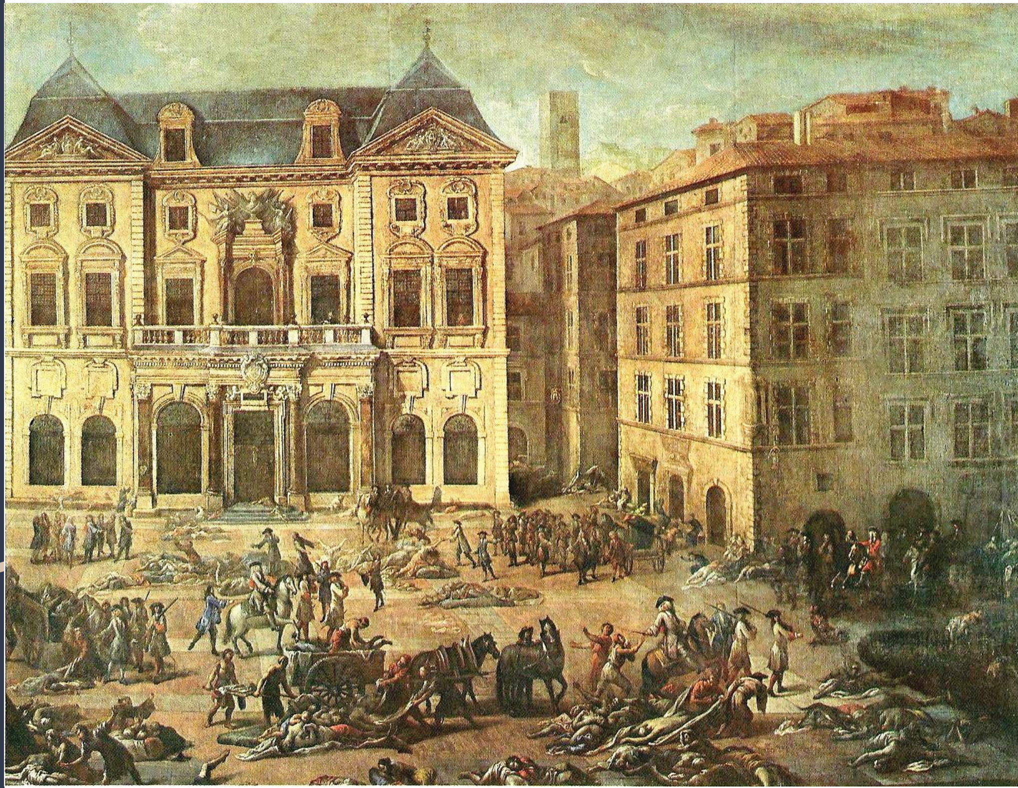
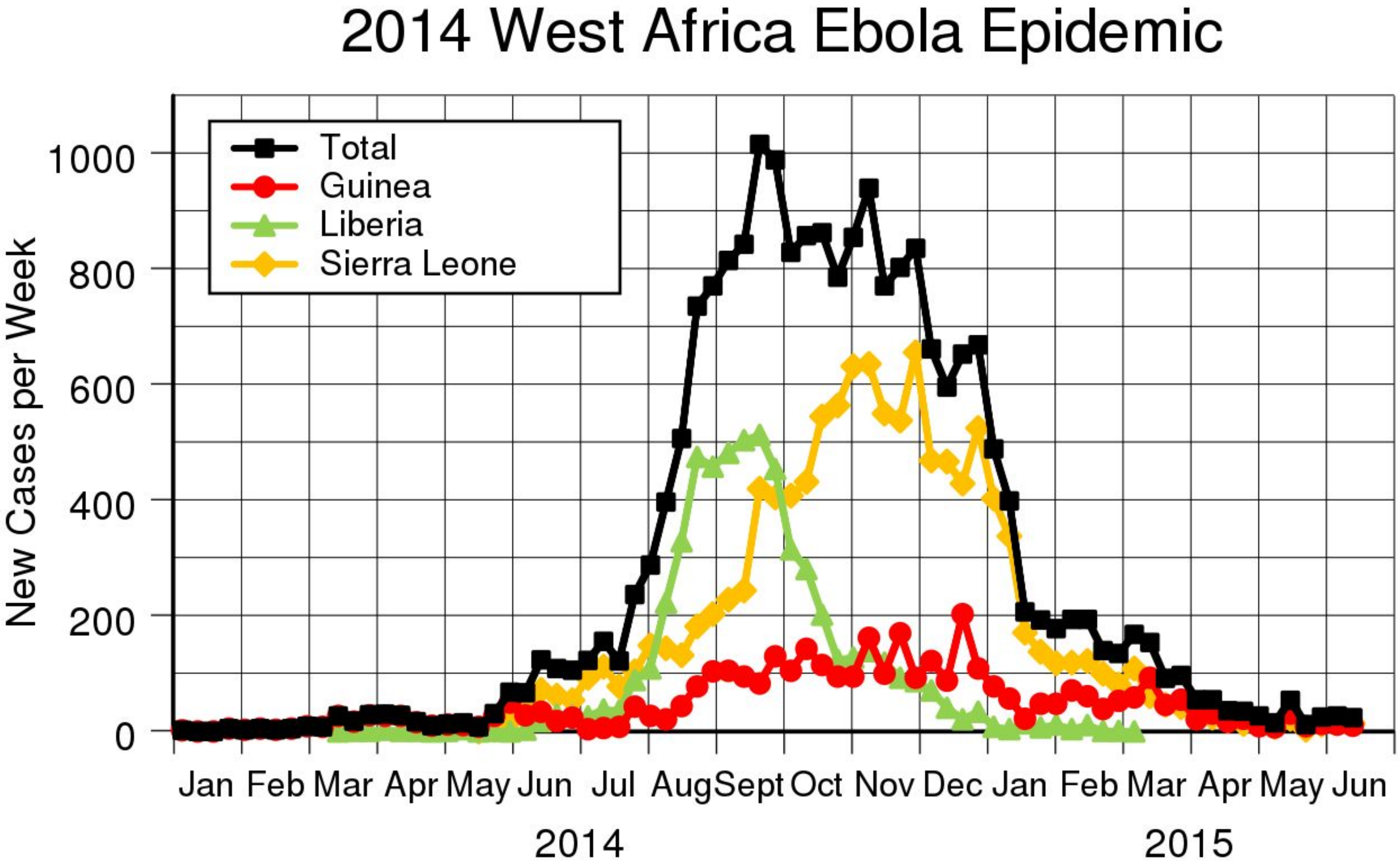
SIR Model on Networks

Luca Mihailescu
Coordinator: Sina Zendehroud

Let’s talk about infections



“L'hôtel de ville de Marseille pendant la peste de 1720”, Michel Serre (1658–1733)



2014, new cases of confirmed Ebola in West Africa each week. Data from WHO Situation reports.
Delphi234, CC0, via Wikimedia Commons.

Health workers carry the body of an Ebola victim for burial at a cemetery in Freetown on Dec. 17, 2014.
Source: IBTimes.com / Reuters / Baz Ratner

The SIR Model

Susceptible

Susceptible individuals can contract the disease by contact with infectious individuals and and transitions to the infectious compartment.

