

Disease spreading on small-world networks

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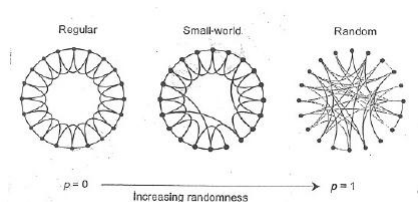
Outline

- 1 Theory
 - Watts-Strogatz models
 - Disease models on networks
- 2 Analysis
 - Infection rates
 - Equilibrium states
- 3 Conclusion and discussion
 - Conclusion
 - Discussion



Construction

- Start with a regular ring graph of size N where each node has K neighbors, $K \gg \log(N)$, $K/2$ at each side.
- Rewire connections with probability p .
- $p = 0$: Completely structured graph.
 $p = 1$: Random graph.



Properties

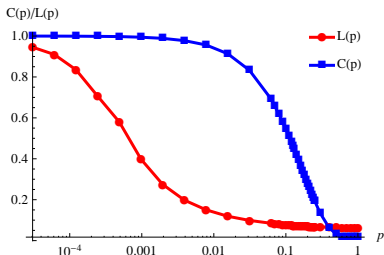
- Average path length $L(p, K)$: The average number of edges between two nodes in the graph.
- Local clustering coefficient $c_i(p, K)$:

$$\frac{\text{Number of connections between neighbors of node } i}{k(k-1)/2}.$$

- Global clustering coefficient $C(p, K)$: $\frac{1}{N} \sum_{i=1}^N c_i(p, K)$.

small-world networks correspond to many realistic networks, e.g.:

- Social networks
- Neural networks
- Distributing networks (e.g. water and electric power grids)



SIR model

- Possible to simulate spreading of a disease on a network by means of assigning states to the nodes; the nodes represent people.
- In this case three possible states: Susceptible (S), Infected (I), Recovered (R).
- Start with all nodes in S state except for one infected node. Infected node can infect neighbors with probability p_{inf} every time step. Infected nodes change state to R and become inactive after t_{inf} steps.
- Small example with $K = 3$, $N = 100$, $p_{\text{inf}} = 0.1$ and $t_{\text{rec}} = 5$:



SIRS model

- Same states as in the SIR model.
- Recovered nodes become susceptible again after t_{rec} .
- In contrast with SIR model this model does not have to reach a steady state.

Parameters used for both models:

$$N = 1000$$

$$K = 5$$

$$p_{\text{inf}} = 0.1$$



Using SIR to determine infection spreading rate

- Use SIR to determine the rate of disease spreading.
- $r_{1/2}$: the number of time steps before half of the population is infected. r_{tot} : the number of time steps before the total population is infected.
- r_{tot} is only slightly bigger than $r_{1/2}$ for every p .
Curves follow the same shape as $L \Rightarrow$ Disease spreading is fast on small-world networks.

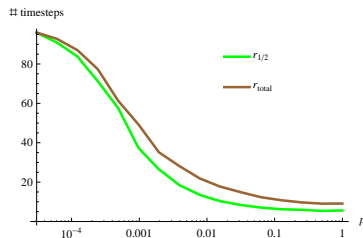
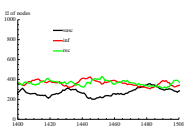


Figure: $t_{\text{inf}} = 4$

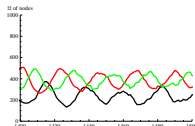


Reaching the equilibrium state

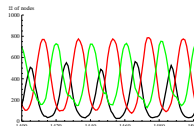
- The SIRS model allows for investigation of a equilibrium state occurring after the initial exponential infection rate.
- Behavior in equilibrium states very different for different values of p .
- Parameters used: $N = 1000$, $K = 5$, $p_{\text{inf}} = 0.1$, $t_{\text{inf}} = 8$, $t_{\text{rec}} = 8$.



(a) $p = 2^{-12}$



(b) $p = 2^{-5}$



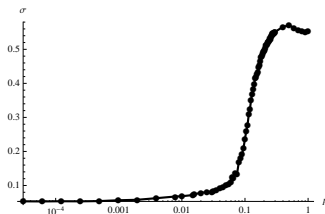
(c) $p = 1$

- Period $\approx t_{\text{inf}} + t_{\text{rec}} + 2$.
- There seems to occur a phase transition: unsynchronized states for low p ; synchronized states for high p .

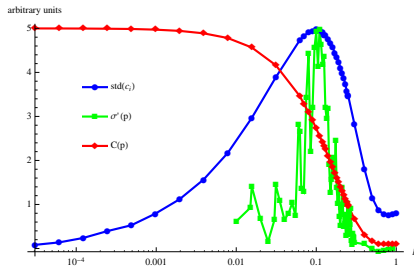


The order parameter

- Capture measure of synchronization in the order parameter:
 $\sigma(t) = \left| \frac{1}{N} \sum_{i=1}^N e^{i\phi_i(t)} \right|$ with $\phi_i(t) = 2\pi \frac{\tau_i - 1}{t_{\text{inf}} + t_{\text{rec}}}$.
- Leave out states with $\tau = 0$ for a clearer signal.



- The derivative of σ is largest when the derivative of $C(p)$ is largest.
- Look at the standard deviation of $c_i(p)$.
- Large standard deviation means large spreading in the amount of clustering.
- Peak of standard deviation coincides with derivative of σ .



- Small-networks have properties that coincide with many real life networks.
- Spreading of diseases on networks scales with $L(p)$.
- Synchronization of states occurs at high values of p , onset of synchronization seems to be coupled with decreasing $C(p)$ and large $\sigma(c_i(p))$.



- Static edges not always very realistic; use dynamic models.
- Outcome highly dependent on N , K , p_{inf} , t_{inf} and t_{rec} , in reality possibly all functions of t .
- Model does not take into account behavioral aspects of people.
- Analytical background of small-world networks still poorly understood.



Software:

- PYTHON: coding
- IGRAPH: package for manipulating, constructing and plotting/animating graphs.
- NUMPY: package for linear algebra in Python.
- Mathematica: graphical output and basic manipulations.

References:

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