Effect of initial seeding in epidemic process on different networks

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Research Question

Given the case count data for a certain period of time, when should one start the simulations? Are the simulations starting from day 1 with initial infections I similar to the simulations started from day T when initial infections are k times I.
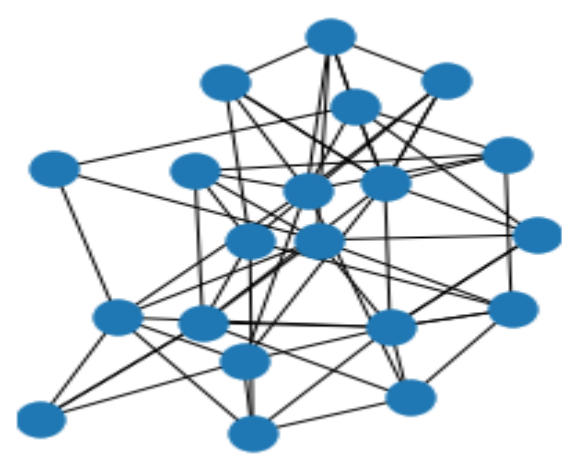
Background

Different networks can model different social situations, and three distinct networks are inspected
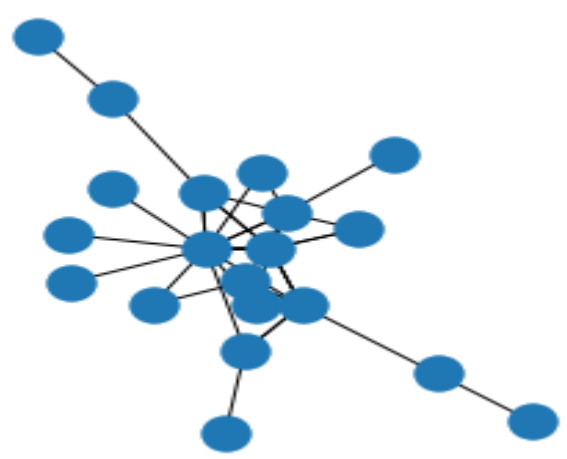
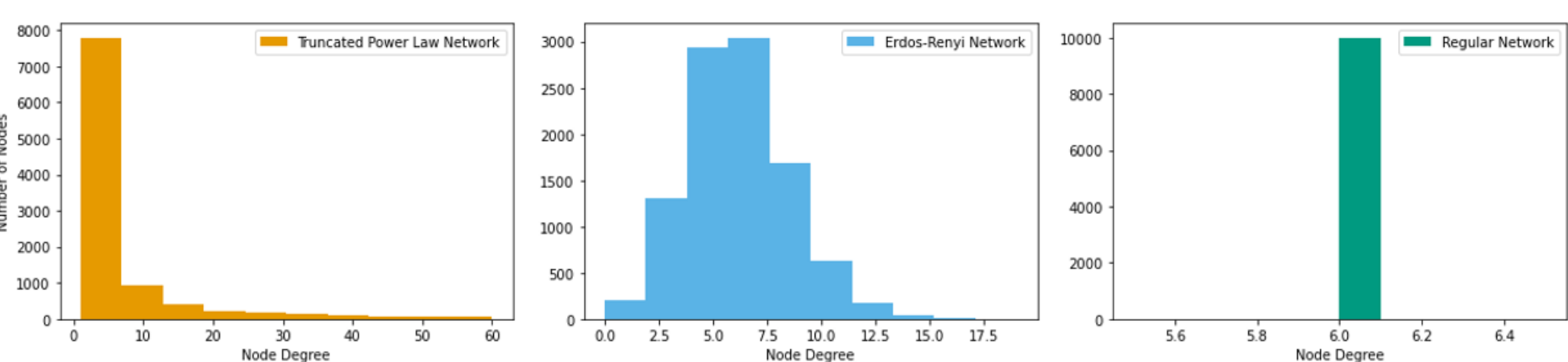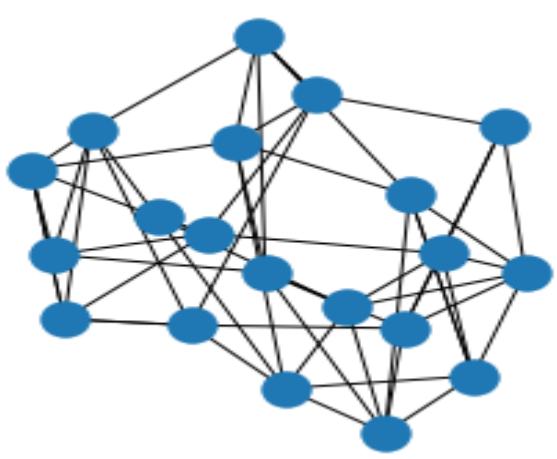**Truncated Power Law Network**   **Erdős–Rényi Network**   **Regular Network**

