Intro to deterministic models

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Pairwise equations

We will develop a system of differential equations which predicts disease spread by tracking the numbers of partnerships involving individuals of various statuses.
These have been developed by [1, 2, 3, 4] among many others.

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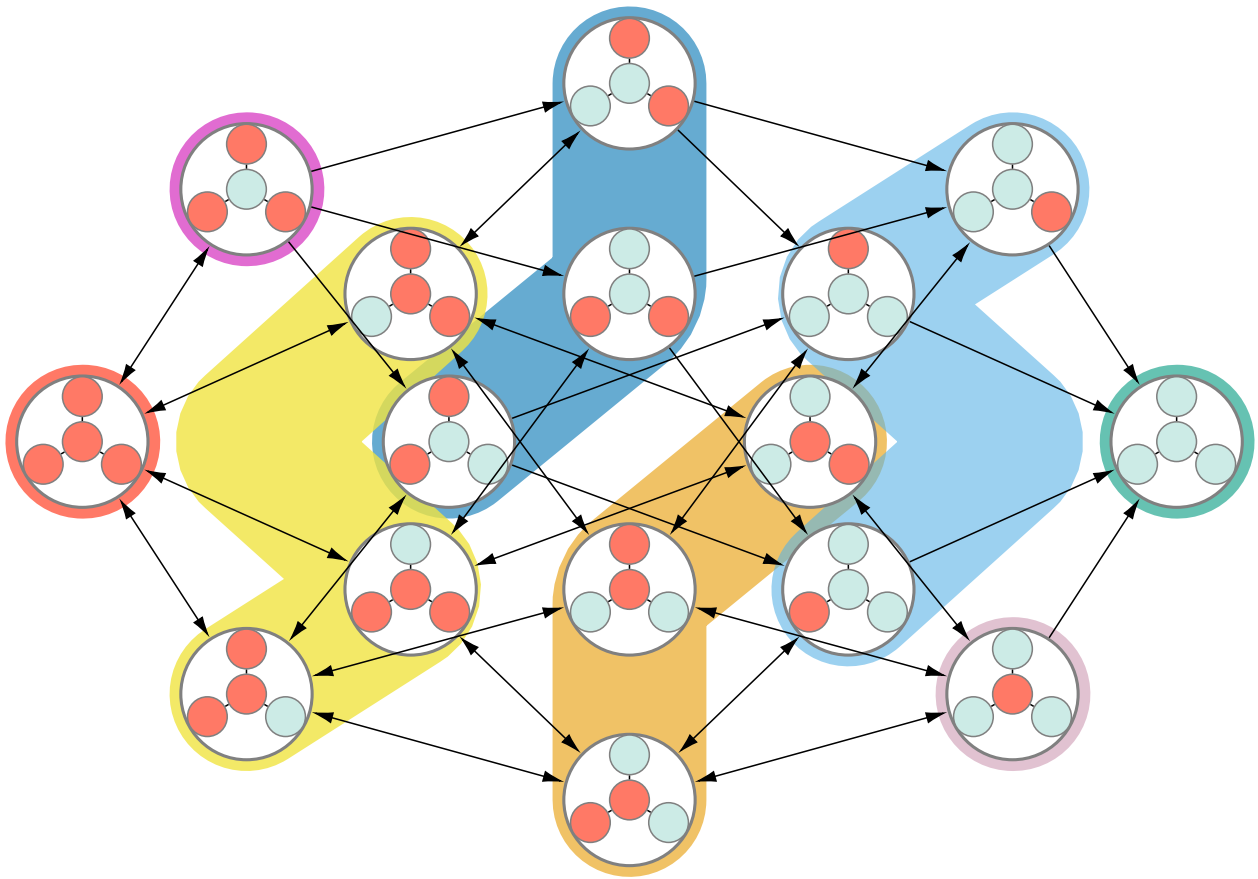

