

Modeling infectious diseases

Networks

Yasaman Asgari

References

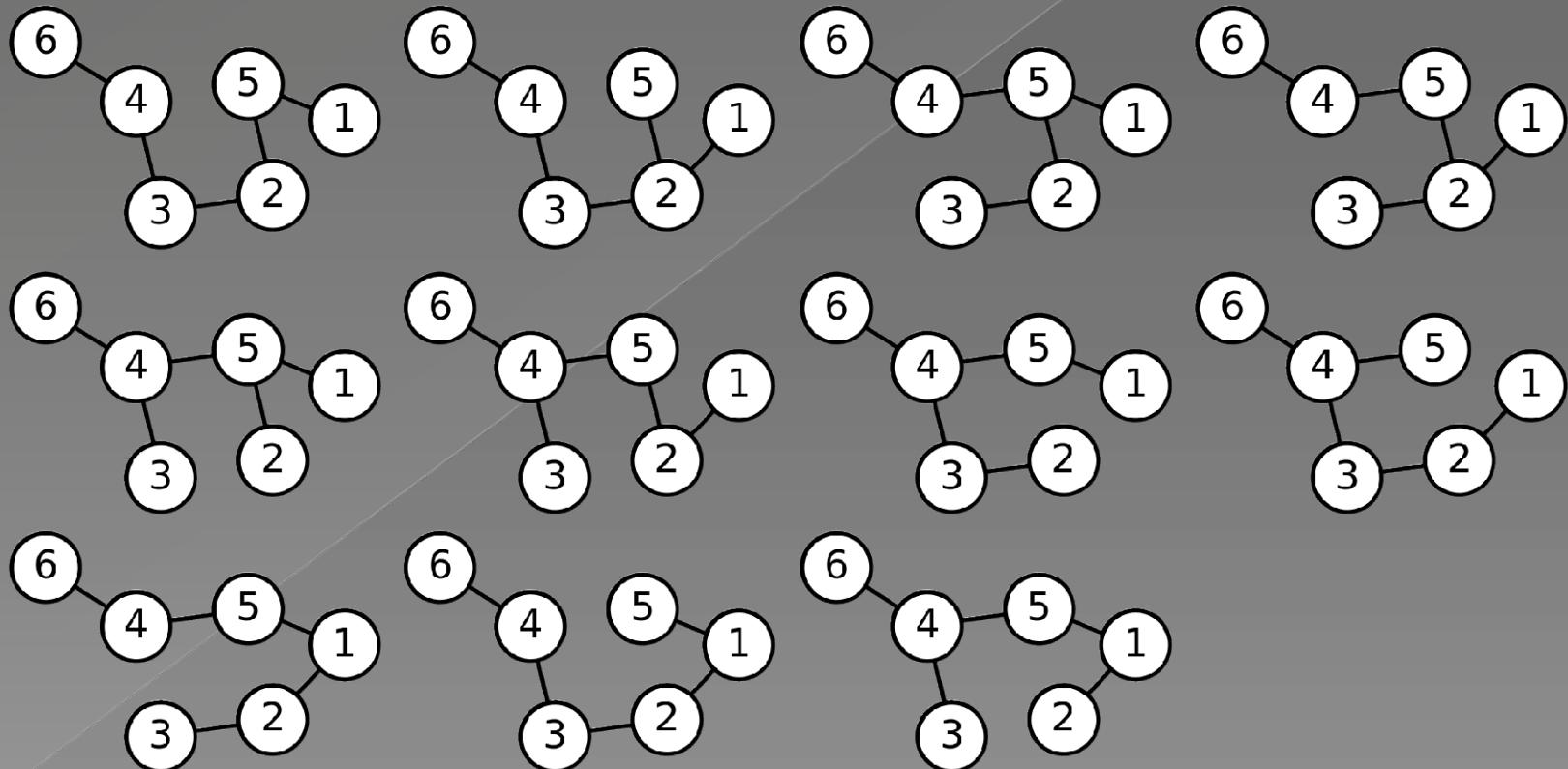
- **Networks , crowds , markets** (David Easley, Jon Kleinberg) :Chapter 21
- **Network Science**(Albert Barabasi): Chapter 1,2 ,3, 10
- **Modeling infectious diseases**(Matt keeling , Pejman Rohani):Chapter7
- **Epidemic spreading in population networks** (Barrat) : Chapter 9