Infectious

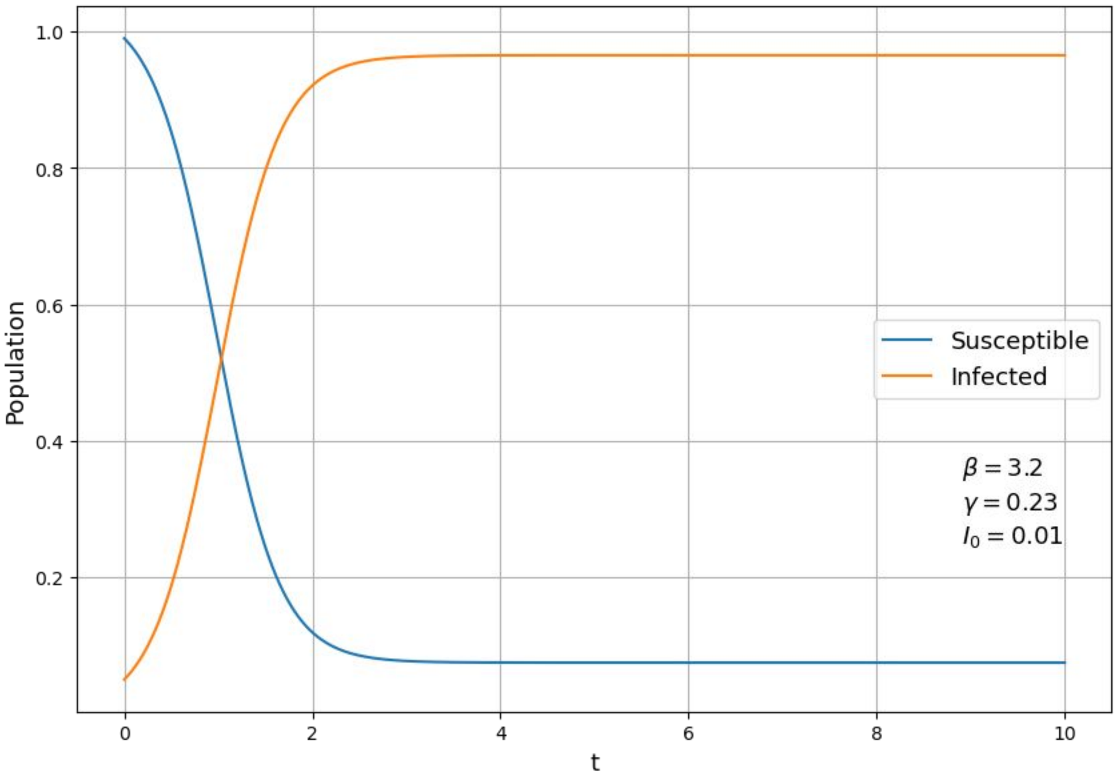
Individuals who have been infected and are capable of infecting susceptible individuals.

Removed

Individuals who have been infected and have either recovered from the disease or died.

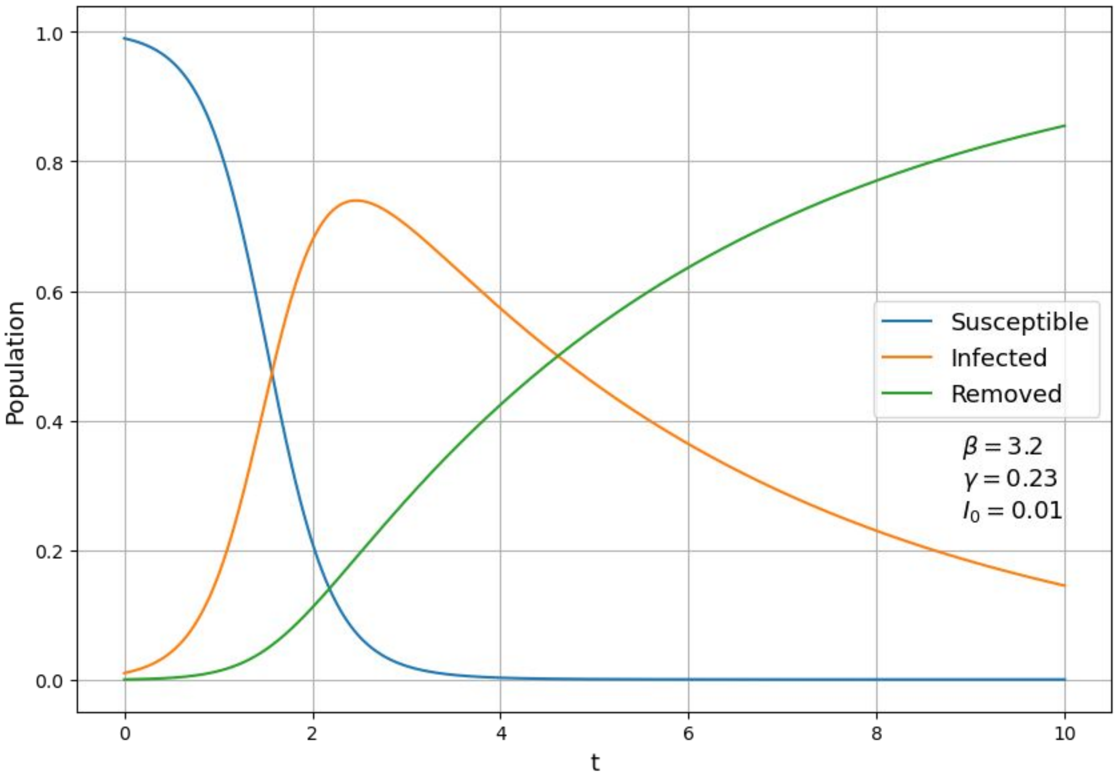
SI (Analytical)

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta I S}{N} + \gamma I \\ \dfrac{dI}{dt} = \dfrac{\beta I S}{N} - \gamma I \end{cases},$$



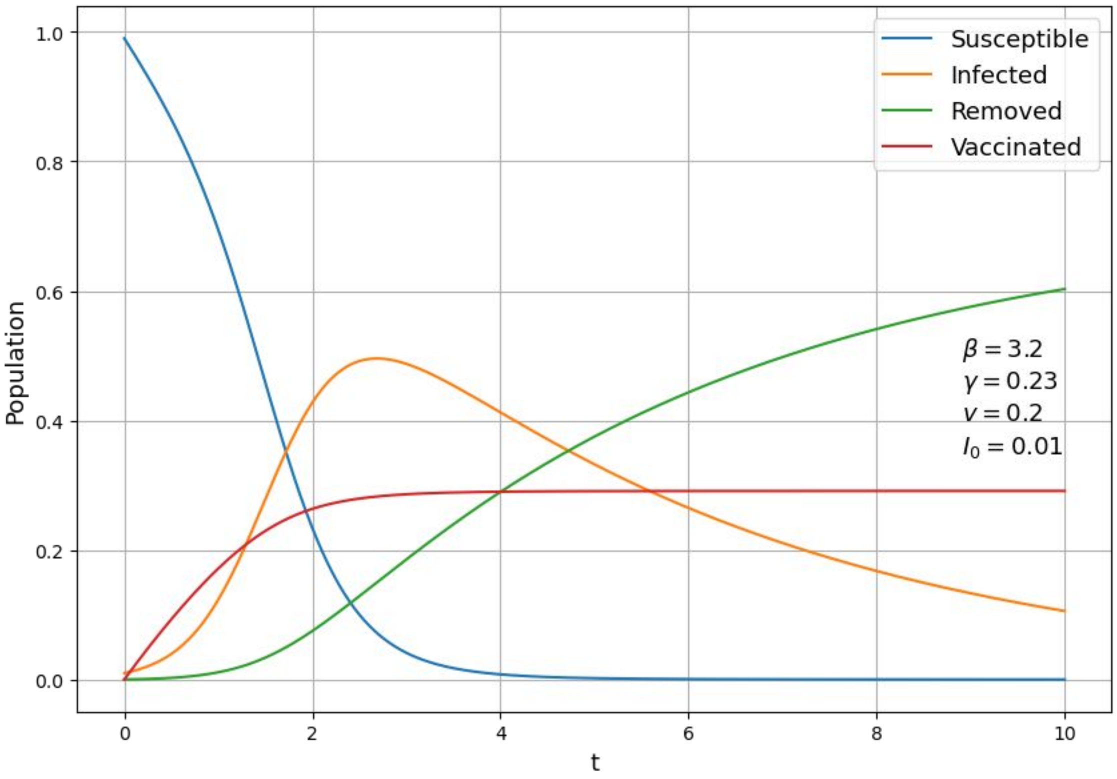
SIR (Analytical)

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta IS}{N} & , \\ \dfrac{dI}{dt} = \dfrac{\beta IS}{N} - \gamma I & , \\ \dfrac{dR}{dt} = \gamma I \end{cases}$$



SIRV (Analytical)

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta IS}{N} - vS & , \\ \frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I & , \\ \frac{dR}{dt} = \gamma I & , \\ \frac{dV}{dt} = vS \end{cases}$$

