

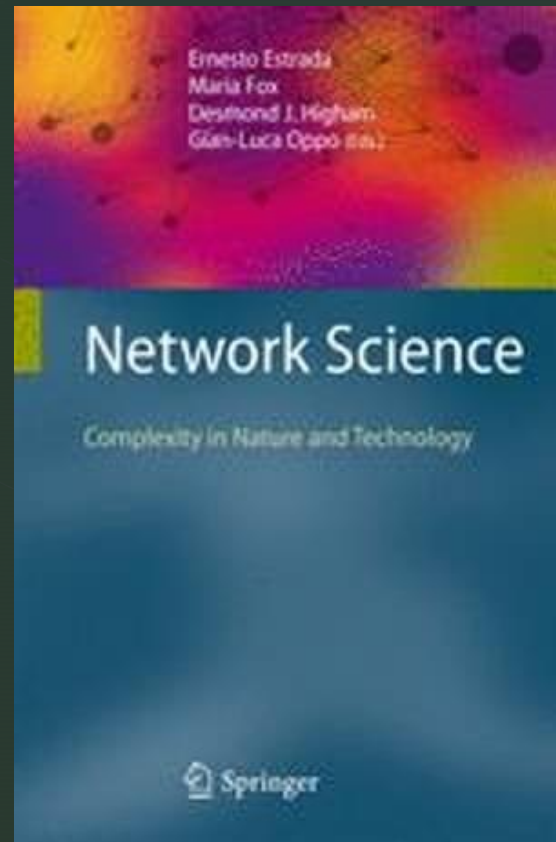
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# Network Science & Epidemiology (1)

▶ *Network Science: Complexity in Nature and Technology (2010)*



## 1.1. SIR Ordinary Differential Equation (ODE) Model

- Susceptible                      Infected                      Resistant (Removed)
- Compartmental model
- Integrated over time

$$\frac{dS}{dt} = -\beta IS,$$

$$\frac{dI}{dt} = \beta IS - \gamma I,$$

$$\frac{dR}{dt} = \gamma I,$$

$$S + I + R = N.$$

$\beta$ : rate of per infected individual at which infections occur.

$\gamma$ : rate at which infected individuals are removed. (4.1)

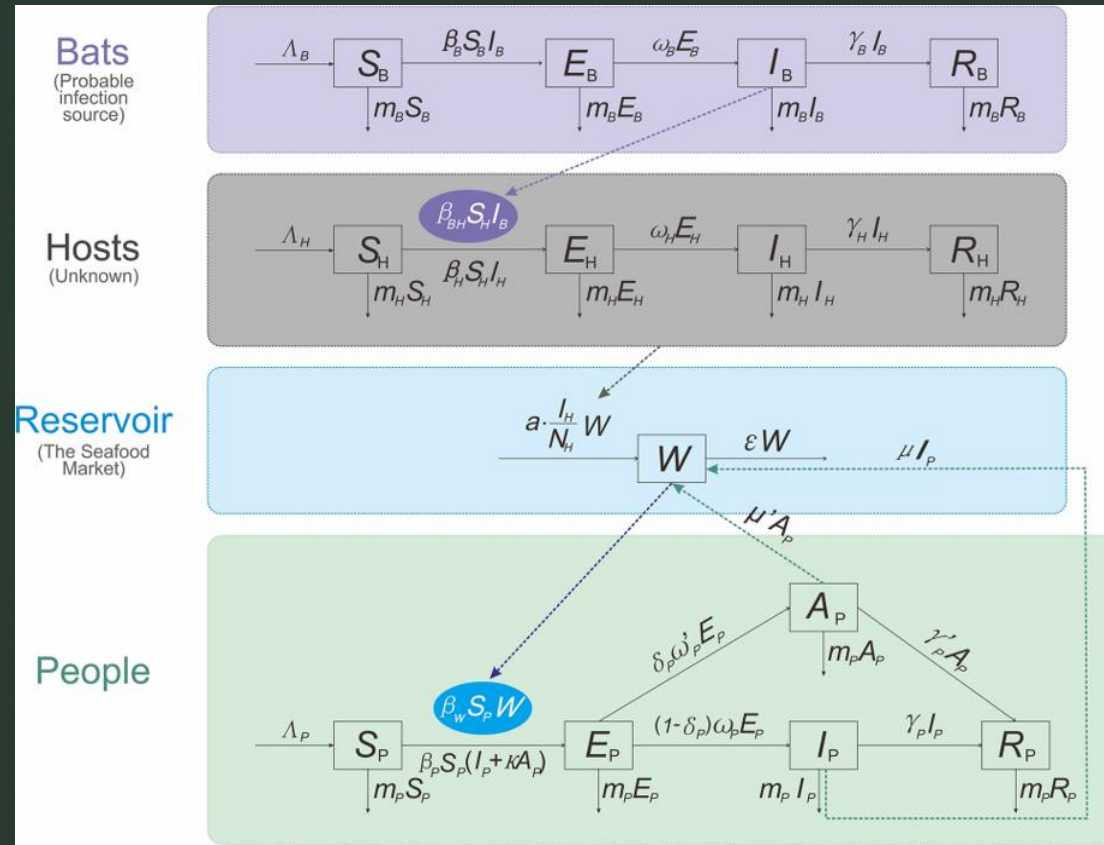
$N$ : total population size (fixed)