First Part

Graph theory

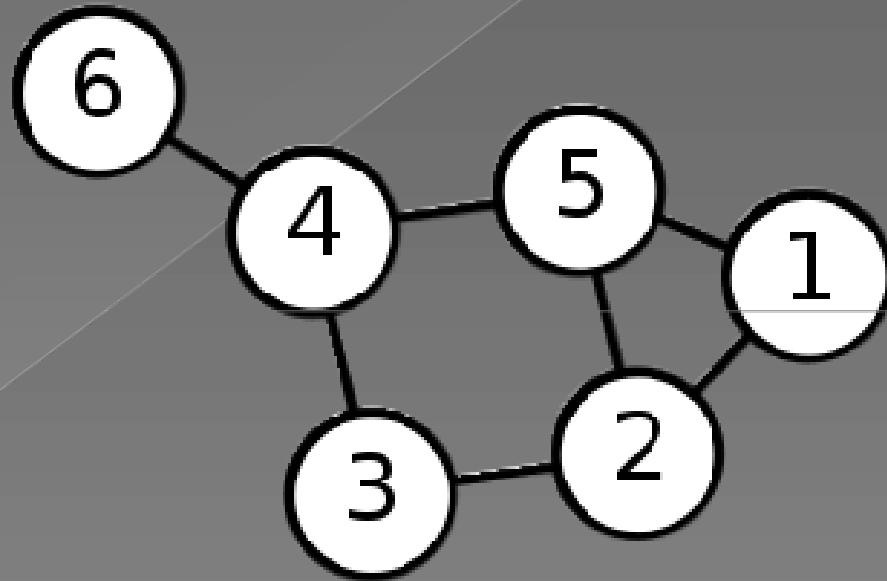
Network

Node , link , degree



Network

Node , link , degree

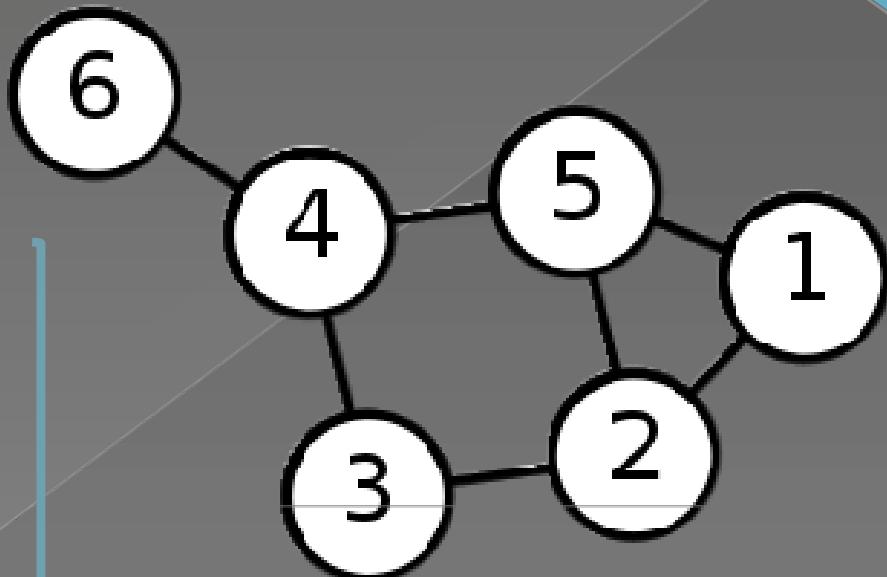


$$V = \{1, 2, 3, 4, 5, 6\}$$

$$E = \{\{1, 2\}, \{1, 5\}, \{2, 5\}, \{2, 3\}, \{3, 4\}, \{4, 5\}, \{6, 4\}\}$$

Adjacency Matrix

0	1	0	0	0	1
1	0	1	0	0	1
0	1	0	1	0	0
0	0	1	0	1	1
1	1	0	1	0	0
0	0	0	1	0	0



Concepts

Overall links

$$L = \frac{1}{2} \sum_{i=1}^N k_i$$

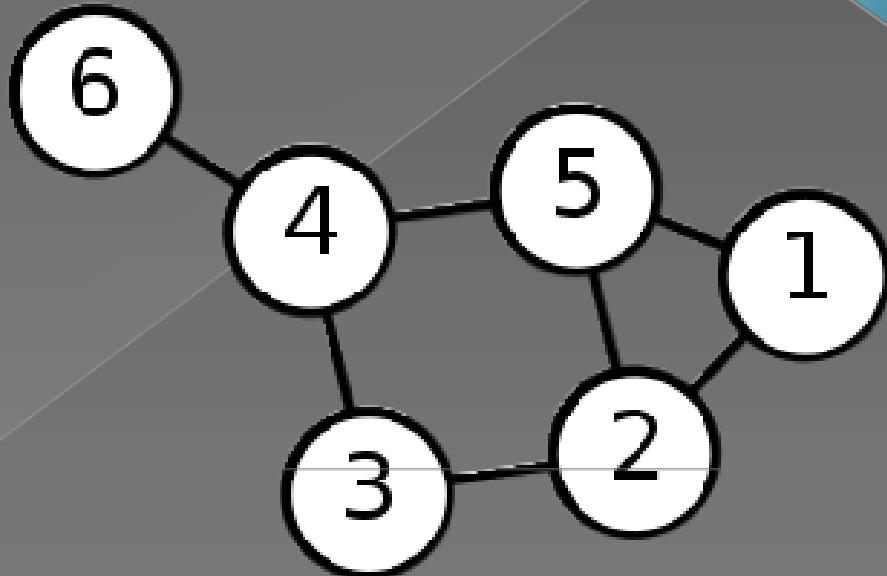
Mean degree

$$\bar{k} = \frac{2L}{N}$$

More On the network

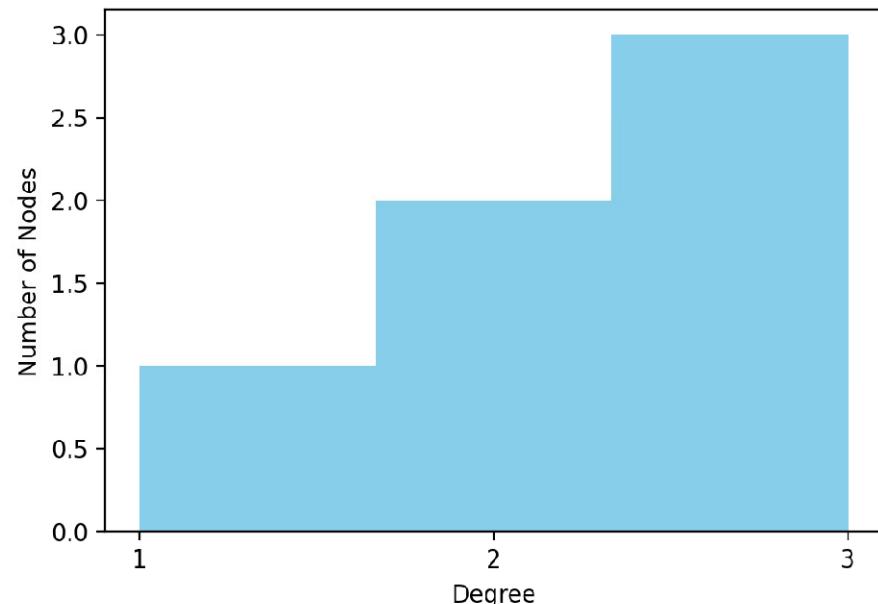
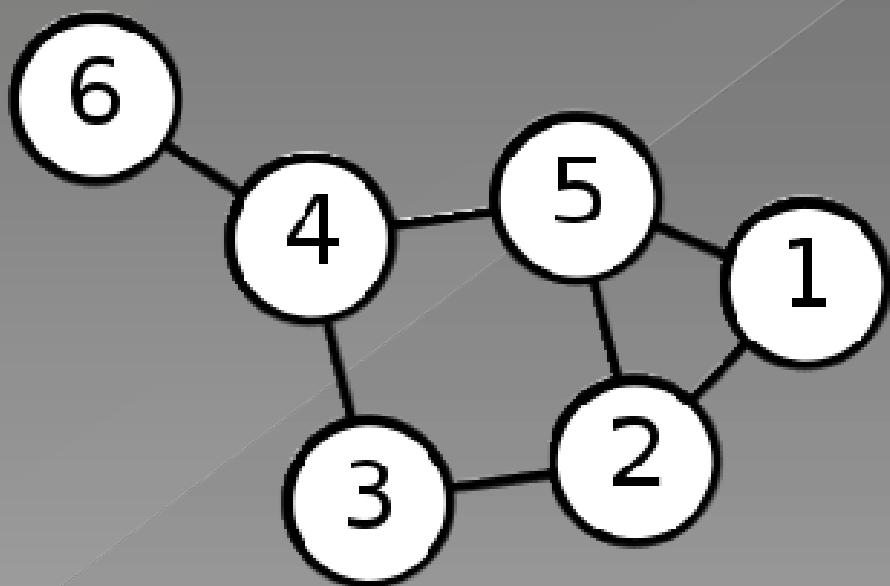
$$\bar{K} = \frac{2 \times 7}{6} = \frac{7}{3}$$