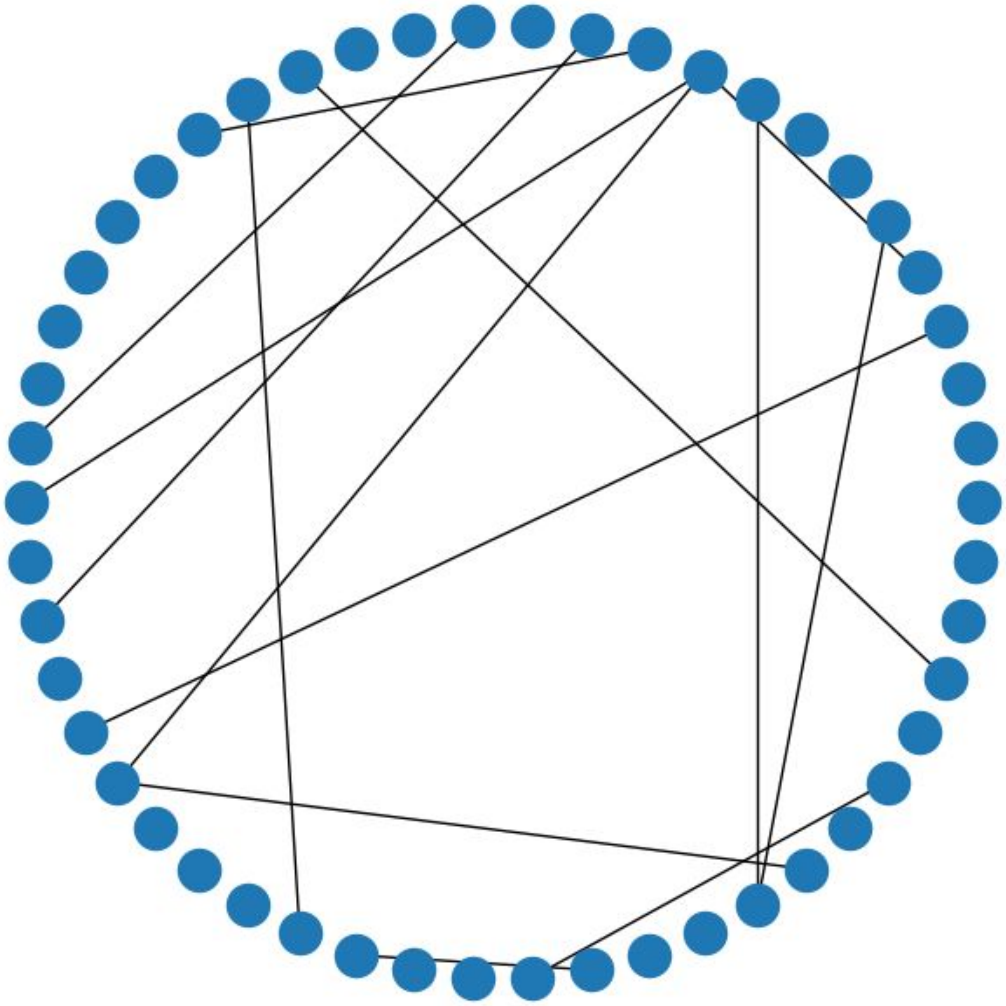


A little about (social) networks

Erdős–Rényi model

- ***G(n,p)*** random network model
- For a given number ***n*** of nodes, each of the possible edges is created with a probability ***p***.
- Here:

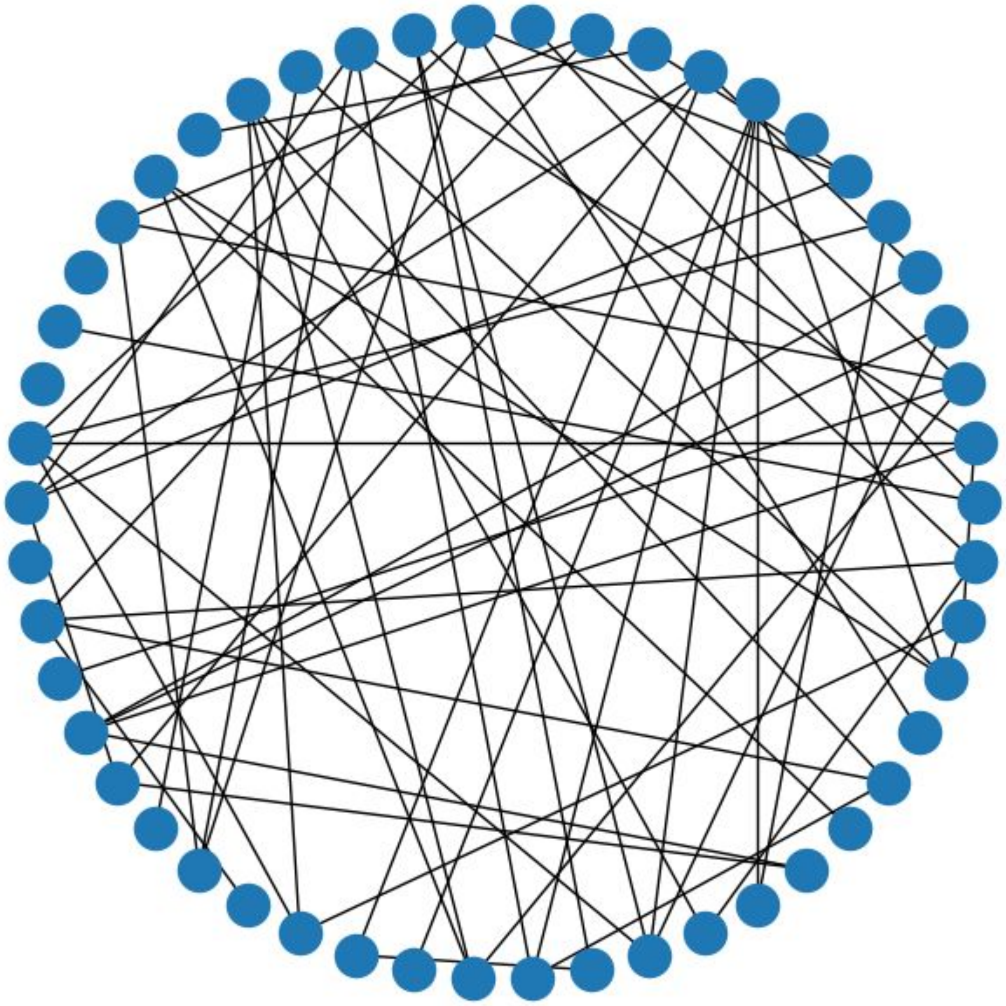
$$G(n = 50, p = 0.01)$$



Random Networks

- Known as the Erdős–Rényi model
- For a given number ***n*** of nodes, each of the possible edges is created with a probability ***p***.
- Here:

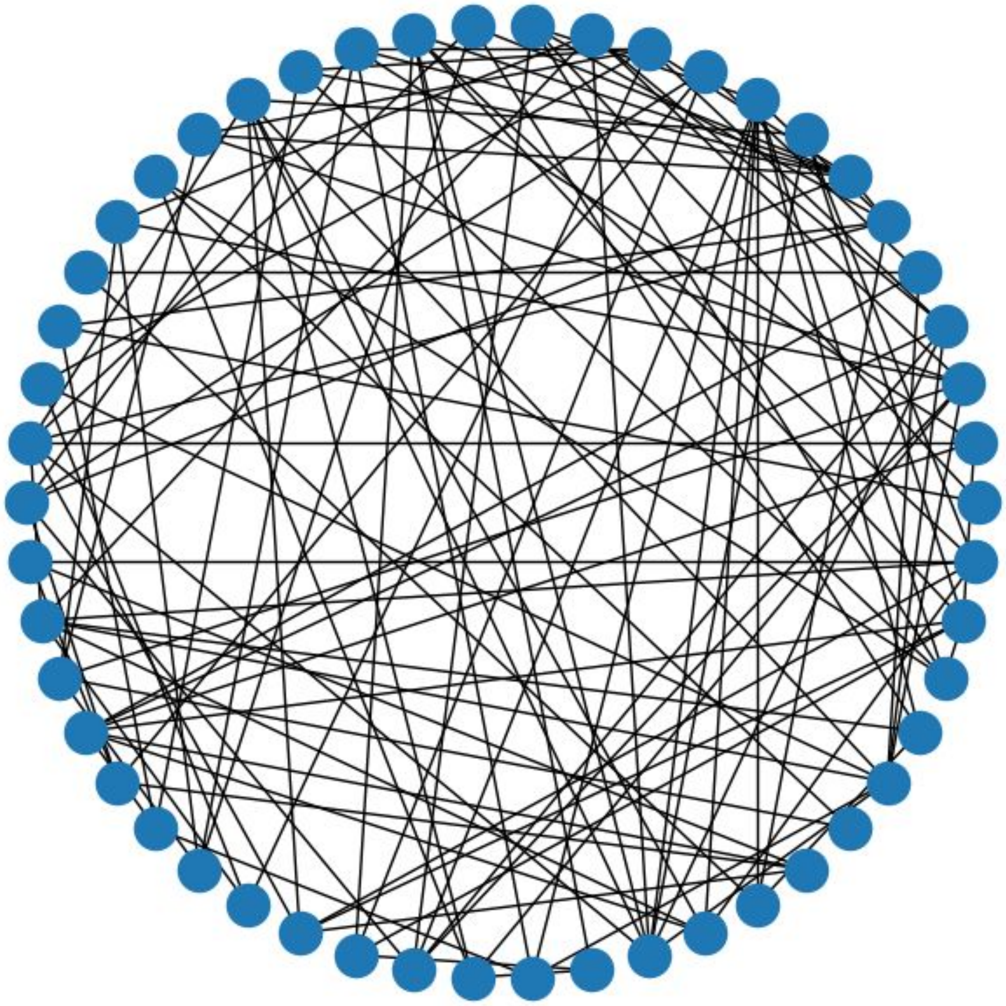
$$G(n = 50, p = 0.05)$$

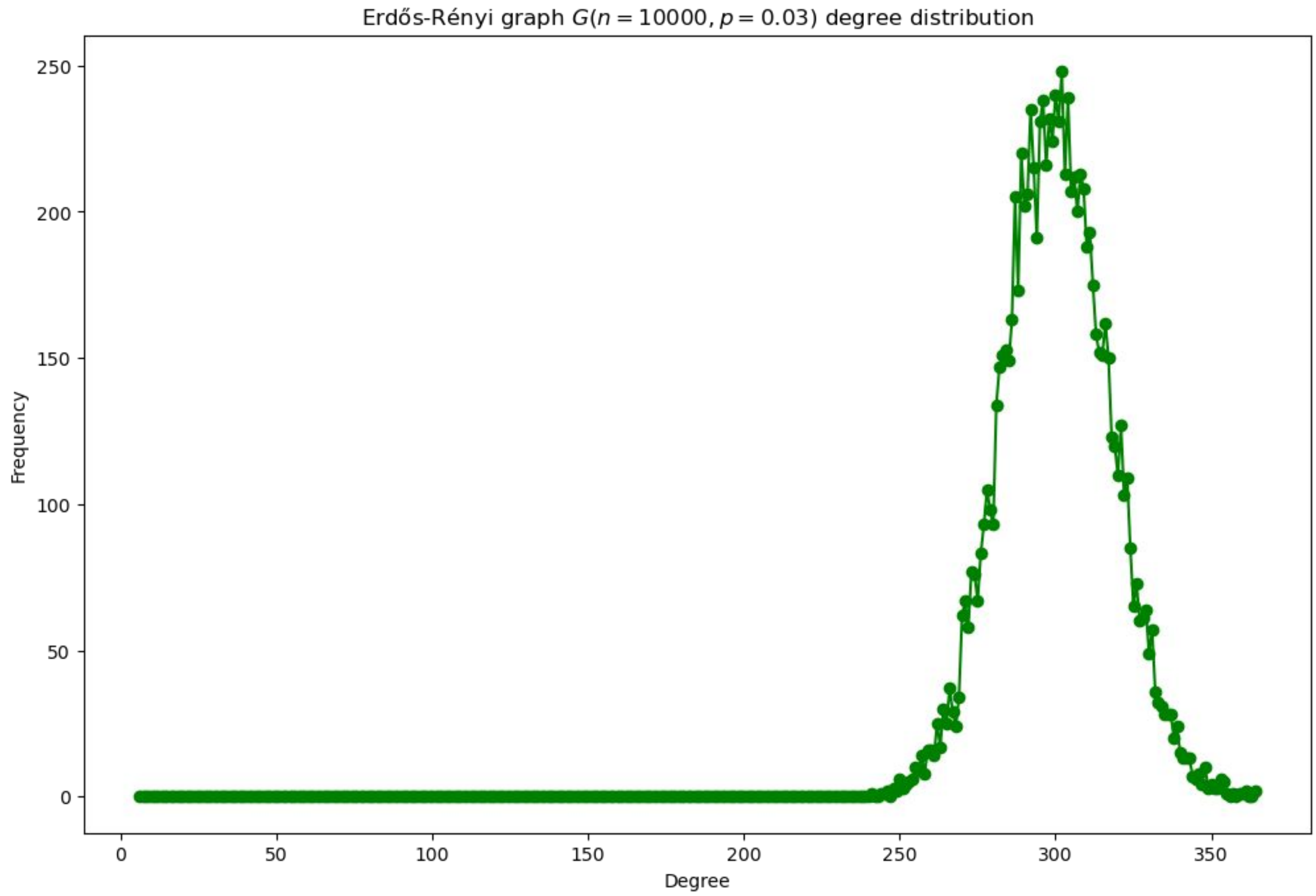


Random Networks

- Known as the Erdős–Rényi model
- For a given number ***n*** of nodes, each of the possible edges is created with a probability ***p***.
- Here:

$$G(n = 50, p = 0.1)$$

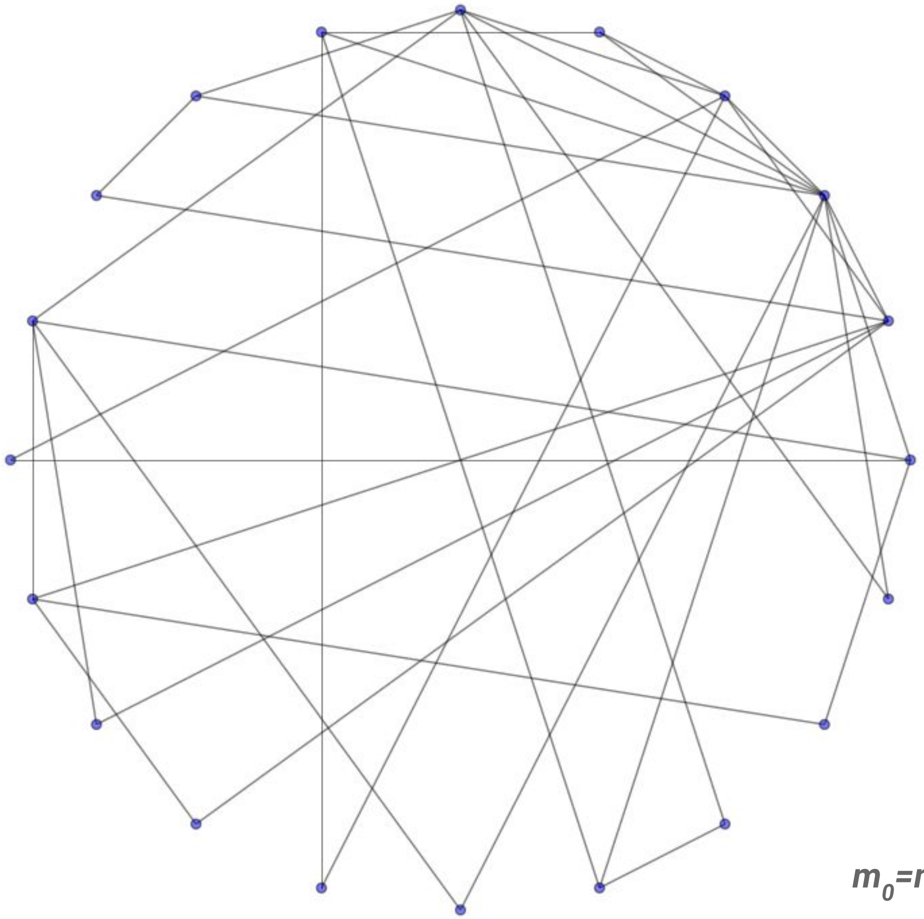




Erdős-Rényi graph $G(n = 10000, p = 0.03)$ degree distribution
Frequency
Degree
0
50
100
150
200
250
300
350

Barabási–Albert Model

1. The network begins with an initial connected network of m_0 nodes.
2. New nodes are added to the network one at a time.
3. Each new node is connected to $m \leq m_0$ existing nodes with a probability that is proportional to the number of links that the existing nodes already have.