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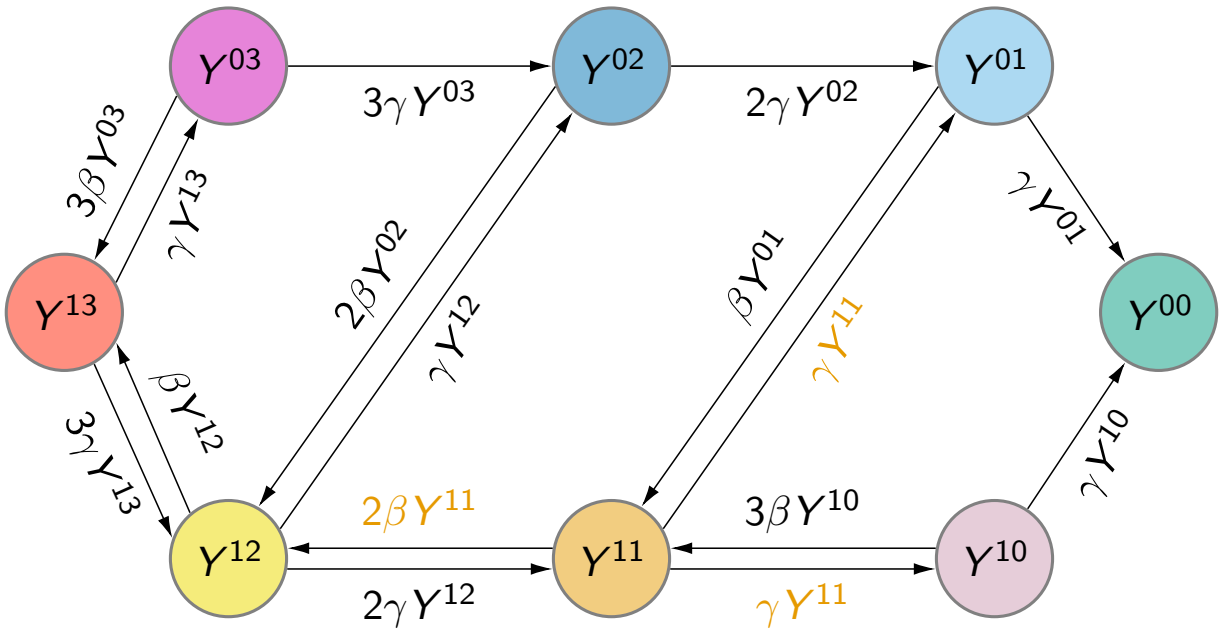

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If we set $[SI]$ to be $1/N$ times the number of SI edges, we have:[1]

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Can you see the problem?