## 1.2. Important Principles

- Interest in the field has concentrated on the nonlinear interactions over time between a host population and a pathogen that exploits it.
- Individuals are treated as indistinguishable except for their disease state.
- The nonlinear terms incorporate the “**mean-field**” assumption, where interactions between members of the population are considered to occur at random, with equal probability that any member will interact with any other element of the system.
- The model operates in continuous time and population-space.

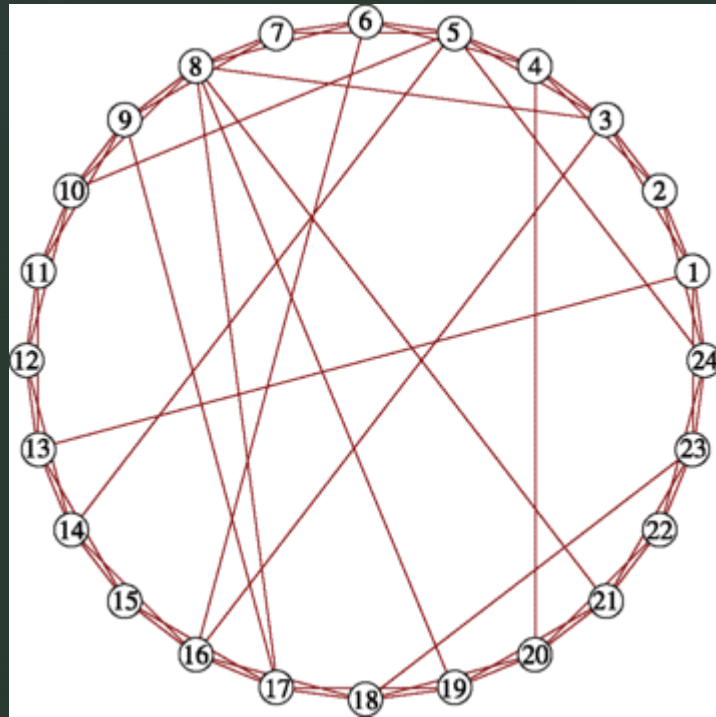
# 1.3. An instance: Bats-Hosts-Reservoir-People (BHRP) Transmission Network Model [1]

$S$ :	susceptible
$E$ :	exposed
$I$ :	infected
$R$ :	removed
$n$ :	birth rate
$m$ :	death rate
$N$ :	total number
$\Lambda$ :	number of newborn
$1/\omega$ :	incubation period of infection
$1/\gamma$ :	infectious period of infection
$\beta$ :	transmission rate (at which $S$ is infected through sufficient contact with $I$ )
$A_P$ :	asymptomatic infected people
$W$ :	SARS-CoV-2 in reservoir
$\delta_P$ :	proportion of asymptomatic infection
$1/\varepsilon$ :	lifetime of the virus



Flowchart of the Bats-Hosts-Reservoir-People transmission network model





## 2.1. Network Model

- nodes  $\rightarrow$  people
- links  $\rightarrow$  potentially infectious contacts
- “mean-field” model  $\approx$  fully-connected network
  - Every individual in the population is connected to any other individual
- $\langle k \rangle \ll N$ 
  - $\langle k \rangle$ : average node degree
  - $N$ : population size
  - In most epidemiologically relevant examples where network structure is important



## 2.2. Comparison

### Mean-field model

- Do have population structure
  - Imposed on the population, rather than being generated from individual properties

### Network model

- Each node only has information about a limited subset of neighbors.
- Displays corresponding “emergent behavior”
- Individuals can no longer be assumed to be in potentially infectious contact with all members of the population.

