Approximation methods for binary-state dynamics on complex networks

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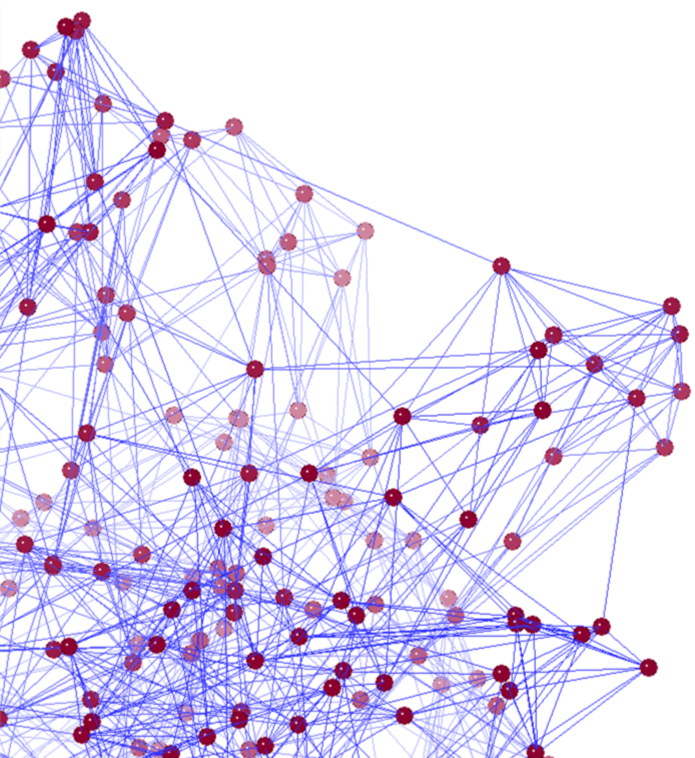

MACSI Mathematics Applications Consortium for Science & Industry

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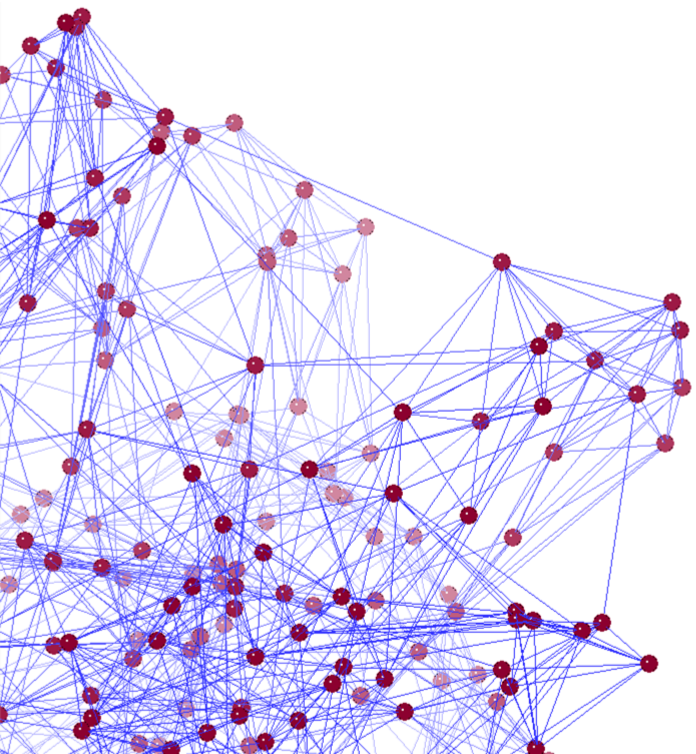
Outline

1. Motivation
2. Models: networks and dynamics
3. Derivation of Approximate Master Equations
4. Hierarchy of approximations: analysis



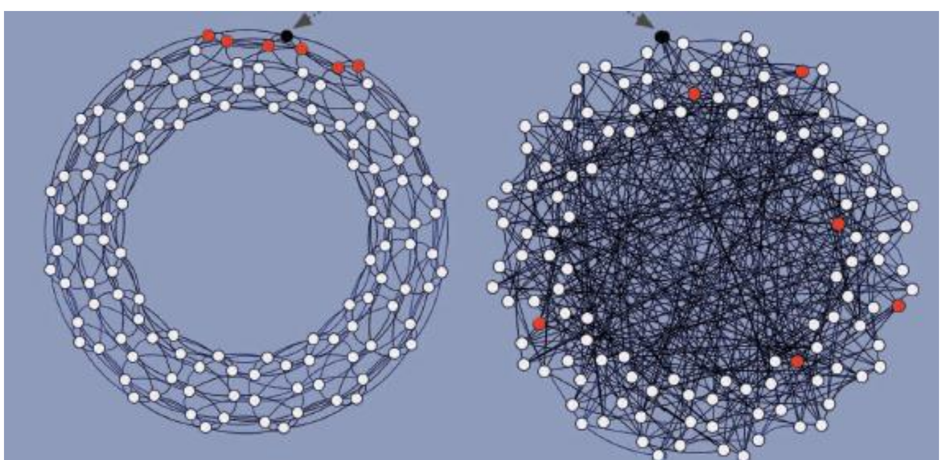
Motivation

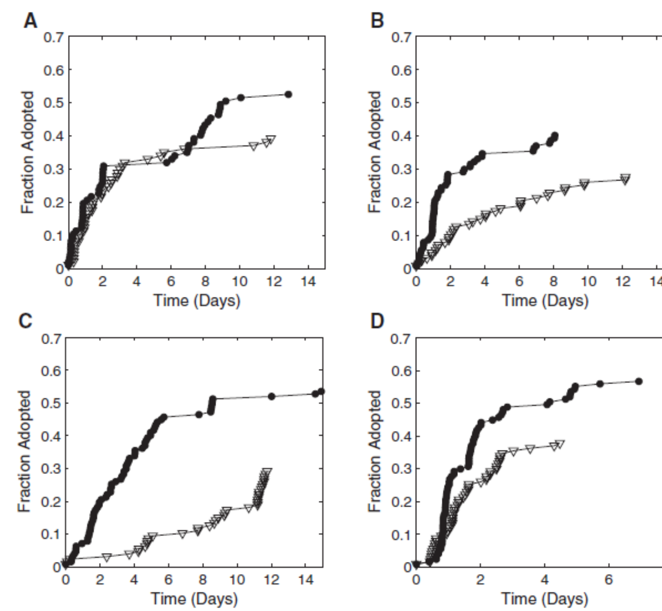
The Spread of Behavior in an Online Social Network Experiment

D. Centola, *Science* 329, 1194 (2010)

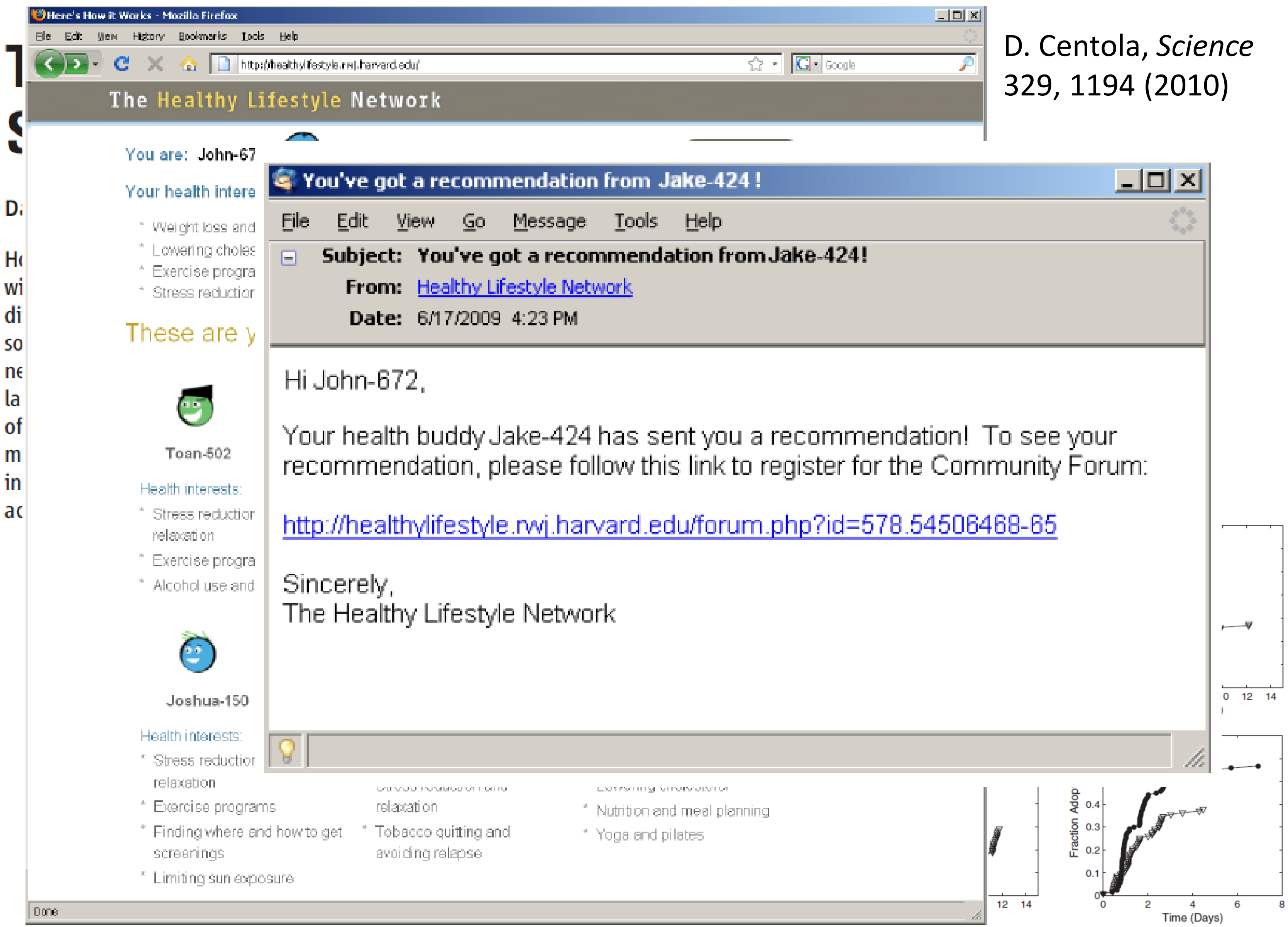
Damon Centola

How do social networks affect the spread of behavior? A popular hypothesis states that networks with many clustered ties and a high degree of separation will be less effective for behavioral diffusion than networks in which locally redundant ties are rewired to provide shortcuts across the social space. A competing hypothesis argues that when behaviors require social reinforcement, a network with more clustering may be more advantageous, even if the network as a whole has a larger diameter. I investigated the effects of network structure on diffusion by studying the spread of health behavior through artificially structured online communities. Individual adoption was much more likely when participants received social reinforcement from multiple neighbors in the social network. The behavior spread farther and faster across clustered-lattice networks than across corresponding random networks.





Motivation



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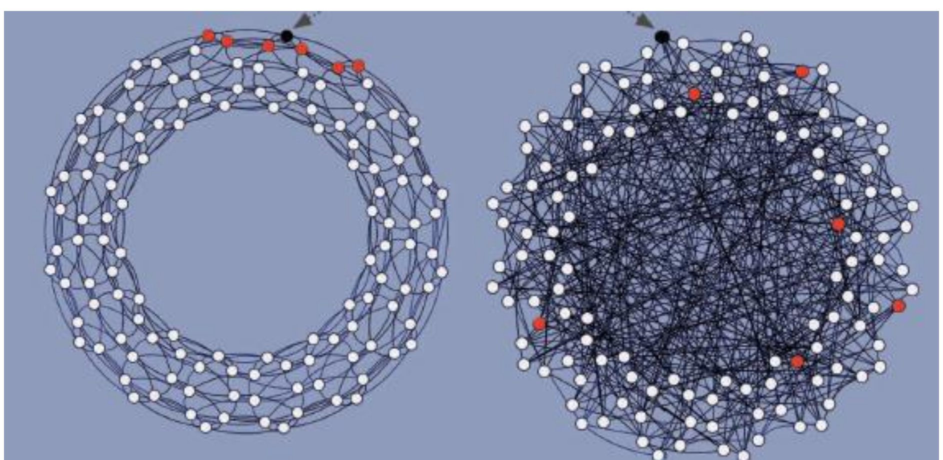
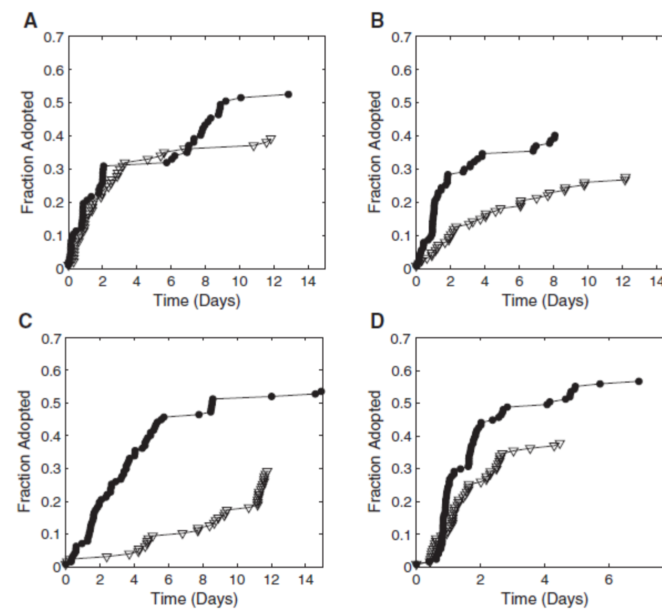




Motivation

Differences in the Mechanics of Information Diffusion Across Topics: Idioms, Political Hashtags, and Complex Contagion on Twitter

Daniel M. Romero Brendan Meeder Jon Kleinberg

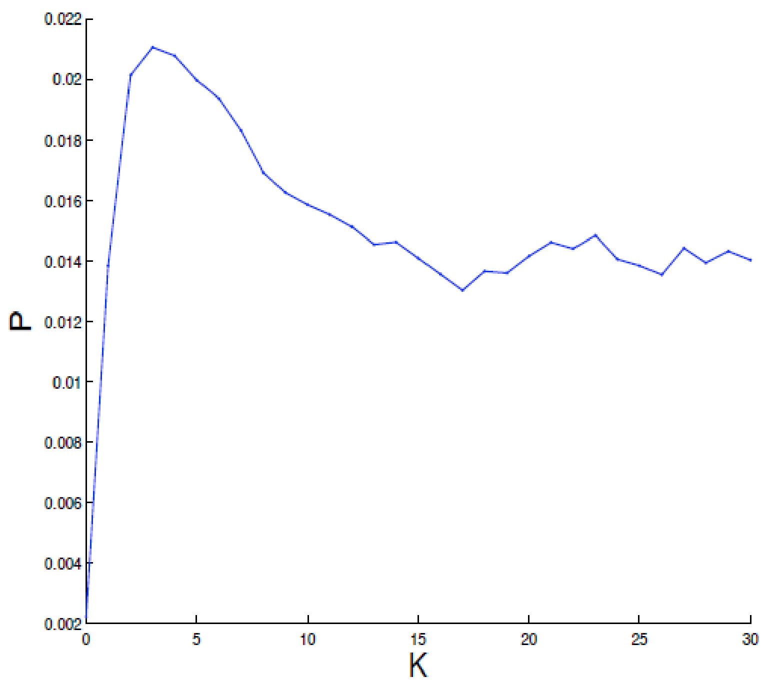
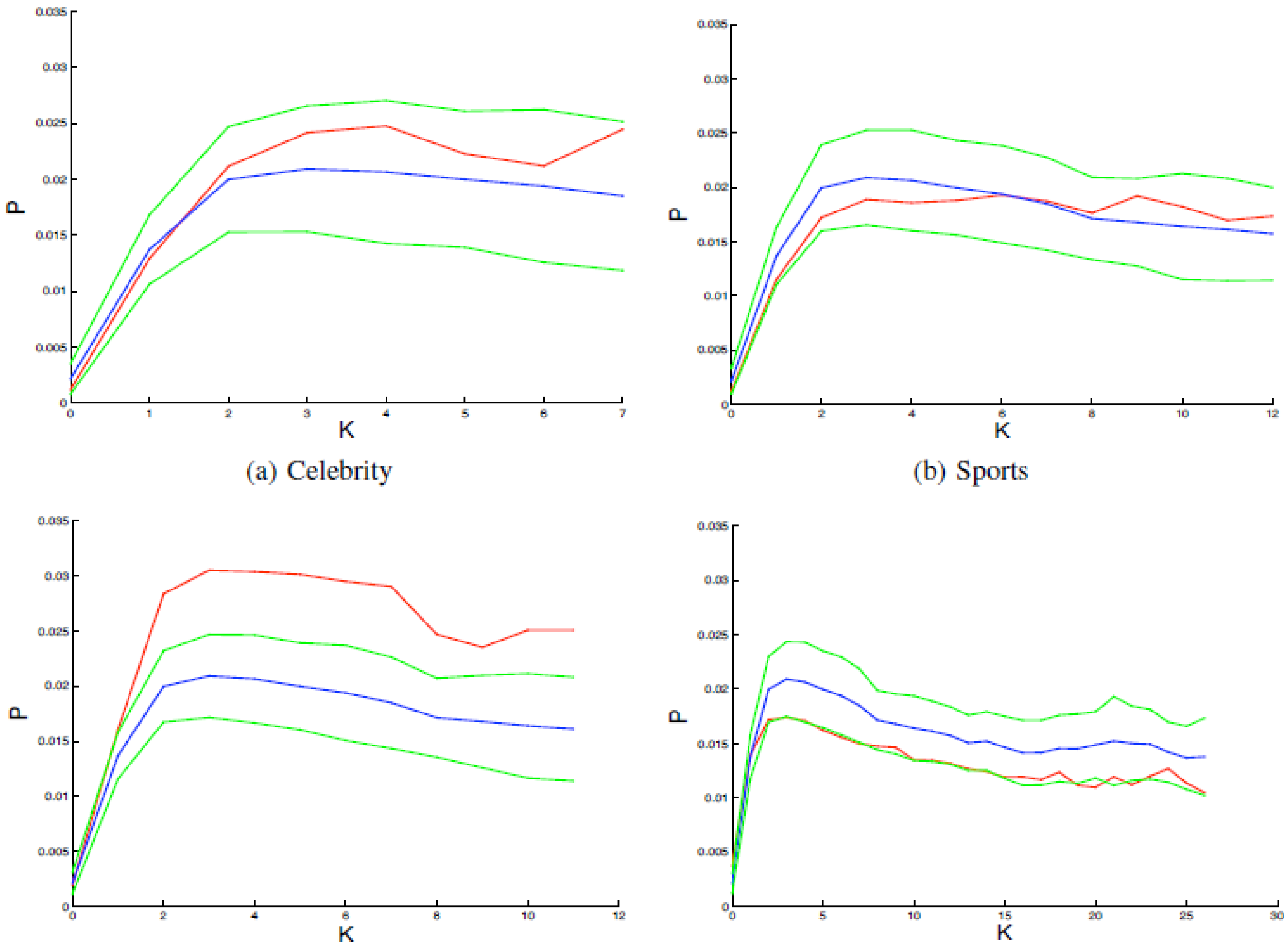


Figure 1: Average exposure curve for the top 500 hashtags. $P(K)$ is the fraction of users who adopt the hashtag directly after their k^{th} exposure to it, given that they had not yet adopted it

Motivation



(a) Celebrity

(b) Sports

(c) Music

(d) Technology

D. M. Romero et al. (2011)

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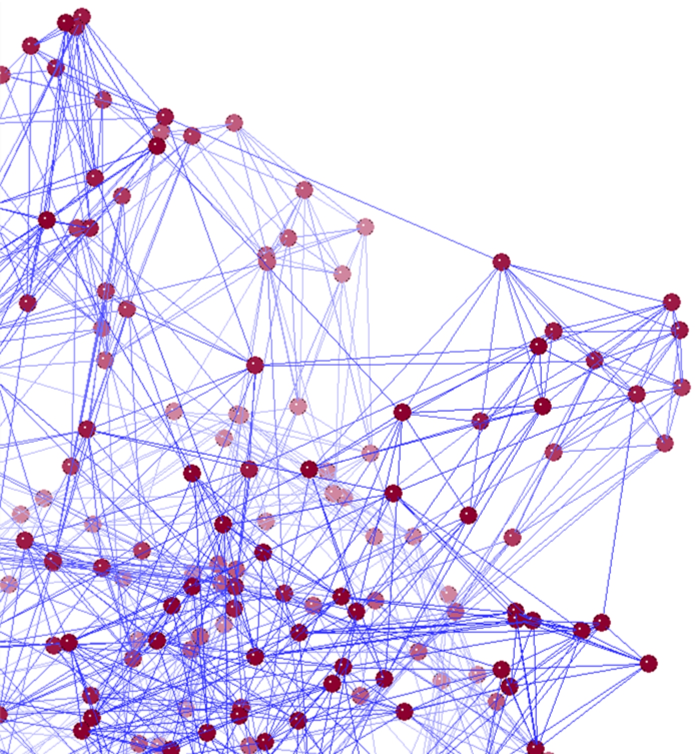
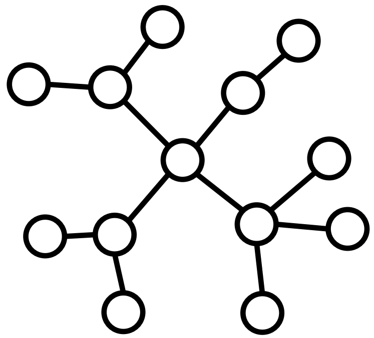
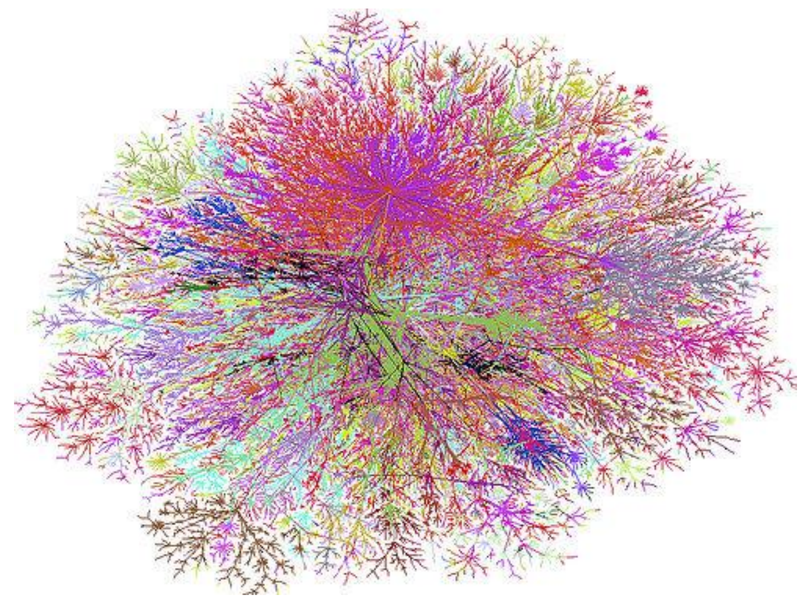