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Need for Closures

We need to find equations for $[SI]$. For the SIS case we have

$$[\dot{SI}] = \beta[SSI] - \beta[ISI] - \beta[SI] - \gamma[SI]$$

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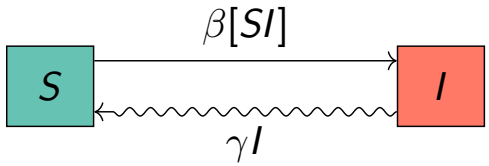
- The third term represents the susceptible node in an SI pair being infected by the infected node in the pair.
- The fourth term represents the infected node in an SI pair recovering.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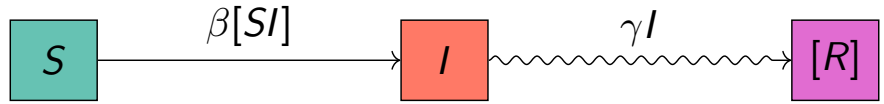
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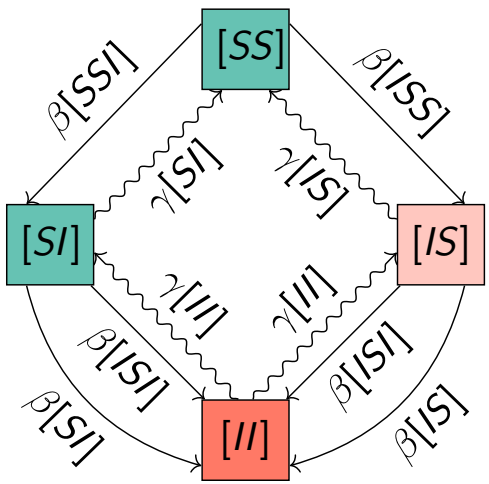
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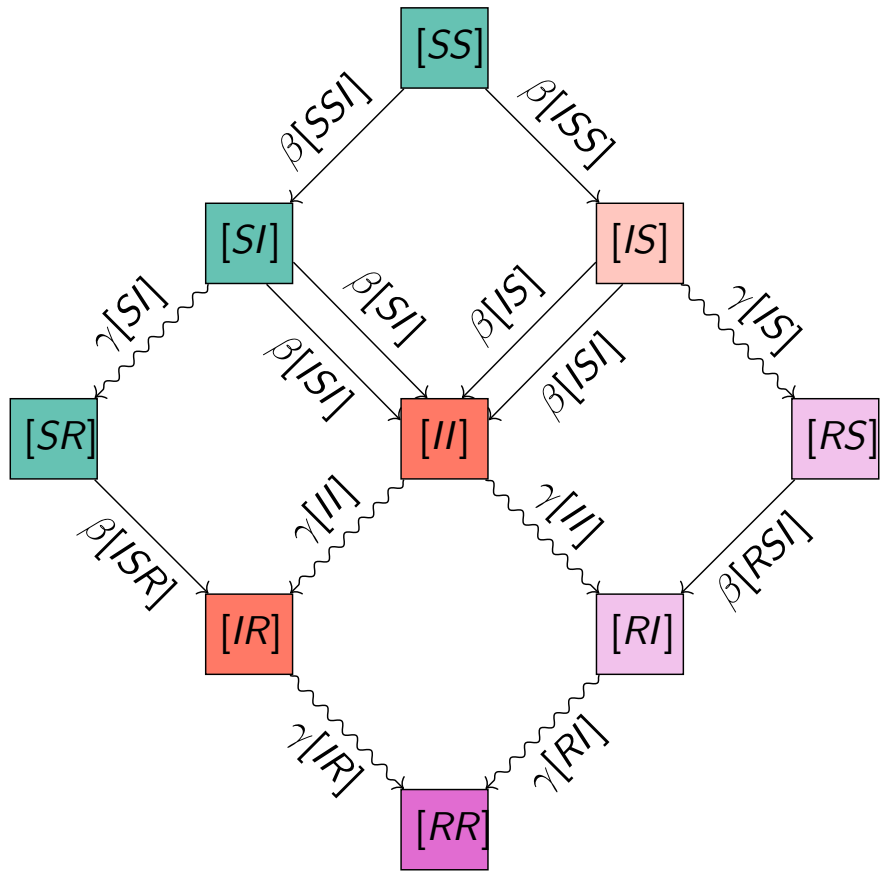
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The equations are equivalent to the Kermack-McKendrick equations

Appropriateness of $[SI] = \langle K \rangle SI$

What assumptions are we making when we set $[SI] = \langle K \rangle SI$?

- We're assuming that nodes are not preferentially infected by degree.
- We're assuming that neighbors of infected nodes are no more likely to be infected than any other node.

When are these assumptions appropriate?

- Same degree, annealed network. Partnerships have zero duration.
- Large very similar degrees, transmission probability per edge very low, and low clustering.
- As a general rule — if the disease will never transmit across the same partnership twice, we can use models that ignore partnership duration.

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- Then

$$\begin{aligned} \dot{S}_k &= -\beta k S_k \pi_I \\ \dot{I}_k &= \beta k S_k \pi_I - \gamma I_k \\ \dot{R}_k &= \gamma I_k \end{aligned}$$

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- This is the same $\mathcal{R}_0$ whether it is SIS or SIR.

