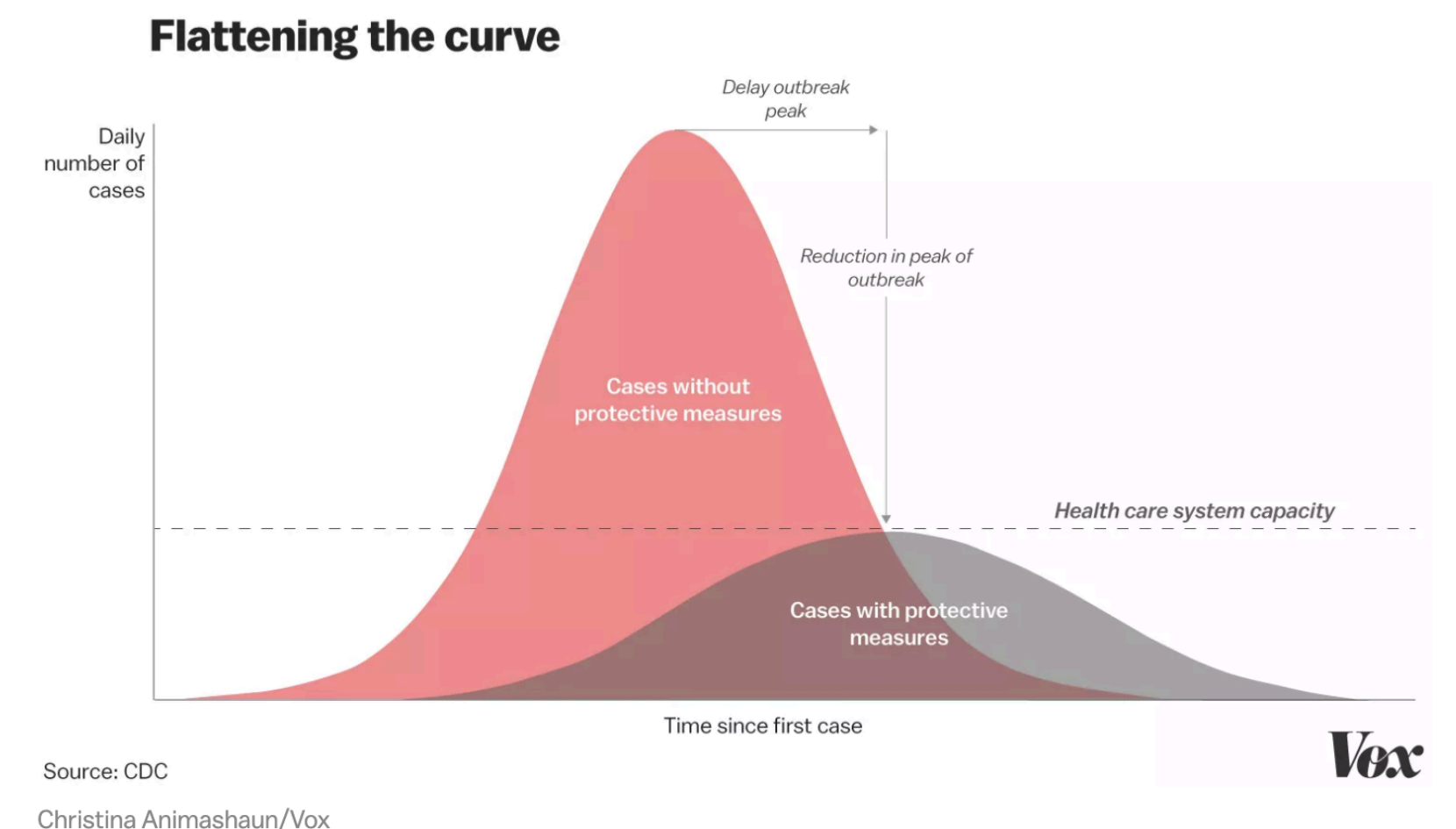
Observed phases



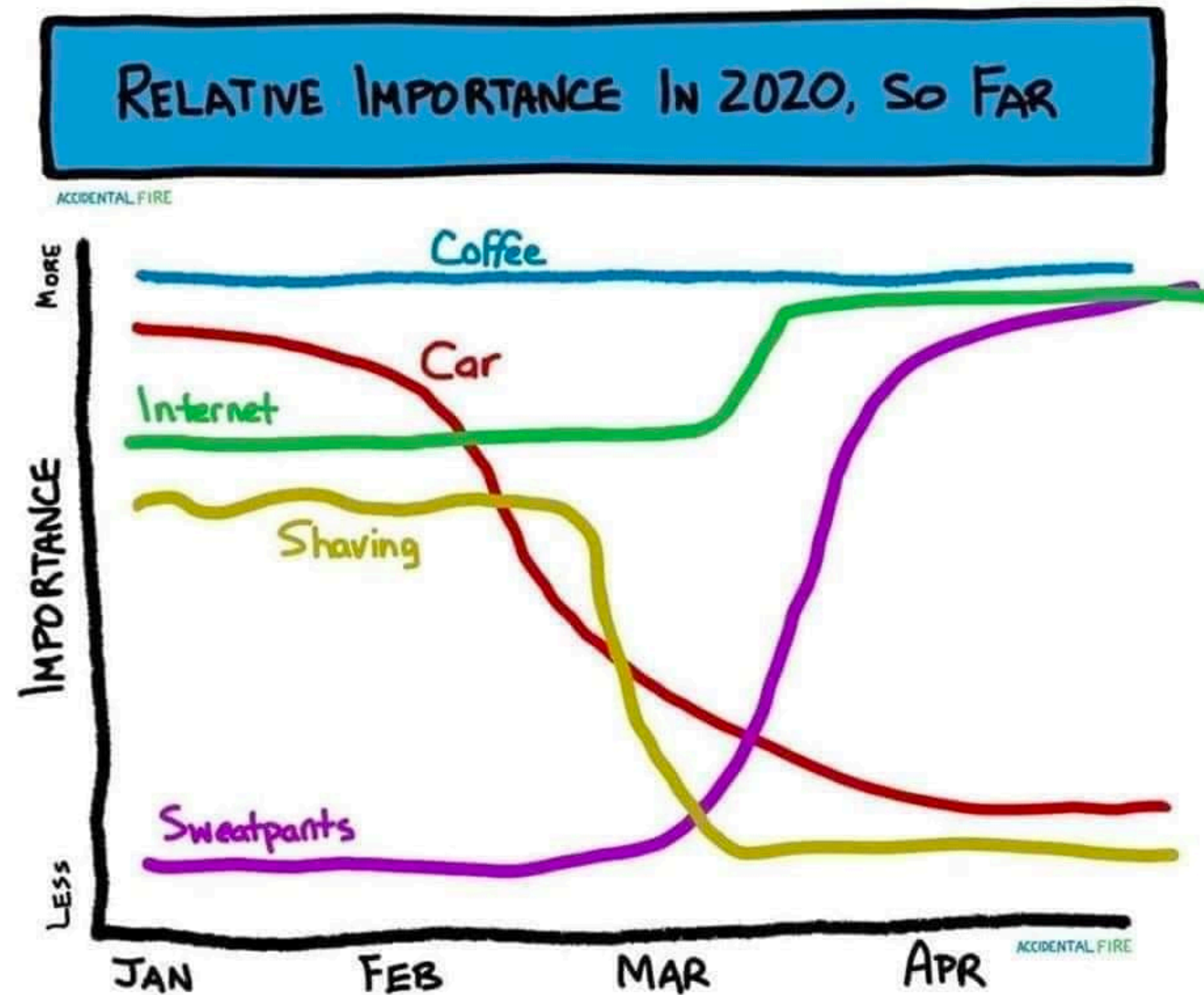
Plot, full SIR simulation



**This should look familiar.
That's the curve we are
trying to flatten.**



Questions?



Recap: Compartmental (SIR) Models

- At the statistical/probabilistic level
- Split population into
 - Susceptible
 - Infectious
 - Recovered
- Simulate the transition from one state to another
 - Characterized by their rate over time
- Formally, should account for time step dt of simulation

Transitions:

- Infection
 - Each infectious can infect a susceptible with with a probability β per unit time per person
 - $\text{new_infectious} = \beta I(t) S(t)/N \, dt$
- Recovery
 - Each infectious transitions to recovered with rate γ
 - $\text{new_recovered} = \gamma I(t) \, dt$

Recap SIR, with time step $dt = 1$

- $\text{new_infectious} = \text{beta } I(t) S(t) / N$
- $\text{new_recovered} = \text{gamma } I(t)$
- $S(t+1) = S(t) - \text{new_infected}(t)$
- $I(t+1) = I(t) + \text{new_infectious} - \text{new_recovered}$
- $R(t+1) = R(t) + \text{new_recovered}$

Links about compartmental models

- https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology
- https://en.wikipedia.org/wiki/Mathematical_modelling_of_infectious_disease#Mathematics_of_mass_vaccination
- <https://www.nature.com/articles/nrmicro1845.pdf>
- https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6990198/pdf/41997_1997_Article_BF03404793.pdf

Link with numbers you may know

- R0
- Typical time until recovery

Link with numbers you may know

- $R_0 = \beta / \gamma$
 - Basic reproduction number
 - Expected number of secondary infectious from one person at beginning of infection (fully susceptible population)
 - (essentially competition between how fast someone infects others and how fast they heal)
- Typical time until recovery = $1 / \gamma$
- At the beginning of the epidemic, $S \sim 1$ and we get an exponential of rate $(R_0 - 1) / D$

Poll: what factors influence R_0 ?

Where does R_0 come from?

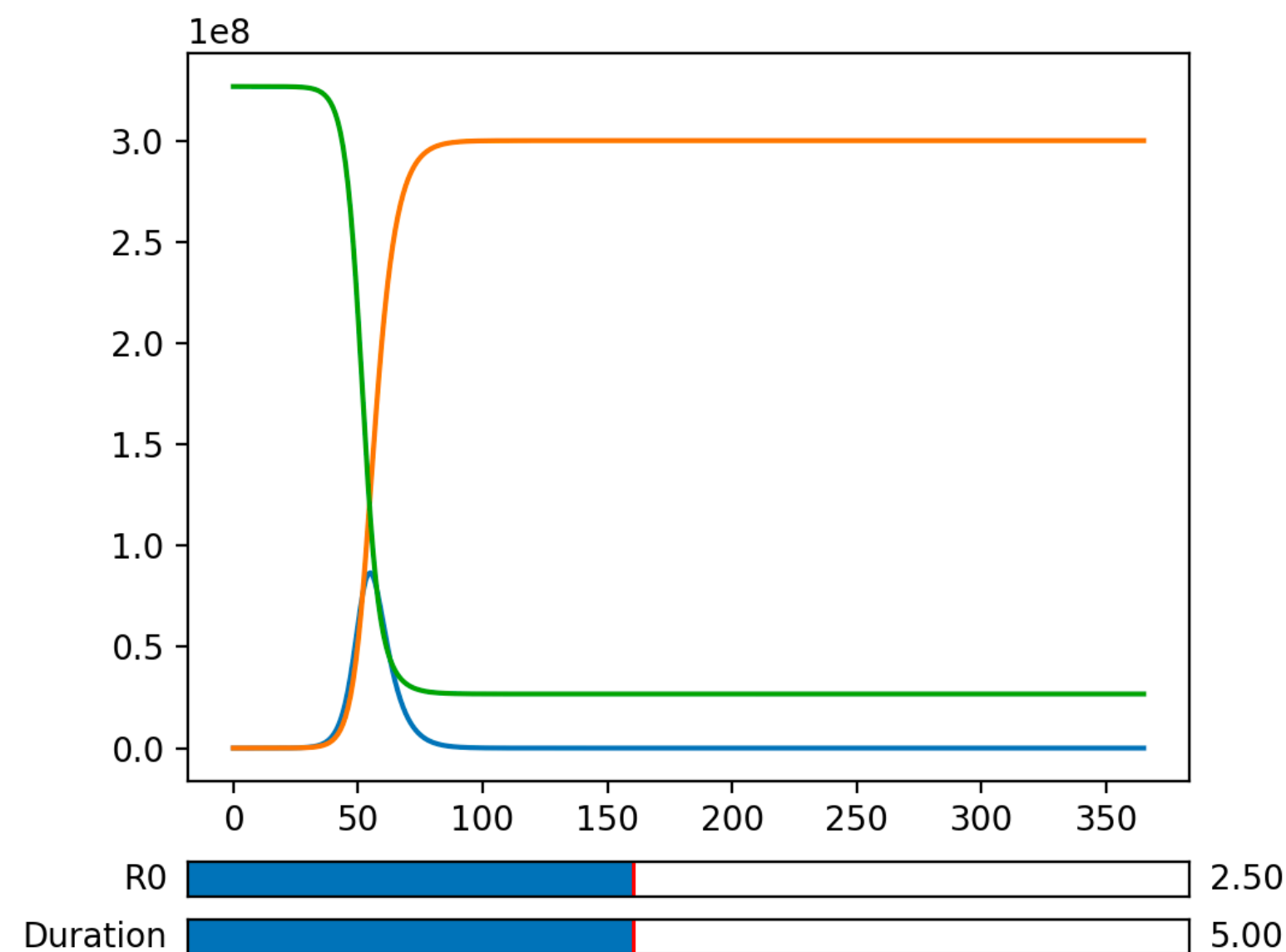
- Biology
- Behavior
 - Social distancing, wearing mask, quarantine, elbow sneeze, hand washing
- Can be thought of as probability of transmission per contact times number of contacts
 - Definition of effective contact depends on disease

R_t

- Expected number of secondary infectious from one person at time t
- (not to be confused with $R(t)$, the number of recovered)
- For SIR $\sim R_0 * S(t) / \text{population}$

Impact of parameters

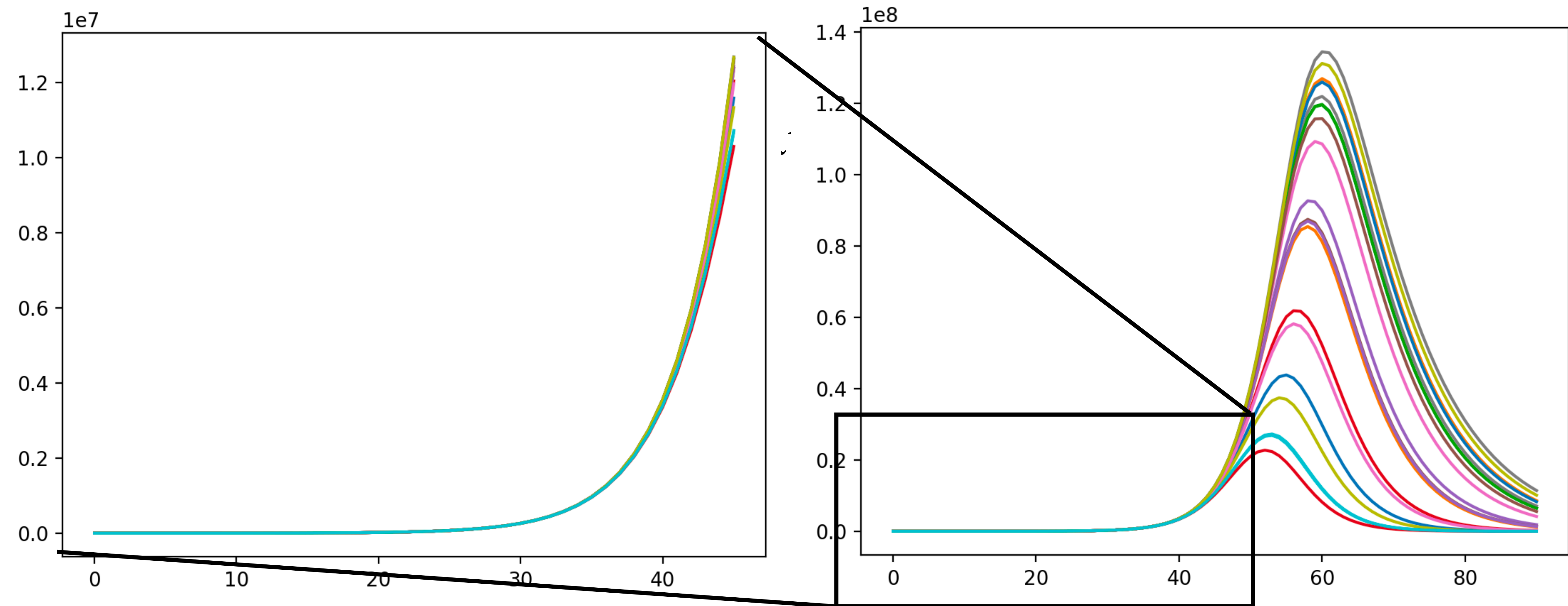
- Matplotlib with sliders: https://matplotlib.org/3.1.1/gallery/widgets/slider_demo.html
 - not expected for class but fun and convenient
 - Requires to change your Spyder parameters, see code



