

# Beyond mean-field theory: High-accuracy approximation of binary-state dynamics on networks

James P. Gleeson

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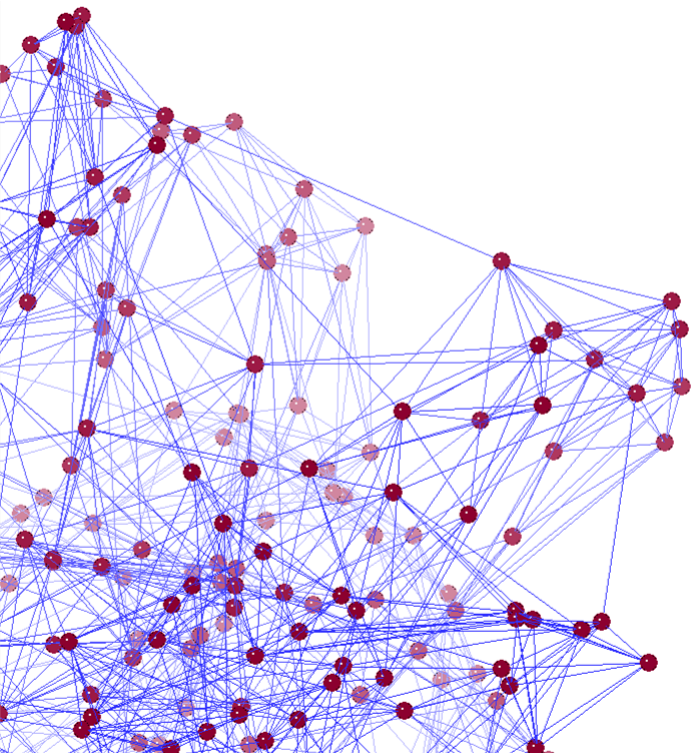
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On the ensemble of (static, undirected,  $N \rightarrow \infty$ ) random networks with degree distribution  $P_k$ : is it possible to accurately predict macroscopic outcomes for given stochastic (binary-state) dynamical processes?

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

Each node is either infected or susceptible.

Infected nodes become susceptible at rate  $\mu$ ;

an infected node infects each of its susceptible neighbours at rate  $\lambda$ .




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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)

On the ensemble of (static, undirected,  $N \rightarrow \infty$ ) random networks with degree distribution  $P_k$ : is it possible to accurately predict macroscopic outcomes for given stochastic (binary-state) dynamical processes?

### **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  $dt = 1/N$ ).
- A 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.

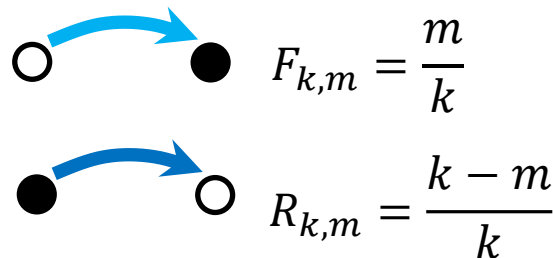


- Similarly:  $R_{k,m} dt =$  recovery probability for a  $k$ -degree infected node with  $m$  infected neighbours.

## Examples

### Voter model

Each node has an opinion (let's call these “infected” or “susceptible”).  
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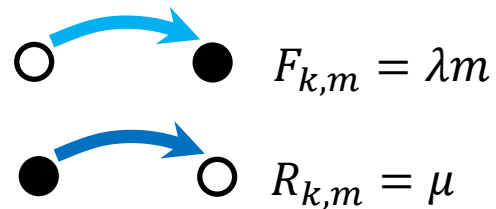
## Examples

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

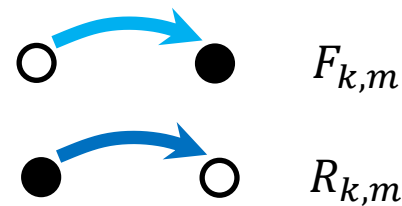
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Infected nodes become susceptible at rate  $\mu$ ;

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## Synergy in Spreading Processes: From Exploitative to Explorative Foraging Strategies

Francisco J. Pérez-Reche,<sup>1,2,\*</sup> Jonathan J. Ludlam,<sup>3</sup> Sergei N. Taraskin,<sup>4</sup> and Christopher A. Gilligan<sup>5</sup>

<sup>1</sup>*Department of Chemistry, University of Cambridge, Cambridge, United Kingdom*

<sup>2</sup>*SIMBIOS Centre, University of Abertay, Dundee, United Kingdom*

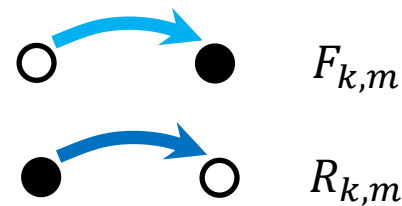
<sup>3</sup>*Churchill College, University of Cambridge, Cambridge, United Kingdom*

<sup>4</sup>*St. Catharine's College and Department of Chemistry, University of Cambridge, Cambridge, United Kingdom*

<sup>5</sup>*Department of Plant Sciences, University of Cambridge, Cambridge, United Kingdom*

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An epidemiological model which incorporates synergistic effects that allow the infectivity and/or susceptibility of hosts to be dependent on the number of infected neighbors is proposed. Constructive synergy induces an exploitative behavior which results in a rapid invasion that infects a large number of hosts. Interfering synergy leads to a slower and sparser explorative foraging strategy that traverses larger distances by infecting fewer hosts. The model can be mapped to a dynamical bond percolation with spatial correlations that affect the mechanism of spread but do not influence the critical behavior of epidemics.



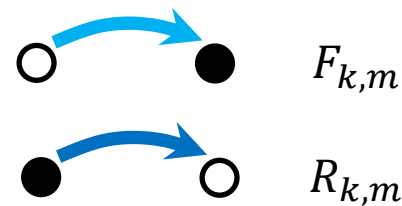
# Infectious Disease Modeling of Social Contagion in Networks

Alison L. Hill<sup>1,2\*</sup>, David G. Rand<sup>1,3</sup>, Martin A. Nowak<sup>1,4,5</sup>, Nicholas A. Christakis<sup>6,7,8</sup>

**1** Program for Evolutionary Dynamics, Harvard University, Cambridge, Massachusetts, United States of America, **2** Biophysics Program and Harvard-MIT Division of Health Sciences and Technology, Harvard University, Cambridge, Massachusetts, United States of America, **3** Department of Psychology and Berkman Center for Internet and Society, Harvard University, Cambridge, Massachusetts, United States of America, **4** Department of Mathematics, Harvard University, Cambridge, Massachusetts, United States of America, **5** Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, Massachusetts, United States of America, **6** Department of Medicine, Harvard Medical School, Boston, Massachusetts, United States of America, **7** Department of Health Care Policy, Harvard Medical School, Boston, Massachusetts, United States of America, **8** Department of Sociology, Harvard University, Cambridge, Massachusetts, United States of America

## Abstract

Many behavioral phenomena have been found to spread interpersonally through social networks, in a manner similar to infectious diseases. An important difference between social contagion and traditional infectious diseases, however, is that behavioral phenomena can be acquired by non-social mechanisms as well as through social transmission. We introduce a novel theoretical framework for studying these phenomena (the SISa model) by adapting a classic disease model to include the possibility for 'automatic' (or 'spontaneous') non-social infection. We provide an example of the use of this framework



## Dynamic Opinion Model and Invasion Percolation

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<sup>1</sup>*Center for Polymer Studies and Department of Physics, Boston University, Boston, Massachusetts 02215, USA*

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We propose a “nonconsensus” opinion model that allows for stable coexistence of two opinions by forming clusters of agents holding the same opinion. We study this nonconsensus model on lattices, several model complex networks, and a real-life social network. We find that the model displays a phase transition behavior characterized by a large spanning cluster of nodes holding the same opinion appearing when the concentration of nodes holding the same opinion (even minority) is above a certain threshold. Because of the clustering (community support) of agents holding the same opinion, these clusters cannot be invaded by the other opinion (similar to incompressible fluids). Our extensive simulations show that the nonconsensus opinion model appears to belong to the same universality class as invasion percolation.

## (Monotone) threshold models of “complex contagion”

[ Granovetter (1978), Watts (2002), Centola & Macy (2007) ]

- Each node  $i$  has a (frozen) threshold  $r_i$ , and a binary state (“susceptible”/“infected”).
- A randomly-chosen fraction  $\rho(0)$  of nodes are initially infected.
- Asynchronous updating: A fraction  $dt$  of nodes update in time step  $dt$ .
- Update rule: compare the fraction of infected neighbours  $m_i/k_i$  to  $r_i$ . Node  $i$  is infected if  $m_i/k_i \geq r_i$ , but unchanged otherwise



- $F_{k,m} dt =$  infection probability for a  $k$ -degree susceptible node with  $m$  infected neighbours.
- For example, if all thresholds are identical ( $r_i = r \ \forall i$ ):

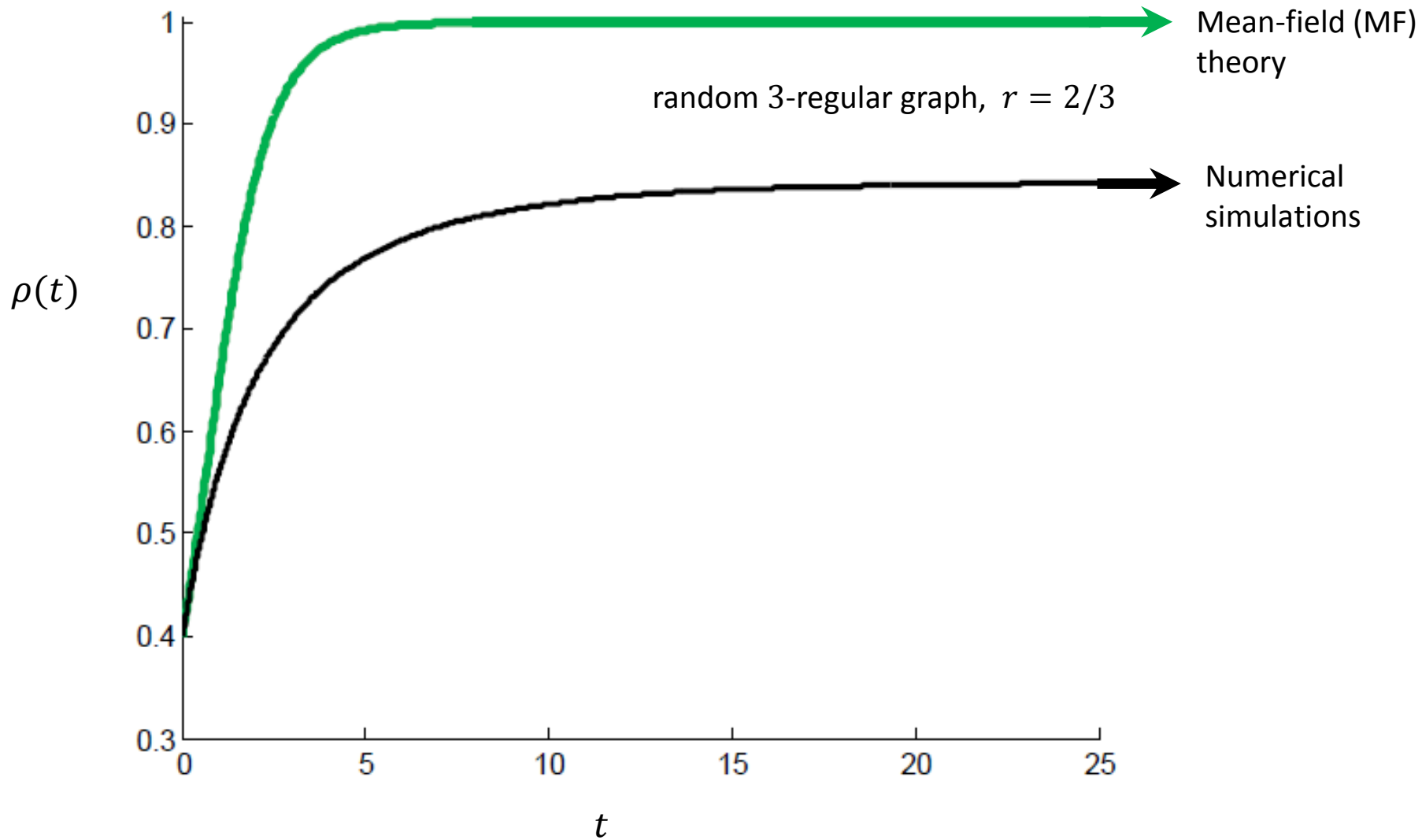
$$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$$

