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

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

www.ul.ie/gleesonj
james.gleeson@ul.ie

PRL 107, 068701 (2011)
PNAS 109, 3682 (2012)
On the ensemble of (static, undirected, $N \to \infty$) random networks with degree distribution $P_k$: is it possible to accurately predict macroscopic outcomes for given stochastic (binary-state) dynamical processes?
On the ensemble of (static, undirected, $N \to \infty$) random networks with degree distribution $P_k$: is it possible to accurately predict macroscopic outcomes for given stochastic (binary-state) dynamical processes?

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

**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 $\lambda$.

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

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

- **Approx. Master Equations (AME):**
On the ensemble of (static, undirected, $N \to \infty$) 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:

  ![Susceptible to infected transition](image)

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

  ![Infected to susceptible transition](image)

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

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

$$R_{k,m} = \frac{k - m}{k}$$
**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 $\lambda$.

\[
F_{k,m} = \lambda m \\
R_{k,m} = \mu
\]
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.
Further examples

\[ F_{k,m} \]
\[ R_{k,m} \]

Infectious Disease Modeling of Social Contagion in Networks

Alison L. Hill\(^1\text{,}^2\text{x} \), David G. Rand\(^1\text{,}^3 \), Martin A. Nowak\(^1\text{,}^4\text{,}^5 \), Nicholas A. Christakis\(^6\text{,}^7\text{,}^8 \)

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 in assessing the role of obesity in the Forced Circle Social Network. The incorporation of non-social transmission mechanisms into social contagion models may aid in understanding a wide variety of behaviors, from obesity and smoking to obesity and social behaviors, and in suggesting new strategies for their control.
Further examples

Dynamic Opinion Model and Invasion Percolation

Jia Shao, 1 Shlomo Havlin, 2 and H. Eugene Stanley 1

1 Center for Polymer Studies and Department of Physics, Boston University, Boston, Massachusetts 02215, USA
2 Minerva Center and Department of Physics, Bar-Ilan University, 52900 Ramat-Gan, Israel
(Received 25 March 2009; published 1 July 2009)

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” 

- 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 3-regular graph, \( r = \frac{2}{3} \)

Numerical simulations

Mean-field (MF) theory
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

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

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

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

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

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

$s_m(t) =$ 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 $t$

$= \sum_{m=0}^{z} ms_m$
\[ \frac{d}{dt} s_m = -F_m s_m + \cdots \]

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

\( F_m \) = infection probability for a susceptible node with \( m \) infected neighbours

\( F_m dt \) = for \( m = 0, 1, \ldots, z \)

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

\[ F_m \equiv F_{z,m} = \begin{cases} 
0 & \text{for } m < zr \\
1 & \text{for } m \geq zr
\end{cases} \]
\[
\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m)s_m + \cdots \quad \text{for } m = 0, 1, \ldots, z
\]
\[
\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0, 1, \ldots, z
\]
\[
\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0, 1, \ldots, z
\]
\[
\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m) s_m + \beta^s (z - m + 1) s_{m-1} \quad \text{for } m = 0, 1, \ldots, z
\]
\[
\frac{d}{dt}s_m = -F_m s_m - \beta^s (z - m)s_m + \beta^s (z - m + 1)s_{m-1} \quad \text{for} \ m = 0, 1, \ldots, z
\]

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

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

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

\[
\rho(t) = 1 - \sum_{m=0}^z s_m(t)
\]
Monotone threshold model

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

random 3-regular graph, \( r = 2/3 \)

Numerical simulations

Mean-field (MF) theory
Monotone threshold model

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

\[ \rho(t) \]

Mean-field (MF) theory

random 3-regular graph, \( r = 2/3 \)

Approximate master equation (AME)
\[
\frac{d}{dt} s_m = -F_m s_m - \beta^s (z - m)s_m + \beta^s (z - m + 1)s_{m-1} \quad \text{for } m = 0, 1, \ldots, z
\]

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

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

\[
\rho = 1 - \sum_{m=0}^{z} s_m
\]
\[ \frac{d}{dt} s_m = -F_m s_m \]

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

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

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

\[ \rho = 1 - \sum_{m=0}^{z} s_m \]
\[ \frac{d s_m}{dt} = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z - m)) s_m + \beta^s (z - m + 1) s_{m-1} + \gamma^s (m + 1) s_{m+1} \]

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

- \( R_m \) \( dt \) = recovery probability for an infected node with \( m \) infected neighbours

- e.g., non-monotone threshold model:

\[ R_{k,m} = \begin{cases} 1 & \text{for } m < kr \\ 0 & \text{for } m \geq kr \end{cases} \]
\[
\frac{d}{dt} s_m = -F_m s_m + R_m i_m - (\gamma^s_m + \beta^s (z - m)) s_m + \beta^s (z - m + 1) s_{m-1} + \gamma^s (m + 1) s_{m+1}
\]