SIS endemic equilibrium prediction

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- This gives the equilibrium infection level.

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- So $I_k = \beta k P(k) \pi_I / (\gamma + \beta k \pi_I)$

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- But $\pi_I = \sum k I_k / \langle K \rangle$. Substituting for I_k yields

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- Not pleasant to solve, but doable. There is a positive solution iff $\mathcal{R}_0 = \beta \left\langle K^2 \right\rangle / \gamma \langle K \rangle > 1$.

SIR final size

Let's derive the final size for

$$\begin{aligned}
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\dot{I}_k &= \beta k S_k \pi_I - \gamma I_k \\
\dot{R}_k &= \gamma I_k \\
\pi_I &= \sum_\ell \ell I_\ell \Big/ \langle K \rangle \ .
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assuming at $t = 0$ a fraction ρ is randomly infected:
$S_k(0) = (1 - \rho)P(k)$ for all k.

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- The integrating factor will have an interpretation which is important later.

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It is convenient to think of θ as the probability that a stub belonging to u has not been responsible for bringing infection to u by time t.

Consolidating and continuing

Our model is now

$$\begin{aligned}
\dot{\theta} &= -\beta \pi_I \theta \\
S_k &= (1-\rho) P(k) \theta^k \\
I_k &= P(k) - S_k - R_k \\
\dot{R}_k &= \gamma I_k \\
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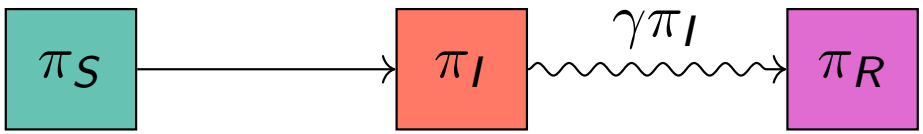
- Setting $\pi_X = \sum_\ell \ell X_\ell / \langle K \rangle$ we have



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- Further $\pi_S = (1 - \rho) \sum_k k P(k) \theta^k / \langle K \rangle = \theta \hat{\psi}(\theta) / \langle K \rangle$.

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- Further $\pi_S = (1-\rho) \sum_k k P(k) \theta^k / \langle K \rangle = \theta \hat{\psi}(\theta) / \langle K \rangle$.
- So $\pi_I = 1 - \pi_S - \pi_R$. Substituting in terms of θ we have

$$\dot{\theta} = -\beta\theta \left(1 - \frac{\theta \hat{\psi}'(\theta)}{\langle K \rangle} + \frac{\gamma \ln \theta}{\beta} \right)$$

$$S = \hat{\psi}(\theta)$$

$$I = 1 - S - R$$

$$\dot{R} = \gamma I$$

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$$\theta(\infty) = \exp\left[-\frac{\beta}{\gamma}\left(1 - \frac{\theta(\infty)\hat{\psi}'(\theta(\infty))}{\langle K \rangle}\right)\right]$$

Then

$$S = \hat{\psi}(\theta), \qquad R = 1 - \hat{\psi}(\theta)$$

Scale-free networks

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- For such a network, $\mathcal{R}_0 = \frac{\beta}{\gamma} \frac{\langle K^2 \rangle}{\langle K \rangle} = \infty$ if $\beta > 0$ — No epidemic threshold!
- But if $\langle K^2 \rangle$ is finite, this predicts there is a β_c below which epidemics are impossible.

