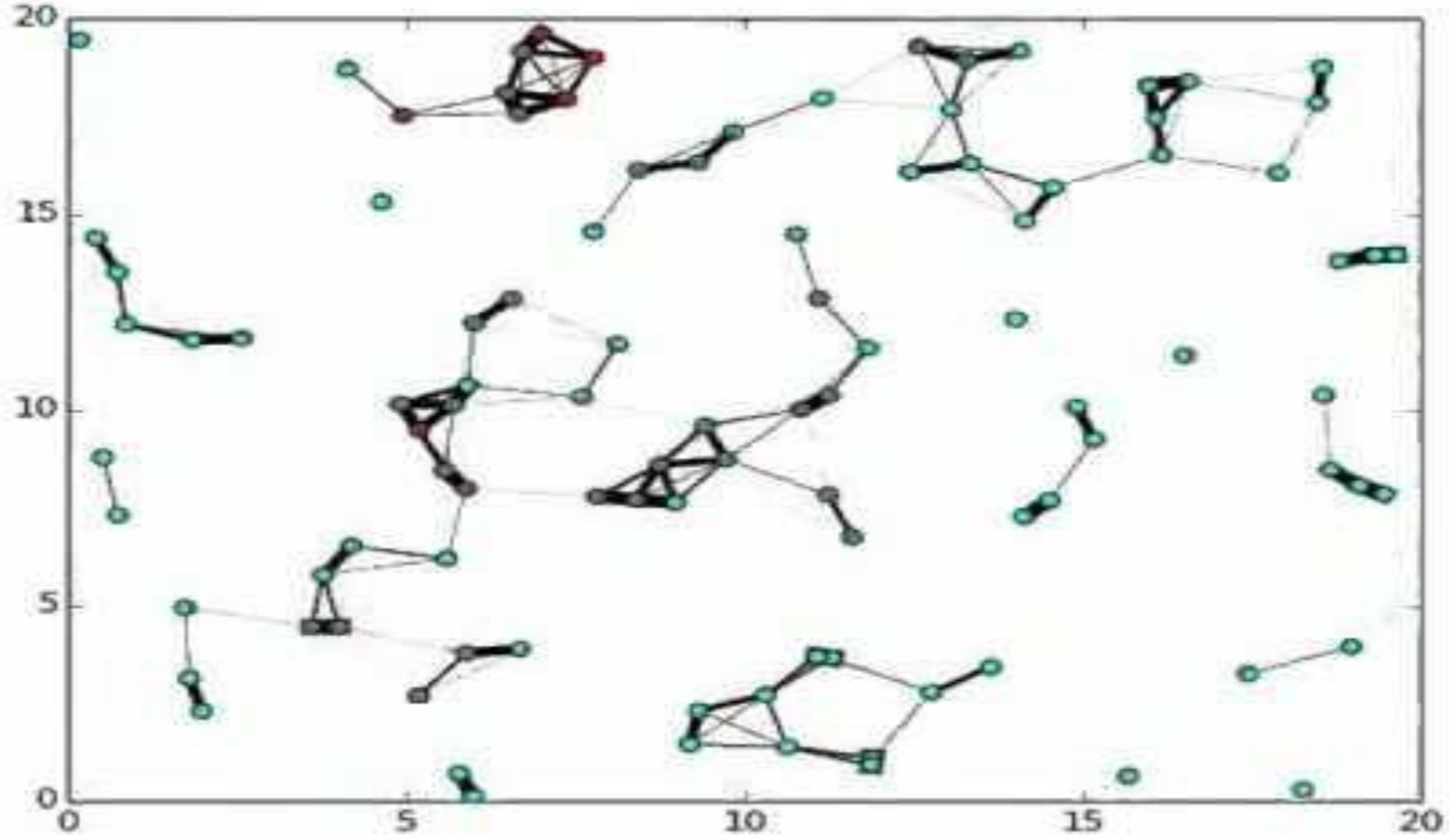
ANU Workshop on Systems and Control

ANU
Dec 7, 2017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Competitive Epidemic Spreading over Networks