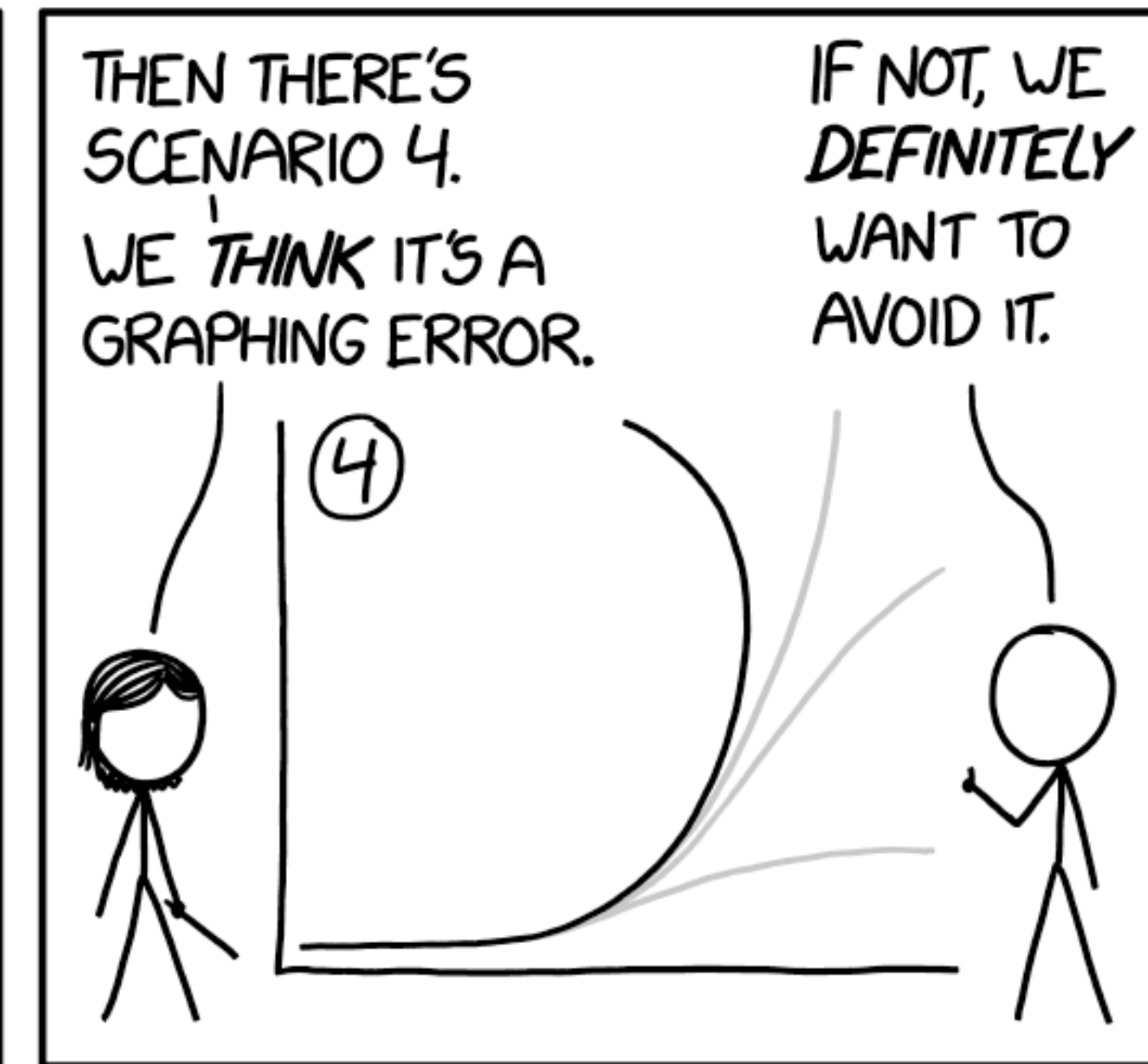
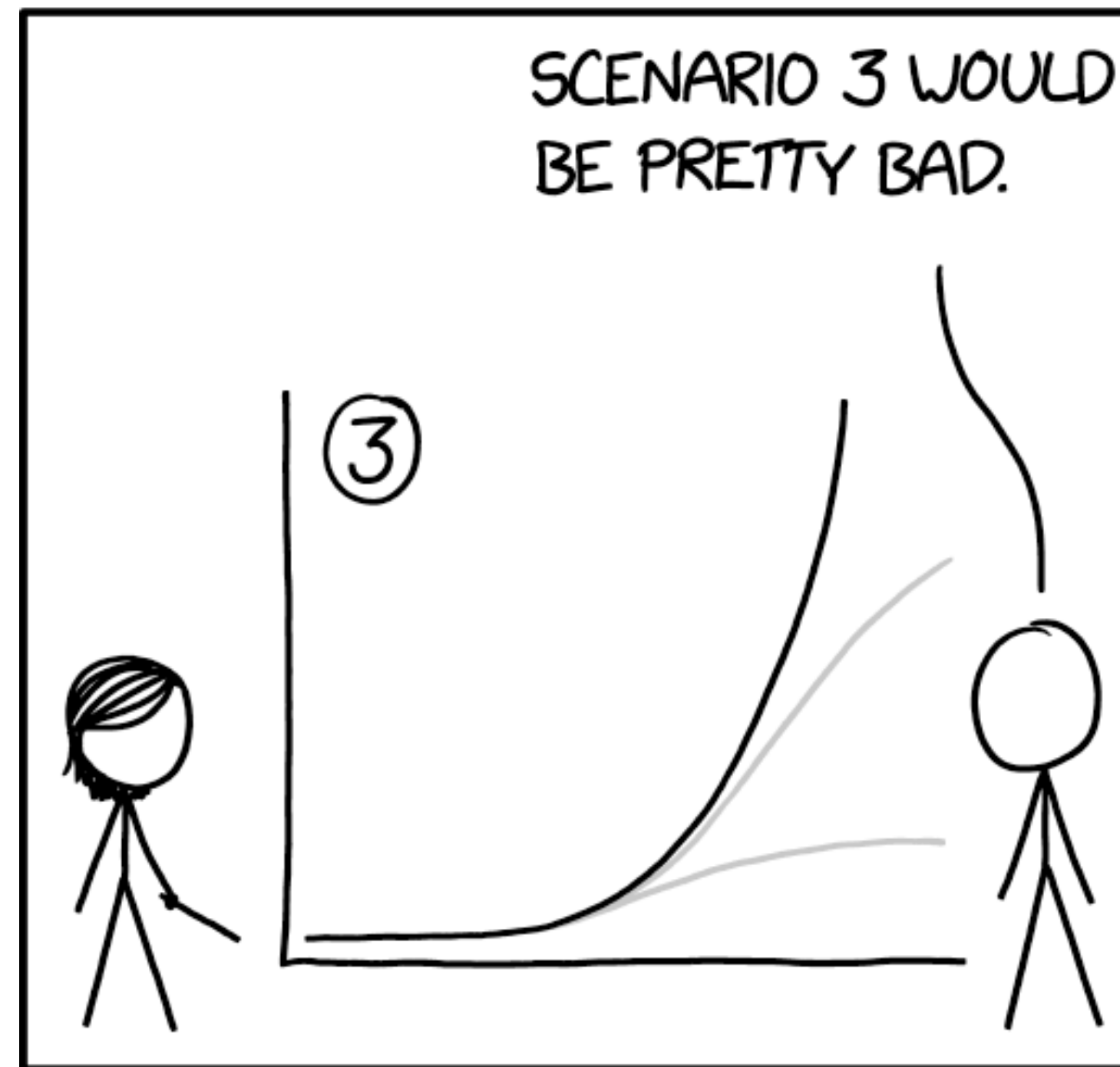
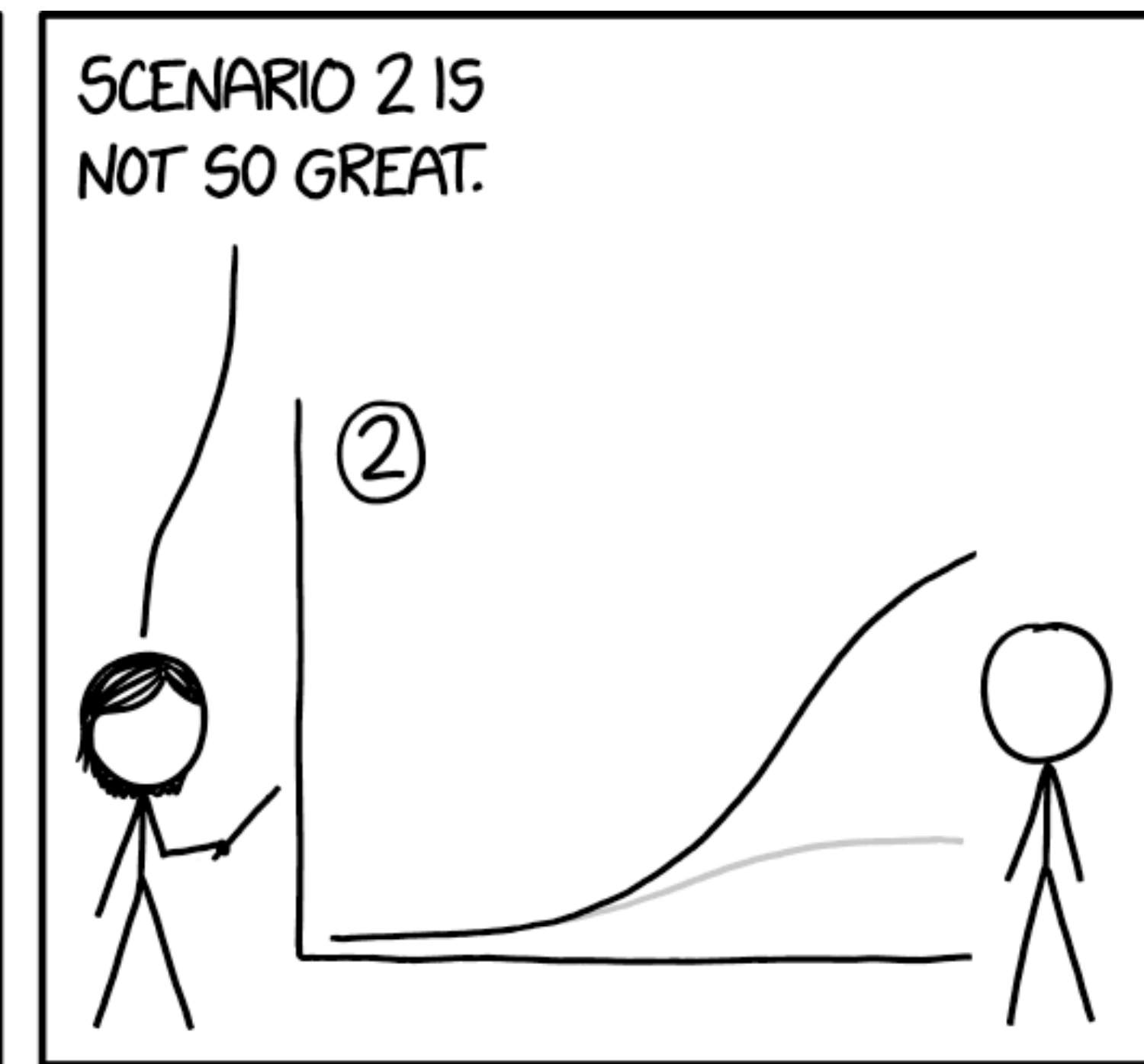
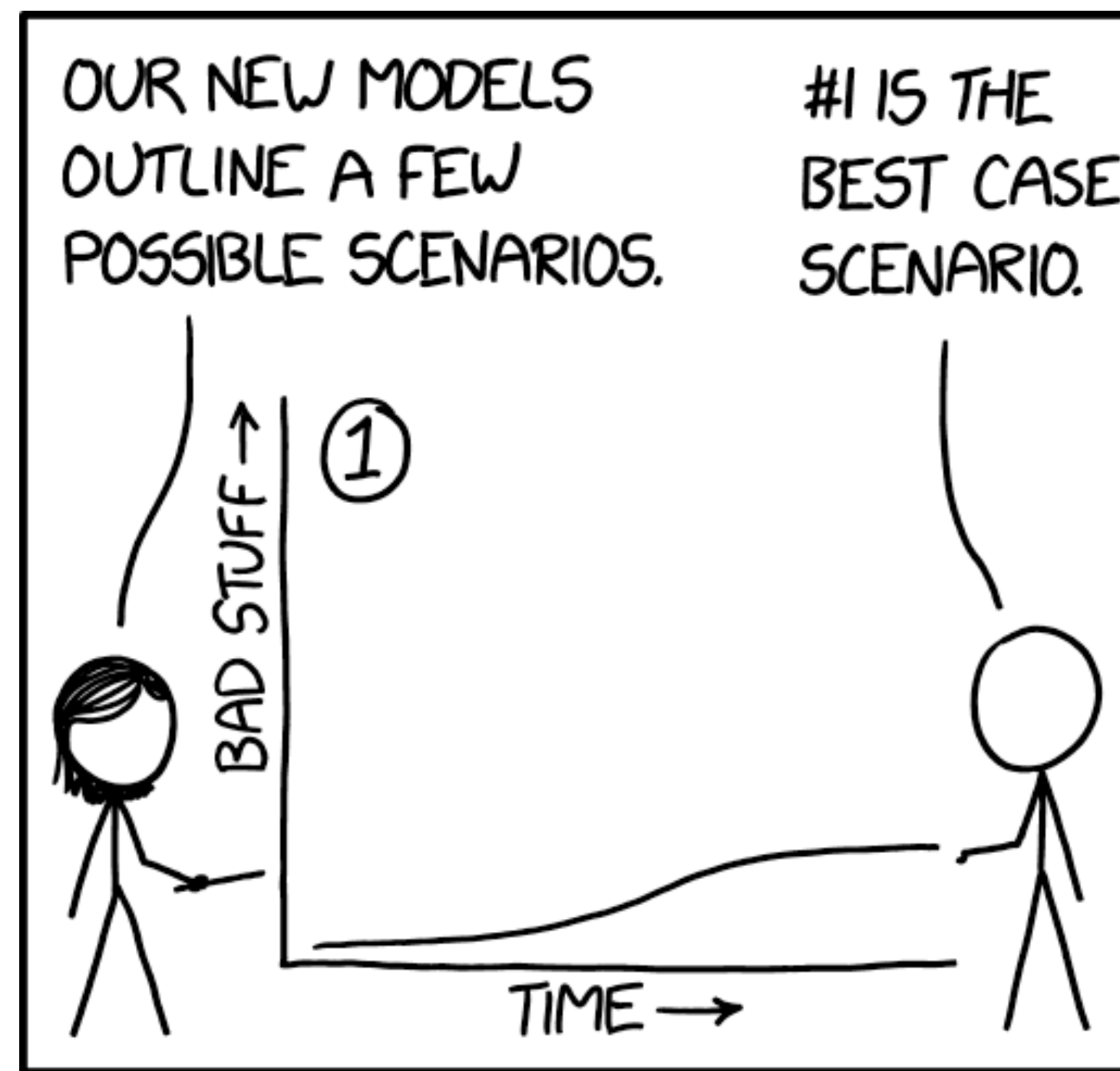
In file SIR-2.py

It is hard to estimate R_0 from curve in early stages

- All D and R_0 such that $D = (R_0 - 1)/k$ have same early rate k
- But very different peaks and total infected



Questions?

