Interplay between Epidemics and Network Topology in a Growing Population

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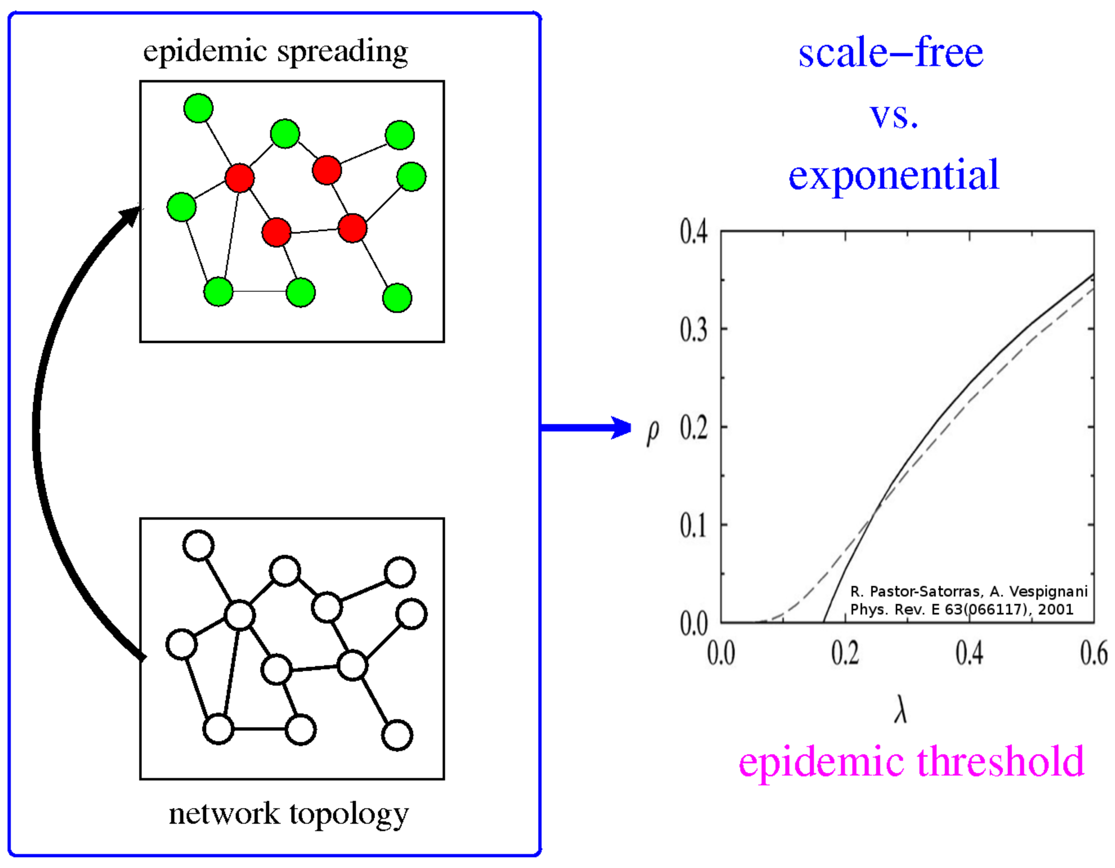
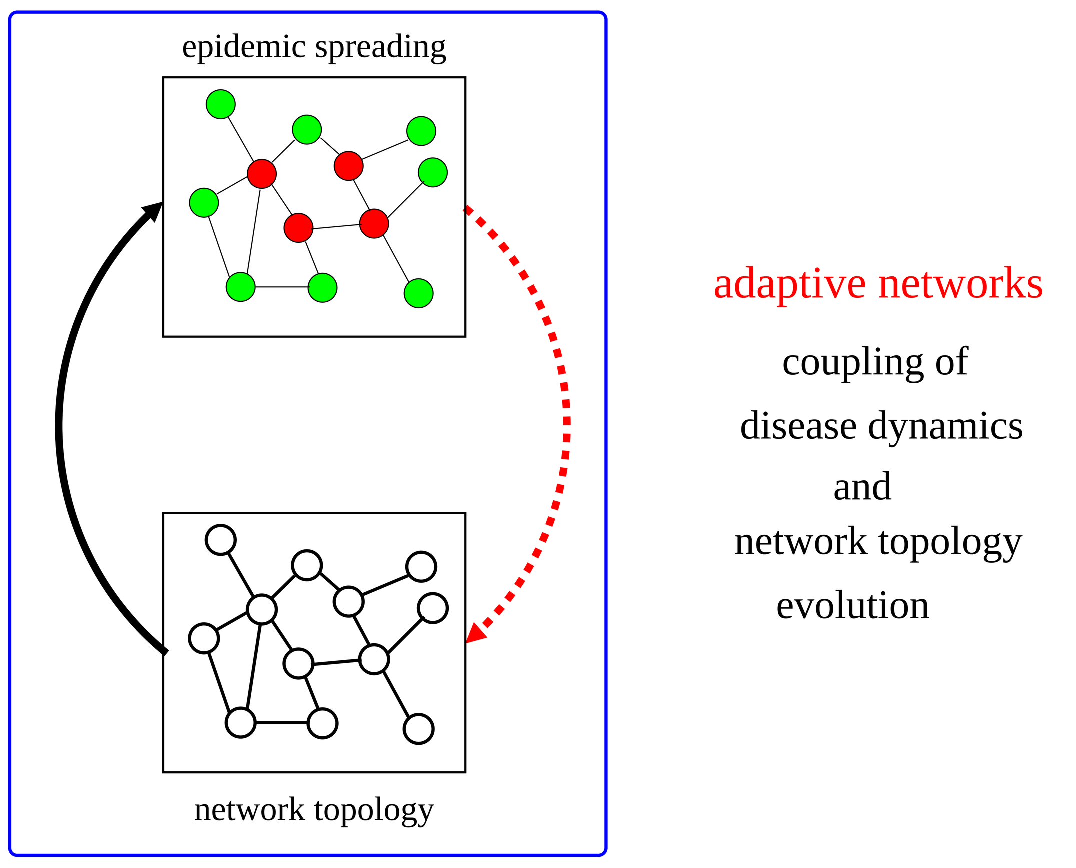
Motivation