Figure #1: Degree Distribution for Truncated Power Law Network (Left), Erdős–Rényi Network (Center), and Regular Network (Right)

SIR Dynamics on Networks

Compartmental modeling is a method to simulate disease transmission
- Susceptible, Infectious, Recovered (SIR) model utilized in this experiment
- This type of modeling can also be utilized on contact networks, where the nodes represent people and edges represent contacts between people
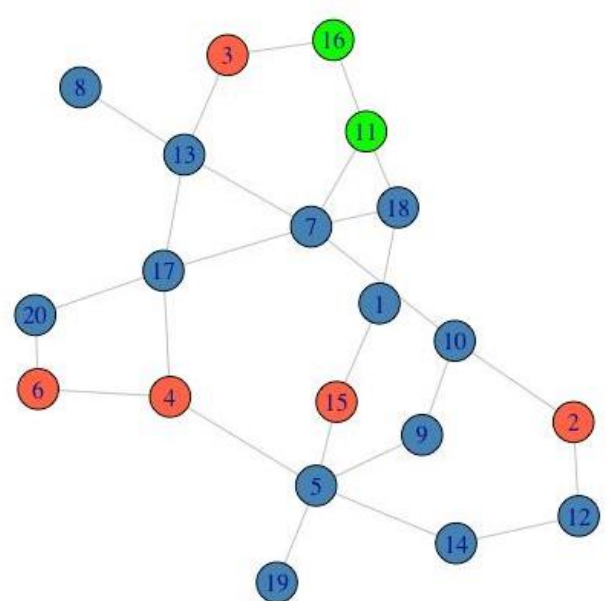
$$\dot{S}(t) = -\tau I(t) S(t)$$
$$\dot{I}(t) = \tau I(t) S(t) - \gamma I(t)$$
$$\dot{R}(t) = \gamma I(t)$$

Figure #3: Susceptible (Blue), Infectious (Red), Recovered (Green) model on a network

Future Work

Explore scaling on different networks, specifically networks that better represent contact networks for disease transmission
- Truncated power law attempts to model the social network of disease transmission, but other networks can also model this network

What happens when the proportion of the population infected, ρ, is held constant and the size of the population, N, increases?
- Is there a scalar limit, k, at which a base population of size N fails to display the same disease dynamics as a population of size kN?

References

- Kiss IZ, Miller JC, Simon P. (Book) Mathematics of epidemics on networks: from exact to approximate models. Springer; 2017.
- Okabe, Y., Shudo, A. Spread of variants of epidemic disease based on the microscopic numerical simulations on networks. Sci Rep 12, 523 (2022). https://doi.org/10.1038/s41598-021-04520-0
- Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. SIAM Review, 42(4), 599–653. http://www.jstor.org/stable/2653135

