Multigroup model and Targeted Control for a Sexually Transmitted Disease

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Outline

1. Introduction
2. Multigroup Model with a Core Group
   - Assumptions
   - n Group Model
3. Type Reproduction Number
4. Two Group Model
   - Case 1: Disease persists in the Core Group
   - Case 2: Disease does not sustain in both groups
5. Illustrative Example: Gonorrhea in a Two Group Model
6. Conclusion and Future Work

Core Group

A Core group in a population can be considered as a group having

(i) a high activity (sexually or commercially)

(ii) a relatively higher contact rate than other groups

(iii) a larger traffic flow than other groups

(iv) a disease sustained but not in other groups

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A Core group is usually a root of spreading disease in a population.

A Core Group Example

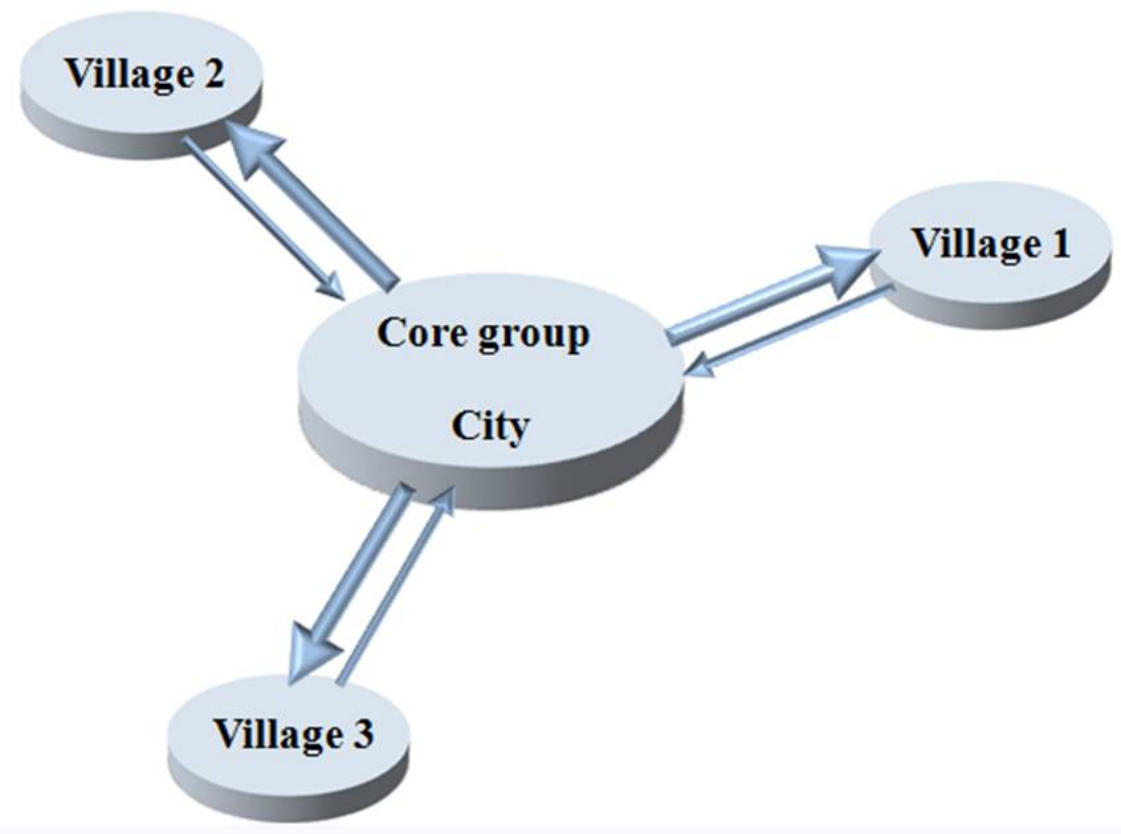

Figure: The city is a hub which connects all villages.

Once a core group is identified, a targeted disease control of such a group could be cost and effort effective.

Our Interest: A Sexully Transmitted Disease with a Core Group

For a sexually transmitted disease, we

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(ii) set or identify a core group as a source of disease spreading,

(iii) construct a control measure for the disease spreading caused either by

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- the core group
- the connection among groups

Assumptions

Consider an n group model with the assumptions:

- N_i : constant population of group i for $i = 1, \cdots, n$ where $N_i = N_i^M + N_i^F$ and N_i^M and N_i^F are the constant male and female populations of group i;
- No disease caused death;
- No immunity and no disease mortality $\Rightarrow$ SIS model
- Only heterosexual contacts can transmit disease;

Assumptions (Cont'd)

- Contact rates within groups are stronger than contract rates across groups, the latter are scaled by $\epsilon \in (0, 1)$;
- Group 1 is a core group that is highly active in spreading the disease within group 1 and to the other $n - 1$ groups;
- The proportions of the susceptible and infectious populations are considered in each group i, i.e.

$$S_i^M + I_i^M = 1 \quad \text{and} \quad S_i^F + I_i^F = 1,$$

(i) $S_i^M(S_i^F)$: proportion of the male (female) susceptible population

(ii) $I_i^M(I_i^F)$: proportion of the male (female) infectious population of group i.