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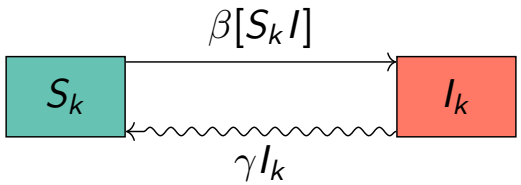
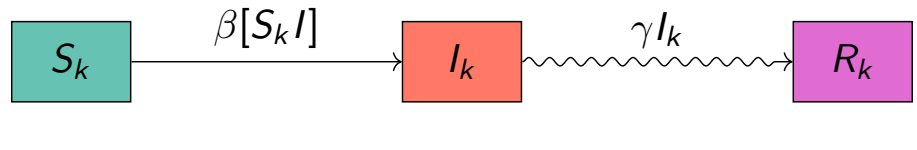
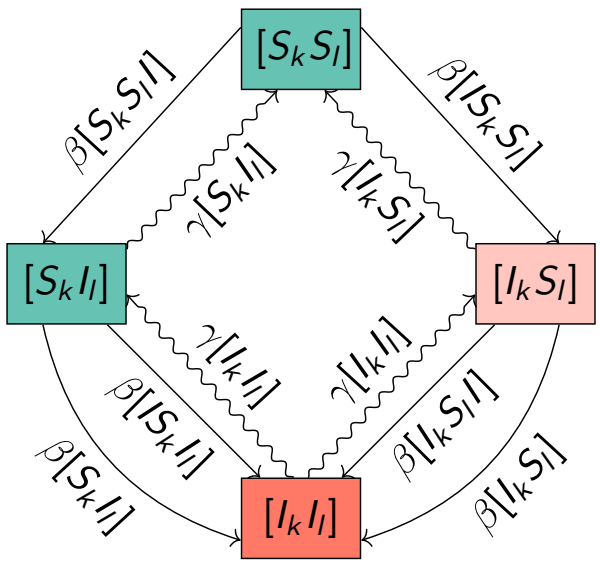
- High degree nodes get infected and infect their neighbors. Then they recover.
- So susceptible high degree nodes tend to have more infected neighbors.
- We expect to see islands of infection surrounding high degree nodes. Eventually the disease spreads to other high degree nodes. So it can persist even if the naive estimate has $\mathcal{R}_0 < 1$.