Epidemic spreading is strongly influenced by the structure of social contact networks.



Adaptive networks combine it with topological evolution.

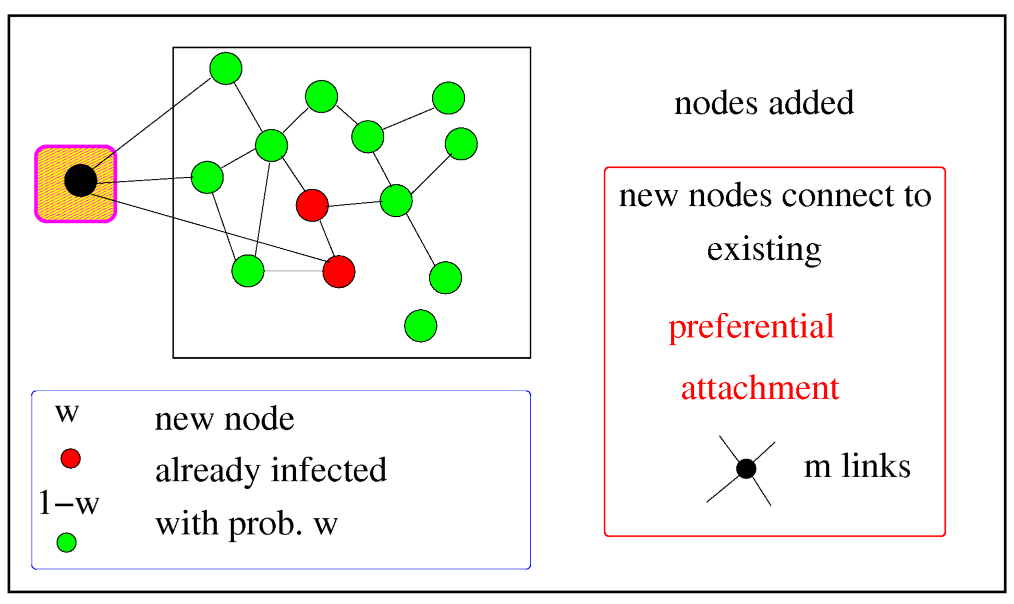


How does the network adaptivity affect the network topology and the disease prevalence in a growing population?