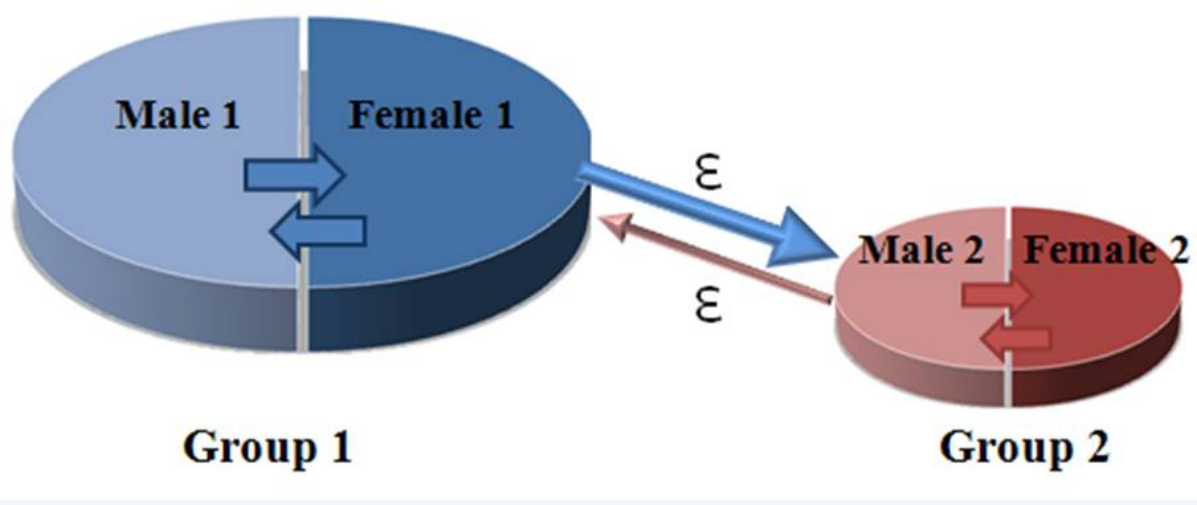

Figure: Male and Female contacts within groups and across groups with the coupling strength ϵ. Group 1 is a core group which contribute the disease spread over the whole network

n Group Model

$$
\begin{aligned}
\frac{dS_i^M}{dt} &= \mu - \mu S_i^M - S_i^M(\beta_i^F I_i^F + \textstyle\sum_{j\neq i}^n \epsilon\beta_j^F I_j^F) + \gamma_M I_i^M \\
\frac{dI_i^M}{dt} &= S_i^M(\beta_i^F I_i^F + \textstyle\sum_{j\neq i}^n \epsilon\beta_j^F I_j^F) - (\gamma_M + \mu) I_i^M \\
\frac{dS_i^F}{dt} &= \mu - \mu S_i^F - S_i^F(\beta_i^M I_i^M + \textstyle\sum_{j\neq i}^n \epsilon\beta_j^M I_j^M) + \gamma_F I_i^F \\
\frac{dI_i^F}{dt} &= S_i^F(\beta_i^M I_i^M + \textstyle\sum_{j\neq i}^n \epsilon\beta_j^M I_j^M) - (\gamma_F + \mu) I_i^F, \quad i = 1, \cdots, n,
\end{aligned}
\tag{1}
$$

- γ_M (γ_F): recovery rate of males (females)
- μ : entry (and exit) rate into the sexually active susceptible classes.

infectious Class

By using $S_i^M + I_i^M = 1$ and $S_i^F + I_i^F = 1$ for $i = 1, \cdots, n$, we consider only the infectious classes such that

$$\begin{aligned} \frac{dI_i^M}{dt} &= (1 - I_i^M)(\beta_i^F I_i^F + \sum_{j \neq i}^n \epsilon \beta_j^F I_j^F) - (\gamma_M + \mu) I_i^M \\ \frac{dI_i^F}{dt} &= (1 - I_i^F)(\beta_i^M I_i^M + \sum_{j \neq i}^n \epsilon \beta_j^M I_j^M) - (\gamma_F + \mu) I_i^F, \end{aligned} \tag{2}$$

where $\beta_1^M > \max_{j \neq 1} \beta_j^M$ and $\beta_1^F > \max_{j \neq 1} \beta_j^F$.

