Contagion in Motion:

Unraveling Emergent Behaviours of Pathogen Mutation in Mobility Networks

27 Apr 2023

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CSC-288: Network Modeling & Diseases

Disease Simulation

Not another COVID work surely

Math Models

- Classic SIR
- ODE vs. Stochastic Simulation

Graphs for Mobility Structures

- Hub-and-spoke architecture
- Power-law distribution

Adding Mutations

- Dynamic infectivity & mortality

Results

Disease Modelling

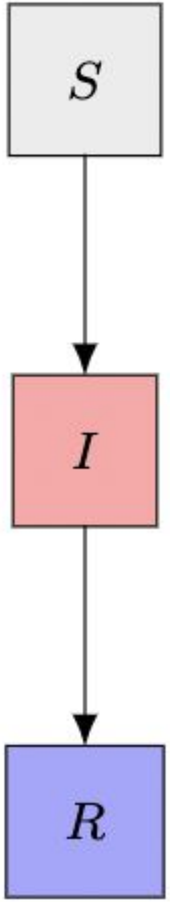
Simple SIR Model

Ordinary Differential Equations &
Stochastic Simulation

Infectious Disease Dynamics: Simple Model

- SIR Model → “Susceptible, Infected, Recovered”
- Total population $n = S + I + R$ remains constant
- Each person interacts with 3 other people per day
- Each S-I interaction results in $S \rightarrow I$ with probability 0.25

How many new infections from S should we expect per day?



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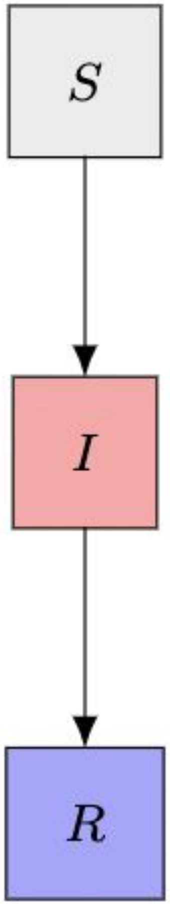
How many new infections from S should we expect per day?

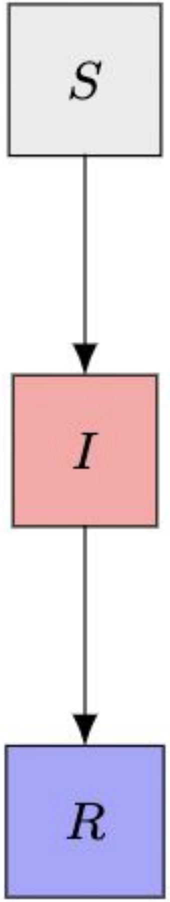
$$\Delta S = -\underbrace{\boxed{3S}}_{\#\text{int.}/day} \times \underbrace{\boxed{\left(\frac{I}{n}\right)}}_{\text{prob. of int with } I} \times \underbrace{\boxed{0.25}}_{\text{prob. of infect} \mid S\text{-}I} = -0.75\ SI/n$$



Infectious Disease Dynamics: Simple Model

- Each infected person remains sick for an average of 8 days.

How many recoveries would we expect from *I* every day?

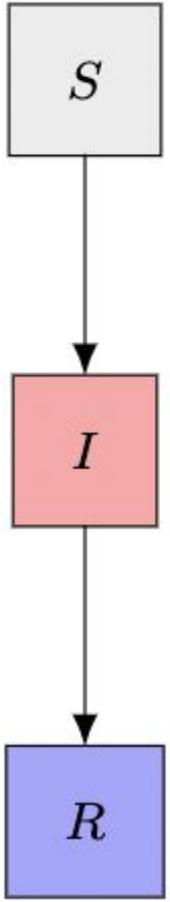


Infectious Disease Dynamics: Simple Model

- Each infected person remains sick for an average of 8 days.

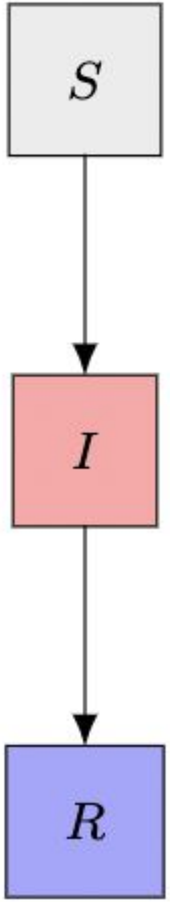
How many recoveries would we expect from *I* every day?

$$\Delta R = \underbrace{\boxed{\frac{1}{8}}}_{\frac{\text{(prob of rec)/day}}{I}} \times \; I$$