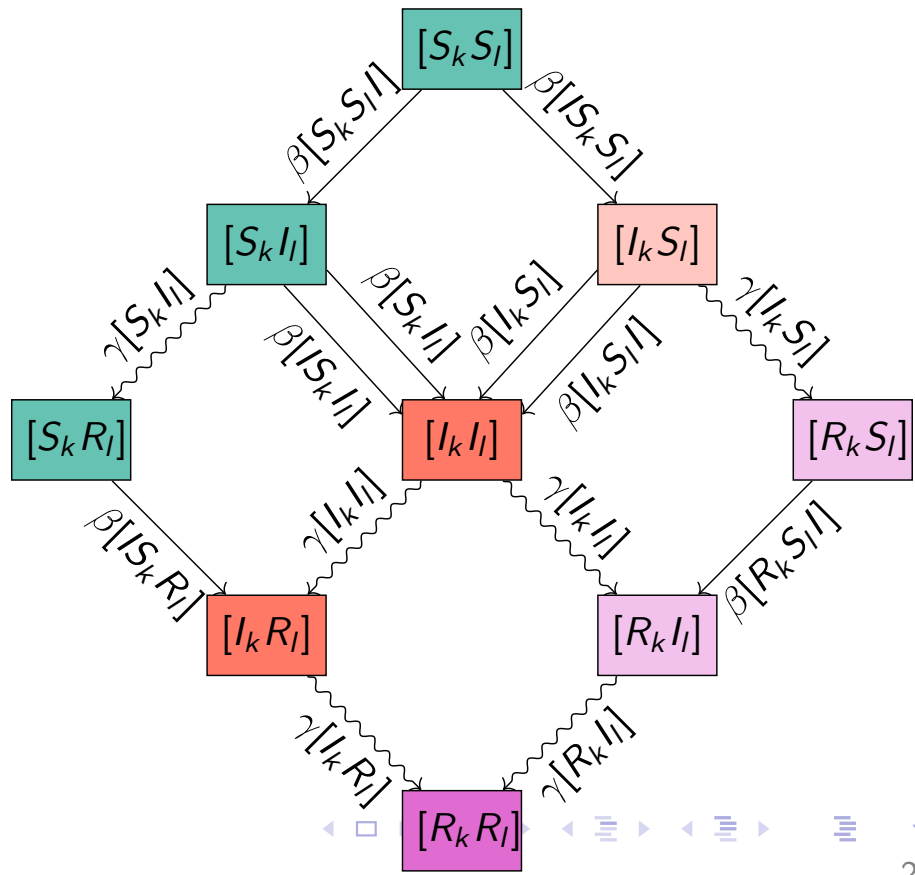
An improved heterogeneous degree model

Use S_k, I_k, and R_k to denote the proportion of the population that is in each state and has degree k: $\sum_k S_k + I_k + R_k = 1$.









Improved closure

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$$[AS_kB] = \frac{k-1}{k}\frac{[AS_k][S_kB]}{S_k}$$

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For SIR on a Configuration Model network, it's a great fit.

SIS system

The SIS model becomes

$$
\begin{aligned}
\dot{[S_k]} &= \gamma[I_k] - \beta[S_k I], \\
\dot{[I_k]} &= \beta[S_k I] - \gamma[I_k], \\
\dot{[S_k I_\ell]} &= \gamma([I_k I_\ell] - [S_k I_\ell]) + \beta\left([S_k S_\ell I] - [I S_k I_\ell] - [S_k I_\ell]\right), \\
\dot{[S_k S_\ell]} &= \gamma([S_k I_\ell] + [I_k S_\ell]) - \beta\left([S_k S_\ell I] + [I S_k S_\ell]\right) \\
\dot{[I_k I_\ell]} &= \beta([S_k I_\ell] + [I_k S_\ell]) - 2\gamma[I_k I_\ell] + \beta\left([I S_k I_\ell] + [I_k S_\ell I]\right)
\end{aligned}
$$

with the closure $[AS_mB] = \frac{m-1}{m}[AS_m][S_mB]/S_m$

SIR system

The SIR model becomes

$$
\begin{aligned}
[\dot{S_k}] &= -\beta[S_k I], \\
[\dot{I_k}] &= \beta[S_k I] - \gamma[I_k], \\
[\dot{R_k}] &= \gamma[I_k], \\
[\dot{S_k I_\ell}] &= -\gamma[S_k I_\ell] + \beta\left([S_k S_\ell I] - [I S_k I_\ell] - [S_k I_\ell]\right), \\
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for some π_I which can be calculated.
This will hold if

1. the network is a Configuration Model network,
2. the disease is introduced to some nodes selected uniformly at random, and
3. the disease is SIR.

Discussion

This "pair approximation" model has some strengths and weaknesses:

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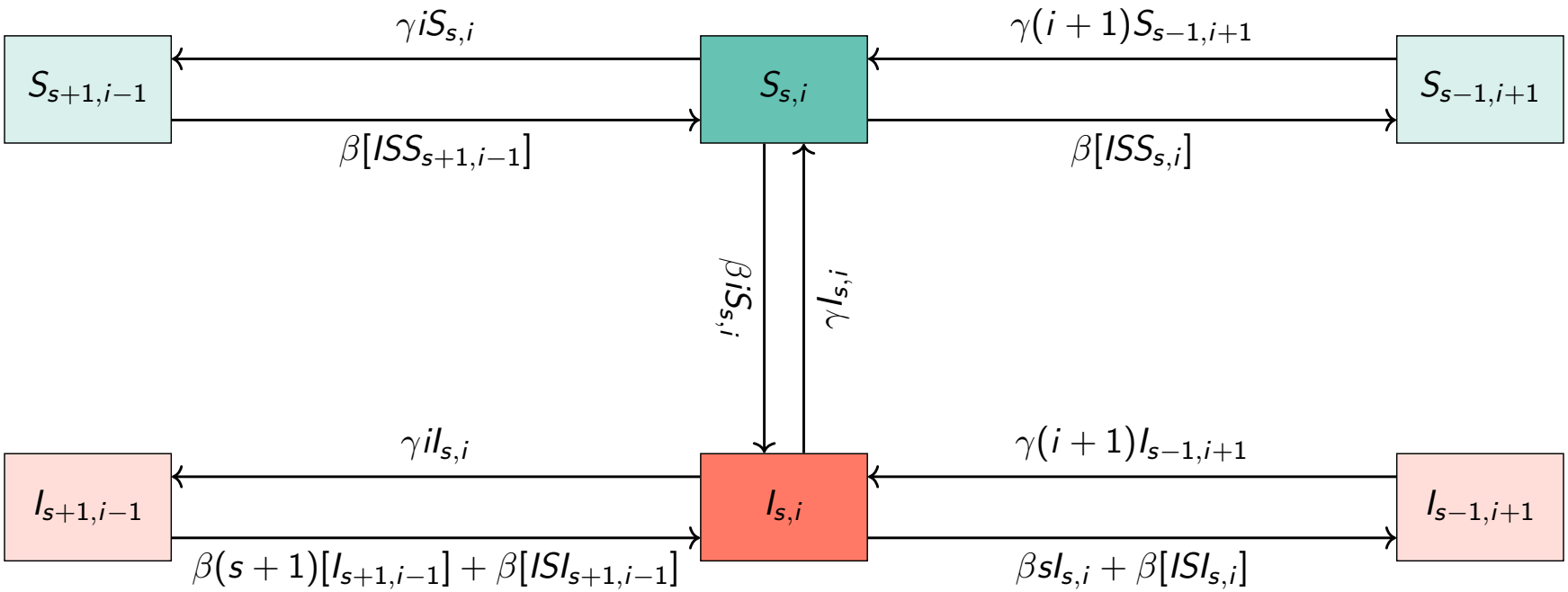
- Attempts to incorporate structures involving more than 3 nodes causes the number of equations to explode.
- Number of equations is like M^2 where M is maximum degree (but in the more simplified model it is like M)

Effective Degree Equations aka Approximate Master Equations

Developed by [6, 7, 8, 9].

- The basic idea is that we can choose a different fundamental unit to study.
- Each node is the center of a "star", and its risk of infection depends on how many infected neighbors it has.
- We use $S_{s,i}$ to denote the proportion of the population that is susceptible and has s susceptible and i infected neighbors. Similarly $I_{s,i}$.
- We can ignore recovered neighbors (hence "effective degree")

SIS model



A term like $[ISS_{s+1,i-1}]$ represents $(1/N$ times) the number of paths that exist from an infected node to a susceptible node to a susceptible node having $s+1$ susceptible partners and $i-1$ infected partners.

We make the closures

$$[ISS_{s,i}] = \frac{[ISS]}{[SS]} sS_{s,i} \qquad [ISI_{s,i}] = \frac{[ISI]}{[SI]} sI_{s,i}$$

Which correspond to assuming that the susceptible neighbors of susceptible nodes are interchangeable and the susceptible neighbors of infected nodes are interchangeable.

SIS effective degree model

We get

$$\dot{S}_{s,i} = -\tau i S_{s,i} + \gamma I_{s,i} + \gamma\big((i+1)S_{s-1,i+1} - iS_{s,i}\big) + \tau\frac{[ISS]}{[SS]}\big((s+1)S_{s+1,i-1} - sS_{s,i}\big),$$

$$\dot{I}_{s,i} = \tau i S_{s,i} - \gamma I_{s,i} + \gamma\big((i+1)I_{s-1,i+1} - iI_{s,i}\big) + \tau\left(\frac{[ISI]}{[SI]} + 1\right)\big((s+1)I_{s+1,i-1} - sI_{s,i}\big),$$