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Dec 7, 2017

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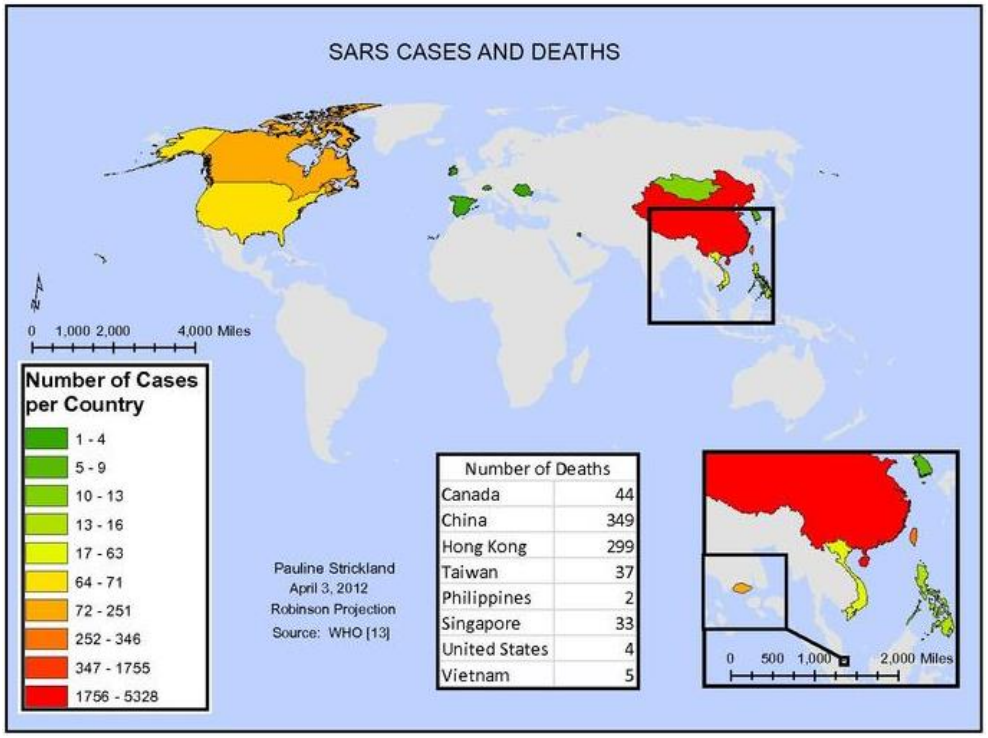
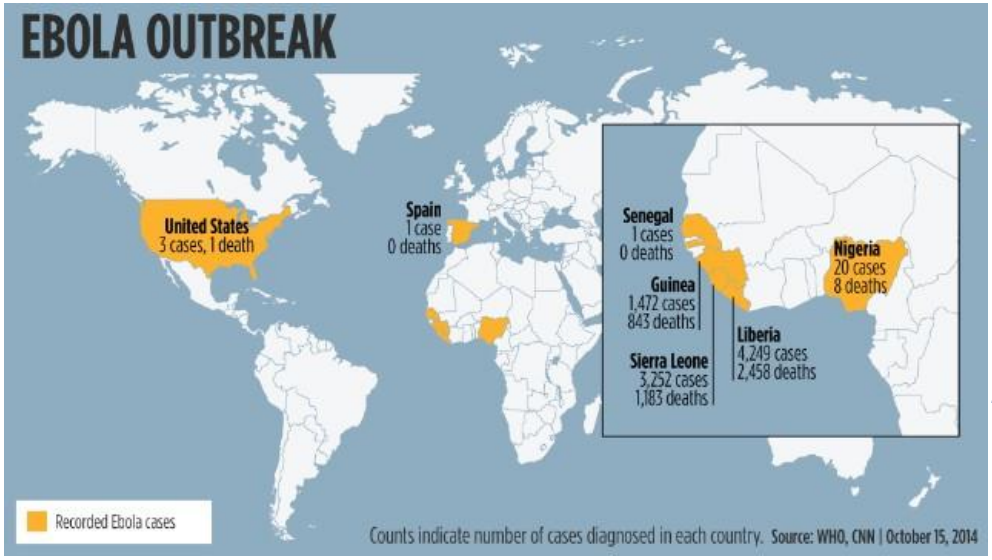




en.wikipedia.org
one.org
abcnews.go.com

- Connections between network parameters and limiting states

  Study an SIS model with more general parameters

- Control of virus spread processes

  Provide an impossibility result of a distributed feedback controller

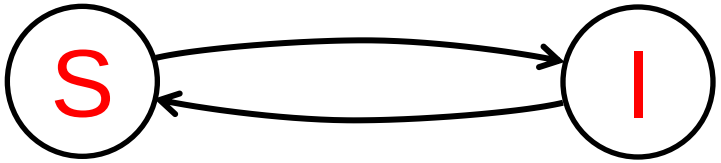
- Competition between different viruses

  Analyze a model of two competing viruses

SIS Model

Susceptible-Infectious-Susceptible

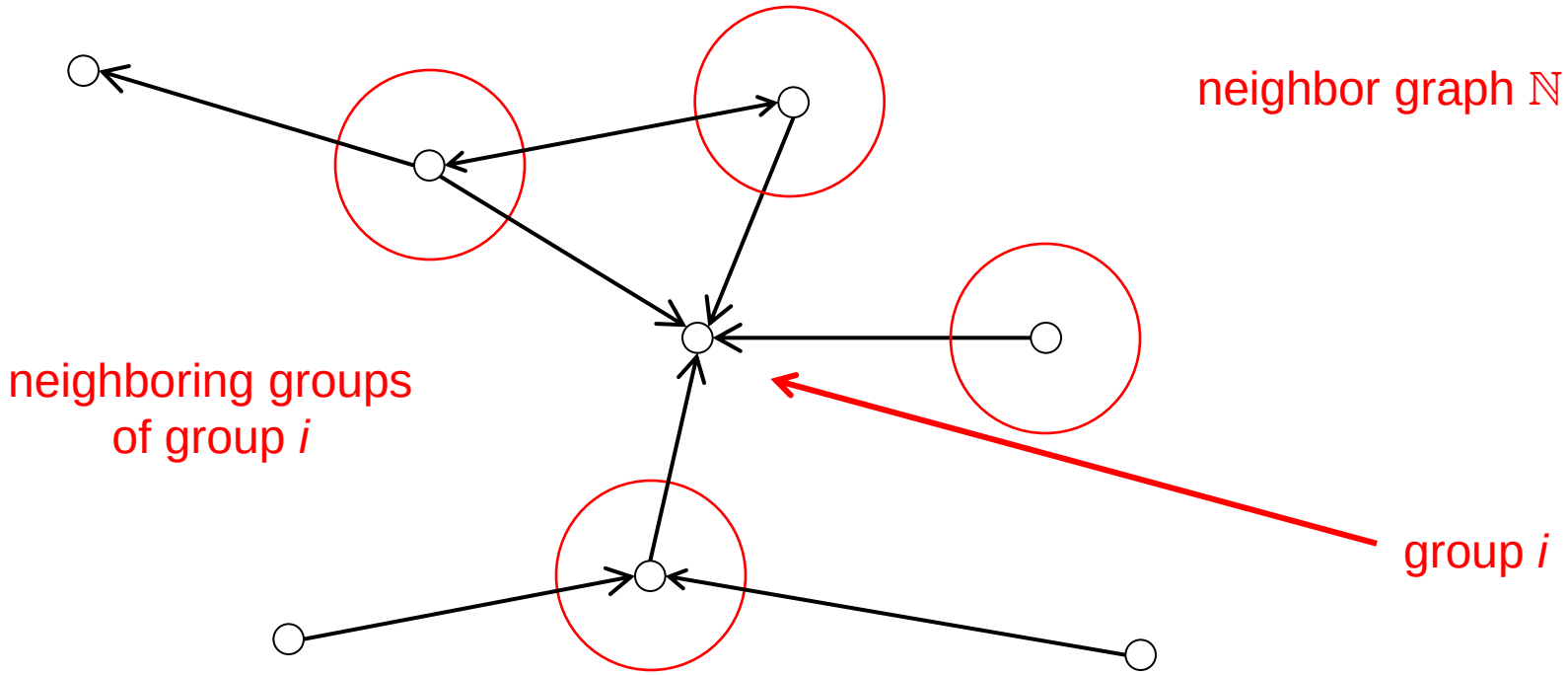
Individuals recover with no immunity to the disease (e.g. common cold).