Network model



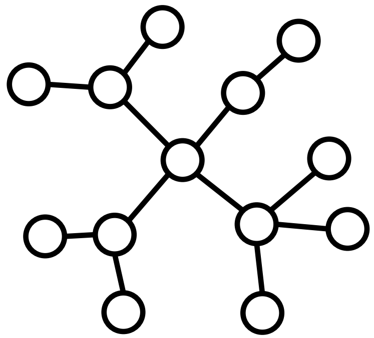


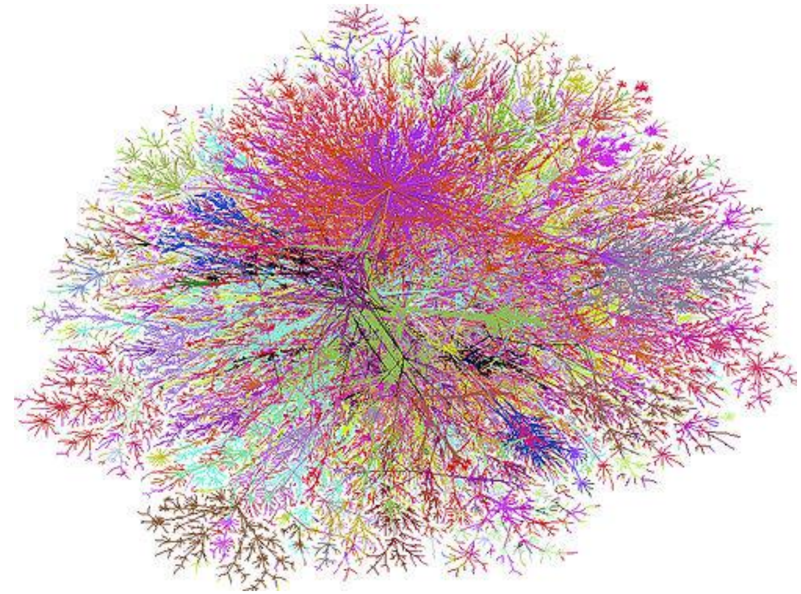
- Network of N nodes (vertices); take limit $N \to \infty$
- Static, undirected, unweighted
- Degree distribution:

  $P_k =$ probability that a randomly-chosen node has degree k
- Mean degree: $z = \langle k \rangle = \sum_{k=0}^{\infty} k\, P_k$

- Configuration model ensemble (uncorrelated, unclustered) for a given P_k

Network model





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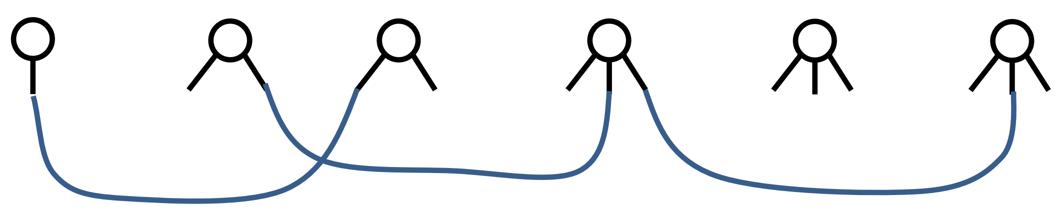

Dynamics: example

SIS (susceptible-infected-susceptible) model for disease spread
Each node is either infected or susceptible.
Infected nodes become susceptible at rate μ;
an infected node infects each of its susceptible neighbours at rate λ.

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→ Mean-field (MF) theory:
Pastor-Satorras and Vespignani (2001)

→ Pair approximation (PA):
Levin and Durrett (1996); Eames and Keeling (2002)

→ Approx. Master Equations (AME):
Marceau et al, PRE (2010), Lindquist et al, J. Math. Biol. (2011)

Dynamics: example

Voter model

Each node has an opinion (let's call these "infected" or "susceptible"). At each time step ($dt = 1/N$), a randomly-chosen node is updated.

The chosen node updates its opinion by picking a neighbour at random and copying the opinion of that neighbour.

→ MF: Sood and Redner (2005)

→ PA: Vazquez and Eguíluz (2008)

General binary-state stochastic dynamics:

- Each node (of N) is in one of two states at any time – call these states "susceptible" and "infected".

- A randomly-chosen fraction $\rho(0)$ of nodes are initially infected.

- In a small time step dt, a fraction dt of nodes are updated (often $dt = 1/N$).

- An updating node that is susceptible becomes infected with probability $F_{k,m}\, dt$, where k is the node's degree and m is the number of its neighbours that are infected:

- Notation: $F_{k,m}\, dt =$ infection probability for a k-degree susceptible node with m infected neighbours.

- Similarly: $R_{k,m}\, dt =$ recovery probability for a k-degree infected node with m infected neighbours.

Examples

Voter model

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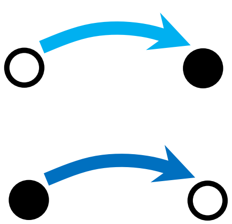


$$F_{k,m} = \frac{m}{k}$$

$$R_{k,m} = \frac{k-m}{k}$$

Examples

SIS (susceptible-infected-susceptible) model for disease spread
Each node is either infected or susceptible.
Infected nodes become susceptible at rate μ;
an infected node infects each of its susceptible neighbours at rate λ.

 $F_{k,m} = \lambda\, m$

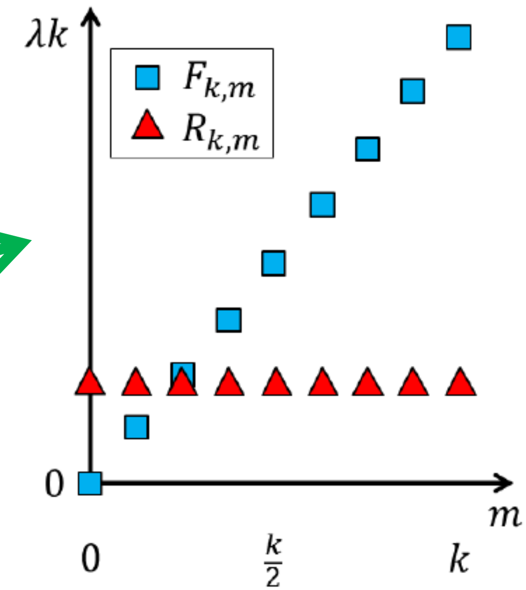
since $1 - (1 - \lambda\, dt)^m \approx \lambda\, m\, dt$
as $dt \to 0$

 $R_{k,m} = \mu$

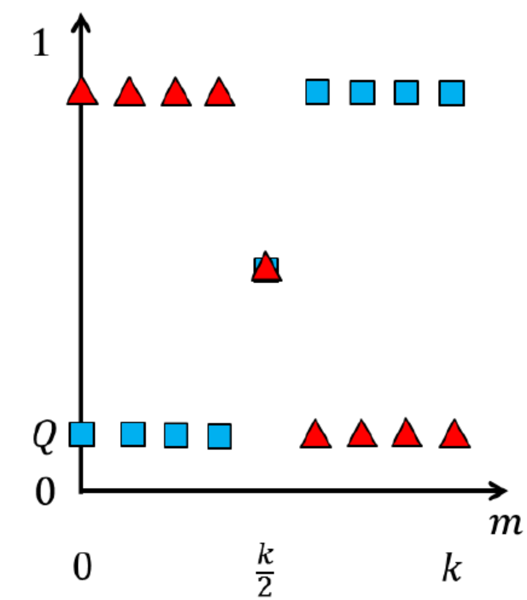
Examples

Process or model	$F_{k,m}$	$R_{k,m}$
SIS	λm	μ
SI	λm	0
Bass	$c + dm$	0
Kirman	$c_1 + dm$	$c_2 + d(k-m)$
voter	$\frac{m}{k}$	$\frac{k-m}{k}$
link update voter	$\frac{m}{z}$	$\frac{k-m}{z}$
majority-vote	$\begin{cases} Q & \text{if } m < k/2 \\ 1/2 & \text{if } m = k/2 \\ 1-Q & \text{if } m > k/2 \end{cases}$	$\begin{cases} 1-Q & \text{if } m < k/2 \\ 1/2 & \text{if } m = k/2 \\ Q & \text{if } m > k/2 \end{cases}$
Ising Glauber	$\frac{1}{1+\exp\left(\frac{2J}{T}(k-2m)\right)}$	$\frac{\exp\left(\frac{2J}{T}(k-2m)\right)}{1+\exp\left(\frac{2J}{T}(k-2m)\right)}$
Ising Metropolis	$\begin{cases} e^{\frac{2J}{T}(2m-k)} & \text{if } m < k/2 \\ 1 & \text{if } m \geq k/2 \end{cases}$	$\begin{cases} 1 & \text{if } m \leq k/2 \\ e^{\frac{2J}{T}(k-2m)} & \text{if } m > k/2 \end{cases}$
threshold	$\begin{cases} 0 & \text{if } m < M_k \\ 1 & \text{if } m \geq M_k \end{cases}$	0

SIS disease-spread



Majority-vote



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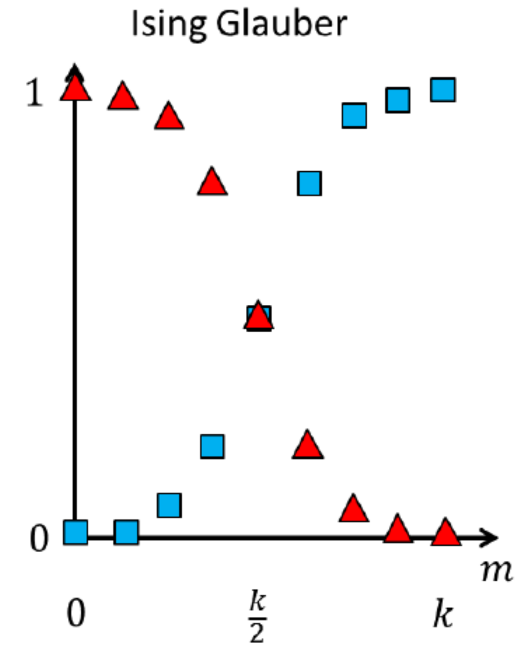
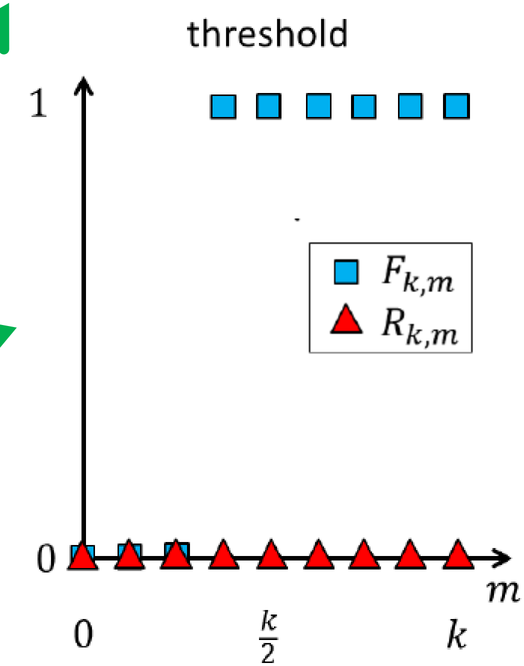
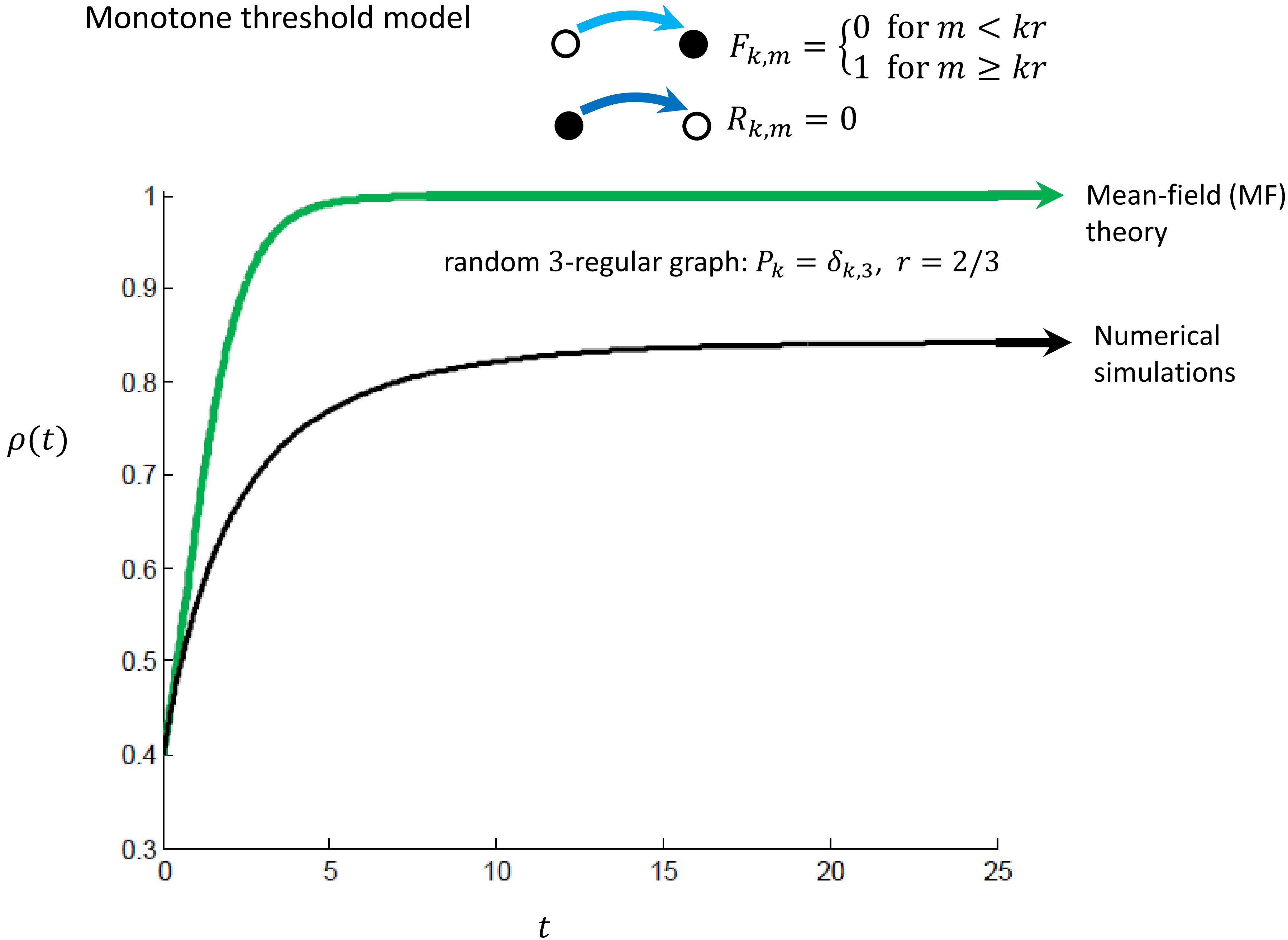
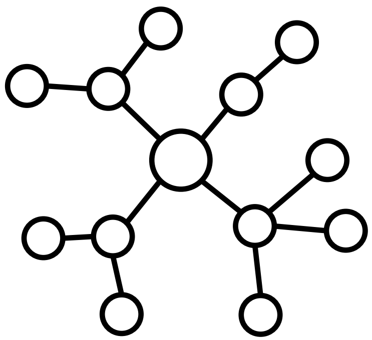




Monotone threshold model



Approximation methods



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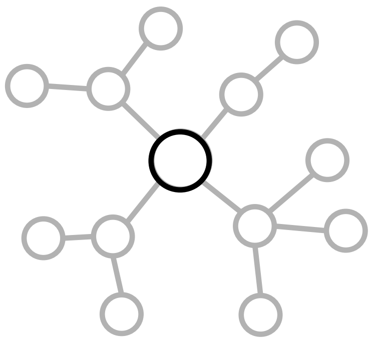
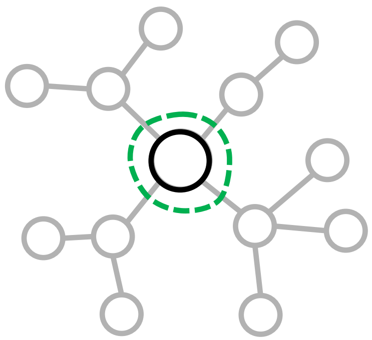


Approximation methods

Mean-field (MF)



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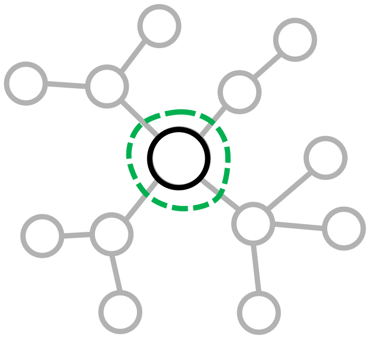

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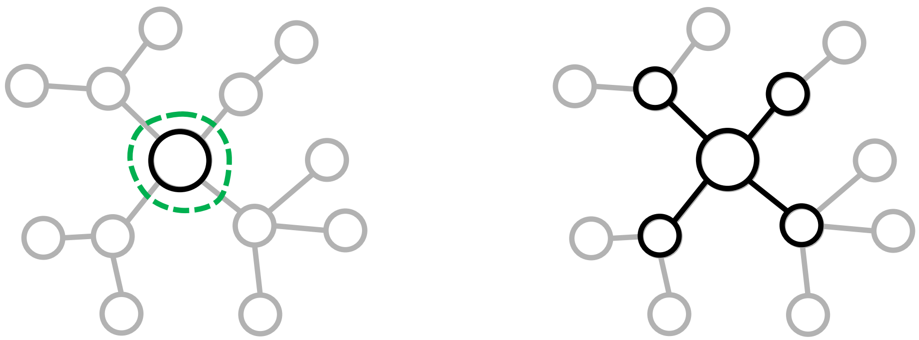

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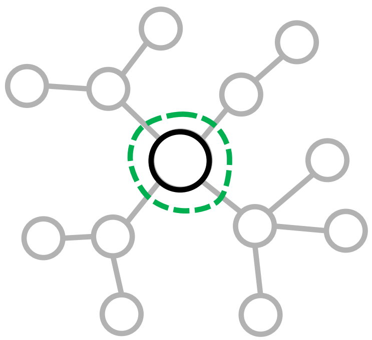
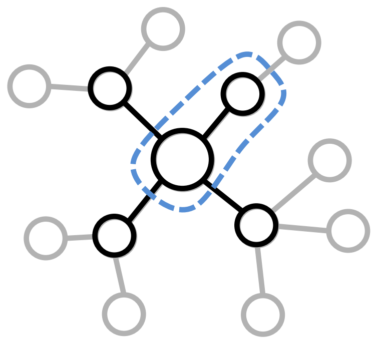


Pair approximation (PA)



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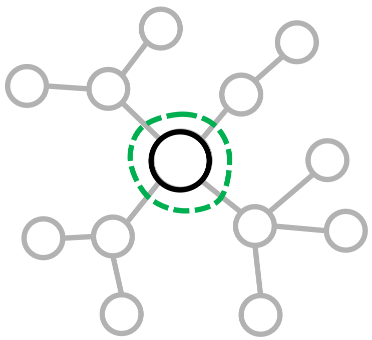

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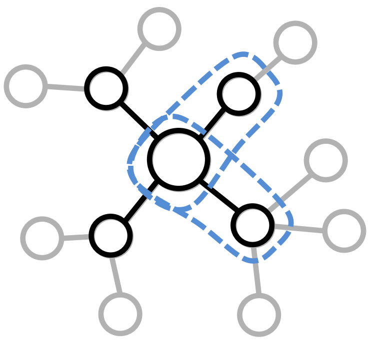

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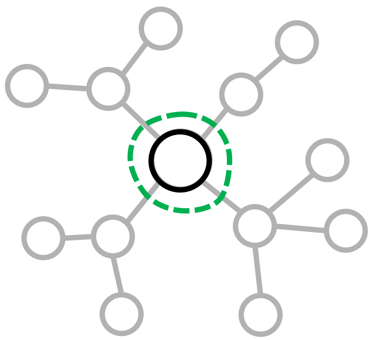

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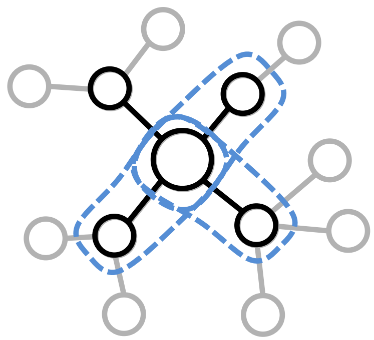

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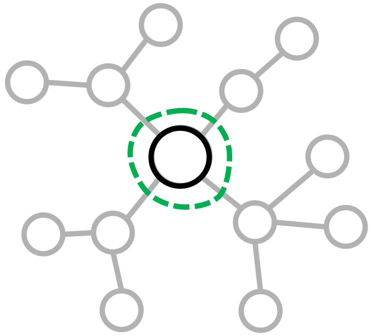

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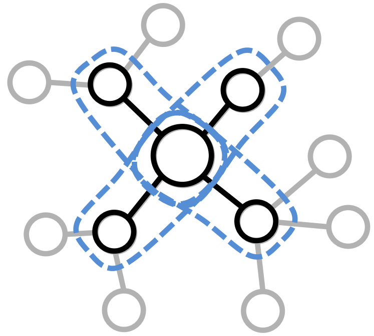