Adaptive SIR Model

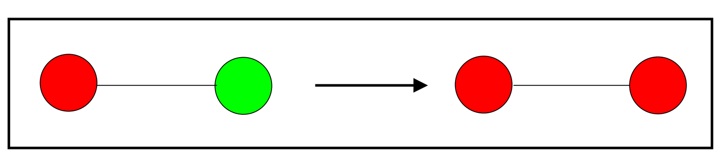
Network growth

- An initial fully connected network of m_0
- Grows with rate **q** due to arrival of new individuals



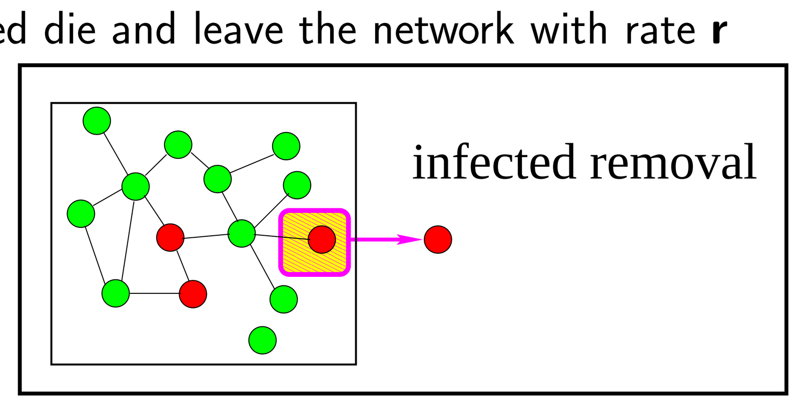
Disease transmission

- Susceptible-Infected-Removed(SIR) disease spreads
- Disease is transmitted on SI links with rate **p**



Deaths/removals

- A potentially fatal disease is considered
- Infected die and leave the network with rate **r**



Moment-Closure Approximation

Heterogeneous node approximation

- Nearest neighbor degree and state correlations are ignored.
- Rate equations for densities of node-degree classes $[S_k]$ and $[I_k]$, i.e.

$$\frac{\mathrm{d}}{\mathrm{d}t}[S_k] = q\left((1-w)\delta_{k,m} + \frac{m}{\langle k\rangle}\Big(-k[S_k] + (k-1)[S_{k-1}]\Big) - [S_k]\right) - p\frac{\langle k_I\rangle[I]}{\langle k\rangle}k[S_k] + r\left(\frac{\langle k_I\rangle[I]}{\langle k\rangle}\Big((k+1)[S_{k+1}] - k[S_k]\Big) + [I][S_k]\right),$$

$$\frac{\mathrm{d}}{\mathrm{d}t}[I_k] = q\left(+w\delta_{k,m} + \frac{m}{\langle k\rangle}\Big(-k[I_k] + (k-1)[I_{k-1}]\Big) - [I_k]\right) + p\frac{\langle k_I\rangle[I]}{\langle k\rangle}k[S_k] + r\left(-[I_k] + \frac{\langle k_I\rangle[I]}{\langle k\rangle}\Big((k+1)[I_{k+1}] - k[I_k]\Big) + [I][I_k]\right), \quad 0 < k < k_{max}$$

Low dimensional approximation

- $\sum_k$ summation and $\langle k_S^2\rangle = \langle k_S\rangle^2 + \langle k_S\rangle$ approximation
- Closed system of equations