SIS Model

A distributed continuous-time Susceptible-Infectious-Susceptible model for groups of individuals (Fall et al. 2007)

n groups of individuals labeled 1 to *n*



SIS Model

A distributed continuous-time Susceptible-Infectious-Susceptible model for groups of individuals

n groups of individuals labeled 1 to *n*

N_i = total number of individuals = $S_i(t) + I_i(t)$ birth rate = death rate

$S_i(t)$ = total number of Susceptible individuals

$I_i(t)$ = total number of Infectious individuals

$$\dot{I}_i(t) = -\gamma_i I_i(t) - \mu_i I_i(t) + \sum_{j=1}^{n} \alpha_{ij} \frac{S_i(t)}{N_i} I_j(t)$$

healing death infection (consistent with neighbor graph $\mathbb{N}$)

SIS Model

A distributed continuous-time Susceptible-Infectious-Susceptible model for groups of individuals

n groups of individuals labeled 1 to *n*

N_i = total number of individuals = $S_i(t) + I_i(t)$

$S_i(t)$ = total number of Susceptible individuals

$I_i(t)$ = total number of Infectious individuals

$$\dot{I}_i(t) = -\gamma_i I_i(t) - \mu_i I_i(t) + \sum_{j=1}^{n} \alpha_{ij} \frac{S_i(t)}{N_i} I_j(t)$$

$$= -(\gamma_i + \mu_i) I_i(t) + \frac{N_i - I_i(t)}{N_i} \sum_{j=1}^{n} \alpha_{ij} N_j \frac{I_j(t)}{N_j}$$

$$\frac{\dot{I}_i(t)}{N_i} = -(\gamma_i + \mu_i) \frac{I_i(t)}{N_i} + \frac{N_i - I_i(t)}{N_i} \sum_{j=1}^{n} \alpha_{ij} \frac{N_j}{N_i} \frac{I_j(t)}{N_j} \qquad z_i(t) = \frac{I_i(t)}{N_i}$$

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

SIS Model

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

curing rate

infection rate

[0, 1] is an invariant set for each $z_i(t)$

$[0, 1]^n$ is an invariant set for $z(t) = \begin{bmatrix} z_1(t) \\ z_2(t) \\ \vdots \\ z_n(t) \end{bmatrix}$

SIS Model

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

$$D = \mathrm{diag}(\delta_1, \delta_2, \ldots, \delta_n), \qquad B = [\beta_{ij}]$$

$$\dot{z}(t) = \Big[-D + B - \mathrm{diag}(z(t))B \Big] z(t)$$

assumptions

B is an irreducible nonnegative matrix

$\delta_i \geq 0$

neighbor graph is strongly connected

s(*M*) denotes the largest real part of eigenvalues of *M*

If *s*(-*D*+*B*) ≤ 0, the model has a unique equilibrium **0**. For any initial condition $z(0) \in [0, 1]^n$, $z(t)$ will asymptotically converge to **0**.

Healthy state is globally stable.

SIS Model

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

$$D = \mathrm{diag}(\delta_1, \delta_2, \ldots, \delta_n), \qquad B = [\beta_{ij}]$$

$$\dot{z}(t) = \Big[-D + B - \mathrm{diag}(z(t))B \Big] z(t)$$

assumptions

B is an irreducible nonnegative matrix

$\delta_i \geq 0$

neighbor graph is strongly connected

s(*M*) denotes the largest real part of eigenvalues of *M*

If *s*(-*D*+*B*) > 0, the model has two equilibria: **0** and positive z^*. For any initial condition $z(0) \in [0, 1]^n \setminus \{\mathbf{0}\}$, $z(t)$ will asymptotically converge to z^*.

A unique epidemic state is almost globally stable.