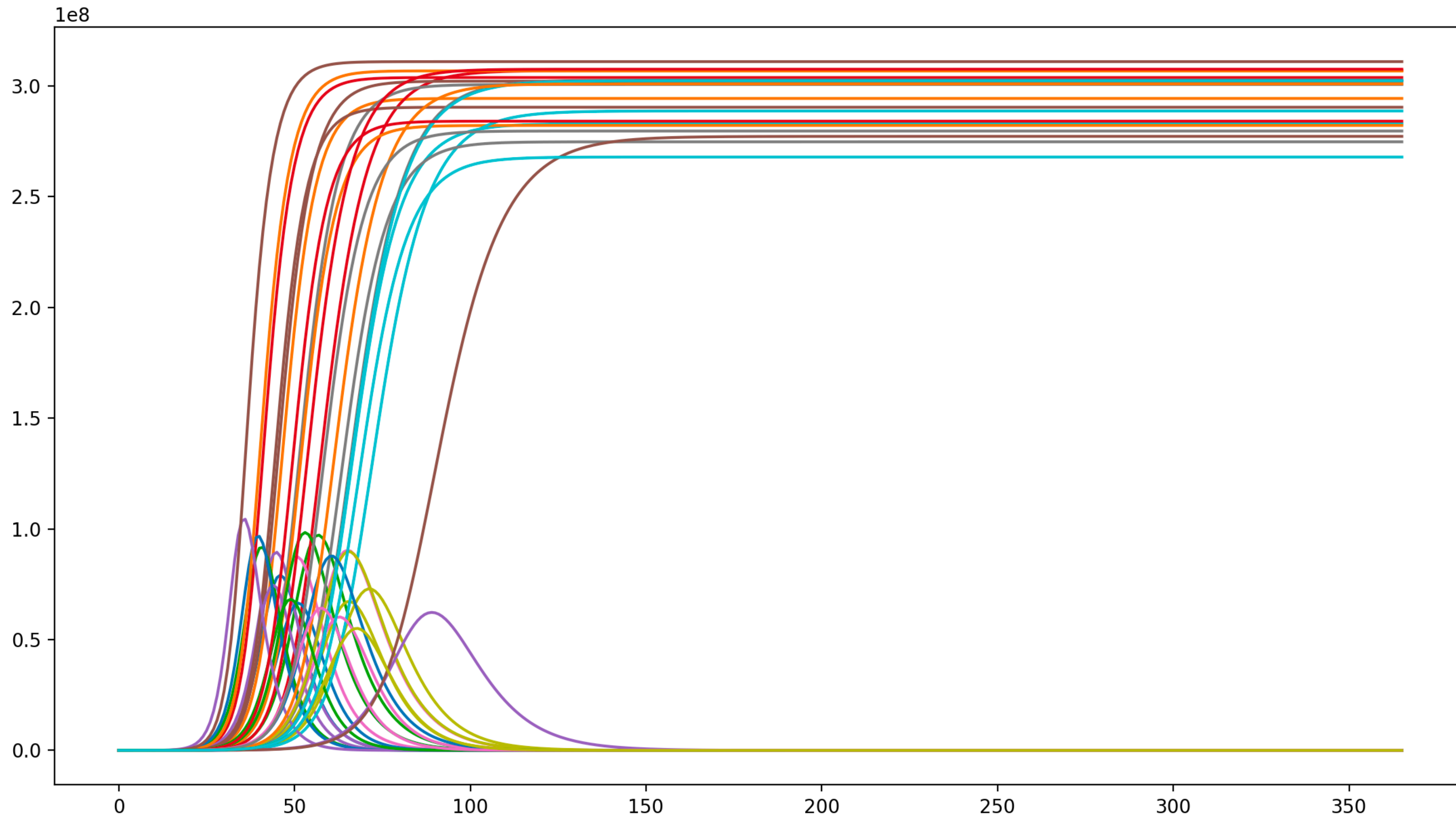


- <https://xkcd.com/2289/>

Parameters for Covid-19

- R_0 : between 2 and 3
- D : between 4 and 8

Stochastic over parameters

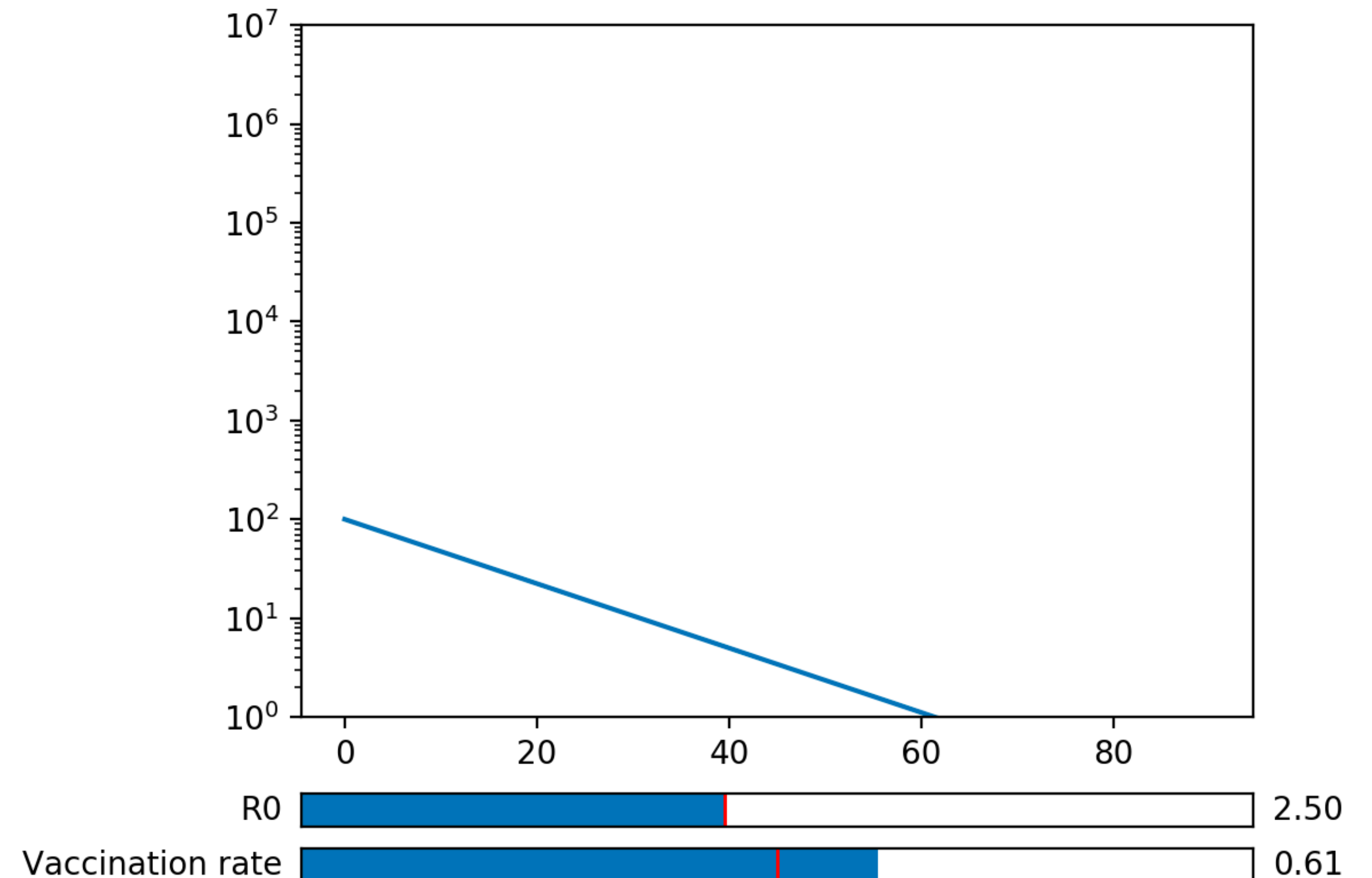


Simulations of covid-19

- <https://www.medrxiv.org/content/10.1101/2020.04.01.20049908v1.full.pdf> The effect of non-pharmaceutical interventions on COVID-19 cases, deaths and demand for hospital services in the UK: a modelling study
- <https://cr.yp.to/papers/gigo-20200330.pdf> Further analysis of the impact of distancing upon the COVID-19 pandemic
- <https://www.nature.com/articles/d41586-020-01003-6> Nature Special report: The simulations driving the world's response to COVID-19
- <https://science.sciencemag.org/content/early/2020/03/24/science.abb3221/tab-figures-data> Science: Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus
- <https://fivethirtyeight.com/features/coronavirus-case-counts-are-meaningless/> 538, simulates testing
- <https://doktormike.gitlab.io/post/covid-19/> educational, Denmark
- <https://www.nature.com/articles/d41586-020-01003-6>
- <https://www.nber.org/papers/w26981.pdf> (with control and economic cost)
- <https://science.sciencemag.org/content/early/2020/04/14/science.abb5793> with seasonal forcing
- [https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(20\)30144-4/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30144-4/fulltext)
- <https://arxiv.org/abs/2003.00122>
- https://www.who.int/bulletin/online_first/20-255158.pdf
- <http://vensim.com/coronavirus/>
- <https://www.thelancet.com/action/showPdf?pii=S1473-3099%2820%2930243-7>
- <https://www.medrxiv.org/content/10.1101/2020.04.01.20049908v1.full.pdf>
- https://www.sciencedirect.com/science/article/pii/S0140673620302609?casa_token=SQSq7RlFU4kAAAAA:F_sJrRpiMfzmrUGq0eft7AZ3a22B9oqqb_Tnx1xJH2t8CM6UtTcuw7ql8y8FdEJzNImsH-_y
- <https://arguablywrong.home.blog/2020/03/27/updated-epidemiological-modeling/>
- <https://covidactnow.org/faq>
- <https://www.aha.org/guidesreports/2020-04-09-compendium-models-predict-spread-covid-19>
- <https://alhill.shinyapps.io/COVID19seir/>
- <https://covid19-scenarios.org/>
-

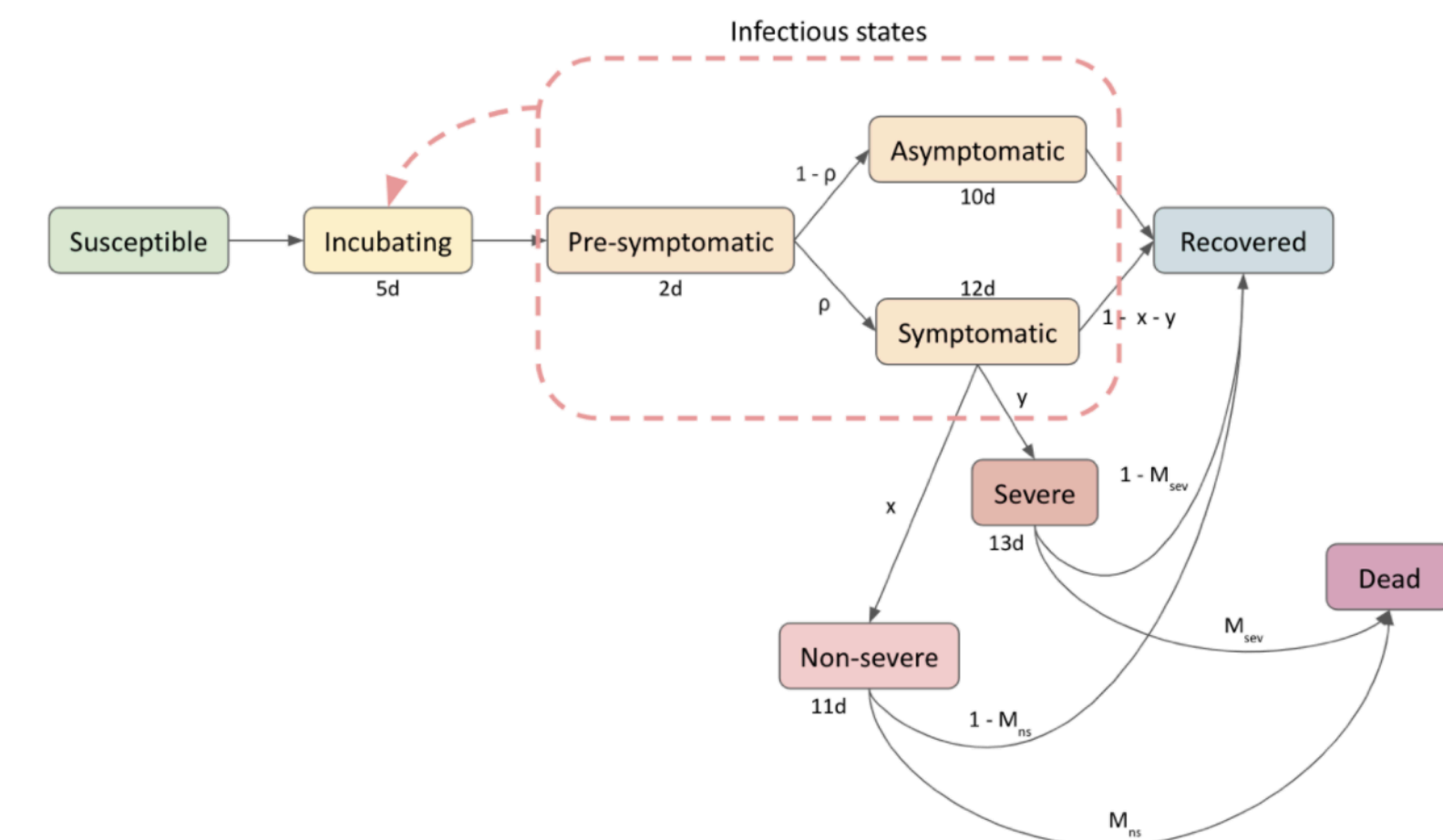
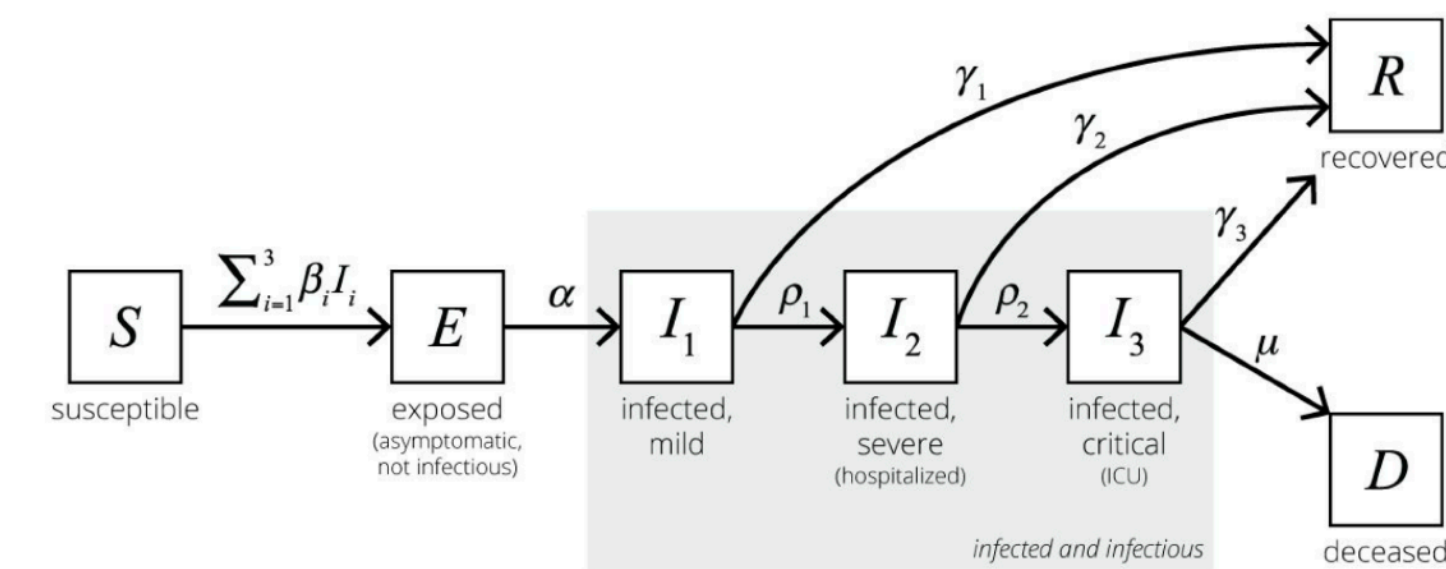
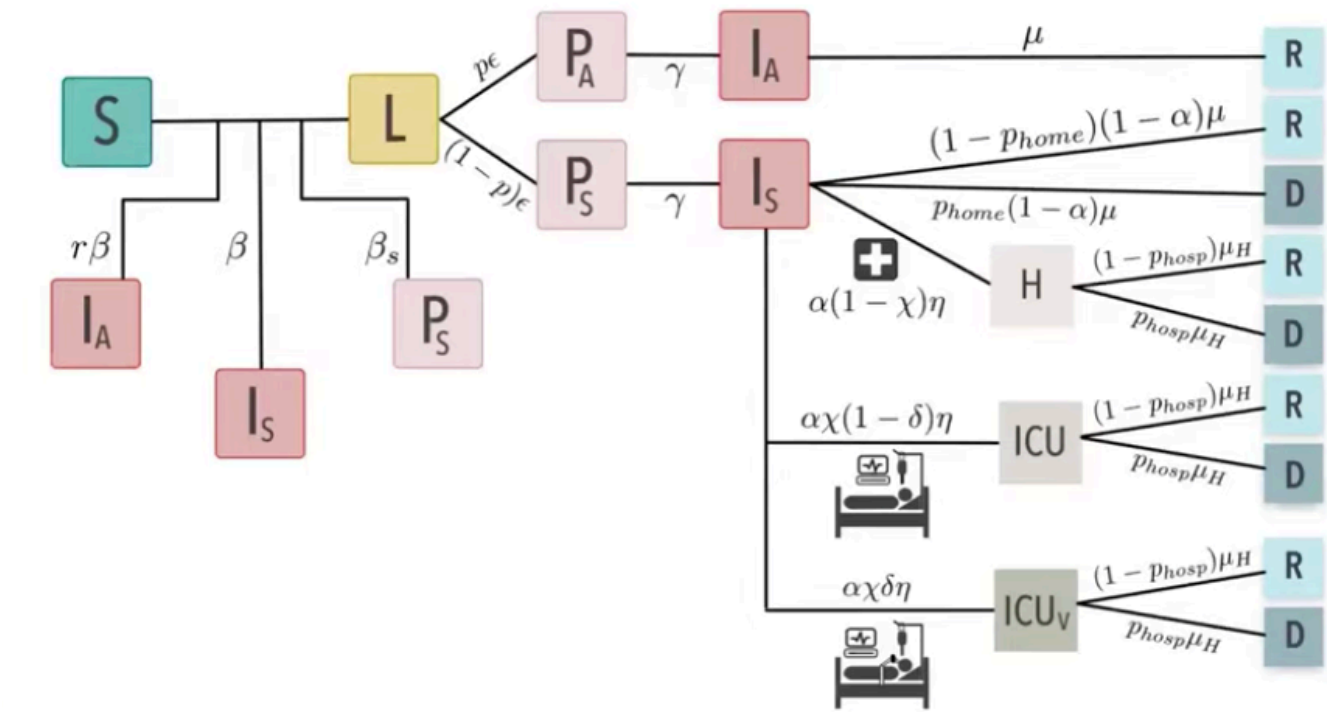
Vaccination, herd immunity

- Just change R at beginning to be the fraction of vaccinated people
- Herd immunity if vaccination rate above $1 - 1/R_0$

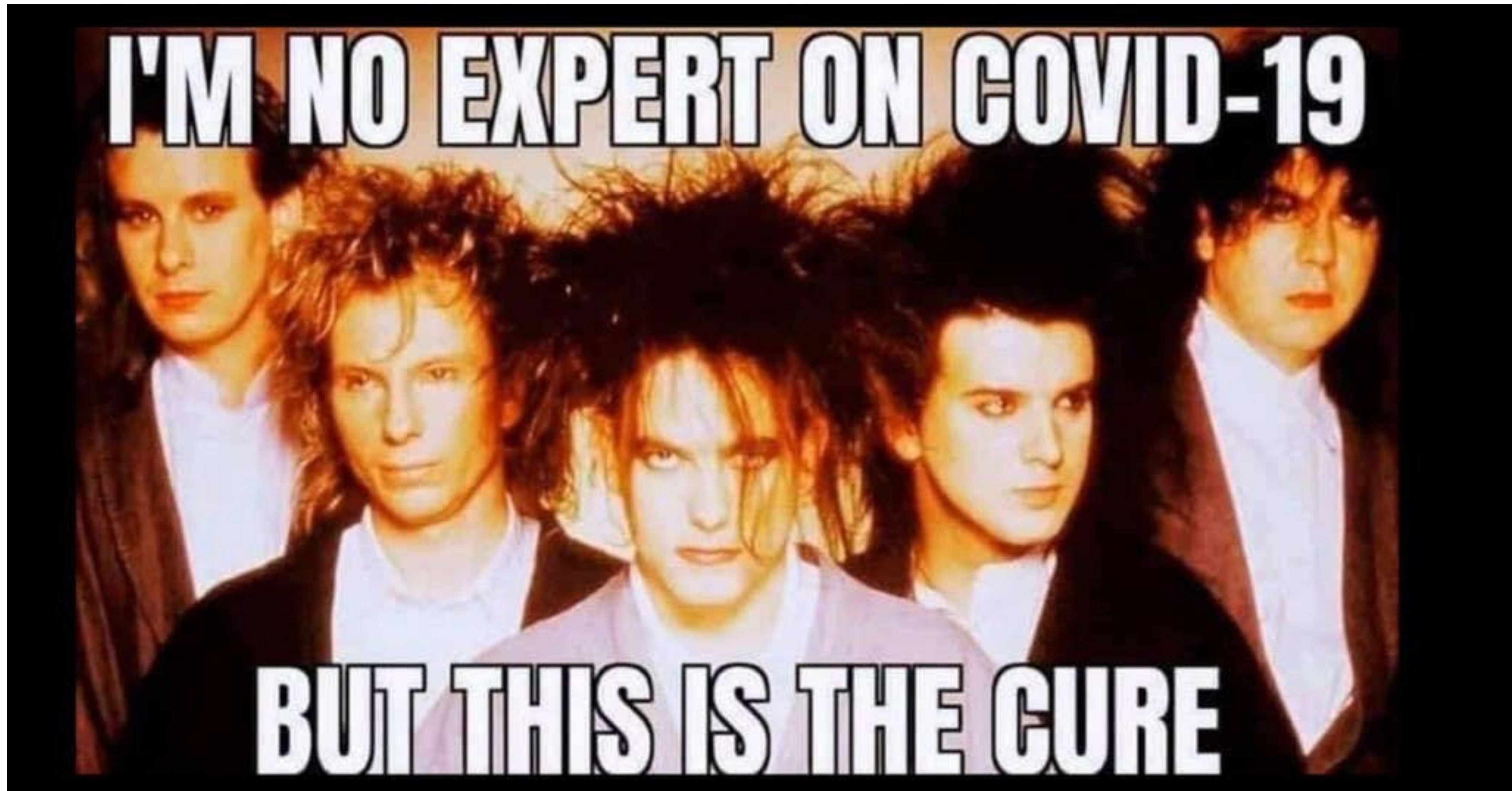


SEIR, SIRS, SEIRS, etc.