$$\bar{L} = \frac{2 \times 2 + 3 \times 3 + 1}{2} = 7$$



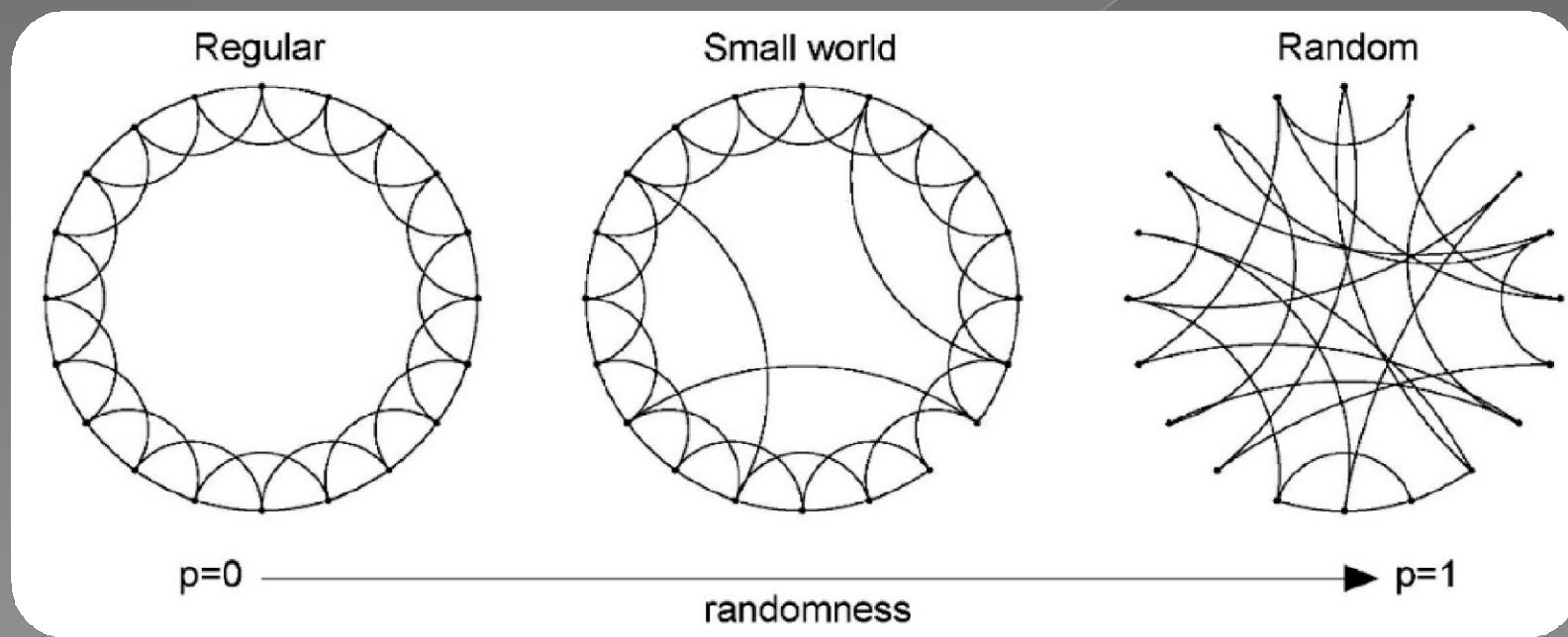
Degree distribution

$$p_k = \frac{N_k}{N}$$



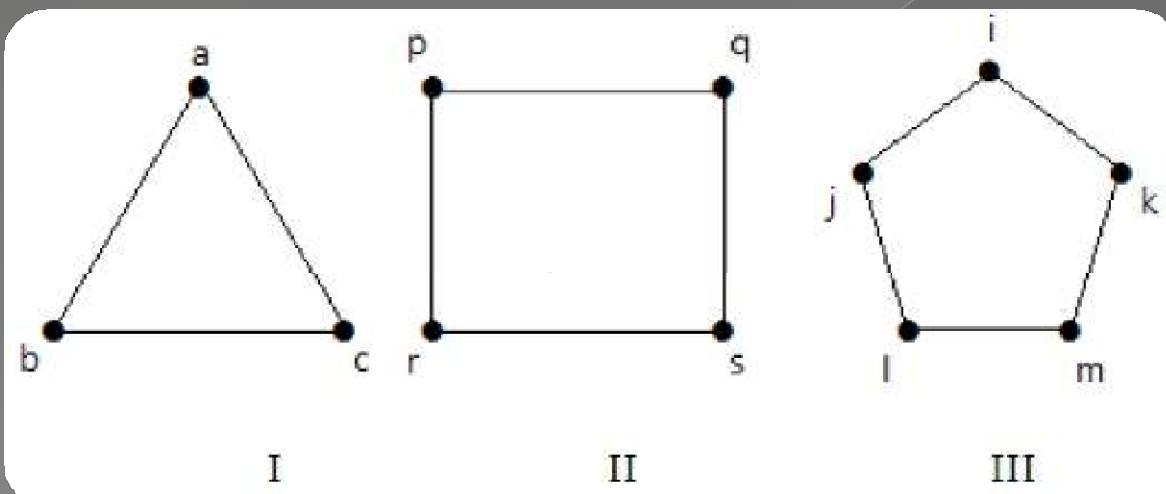
Types of network

We have different types of network!