- Monotone case: no recovery, so  $R_{k,m} \equiv 0$

Monotone threshold model

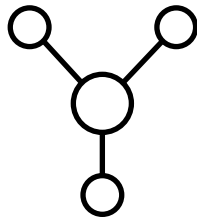


$$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$$

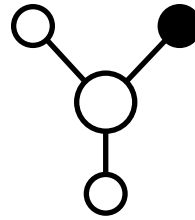


Random  
z-regular  
graphs

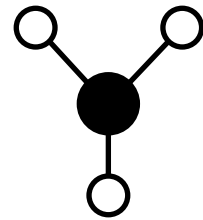
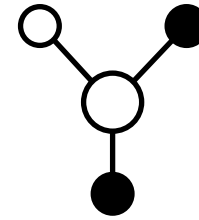
$S_{m-1}$  class



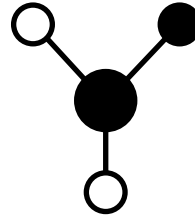
$S_m$  class



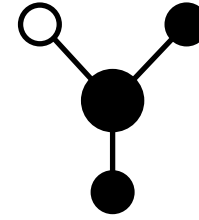
$S_{m+1}$  class



$I_{m-1}$  class



$I_m$  class



$I_{m+1}$  class

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

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

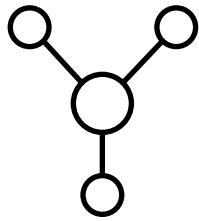
$i_m(t)$  = fraction of nodes which are infected and have  $m$  infected neighbours at time  $t$

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

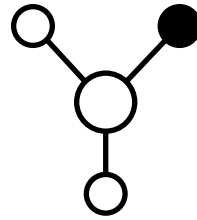
$$i_m(0) = \rho(0)B_{z,m}(\rho(0))$$

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

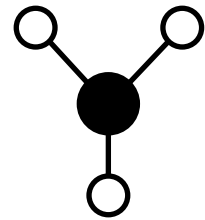
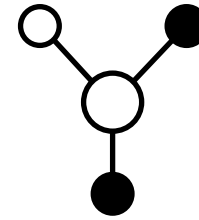
$S_{m-1}$  class



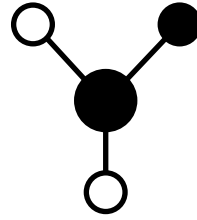
$S_m$  class



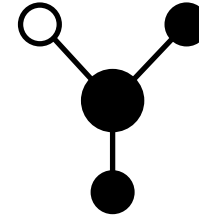
$S_{m+1}$  class



$I_{m-1}$  class



$I_m$  class



$I_{m+1}$  class

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

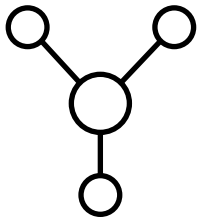
$i_m(t)$  = fraction of nodes which are infected and have  $m$  infected neighbours at time  $t$



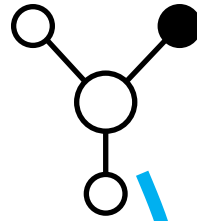
= number of S-I edges

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

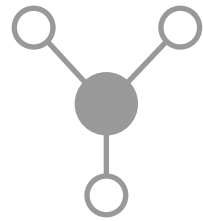
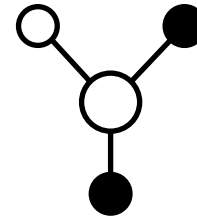
$S_{m-1}$  class



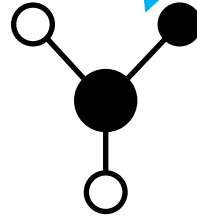
$S_m$  class



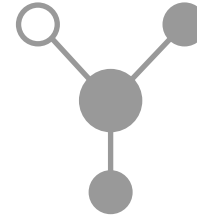
$S_{m+1}$  class



$I_{m-1}$  class



$I_m$  class



$I_{m+1}$  class

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

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

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

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

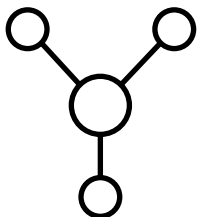
$$F_m \equiv F_{z,m} = \begin{cases} 0 & \text{for } m < zr \\ 1 & \text{for } m \geq zr \end{cases}$$