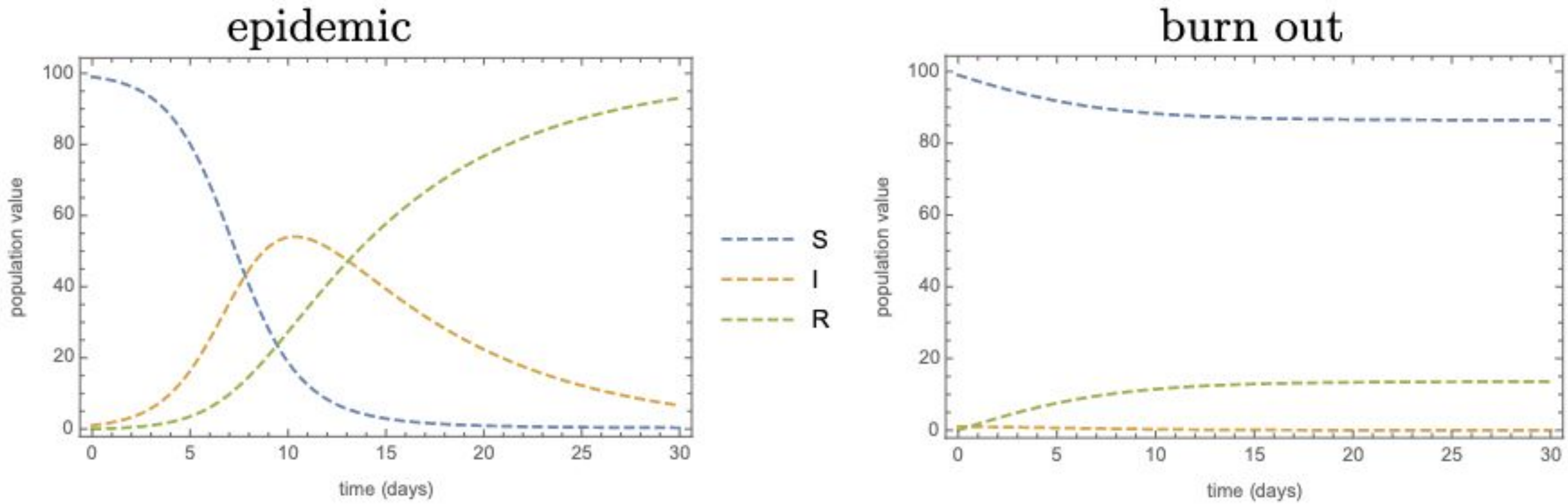
Infectious Disease Dynamics: Simple Model

$$\begin{cases} \dfrac{dS}{dt} = -0.75\ SI/n \\ \dfrac{dI}{dt} = 0.75\ SI/n - 0.125I \\ \dfrac{dR}{dt} = 0.125I \end{cases}$$



Initial conditions $S(0) = s_0$, $I(0) = i_0$, and $R(0) = r_0$

ODE Model: Different Parameters, Different Outcomes!



ODE Model vs Stochastic Simulation

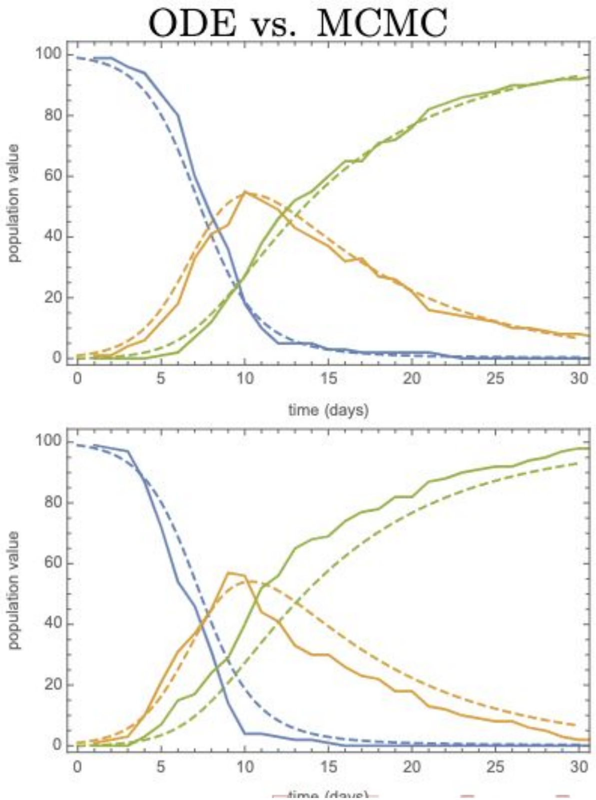
ODE: Populations are continuous, parameters are rates, and the solution is deterministic (i.e. there is *the* solution)

Stochastic: As a Markov Chain Monte Carlo simulation, populations are discrete, parameters are probabilities, and we have a distribution of solutions.