Regular Networks

- Cycles



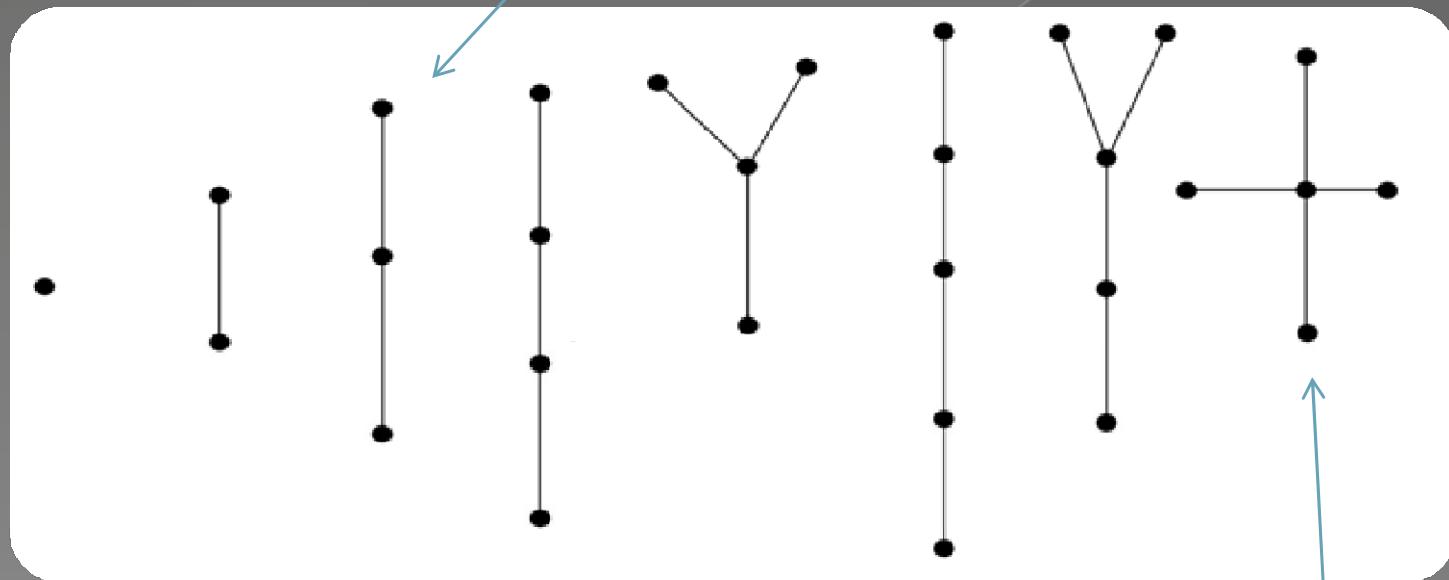
$$L=N$$

$$\bar{K}=N-1$$

Regular Networks

- Cycles
- Trees

Paths



$$L=N-1$$

$$\bar{K}=2(1-1/N)$$

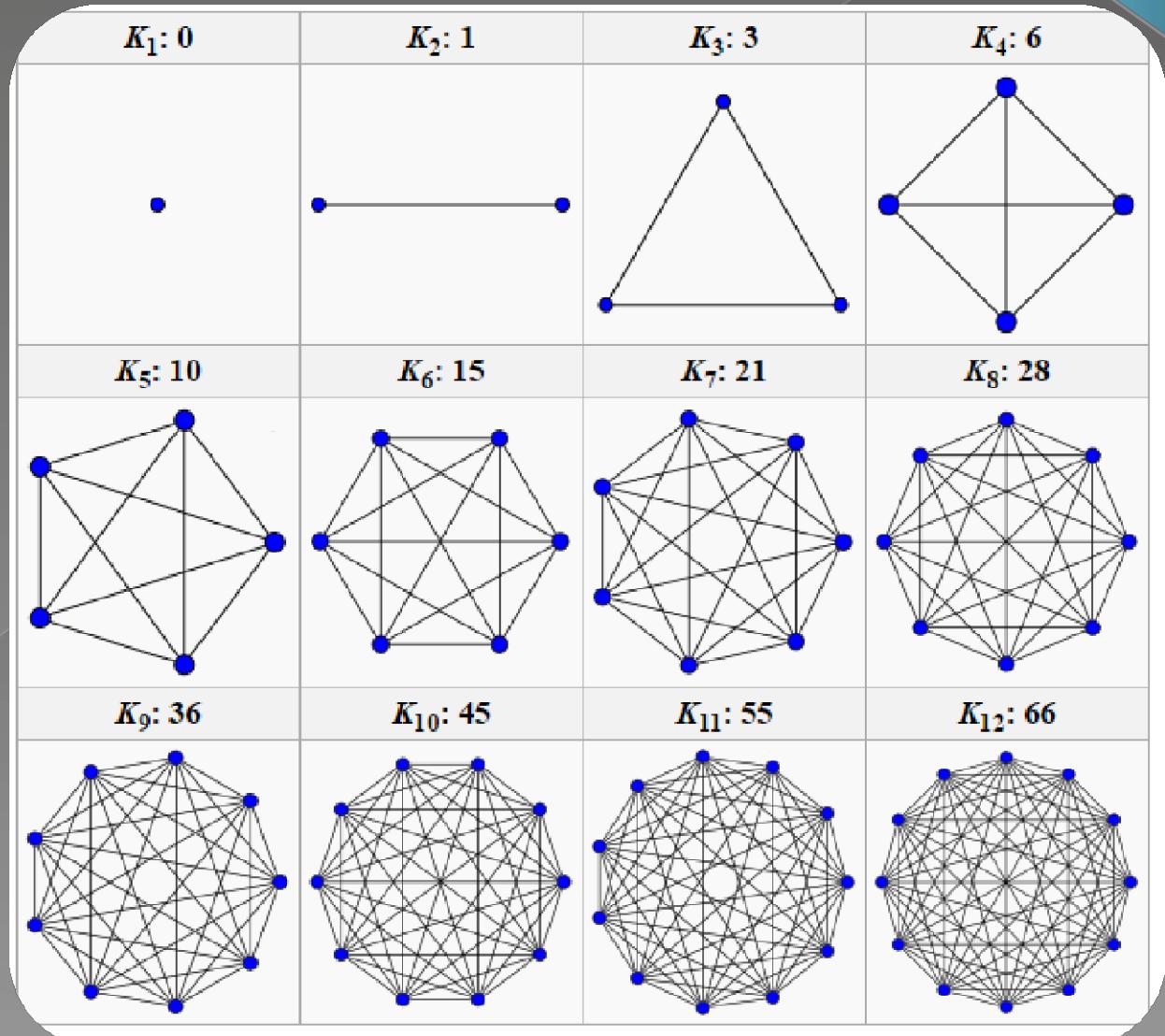
Stars

Regular Networks

- Cycles
- Trees
- Complete

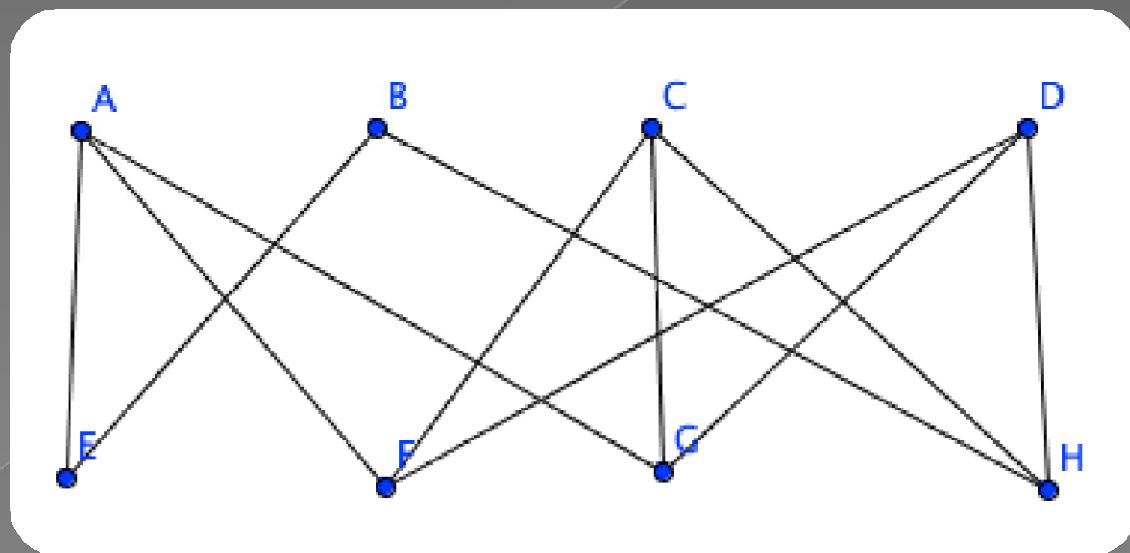
$$L = N(N-1)/2$$

$$\bar{K} = N-1$$



Regular Networks

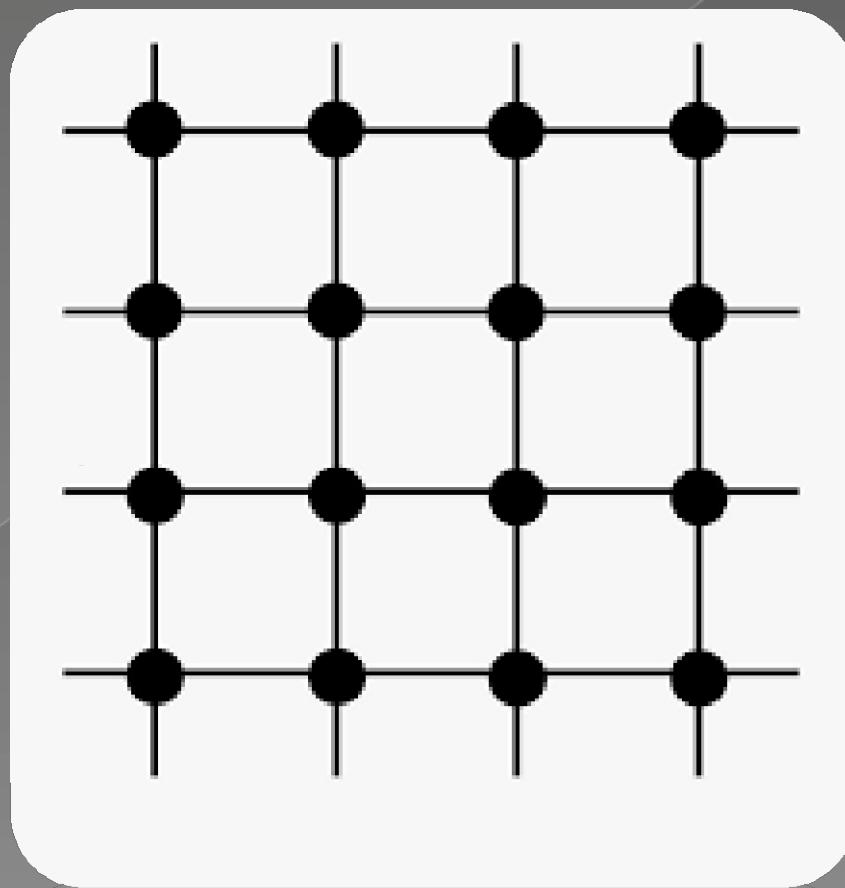
- Cycles
- Trees
- Complete
- bipartite



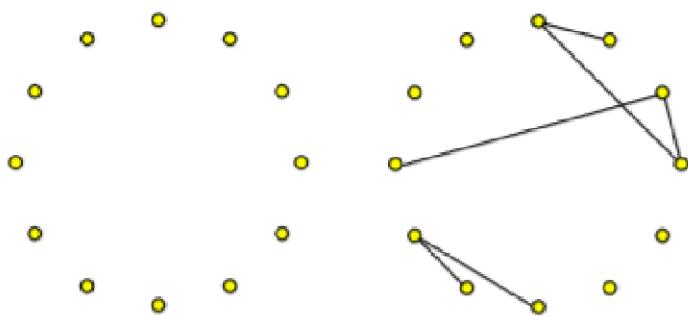
Regular Networks

- Cycles
- Trees
- Complete
- Bipartite
- Lattice

$\overline{K}=4$ or 8

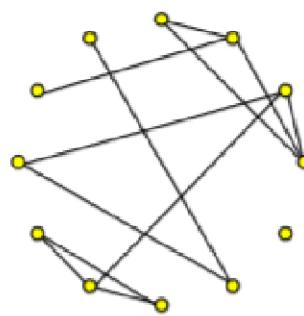


Erdos Renyi

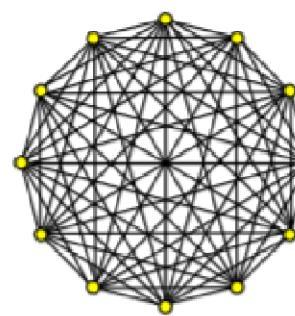


$p = 0.0 ; k = 0$

$p = 0.045 ; k = 0.5$



$p = 0.09 ; k = 1$



$p = 1.0 ; k \approx \frac{1}{2}N^2$

Size of largest component

1

5

11

12

Diameter of largest component

0

4

7

1

Average path length between nodes

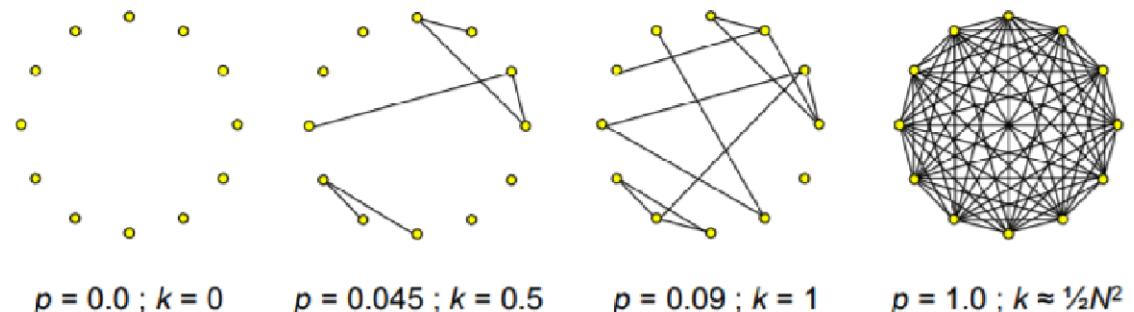
0.0

2.0

4.2

1.0

Erdos Renyi



Size of largest component

1

5

11

12

Diameter of largest component

0

4

7

1

Average path length between nodes

0.0

2.0

4.2

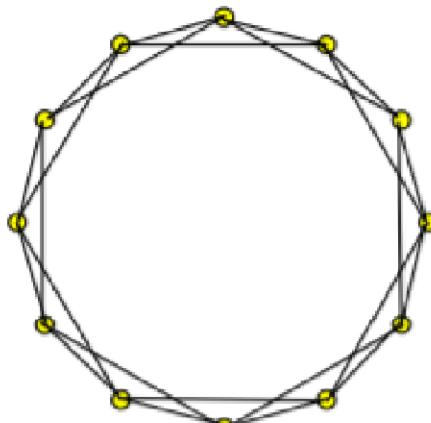
1.0

$$P(\deg(v) = k) = \binom{n-1}{k} p^k (1-p)^{n-1-k},$$