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

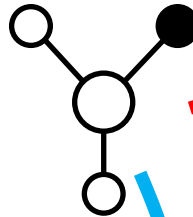




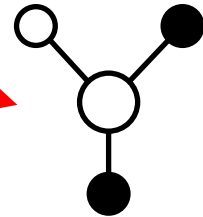
$S_{m-1}$  class



$S_m$  class



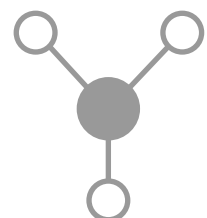
$S_{m+1}$  class



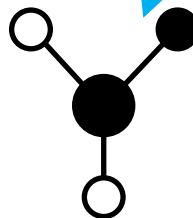
$\beta^s$



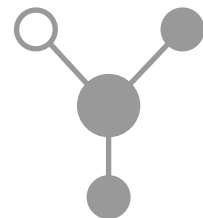
$F_m$



$I_{m-1}$  class



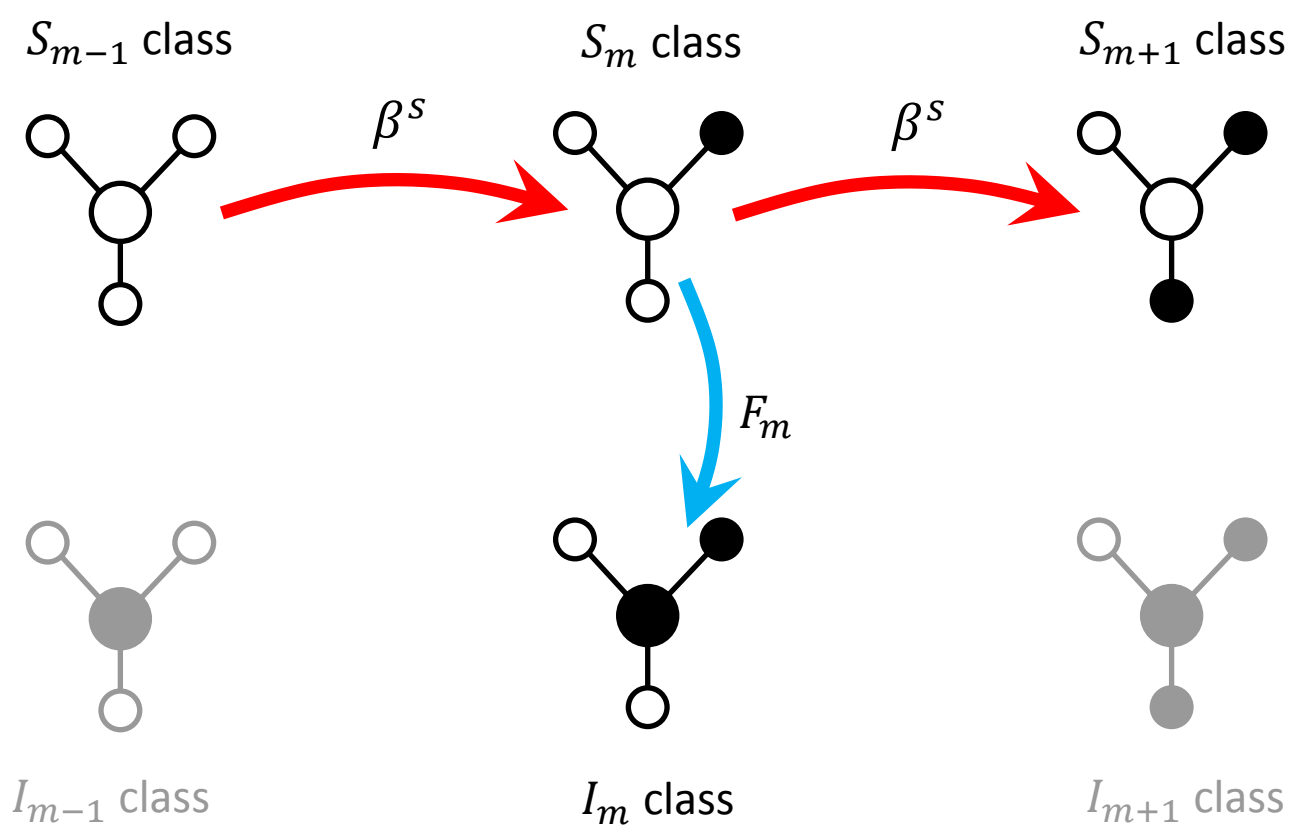
$I_m$  class



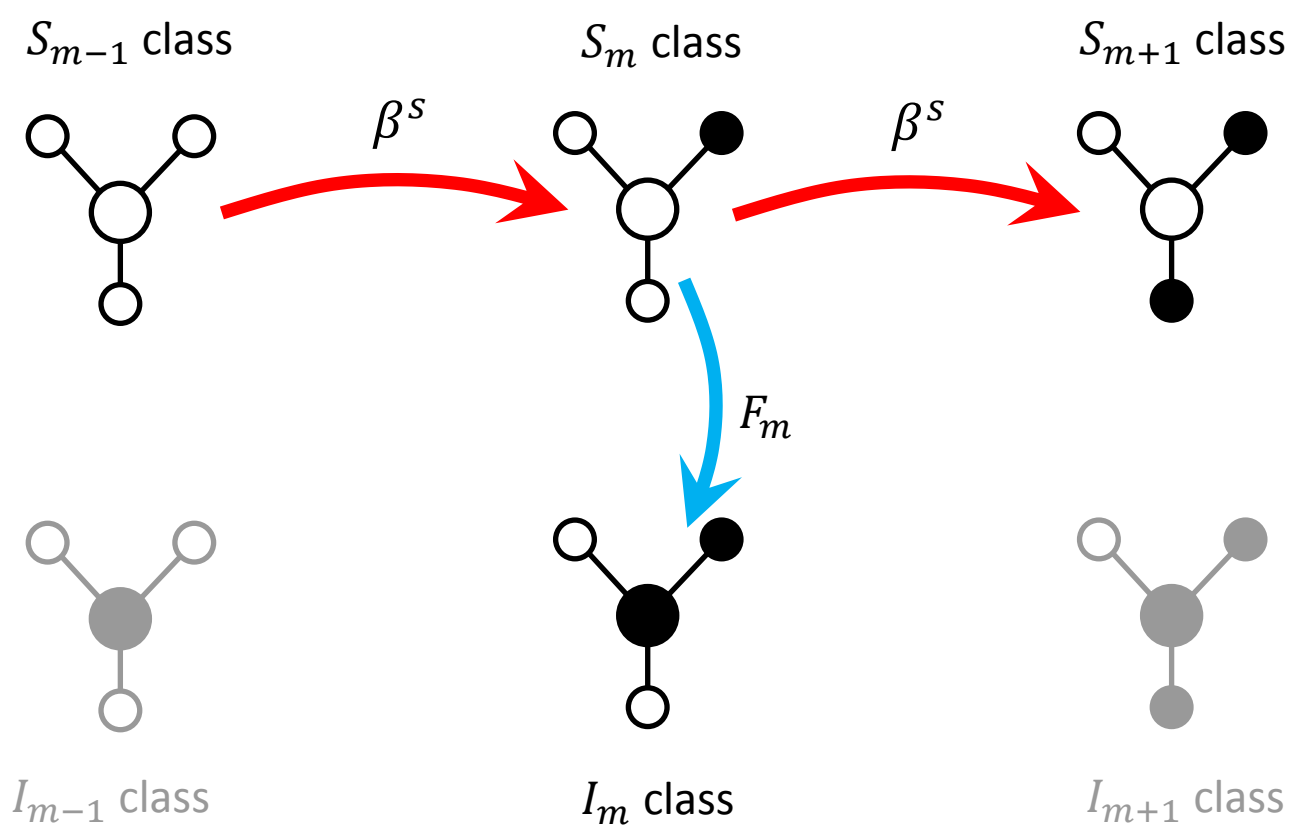
$I_{m+1}$  class

$$\frac{d}{dt} S_m = -F_m S_m - \beta^s (z - m) S_m + \dots$$

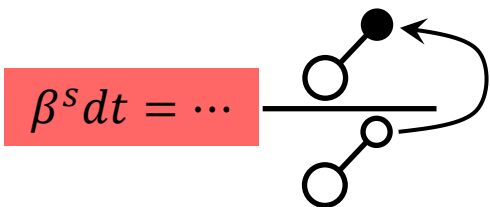
for  $m = 0, 1, \dots, z$

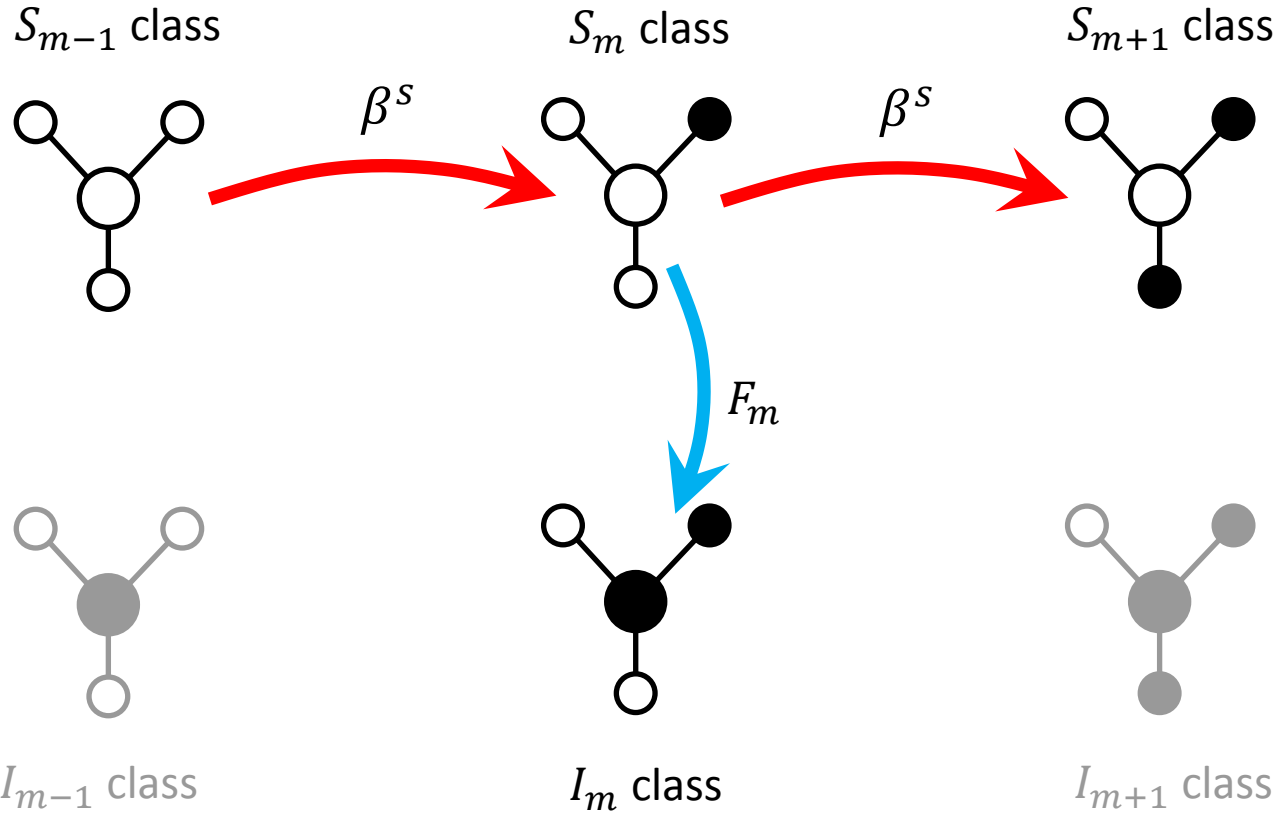


$$\frac{d}{dt} S_m = -F_m S_m - \beta^s (z - m) S_m + \beta^s (z - m + 1) S_{m-1} \quad \text{for } m = 0, 1, \dots, z$$

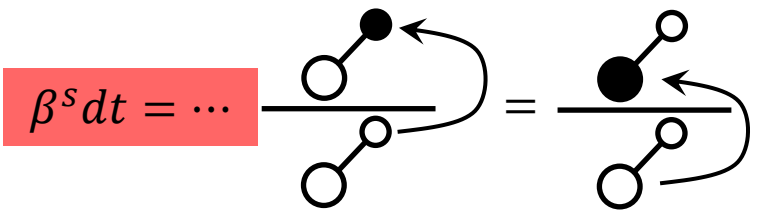


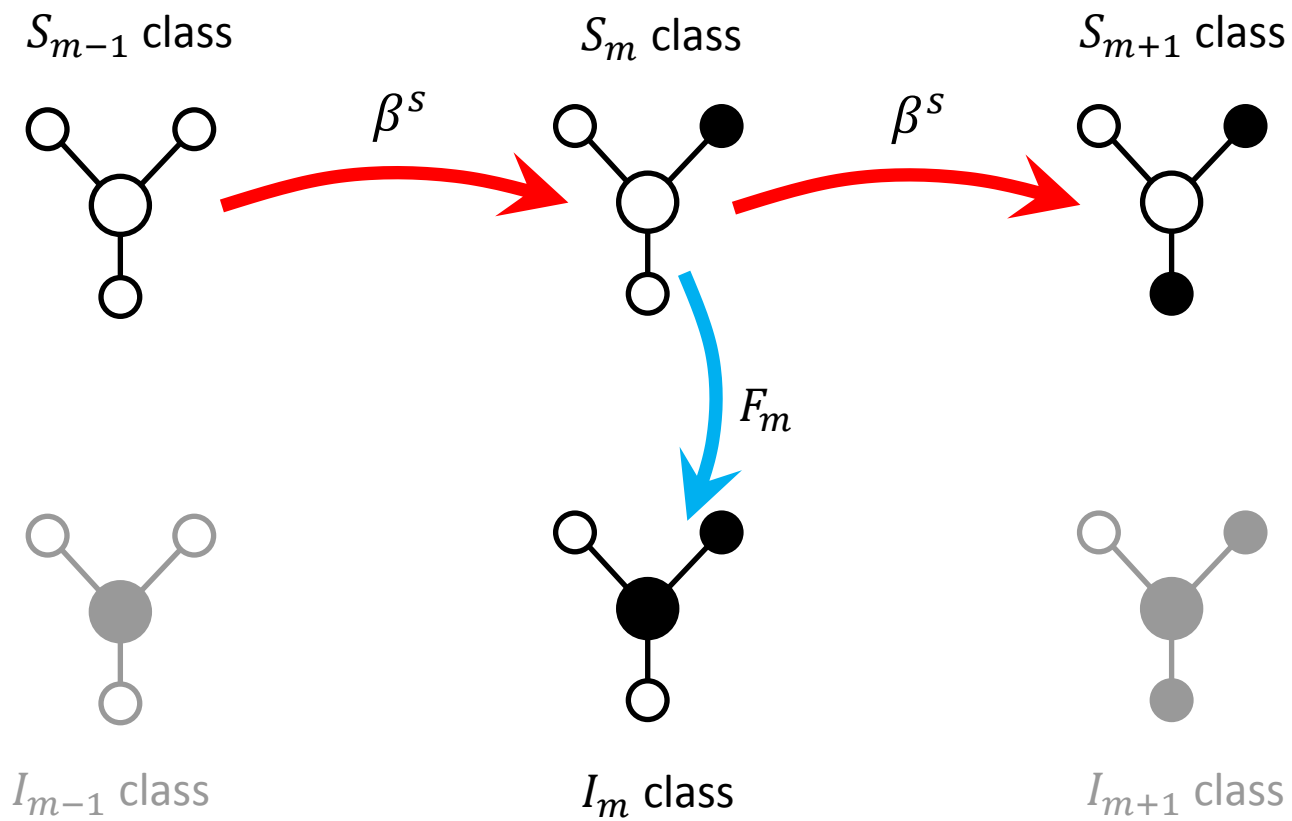
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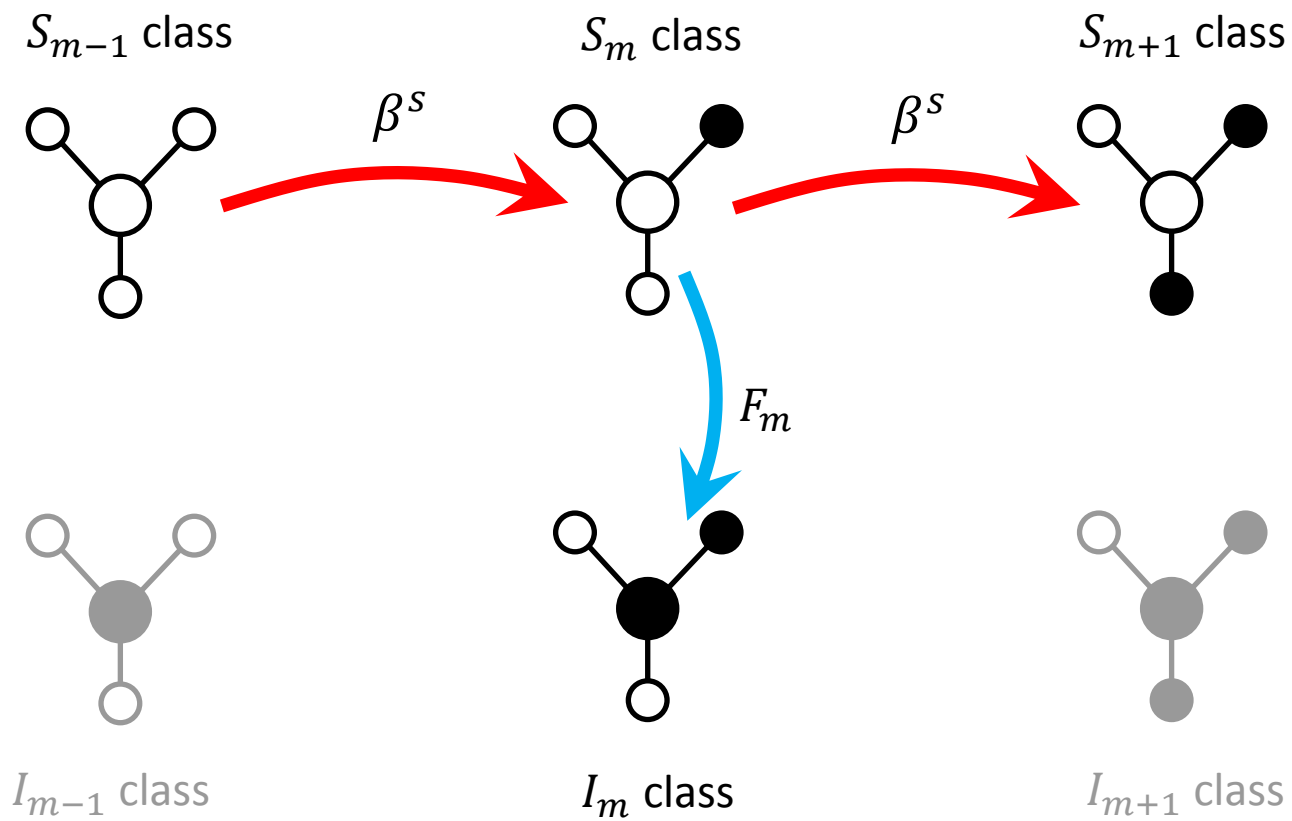
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$$\frac{d}{dt} S_m = -F_m S_m - \beta^s (z - m) S_m + \beta^s (z - m + 1) S_{m-1} \quad \text{for } m = 0, 1, \dots, z$$

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



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

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

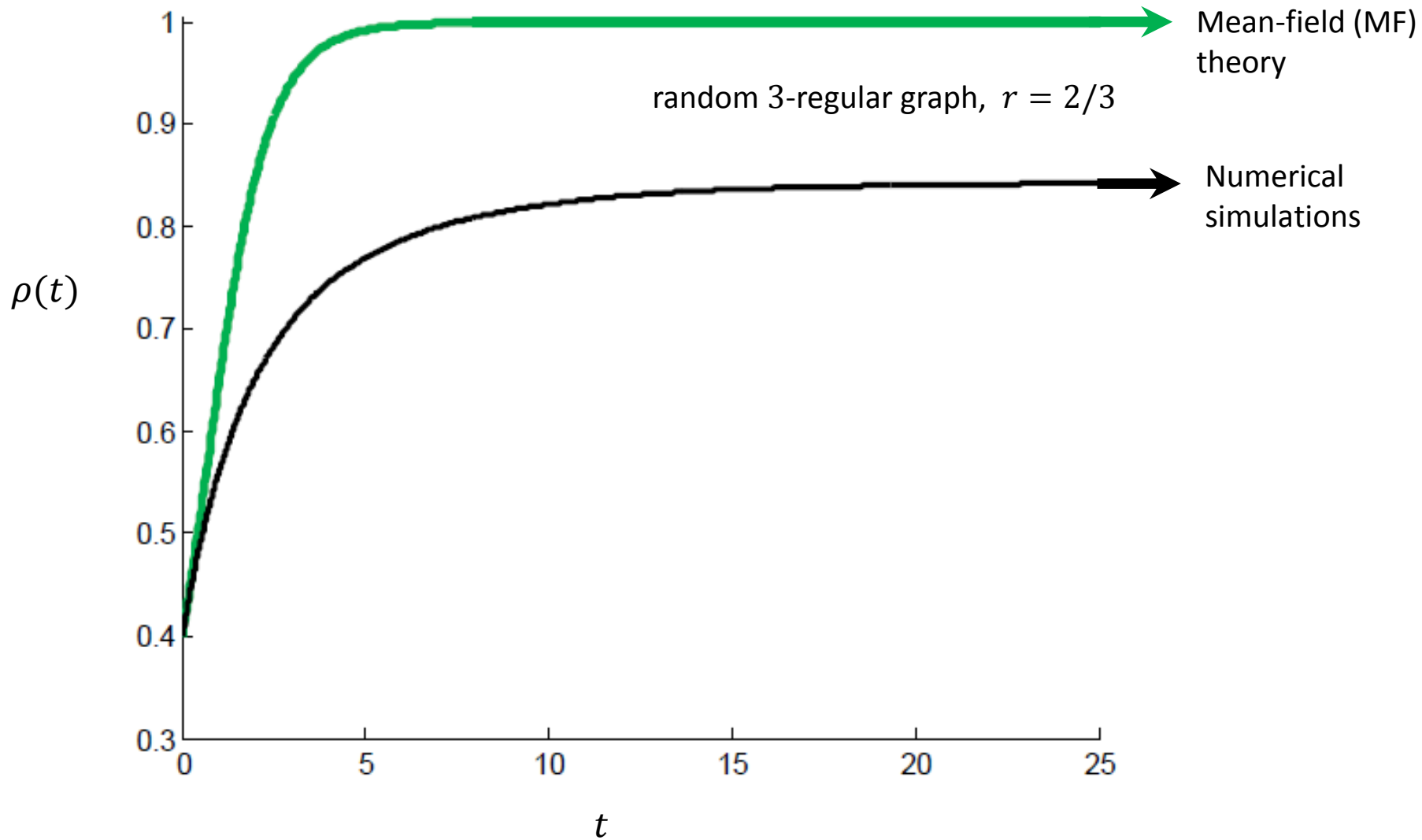
$$s_m(0) = (1 - \rho(0)) B_{z,m}(\rho(0))$$