SIS Model

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

$$D = \mathrm{diag}(\delta_1, \delta_2, \ldots, \delta_n), \qquad B = [\beta_{ij}]$$

$$\dot{z}(t) = \Big[-D + B - \mathrm{diag}(z(t))B \Big] z(t)$$

assumptions

B is an irreducible nonnegative matrix

$\delta_i \geq 0$

neighbor graph is strongly connected

s(*M*) denotes the largest real part of eigenvalues of *M*

If *s*(-*D*+*B*) > 0, each entry of the unique epidemic equilibrium *z** is a strictly decreasing function of each δ_i, and a strictly increasing function of each β_{ij}.

U.S. health care spending in 2015
reached $3.2 trillion or $9,990 per person.

Control of Virus Spreading

$$\dot{z}_i(t) = -\delta_i z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

$$\dot{z}(t) = \Big[-D + B - \mathrm{diag}(z(t))B \Big] z(t)$$

If $s(-D+B) \leq 0$, the model has a unique equilibrium **0**. For any initial condition $z(0) \in [0, 1]^n$, $z(t)$ will asymptotically converge to **0**.

Regard each δ_i as a control input.

Sufficient large δ_i can lead to healthy state, but it is inefficient.

A Simple Distributed Feedback Control

$$\dot{z}_i(t) = -(k_i z_i(t)) z_i(t) + (1 - z_i(t)) \sum_{j=1}^{n} \beta_{ij} z_j(t)$$

$$\dot{z}(t) = \Big[- K\,\mathrm{diag}(z(t)) + B - \mathrm{diag}(z(t))B \Big] z(t)$$

$$= \Big[- \mathrm{diag}(z(t))K + B - \mathrm{diag}(z(t))B \Big] z(t)$$

$$= \Big[B - \mathrm{diag}(z(t))(K + B) \Big] z(t)$$

$$= \Big[\underbrace{- K + (K + B)}_{s(B) > 0} - \mathrm{diag}(z(t))(K + B) \Big] z(t)$$

The distributed feedback control can never stabilize healthy state **0**.

Healthy state **0** is a repeller.

The SIS model can be used to describe virus or worm spreading in computer networks or drone fleets.

The state of each agent then represents the probability of the agent being infected.

The discrete-time counterpart model is probably more appropriate, whose analysis is more challenging.

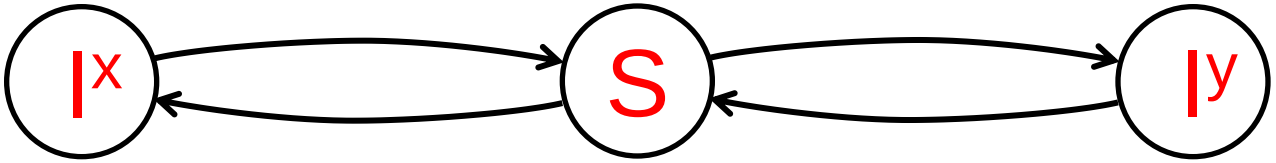
Bi-Virus Model

Two competing SIS viruses

Each individual cannot be simultaneously infected by the two viruses.
(e.g. common flu vs. avian flu)

Two competing products (e.g. Apple vs. Android)

Two competing species (e.g. lion vs. spotted hyena)