$$P(\deg(v) = k) \rightarrow \frac{(np)^k e^{-np}}{k!} \quad \text{as } n \rightarrow \infty \text{ and } np = \text{constant},$$

Small world

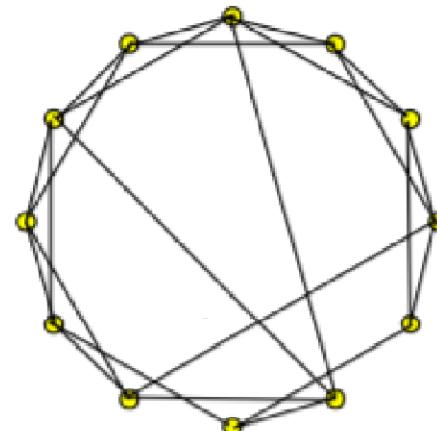
Watts and Strogatz (1998)



$$\beta = 0$$

People know
their **neighbors**.

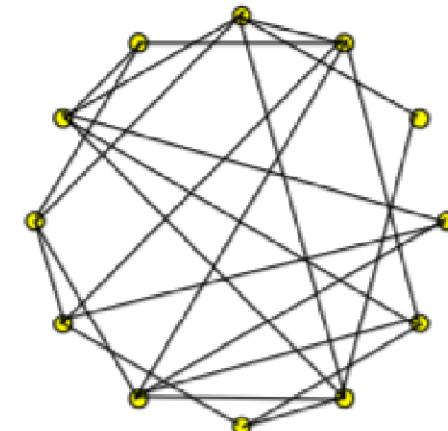
Clustered, but
not a “small world”



$$\beta = 0.125$$

People know
their neighbors,
and a few distant people.

Clustered and
“small world”

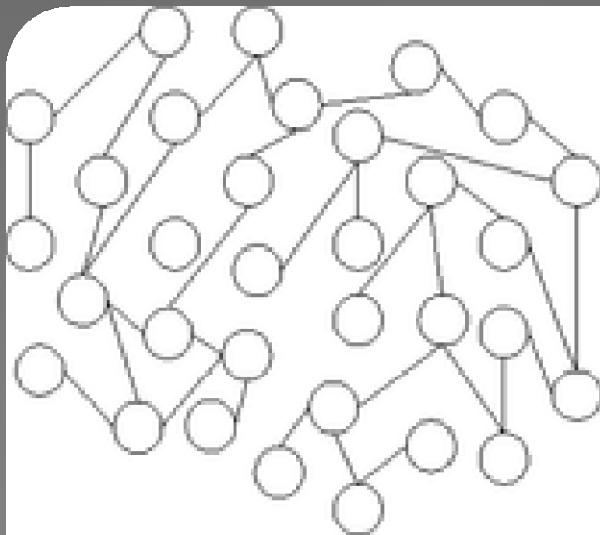


$$\beta = 1$$

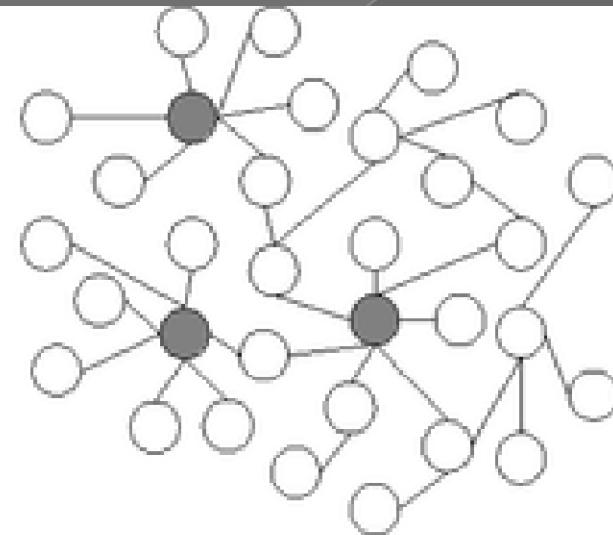
People know
others at
random.

Not clustered,
but “small world”

Scale-free



(a) Random network



(b) Scale-free network

Part two

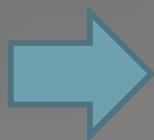
Infectious Disease modeling

Agent Based models

PHENOMENA	AGENT	NETWORK
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malwares, Digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social Network/Proximity Network
Bedbugs	Parasitic Insects	Hotel - Traveler Network
Malaria	Plasmodium	Mosquito - Human network

Homogenous Mixing

Each individual has the **same chance** of coming into contact with an infected individual !



It doesn't need precise contact network!

Which models?