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

Monotone threshold model



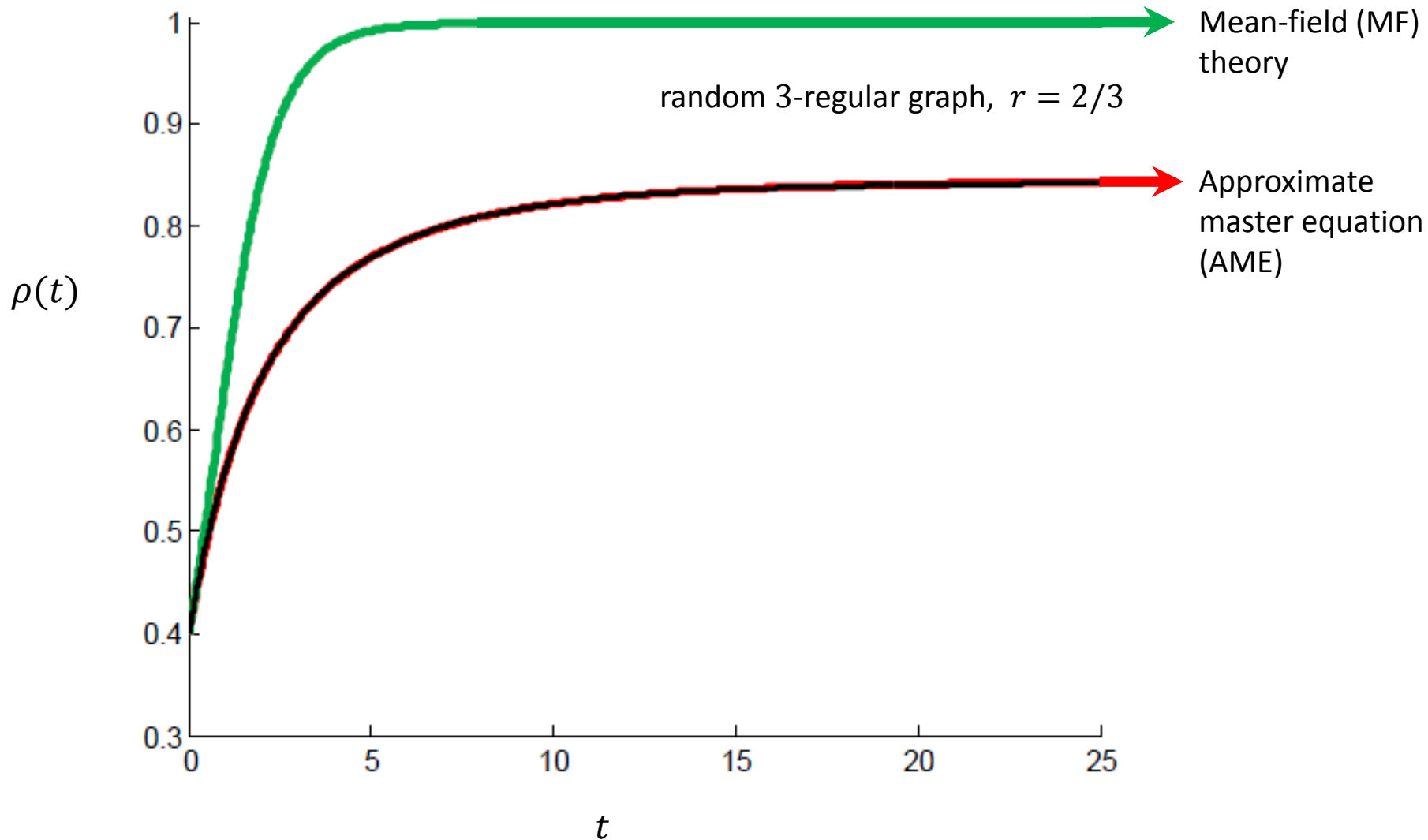
$$F_{k,m} = \begin{cases} 0 & \text{for } m < kr \\ 1 & \text{for } m \geq kr \end{cases}$$