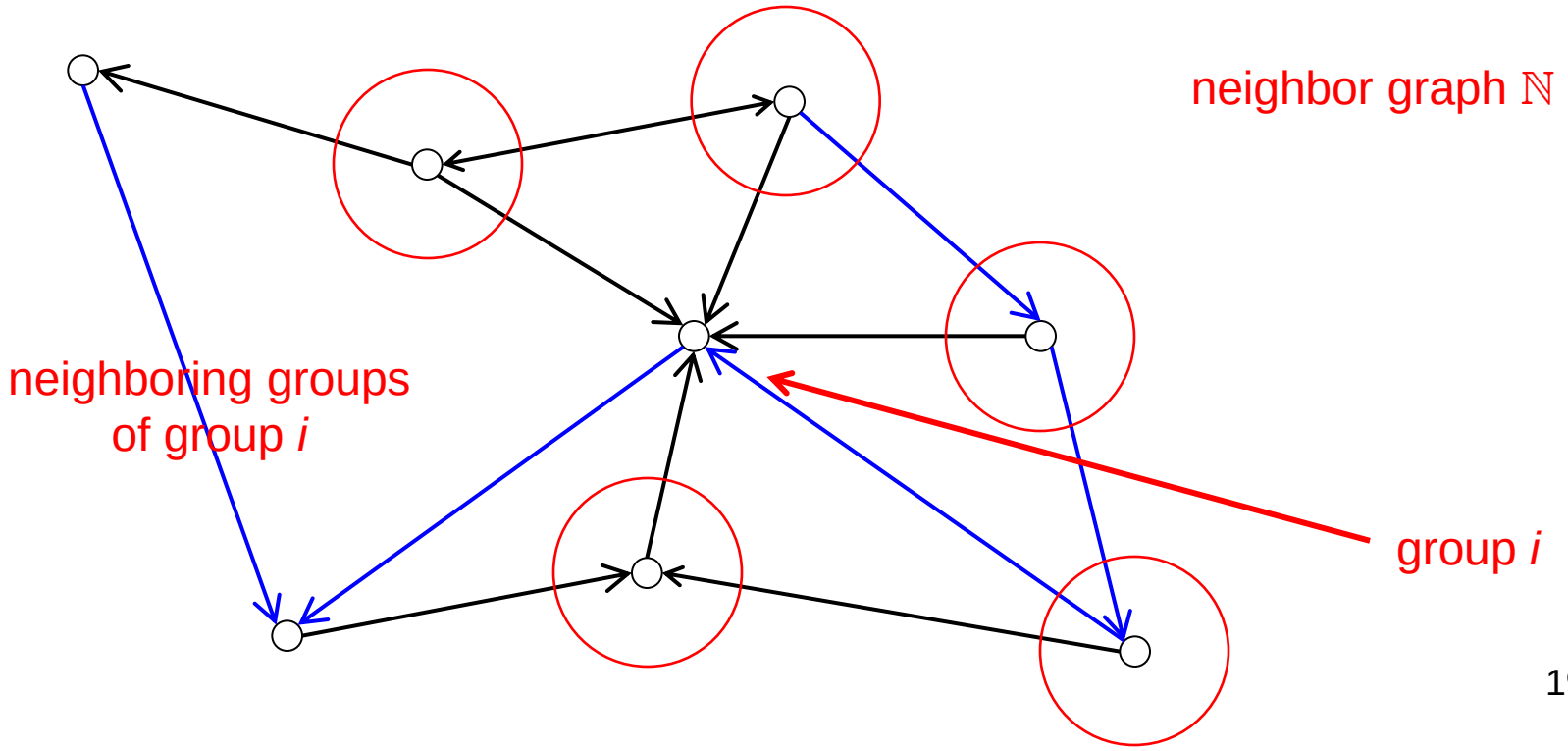
Bi-Virus Model

Two competing SIS viruses in *n* groups of individuals (Prakash et al. 2012)

Each individual cannot be simultaneously infected by the two viruses.

Two viruses spread over two directed graphs.

neighbor graph $\mathbb{N}$ = spreading graph of virus *x* + spreading graph of virus *y*



Bi-Virus Model

Two competing SIS viruses in *n* groups of individuals

Each individual cannot be simultaneously infected by the two viruses.

N_i = total number of individuals = $S_i(t) + I^x_i(t) + I^y_i(t)$

$S_i(t)$ = total number of Susceptible individuals

$I^x_i(t)$ = total number of Infectious individuals by virus *x*

$I^y_i(t)$ = total number of Infectious individuals by virus *y*

$$x_i(t) = \frac{I_i^x(t)}{N_i}$$

$$y_i(t) = \frac{I_i^y(t)}{N_i}$$

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

[0, 1] is an invariant set for each $x_i(t)$, $y_i(t)$, and $x_i(t)+y_i(t)$.

Domain

$$\mathcal{D} = \left\{ (x, y) \mid x \in R^n,\ y \in R^n,\ x_i \geq 0,\ y_i \geq 0,\ x_i + y_i \leq 1 \right\}$$

Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

$$\dot{x}(t) = \left[-D^x + B^x - \mathrm{diag}(x(t))B^x - \mathrm{diag}(y(t))B^x \right] x(t)$$

$$\dot{y}(t) = \left[-D^y + B^y - \mathrm{diag}(x(t))B^y - \mathrm{diag}(y(t))B^y \right] y(t)$$

Two viruses can have different spreading graphs.

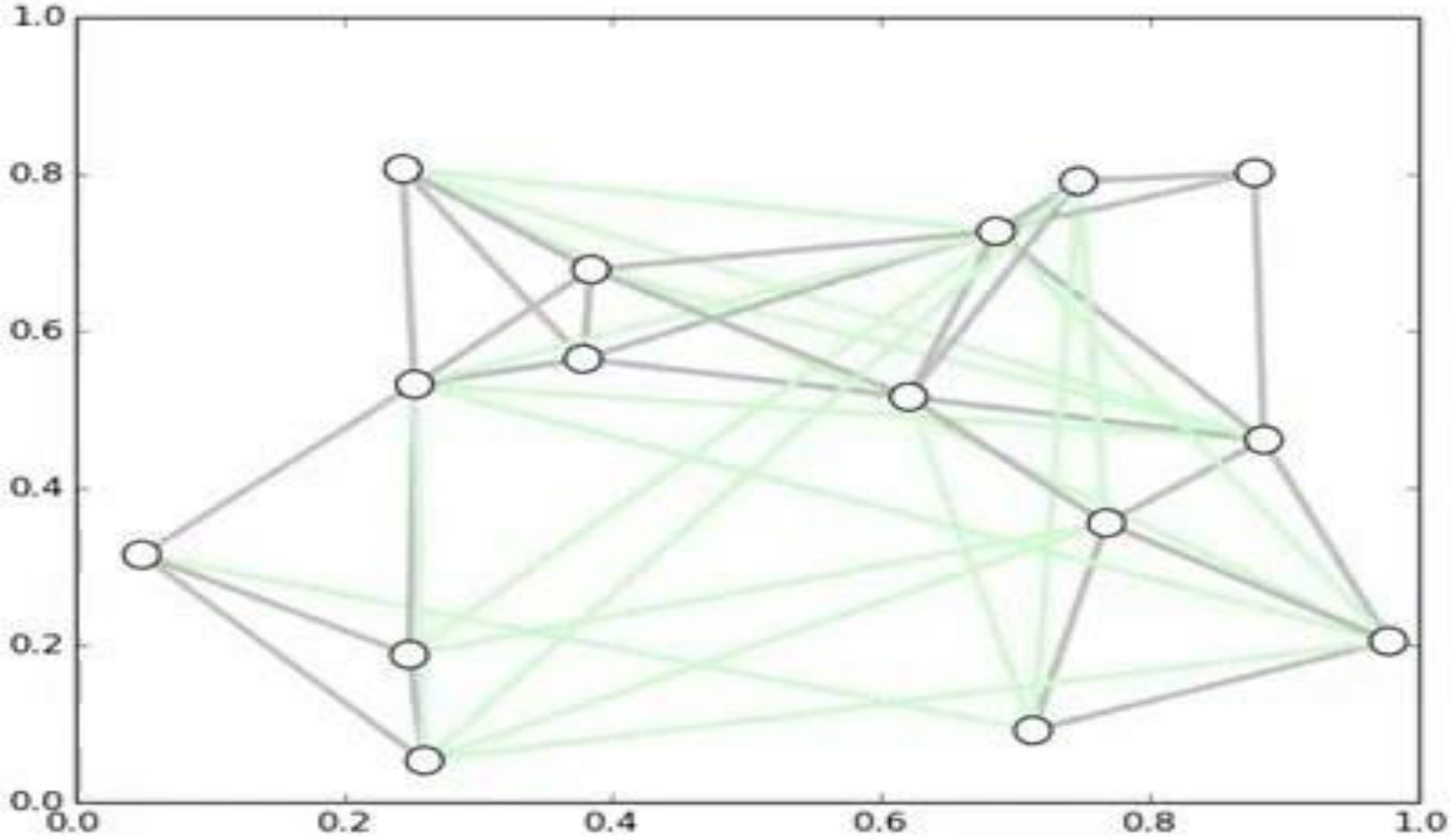
If $s(-D^x+B^x) \leq 0$ and $s(-D^y+B^y) \leq 0$, the model has a unique equilibrium (**0**, **0**). For any initial condition $(x(0), y(0)) \in \mathcal{D}$, $(x(t), y(t))$ will asymptotically converge to (**0**, **0**).