Let U be a **unif**$(0, 1)$ Random Variable

```
Initialize:  day=1, S=99, I=1, R=0
```

```
for( day = 1, 2, ..., finalDay )
    for( s = 1, 2, ..., S )
        if( β*I*/n < U  )
            S=S-1
            I=I+1
        end if
    end for
    for( i = 1, 2, ..., I )
        if( γ < U  )
            I=I-1
            R=R+1
        end if
    end for
end for
```

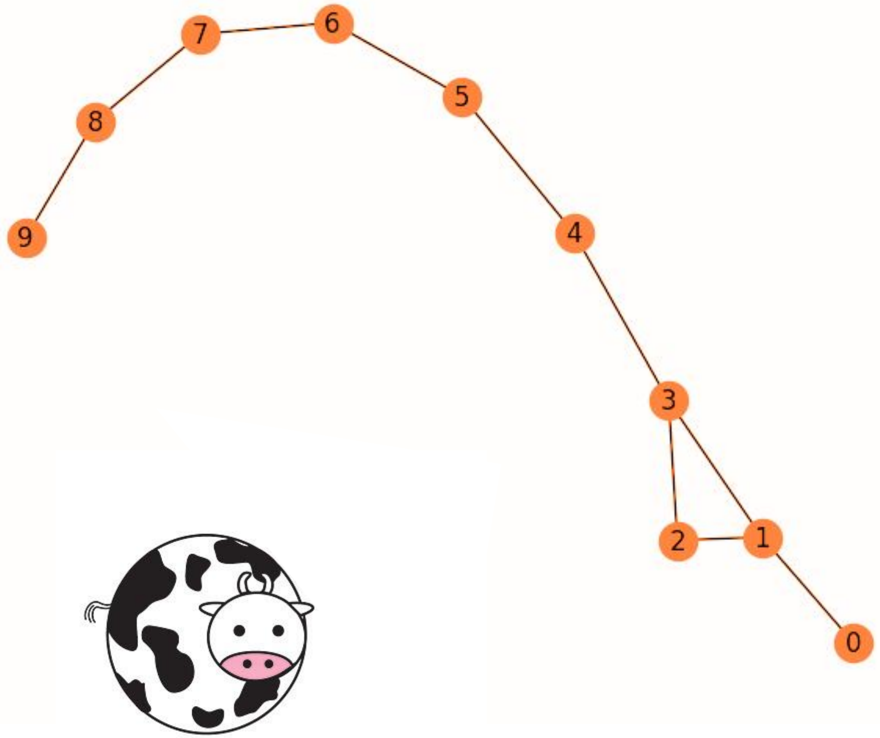


Disease Modelling

Differential Systems