- Can also add a compartment for exposed but not yet infectious $E(t) \rightarrow$ SEIR model
- If immunity is temporary, add transitions from R to S \rightarrow SEIRS or SIRS model
- Can also add compartments for finer-grained stages and different severity
- Depends on biology of infection and goals of a study



Questions?



Interventions

- Wash hands, mask, social distancing, etc.
- All seek to reduce transmission rate
- Simulate with factor over β


```

def simulation_sir_triggered_intervention(beta, gamma,
                                         number_cases_intervention=100000,
                                         fraction=0.5,
                                         population = 327e6, initial_I=1000,
                                         duration = 365):

    I = [initial_I]
    S = [population - initial_I]
    R = [0]
    intervention = False

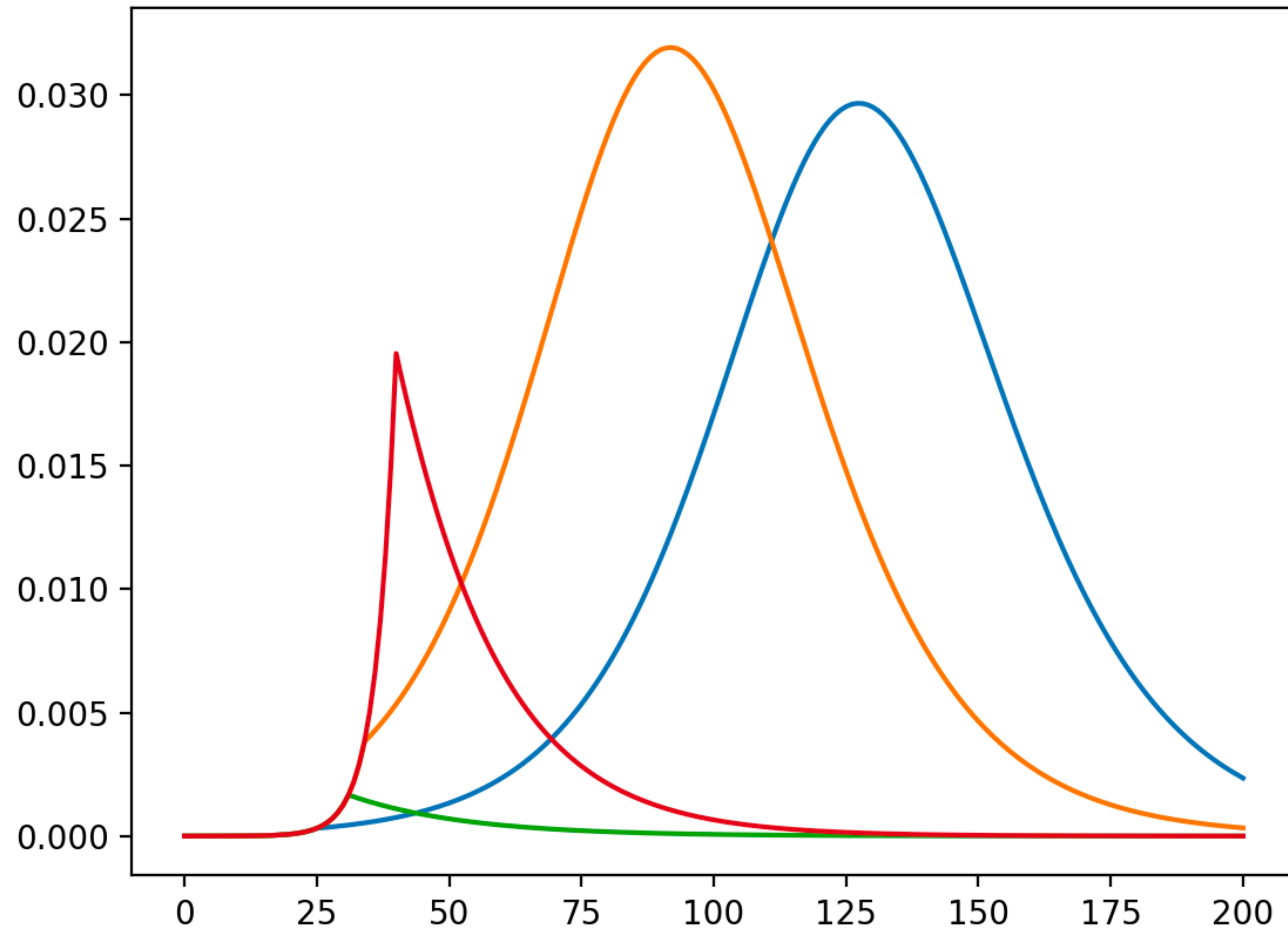
    for t in range(duration):
        if not intervention and I[-1]>number_cases_intervention:
            intervention = True
        if intervention:
            effective_beta = beta*fraction
        else:
            effective_beta = beta

        new_infected = effective_beta*I[-1]*S[-1] / population
        new_recovered = gamma * I[-1]
        I.append( I[-1] + new_infected - new_recovered )
        S.append( S[-1] - new_infected)
        R.append( R[-1] + new_recovered)

    return S, I, R

```

Intervention: when, how much?

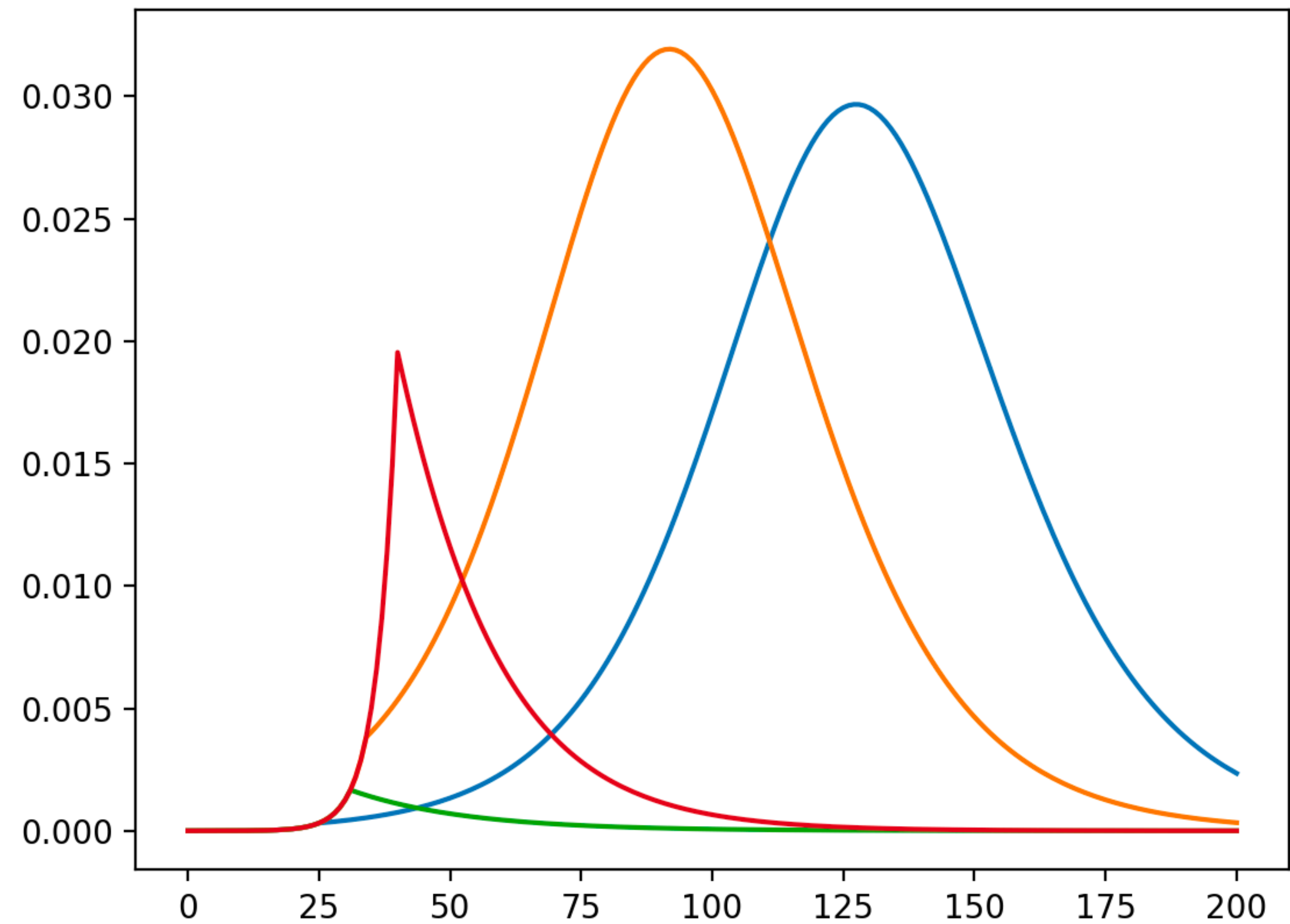


Interventions

- Different places appear to have reduced R_0 from ~ 2.5 to ~ 0.8 - ~ 1.4

Discussion

- If intervention is weak, timing doesn't matter as much
 - You're not doing something as useful anyway
- If intervention is strong, timing is critical
 - Rate goes down immediately, max is at time of intervention
 - If intervention is during exponential growth, any delay has an exponential effect



Heterogeneity

- Unfortunately, reducing by 50% on average is not the same as reducing by 50% for everyone
 - High-contact individuals have a predominant effect.
 - You must add a term \sim relative variance
- Can be simulated with multiple compartments
 - See code in SIR-2.py
- Can also be analyzed with linear algebra eigenvalues

What happens when you stop?

```

def simulation_sir_intervention (beta, gamma,
                                time_begin_intervention =30,
                                time_end_intervention =60,
                                fraction=0.5,
                                population = 327e6, initial_I=1000,
                                duration = 365):

    I = [initial_I]
    S = [population - initial_I]
    R = [0]

    for t in range(duration):
        effective_beta = beta
        if t>time_begin_intervention and t<time_end_intervention:
            effective_beta = beta * fraction

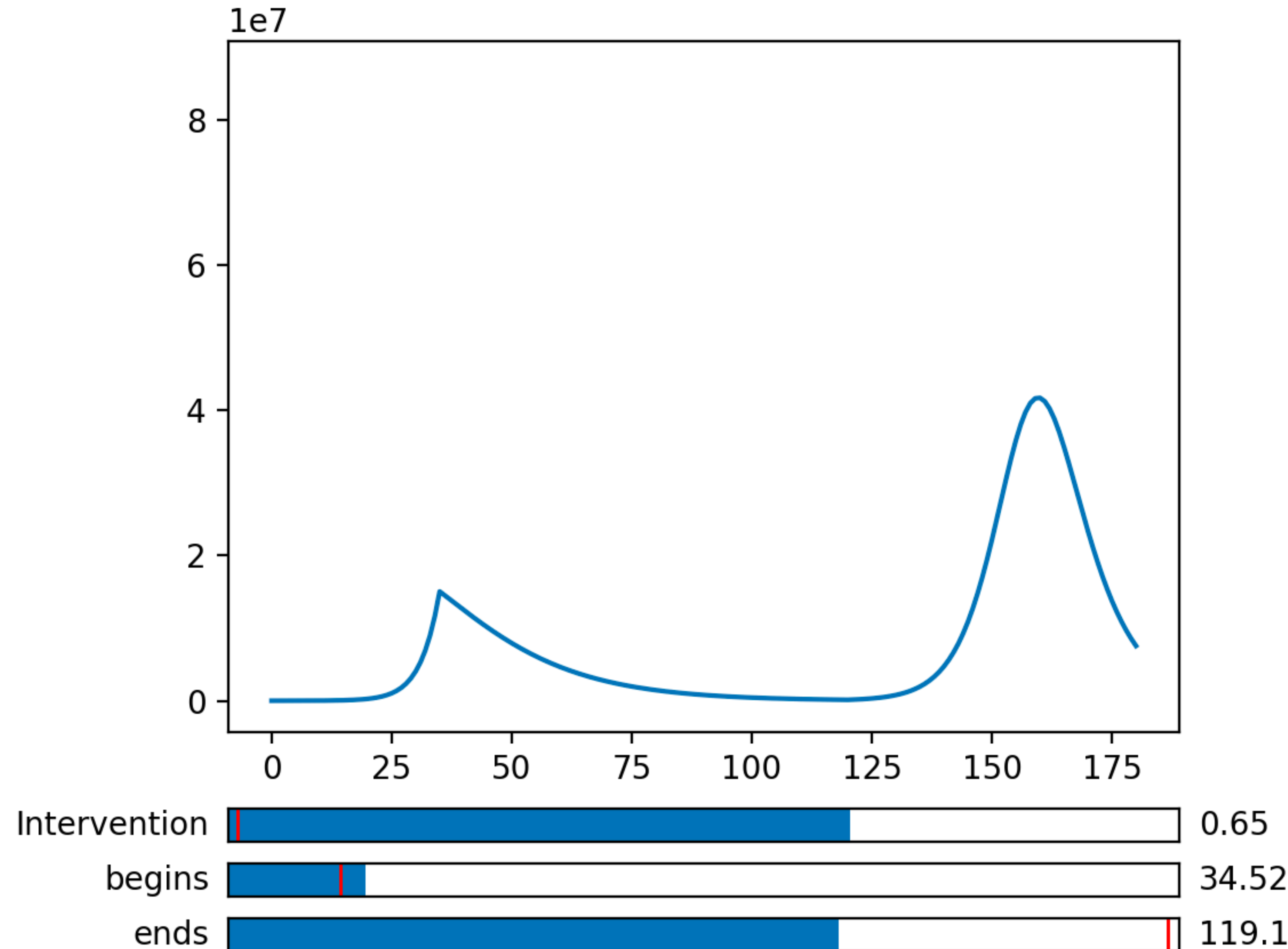
        new_infected = effective_beta*I[-1]*S[-1] / population
        new_recovered = gamma * I[-1]
        I.append( I[-1] + new_infected - new_recovered )
        S.append( S[-1] - new_infected)
        R.append( R[-1] + new_recovered)

    return S, I, R

```

What happens when you stop?

- Nothing good
- The epidemic restarts with the original R_0
- Unless we test, trace and quarantine (aka not stopping)



Questions?