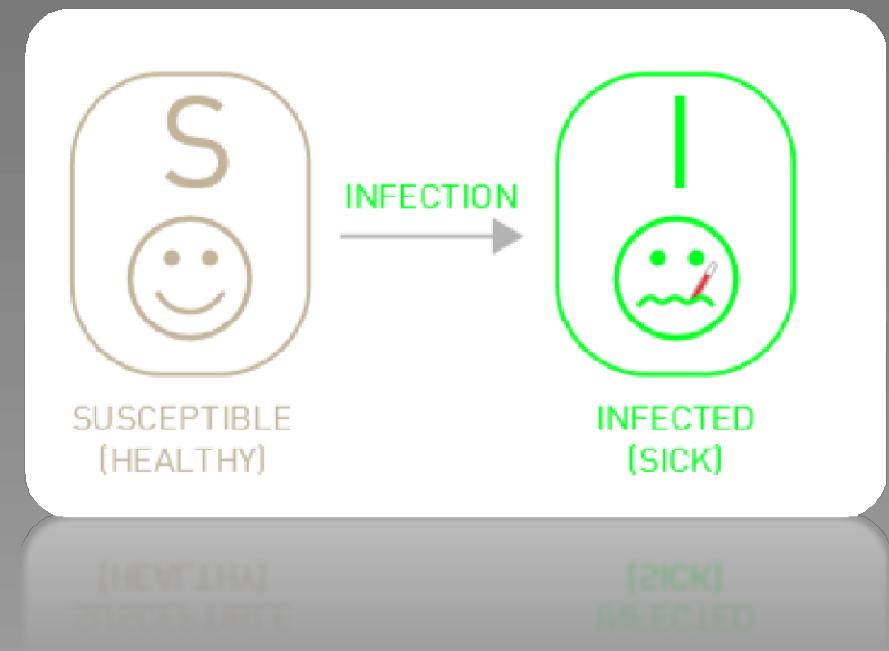
- SI
- SIS
- SIR

SI Model

- N individuals
- $S(t)$ the number of individuals who are susceptible
- $I(t)$ the number individuals that have been already infected

$$\left. \begin{array}{l} S(t=0)=1 \\ I(t=0)=0 \end{array} \right\} t=0$$

- typical individual has $\langle k \rangle$ contacts
- Transmission rate is β



SI Model-1

- Homogenous mixing hypothesis

→ **probability** that the infected person encounters a susceptible individual is $S(t)/N$.

- Number of susceptible contacts per time → $\langle k \rangle S(t)/N$

- So:

$$\frac{dI}{dt} = \beta \langle k \rangle I(t)S(t)$$

SI Model-1

- If we normalize population to 1 and assume that $s(t)=S(t)/N$ and $i(t)=I(t)/N$, we have:

$$\frac{di}{dt} = \beta \langle k \rangle i(t)s(t) = \beta \langle k \rangle i(t)(1 - i(t))$$

- where the product $\beta\langle k \rangle$ is called the **transmission rate** or **transmissibility**

SI Model-1

- If we rewrite the Equation, we have:

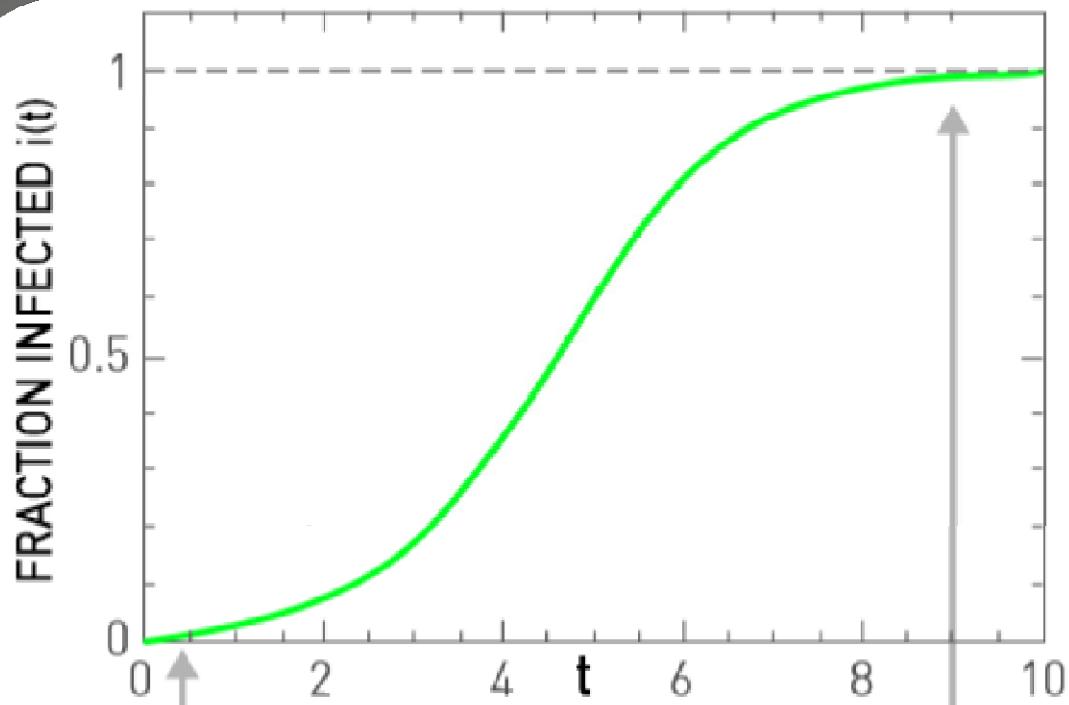
$$\frac{di}{i(t)(1 - i(t))} = \beta <k> dt$$

1  $\int \frac{di}{i(t)} + \int \frac{di}{(1 - i(t))} = \int \beta <k> dt$

2 
$$\begin{cases} \ln i - \ln(1 - i) + C = \beta <k> t \\ C = \frac{i_0}{1 - i_0} \end{cases}$$

SI Model-1

$$i = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$



exponential regime

If i is small,

$$i \approx i_0 e^{\beta \langle k \rangle t}$$

saturation regime

If $i \rightarrow 1$,

$$\frac{di}{dt} \rightarrow 0$$

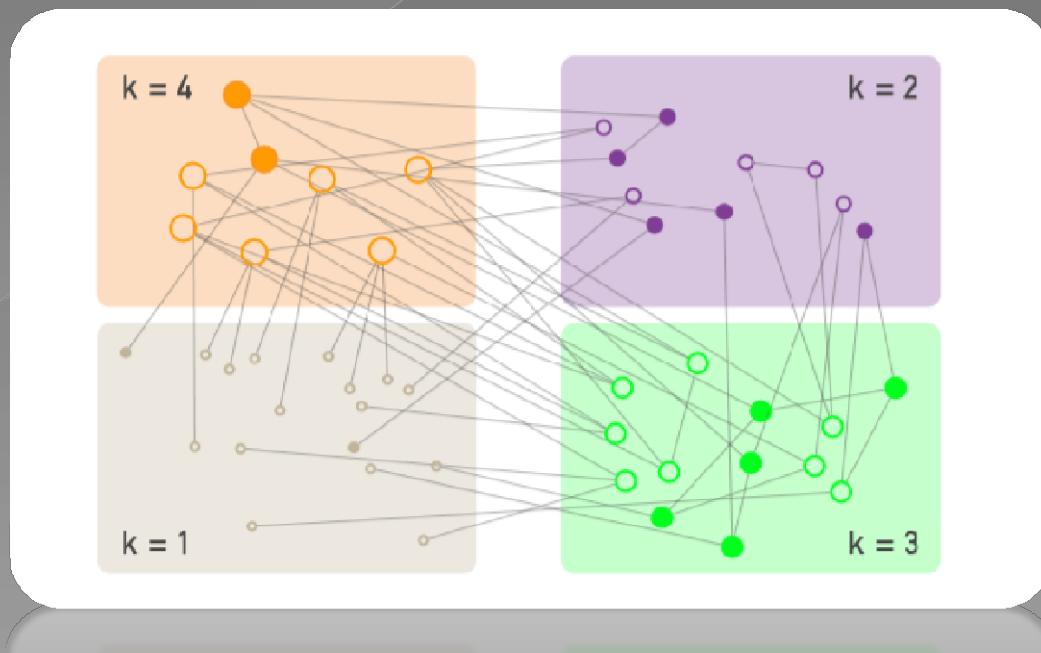
SI Model-2

- But what happens if there is no homogeneity?



Degree Block approximation

- Groups **nodes** based on their **degree** and assumes that nodes with the same degree are **statistically equivalent**!