Healthy state is globally stable.

Simulation

SIZE: total infectious density $x_i(t) + y_i(t)$ in group i

COLOR = $\frac{x_i(t)}{x_i(t) + y_i(t)}$ red + $\frac{y_i(t)}{x_i(t) + y_i(t)}$ blue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Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

$$\dot{x}(t) = \Big[- D^x + B^x - \mathrm{diag}(x(t))B^x - \mathrm{diag}(y(t))B^x \Big] x(t)$$

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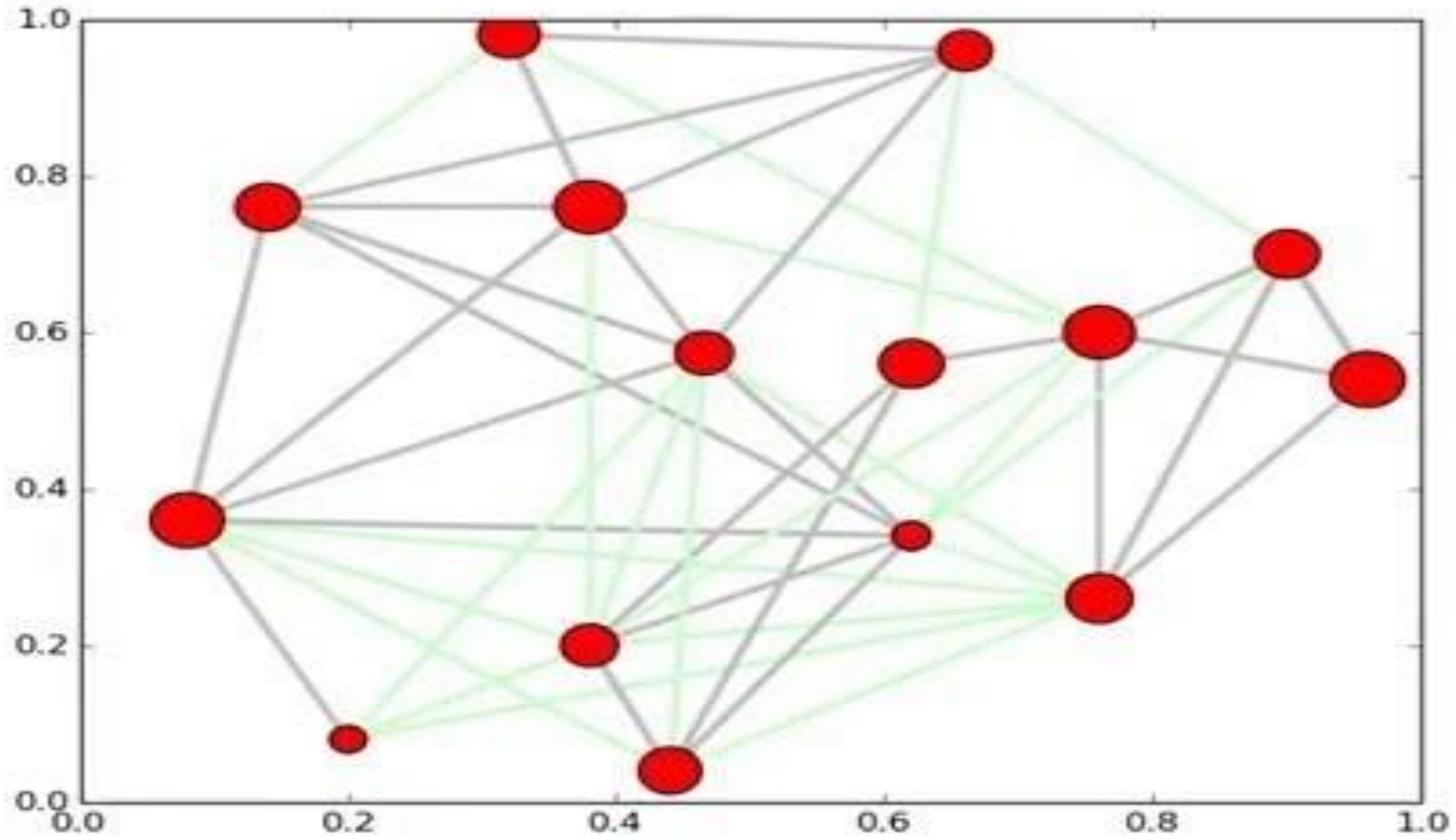
Two viruses can have different spreading graphs.