## 2.3. Connection from SIR ODE to Network Models

- A closer examination of the contact structure
- $\beta SI \rightarrow \tau C(N)I \frac{S}{N}$ 
  - $\tau$ : infectious probability
  - $C(N)$ : # potential infectious contacts each individual has
    - For density dependent contact:  $C(N) = N$
    - For frequency dependent contact:  $C(N) = \kappa$  (a constant)



## 2.4. Why Concentrate on Simplify Compartments

- Observational data on **overall disease incidence** and detailed data describing the **time course of individual infection states** have historically been more **available** than meaningful population **contact** structure data, particularly for humans.
- Now it is easier to collect meaningful population contact structure data (e.g. by trajectory tracing technologies)

## 2.5. Frequency Dependent Model (FDM) vs. Network Models (NM)

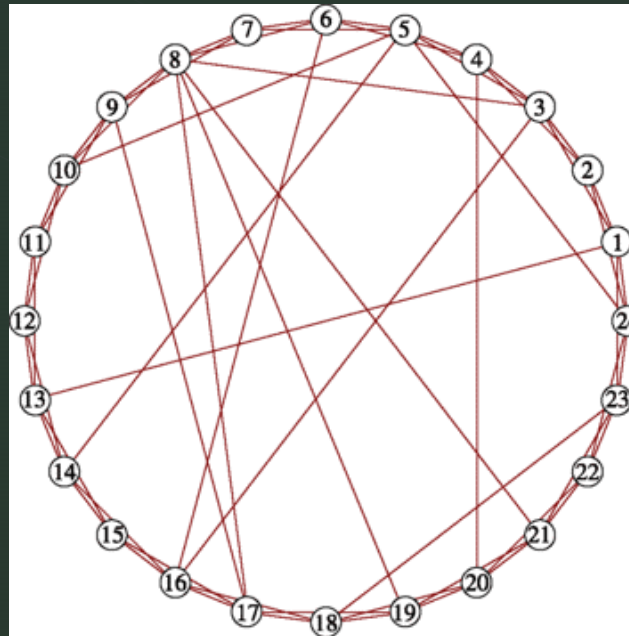
- In FDM
  - # contacts is independent of population size.
  - Contact is made with a random individual in the population.
  - Any infected individual still has  $\kappa$  outward potentially infectious contacts
- In static NM with bi-directional links
  - At least one of potentially infectious contacts is “used up” because the node was infected along one of its existing links.
- The two are only equivalent in the case of a dynamic network with links that switch to new partners at an infinite rate.

### 3. Basic Reproduction Number ( $R_0$ )

- Definition: the number of new infections generated by a single infected individual introduced into a wholly susceptible, homogeneously mixed population at equilibrium.
- For the system of SIR ODE:  $R_0 = \frac{\beta N}{\gamma}$ .

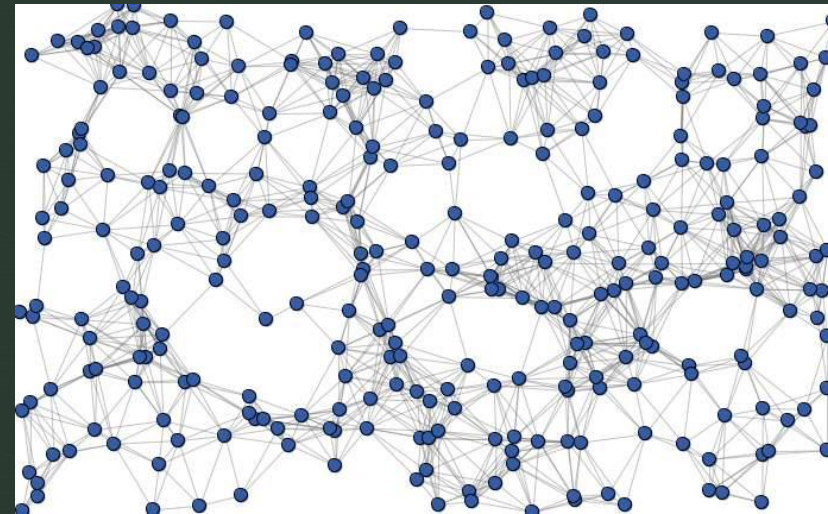
## 4. “Small-World Network” (SWN) model

- Watts and Strogatz (1998) [2]
- It is a very specific, illustrative example of a highly clustered network.