Mobility Networks

Graphs, Graphs, and more Graphs

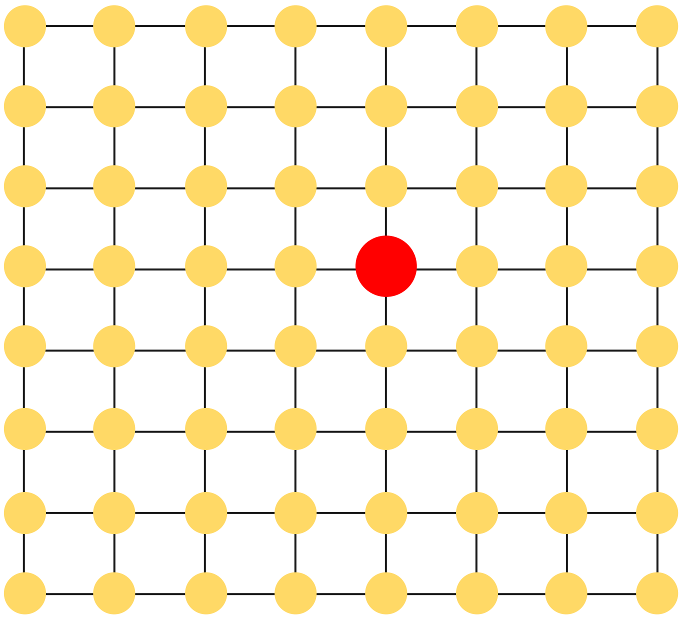


Graphs Objects

Nodes, Edges,
and all the fun stuff
and spherical cows

Grid network

Simply perfect



Grid network illustration

Topologically it’s a doughnut

Grid is unrealistic

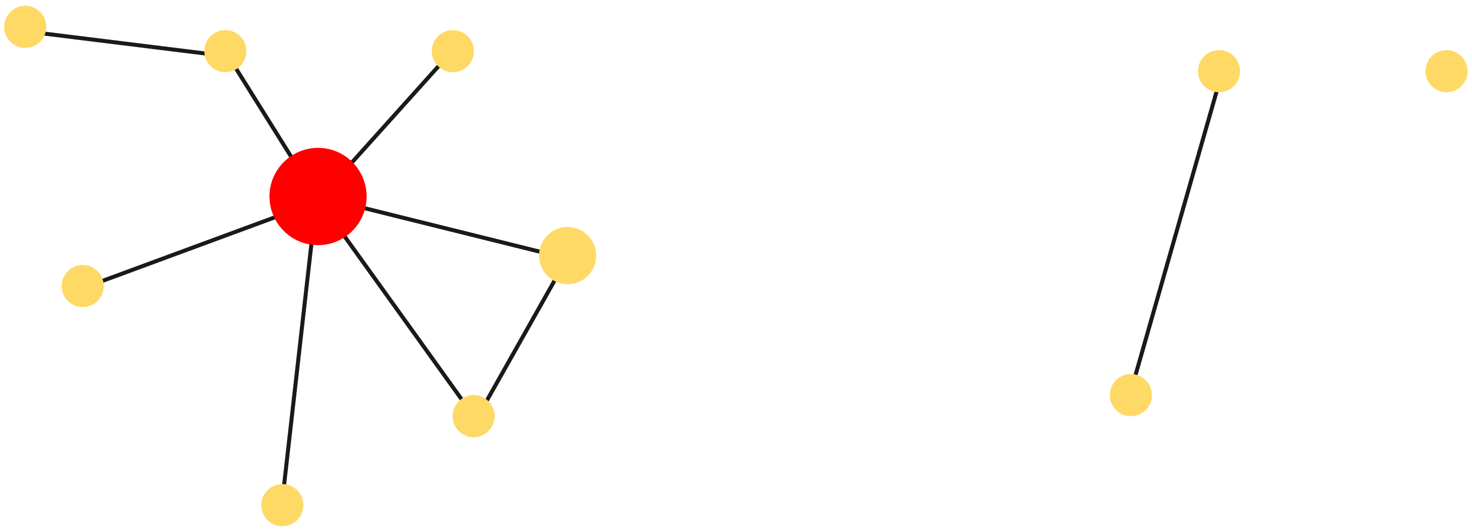
Spherical cows are cute

Can we do better?

How to modify the connectivity?

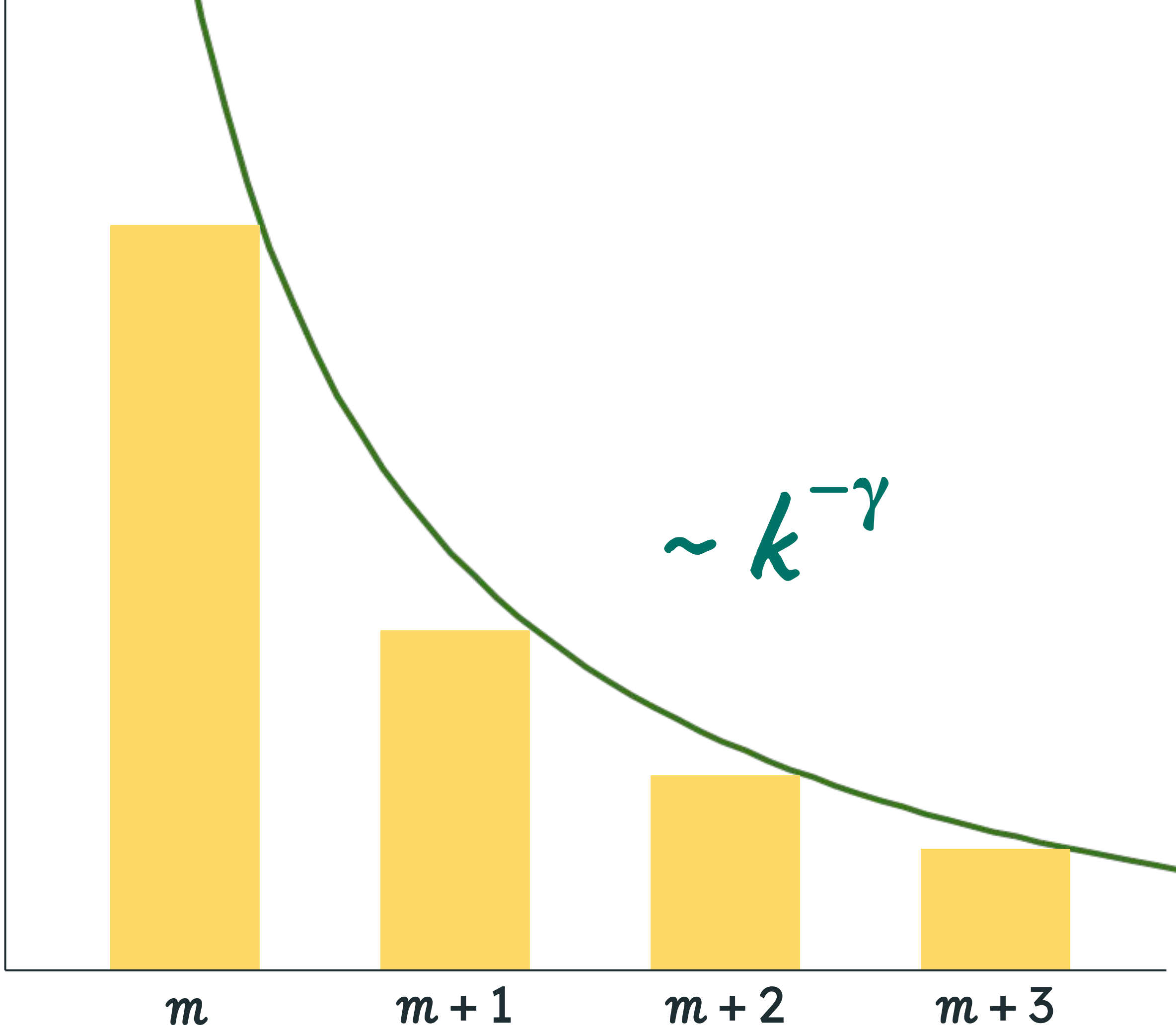
Rewiring...