Building up (but we won't cover)

- Heterogenous populations
- Different severity
- Vector, Malaria
- Multiple diseases

Putting it all together with bells and whistles:

A recent Science paper

- <https://science.sciencemag.org/content/early/2020/04/14/science.abb5793>

Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period

Stephen M. Kissler^{1,*}, Christine Tedijanto^{2,*}, Edward Goldstein², Yonatan H. Grad^{1,†,‡}, Marc Lipsitch^{2,†,‡}

+ See all authors and affiliations

Science 14 Apr 2020:

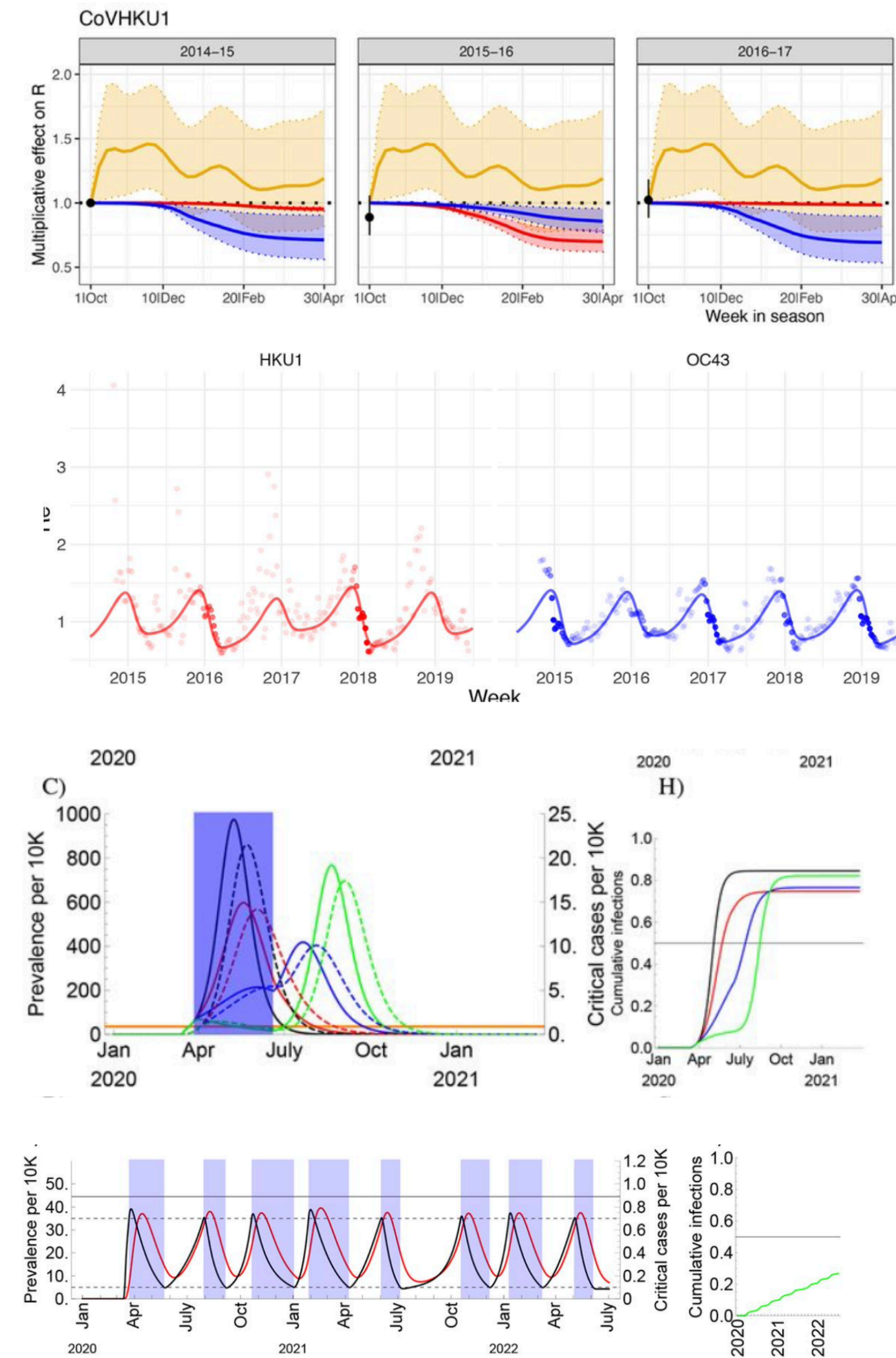
eabb5793

DOI: 10.1126/science.abb5793

Putting it all together with bells and whistles:

A recent Science paper

- SEIRS
- Exposed but not infectious group
- Different durations of immunity
- Seasonal variation
- Social distancing effect (possibly recurring)
- Cross immunity with other coronaviruses
- Sensitivity analysis of all parameters
 - Run simulation with different parameters, compute variance, confidence intervals
- Emphasizes uncertainty about everything



Questions?



Another case: measles before vaccination

- Very contagious:
 $R_0 \sim 17$
- Recurring outbreaks,
mostly affects
children
- Seasonal,
because vacations
- Appears to depend
on town population

A stochastic model for extinction and recurrence of epidemics

495

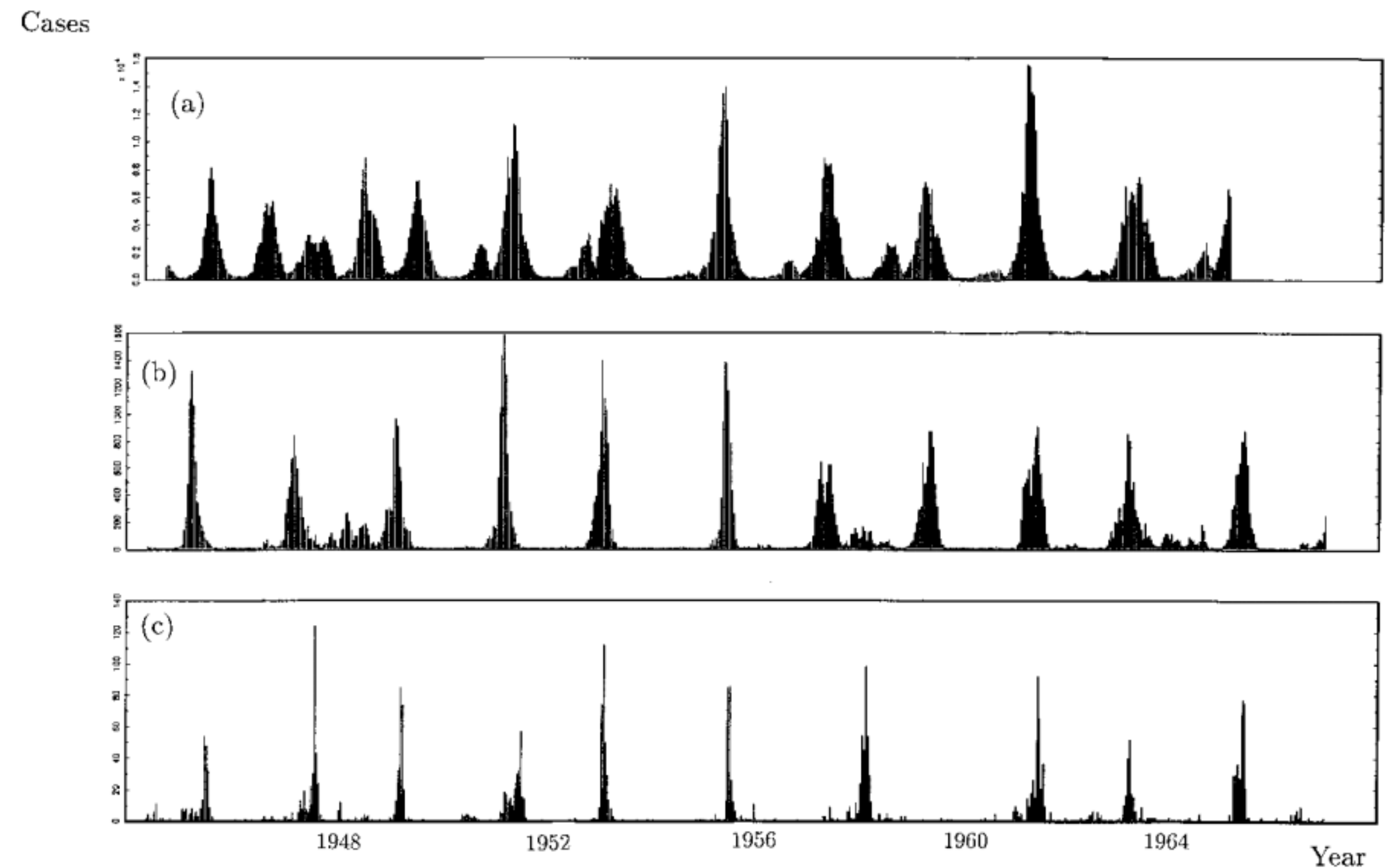
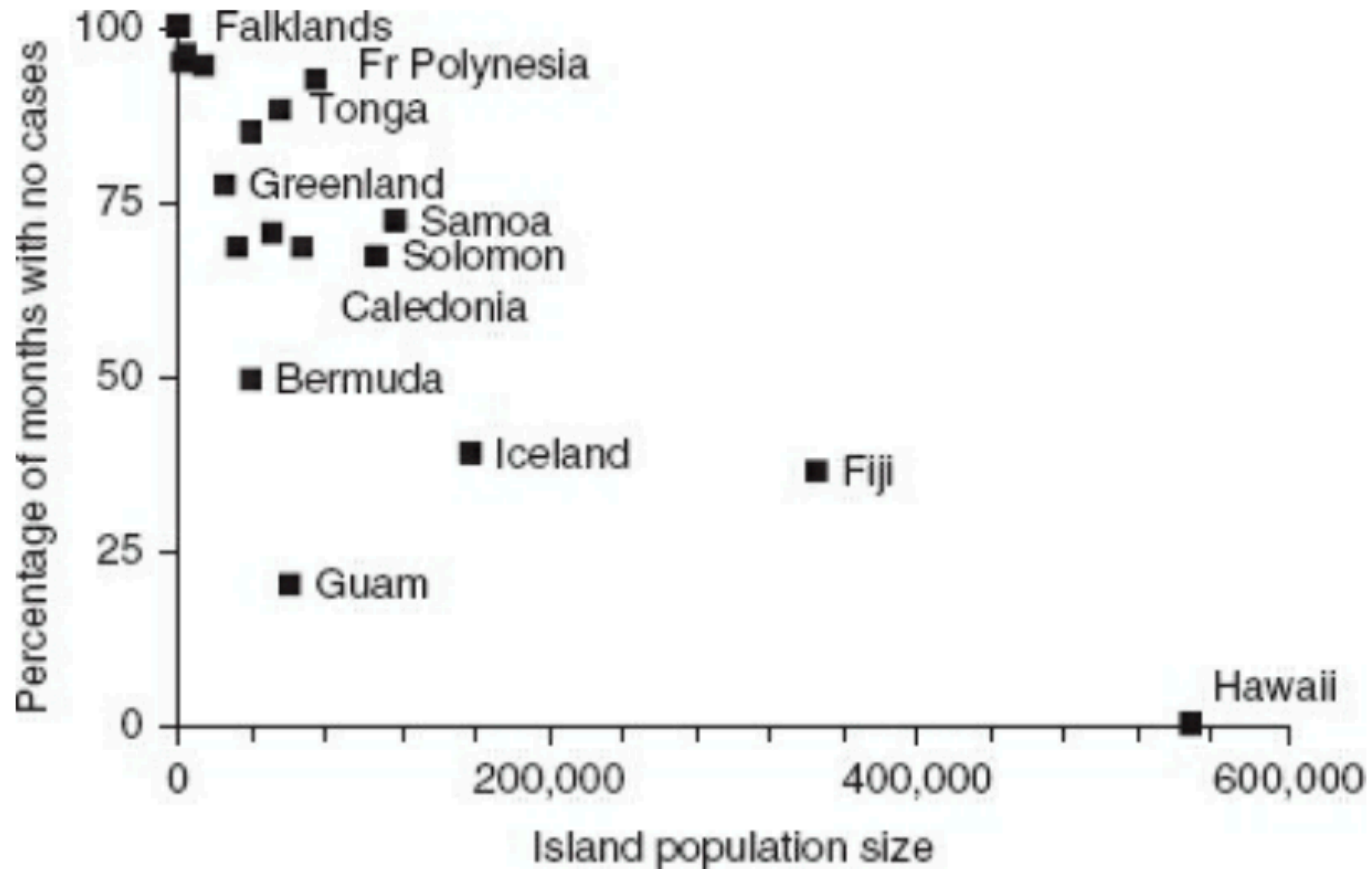


Fig. 1. Time series plots of reported cases corrected for temporal under-reporting for (a) London (3.3 million inhabitants), (b) Plymouth (210 000 inhabitants), (c) Teignmouth (10 000 inhabitants) during the pre-vaccination time from 1944 to 1966. The population sizes stated in brackets are the approximate median yearly sizes for this time period.

Month without measles vs. population



Building up: long term measles

- Seasonal variation due to school vacation
vary beta over time, reduce by factor 0.2 in summer
- Add demographics effect (birth, death)
at rate $\mu = 1 / (\text{life expectancy})$
- Take into account randomness:
each susceptible in $S(t)$ is infected with probability given by rate $\beta * I(t)$
 - similar to $S(t)$ biased coin tosses, either simulate or use binomial distribution
- Add random transmission from external travelers

Code

```
def simulation_sir_stochastic(beta, gamma, mu=1/50/365, noise_level=1, gamma_external=1e-3,
                             initial_I=1, population=5000, initial_S=0, duration=100):

    total_birth=0
    N = [population]
    I =[initial_I]
    S =[initial_S]
    R =[N[0] - I[0] - S[0]]

    for t in range(duration):

        new_infected = randomize(vacation_factor(t)*beta*I[-1]/N[-1], S[-1])

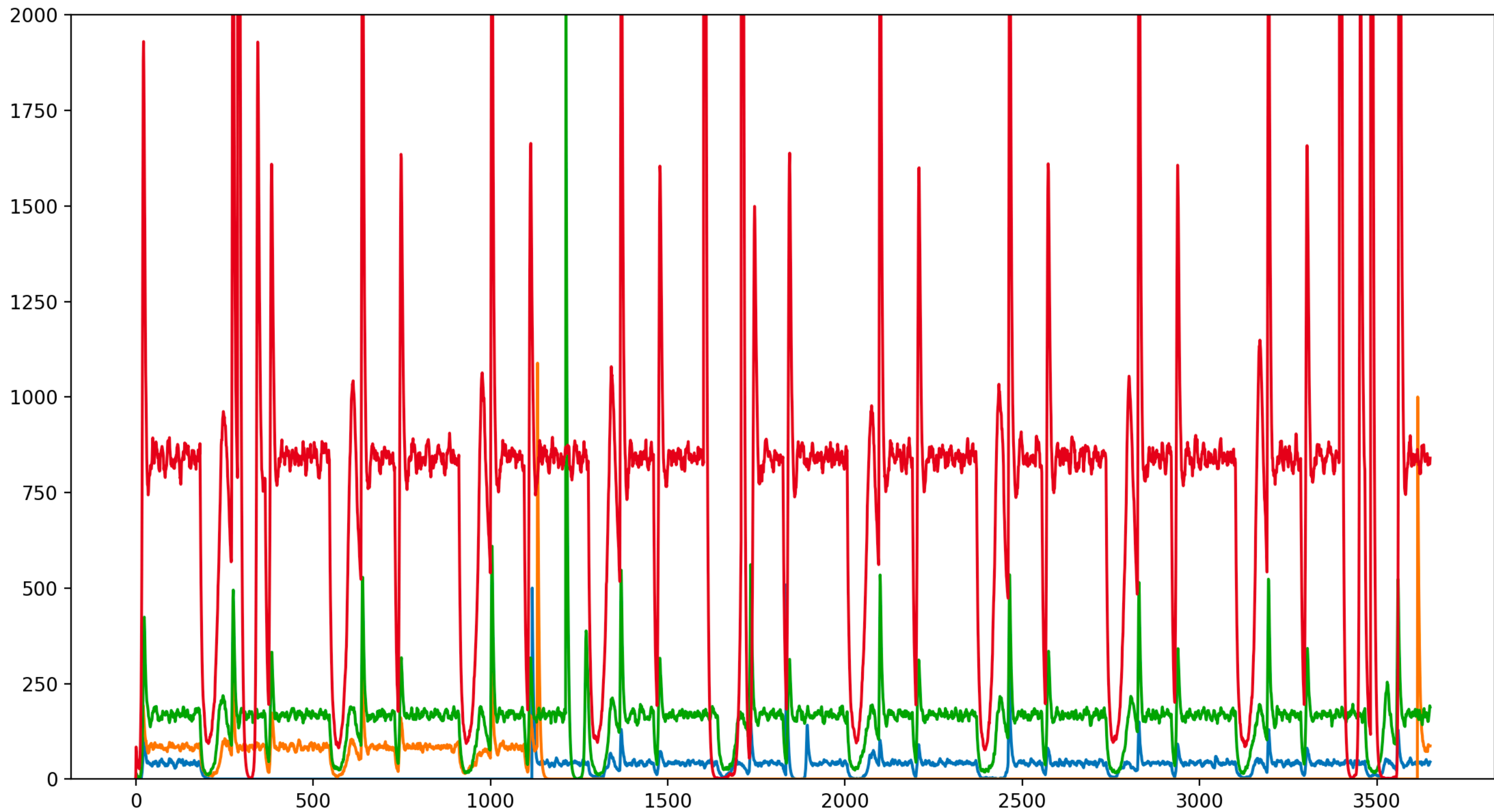
        new_infected += randomize(gamma_external, S[-1])

        new_recovered = randomize(gamma, I[-1])

        birth = randomize(mu, N[-1])
        total_birth += birth

        I.append(max(0, I[-1] + new_infected - new_recovered ))
        S.append(max(0, S[-1] - new_infected + birth))
        R.append(max(0, R[-1] + new_recovered -birth))
        N.append(I[-1]+S[-1]+R[-1])

    return S, I, R
```