## 5. Clustering

- Clustering: the probability of two friends of any one individual being themselves friends of each other.
- A population can be described in terms of the frequency of clusters of individuals of various types (e.g.  $S, I, R$ ) and of various sizes.





## 5. Clustering

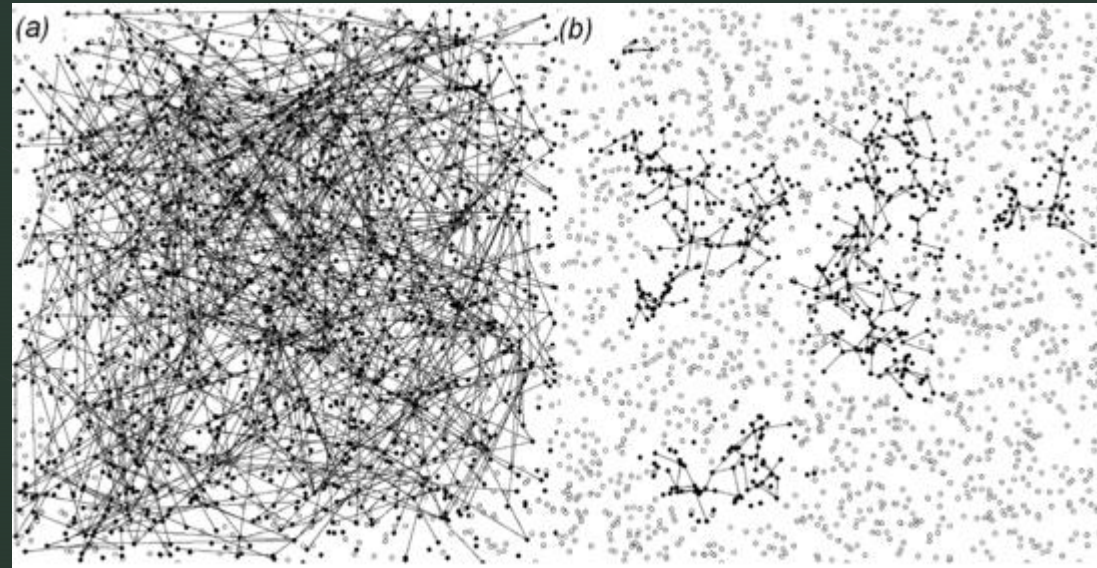
- It is illustrated in the classic signature of the small world effect, which is the rapid decline in the average path length between nodes, when the clustering coefficient remains high.
  - distance: the minimum number of hops between two individuals in a network
  - Clustering coefficient: a measure of localization
- Clustering and its extensions allows for the description of heterogeneous structures in network, but it does not create an analytical tool for describing the effect on disease transmission.



## 6.1. Closure

- Disease transmission is dependent on whether one of the pairs is connected to an infectious individual.
- The closure has been successful in accounting for correlations that form due to diseases spreading amongst clusters of connected individuals.
- An important feature of even moderate levels of clustering is the rapid decrease in the average number of new infections produced by each infectious individual.  
**Largely due to the depletion of the susceptible neighborhood.**

## 6.2. Moment Closure



Transmission on unclustered and spatially clustered networks. Transmission on unclustered networks fills the picture (above percolation threshold) while on clustered networks, the epidemic is **self-limiting** (below the percolation threshold). Figure courtesy of Dr. D.M. Green, Stirling University

## 6.2. Moment Closure

- Explore the relationship between clustering and epidemic spread, showing how clustering can lead to a dramatic reduction in the value of  $R_0$ .
- Using additional equations incorporating links between nodes along which tracing takes place, the moment closure approach can also be used to explore the effect of network dependent disease control, such as contact tracing, i.e. identifying potentially infectious connections from infected individuals.
- Practice: Exploring the consequences of exploiting spatial proximity in the case of the Great Britain 2001 foot-and-mouth disease epidemic.

## 7. Reference

- [1] Chen, T., Rui, J., Wang, Q. *et al.* A mathematical model for simulating the phase-based transmissibility of a novel coronavirus. *Infect Dis Poverty* **9**, 24 (2020).  
<https://doi.org/10.1186/s40249-020-00640-3>
- [2] Watts, D.J., Strogatz, S.H.: Collective dynamics of ‘small-world’ networks. *Nature* 393, 440– 442 (1998)



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Thank you for  
your listening!