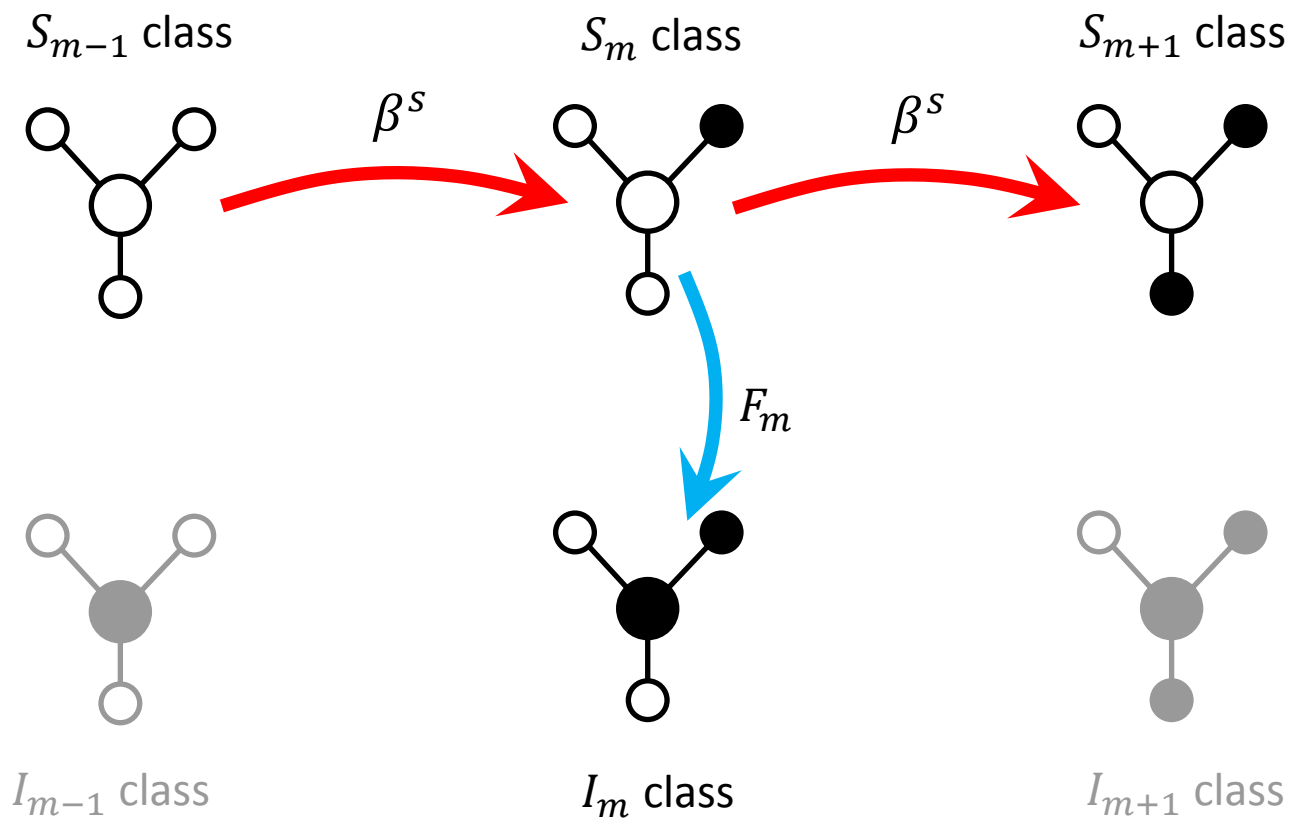
Monotone threshold model



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





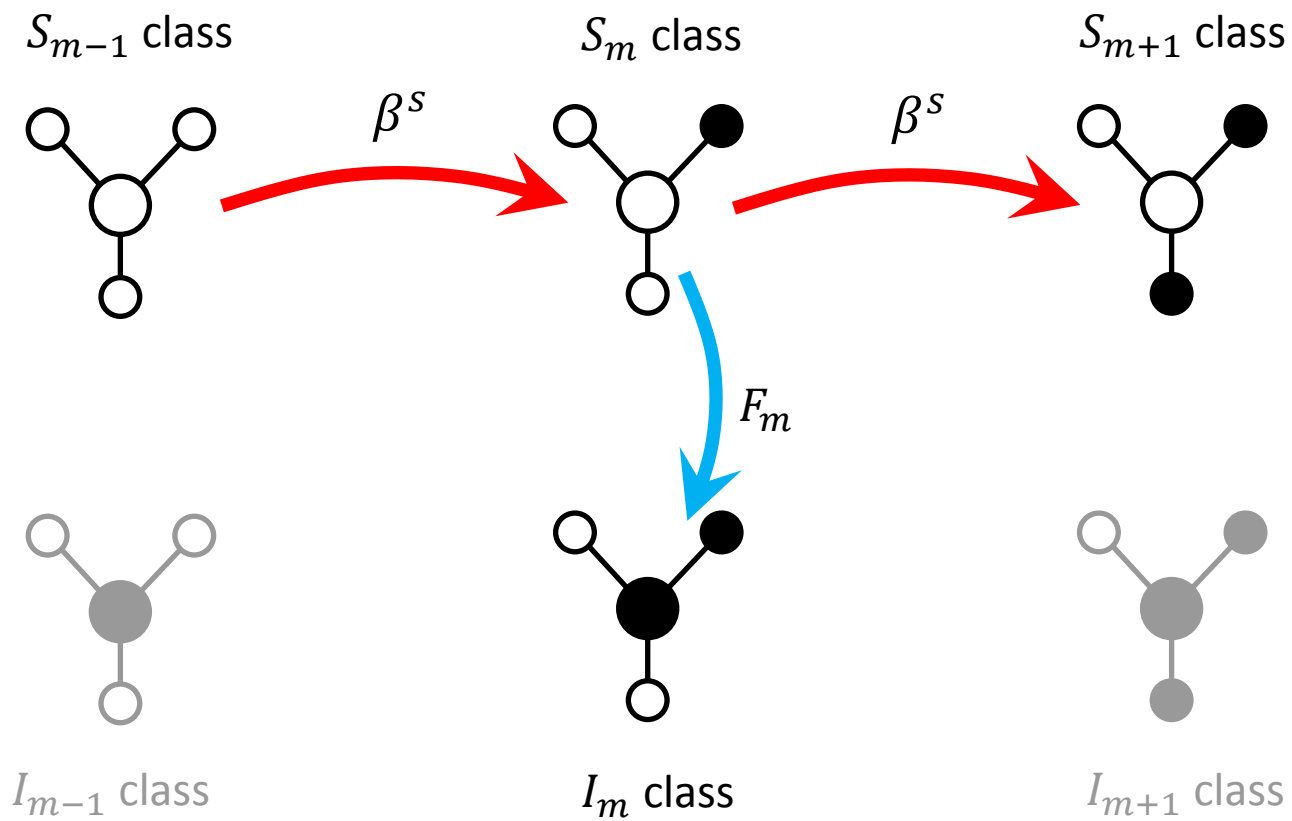


$$\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0, 1, \dots, z$$

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

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

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



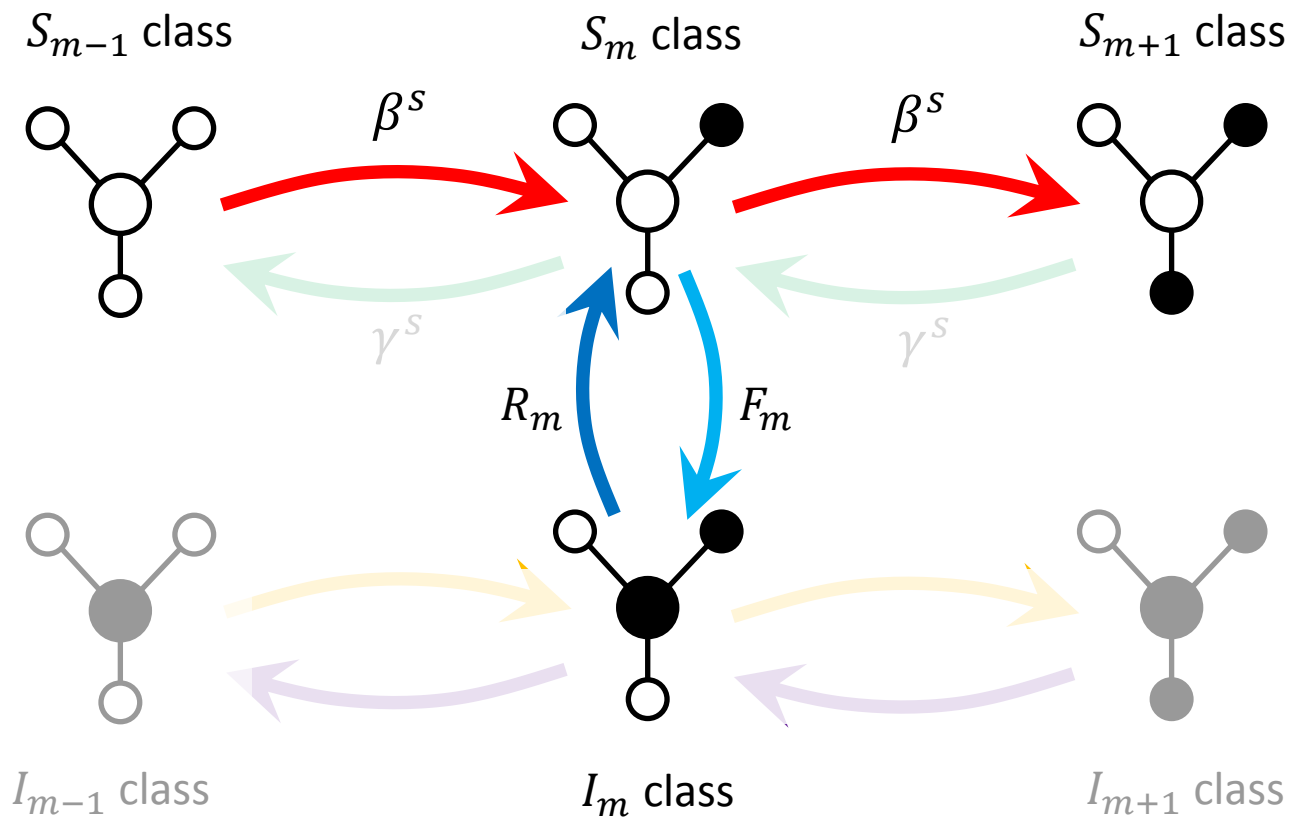
$$\frac{d}{dt} s_m = -F_m s_m$$

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

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

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

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



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

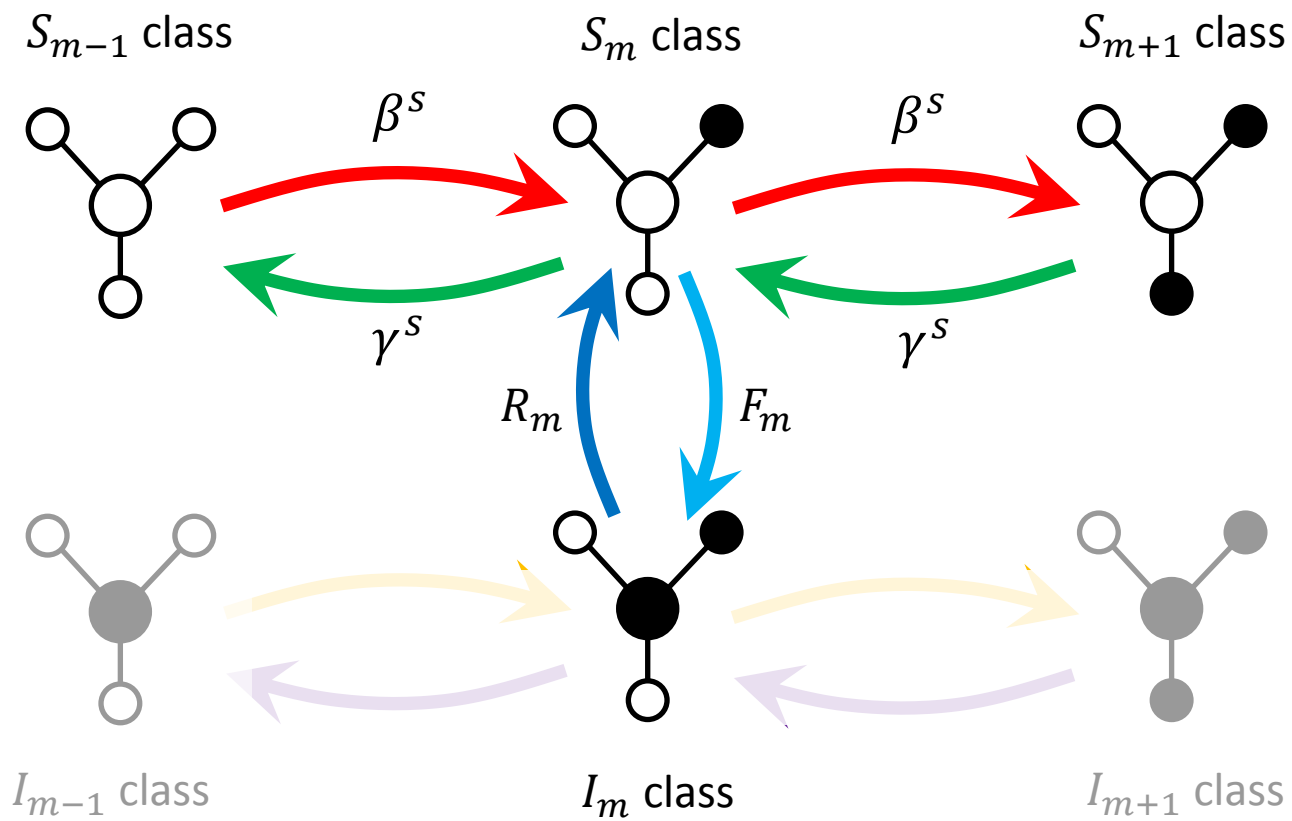


$R_m dt =$  recovery probability for an infected node with  $m$  infected neighbours

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

e.g., non-monotone threshold model:

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

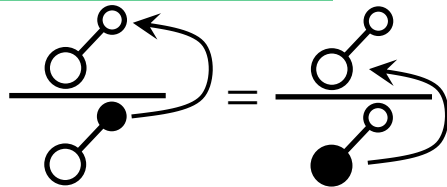


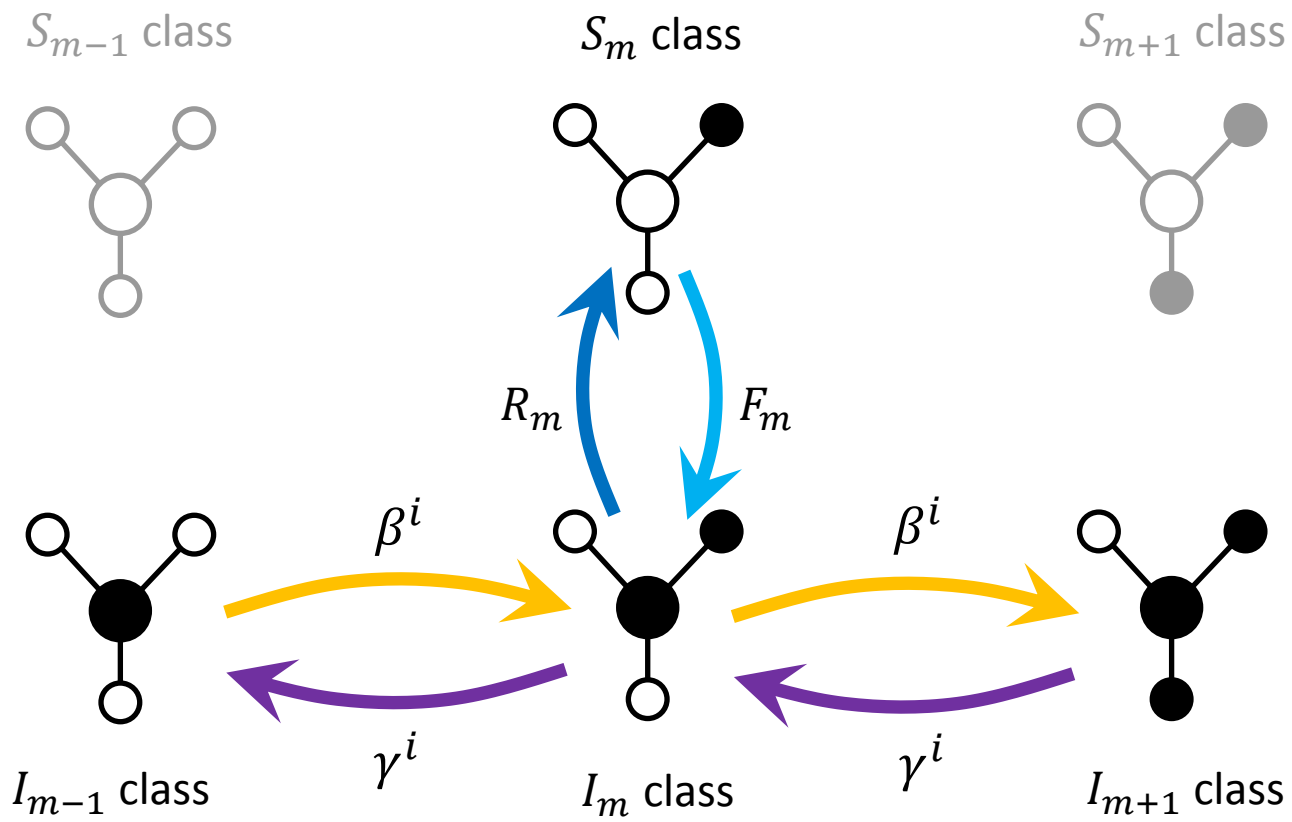
$$\frac{d}{dt} s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z - m)) s_m + \beta^s (z - m + 1) s_{m-1} + \gamma^s (m + 1) s_{m+1}$$