Hub-and-Spoke Structure



Power-law distribution

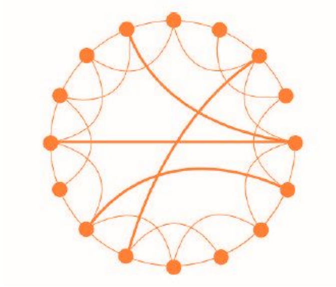
- Most will have few connections
- Superspreaders few & far between
- Minimum degree of connectivity m
- Decay exponent γ



Hub-and-Spoke Structure

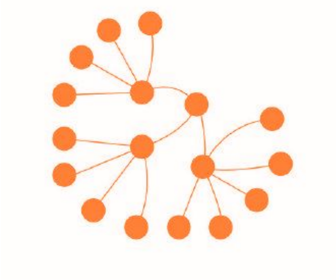
Random

Average distributions.
No structural or hierarchical patterns.



Small-world

High **local clustering** and
short average path lengths.
Hub-and-spoke architecture.



Scale-free

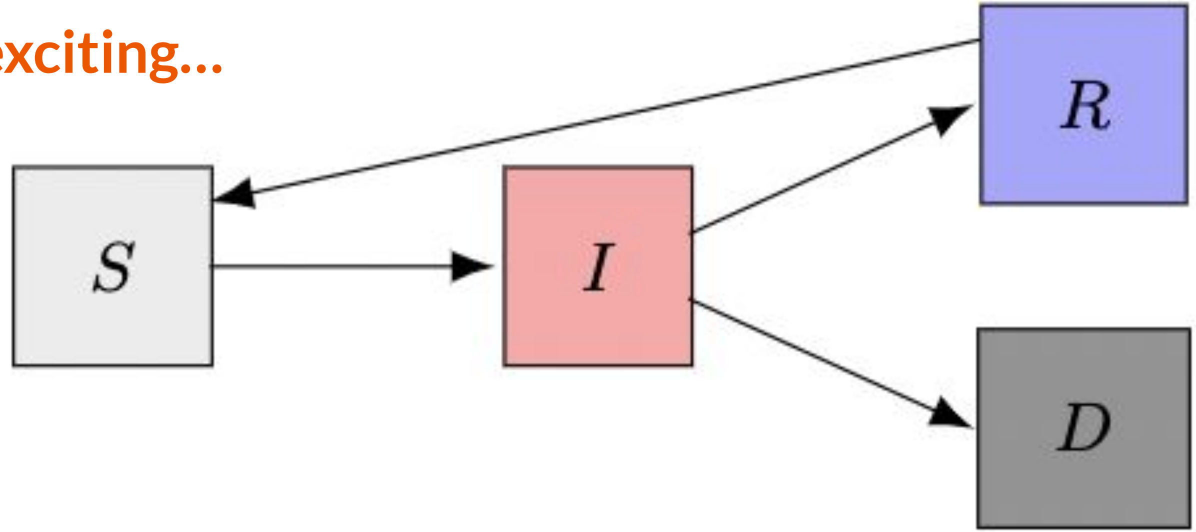
Hub-and-spoke architecture
preserved at multiple scales.
High **power-law distribution**

Disease Modelling

Differential Systems

Expanding our Model

Making it more exciting…



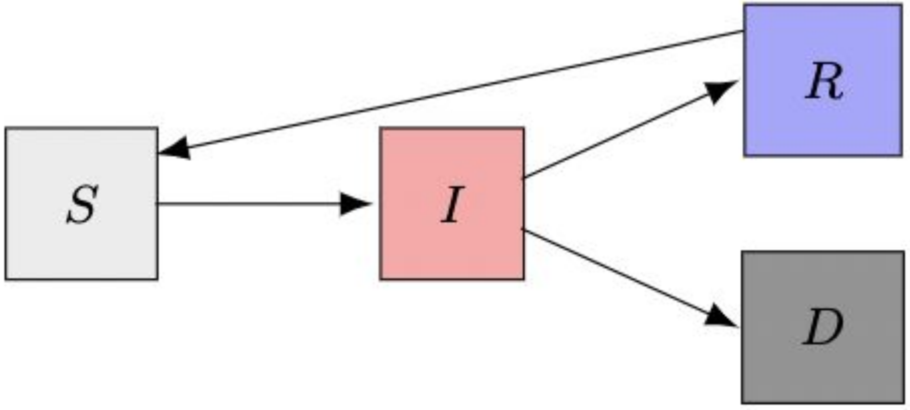
Now Four Categories:

- S → “Susceptible”
- I → “Infected”
- R → “Recovered”
- D → “Dead”

(Notice the Waning Immunity)

Infectious Disease Dynamics: Ordinary Differential Equations Model

$$
\begin{cases}
\dfrac{dS}{dt} = -\dfrac{\beta}{n} SI + \gamma R \\
\dfrac{dI}{dt} = \dfrac{\beta}{n} SI - \rho I - \delta I \\
\dfrac{dR}{dt} = \rho I - \gamma R \\
\dfrac{dD}{dt} = \delta I
\end{cases}
$$



Mutations: Hypothesis

Letting Our Disease Develop…

What if we allow our disease's infectivity and death rate to mutate unbiasedly on a local scale? Will there be an emergent bias on a global scale?