SI Model-2

- Fraction of nodes with degree k that are infected among all N_k (degree- k nodes) in the network.

$$i_k = \frac{I_k}{N_k}$$

- We sum over degrees and use degree distribution:

$$i = \sum_k p_k i_k$$

SI Model-2

- We revise the equation in SI Model-1:
- Now we have k max coupled equations!

$$\frac{di_k}{dt} = \beta k (1 - i_k) \theta_k$$

- The **density function** (θ_k): fraction of infected neighbors of a susceptible node k. It depends on:

- 1. Time
- 2. Node degree
- 3. Network Topology

SI Model-2

- It's not easy to find and answer for those Equations.



Early stage Approximation

- i_k is small. So:

$$\frac{di_k}{dt} \approx \beta k \theta_k$$

- Still a problem: What's Θ_k ?



No degree-correlations

No degree-Correlations

- The **probability** that a **link** points from a node with **degree k** to a node with **degree k'** is independent of k !
- The **probability** that a randomly chosen link points to a node with degree k' is:

$$\frac{k' p_{k'}}{\sum_k k p_k} = \frac{k' p_{k'}}{< k >}$$

- At least **one link** of each infected node is connected to another infected node . So:

$$\theta_k = \frac{\sum_{k'} (k' - 1) p_{k'} i_{k'}}{< k >} = \theta$$

Independency

No degree-Correlations

- Differentiate Both Sides:

$$\frac{d\theta_k}{dt} = \frac{1}{\langle k \rangle} \sum_k (k - 1)p_k \frac{di_k}{dt}$$

- Now we use SI Model and rewrite:

$$\frac{d\theta}{dt} = \frac{1}{\langle k \rangle} \sum_k (k^2 - k)p_k \beta (1 - i_k)\theta$$

No degree-Correlations

- Now we append **early stage approximation** : $I_{k=0}$

$$\frac{d\theta}{dt} = \frac{1}{\langle k \rangle} \sum_k (k^2 - k) p_k \beta \theta = \beta \theta \left(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1 \right)$$

- Integrate the Equation:

$$\theta(t) = \theta_0 e^{\beta \left(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1 \right) t} \quad \theta_0 = i_0 \frac{\langle k \rangle - 1}{\langle k \rangle}$$

Uniform distribution

SI Model-2

- Then substitute last equation to coupled differential equations:

$$\frac{di_k}{dt} \approx \beta k \theta_0 e^{\beta(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1)t} \quad \theta_0 = i_0 \frac{\langle k \rangle - 1}{\langle k \rangle}$$

- A really easy Integration over time!

$$i_k(t) = i_0 \left(1 + \frac{k(\langle k \rangle - 1)}{\langle k^2 \rangle - \langle k \rangle} \left(e^{\beta(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1)t} - 1 \right) \right)$$

SI Model-2

the total fraction of infected nodes grows with time as:

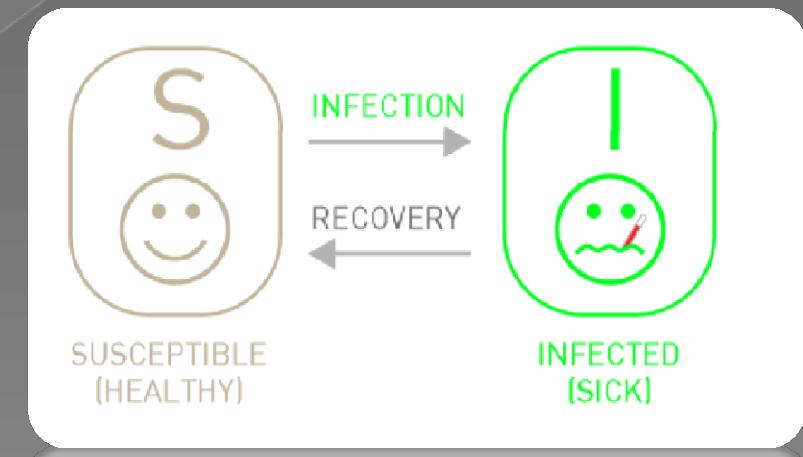
$$i = \int_{k=0}^{k=\max} p_k i_k(t) dk = i_0 \left(1 + \frac{(\langle k \rangle^2 - \langle k \rangle)}{\langle k^2 \rangle - \langle k \rangle} \left(e^{\beta \left(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1 \right) t} - 1 \right) \right)$$



SIS Model-1

- N individuals
- $S(t)$ the number of individuals who are susceptible
- $I(t)$ the number individuals that have been already infected

$$\left. \begin{array}{l} S(t=0)=1 \\ I(t=0)=0 \end{array} \right\} t=0$$



- typical individual has $\langle k \rangle$ contacts
- Transmission rate is β
- infected individuals recover at a fixed rate μ , becoming susceptible again

SIS Model-1

- We write the differential equations as usual:

$$\frac{di}{dt} = \beta \langle k \rangle i(1 - i) - \mu i$$

- Then Solve it over time:

$$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{C e^{(\beta \langle k \rangle - \mu)t}}{1 + C e^{(\beta \langle k \rangle - \mu)t}}$$
$$C = \frac{i_0}{1 - i_0 - \frac{\mu}{\beta \langle k \rangle}}$$

SIS States

- Endemic state \rightarrow There is an equilibrium !

$$(\mu < \beta\langle k \rangle)$$

$$i(\infty) = 1 - \frac{\mu}{\beta \langle k \rangle}$$

- Disease-free state $\rightarrow I(t)$ will go to zero

$$(\mu \geq \beta\langle k \rangle)$$

$$i(\infty) = 0$$

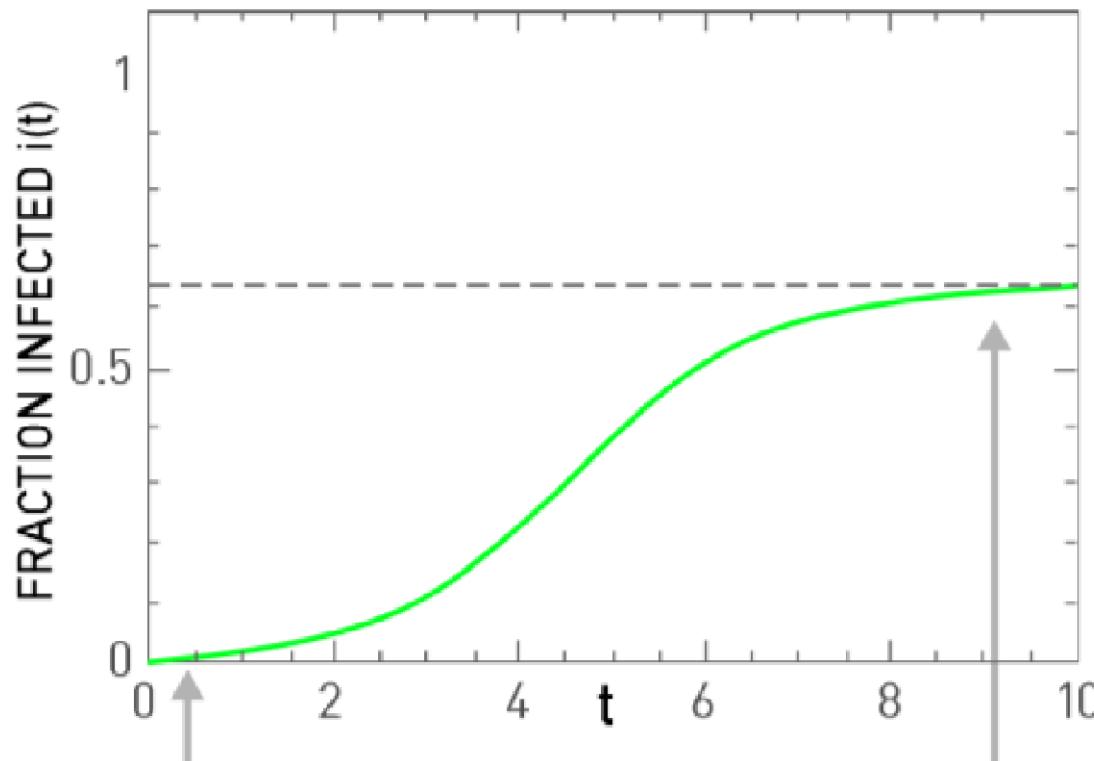
- Basic reproductive number

$$R_0 = \frac{\beta\langle k \rangle}{\mu}$$

SIS Model-1

$$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{C e^{(\beta \langle k \rangle - \mu)t}}{1 + C e^{(\beta \langle k \rangle - \mu)t}}$$

$$C = \frac{i_0}{1 - i_0 - \frac{\mu}{\beta \langle k \rangle}}$$



exponential
outbreak

If i is small,
 $i \approx i_0 e^{(\beta \langle k \rangle t - \mu)t}$

endemic
state

$$i(\infty) = 1 - \frac{\mu}{\beta \langle k \rangle}$$

SIS Model-2

- For a no homogenous network we have **Degree Block approximation.**

$$\frac{di_k}{dt} = \beta k \theta_k (1 - i_k) - \mu i_k$$

- We use **early stage approximation.**

$$\frac{di_k}{dt} = \beta k \theta_k - \mu i_k$$

SIS Model-2

- And now **No degree correlations** method!