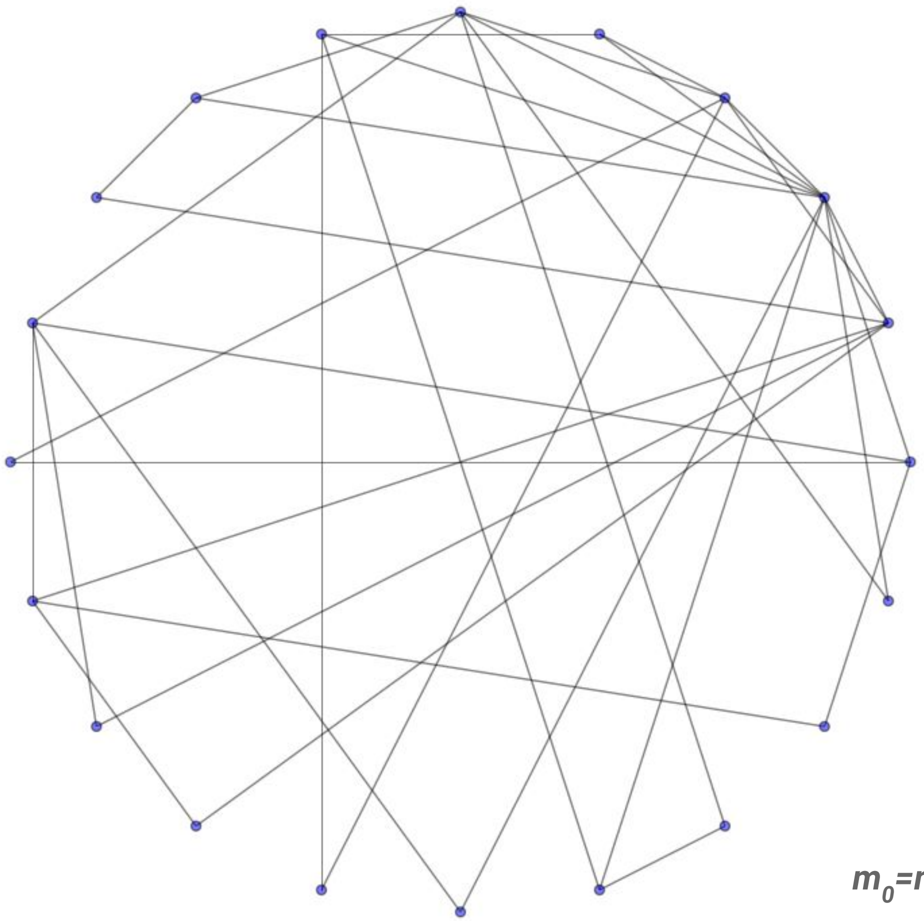
$m_0 = m = 2$

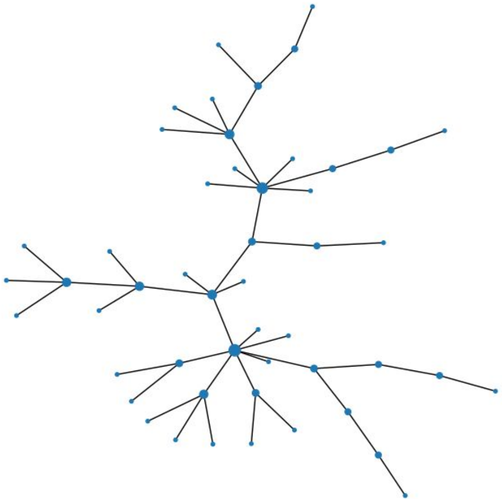
Barabási–Albert Model

Formally, the probability p_i that the new node will be connected to node i is:

$$p_i = \frac{k_i}{\Sigma_j k_j}$$

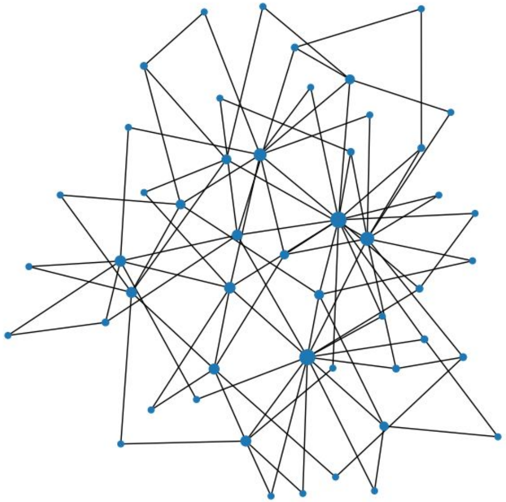
where k_i is the degree of node **i** and the sum is made over all pre-existing nodes **j**