What might we *expect* to happen?

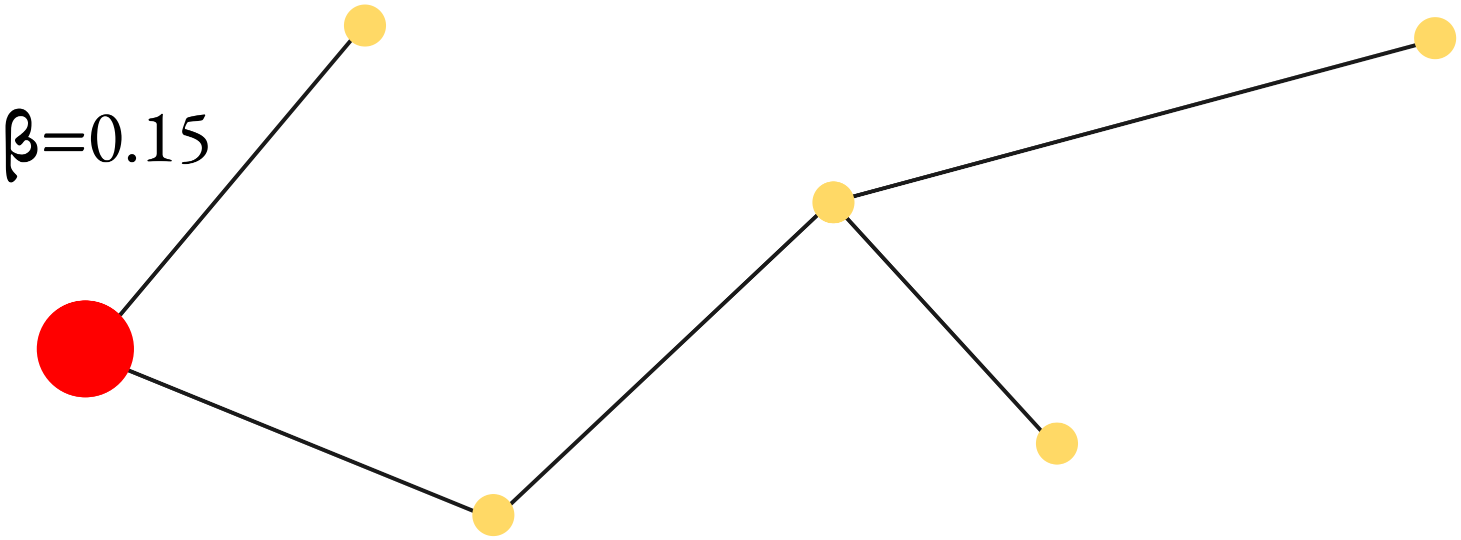
Intuitively, we may expect more infectivity…

- Think about how a more infectious disease would spread to more people, becoming more "dominant" than a less infectious one.

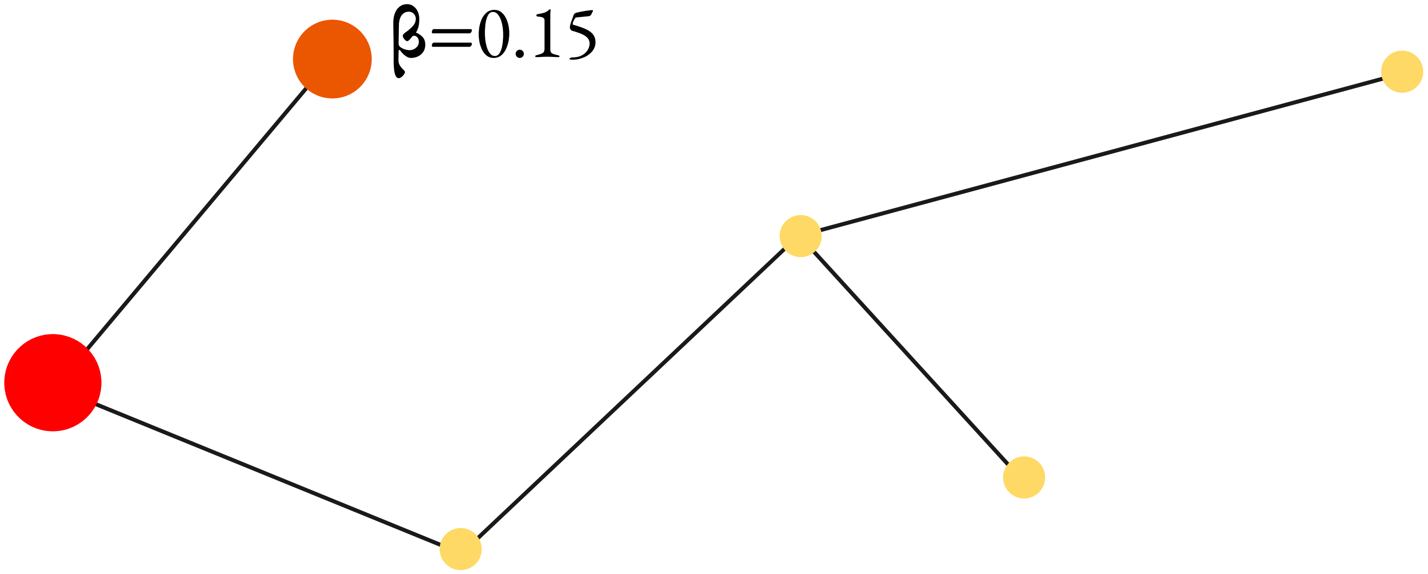
Intuition might also suggest less mortality…