Current Work

Exploration of how network structure affect disease dynamics:
- After generating networks, running SIR models on those networks to simulate a contagion with a fixed number of initial infections distributed uniformly on the network
- Examined how the network structure and initial number of infections affects disease dynamics of the SIR simulation
  - **Fixed Seeding** - Determined how the initial seeding of infected nodes (I_0) within a *specific network affects* disease dynamics
  - **Fixed Network** - Compared disease dynamics with initial infections (I_0) and scaled initial infections ($k\ I_0$)
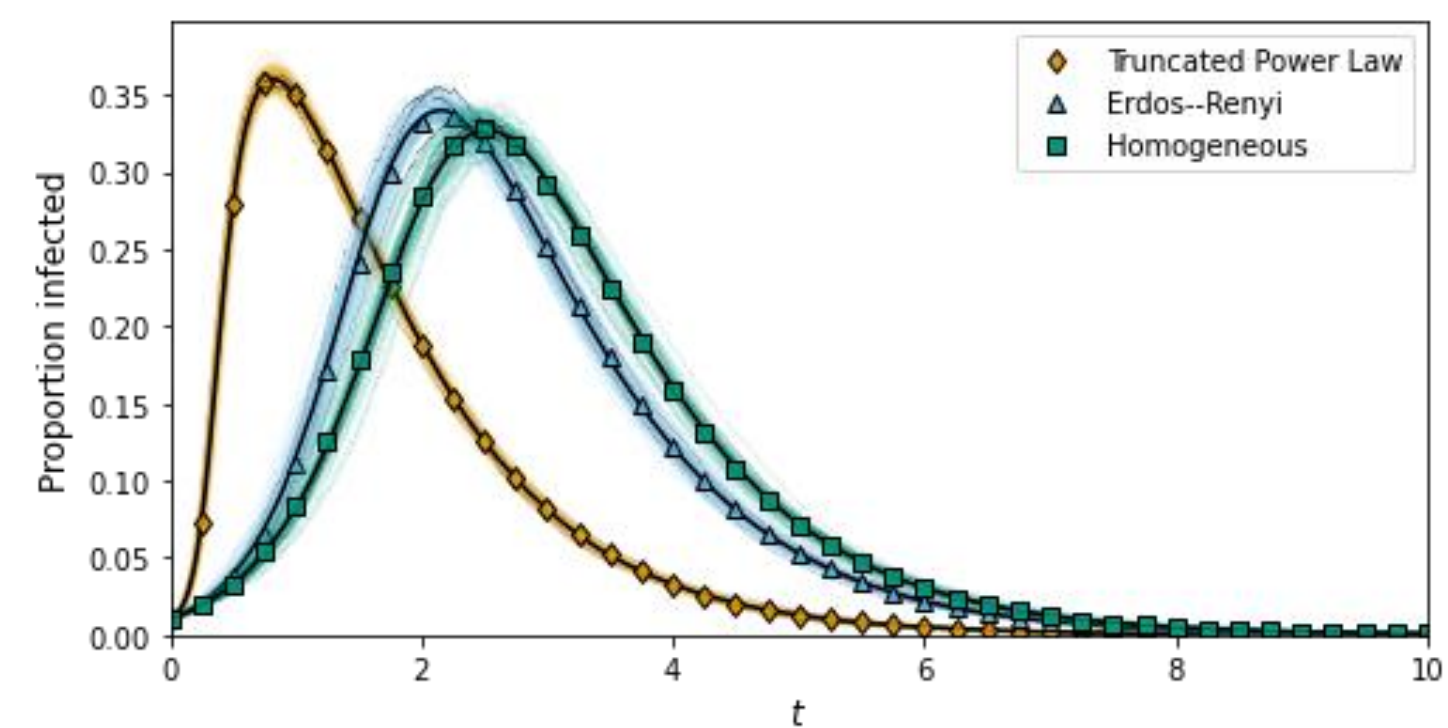
Figure #2: Mean epi curve for 50 SIR simulations on a network of size 10,000, $\tau = 0.5, \gamma = 1$

Design

- Generated previously described networks and ran SIR simulations with uniformly selected initial infected nodes (I_0)
- Altered the number of infected nodes (I_0) by a scalar, k, and the transmission rate, τ

Experiment

1. Generate truncated power law network and Erdős–Rényi Network
2. Run SIR simulations with I_0 and $k\ I_0$ infected nodes
3. Inspected the mean infection curves for different k and τ,
4. Determined the shift (Δ_k) at which the unit epi curve ($k = 1$) reaches $k\ I_0$
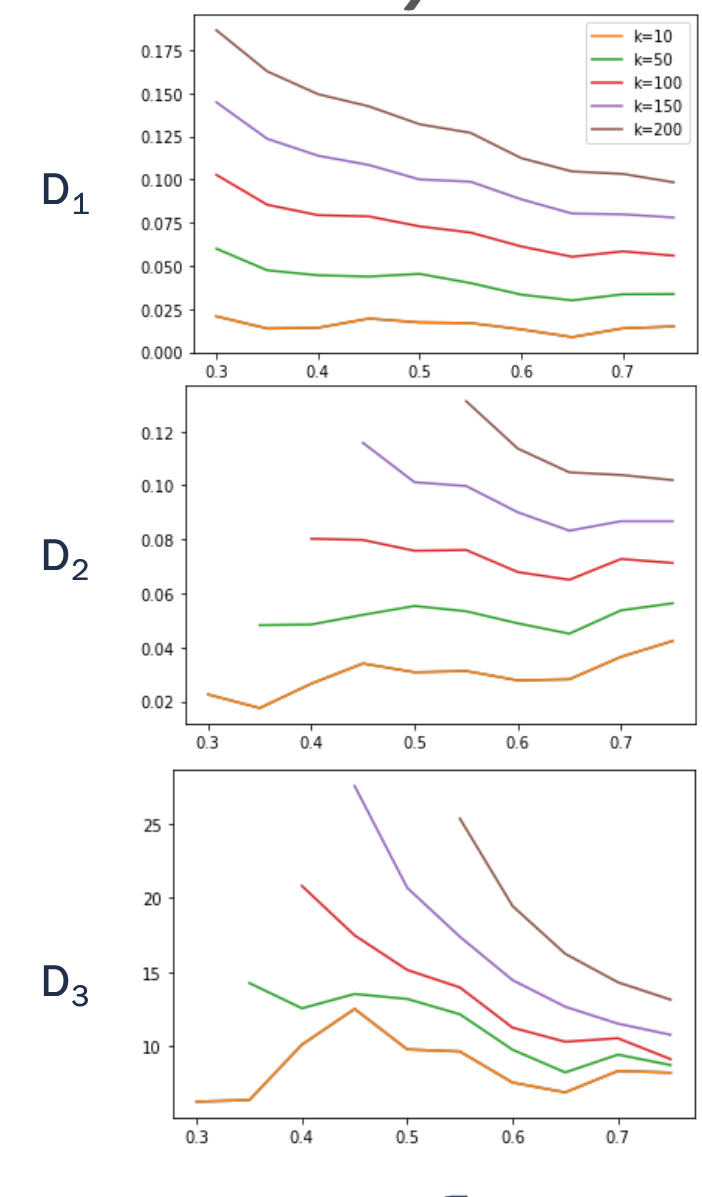
Results