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

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

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





$$\frac{d}{dt} S_m = -F_m S_m + R_m I_m - (\gamma^S m + \beta^S (z - m)) S_m + \beta^S (z - m + 1) S_{m-1} + \gamma^S (m + 1) S_{m+1}$$

$$\frac{d}{dt} I_m = -R_m I_m + F_m S_m - (\gamma^I m + \beta^I (z - m)) I_m + \beta^I (z - m + 1) I_{m-1} + \gamma^I (m + 1) I_{m+1}$$

$$\beta^S = \frac{\sum_{m=0}^Z (z-m) F_m S_m}{\sum_{m=0}^Z (z-m) S_m}$$

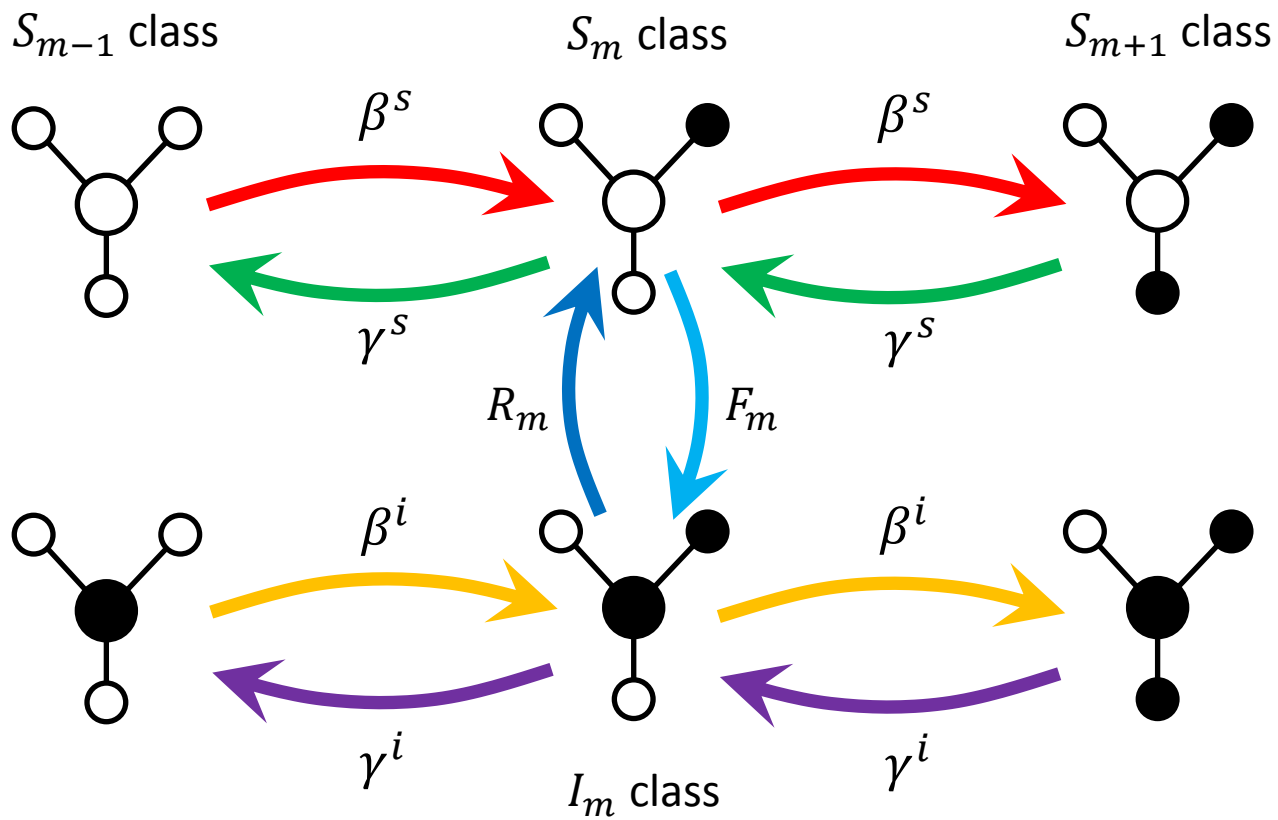
$$\gamma^S = \frac{\sum_{m=0}^Z (z-m) R_m I_m}{\sum_{m=0}^Z (z-m) I_m}$$

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

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

$$\beta^I = \frac{\sum_{m=0}^Z m F_m S_m}{\sum_{m=0}^Z m S_m}$$

$$\gamma^I = \frac{\sum_{m=0}^Z m R_m I_m}{\sum_{m=0}^Z m I_m}$$



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

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

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

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

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

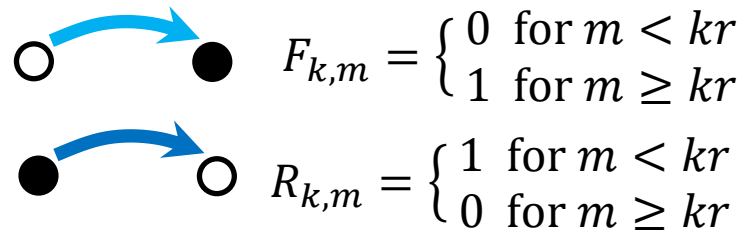
$$i_m(0) = \rho(0) B_{z,m}(\rho(0))$$

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

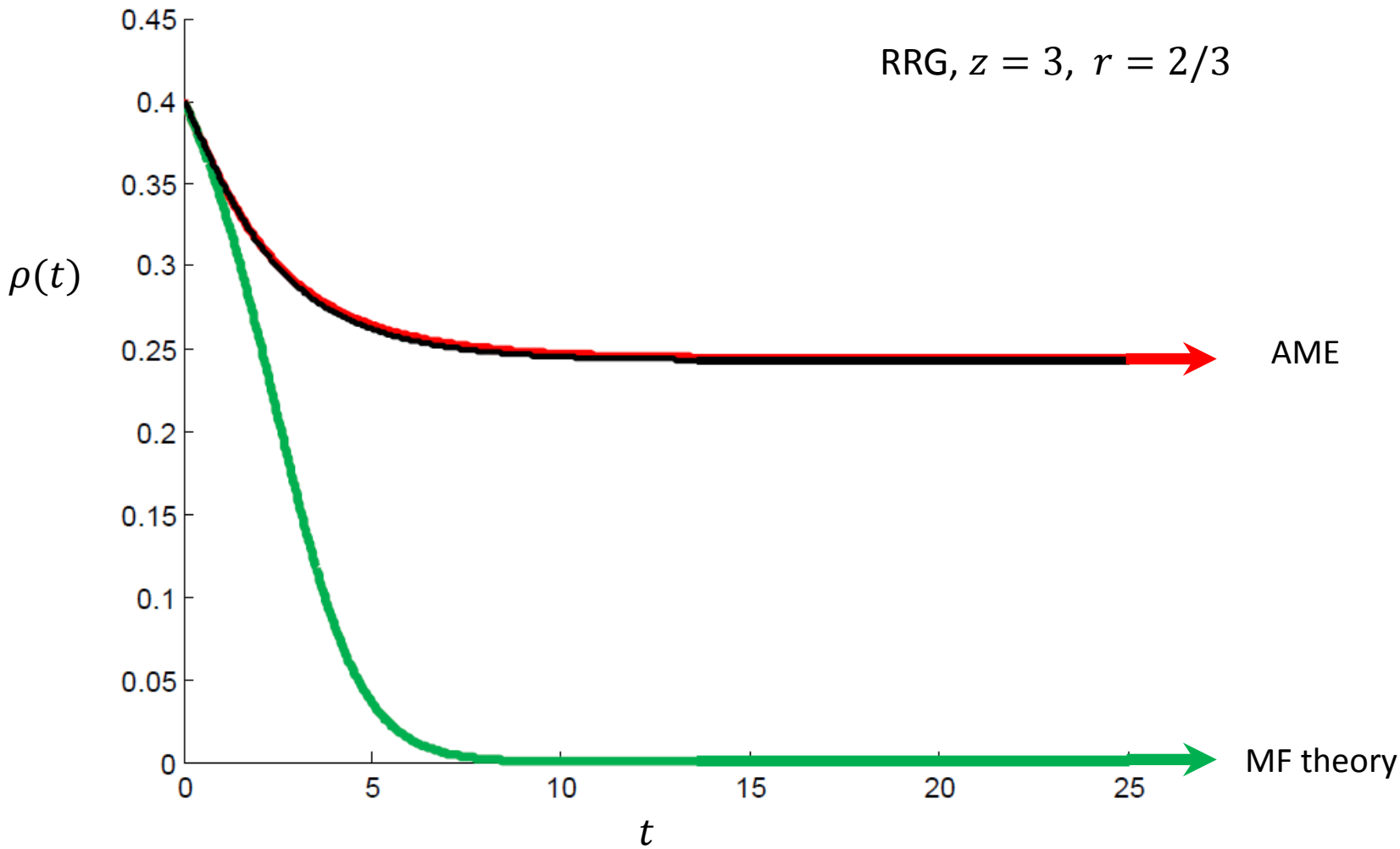
$$\gamma^i = \frac{\sum_{m=0}^z m R_m i_m}{\sum_{m=0}^z m i_m}$$

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

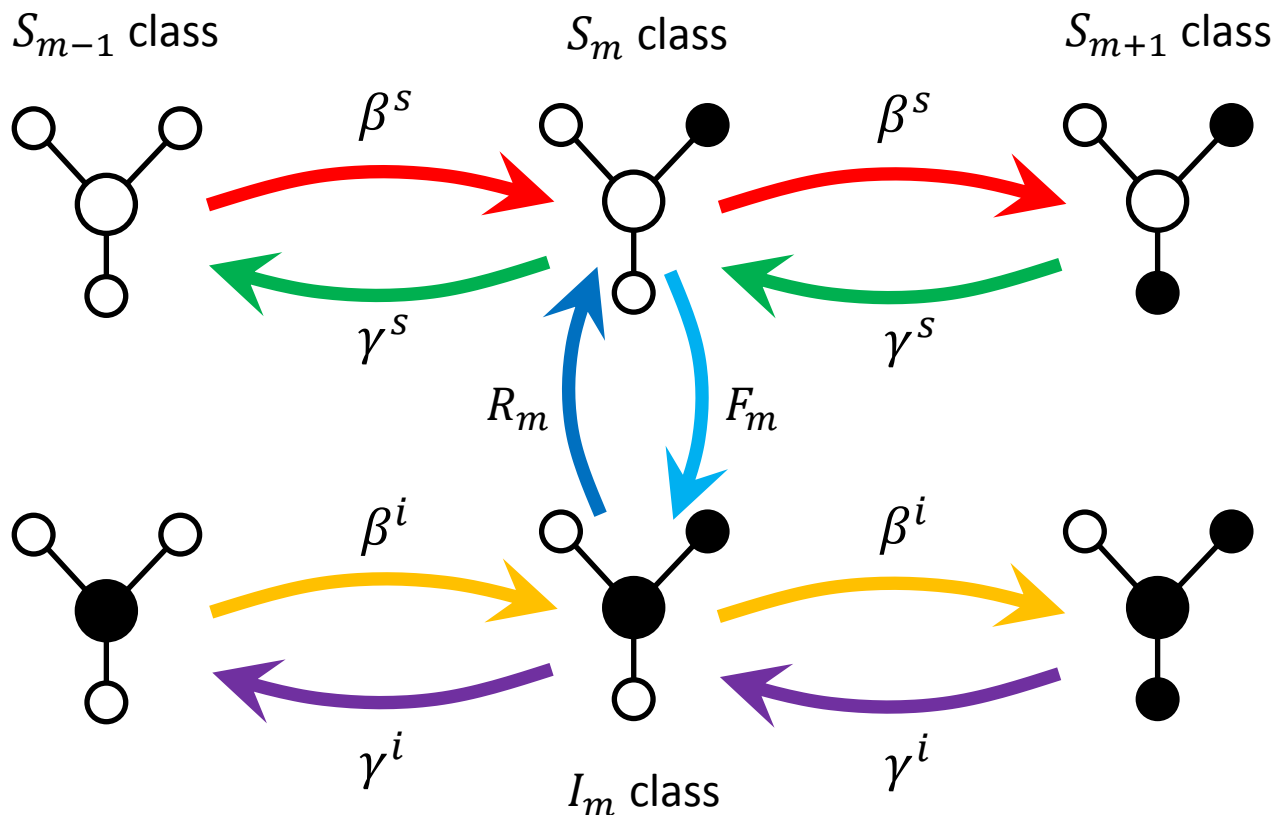
# Non-monotone threshold model



RRG,  $z = 3, r = 2/3$



Random  
z-regular  
graphs



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

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

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

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

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

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

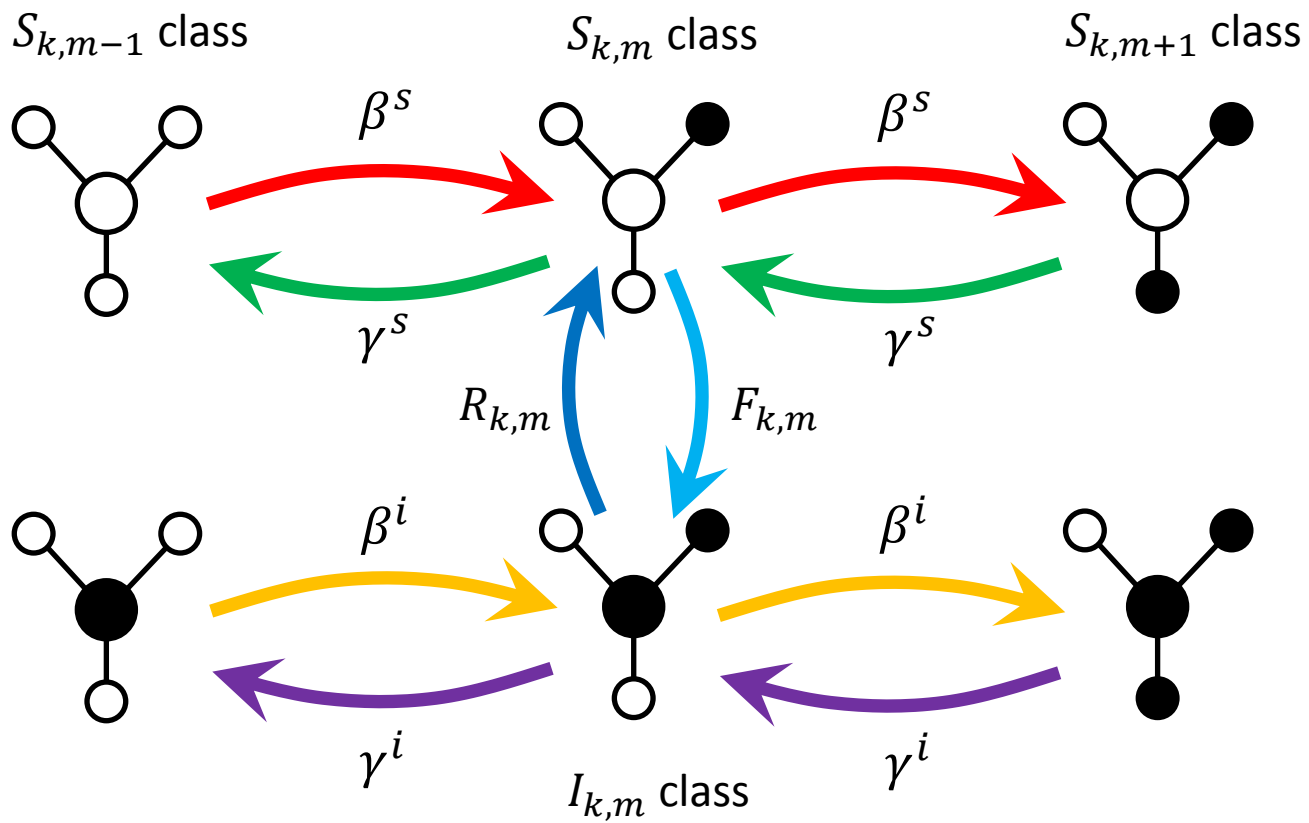
$$\beta^i = \frac{\sum_{m=0}^z m F_m s_m}{\sum_{m=0}^z m s_m}$$