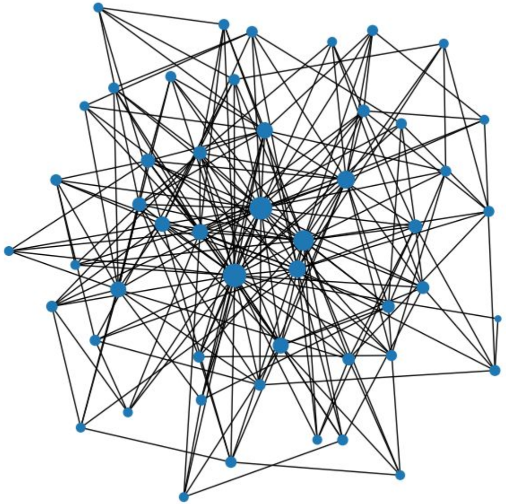
n=50

m_0=m=1



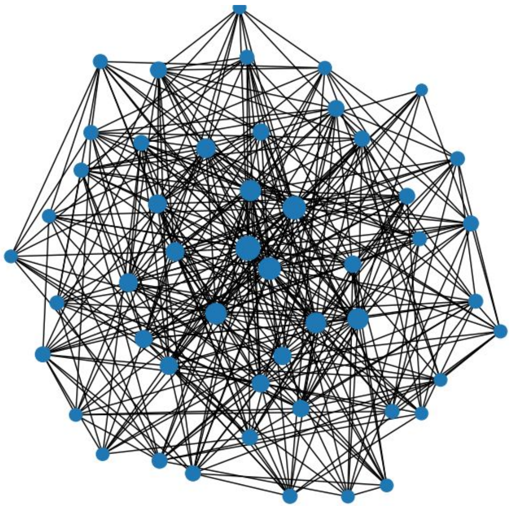
n=50

m_0=m=2



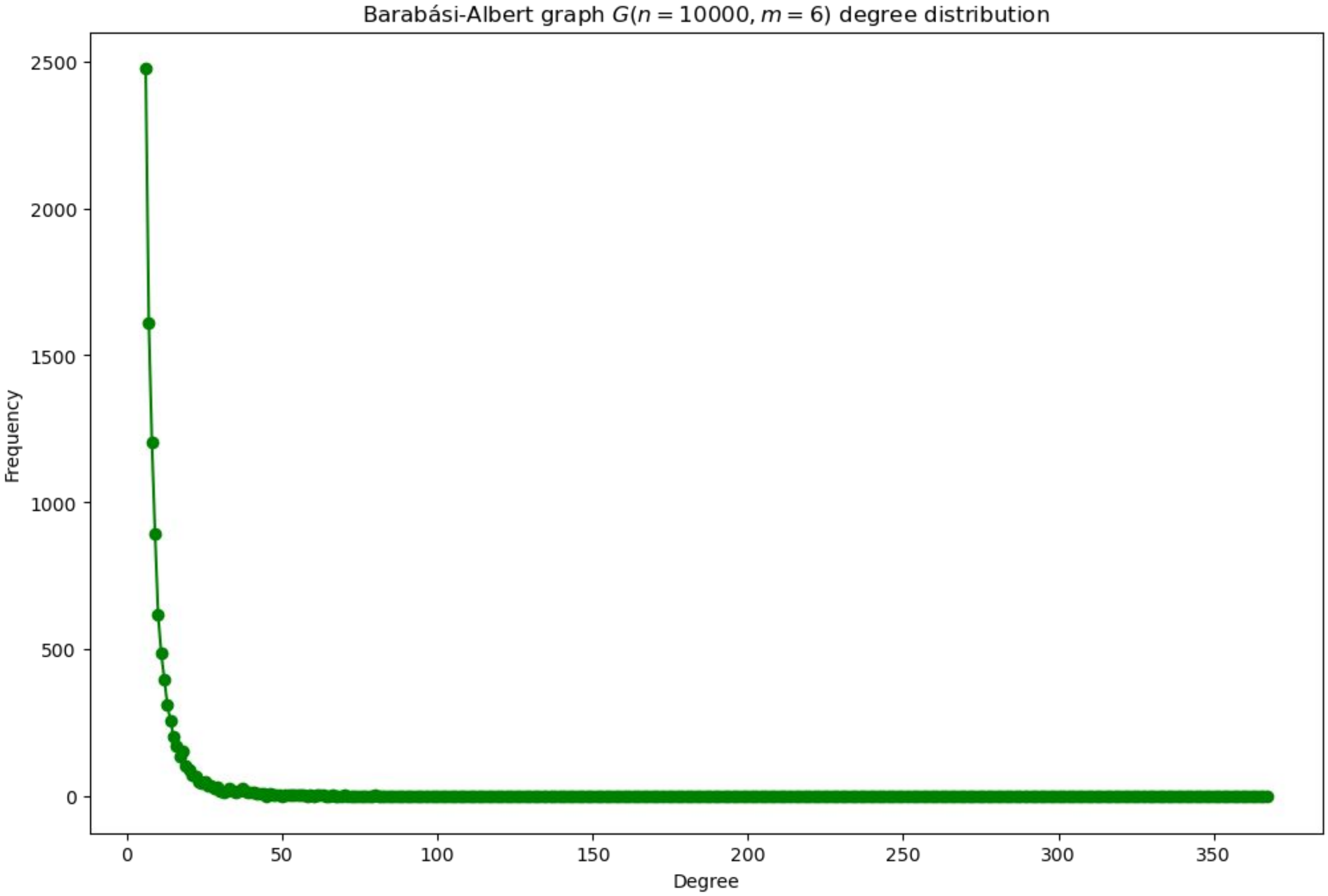
n=50

m_0=m=5



n=50

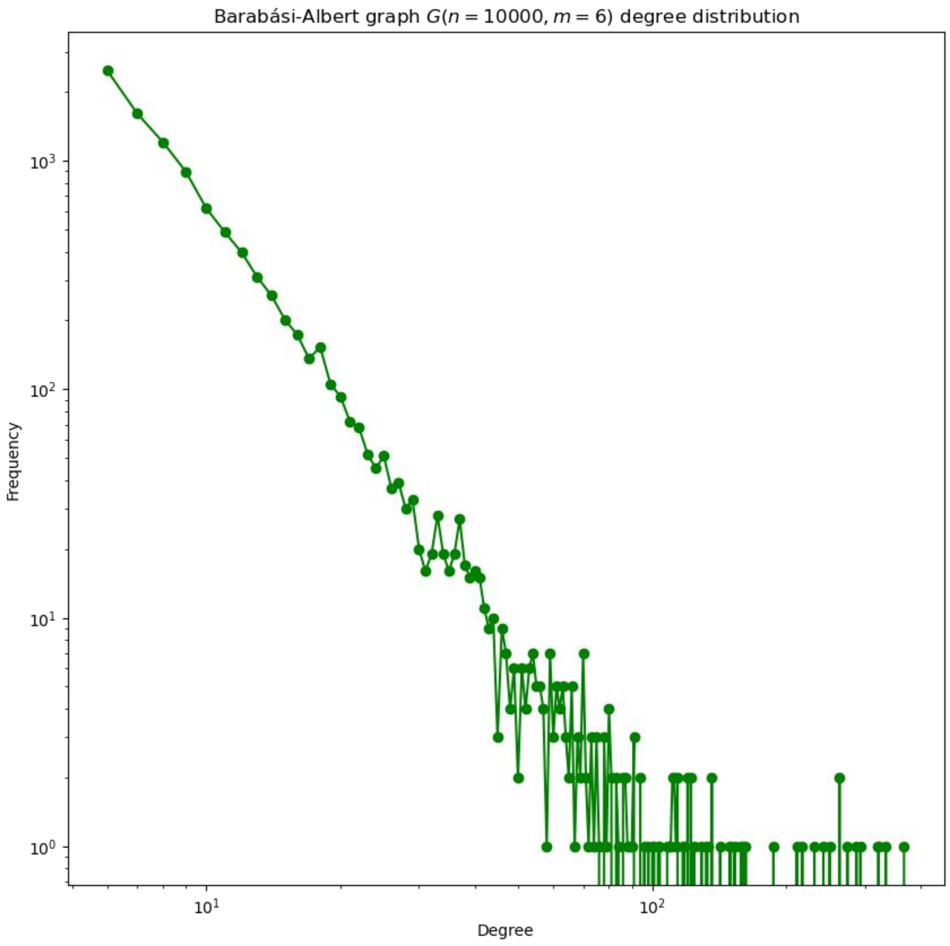
m_0=m=10


Barabási-Albert graph $G(n = 10000, m = 6)$ degree distribution
Frequency
2500
2000
1500
1000
500
0
0
50
100
150
200
250
300
350
Degree

Barabási–Albert Is Scale-free

Scale-free networks have degree distributions following a power law (at least asymptotically):