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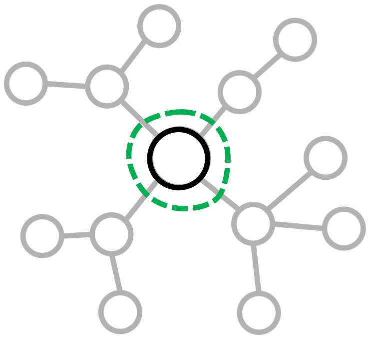

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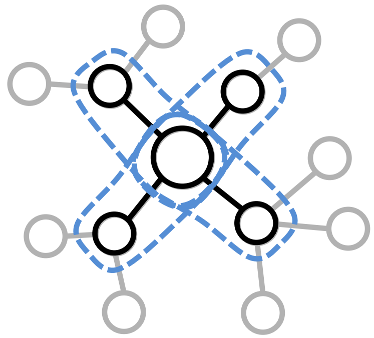

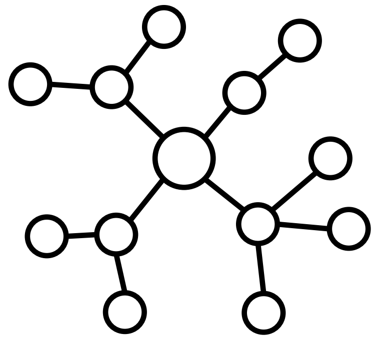

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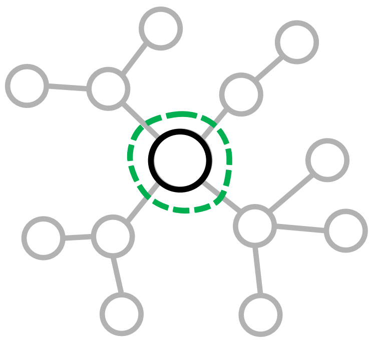

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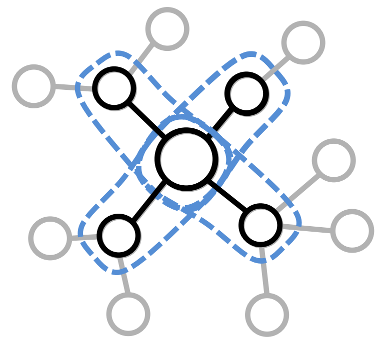
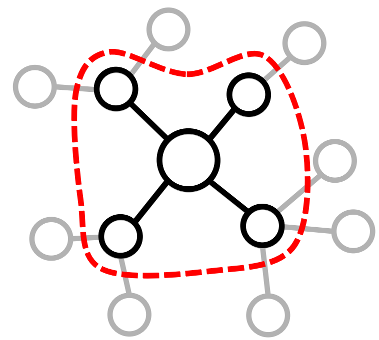


Approx. Master Eqn. (AME)



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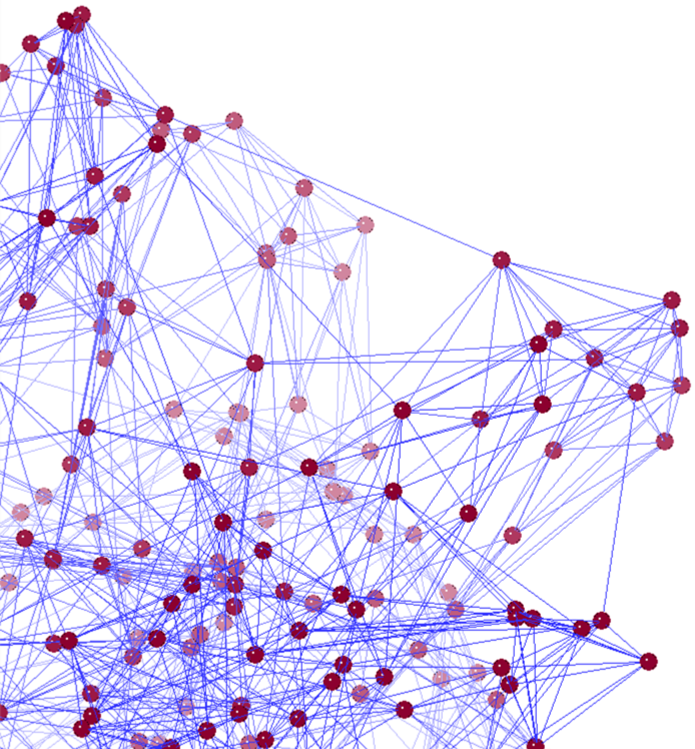
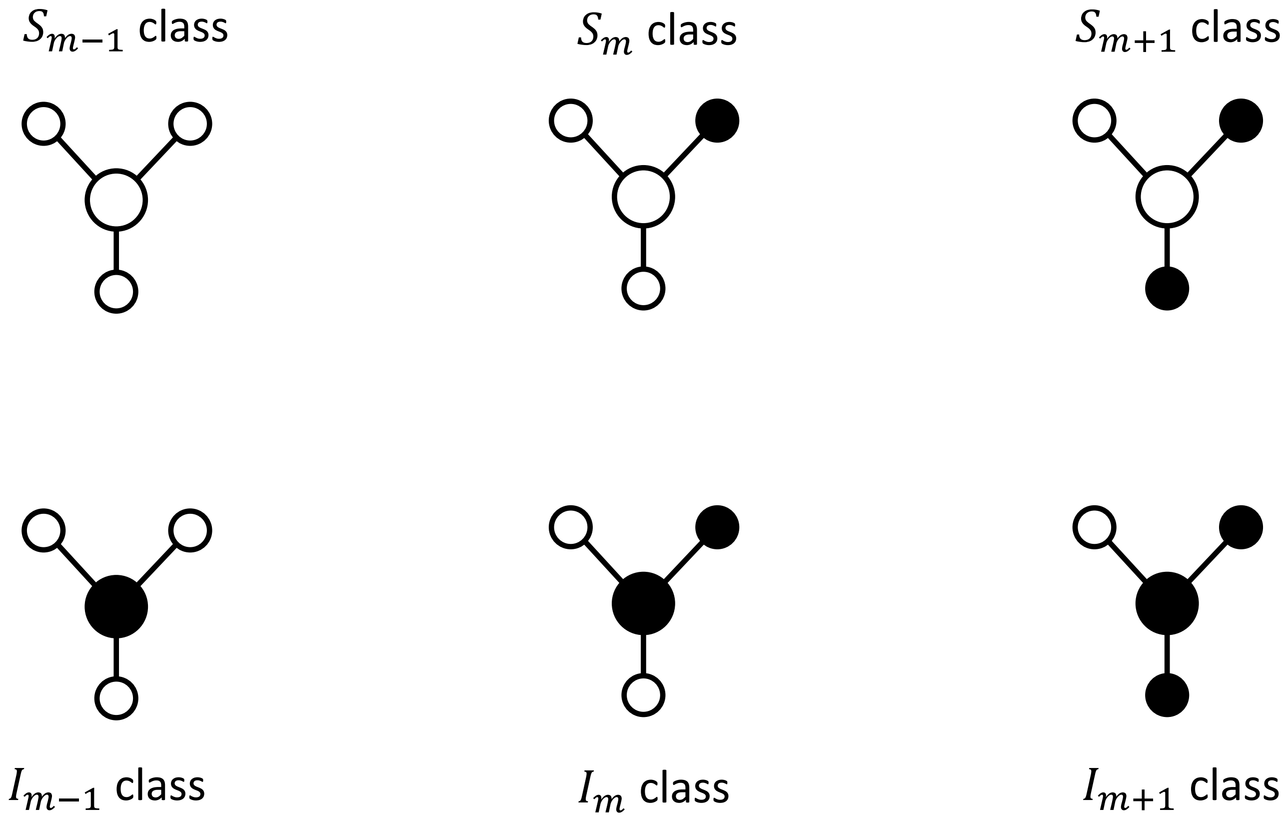


Approx. Master Equations (AME) for SIS:
Marceau et al, PRE (2010),
Lindquist et al, J. Math. Biol. (2011)

Random z-regular graphs



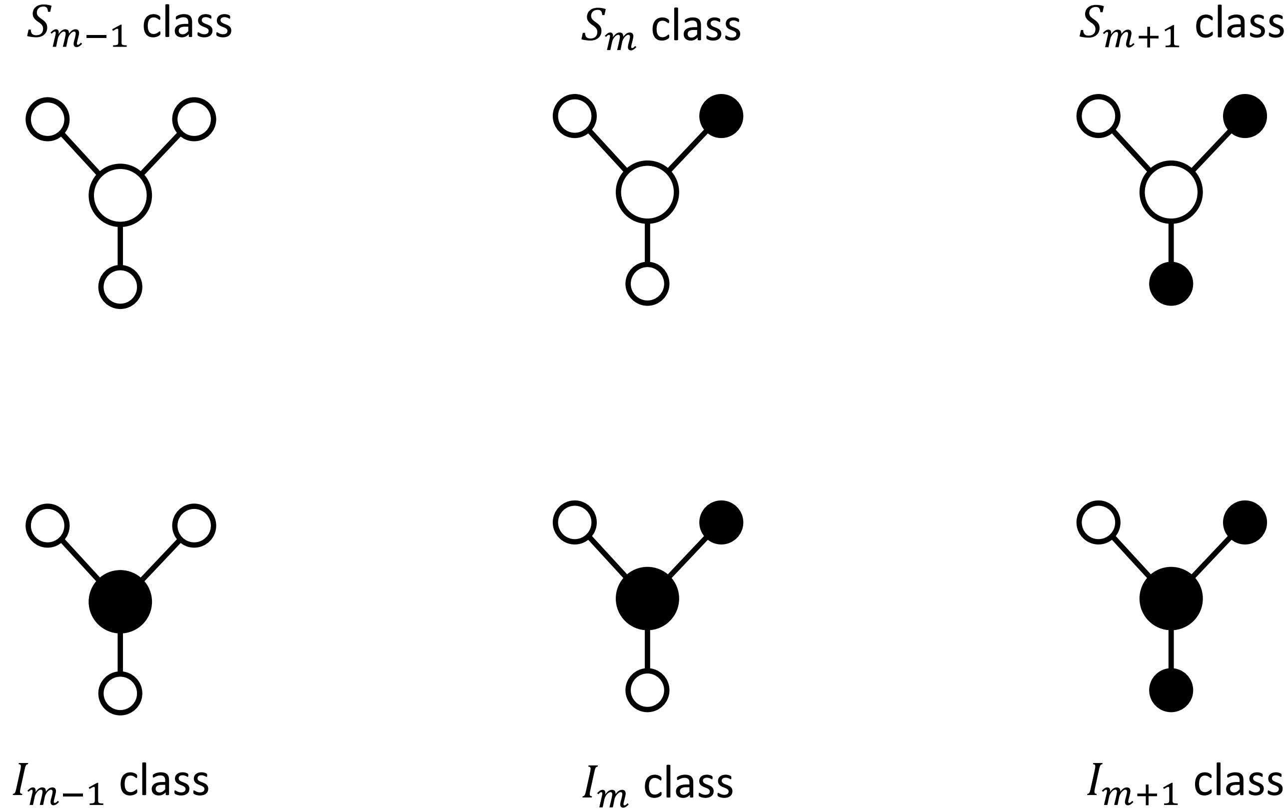
$s_m(t) =$ size of S_m class at time t (for $m = 0, 1, \ldots, z$)

$=$ fraction of nodes which are susceptible and have m infected neighbours at time t

$i_m(t) =$ fraction of nodes which are infected and have m infected neighbours at time t

$$s_m(0) = (1 - \rho(0))B_{z,m}(\rho(0))$$

$$i_m(0) = \rho(0)B_{z,m}(\rho(0))$$



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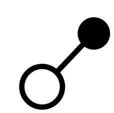
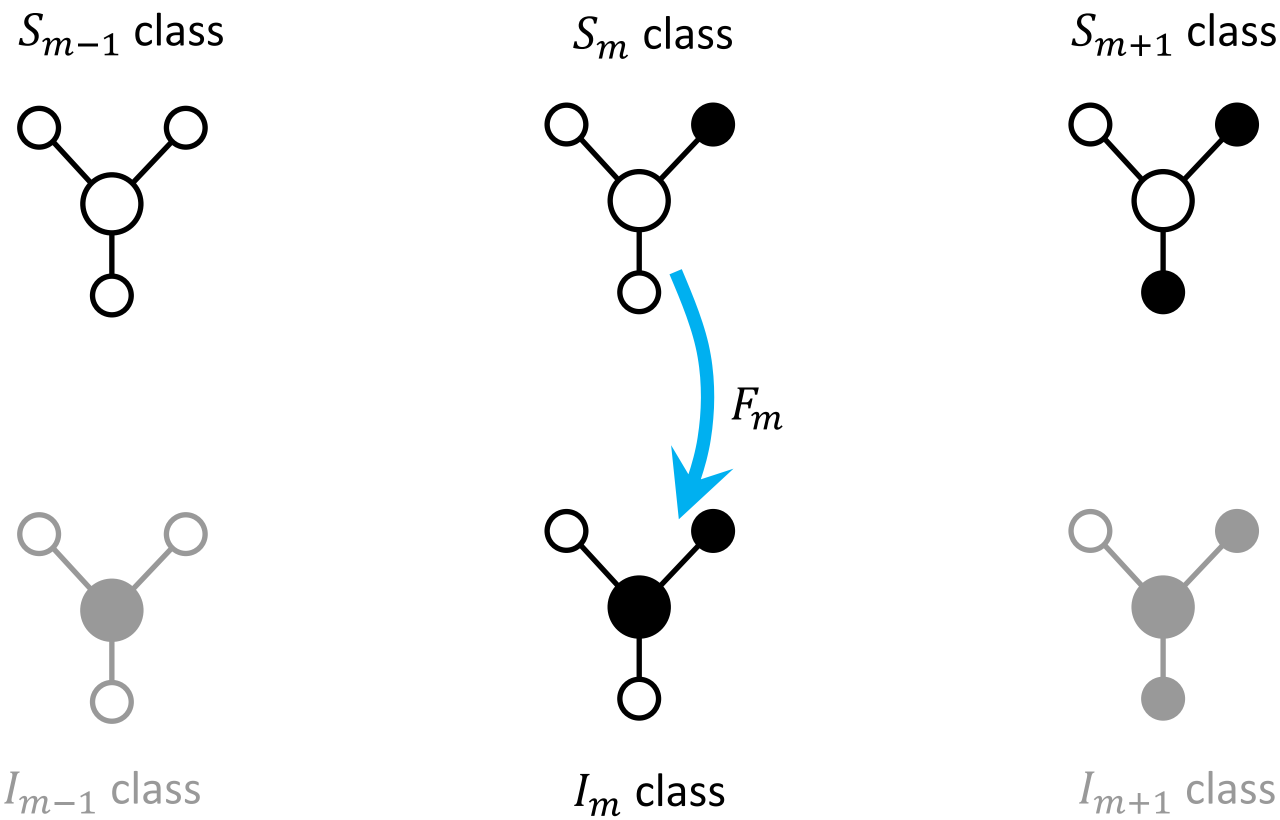


$= \text{number of S-I edges}$

$$= N \sum_{m=0}^{z} m s_m$$

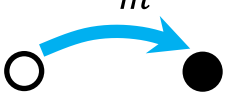


$$\frac{d}{dt} s_m = -F_m s_m + \cdots$$

for $m = 0, 1, \ldots, z$

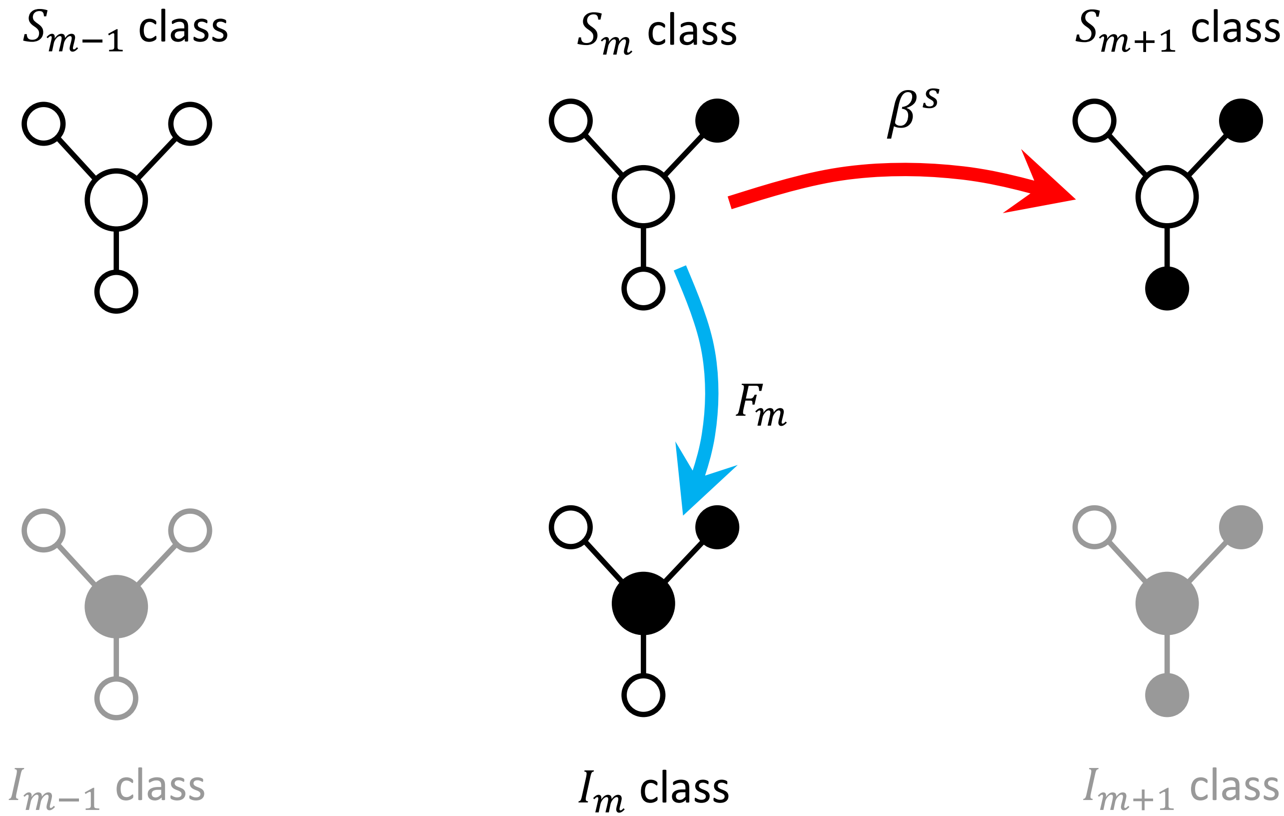
$s_m(t)$ = fraction of nodes which are susceptible and have m infected neighbours at time t

$F_m \, dt$ = infection probability for a susceptible node with m infected neighbours

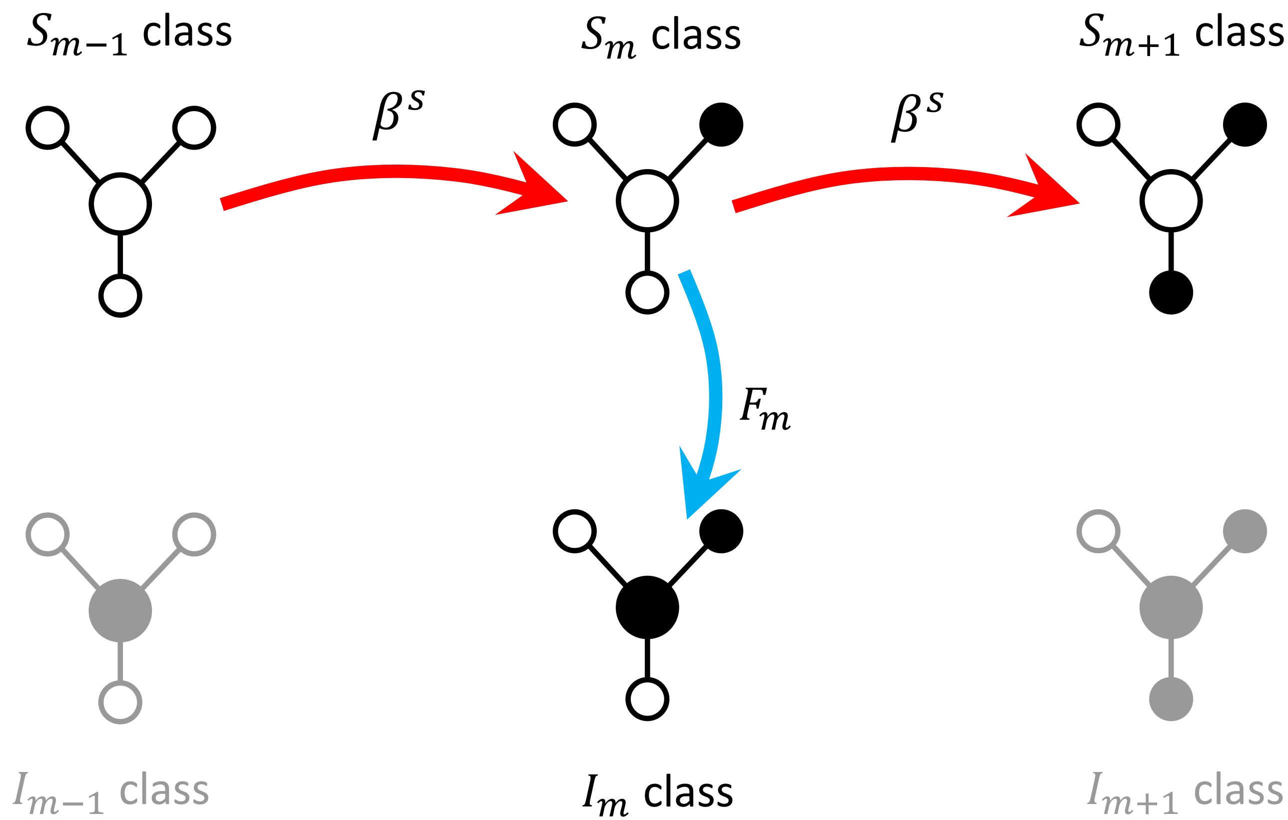


e.g., threshold model on random z-regular graph:

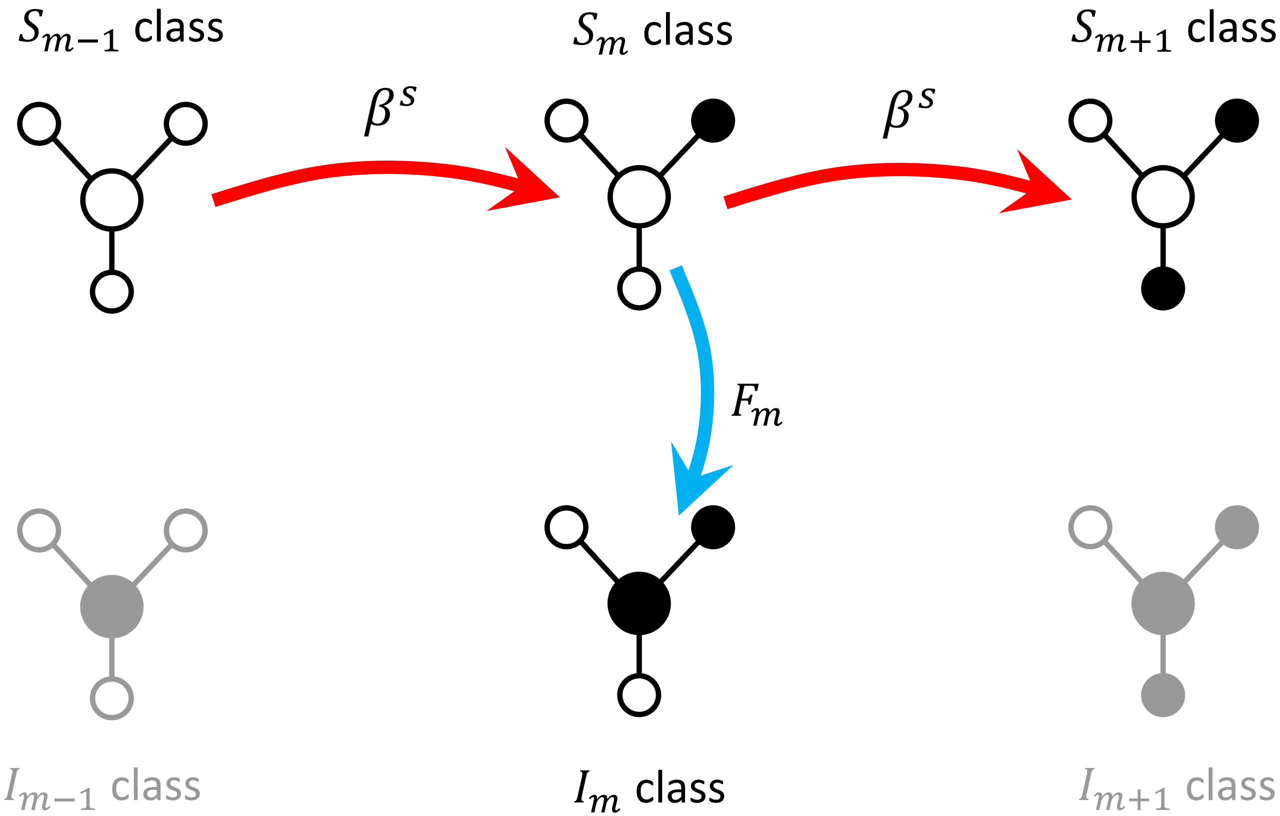
$$F_m \equiv F_{z,m} = \begin{cases} 0 & \text{for } m < zr \\ 1 & \text{for } m \geq zr \end{cases}$$



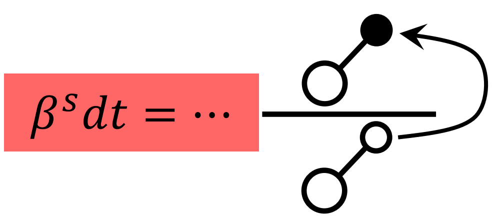
$$\frac{d}{dt}s_m = -F_m s_m - \beta^s(z-m)s_m + \cdots$$ for $m = 0,1,\ldots,z$

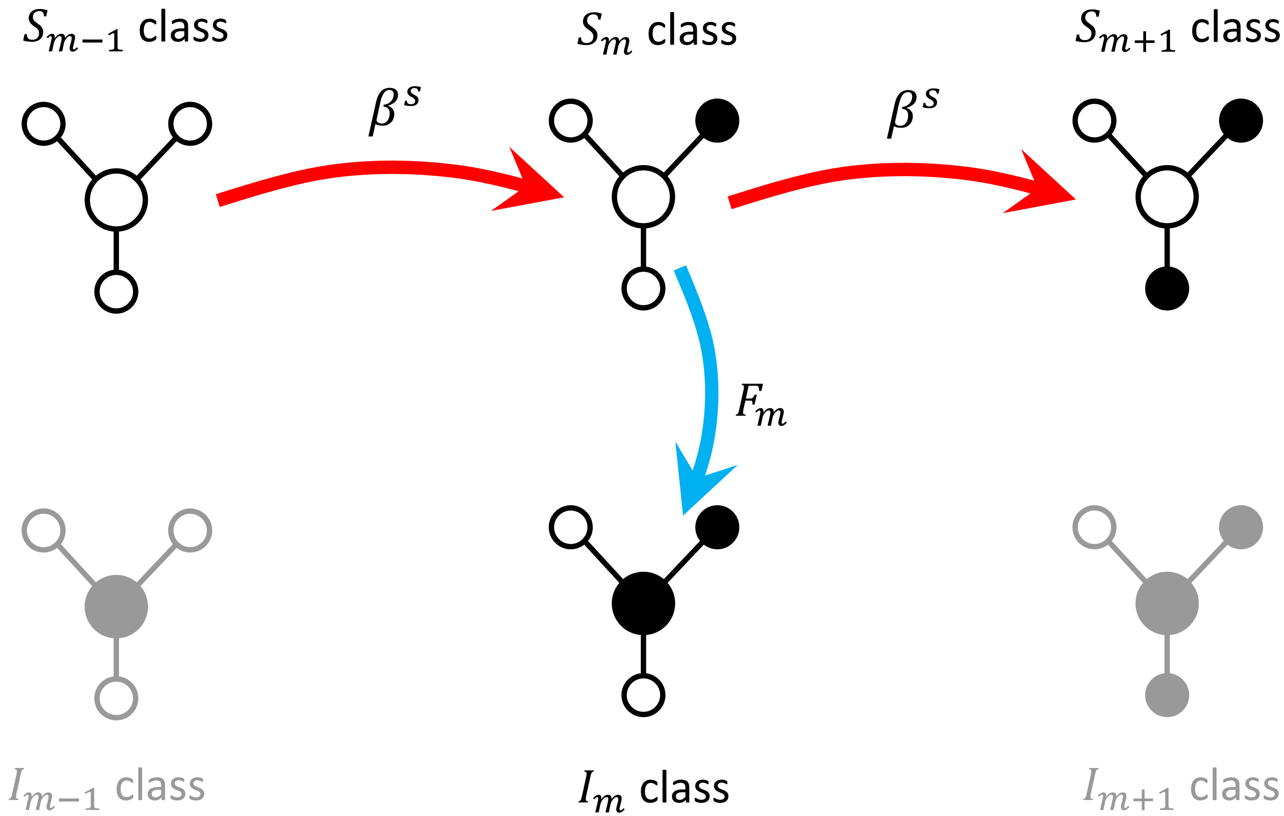


$$\frac{d}{dt} s_m = -F_m s_m - \beta^s(z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0,1, \ldots, z$$

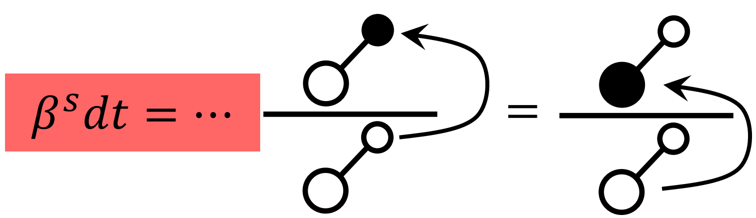


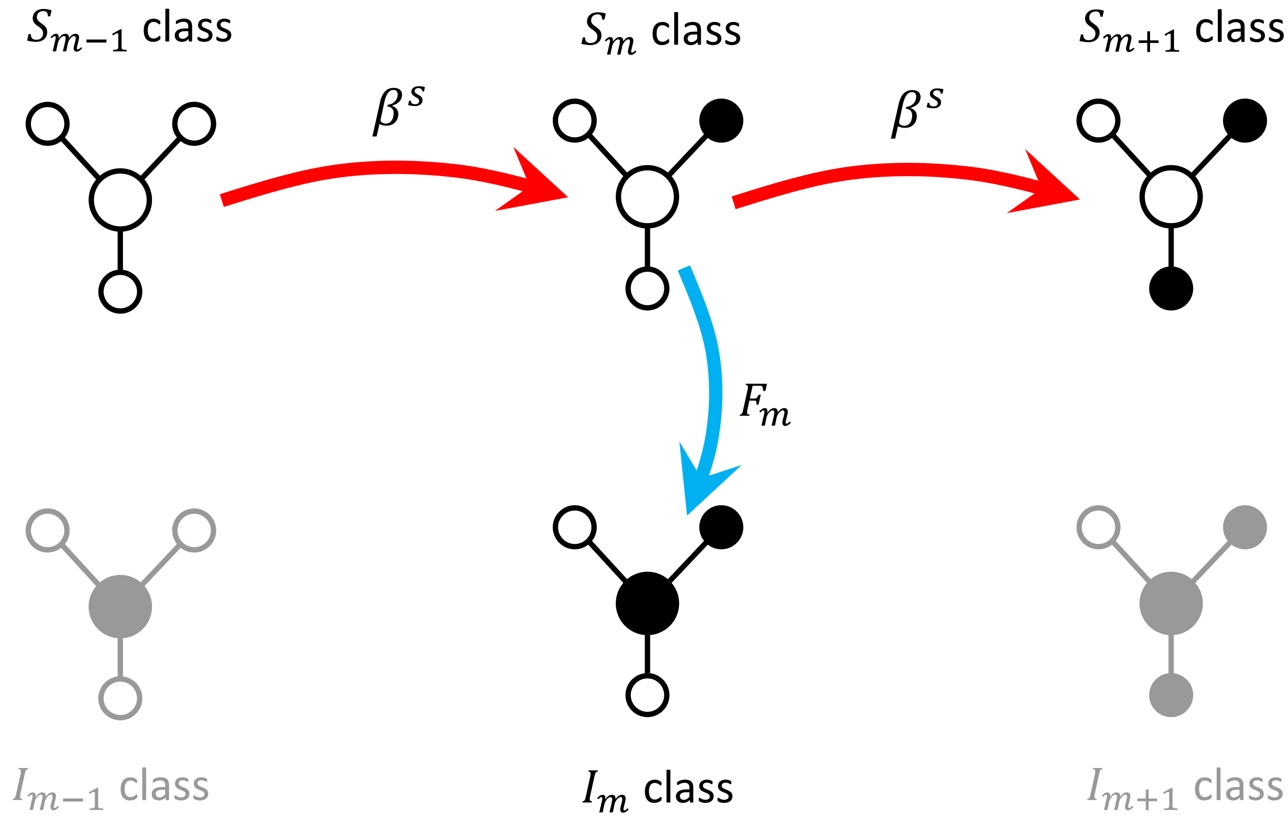
$$\frac{d}{dt} s_m = -F_m s_m - \beta^s (z-m) s_m + \beta^s (z-m+1) s_{m-1} \quad \text{for } m = 0,1,\ldots,z$$





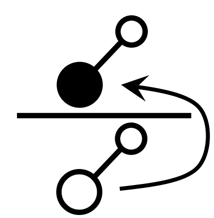
$$\frac{d}{dt} s_m = -F_m s_m - \beta^s (z-m) s_m + \beta^s (z-m+1) s_{m-1} \quad \text{for } m = 0,1,\ldots,z$$

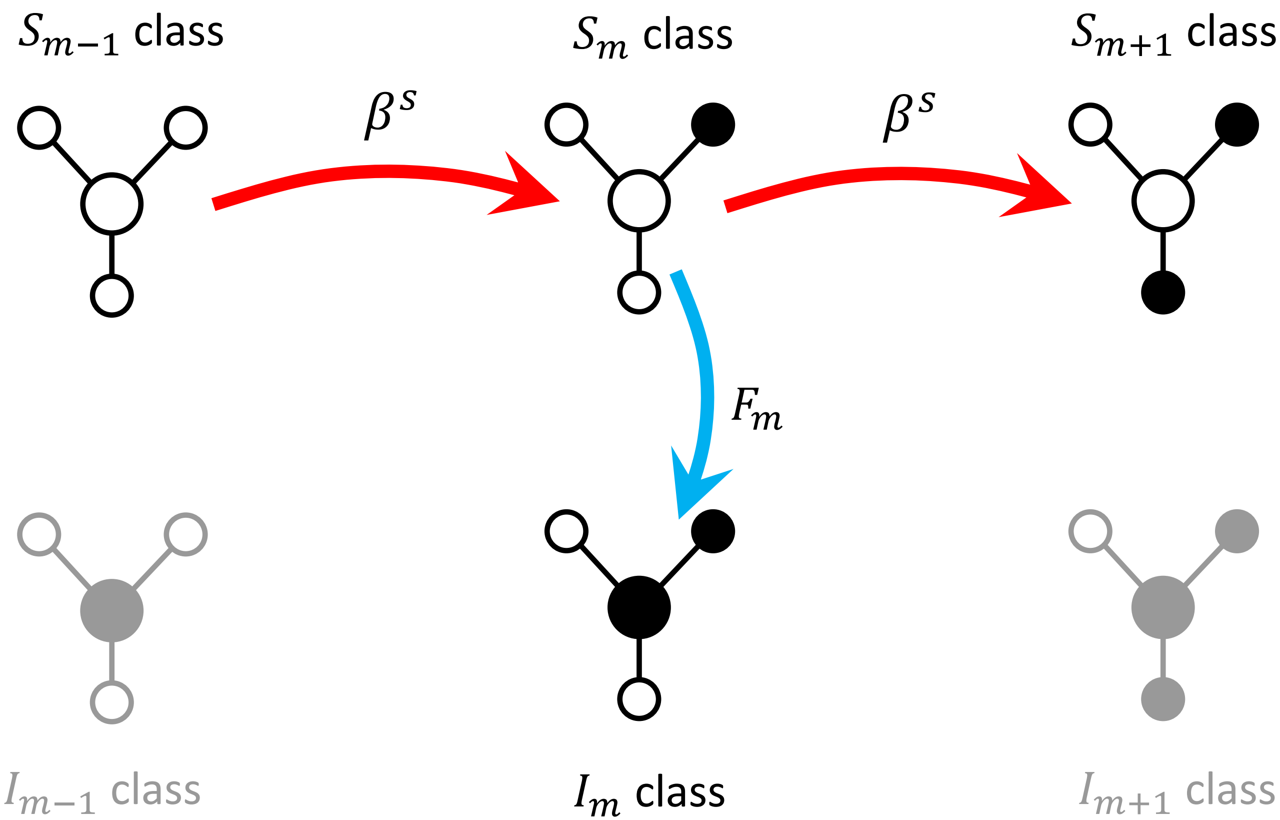




$$\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0,1, \dots, z$$

$$\beta^s = \frac{\sum_{m=0}^{z} (z-m) F_m s_m}{\sum_{m=0}^{z} (z-m) s_m} =$$





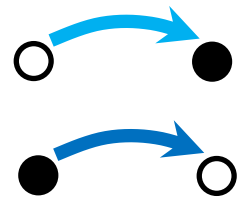
$$\frac{d}{dt}s_m = -F_m s_m - \beta^s(z-m)s_m + \beta^s(z-m+1)s_{m-1} \quad \text{for } m = 0,1,\dots,z$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m}$$