Then, the basic reproduction number $\mathcal{R}_o$ can be used to determine whether or no the disease dies out. However, for a large system, it is in general hard to calculate $\mathcal{R}_o$.

Core Group, a Contributor of the Disease Spread

The Core group, *group 1*

$\Rightarrow$ major contribution of the disease spread

$\Rightarrow$ should be targeted to control

$\Rightarrow$ hence, natural to consider the expected number of secondary infections of the core group arising from core group infections to determine the disease spread over the network

$\Rightarrow$ called a **type reproduction number** developed by Roberts and Heesterbeek (2003)

Type Reproduction Number

Expected number of the secondary male infection in group 1

after introducing one infectious male of group 1

to the entirely susceptible population:

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1. Number of new male infectious cases in group 1 caused by a single infectious male in the next infection generation

plus

2. Number of new infectious male cases in group 1 resulted from the infectious of other groups in all future infection generations

Type Reproduction Number (Cont'd)

- $K \in \mathbb{R}^{2n \times 2n}$: next generation matrix to determine the expected number of infectious hosts of all groups
- $e = (1, 0 \cdots, 0)^T \in \mathbb{R}^{2n} = (I_1^M, I_1^F, I_2^M, I_2^F, \cdots, I_n^M, I_n^F)^T$: one male infectious of group 1 to introduce
- $P = diag(1, 0 \cdots, 0) \in \mathbb{R}^{2n \times 2n}$; projection matrix of group 1, i.e. $I - P$ that of other $n - 1$ groups
- $I \in \mathbb{R}^{2n \times 2n}$: $2n \times 2n$ Identity matrix

Type Reproduction Number (Cont'd)

Then, the type reproduction number $\mathcal{T}_{10}$ when one infectious male of group 1 is introduced:

1. $e^T K e$

   expected number of new infectious males of group 1 in the **next infection generation**

2. $e^T K((I-P)K)^{j-1}e$

   expected number of new infectious males of group 1 cause by infectious people of the other $n-1$ groups at the **jth infection generation** ,

   where $(I-P)Ke$ represents the transmission paths not yielding a core group infection

The total expected number $\mathcal{T}_{10}$ of secondary male infections in group 1:

$$\mathcal{T}_{10} = e^T K \sum_{j=0}^{\infty} ((I-P)K)^{j-1} e = e^T K (I-(I-P)K)^{-1} e \quad (3)$$

provided that $\rho((I-P)K) < 1$

Relation with $\mathcal{R}_o$: (Roberts and Heesterbeek (2003))

$$\mathcal{T}_{10} > 1 \quad \Longleftrightarrow \quad \mathcal{R}_o > 1 \quad (4)$$

In the presence of a core group, the type reproduction number can be used to determine the status of the disease spread.

Two Group Model

We consider two group model with group 1 as a core group. From (2), the next generation matrix K is obtained as

$$K = \begin{bmatrix} 0 & \frac{\beta_1^F}{\gamma_F+\mu} & 0 & \frac{\epsilon\beta_2^F}{\gamma_F+\mu} \\ \frac{\beta_1^M}{\gamma_M+\mu} & 0 & \frac{\epsilon\beta_1^M}{\gamma_M+\mu} & 0 \\ 0 & \frac{\epsilon\beta_1^F}{\gamma_F+\mu} & 0 & \frac{\beta_2^F}{\gamma_F+\mu} \\ \frac{\epsilon\beta_1^M}{\gamma_M+\mu} & 0 & \frac{\beta_1^M}{\gamma_M+\mu} & 0 \end{bmatrix} \tag{5}$$

$$= \begin{bmatrix} 0 & a_1 & 0 & \epsilon a_2 \\ b_1 & 0 & \epsilon b_2 & 0 \\ 0 & \epsilon a_1 & 0 & a_2 \\ \epsilon b_1 & 0 & b_2 & 0 \end{bmatrix}$$

where $a_i = \dfrac{\beta_i^F}{\gamma_F+\mu}$, $b_i = \dfrac{\beta_i^M}{\gamma_M+\mu}$, $i = 1, 2$.

The type reproduction number of group 1 is

$$\mathcal{T}_{10} = \frac{b_1(a_1 + a_2\epsilon^2 - a_1 a_2 b_2(1-\epsilon^2)^2)}{1 - b_2(a_2 + \epsilon^2 a_1)} \tag{6}$$

provided that $1 - b_2(a_2 + \epsilon^2 a_1) > 0$, i.e. the disease cannot sustain in the absence of males in group 1.