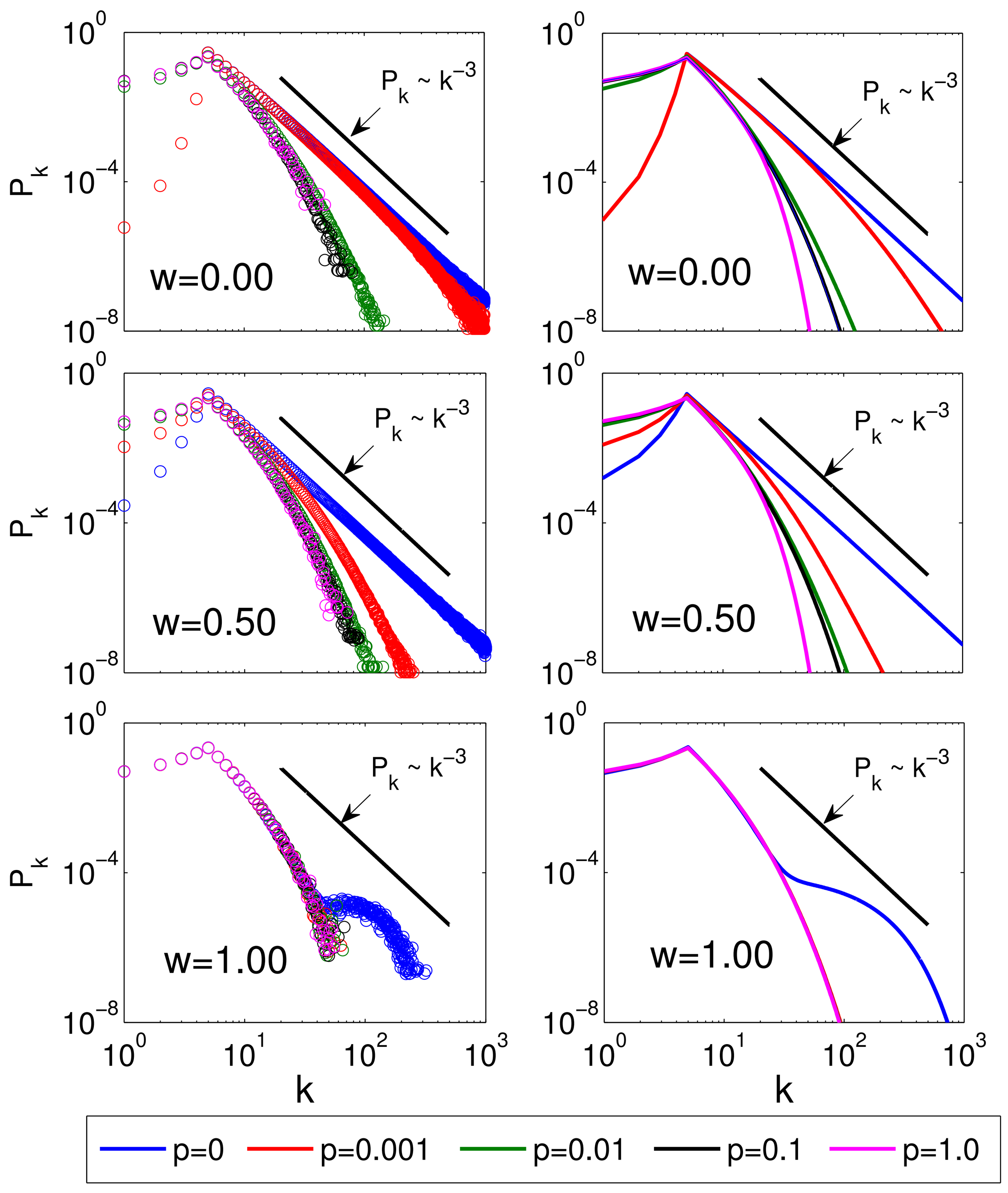
$$\frac{\mathrm{d}}{\mathrm{d}t}[S] = q(1-w-[S]) - p\frac{\langle k_S\rangle\langle k_I\rangle}{\langle k\rangle}[S][I] + r[S][I]$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\langle k\rangle = q(2m - \langle k\rangle) + r(2\langle k_S\rangle[S] - \langle k\rangle(1+[S]))$$

$$\frac{\mathrm{d}}{\mathrm{d}t}\langle k_S\rangle = q\left(\frac{(1-w)(m-\langle k_S\rangle)}{[S]} + m\frac{\langle k_S\rangle}{\langle k\rangle}\right) - p\frac{\langle k_S\rangle\langle k_I\rangle[I]}{\langle k\rangle} - r\frac{\langle k_S\rangle\langle k_I\rangle}{\langle k\rangle}[I]$$