$$s_m(0) = (1-\rho(0))B_{z,m}(\rho(0))$$

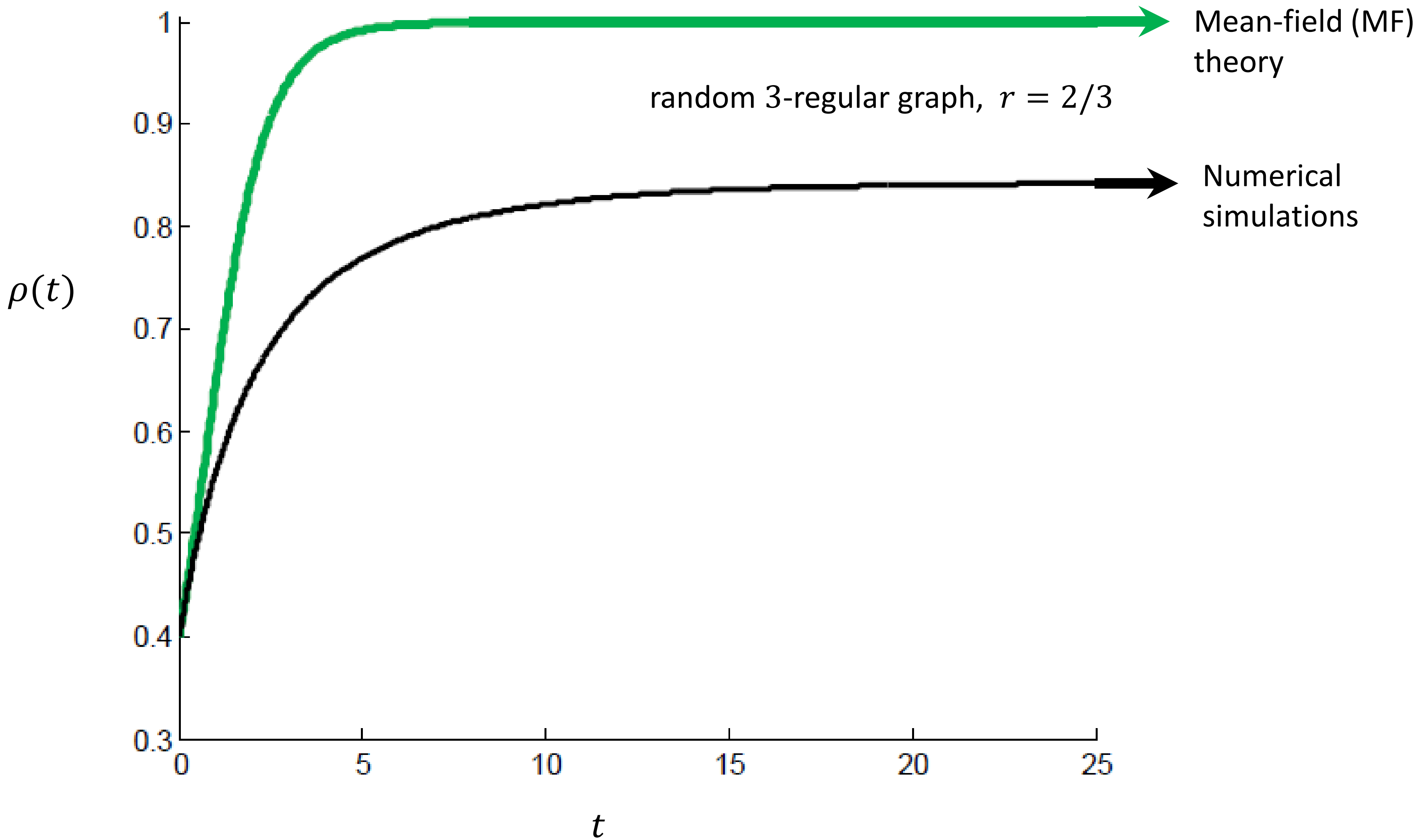
$$\rho(t) = 1 - \sum_{m=0}^{z} s_m(t)$$

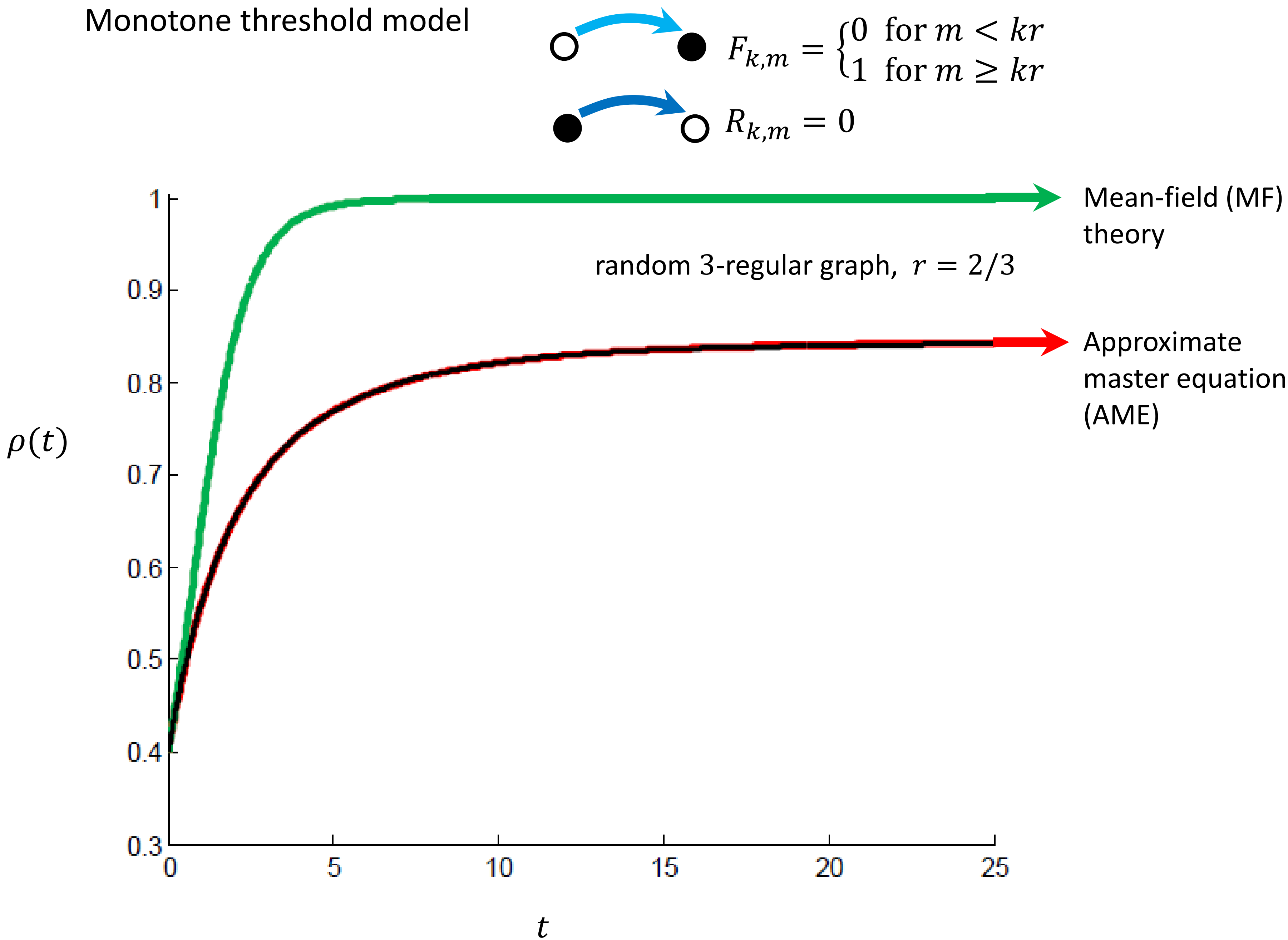
Monotone threshold model



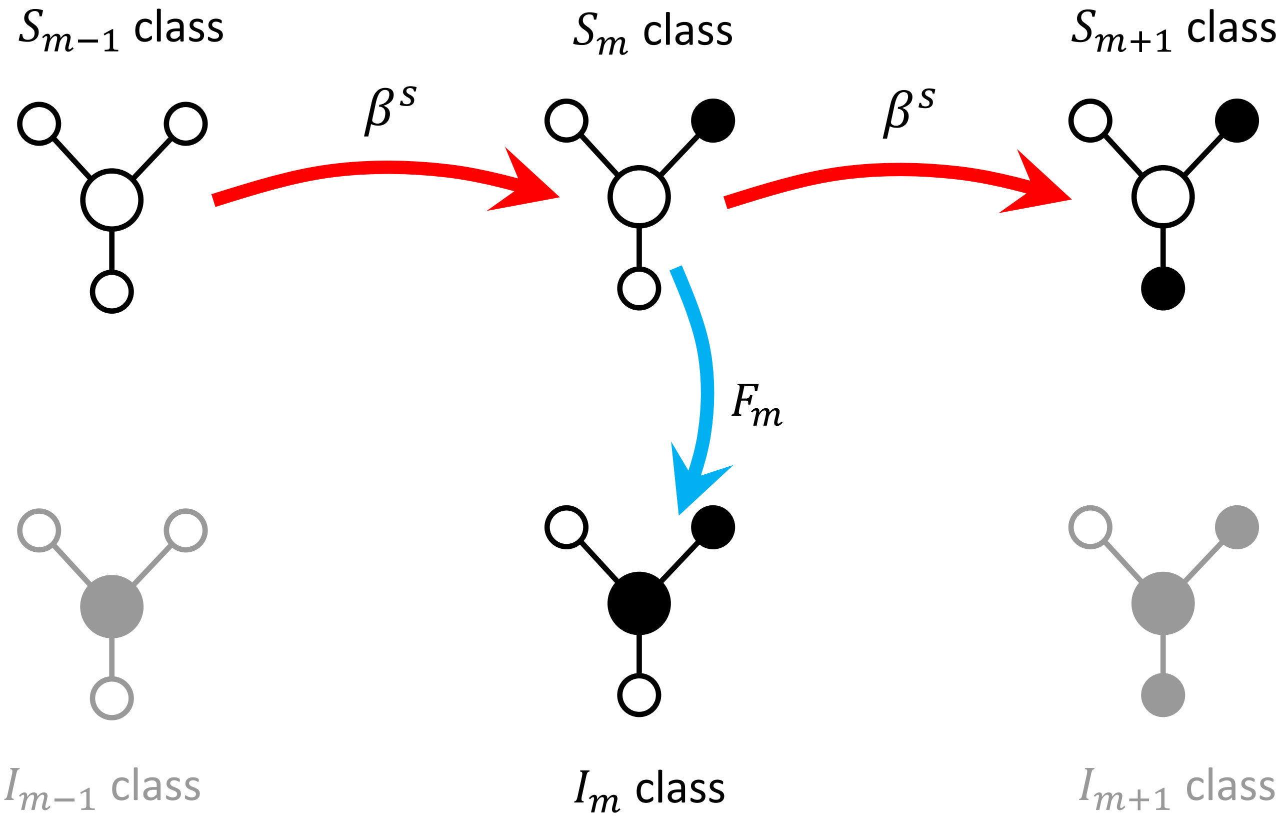
$$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$$

$$R_{k,m} = 0$$





Monotone threshold model
$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$
$R_{k,m} = 0$
Mean-field (MF) theory
random 3-regular graph, $r = 2/3$
Approximate master equation (AME)
$\rho(t)$
t
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0
5
10
15
20
25

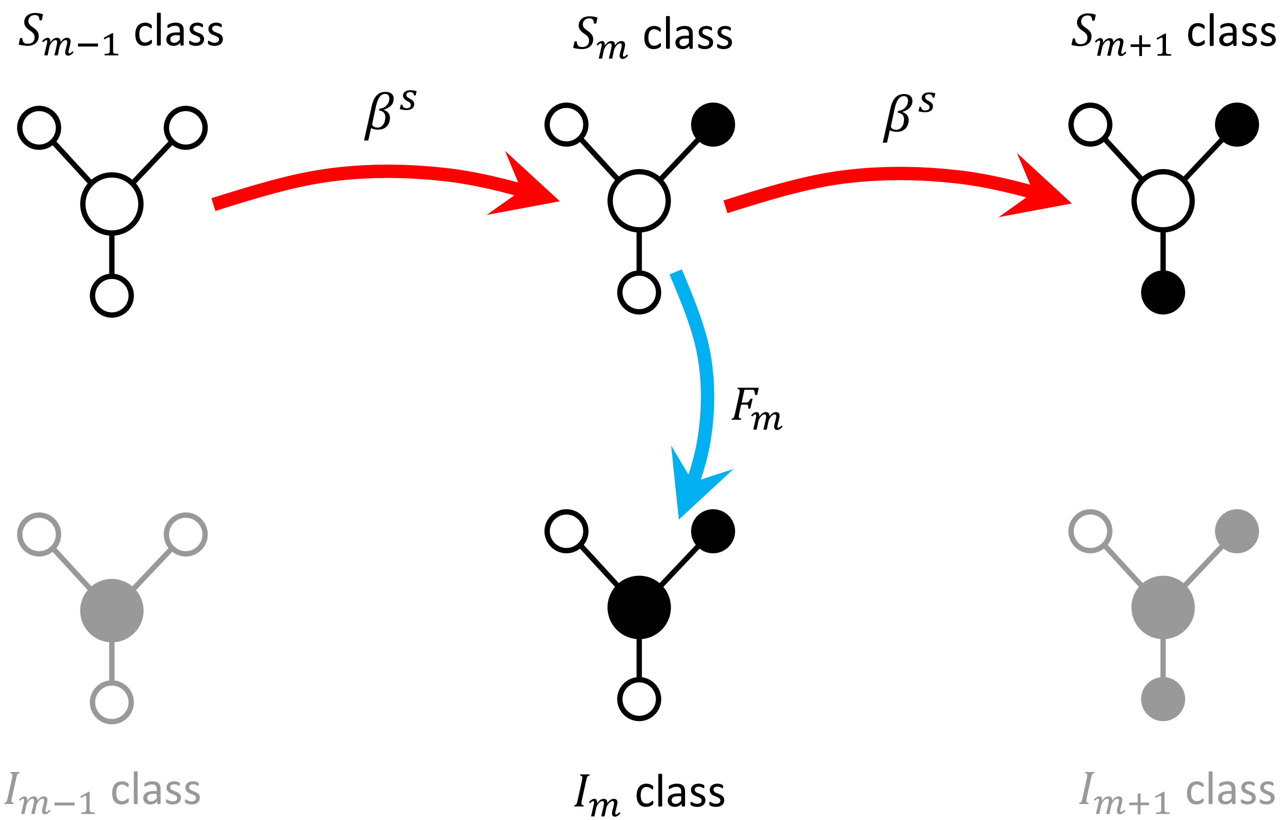


$$\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0,1, \dots, z$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m) F_m s_m}{\sum_{m=0}^{z}(z-m) s_m}$$

$$s_m(0) = (1 - \rho(0)) B_{z,m}(\rho(0))$$

$$\rho = 1 - \sum_{m=0}^{z} s_m$$

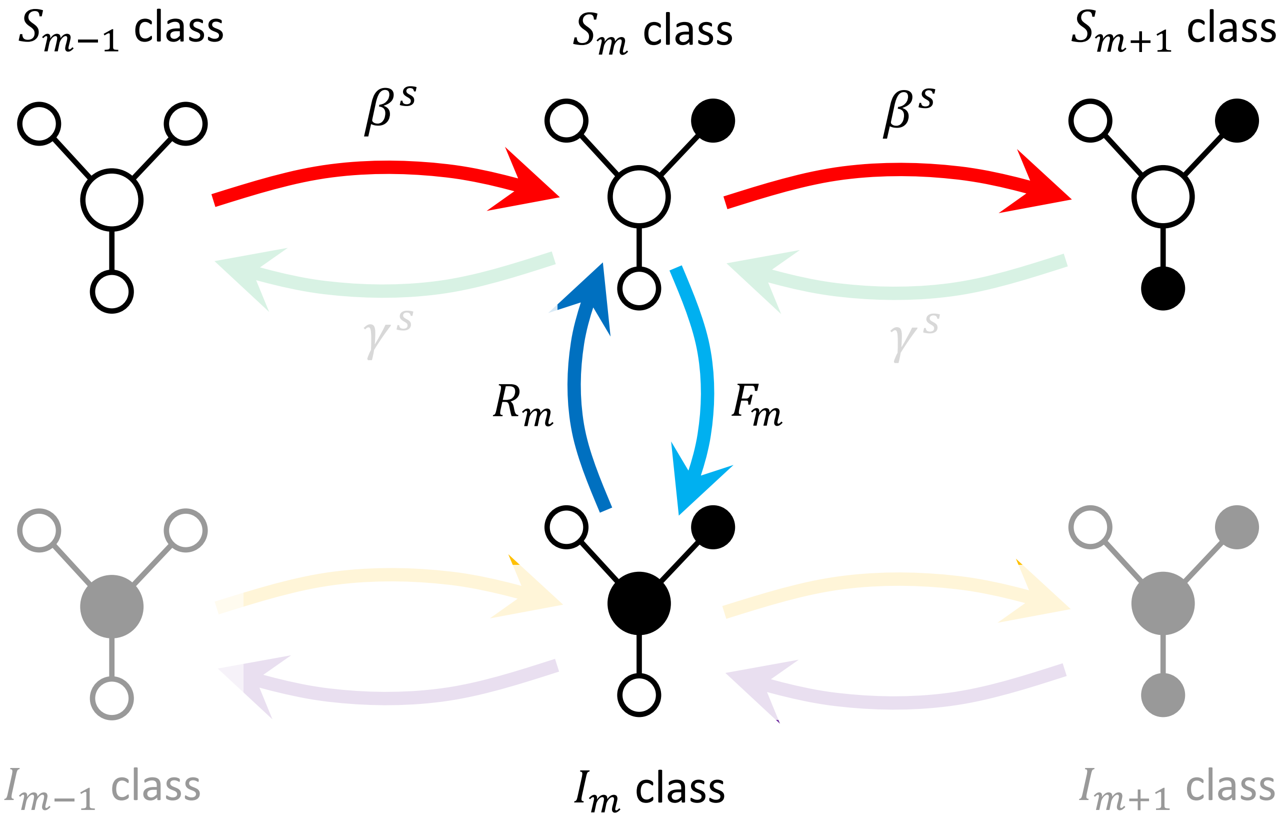


$$\frac{d}{dt}s_m = -F_m s_m \quad -\beta^s(z-m)s_m+\beta^s(z-m+1)s_{m-1} \quad \text{for } m=0,1,\ldots,z$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m}$$

$$s_m(0) = (1-\rho(0))B_{z,m}(\rho(0))$$

$$\rho = 1-\sum_{m=0}^{z} s_m$$



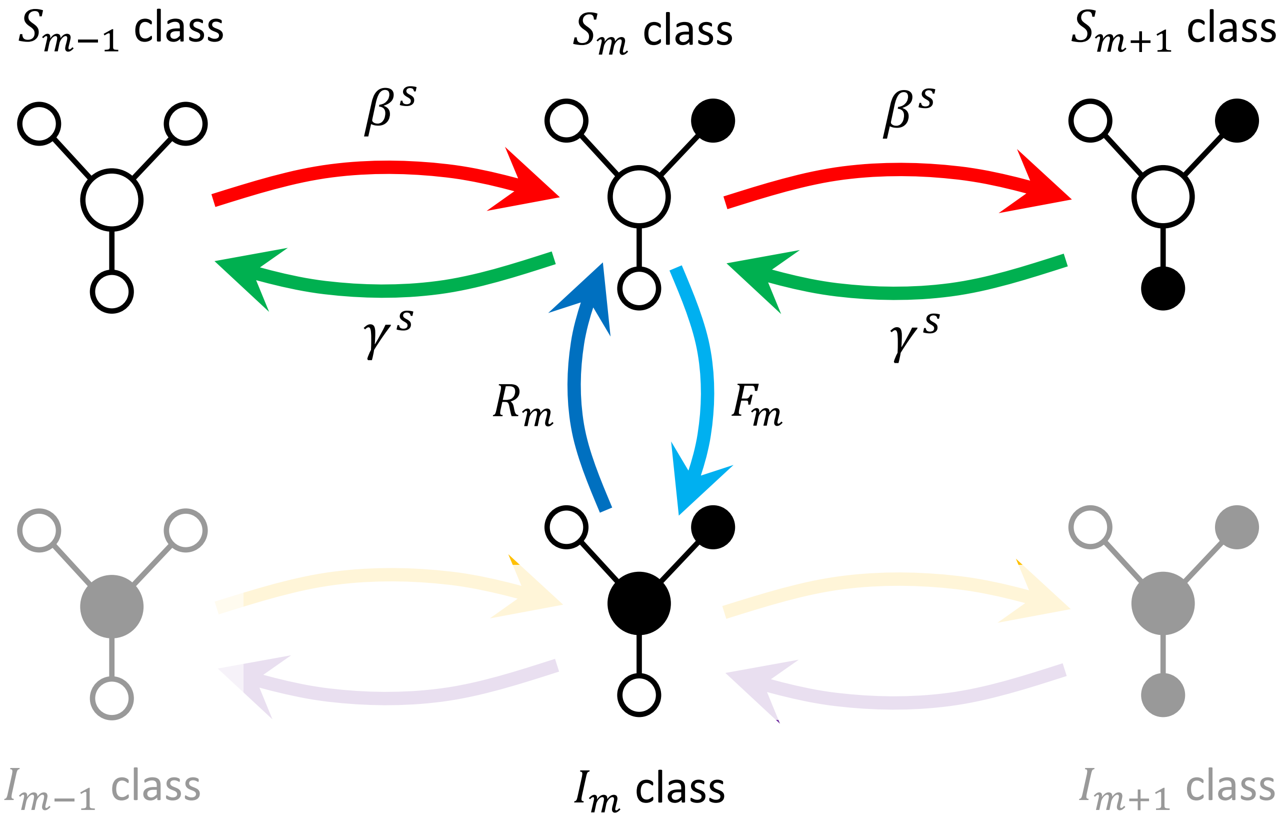
$$\frac{d}{dt} s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z-m)) s_m + \beta^s (z-m+1) s_{m-1} + \gamma^s (m+1) s_{m+1}$$

$R_m\, dt =$ recovery probability for an infected node with m infected neighbours

$$\beta^s = \frac{\sum_{m=0}^{z} (z-m) F_m s_m}{\sum_{m=0}^{z} (z-m) s_m}$$

e.g., non-monotone threshold model:

$$R_{k,m} = \begin{cases} 1 & \text{for } m < kr \\ 0 & \text{for } m \geq kr \end{cases}$$

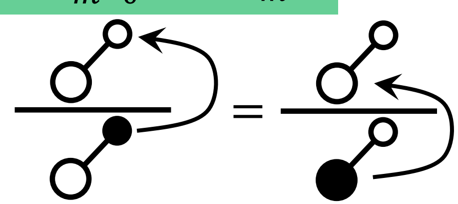


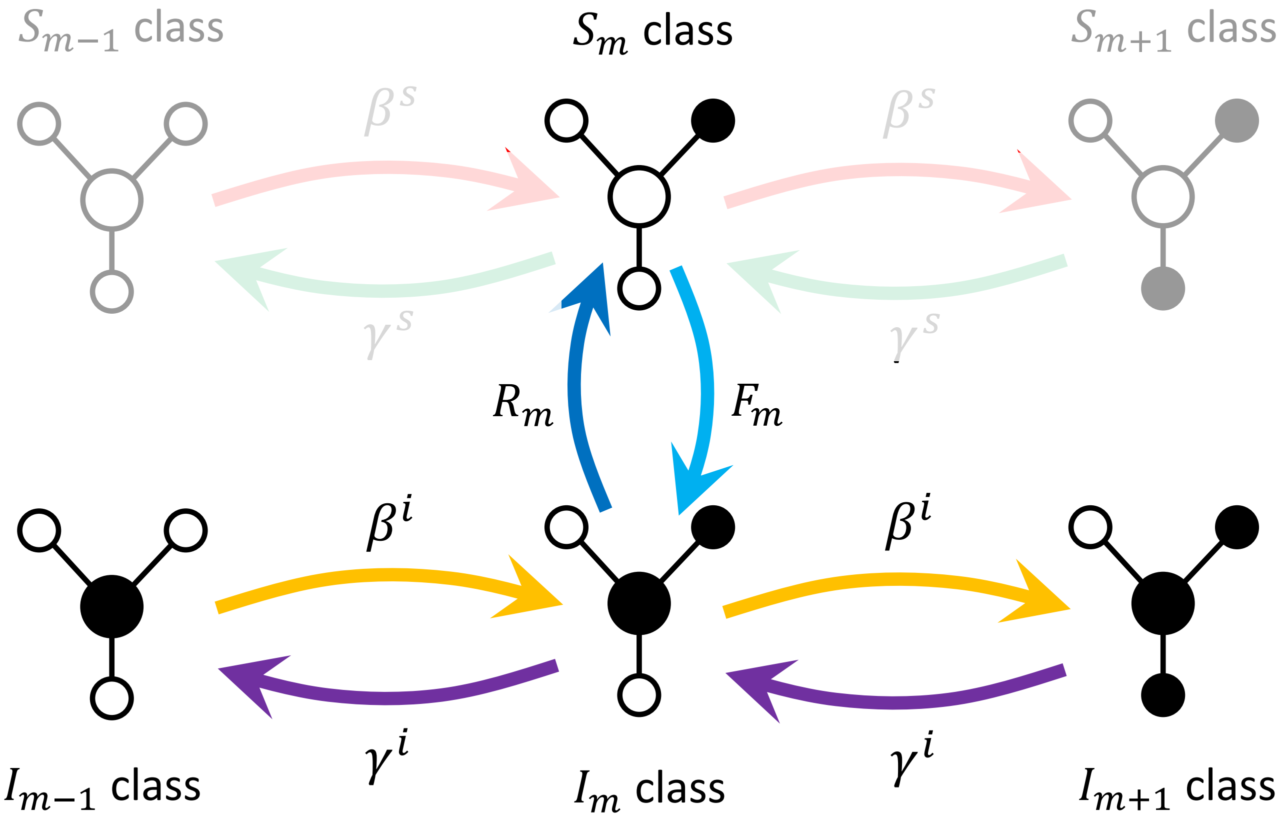
$$\frac{d}{dt}s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z-m))s_m + \beta^s (z-m+1)s_{m-1} + \gamma^s (m+1)s_{m+1}$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m}$$

$$\gamma^s = \frac{\sum_{m=0}^{z}(z-m)R_m i_m}{\sum_{m=0}^{z}(z-m)i_m}$$

$$s_m(0) = (1-\rho(0))B_{z,m}(\rho(0))$$





$$\frac{d}{dt}s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z-m)) s_m + \beta^s (z-m+1) s_{m-1} + \gamma^s (m+1) s_{m+1}$$

$$\frac{d}{dt}i_m = -R_m i_m + F_m s_m - (\gamma^i m + \beta^i (z-m)) i_m + \beta^i (z-m+1) i_{m-1} + \gamma^i (m+1) i_{m+1}$$