If $s(-D^x+B^x) > 0$ and $s(-D^y+B^y) \leq 0$, the model has two equilibria: (**0**, **0**) and (x^*, **0**) with positive x^*. For any initial condition $(x(0), y(0)) \in \mathcal{D}$ and $x(0) \neq \mathbf{0}$, $(x(t), y(t))$ will asymptotically converge to (x^*, **0**).

A unique epidemic state is almost globally stable.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Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

$$\dot{x}(t) = \Big[- D^x + B^x - \mathrm{diag}(x(t))B^x - \mathrm{diag}(y(t))B^x \Big] x(t)$$

$$\dot{y}(t) = \Big[- D^y + B^y - \mathrm{diag}(x(t))B^y - \mathrm{diag}(y(t))B^y \Big] y(t)$$

Two viruses can have different spreading graphs.

If $s(-D^x+B^x) > 0$ and $s(-D^y+B^y) > 0$, the model has at least three equilibria: (**0**, **0**), (x^*, **0**) and (**0**, y^*) with positive x^* and y^*.

Bi-epidemic equilibrium (x^*, y^*) may not occur.

Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

Two viruses have the same directed spreading graph.

$$\delta_i^x = \delta^x, \quad \delta_i^y = \delta^y, \quad \beta_{ij}^x = \beta^x, \quad \beta_{ij}^y = \beta^y$$

If $\delta^x / \beta^x \neq \delta^y / \beta^y$, then (x^*, y^*) with positive x^* and y^* cannot be an equilibrium of the model.

If $\delta^x / \beta^x < \delta^y / \beta^y$, then $(x^*, \mathbf{0})$ with positive x^* is exponentially stable, and $(\mathbf{0}, y^*)$ with positive y^* is unstable.

Bi-Virus Model

$$\dot{x}_i(t) = -\delta_i^x x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^x x_j(t)$$

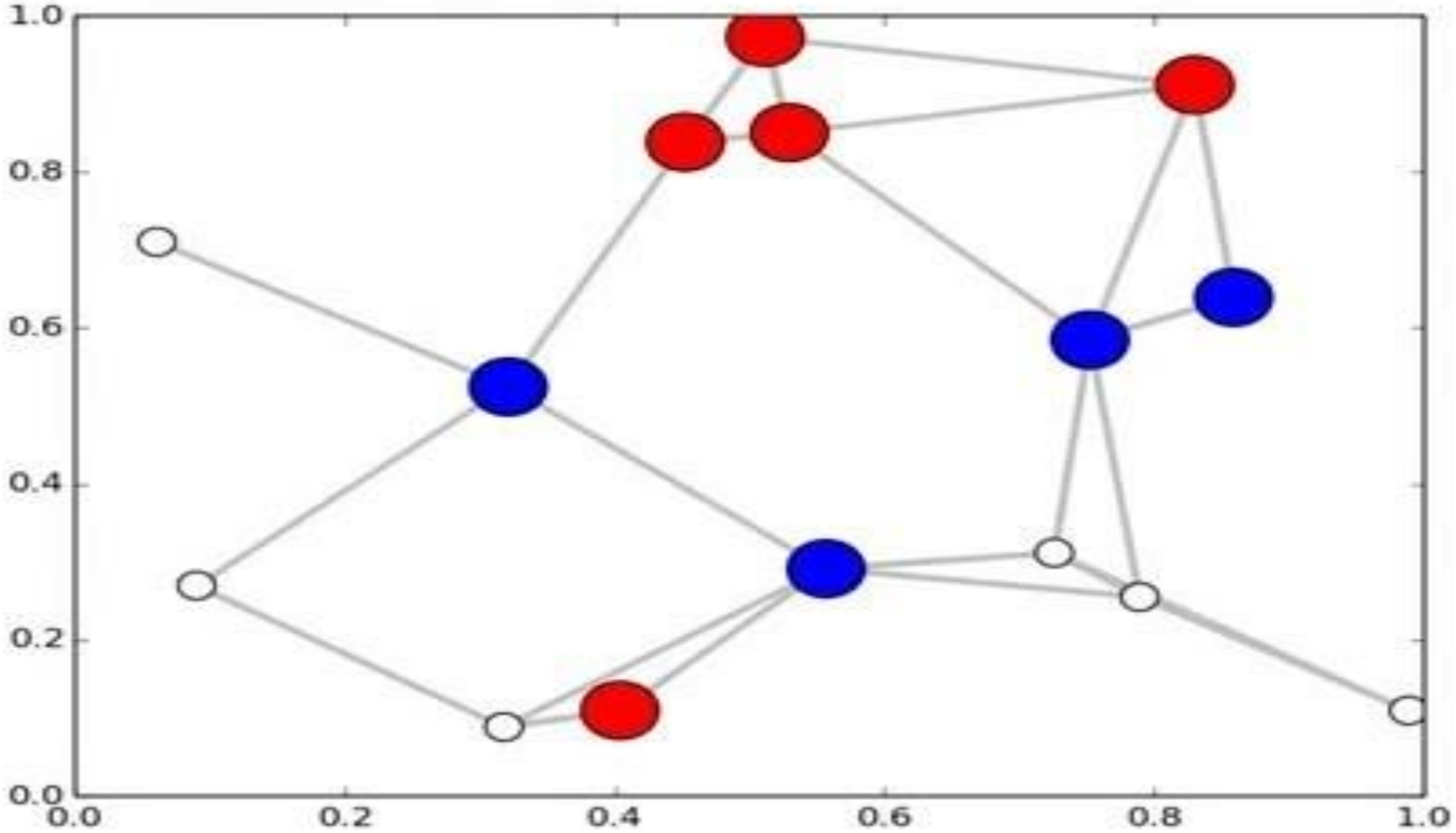
$$\dot{y}_i(t) = -\delta_i^y y_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta_{ij}^y y_j(t)$$