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

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

\[s_m(0) = (1 - \rho(0))B_{z,m}(\rho(0))\]
\[
\frac{d}{dt} s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z - m)) s_m + \beta^s (z - m + 1) s_{m-1} + \gamma^s (m + 1) s_{m+1}
\]

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

\[
\beta^s = \frac{\sum^z_{m=0}(z-m)F_m s_m}{\sum^z_{m=0}(z-m)s_m}
\]

\[
\gamma^s = \frac{\sum^z_{m=0}(z-m)R_m i_m}{\sum^z_{m=0}(z-m)i_m}
\]

\[
\beta^i = \frac{\sum^z_{m=0}mF_m s_m}{\sum^z_{m=0}m s_m}
\]

\[
\gamma^i = \frac{\sum^z_{m=0}mR_m i_m}{\sum^z_{m=0}m i_m}
\]

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

\[
i_m(0) = \rho(0)B_{z,m}(\rho(0))
\]
\[
\begin{align*}
\frac{d}{dt} s_m &= -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z - m)) s_m + \beta^s (z - m + 1) s_{m-1} + \gamma^s (m + 1) s_{m+1} \\
\frac{d}{dt} i_m &= -R_m i_m + F_m s_m - (\gamma^i m + \beta^i (z - m)) i_m + \beta^i (z - m + 1) i_{m-1} + \gamma^i (m + 1) i_{m+1}
\end{align*}
\]

\[
\begin{align*}
\beta^s &= \frac{\sum_{m=0}^{z}(z-m)F_m s_m}{\sum_{m=0}^{z}(z-m)s_m} \\
\gamma^s &= \frac{\sum_{m=0}^{z}(z-m)R_m i_m}{\sum_{m=0}^{z}(z-m)i_m} \\
\beta^i &= \frac{\sum_{m=0}^{z}mF_m s_m}{\sum_{m=0}^{z}ms_m} \\
\gamma^i &= \frac{\sum_{m=0}^{z}mR_m i_m}{\sum_{m=0}^{z}mi_m} \\
s_m(0) &= (1 - \rho(0))B_{z,m}(\rho(0)) \\
i_m(0) &= \rho(0)B_{z,m}(\rho(0)) \\
\rho &= \sum_{m=0}^{z} i_m = 1 - \sum_{m=0}^{z} s_m
\end{align*}
\]
Non-monotone threshold model

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

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

RRG, \( z = 3, \ r = 2/3 \)
\[
\frac{d}{dt} s_m = -F_m s_m + R_m i_m - (\gamma^s m + \beta^s (z - m))s_m + \beta^s (z - m + 1)s_{m-1} + \gamma^s (m + 1)s_{m+1}
\]

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

\[
\beta^s = \frac{\sum_{m=0}^{z} (z-m)F_ms_m}{\sum_{m=0}^{z} (z-m)s_m}
\]

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

\[
\beta^i = \frac{\sum_{m=0}^{z} mF_ms_m}{\sum_{m=0}^{z} ms_m}
\]

\[
\gamma^i = \frac{\sum_{m=0}^{z} mR_m i_m}{\sum_{m=0}^{z} mi_m}
\]

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

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

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

Random \(z\)-regular graphs
\[ \begin{align*}
\frac{d}{dt} s_{k,m} &= -F_{k,m} s_{k,m} + R_{k,m} i_{k,m} - (\gamma^s m + \beta^s (k - m)) s_{k,m} + \beta^s (k - m + 1) s_{k,m-1} + \gamma^s (m + 1) s_{k,m+1} \\
\frac{d}{dt} i_{k,m} &= -R_{k,m} i_{k,m} + F_{k,m} s_{k,m} - (\gamma^i m + \beta^i (k - m)) i_{k,m} + \beta^i (k - m + 1) i_{k,m-1} + \gamma^i (m + 1) i_{k,m+1} \\
\beta^s &= \frac{\sum P_k \sum_{m=0}^k (k-m) F_{k,m} s_{k,m}}{\sum P_k \sum_{m=0}^k (k-m) s_{k,m}} \\
\gamma^s &= \frac{\sum P_k \sum_{m=0}^k (k-m) R_{k,m} i_{k,m}}{\sum P_k \sum_{m=0}^k (k-m) i_{k,m}} \\
\beta^i &= \frac{\sum P_k \sum_{m=0}^k m F_{k,m} s_{k,m}}{\sum P_k \sum_{m=0}^k m s_{k,m}} \\
\gamma^i &= \frac{\sum P_k \sum_{m=0}^k m R_{k,m} i_{k,m}}{\sum P_k \sum_{m=0}^k m i_{k,m}} \\
\rho &= \sum_k P_k \sum_{m=0}^k i_{k,m} \\
\end{align*} \]
Non-monotone threshold model

Poisson degree distribution

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

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

PRG, \( z = 3 \), \( r = 1/2 \)
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 $\lambda$.

\[ F_{k,m} = \lambda m \]
\[ R_{k,m} = \mu \]

[cf. Marceau et al, PRE (2010),
SIS (contact process):

\[ F_{k,m} = \lambda m \]

\[ R_{k,m} = \mu \]

\( RRG, z = 3, \lambda = 1, \mu = 1.4 \)

MF theory of Pastor-Satorras and Vespignani (2001)

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

AME
SIS (contact process): \[ F_{k,m} = \lambda m \]
\[ R_{k,m} = \mu \]

RRG, \( z = 3 \), \( \lambda = 1 \), \( \mu = 1.7 \)

MF theory of Pastor-Satorras and Vespignani (2001)

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

AME
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.