- If a disease has too high of a mortality rate, the infected would die before having an opportunity to pass on their strain of the disease.

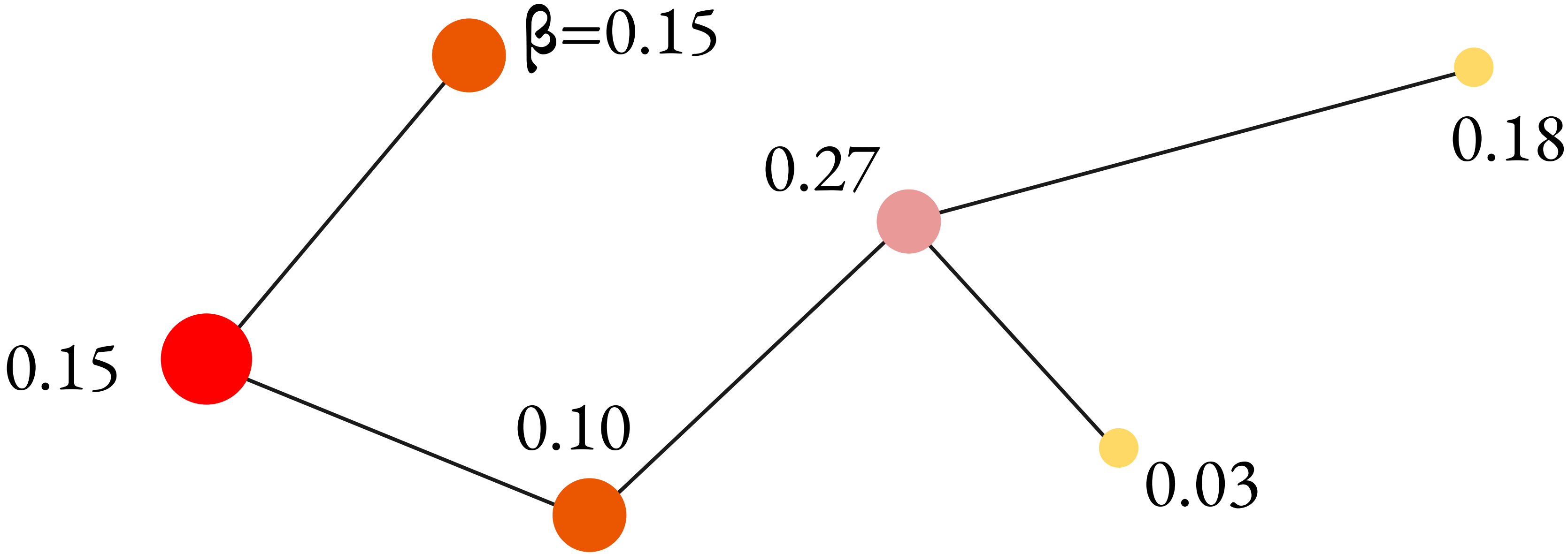
Edge Attributes ⟵ Individual Quirks



Node Attributes ⟵ Individual Quirks



Emergence? ⟵ Individual Quirks

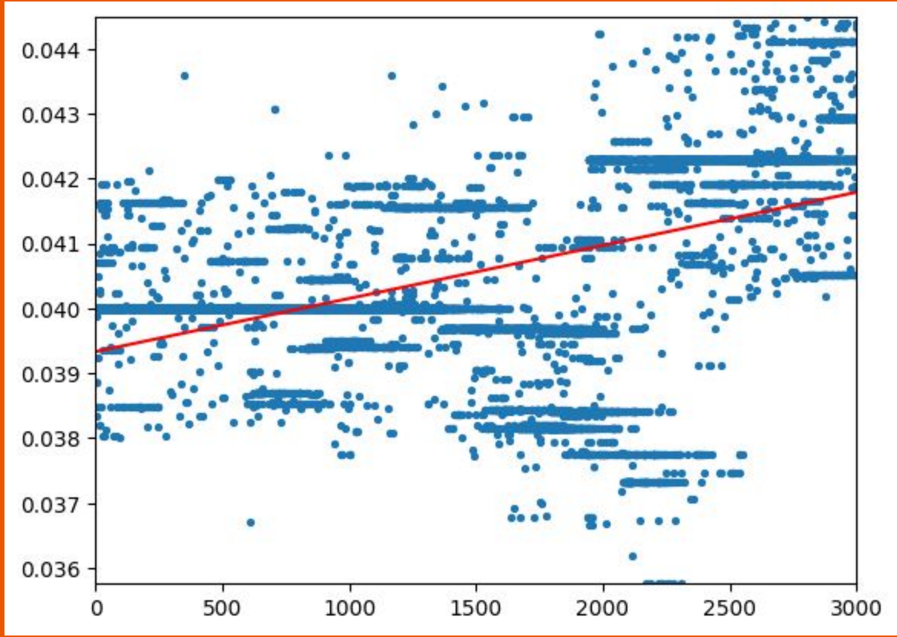


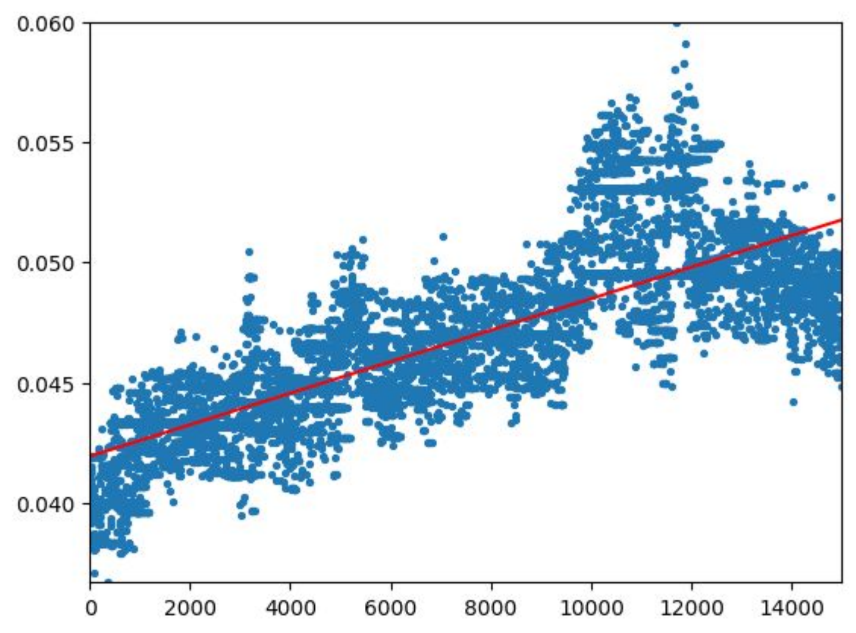
Illustrative Case:

Scale-free graph with an average degree of 6.124, $\beta = 0.04$ (infectivity), $\delta = 0.01$ (death rate)

Beta: 5% chance of mutating between 0 and 5% of original amount

Delta: 5% chance of mutating between 0 and 1% of original amount





Beta's Mutation Slope: 8.18×10^{-7}

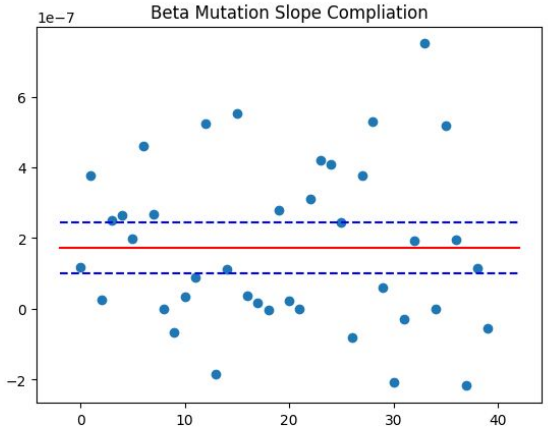
Mutations: Results