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

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



General degree distribution  $P_k$



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

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

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

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

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

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

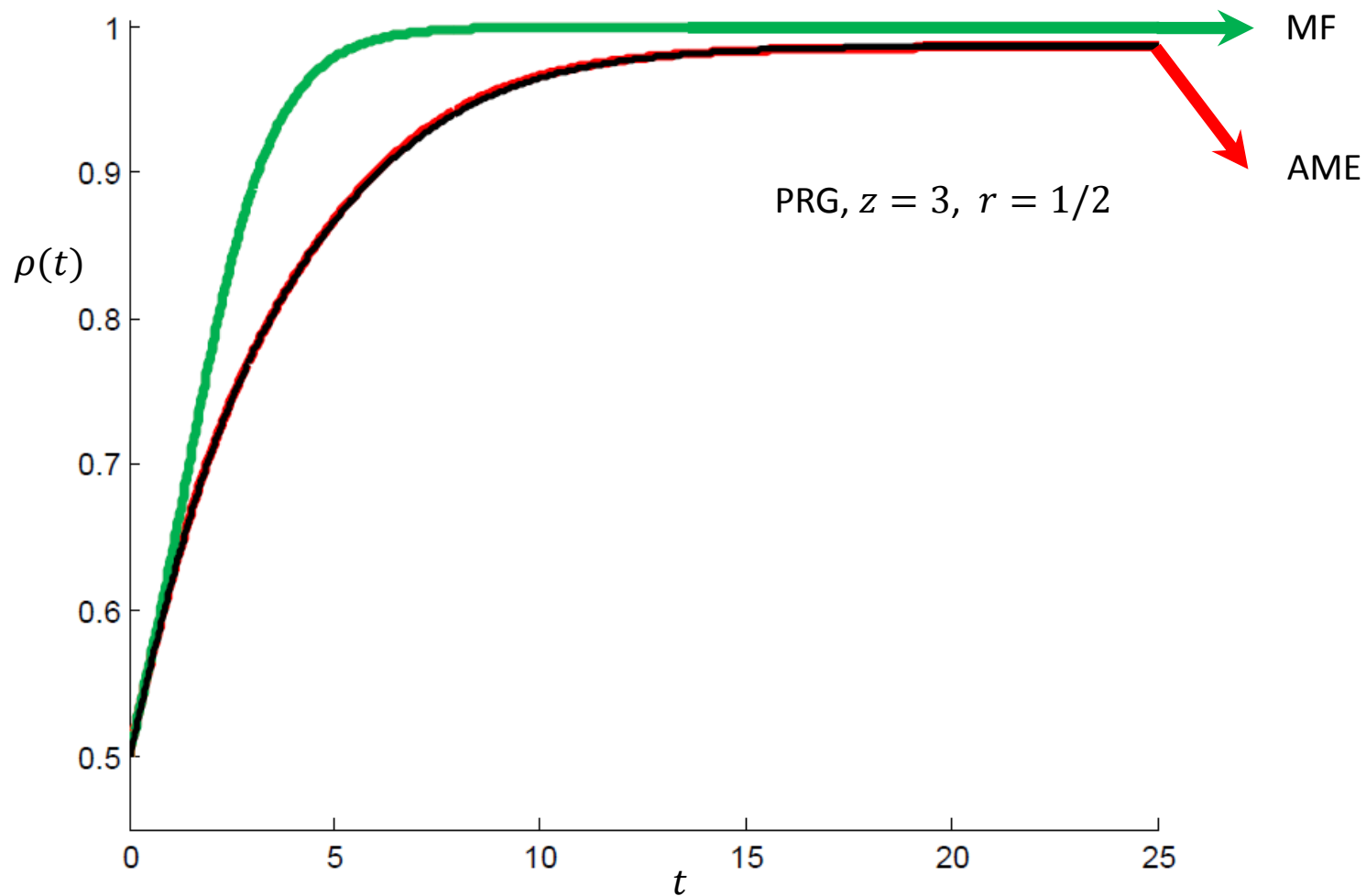
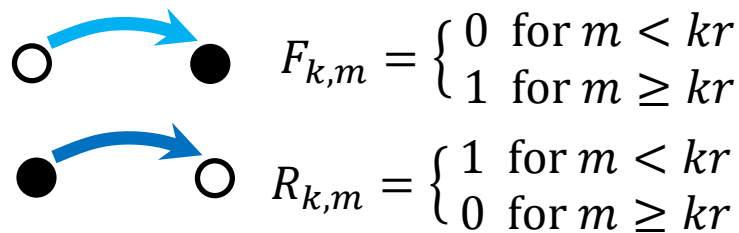
$$\beta^i = \frac{\sum P_k \sum_{m=0}^k m F_{k,m} S_{k,m}}{\sum P_k \sum_{m=0}^k m S_{k,m}}$$

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

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

Non-monotone threshold model

Poisson degree distribution

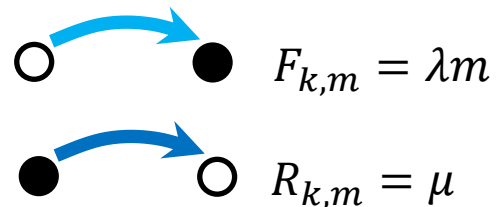


## SIS (susceptible-infected-susceptible) model for disease spread

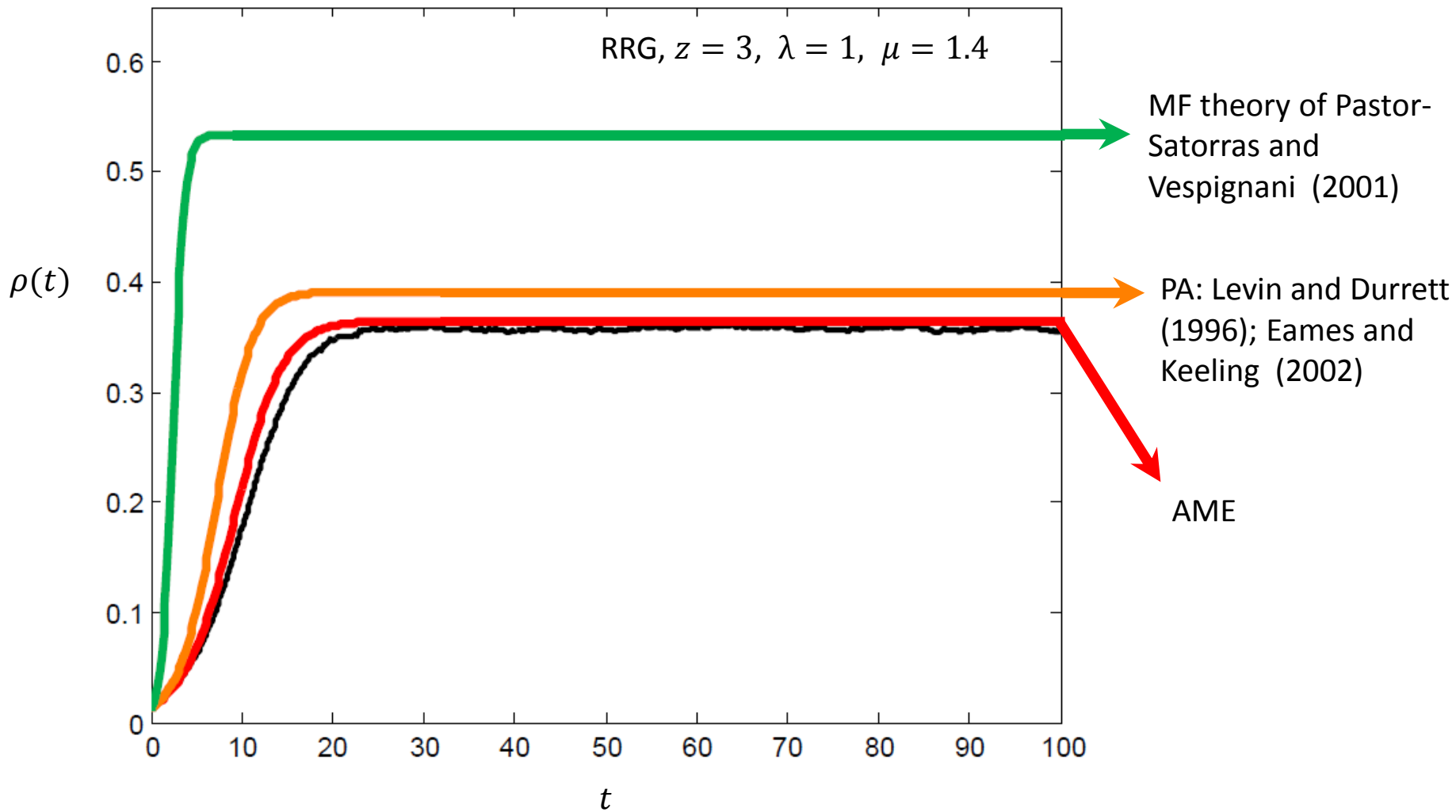
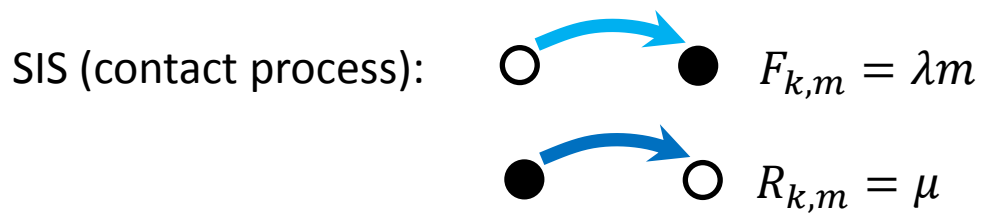
Each node is either infected or susceptible.