Topological transition

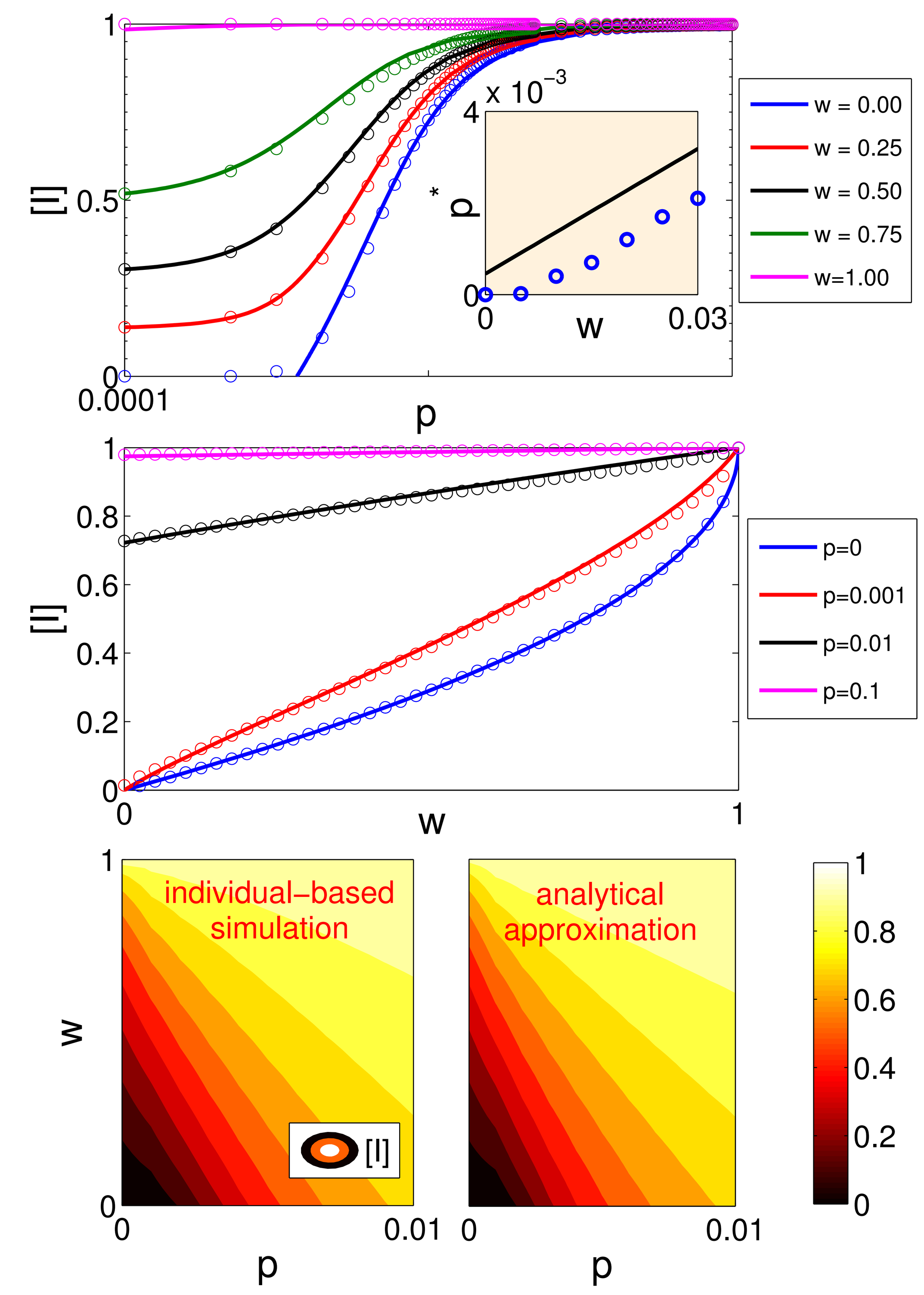
Degree distribution



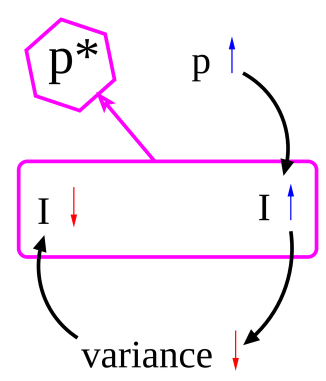
- For $w = 0$, topological transition with increasing p from scale-free to exponential
- Similar behavior as long as some new comers are susceptible ($w < 1$) and transition is faster for higher w
- Bimodal form when all new comers are infected ($w = 1$)
- Good agreement between approximation(solid lines) and simulations(points)