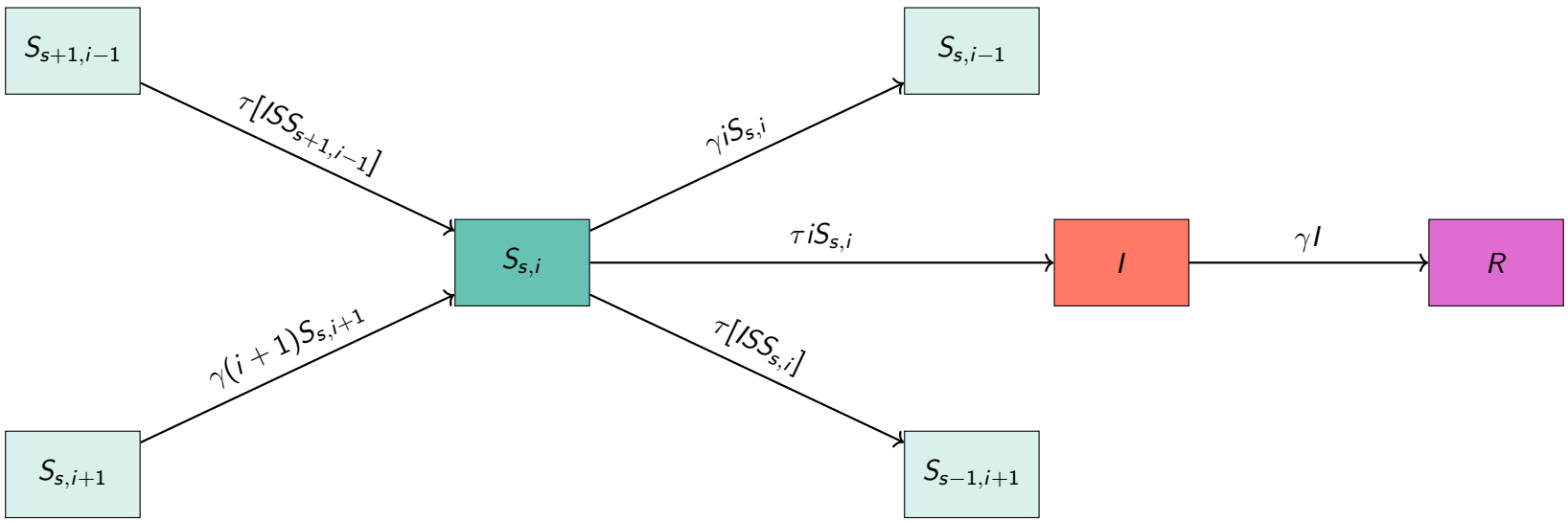
$$S = \sum_{s,i} S_{s,i}, \qquad I = \sum_{s,i} I_{s,i},$$

with

$$[SS] = \sum_{s,i} sS_{s,i}, \qquad [SI] = \sum_{s,i} iS_{s,i},$$

$$[ISS] = \sum_{s,i} isS_{s,i}, \qquad [ISI] = \sum_{s,i} i(i-1)S_{s,i}.$$

SIR effective degree model



SIR effective degree equations

$$\dot{S}_{s,i} = -\tau i S_{s,i} + \gamma((i+1)S_{s,i+1} - iS_{s,i}) + \tau \frac{[ISS]}{[SS]}[(s+1)S_{s+1,i-1} - sS_{s,i}]$$

$$\dot{R} = \gamma I,$$

$$S = \sum_{s,i} S_{s,i},$$

$$I = N - S - R,$$

Further simplifications

If we assume that the number of infected neighbors a susceptible node has is binomially distributed, we get a reduced model.
This reduced model is exact for the $N \to \infty$ limit of SIR disease in Configuration Model networks.

DIscussion

- Problems for SIS, but not as bad.
  - If a node becomes infected, we get an $I_{s,i}$ with i growing and s shrinking.
  - If it recovers with a given s_0 and i_0, it becomes S_{s_0,i_0}.
  - It doesn't capture the correlations between the neighbors of the neighbors.
- Problems for clustered networks.
- Cannot handle degree correlations.
- For SIR disease in Configuration Model network it is exact in $N \to \infty$ limit.
- Number of equations scales like M^2 where M is the maximum degree (but in the simplified model it is like M).

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