Run the simulation, get a Gaussian distribution…

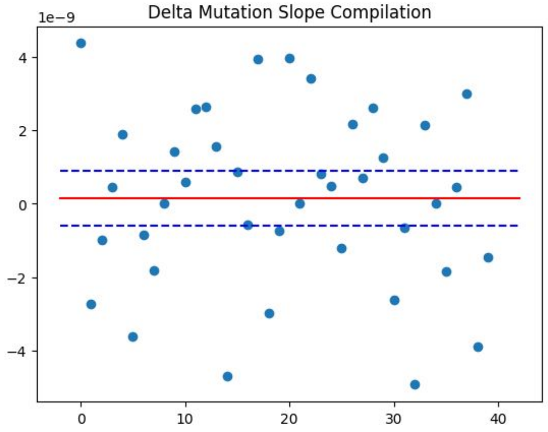
(These example results for initial parameters of beta = 0.030, delta=0.005)

(Consistent results with other initial probabilities)

Beta: (1.73 +- 0.73) × 10^{-8} (95% CI, Gaussian Distribution)



Delta: (1.44 +- 7.48) × 10^{-10} (95% CI, Gaussian Distribution)



Future Directions and Remaining Questions...

- Why didn’t delta’s slope didn’t have any trends?
- What if we let a community’s connections change with time?
- What if we let two diseases of different parameters “compete?” Would *that* then show some preference for less deadly diseases?

Thank you!

Q & A session

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