$$\beta^s = \frac{\sum_{m=0}^{z} (z-m) F_m s_m}{\sum_{m=0}^{z} (z-m) s_m}$$

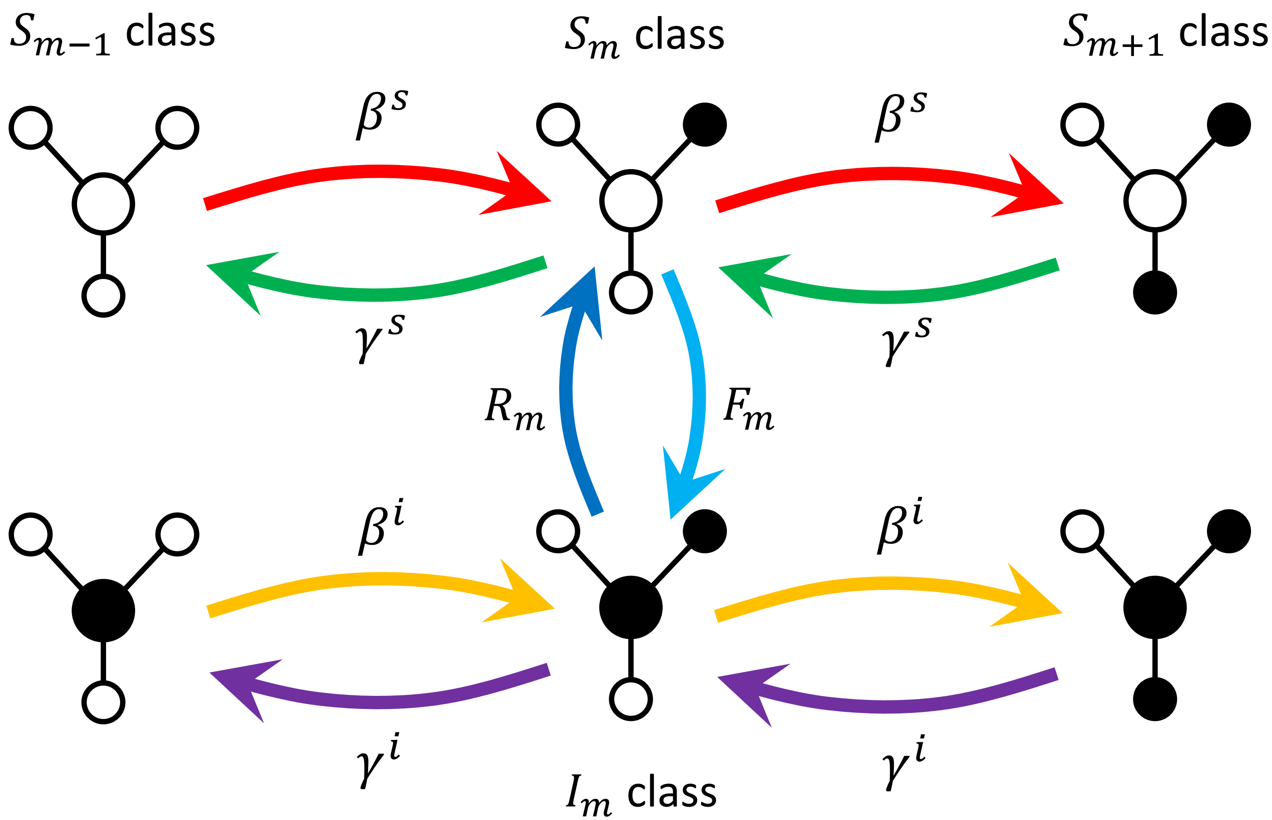
$$\gamma^s = \frac{\sum_{m=0}^{z} (z-m) R_m i_m}{\sum_{m=0}^{z} (z-m) i_m}$$

$$s_m(0) = (1-\rho(0)) B_{z,m}(\rho(0))$$

$$i_m(0) = \rho(0) B_{z,m}(\rho(0))$$

$$\beta^i = \frac{\sum_{m=0}^{z} m F_m s_m}{\sum_{m=0}^{z} m s_m}$$

$$\gamma^i = \frac{\sum_{m=0}^{z} m R_m i_m}{\sum_{m=0}^{z} m i_m}$$



$$\frac{d}{dt}s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s(z-m))s_m + \beta^s(z-m+1)s_{m-1} + \gamma^s(m+1)s_{m+1}$$

$$\frac{d}{dt}i_m = -R_m i_m + F_m s_m - \left(\gamma^i m + \beta^i(z-m)\right)i_m + \beta^i(z-m+1)i_{m-1} + \gamma^i(m+1)i_{m+1}$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m} \qquad \gamma^s = \frac{\sum_{m=0}^{z}(z-m)R_m i_m}{\sum_{m=0}^{z}(z-m)i_m}$$

$$s_m(0) = (1-\rho(0))B_{z,m}(\rho(0))$$

$$i_m(0) = \rho(0)B_{z,m}(\rho(0))$$

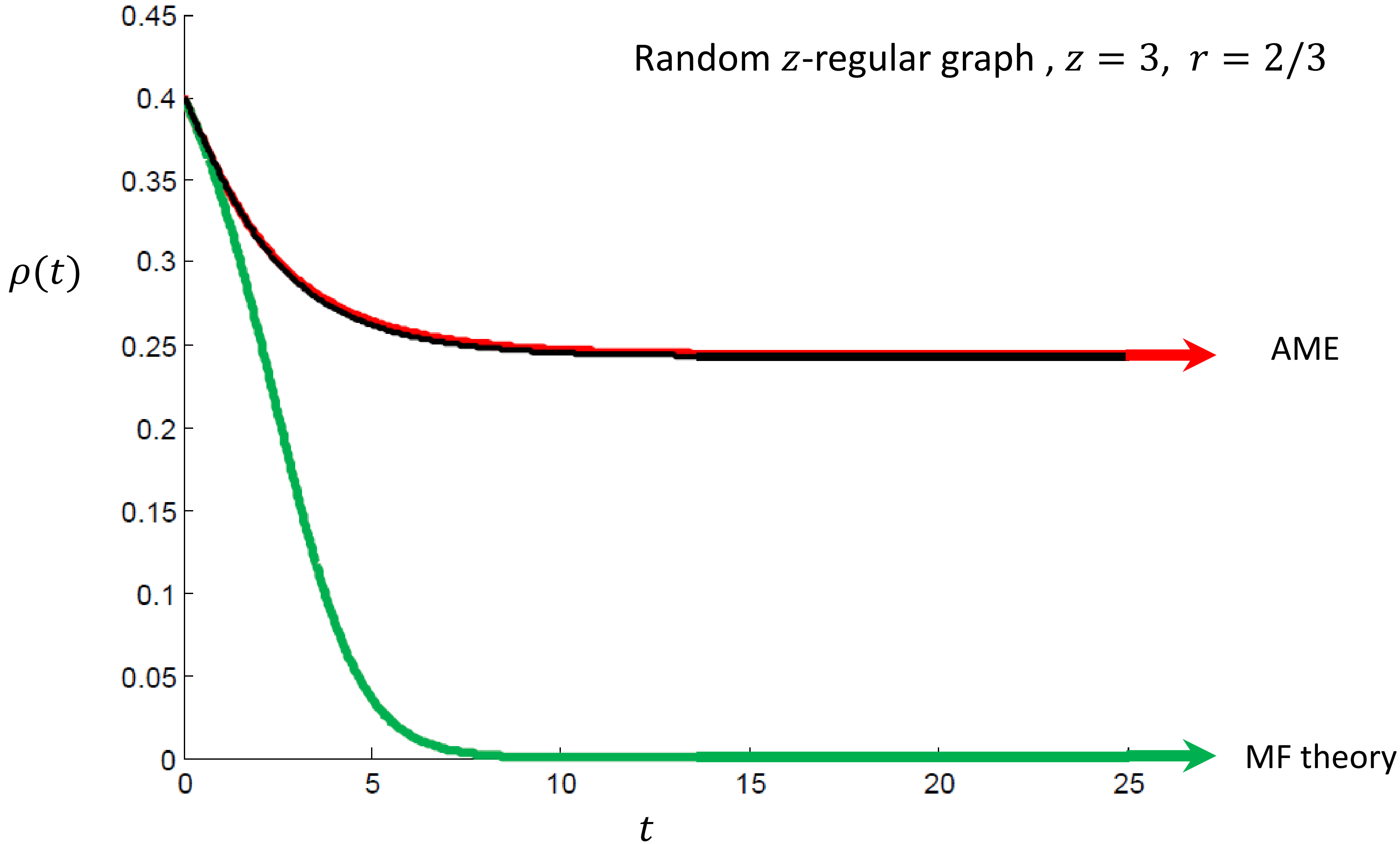
$$\beta^i = \frac{\sum_{m=0}^{z} mF_m s_m}{\sum_{m=0}^{z} m s_m} \qquad \gamma^i = \frac{\sum_{m=0}^{z} mR_m i_m}{\sum_{m=0}^{z} m i_m}$$

$$\rho = \sum_{m=0}^{z} i_m = 1 - \sum_{m=0}^{z} s_m$$

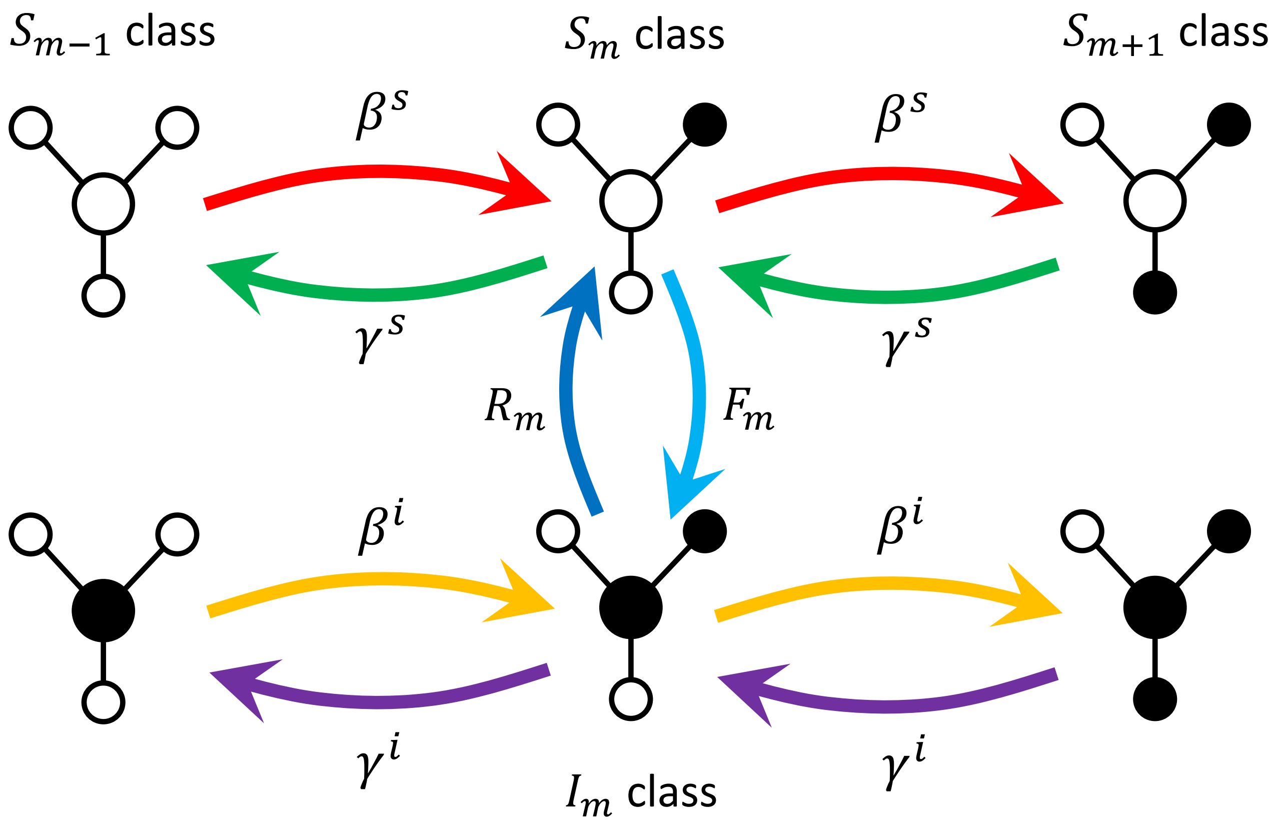
Non-monotone threshold model

$$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$$

$$R_{k,m} = \begin{cases} 1 & \text{for } m < kr \\ 0 & \text{for } m \geq kr \end{cases}$$



Random z-regular graphs



$$\frac{d}{dt}s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s(z-m))s_m + \beta^s(z-m+1)s_{m-1} + \gamma^s(m+1)s_{m+1}$$

$$\frac{d}{dt}i_m = -R_m i_m + F_m s_m - \left(\gamma^i m + \beta^i(z-m)\right)i_m + \beta^i(z-m+1)i_{m-1} + \gamma^i(m+1)i_{m+1}$$

$$\beta^s = \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m}$$

$$\gamma^s = \frac{\sum_{m=0}^{z}(z-m)R_m i_m}{\sum_{m=0}^{z}(z-m)i_m}$$

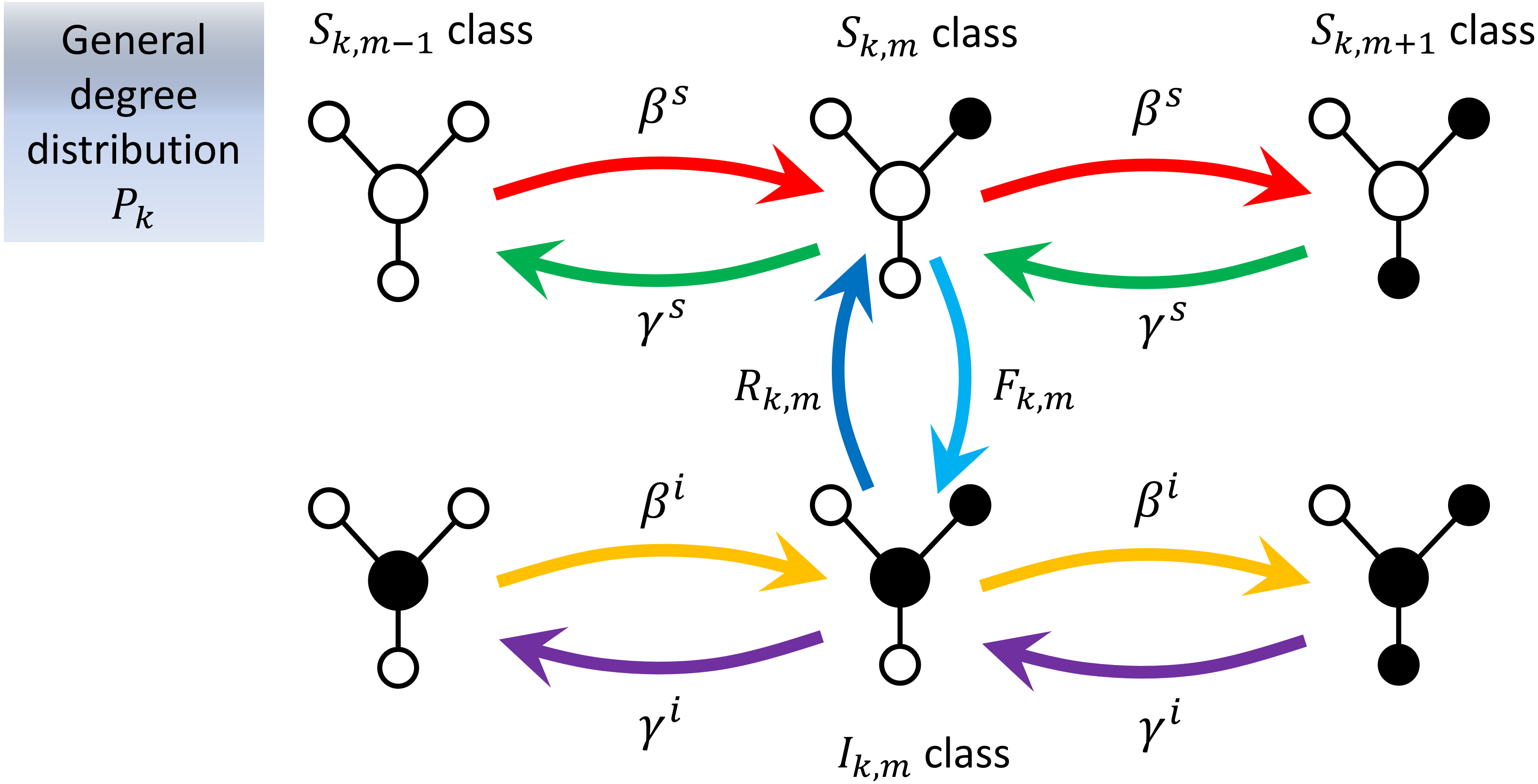
$$s_m(0) = (1-\rho(0))B_{z,m}(\rho(0))$$

$$i_m(0) = \rho(0)B_{z,m}(\rho(0))$$

$$\beta^i = \frac{\sum_{m=0}^{z} m F_m s_m}{\sum_{m=0}^{z} m s_m}$$

$$\gamma^i = \frac{\sum_{m=0}^{z} m R_m i_m}{\sum_{m=0}^{z} m i_m}$$

$$\rho = \sum_{m=0}^{z} i_m = 1 - \sum_{m=0}^{z} s_m$$



$$\frac{d}{dt}s_{k,m} = -F_{k,m}s_{k,m} + R_{k,m}i_{k,m} - (\gamma^s m + \beta^s(k-m))s_{k,m} + \beta^s(k-m+1)s_{k,m-1} + \gamma^s(m+1)s_{k,m+1}$$

$$\frac{d}{dt}i_{k,m} = -R_{k,m}i_{k,m} + F_{k,m}s_{k,m} - \left(\gamma^i m + \beta^i(k-m)\right)i_{k,m} + \beta^i(k-m+1)i_{k,m-1} + \gamma^i(m+1)i_{k,m+1}$$

$$\beta^s = \frac{\sum P_k \sum_{m=0}^{k}(k-m)F_{k,m}s_{k,m}}{\sum P_k \sum_{m=0}^{k}(k-m)s_{k,m}}$$

$$\gamma^s = \frac{\sum P_k \sum_{m=0}^{k}(k-m)R_{k,m}i_{k,m}}{\sum P_k \sum_{m=0}^{k}(k-m)i_{k,m}}$$

$$s_{k,m}(0) = (1-\rho_k(0))B_{k,m}(\rho_k(0))$$

$$i_{k,m}(0) = \rho_k(0)B_{k,m}(\rho_k(0))$$

$$\beta^i = \frac{\sum P_k \sum_{m=0}^{k} mF_{k,m}s_{k,m}}{\sum P_k \sum_{m=0}^{k} m\, s_{k,m}}$$

$$\gamma^i = \frac{\sum P_k \sum_{m=0}^{k} mR_{k,m}i_{k,m}}{\sum P_k \sum_{m=0}^{k} m\, i_{k,m}}$$

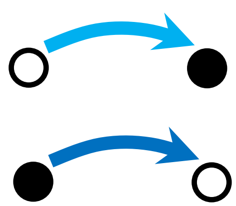
$$\rho = \sum_k P_k \sum_{m=0}^{k} i_{k,m}$$

SIS (susceptible-infected-susceptible) model for disease spread

Each node is either infected or susceptible.

Infected nodes become susceptible at rate μ;

an infected node infects each of its susceptible neighbours at rate λ.

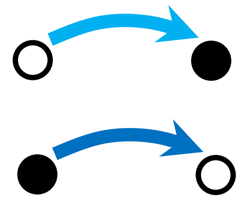


$$F_{k,m} = \lambda m$$

$$R_{k,m} = \mu$$

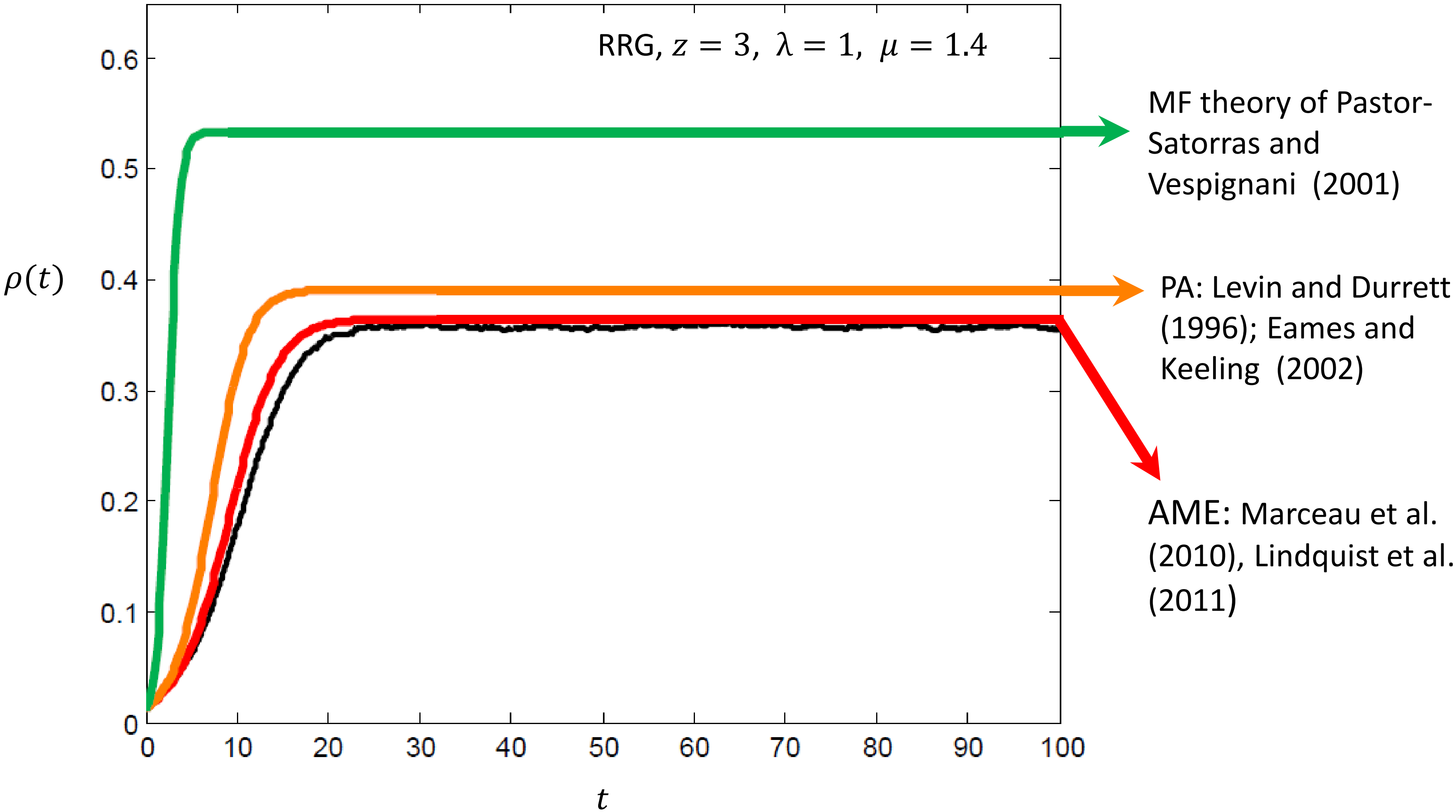
[cf. Marceau et al, PRE (2010),
Lindquist et al, J. Math. Biol. (2011)]

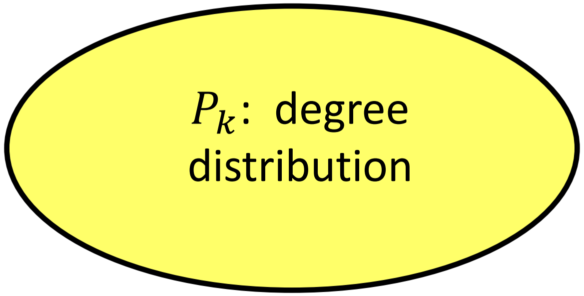
SIS disease spread:

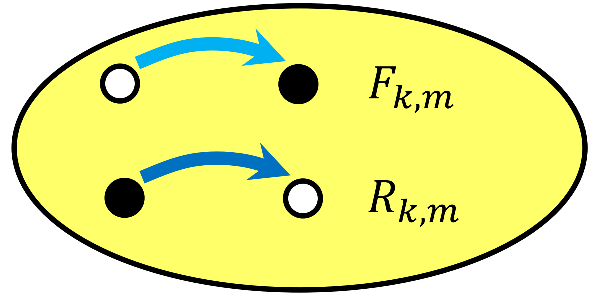


$F_{k,m} = \lambda m$

$R_{k,m} = \mu$

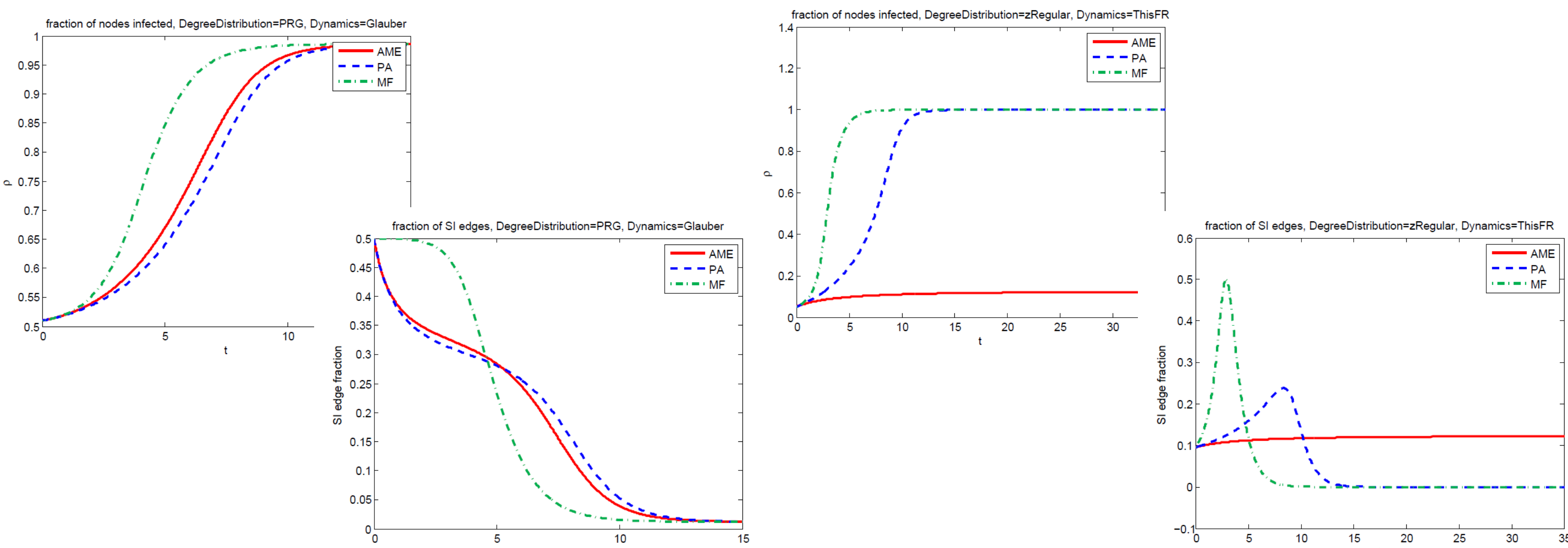






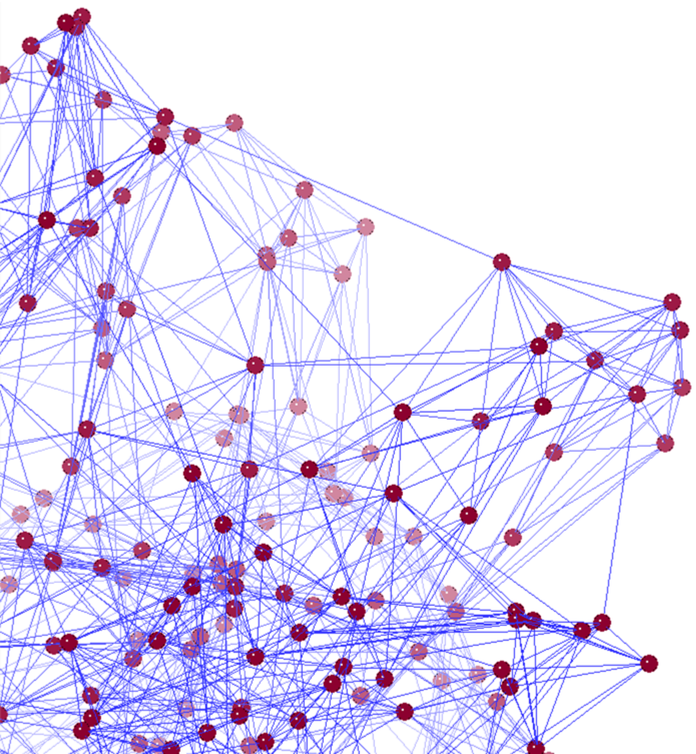
Octave/Matlab m-files for solving the approximate master equations, pair approximation, and mean-field theory equations for given degree distribution and transition rates (P_k, $F_{k,m}$ and $R_{k,m}$):

available to download from www.ul.ie/gleesonj



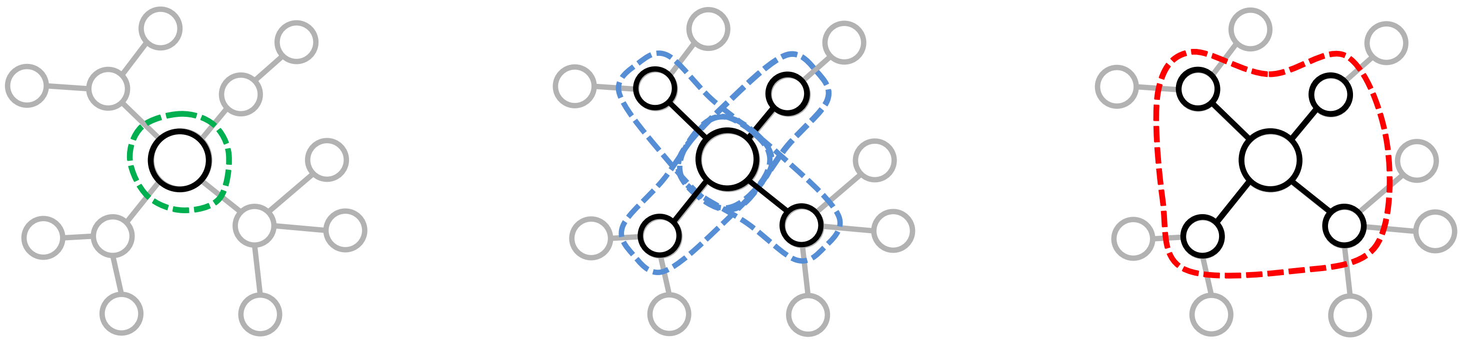
Outline

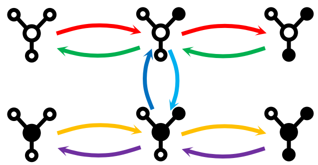
1. Motivation
2. Models: networks and dynamics
3. Derivation of Approximate Master Equations
4. Hierarchy of approximations: analysis



Approximation methods

Mean-field (MF) | Pair approximation (PA) | Approx. Master Eqn. (AME)





$$\frac{d}{dt}s_{k,m} = -F_{k,m}s_{k,m} + R_{k,m}i_{k,m} - (\gamma^s m + \beta^s (k-m))s_{k,m} + \beta^s (k-m+1)s_{k,m-1} + \gamma^s (m+1)s_{k,m+1}$$

$$\frac{d}{dt}i_{k,m} = -R_{k,m}i_{k,m} + F_{k,m}s_{k,m} - \left(\gamma^i m + \beta^i (k-m)\right)i_{k,m} + \beta^i (k-m+1)i_{k,m-1} + \gamma^i (m+1)i_{k,m+1}$$

Pair Approximation: using the binomial ansatz

$$s_{k,m}(t) = \big(1-\rho_k(t)\big)B_{k,m}\big(p(t)\big),$$
$$i_{k,m}(t) = \rho_k(t)B_{k,m}\big(q(t)\big),$$

moments of the approximate master equation give equations for $\rho_k(t)$, $q(t)$ and $p(t)$.

Note: in general, this does *not* give an exact solution of the AME.

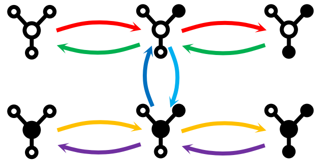
$$\frac{d}{dt}\rho_k = -\rho_k \sum_m R_{k,m}B_{k,m}(q) + (1-\rho_k)\sum_m F_{k,m}B_{k,m}(p)$$

$$\frac{d}{dt}p = \frac{1}{1-\omega}\sum_k \frac{k}{z}P_k \sum_m \left(1+p-2\frac{m}{k}\right)\left((1-\rho_k)F_{k,m}B_{k,m}(p) - \rho_k R_{k,m}B_{k,m}(q)\right)$$

$$\omega = \sum_k \frac{k}{z}P_k\rho_k \qquad (1-q)\omega = p(1-\omega) \qquad \rho = \sum_k P_k\rho_k$$

Further approximating $p(t)$ and $q(t)$ by $\omega(t)$ gives a Mean Field approximation:

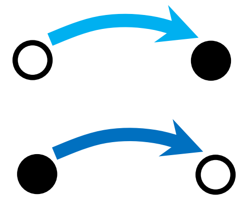
$$\frac{d}{dt}\rho_k = -\rho_k \sum_m R_{k,m}B_{k,m}(\omega) + (1-\rho_k)\sum_m F_{k,m}B_{k,m}(\omega)$$



$$\frac{d}{dt}s_{k,m} = -F_{k,m}s_{k,m} + R_{k,m}i_{k,m} - (\gamma^s m + \beta^s(k-m))s_{k,m} + \beta^s(k-m+1)s_{k,m-1} + \gamma^s(m+1)s_{k,m+1}$$

$$\frac{d}{dt}i_{k,m} = -R_{k,m}i_{k,m} + F_{k,m}s_{k,m} - \left(\gamma^i m + \beta^i(k-m)\right)i_{k,m} + \beta^i(k-m+1)i_{k,m-1} + \gamma^i(m+1)i_{k,m+1}$$

SIS disease spread:



$$F_{k,m} = \lambda m$$

$$R_{k,m} = \mu$$

$$\frac{d}{dt}\rho_k = -\rho_k \sum_m R_{k,m}B_{k,m}(q) + (1-\rho_k)\sum_m F_{k,m}B_{k,m}(p)$$

$$\frac{d}{dt}p = \frac{1}{1-\omega}\sum_k \frac{k}{z}P_k \sum_m \left(1 + p - 2\frac{m}{k}\right)\left((1-\rho_k)F_{k,m}B_{k,m}(p) - \rho_k R_{k,m}B_{k,m}(q)\right)$$

$$\omega = \sum_k \frac{k}{z}P_k\rho_k \qquad (1-q)\omega = p(1-\omega) \qquad \rho = \sum_k P_k\rho_k$$

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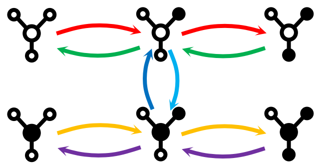

$$\frac{d}{dt}s_{k,m} = -F_{k,m}s_{k,m} + R_{k,m}i_{k,m} - (\gamma^s m + \beta^s(k-m))s_{k,m} + \beta^s(k-m+1)s_{k,m-1} + \gamma^s(m+1)s_{k,m+1}$$

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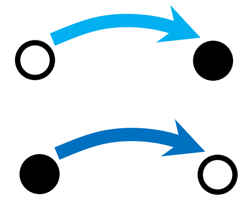
SIS disease spread :



$$F_{k,m} = \lambda m$$

$$R_{k,m} = \mu$$

$$\frac{d}{dt}\rho_k = -\mu\rho_k + \lambda(1-\rho_k)kp$$

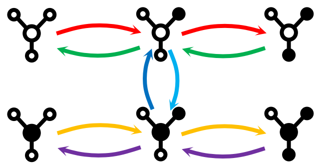
$$\frac{d}{dt}p = -2\lambda p(1-p) + \frac{1}{1-\omega}[\lambda p(1-p)\omega_2 + \mu(\omega + p\omega - 2p)]$$

$$\omega = \sum_k \frac{k}{z}P_k\rho_k \qquad \omega_2 = \sum_k \frac{k^2}{z}P_k(1-\rho_k)$$

PA of House and Keeling (2010)

$$\frac{d}{dt}\rho_k = -\mu\rho_k + \lambda(1-\rho_k)k\omega$$

MF theory of Pastor-Satorras and Vespignani (2001)



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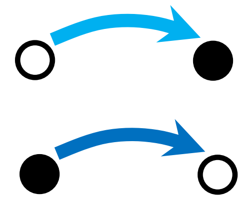
Voter model:



$$F_{k,m} = \frac{m}{k}$$

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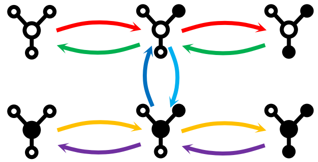

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Voter model:

$$F_{k,m} = \frac{m}{k}$$

$$R_{k,m} = \frac{k-m}{k}$$

$$\frac{d}{dt}\rho_k = \frac{p}{\omega}(\omega - \rho_k)$$

$$\frac{d}{dt}p = -\frac{2p}{z\omega}\left(p(z-1) - (z-2)\omega\right)$$

PA of Vazquez and Eguíluz (2008)

$$\frac{d}{dt}\rho_k = -\rho_k + \rho(0)$$

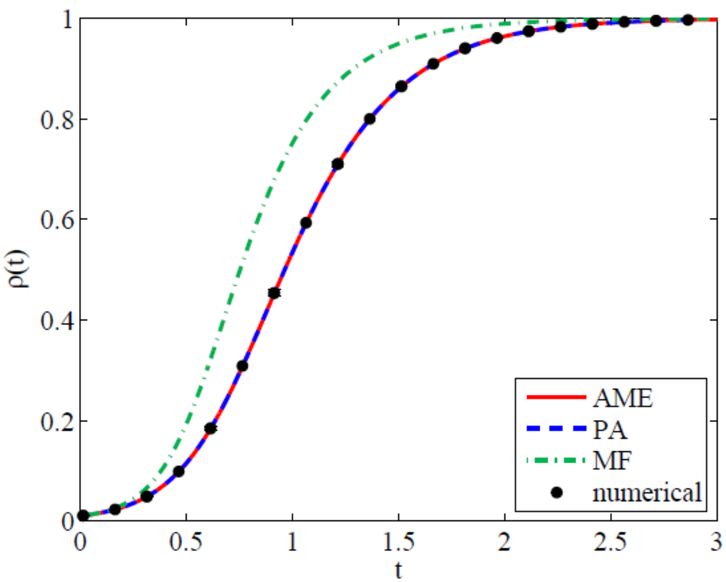
MF theory of Sood and Redner (2005)

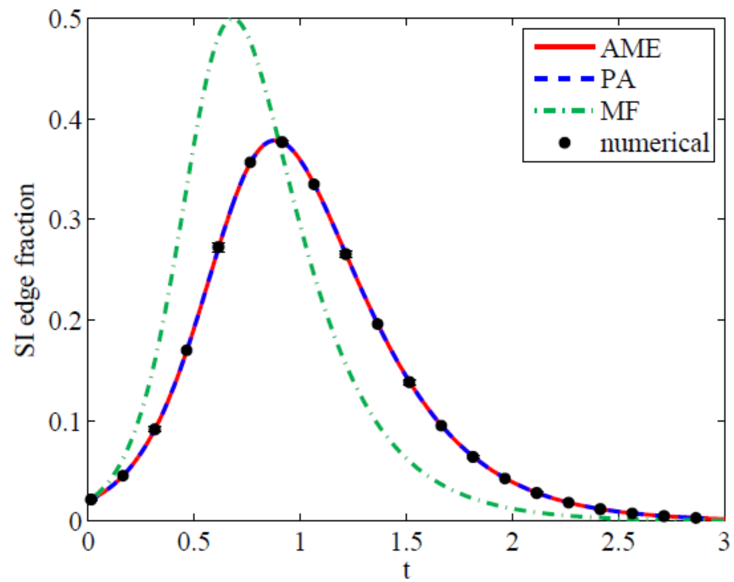
Insights into PA accuracy I

Pair approximation solutions and AME solutions for $\rho(t)$ are identical for all time if:

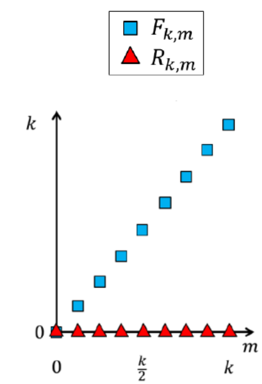
$$R_{k,m} = 0 \qquad \text{and} \qquad F_{k,m} = A(k) + B(k)m$$

e.g., SI disease-spread model ($A = 0$).





$$F_{k,m} = m$$



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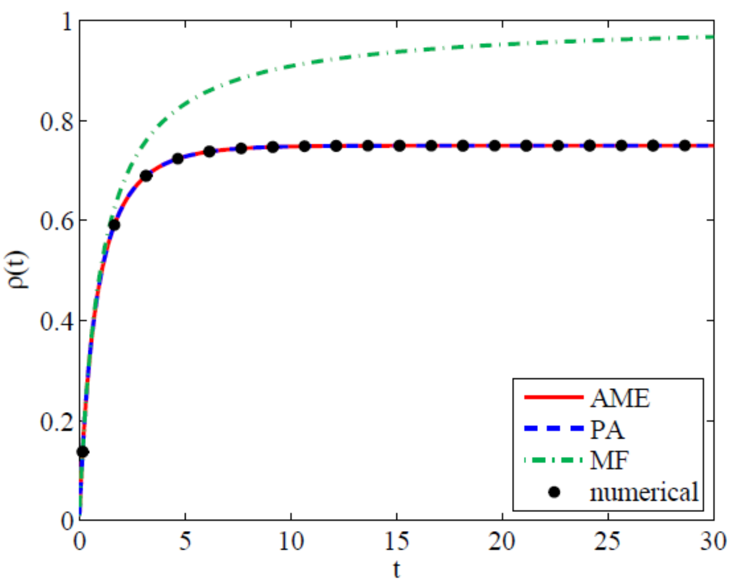

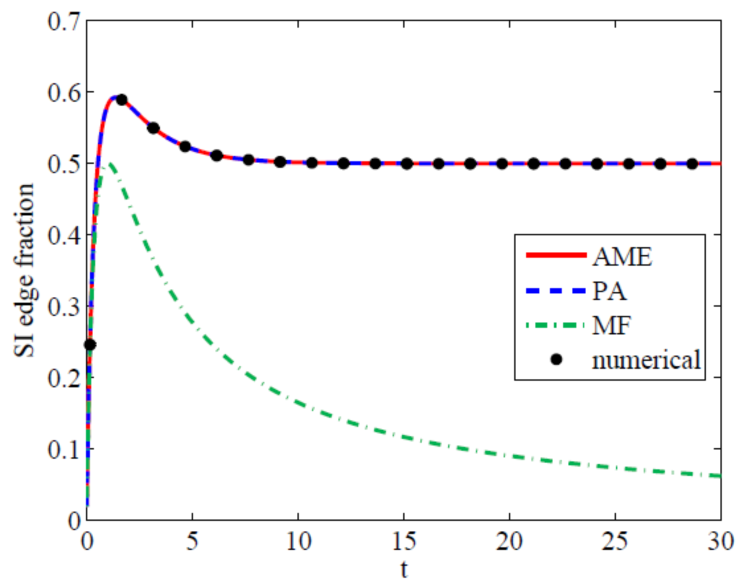

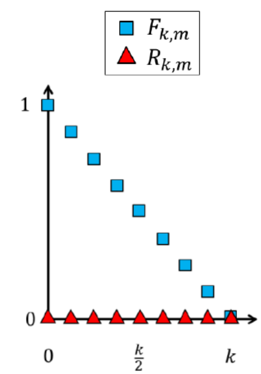

$$P_k = \delta_{k,4} \qquad F_{k,m} = 1 - m/4$$

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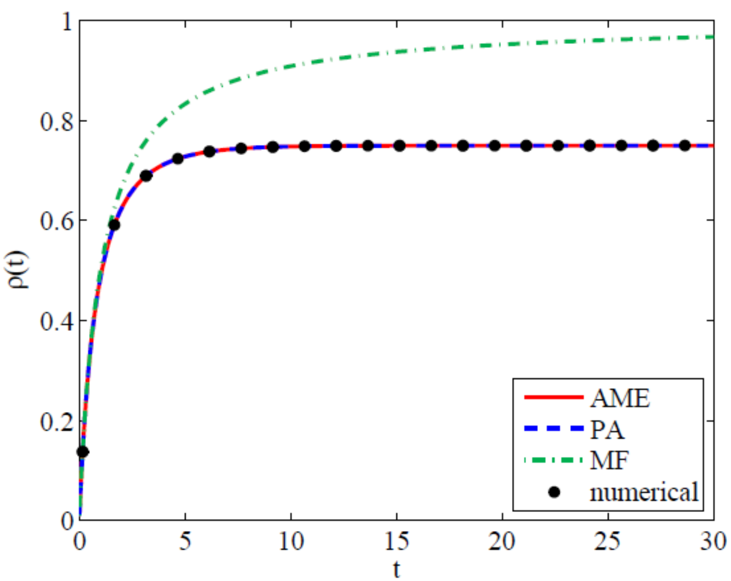
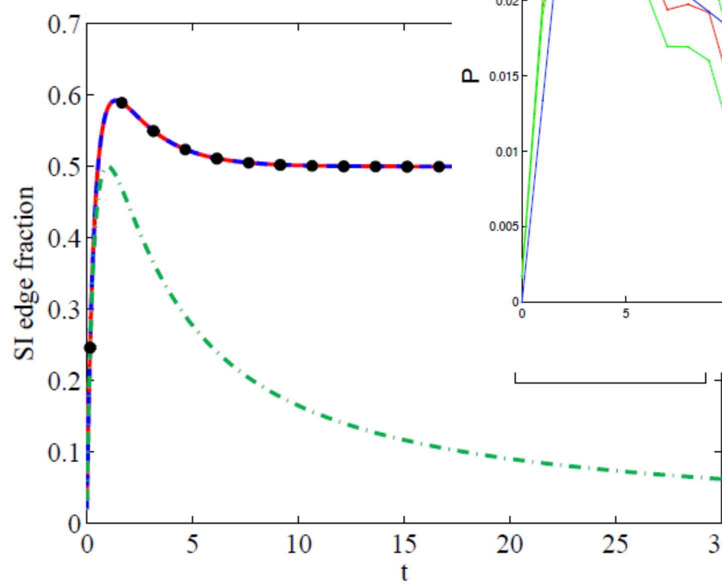
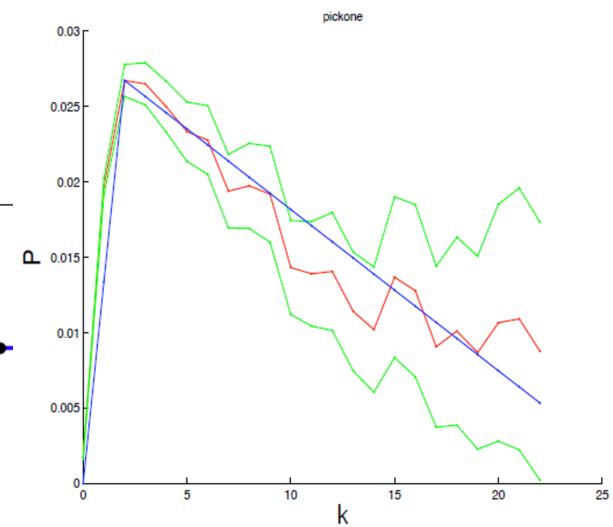
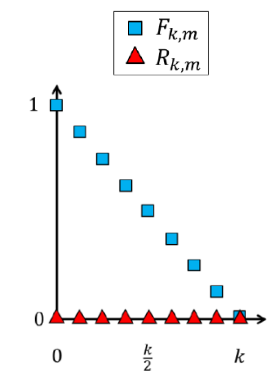