Further approximating \( p(t) \) and \( q(t) \) by \( \omega(t) \) gives a Mean Field approximation:
Number of differential equations, if $P_k \neq 0$ for $k = 0, 1, 2, \ldots, K$:

$$(K + 2)(K + 1)$$
\[
\begin{align*}
\frac{d}{dt}s_{k,m} &= -F_{k,m}s_{k,m} + R_{k,m}i_{k,m} - (\gamma s_{k,m} + \beta (k-m))s_{k,m} + \beta s_{k,m-1} + \gamma s_{k,m+1} \\
\frac{d}{dt}i_{k,m} &= -R_{k,m}i_{k,m} + F_{k,m}s_{k,m} - (\gamma s_{k,m} + \beta (k-m))i_{k,m} + \beta i_{k,m-1} + \gamma i_{k,m+1}
\end{align*}
\]

SIS (contact process):
\[
\begin{align*}
F_{k,m} &= \lambda m \\
R_{k,m} &= \mu
\end{align*}
\]

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

\[
\begin{align*}
\frac{d}{dt} \rho_k &= -\rho_k \sum_m R_{k,m}B_{k,m}(\omega) + (1 - \rho_k) \sum_m F_{k,m}B_{k,m}(\omega)
\end{align*}
\]
SIS (contact process):

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

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

MF theory of Pastor-Satorras and Vespignani (2001)

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

PA of House and Keeling (2010)

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

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

\[
\omega = \sum_k k P_k \rho_k \quad \omega_2 = \sum_k \frac{k^2}{z} P_k (1 - \rho_k)
\]
\[
\frac{d}{dt} s_{k,m} = -F_{k,m} s_{k,m} + R_{k,m} l_{k,m} - \left( \gamma s_{m} + \beta (k - m) s_{k,m} \right) s_{k,m} + \beta (k - m + 1) s_{k,m-1} + \gamma s_{m} + \beta (m + 1) s_{k,m+1}
\]

Voter model:

\[
F_{k,m} = \frac{m}{k}
\]

\[
R_{k,m} = \frac{k - m}{k}
\]

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

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

\[
\omega = \sum_k P_k \rho_k \quad (1 - q) \omega = p (1 - \omega) \quad \rho = \sum_k P_k \rho_k
\]

\[
\frac{d}{dt} \rho_k = -\rho_k \sum_m R_{k,m} B_{k,m}(\omega) + (1 - \rho_k) \sum_m F_{k,m} B_{k,m}(\omega)
\]
\[
\frac{d}{dt} s_{k,m} = -F_{k,m} s_{k,m} + R_{k,m} i_{k,m} - (\gamma + \beta (k-m)) s_{k,m} + \beta \delta (k-m+1) s_{k,m+1}
\]

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

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

Other example of binary-state dynamics:

<table>
<thead>
<tr>
<th>Process</th>
<th>$F_{k,m}$</th>
<th>$R_{k,m}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>SIS</td>
<td>$\lambda m$</td>
<td>$\mu$</td>
</tr>
<tr>
<td>Voter model</td>
<td>$m/k$</td>
<td>$1 - F_{k,m}$</td>
</tr>
<tr>
<td>Glauber dynamics</td>
<td>$[1 + \exp\left(\frac{2f}{T}(k-2m)\right)]^{-1}$</td>
<td>$1 - F_{k,m}$</td>
</tr>
<tr>
<td>Majority-vote</td>
<td>$\begin{cases} Q &amp; \text{if } m &lt; k/2 \ 1/2 &amp; \text{if } m = k/2 \ 1 - Q &amp; \text{if } m &gt; k/2 \end{cases}$</td>
<td>$1 - F_{k,m}$</td>
</tr>
</tbody>
</table>
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)
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

- 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 $t \to \infty$ for Ising model Glauber dynamics, but not for other (non-equilibrium) spin systems.
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) ]
Collaborators and funding

- Adam Hackett, UL
- 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

Seeking PhD students and (soon) postdoctoral researchers: see www.ul.ie/gleesonj
Beyond mean-field theory: High-accuracy approximation of binary-state dynamics on networks

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

www.ul.ie/gleesonj
james.gleeson@ul.ie

PRL 107, 068701 (2011)
PNAS 109, 3682 (2012)