$$P(k) \sim k^{-\gamma}$$



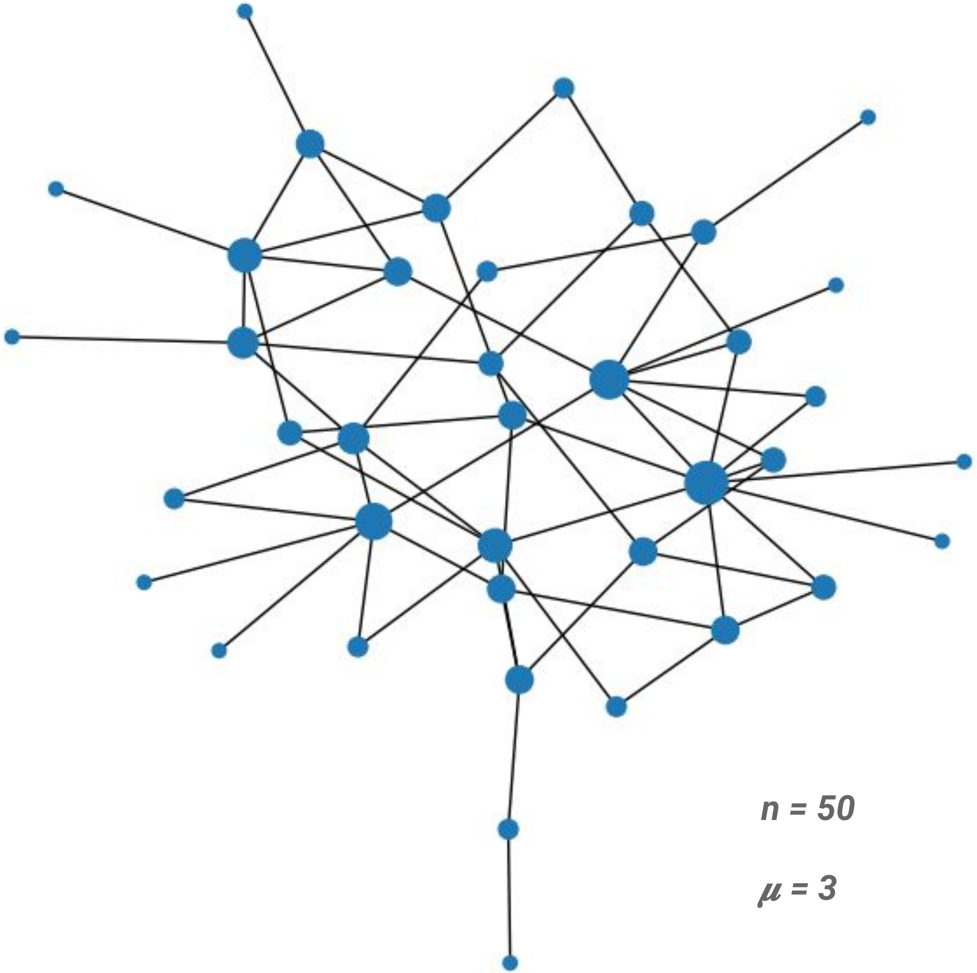
Poisson Distribution Graphs

1. Generate sequence of size ***n*** of Poisson distributed degrees, with expected degree μ:

$$W = (w_0, w_1, \ldots, w_{n-1})$$

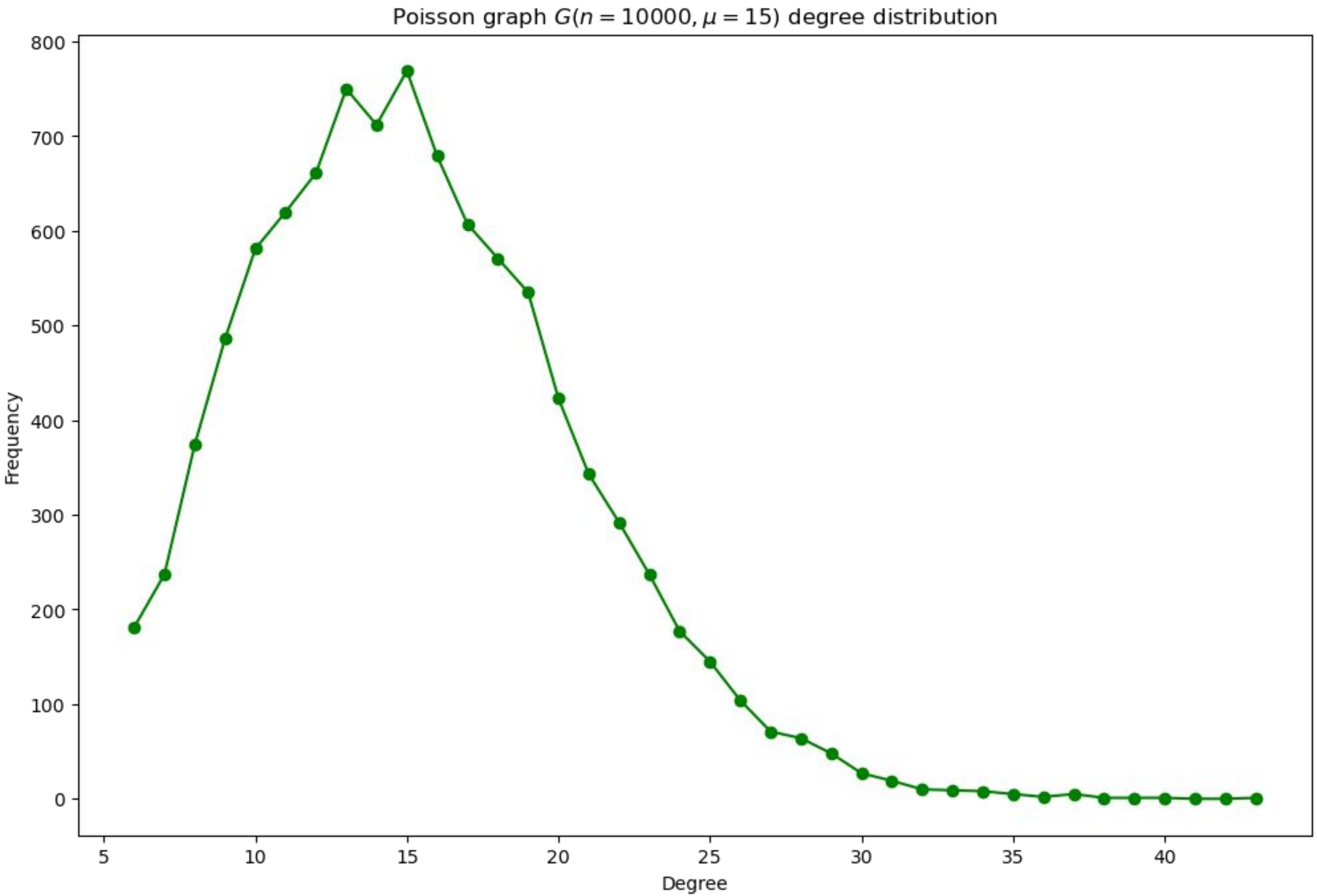
2. Assign an edge between node ***u*** and node ***v*** with probability:

$$p_{uv} = \frac{w_u w_v}{\Sigma_k w_k}$$



n = 50

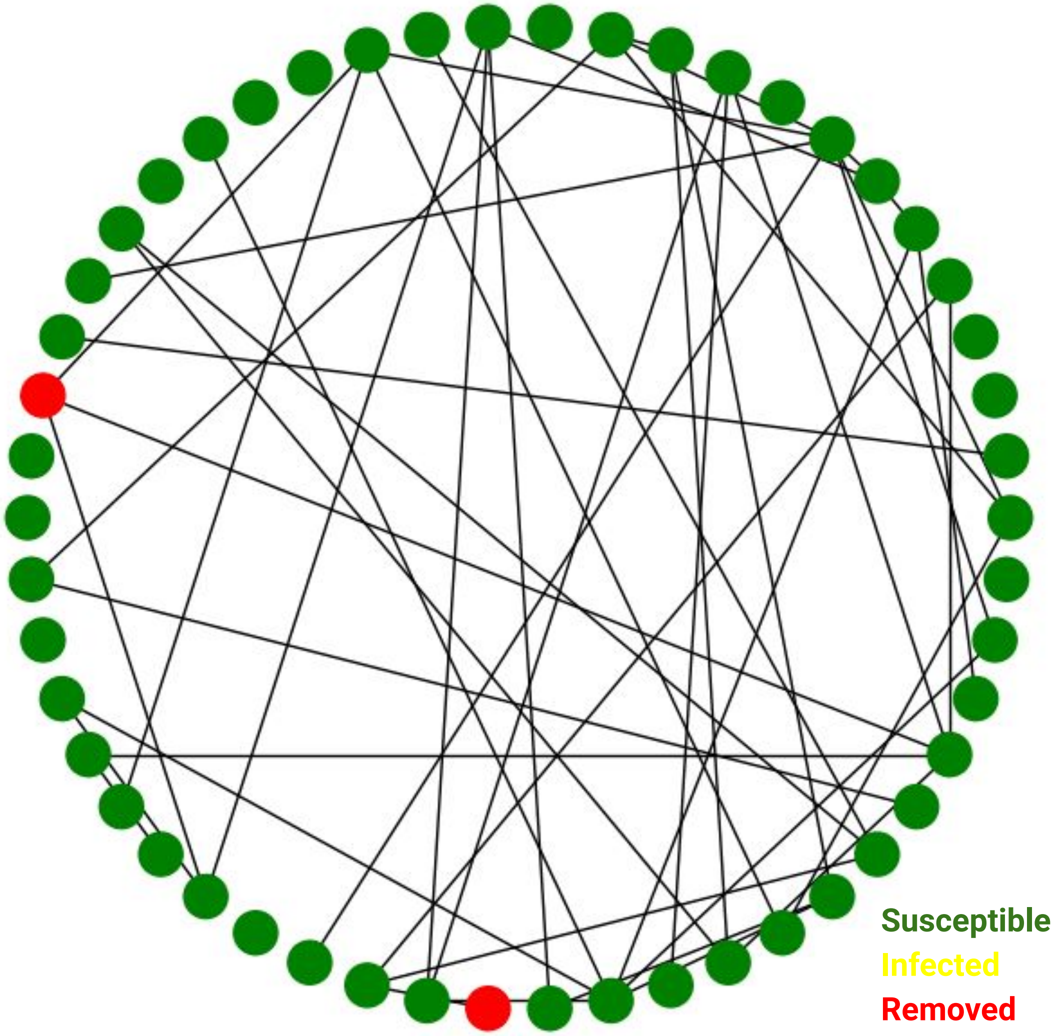
μ *= 3*

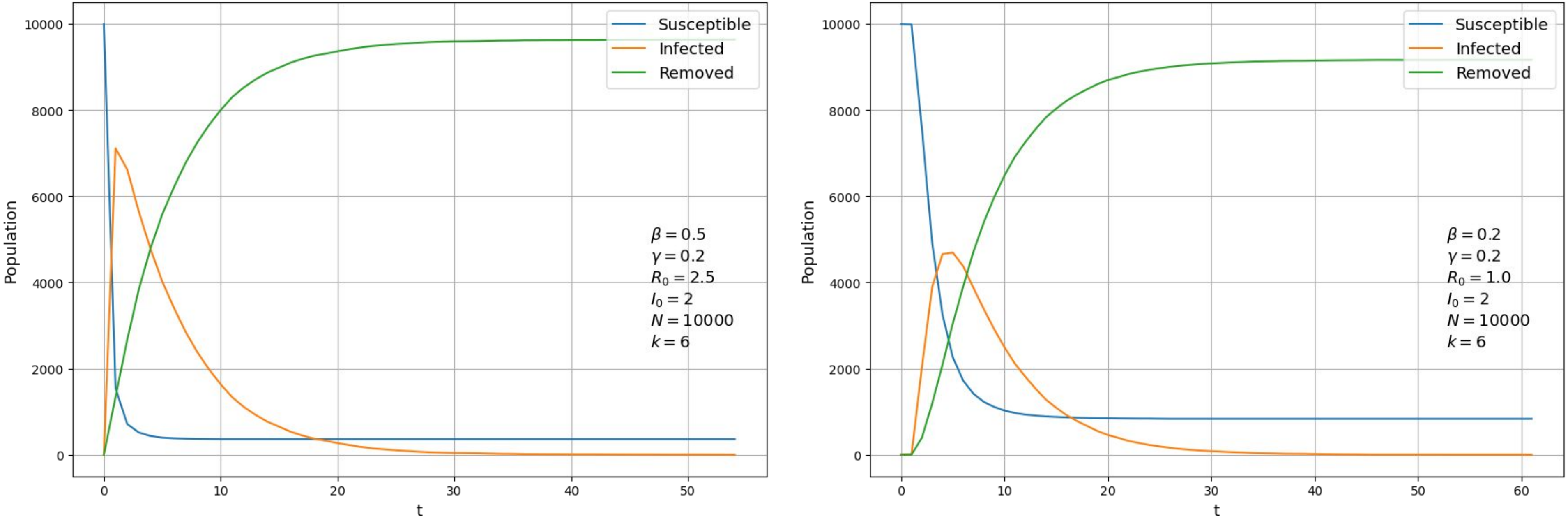

Poisson graph $G(n = 10000, \mu = 15)$ degree distribution
Frequency
Degree
0
100
200
300
400
500
600
700
800
5
10
15
20
25
30
35
40