Monte-Carlo

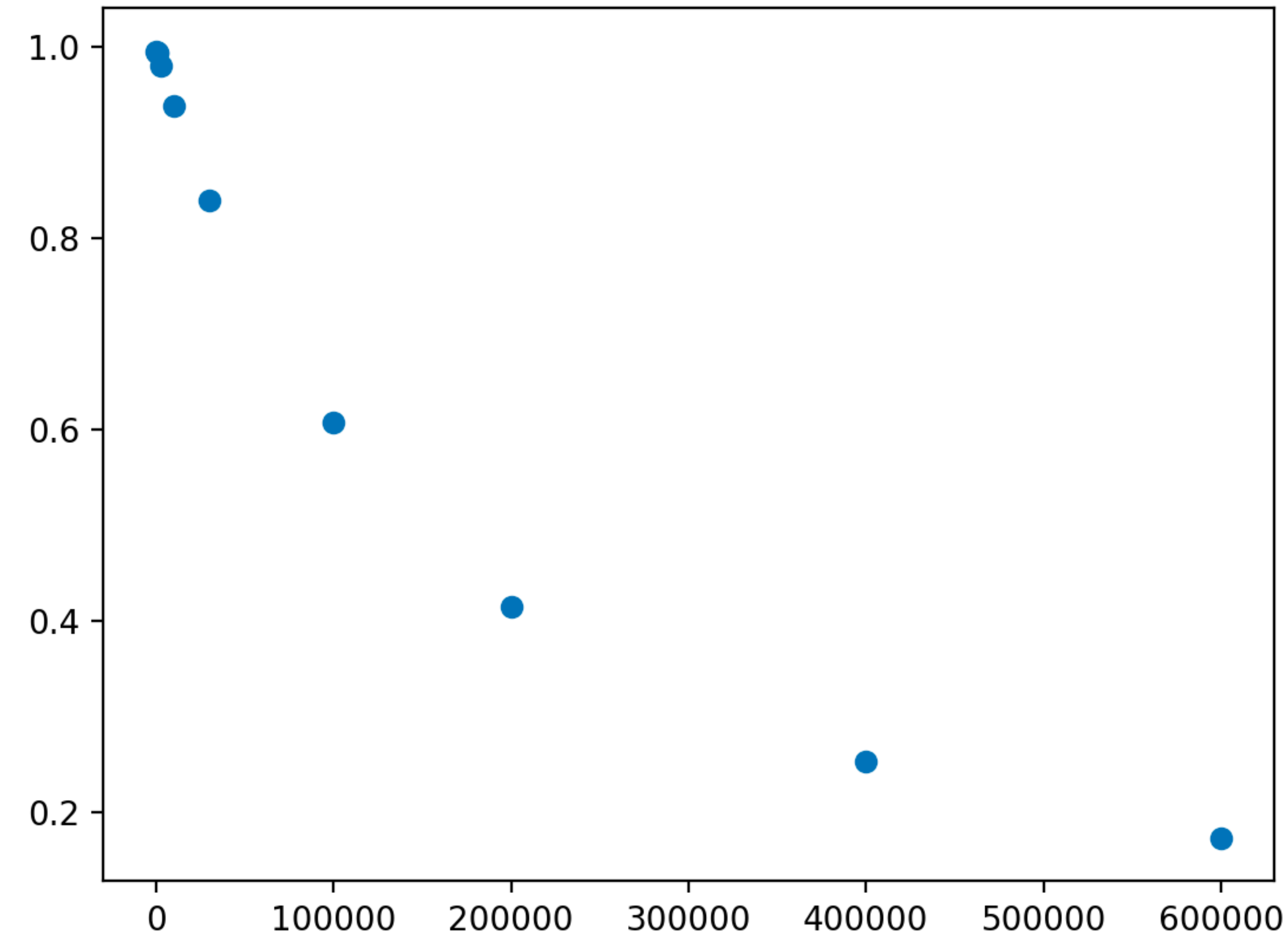
- Days without measles as function of population

```
for population in [100, 1000, 10000, 30000, 100000, 200000, 400000, 600000]:
    total = 0
    for i in range(numtrials):
        L_S, L_I, L_R = simulation_sir_stochastic(beta, gamma, \
                                                    gamma_external=0.01/365, \
                                                    noise_level=1, \
                                                    population = population,
                                                    duration=duration)

        empty_days = len([True for x in L_I if x==0])
        total+=empty_days/duration
    Lx.append(population)
    Ly.append(total/numtrials)
    print(population)
print(Ly)
plt.scatter(Lx, Ly)
```

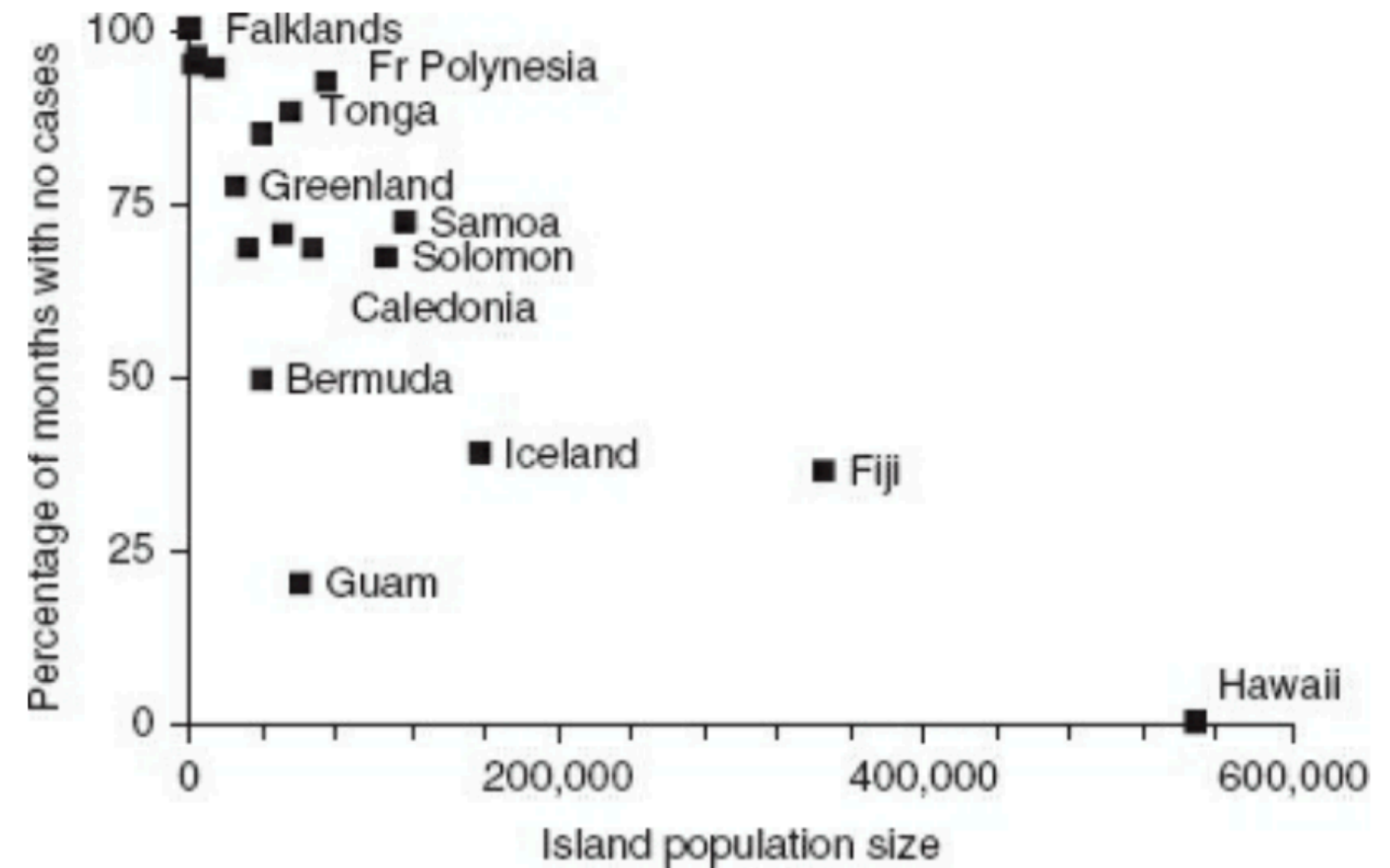
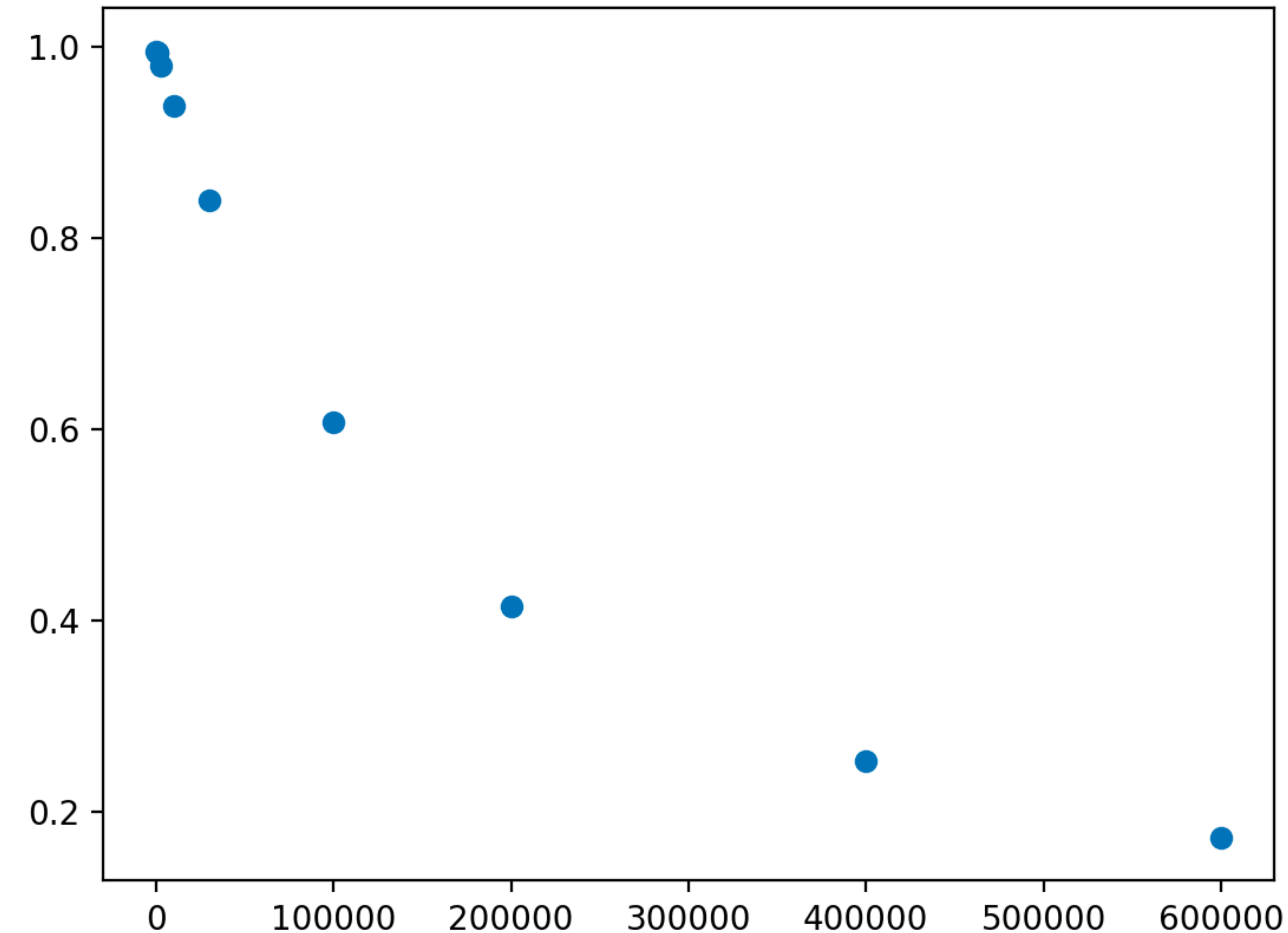
Monte-Carlo

- Days without measles as function of population



Monte-Carlo

- Days without measles as function of population



Questions?

- I spent my childhood worrying about Zombies, Piranhas and Cooties. I should have focused more on cooties.
 - Meme I can't quite remember:

Sources of error

- dt, integrator
- Exponential distribution
- Compartments, SEIR vs SIR VS SEIRS, etc.
- Spatial effects, stochasticity
- Homogeneity of population
- PARAMETERS, REAL DATA USED FOR CALIBRATION

Discussion

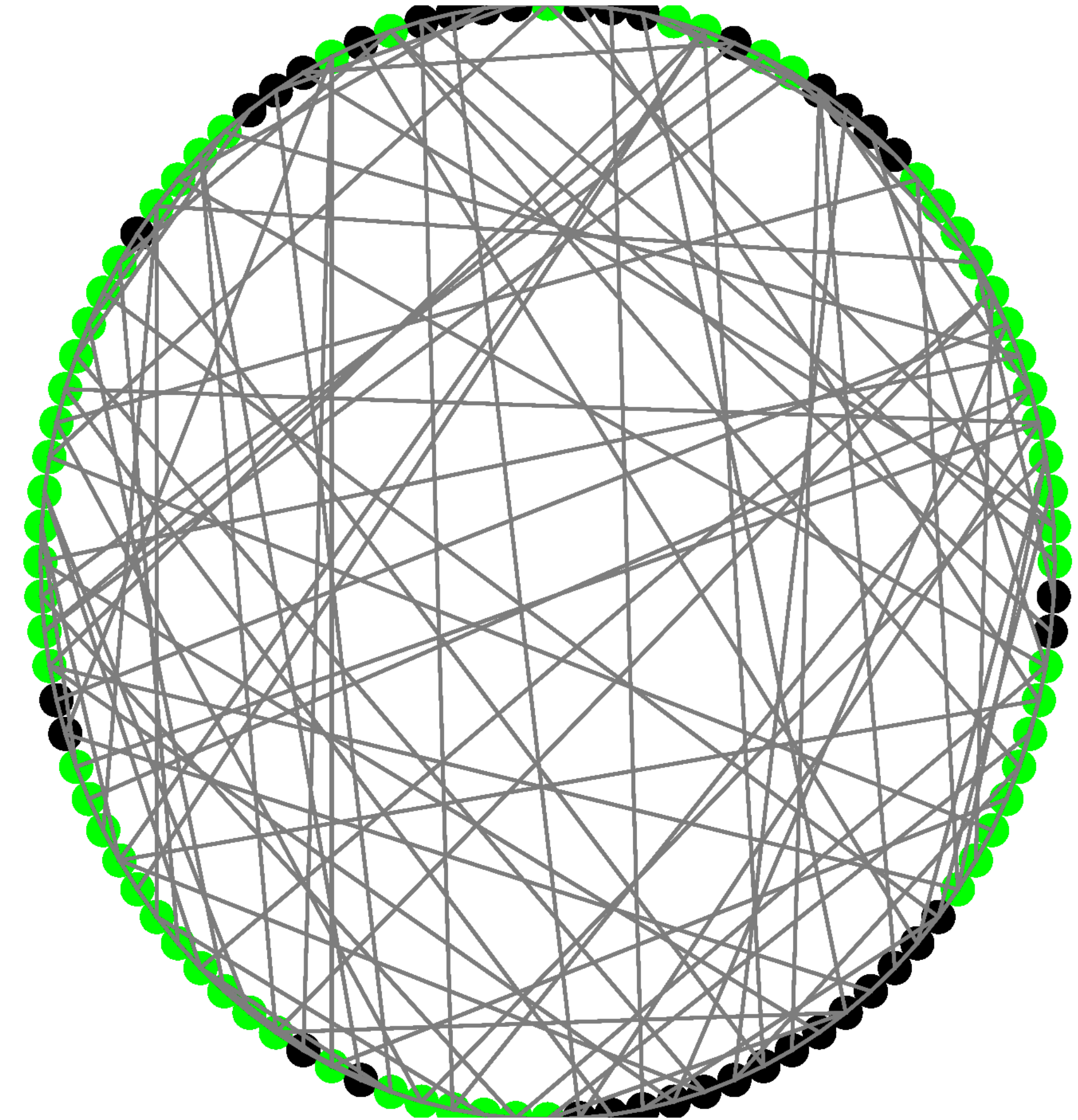
- Pros
 - Easy to run
 - Easy to build up
 - Often easy to analyze analytically
 - Small number of parameters
- Cons:
 - Ergodicity/panmixia assumption
 - Predictions are noisy at best, especially early and late (small numbers -> stochastic)
 - Missing parameters
 - Can miss spatial aspects
 - Hard to get fine-grained modeling of complex human behavior
- Heterogeneity is important
- Remember: humility, bad data

Worth repeating

- The tendency of some modelers to present them as scientific predictions of the future rather than models does not help. Models are widely used in government, and some models arguably have too much influence. They are generally most useful when they identify impacts of policy decisions which are not predictable by commonsense; the key is usually not that they are ‘right’, but that they provide an unpredicted insight.
- <https://bmcmmedicine.biomedcentral.com/articles/10.1186/s12916-015-0544-8> What makes an academic paper useful for health policy? Chris Whitty

Graph-based: basic

- Node :
individual, is either S, I or R
- Edge: contact
- At each time step, each edge has a probability of transition