Disease prevelance

Reemergence of an epidemic threshold

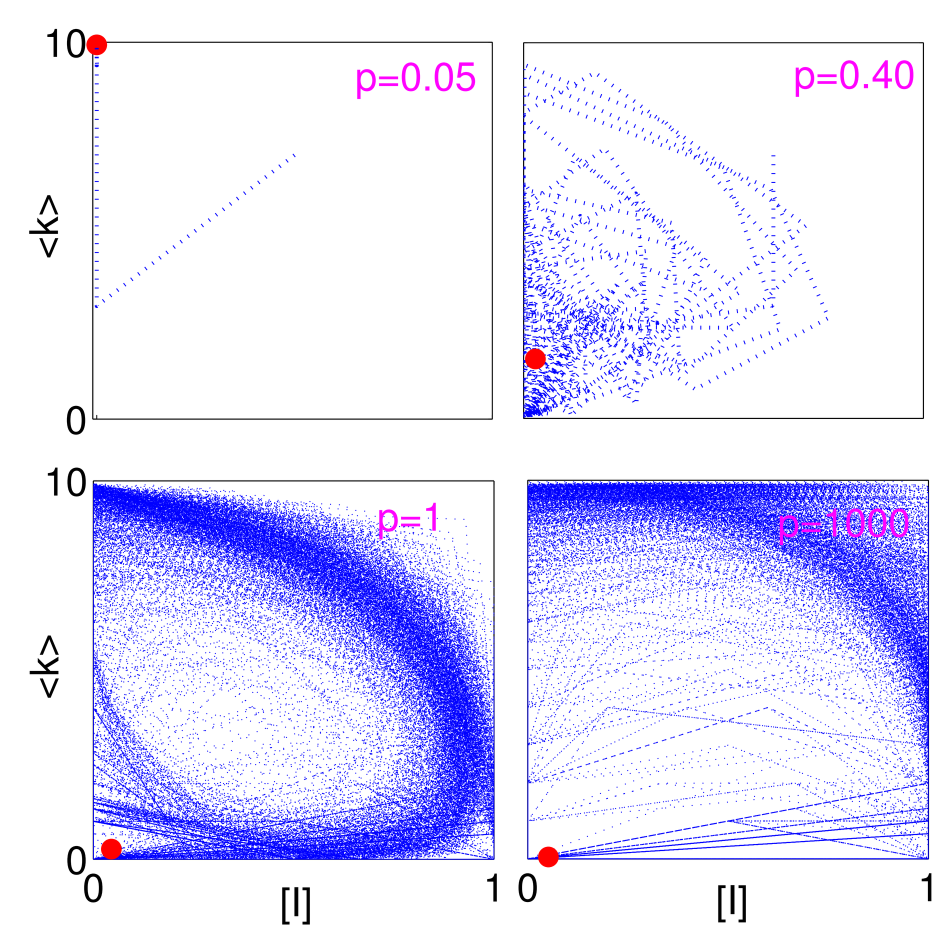


- $[I]^*$ increases with p and w
- Good agreement between approximation(solid lines) and simulations(points)
- For $w = 0$, an epidemic threshold reemerges



Cyclic Trajectories

Population cvcles



- low p, network keeps growing, stable $[I]^*$ is reached ⇒ good analytical approximation
- high p, network grows and shrinks periodically due to frequent deaths ⇒ analytical approximation fails

Summary

- A transition from scale-free to exponential degree distribution is observed for increasing transmission rate.
- An epidemic threshold reemerges due to the interplay between node dynamics and topology.
- Analytical approximation confirms simulation results.