Let’s add infections to the mix

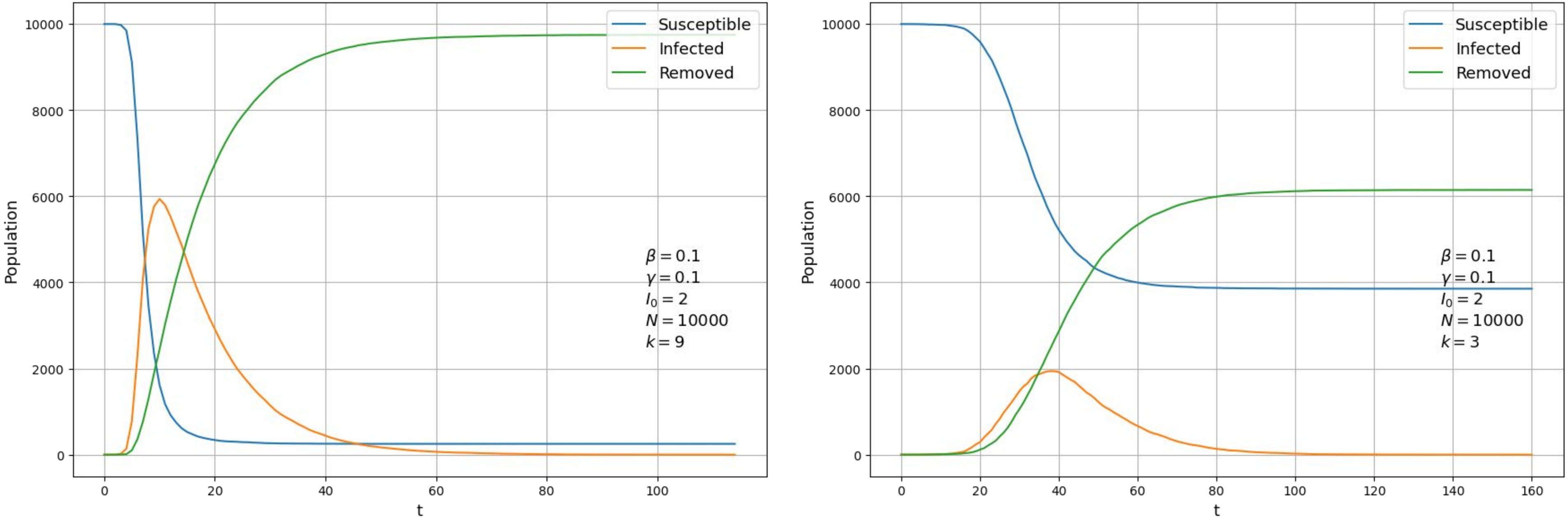
Simulation of SIR on Networks

1. A random network of size ***N*** and average degree ***k*** is generated.
2. A number I_0 of nodes are randomly selected as initial infected.
3. Infected nodes will infect their neighbors with a probability β.
4. Infected nodes will be removed with a probability γ.
5. Steps 3-4 are repeated until there are no infected nodes left.

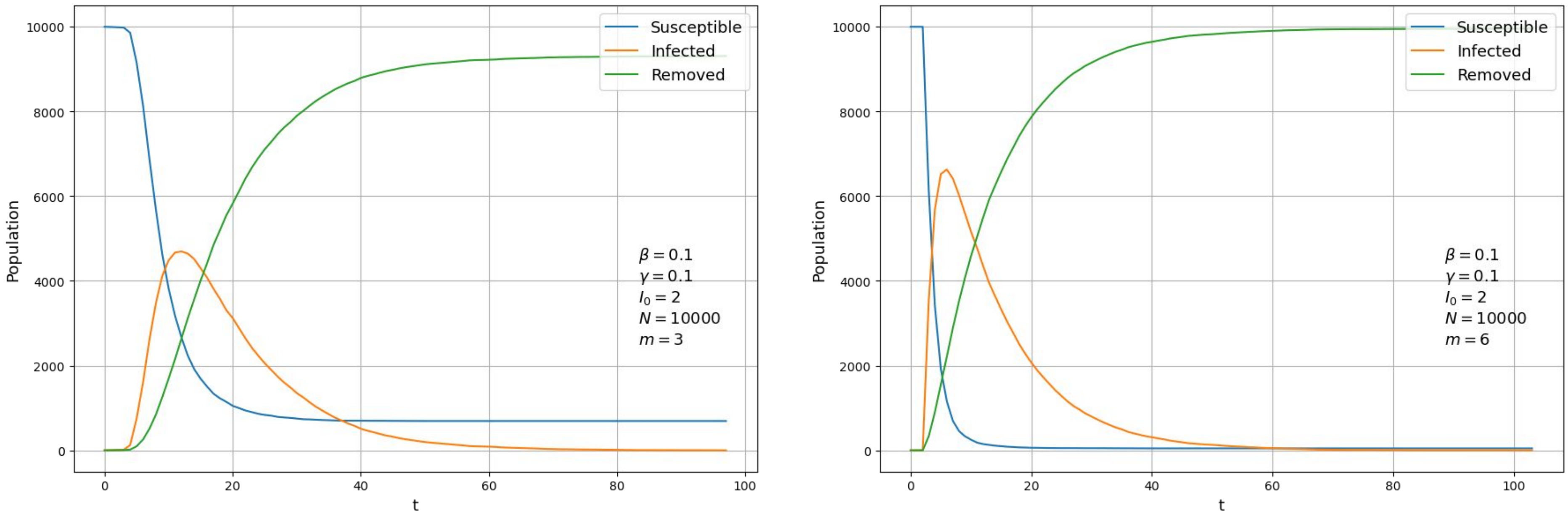




Disease parameter comparison (Poisson graph)



Network parameter comparison (Poisson graph)



Network parameter comparison (Barabási–Albert graph)

Some thoughts on Surrogate Models

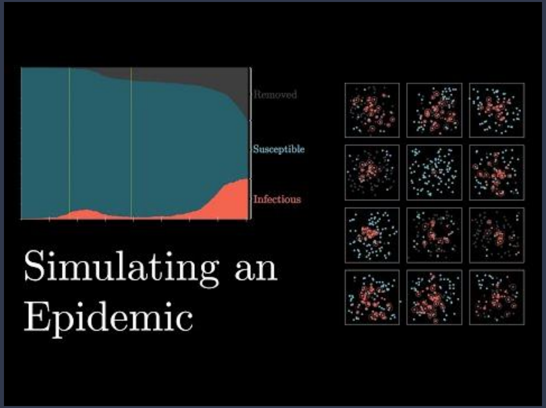
- Surrogate models are simpler, faster models that achieve approximately the same result
- The SIR system of differential equations is a surrogate model
- The dynamics of surrogate models might of more interest to field specialists

$$\begin{cases} \dfrac{dS}{dt} = -\dfrac{\beta I S}{N}, \\ \dfrac{dI}{dt} = \dfrac{\beta I S}{N} - \gamma I, \\ \dfrac{dR}{dt} = \gamma I \end{cases}$$

Conclusions

- ➔ We don’t like epidemics
- ➔ Compartmental models in epidemiology: SI, SIR, SIRV, etc.
- ➔ SIR simulations are affected by network topology

Further ~~reading~~ watching



Simulating an epidemic

3Blue1Brown