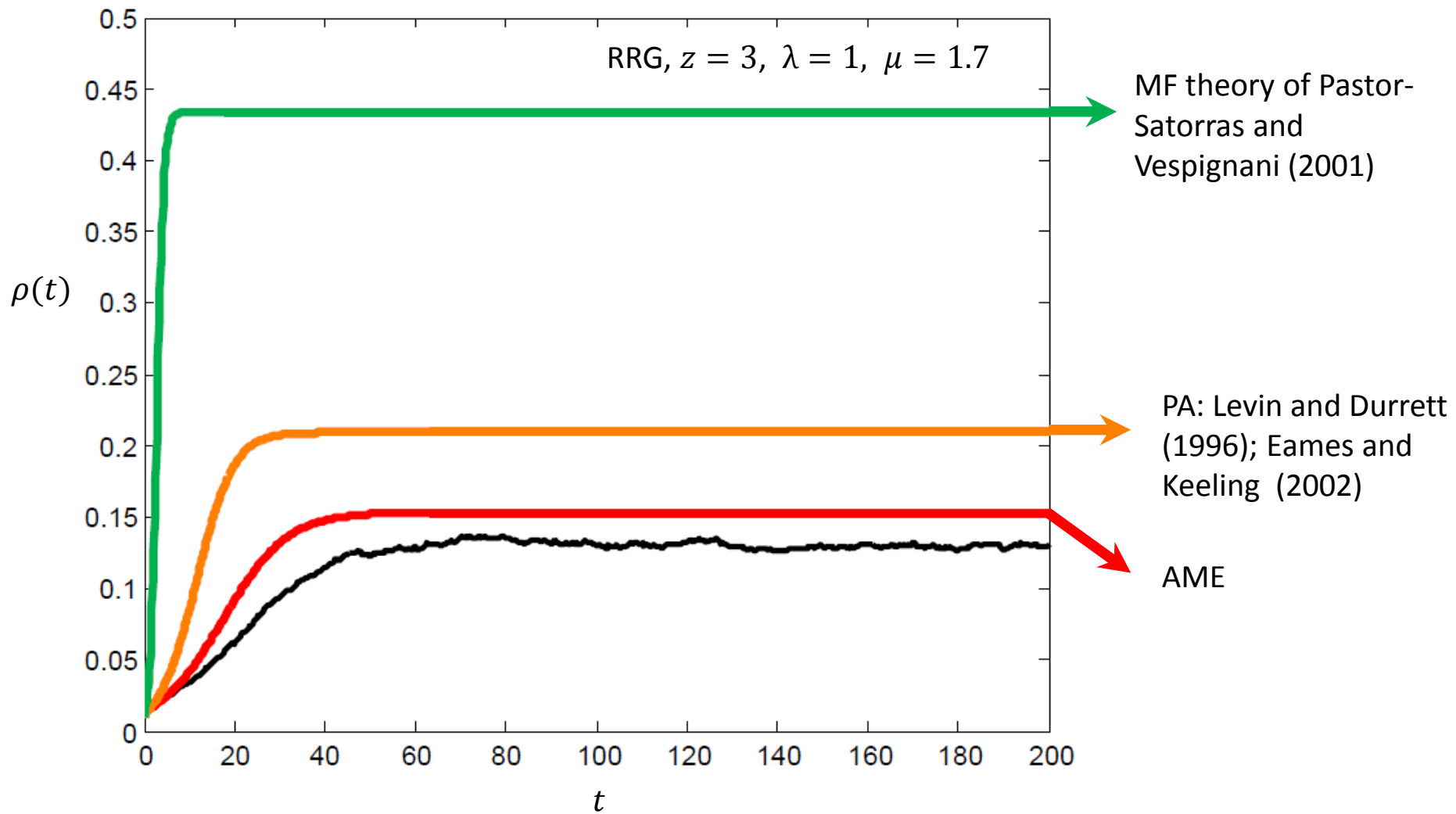
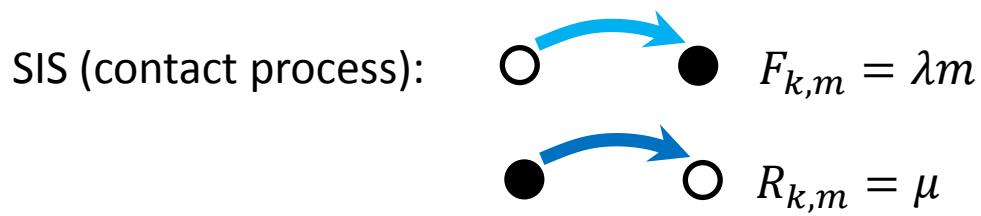
Infected nodes become susceptible at rate  $\mu$ ;

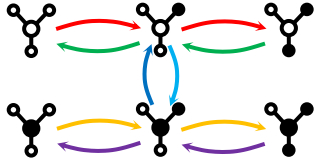
an infected node infects each of its susceptible neighbours at rate  $\lambda$ .



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







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

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

Pair Approximation: using the binomial ansatz

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

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

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.

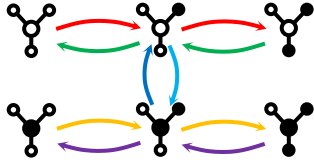
$$\frac{d}{dt} \rho_k = -\rho_k \sum_m R_{k,m} B_{k,m}(q) + (1 - \rho_k) \sum_m F_{k,m} B_{k,m}(p)$$

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

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

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

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



Number of differential equations, if  $P_k \neq 0$  for  $k = 0, 1, 2, \dots, K$ :

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

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

$(K+2)(K+1)$

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

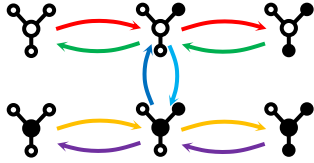
$$\frac{d}{dt} p = \frac{1}{1 - \omega} \sum_k \frac{k}{Z} P_k \sum_m \left(1 + p - 2 \frac{m}{k}\right) \left( (1 - \rho_k) F_{k,m} B_{k,m}(p) - \rho_k R_{k,m} B_{k,m}(q) \right)$$

$K+2$

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

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

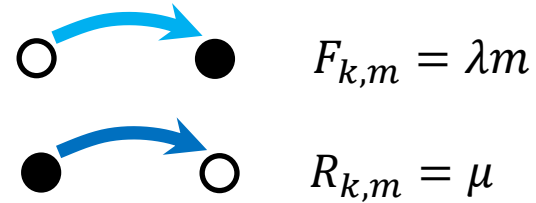
$K+1$



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

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

SIS (contact process):



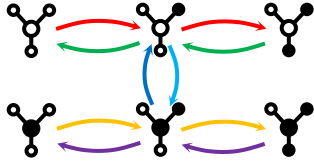
$$\frac{d}{dt} \rho_k = -\rho_k \sum_m R_{k,m} B_{k,m}(q) + (1 - \rho_k) \sum_m F_{k,m} B_{k,m}(p)$$

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

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

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

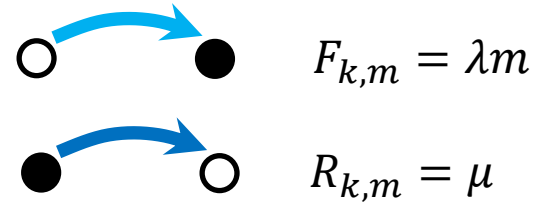




$$\frac{d}{dt} s_{k,m} = -F_{k,m} s_{k,m} + R_{k,m} i_{k,m} - (\gamma^s m + \beta^s (k-m)) s_{k,m} + \beta^s (k-m+1) s_{k,m-1} + \gamma^s (m+1) s_{k,m+1}$$

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

SIS (contact process):



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

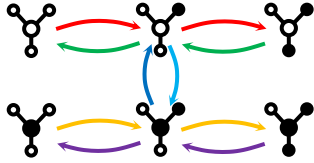
$$\frac{d}{dt} p = -2\lambda p (1 - p) + \frac{1}{1 - \omega} [\lambda p (1 - p) \omega_2 + \mu (\omega + p \omega - 2p)]$$

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

PA of House and Keeling (2010)

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

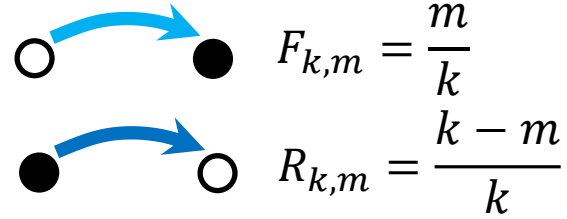
MF theory of Pastor-Satorras and Vespignani (2001)



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

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

Voter model:



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

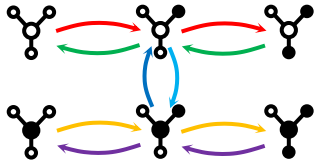
$$R_{k,m} = \frac{k-m}{k}$$

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

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

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

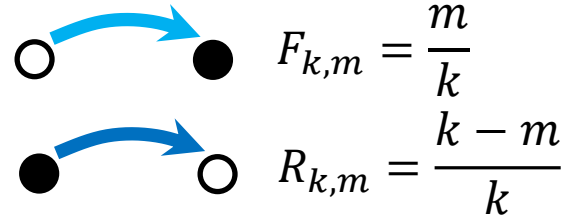
$$\frac{d}{dt} \rho_k = -\rho_k \sum_m R_{k,m} B_{k,m}(\omega) + (1 - \rho_k) \sum_m F_{k,m} B_{k,m}(\omega)$$



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

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

Voter model:



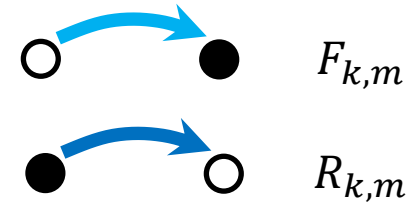
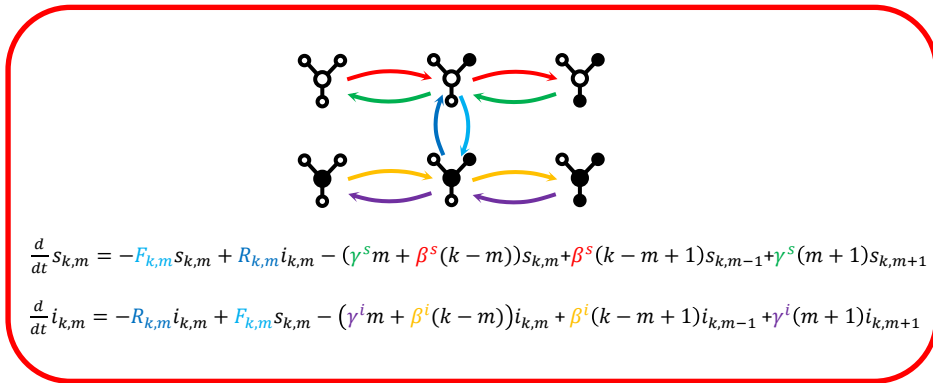
$$\frac{d}{dt} \rho_k = \frac{p}{\omega} (\omega - \rho_k)$$

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

PA of Vazquez and Eguíluz (2008)

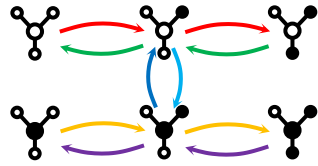
$$\frac{d}{dt} \rho_k = -\rho_k + \rho(0)$$

MF theory of Sood and Redner (2005)



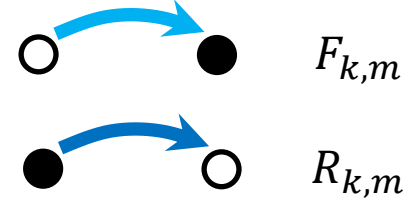
Other example of binary-state dynamics:

| Process          | $F_{k,m}$                                                                                                    | $R_{k,m}$     |
|------------------|--------------------------------------------------------------------------------------------------------------|---------------|
| SIS              | $\lambda m$                                                                                                  | $\mu$         |
| Voter model      | $m/k$                                                                                                        | $1 - F_{k,m}$ |
| Glauber dynamics | $[1 + \exp(\frac{2J}{T}(k - 2m))]^{-1}$                                                                      | $1 - F_{k,m}$ |
| Majority-vote    | $\begin{cases} Q & \text{if } m < k/2 \\ 1/2 & \text{if } m = k/2 \\ 1 - Q & \text{if } m > k/2 \end{cases}$ | $1 - F_{k,m}$ |



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

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



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

Moreover, it:

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

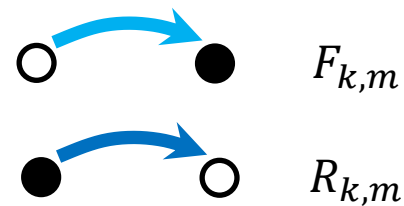
[ Durrett et al. (2012) ]

PRL 107, 068701 (2011)

PNAS 109, 3682 (2012)

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

Further results (in progress)



- Matlab m-files for solving the approximate master equations, pair approximation, and mean-field theory equations for given  $P_k$ ,  $F_{k,m}$  and  $R_{k,m}$ :

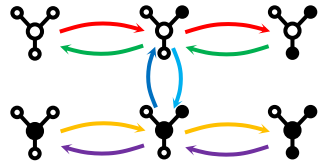
now available to download from [www.ul.ie/gleesonj](http://www.ul.ie/gleesonj)

- Pair approximation solutions and master equation solutions are identical for all time if:

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

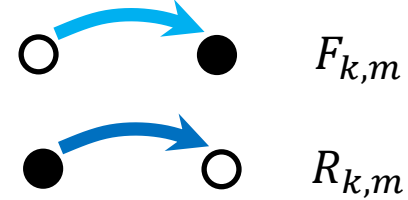
e.g., SI disease-spread model ( $A = 0$ ). Note  $B$  may be negative...

- Spin systems: pair approximation solutions and master equation solutions are identical in the limit  $t \rightarrow \infty$  for Ising model Glauber dynamics, but not for other (non-equilibrium) spin systems.



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

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



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

Moreover, it:

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

[ Durrett et al. (2012) ]

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

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- Rick Durrett, Duke

Seeking PhD students and (soon) postdoctoral researchers: see [www.ul.ie/gleesonj](http://www.ul.ie/gleesonj)





# Beyond mean-field theory: High-accuracy approximation of binary-state dynamics on networks

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