Two viruses have the same directed spreading graph.

$$\delta_i^x = \delta^x, \quad \delta_i^y = \delta^y, \quad \beta_{ij}^x = \beta^x, \quad \beta_{ij}^y = \beta^y$$

If $\delta^x / \beta^x = \delta^y / \beta^y$, the model may have multiple equilibria of the form (x^*, y^*) with positive x^* and y^*, and $x^* = \alpha y^*$ for any positive constant α.

Different sets of initial conditions may lead to different equilibria.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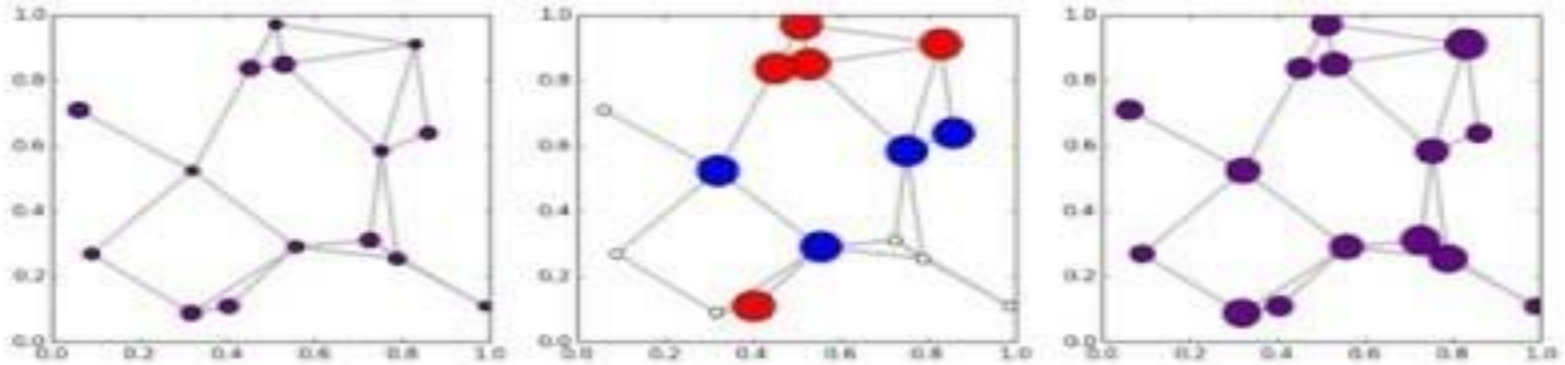
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Future Work

- Evolution of neighbor graphs
- Efficient distributed control
- Effects of human awareness and behaviors

Thank You !

Bi-Virus Model

Two competing SIS viruses in *n* groups of individuals

Each individual cannot be simultaneously infected by the two viruses.

N_i = total number of individuals = $S_i(t) + I^x_i(t) + I^y_i(t)$

$S_i(t)$ = total number of Susceptible individuals

$I^x_i(t)$ = total number of Infectious individuals by virus *x*

$I^y_i(t)$ = total number of Infectious individuals by virus *y*

$$x_i(t) = \frac{I^x_i(t)}{N_i}$$

$$y_i(t) = \frac{I^y_i(t)}{N_i}$$

$$\dot{I}^x_i(t) = -\gamma_i I^x_i(t) - \mu_i I^x_i(t) + \sum_{j=1}^{n} \alpha_{ij} \frac{S_i(t)}{N_i} I^x_j(t)$$

$$= -(\gamma_i + \mu_i) I^x_i(t) + \frac{N_i - I^x_i(t) - I^y_i(t)}{N_i} \sum_{j=1}^{n} \alpha_{ij} N_j \frac{I^x_j(t)}{N_j}$$

$$\frac{\dot{I}^x_i(t)}{N_i} = -(\gamma_i + \mu_i) \frac{I^x_i(t)}{N_i} + \frac{N_i - I^x_i(t) - I^y_i(t)}{N_i} \sum_{j=1}^{n} \alpha_{ij} \frac{N_j}{N_i} \frac{I^x_j(t)}{N_j}$$

$$\dot{x}_i(t) = -\delta^x_i x_i(t) + (1 - x_i(t) - y_i(t)) \sum_{j=1}^{n} \beta^x_{ij} x_j(t)$$