Three distances to represent how similar the scaled epi curve is to the unit epi curve:
- Difference in Total Proportion Infected (D_1)
  - $D_1(i_k, i_1) = \left| \sum_{\Delta_k < t} i_k(t + \Delta_k) - \sum_{\Delta_k < t} i_1(t) \right|$
- Maximum Distance between Curves (D_2)
  - $D_2(i_k, i_1) = \max_{\Delta_k < t} |i_k(t + \Delta_k) - i_1(t)|$
- Area between Curves (D_3)
  - $D_3(i_k, i_1) = \sum_{\Delta_k < t} |i_k(t + \Delta_k) - i_1(t)|$
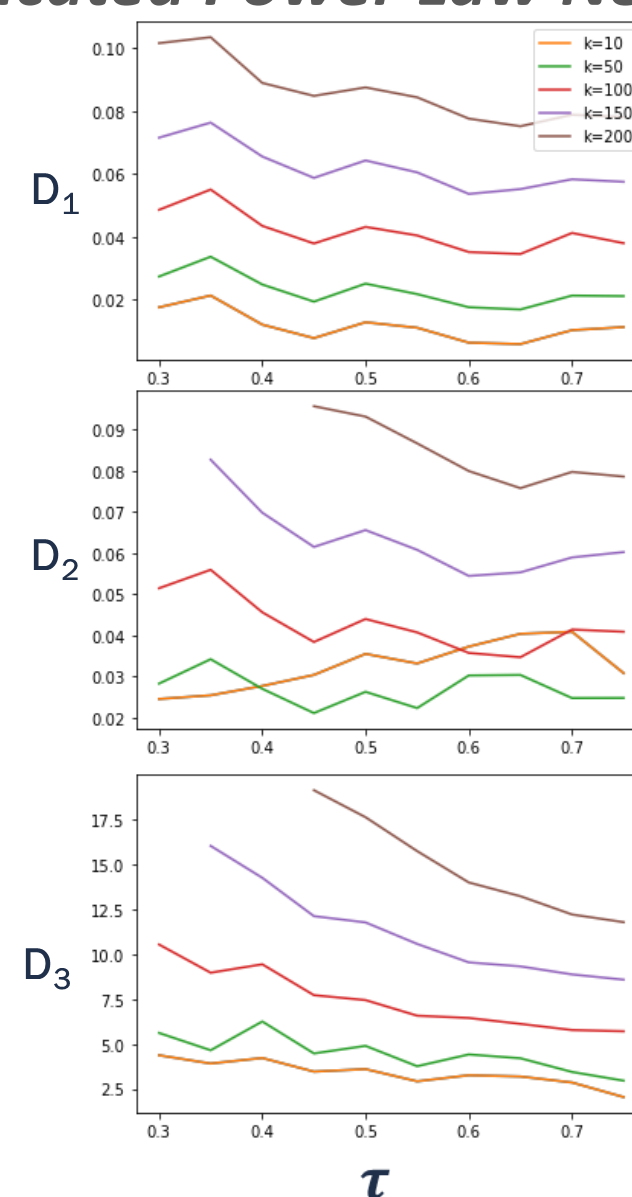
Truncated Power Law Network   **Erdős–Rényi Network**

Conclusion

- For both networks, as τ increases, the distance between the unit epi curve and the scaled epi curve decreases. Therefore, for higher values of τ the scaled disease can be more accurately predicted.
- Additionally, for small scale factors (k<50) the scaled base curve is a close estimate of the true curve.