In file `simple-graph.py`

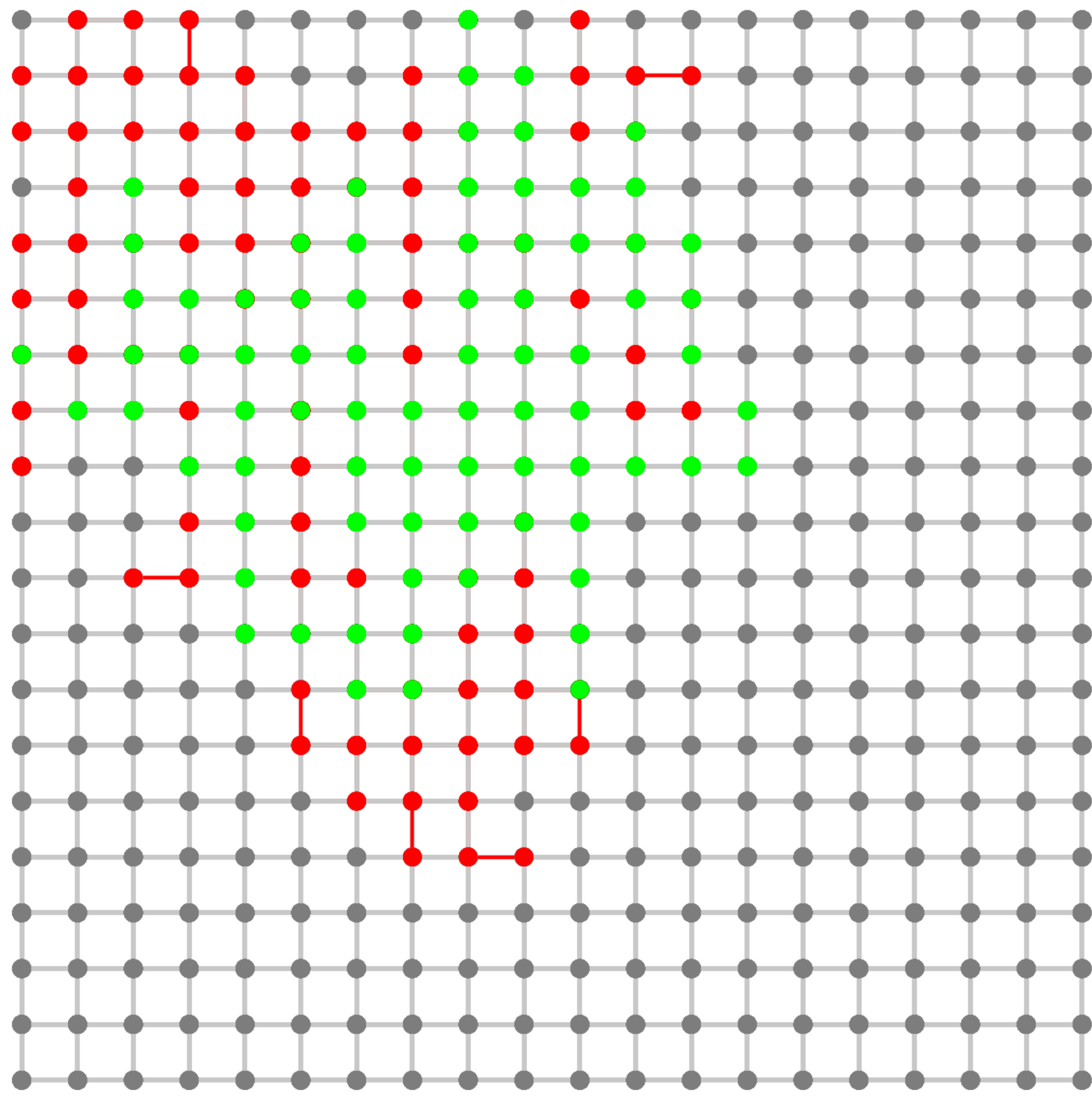
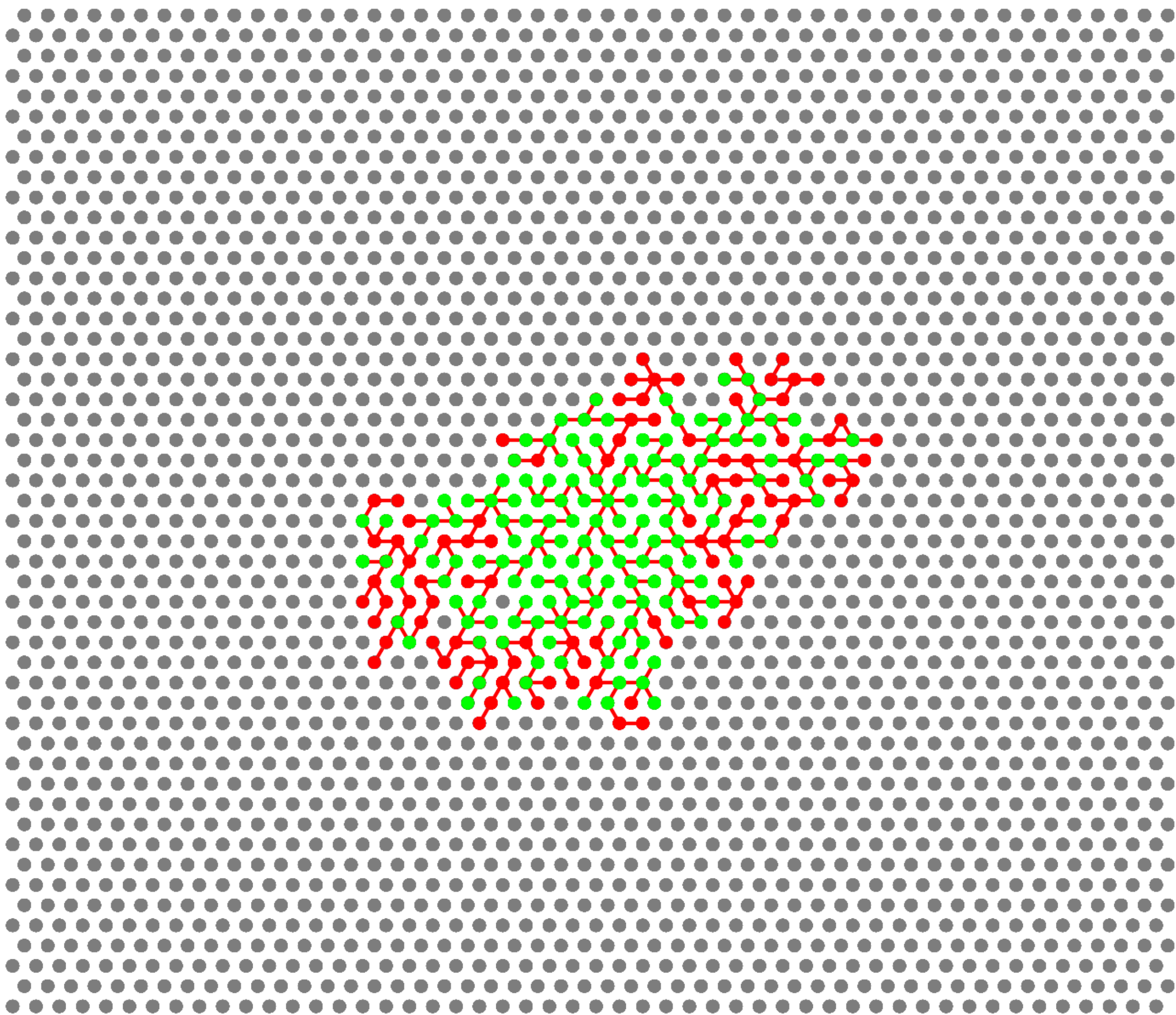
```
def simulate_one_step(vertices, edges, beta, gamma, dt):  
    # count people  
    L_contagion_edges = []  
    I, S, R=0,0,0  
    for i in vertices:  
        if i.get_status()=='I': I+=1  
        if i.get_status()=='S': S+=1  
        if i.get_status()=='R': R+=1  
    L_I.append(I)  
    L_S.append(S)  
    L_R.append(R)  
  
    for e in edges:  
        if e[0].get_status()=='I' and e[1].get_status()=='S':  
            if random.random()<beta*dt:  
                e[1].set_status('I')  
                L_contagion_edges.append(e)  
    for i in vertices:  
        if i.get_status()=='I' and random.random()<gamma*dt:  
            i.set_status('R')  
    return L_contagion_edges
```


Graph, better keep track of previous state

```
def simulate_one_step(vertices, edges, beta, gamma, dt):
    current_time = len(vertices[0]._status)-1
    L_contagion_edges = []

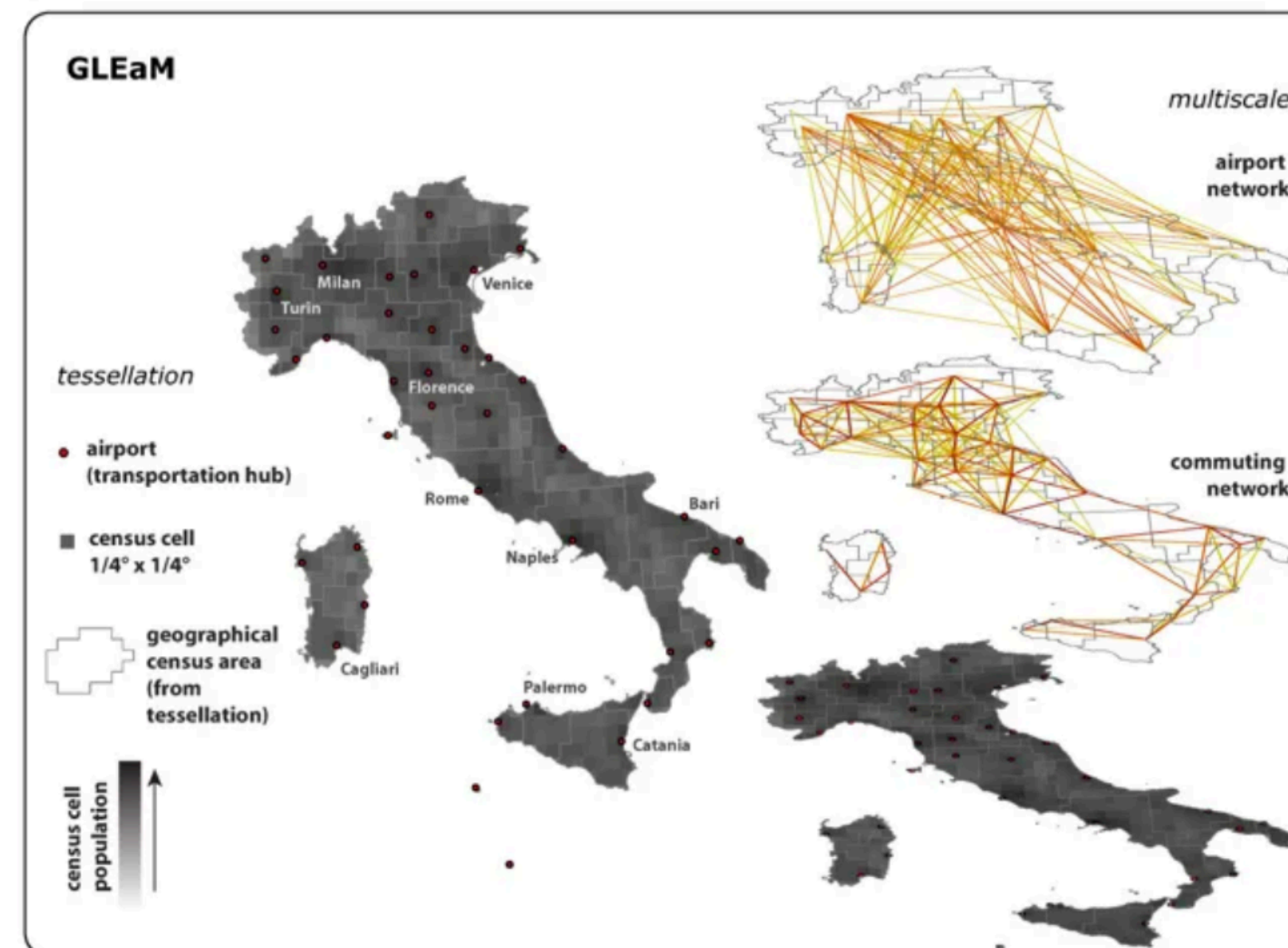
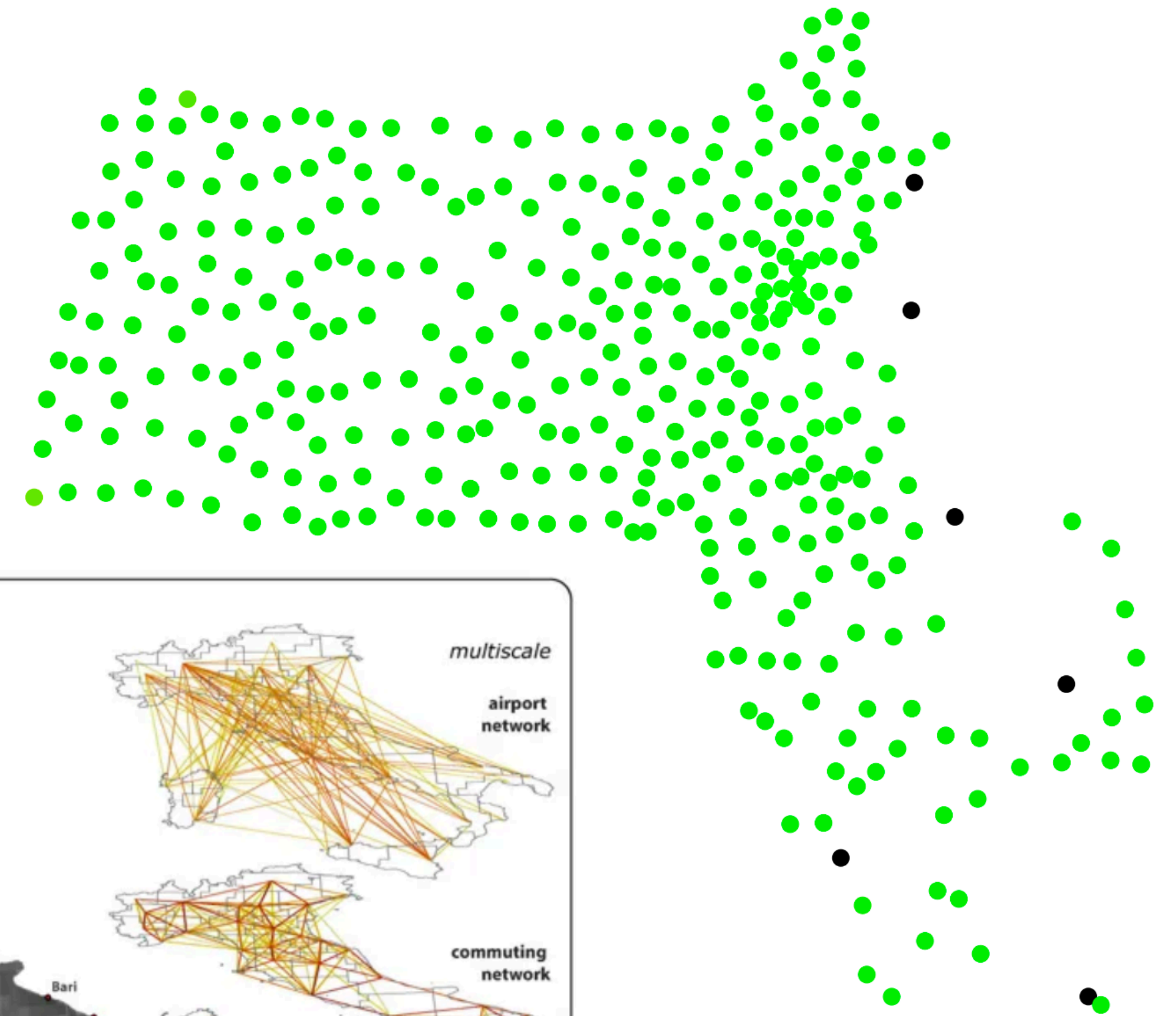
    # count people
    I, S, R=0,0,0
    for i in vertices:
        if i.get_status()=='I': I+=1
        if i.get_status()=='S': S+=1
        if i.get_status()=='R': R+=1
    L_I.append(I)
    L_S.append(S)
    L_R.append(R)
    for i in vertices:
        i.copy_previous_status()

    for e in edges:
        if e[0].get_status(current_time)=='I' and e[1].get_status(current_time)=='S':
            if random.random()<beta*dt:
                e[1].set_status('I')
                L_contagion_edges.append(e)
    for i in vertices:
        if i.get_status(current_time)=='I' and random.random()<gamma*dt:
            i.set_status('R')
    return L_contagion_edges
```



Alternative: Graph + SIR

- Each vertex keeps track of SIR
- Different gamma between nodes
(based on distance,
population,
road and other
transportation)

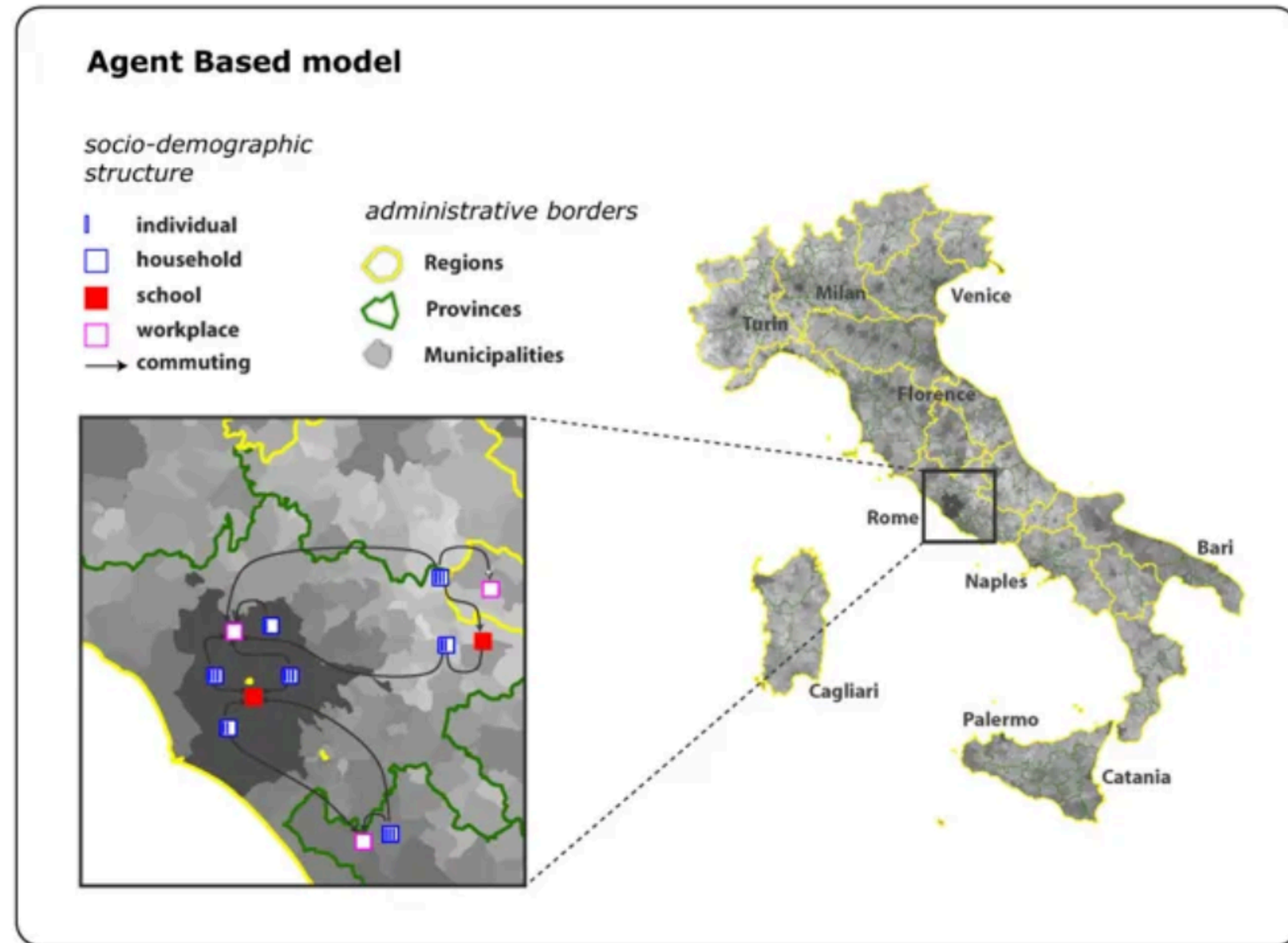


Graph, links

- https://www.researchgate.net/publication/6937027_Networks_and_Epidemic_Models
- <http://downloads.hindawi.com/journals/ipid/2011/284909.pdf>
- <http://systems-sciences.uni-graz.at/etextbook/networks/sirnetwork.html>
- <https://github.com/vrdi/Networks-Breakout> Daryl
- <http://people.csail.mit.edu/ddeford/epi.html> Daryl
-