D. M. Romero et al. (2011)





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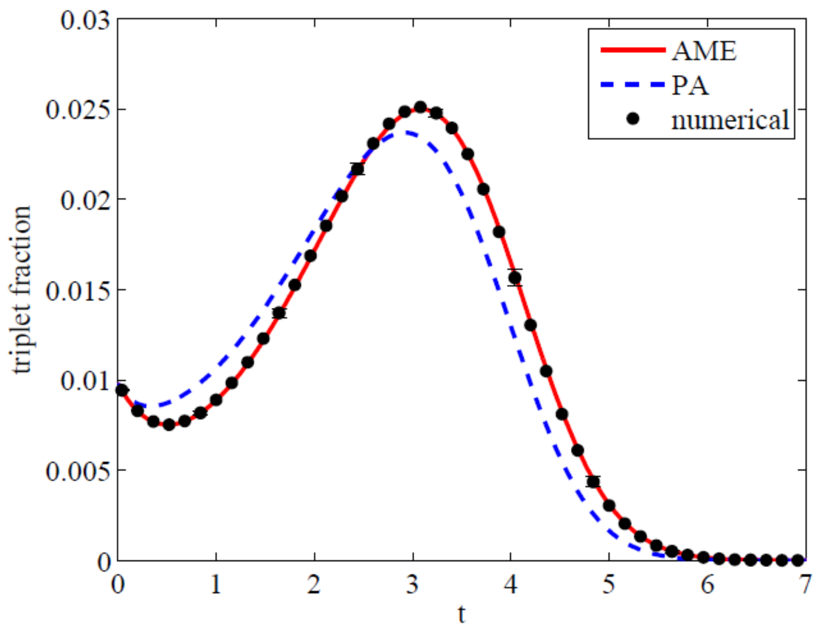
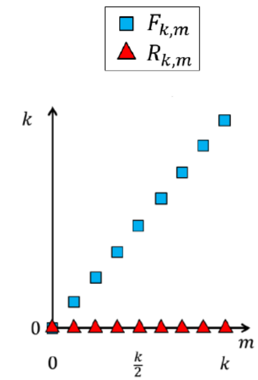
Pair approximation solutions and AME solutions for $\rho(t)$ are identical for all time if:

$$R_{k,m} = 0 \qquad \text{and} \qquad F_{k,m} = A(k) + B(k)m$$

… but not identical for triplets of node states:



$$F_{k,m} = m$$

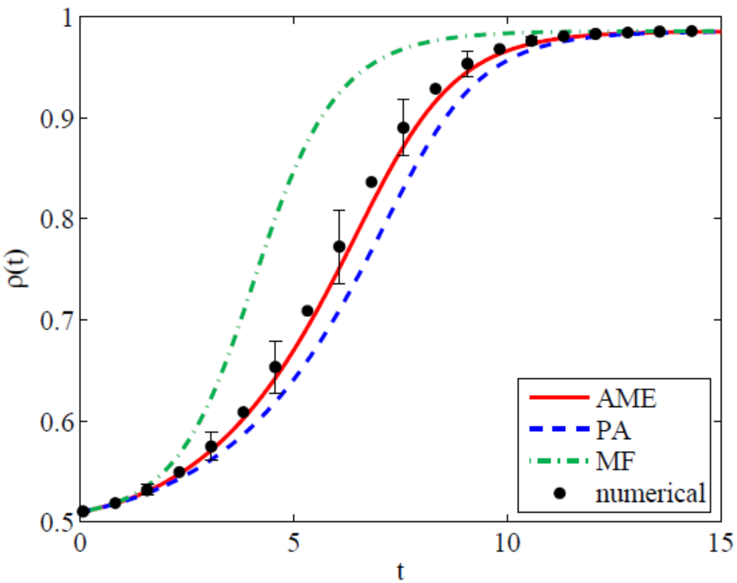


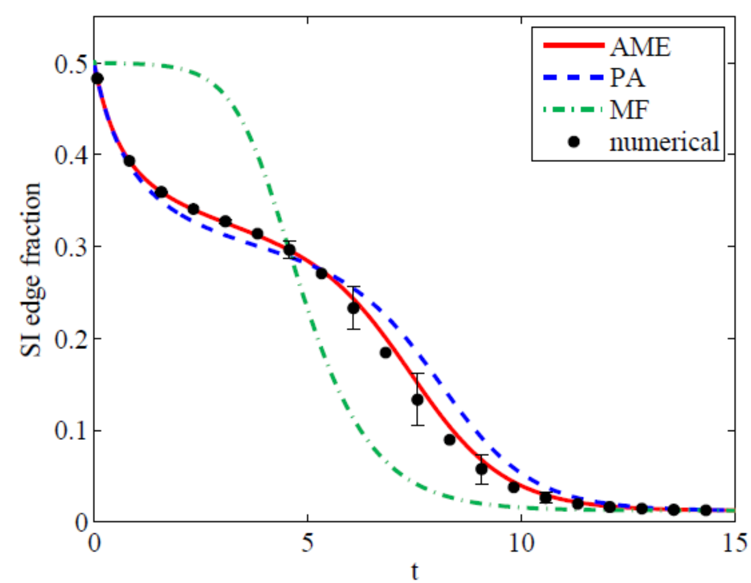
Insights into PA accuracy II

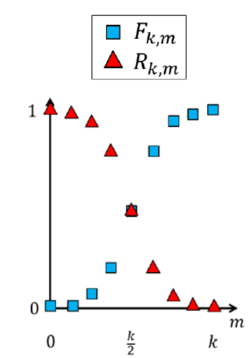
Pair approximation solutions and AME solutions are identical in the limit $t \to \infty$ if:

$$\frac{F_{k,m}}{R_{k,m}} = b_k a^m$$ for some constants b_k and a

e.g., Glauber/Metropolis dynamics for the Ising spin model on a network.







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e.g., Glauber/Metropolis dynamics for the Ising spin model on a network.

For systems that also possess up-down symmetry, this permits a one-dimensional bifurcation analysis of the steady-states of the system.

A pitchfork bifurcation occurs at a critical value of a that depends on the network topology:

$$a_c = \left(\frac{\langle k^2\rangle}{\langle k^2\rangle - 2\langle k\rangle}\right)^2$$

[cf. critical temperature for Ising model,
Dorogovtsev et al. 2004, Leone et al. 2004]

Insights into PA accuracy II

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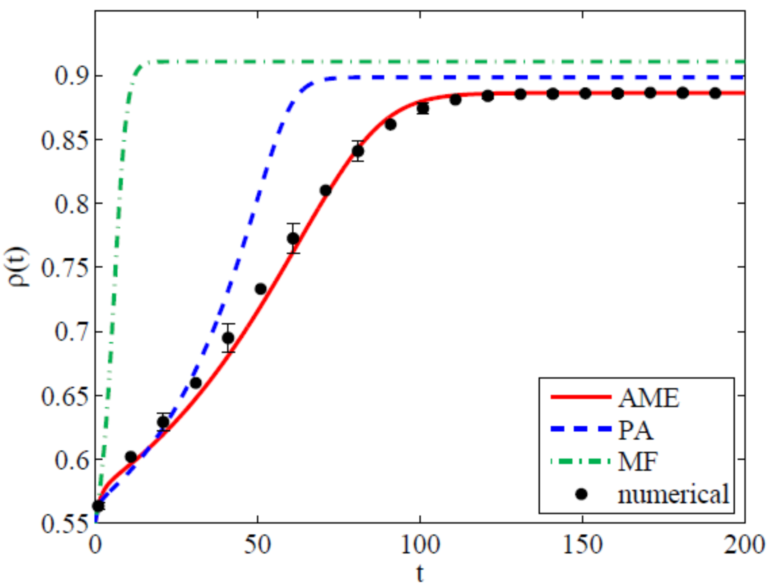
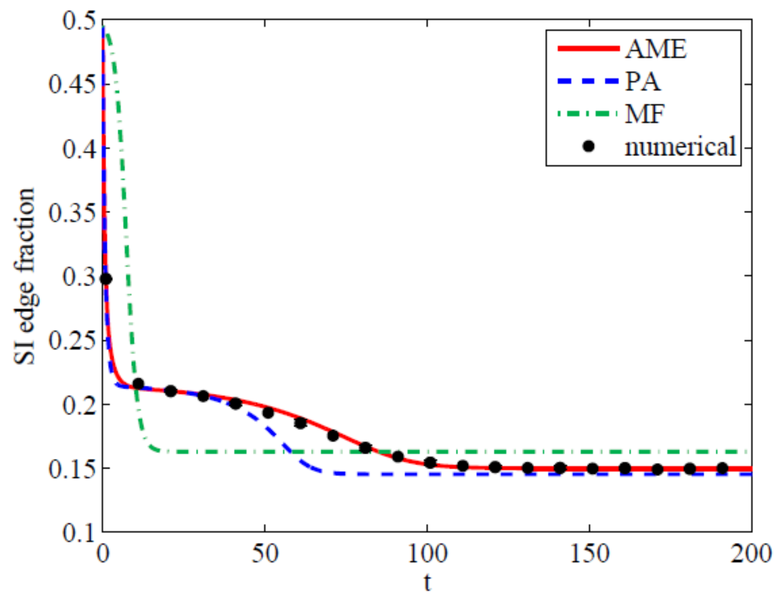
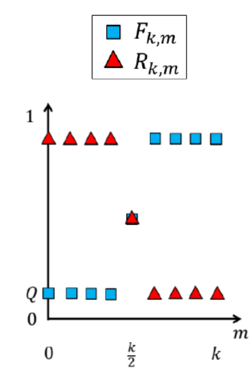
Contrast to, e.g., majority-vote model:







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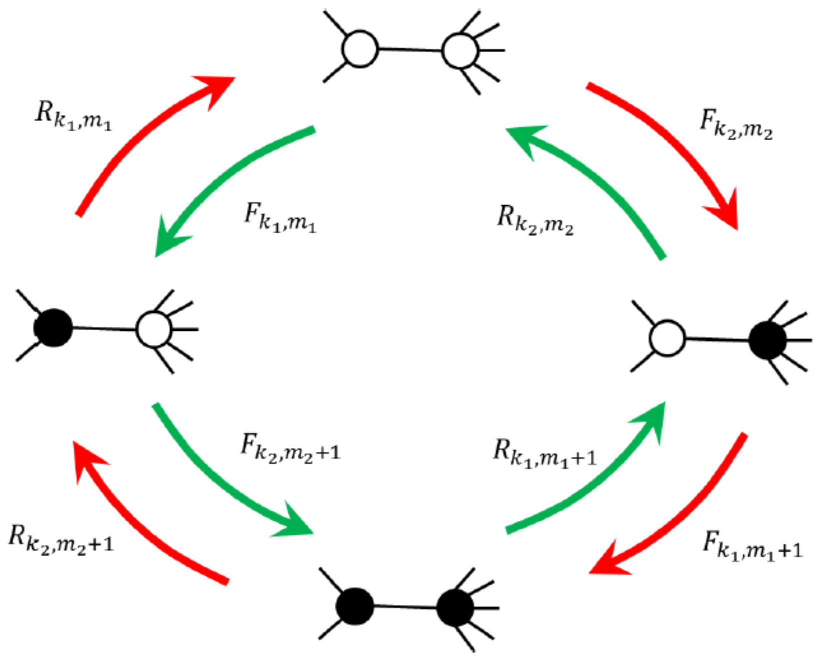
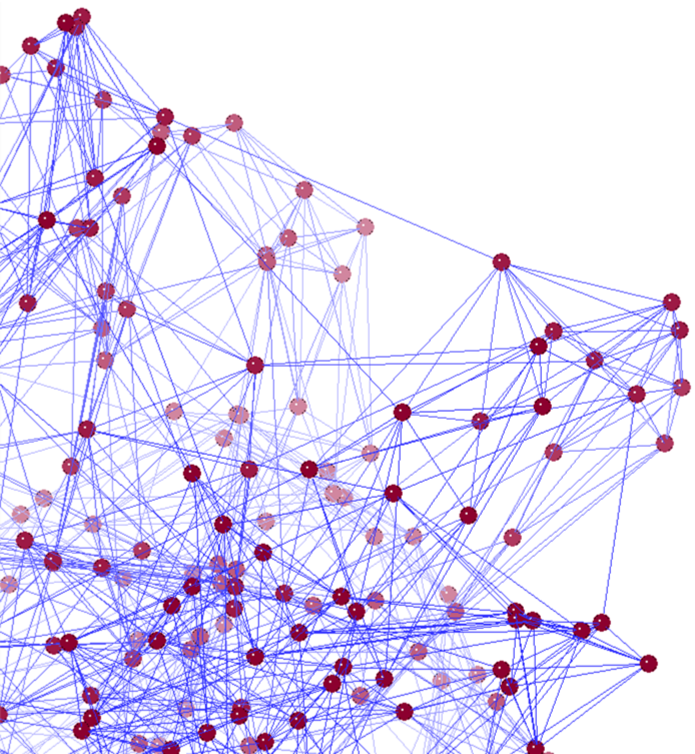
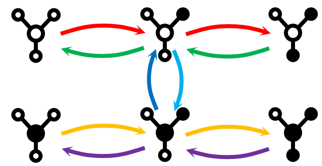
This condition proves equivalent to microscopic reversibility of the dynamics



Outline

1. Motivation
2. Models: networks and dynamics
3. Derivation of Approximate Master Equations
4. Hierarchy of approximations: analysis





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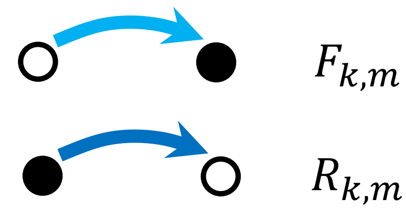

Approximate master equation approach gives high-accuracy approximations for a range of stochastic binary dynamics (defined by $F_{k,m}$ and $R_{k,m}$).

Moreover, it:

- “Automatically” generates pair approximation and mean-field equations.
- Gives insight into accuracy regimes for pair approximation.
- Enables dynamical systems analysis (e.g. bifurcation theory).
- Allows extensions to coevolving dynamics and networks.

Octave/Matlab files for solving differential equation systems available from www.ul.ie/gleesonj

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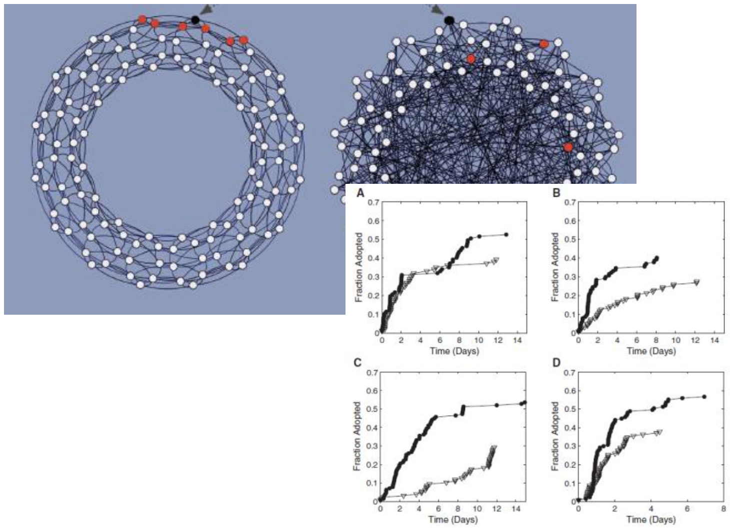
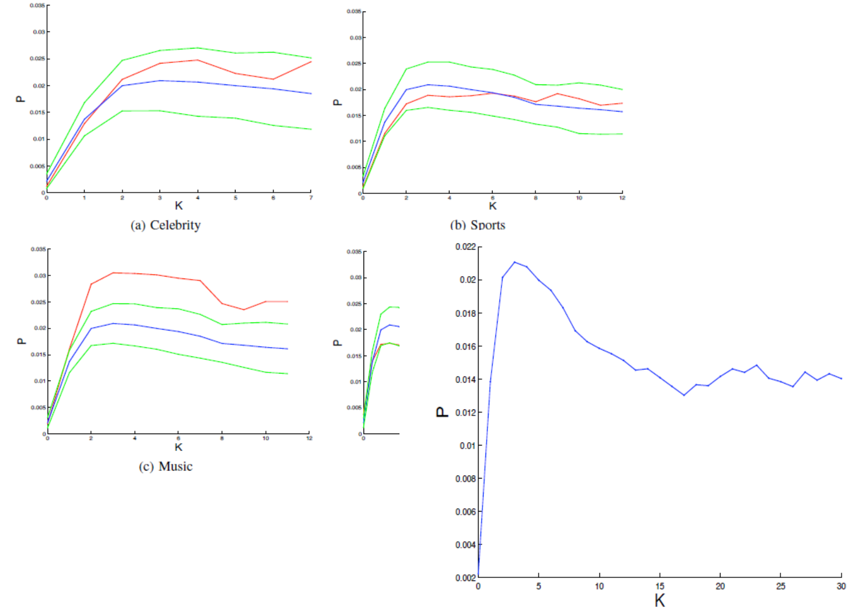
The challenge





Data-driven mathematical modelling of behaviour at population level

- Influence of neighbours
- Effects of clustering and network topology
- Memory effects in decision-making
- Impact of finite-size systems: fluctuations
- Non-binary choices
- ....
- ....
- ....

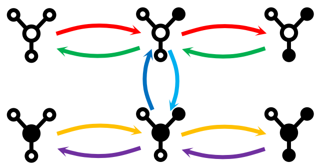
Collaborators and funding

- Peter Fennell, UL
- Adam Hackett, Hamilton Inst.
- Diarmuid Cahalane, Cornell
- Sergey Melnik, UL
- Davide Cellai, UL
- Jonathan Ward, Reading

- Mason Porter, Oxford
- Peter Mucha, U. North Carolina
- Rick Durrett, Duke

- Science Foundation Ireland
- MACSI: Mathematics Applications Consortium for Science & Industry
- IRCSET Inspire
- FP7 FET Proactive PLEXMATH

- SFI/HEA Irish Centre for High-End Computing (ICHEC)



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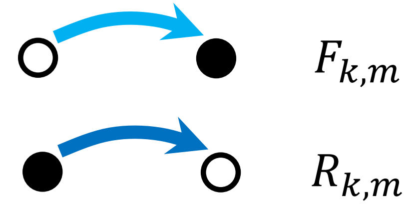

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Approximation methods for binary-state dynamics on complex networks

James P. Gleeson
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Department of Mathematics and Statistics,
University of Limerick,
Ireland

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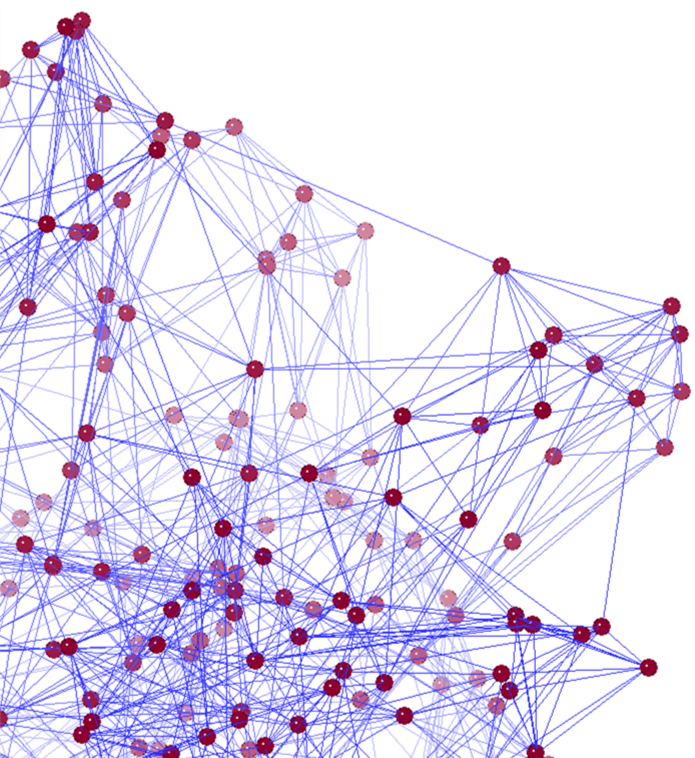

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