$$\frac{d\theta_k}{dt} = \frac{1}{\langle k \rangle} \sum_k (k - 1) p_k \frac{di_k}{dt}$$

- We put in the SIS differential equation.

$$\frac{d\theta}{dt} = \left(\beta \frac{\langle k^2 \rangle}{\langle k \rangle} - \mu \right) \theta$$

SIS Model-2

- Solve the equation and put in the SIS equation

$$\theta(t) = Ce^{\frac{t}{\tau}}$$

$$\tau = \frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle}$$

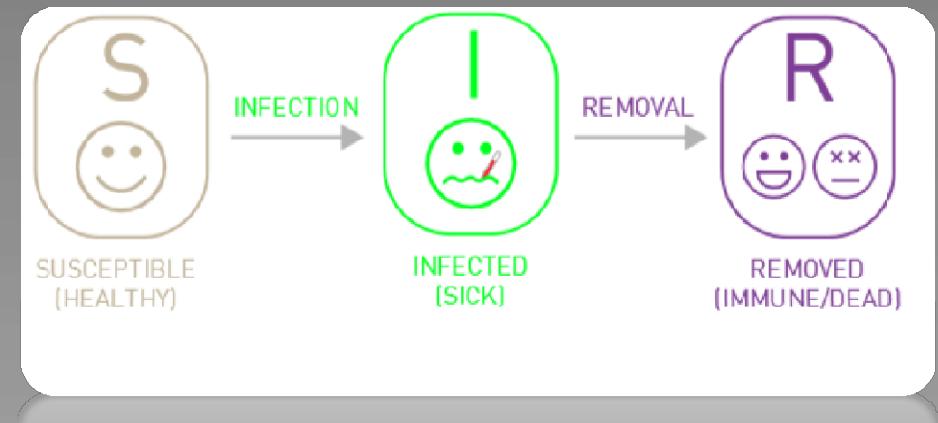
- We have epidemic outbreak if $\tau > 0$.

$$\lambda_c = \frac{\beta}{\mu} = \frac{\langle k \rangle}{\langle k^2 \rangle}$$

SIR Model-1

Groups:

- **Susceptible** (S): Healthy individuals who have not yet contacted the pathogen
- **Infectious** (I): Contagious individuals who have contacted the pathogen and hence can infect others.
- **Recovered** (R): Individuals who have been infected before, but have recovered from the disease, hence are not infectious



SIR Model-1

- We write equation as usual and we know that there is no easy open solution for them!

$$\frac{ds}{dt} = -\beta \langle k \rangle i [I - r - i]$$

$$\frac{di}{dt} = -\mu i + \beta \langle k \rangle i [I - r - i]$$

$$\frac{dr}{dt} = \mu i$$

SIR States

- Endemic state \rightarrow There is an equilibrium !

$$(\mu < \beta\langle k \rangle)$$

- Disease-free state $\rightarrow I(t)$ will go to zero

$$(\mu \geq \beta\langle k \rangle)$$

- Basic reproductive number

$$R_0 = \frac{\beta\langle k \rangle}{\mu}$$

SIR Model-2

- And now **No degree correlations** method!

$$\frac{d\theta_k}{dt} = \frac{1}{\langle k \rangle} \sum_k (k - 1) p_k \frac{di_k}{dt}$$

- We put in the SIS differential equation.

$$\frac{di_k}{dt} = \beta k \theta_k (1 - i_k) - \mu i_k$$

$$\frac{d\theta}{dt} = \left(\beta \left(\frac{\langle k^2 \rangle}{\langle k \rangle} - 1 \right) - \mu \right) \theta$$

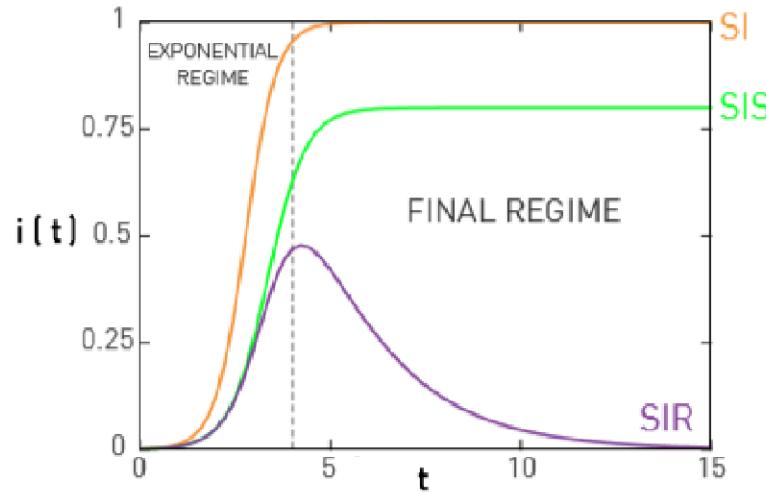
SIR Model-2

$$\theta(t) = Ce^{\frac{t}{\tau}} \quad \tau = \frac{<k>}{\beta <k^2> - \mu(<k> + \beta)}$$

- We have epidemic outbreak if $\tau > 0$.

$$\lambda_c = \frac{\beta}{\mu} = \frac{<k>}{<k^2> - <k>}$$

Summary



	SI	SIS	SIR
Exponential Regime: Number of infected individuals grows exponentially	$i = \frac{i_0 e^{\beta(k)t}}{1 - i_0 e^{\beta(k)t}}$	$i = \left(1 - \frac{\mu}{\beta(k)}\right) \frac{C e^{(\beta(k) - \mu)t}}{1 + C e^{(\beta(k) - \mu)t}}$	No closed solution
Final Regime: Saturation at $t \rightarrow \infty$	$i(\infty) = 1$	$i(\infty) = 1 - \frac{\mu}{\beta(k)}$	$i(\infty) = 0$
Epidemic Threshold: Disease does not always spread	No threshold	$R_0 = 1$	$R_0 = 1$

Summary

MODEL	CONTINUUM EQUATION	τ	λ_c
SI	$\frac{di_k}{dt} = \beta[1 - i_k]k\theta_k$	$\frac{\langle k \rangle}{\beta(\langle k^2 \rangle - \langle k \rangle)}$	0
SIS	$\frac{di_k}{dt} = \beta[1 - i_k]k\theta_k - \mu i_k$	$\frac{\langle k \rangle}{\beta\langle k^2 \rangle - \mu\langle k \rangle}$	$\frac{\langle k \rangle}{\langle k^2 \rangle}$
SIR	$\frac{di_k}{dt} = \beta s_k \theta_k - \mu i_k$ $s_k = 1 - i_l - r_k$	$\frac{\langle k \rangle}{\beta\langle k^2 \rangle - (\mu + \beta)\langle k \rangle}$	$\frac{1}{\langle k^2 \rangle - 1}$

Thanks!