Most complex: Agent-based

- Keep track of individual humans (simulation, GPS traces)
- Imperial College/Ferguson model
<https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-NPI-modelling-16-03-2020.pdf> (see critique at <https://static1.squarespace.com/static/5b68a4e4a2772c2a206180a1/t/5e70eb32b16229792eb14836/1584458547530/ReviewOfFergusson.pdf>)
- <https://covid-19-sds.github.io/> (Pentland, Moro et al.)
- Can be used to set up an SEIR model
- <https://bmcinfectdis.biomedcentral.com/articles/10.1186/1471-2334-10-190> comparison between agents and meta population
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5594572/> Lessons from a decade of individual-based models for infectious disease transmission: a systematic review (2006-2015)
- <http://jasss.soc.surrey.ac.uk/20/3/2.html> A Taxonomy for Agent-Based Models in Human Infectious Disease Epidemiology
- <https://fred.publichealth.pitt.edu>



Curve fitting (e.g. IHME)

- But remember, all exponentials look the same at the beginning
- <https://covid19.healthdata.org/>
- <https://www.medrxiv.org/content/10.1101/2020.03.27.20043752v1>
- Critique at <https://arguablywrong.home.blog/2020/04/02/ihme-projections-are-absurdly-optimistic/>
- <https://www.balloon-juice.com/2020/04/07/the-ihme-epidemiological-model/>
- https://twitter.com/CT_Bergstrom/status/1247645708741566465 more critique
- <https://www.covid-projections.com/>
- <https://annals.org/aim/fullarticle/2764774/caution-warranted-using-institute-health-metrics-evaluation-model-predicting-course>
- https://covid-19.tacc.utexas.edu/media/filer_public/d8/c1/d8c133e3-8814-4b30-9d3f-f0992ca66886/ut_covid-19_mortality_forecasting_model.pdf

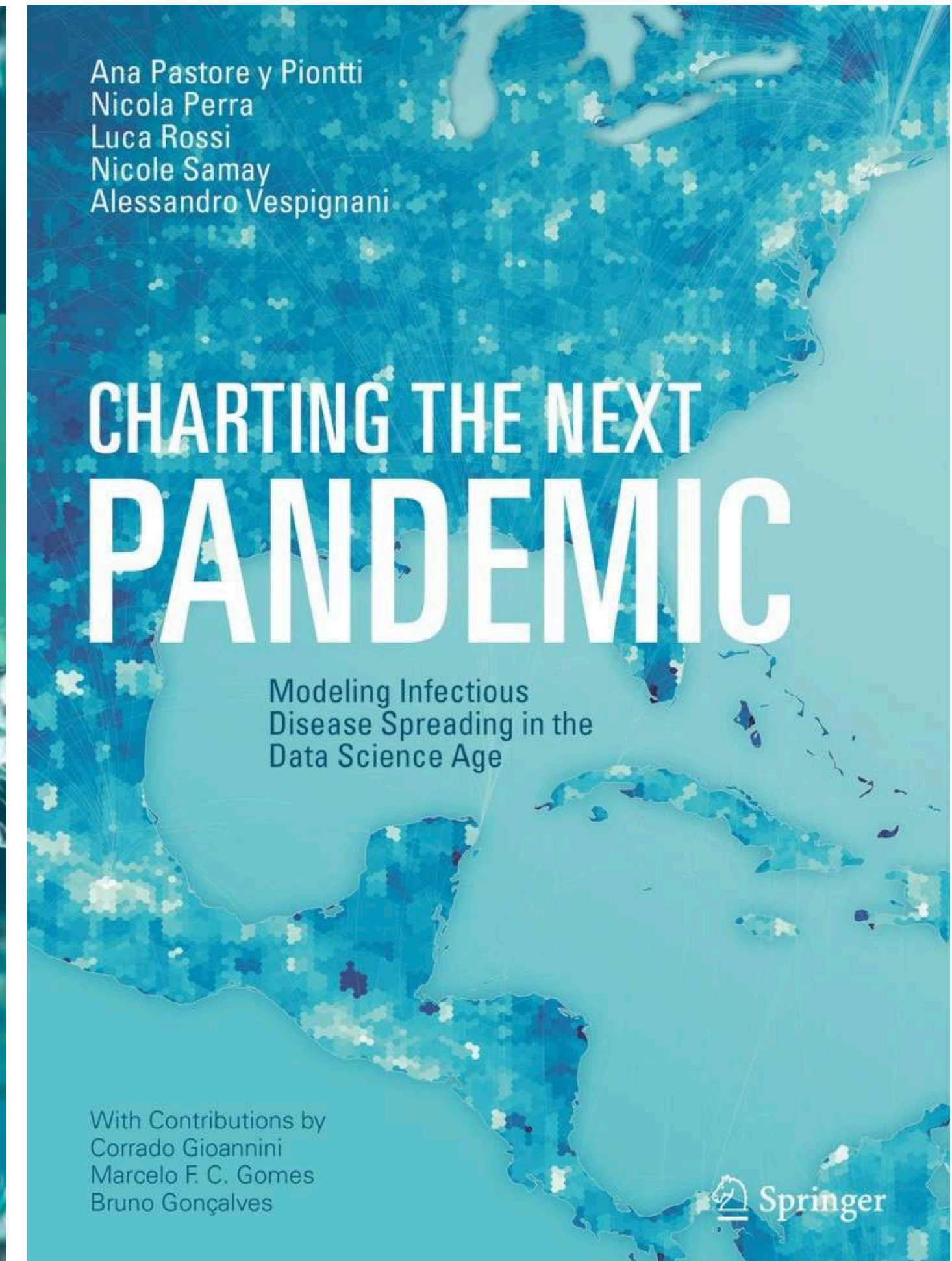
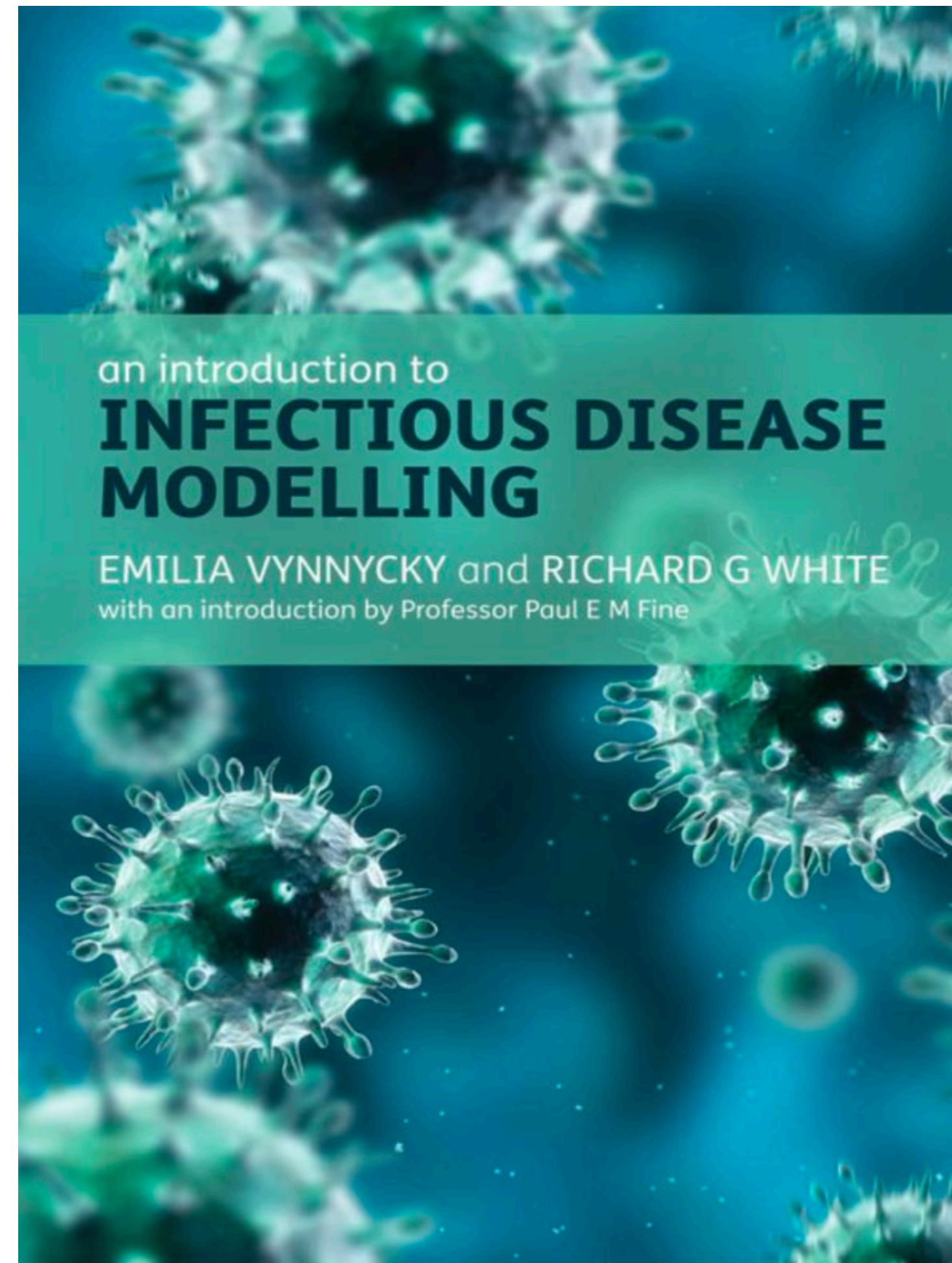
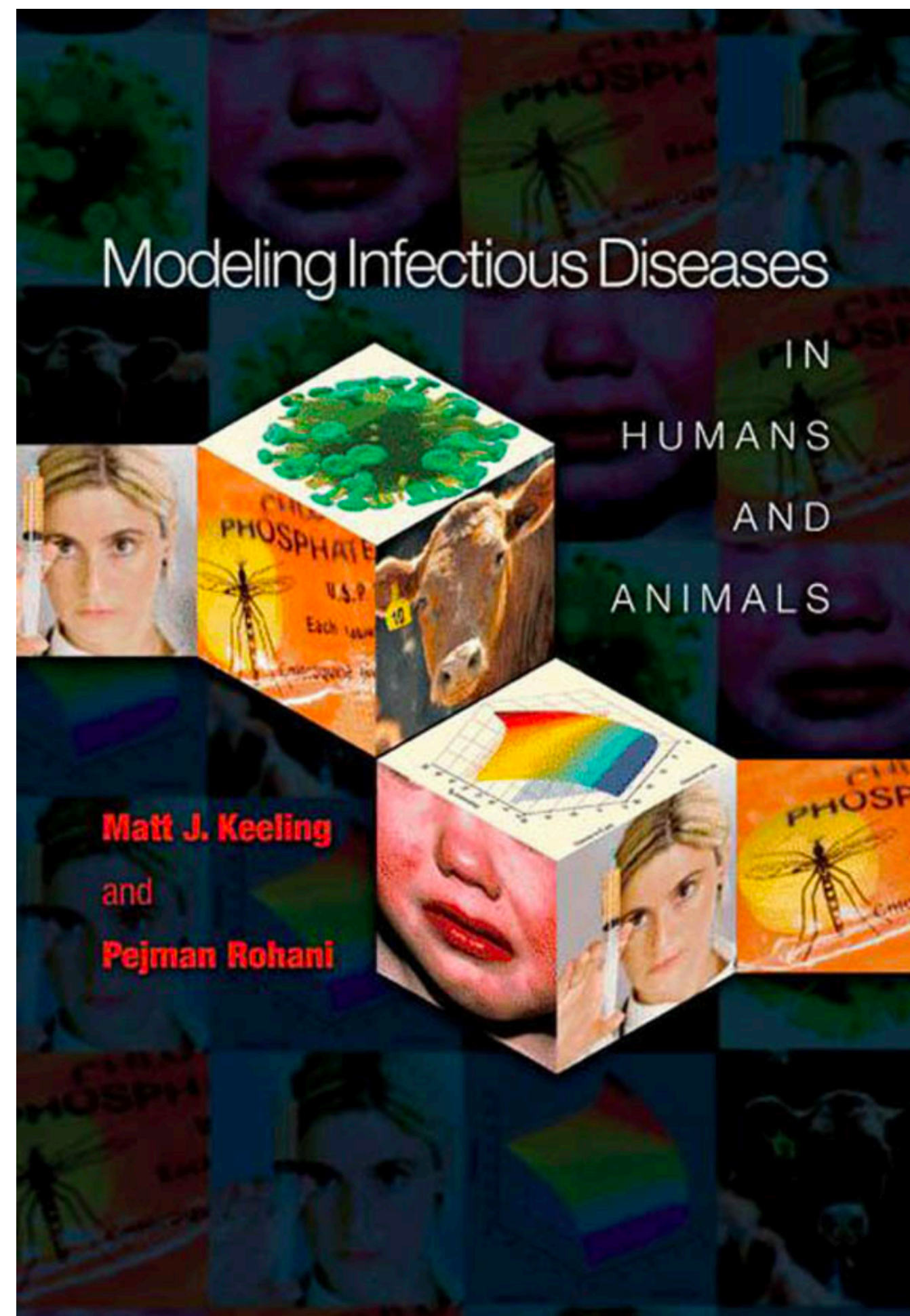
Other tools from 6.0002

- Clustering
- Regression
- Confidence intervals
- Optimization
- Random walk

In summary: We need better data

- Randomize/systematic virus and serology tests
- Then we have good computational models to analyze behavior and assess interventions

Books and intro material



Decent sources of information

- <https://www.nature.com/>
- <https://www.cdc.gov/coronavirus/2019-ncov/index.html>
- <https://coronavirus.jhu.edu/>
- <https://covid19.mit.edu/>
- <https://fivethirtyeight.com/science/>
- <https://www.economist.com/>
- <https://www.scientificamerican.com/tag/The+Coronavirus+Outbreak/>
- <https://www.statnews.com/>
- <https://medium.com/@tomaspueyo>

More links

- Weekly expert survey <https://works.bepress.com/mcandrew/4/>
- In favor of masks <https://medium.com/@Cancerwarrior/covid-19-why-we-should-all-wear-masks-there-is-new-scientific-rationale-280e08ceee71>
- Where do people social distance in US? <https://www.nytimes.com/interactive/2020/04/02/us/coronavirus-social-distancing.html>
- 538: why it's hard <https://fivethirtyeight.com/features/why-its-so-freaking-hard-to-make-a-good-covid-19-model/>
- 538: counts are meaningless <https://fivethirtyeight.com/features/coronavirus-case-counts-are-meaningless/>
- Google mobility data <https://www.google.com/covid19/mobility/>
- <https://medium.com/@tomaspueyo> Tomas Pueyo, always good
- <https://fivethirtyeight.com/videos/why-forecasting-covid-19-is-harder-than-forecasting-elections/> 538, video, why cover is hard to model
- <https://blogs.scientificamerican.com/observations/leading-with-the-unknowns-in-covid-19-models/> uncertainty
- <https://www.nature.com/articles/s42254-020-0175-7> How you can help with COVID-19 modelling
- <https://www.youtube.com/watch?v=54XLXg4fYsc> minute physics
- <https://www.nber.org/papers/w26917.pdf> Is NYC flattening the curve? Good discussion of potential biases and alternative explanations
- <https://www.newyorker.com/news/q-and-a/what-have-epidemiologists-learned-about-the-coronavirus>
- <https://www.youtube.com/watch?v=MZ957qhzcjI> UC Berkeley/London school of hygiene

Videos and demos

- https://www.youtube.com/watch?v=gxAaO2rsdIs&feature=emb_logo (floating “pi’s”)
- <https://meltingasphalt.com/interactive/outbreak/> (grid)
- <https://www.washingtonpost.com/graphics/2020/world/corona-simulator/> (wapo)
- <http://gabgoh.github.io/COVID/index.html> (has sampling parameters, SEIR with different strength of patients plus intervention)
- <https://www.youtube.com/watch?v=NKMHhm2Zbkw> intro to SIR
- <https://www.youtube.com/watch?v=Qrp40ck3WpI> intro to SIR
- <https://towardsdatascience.com/will-we-survive-the-covid-19-pandemic-d86e8f3c1846>
- <https://towardsdatascience.com/building-your-own-covid-19-epidemic-simple-model-using-python-e39788fbda55>
- <https://github.com/jckantor/covid-19>
- https://github.com/paulvangentcom/python_corona_simulation
- <https://www.lewuathe.com/covid-19-dynamics-with-sir-model.html>
- <https://github.com/covid-projections/covid-data-model>
- <https://neherlab.org/covid19/>
- https://art-bd.shinyapps.io/nCov_control/

Me reading about covid-19

- <https://xkcd.com/386/>