Note that the basic reproduction number $\mathcal{R}_o^{(i)}$ for each group is

$$\mathcal{R}_o^{(i)} = \sqrt{a_i b_i} \quad \text{for } i = 1, 2. \tag{7}$$

Two Cases

Case 1. The disease can sustain only in the core group in isolation, but not in the non-core group.

Case 2. The disease does not sustain in either group in isolation, but it can sustain in the whole network.

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Actions required:

- For Case 1, treating or controlling the infection in the core group is the top priority
- For Case 2, although the disease cannot persist in either of the groups independently, coupling two groups enhances the level of infection over the network

$\Rightarrow$ Reducing the coupling strength may control disease spread

Case 1: Disease persists in the Core Group

Unfortunately, $\mathcal{R}_o \geq \mathcal{R}_o^{(i)} = \sqrt{a_i b_i} > 1$ for $\epsilon > 0$ and the coupling of two groups via $\epsilon \in (0, 1)$ only enhances the disease spread over the network. Thus, $\mathcal{T}_{10} > 1$.

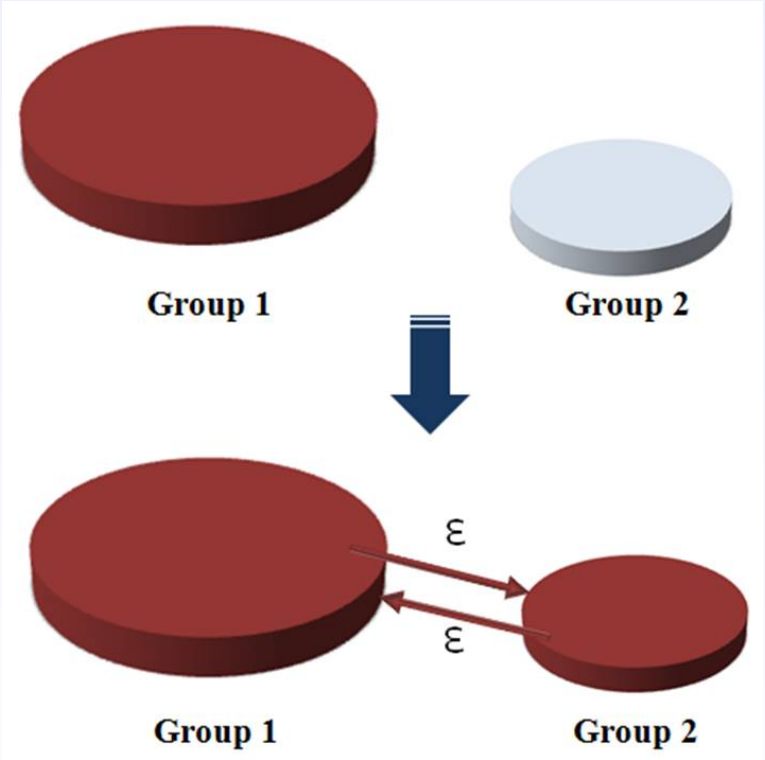

Figure: Case 1: The disease sustains in Group 1 and the coupling two groups results in the disease spread over the network.

Controlled Type Reproduction Number $\mathcal{T}_c$

In fact, $\mathcal{T}_{10} = a_1 b_1 > 1$ for $\epsilon = 0$

$\Rightarrow$ Disease invasion cannot be controlled by reducing the coupling between the two groups.

Hence, to control the spread of the disease in order to obtain $\mathcal{T}_c < 1$, either

1. the male contact rate of group 1 should be reduced by $\sigma > 0$ or
2. the infectious males of group 1 should be treated at a rate by $1/\sigma$, where

$$\sigma < \frac{1 - b_2(a_2 + \epsilon^2 a_1)}{b_1(a_1 + a_2\epsilon^2 - a_1 a_2 b_2(1-\epsilon^2)^2)}. \tag{8}$$

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1. **Reducing the male contact rate of group 1** via sex education or an increase of condome use;

2. **Treating the infectious males of group 1** at a rate greater than the rate of the disease spreading

Case 2: Disease does not sustain in both groups

(i) $\mathcal{R}_o^{(2)} < \mathcal{R}_o^{(1)} < 1$ in isolation $\Rightarrow$ group 1 acting as a core group

(ii) consider the possibility of $\mathcal{T}_{10} > 1$ when the two groups are coupled via $\epsilon \in (0, 1)$.

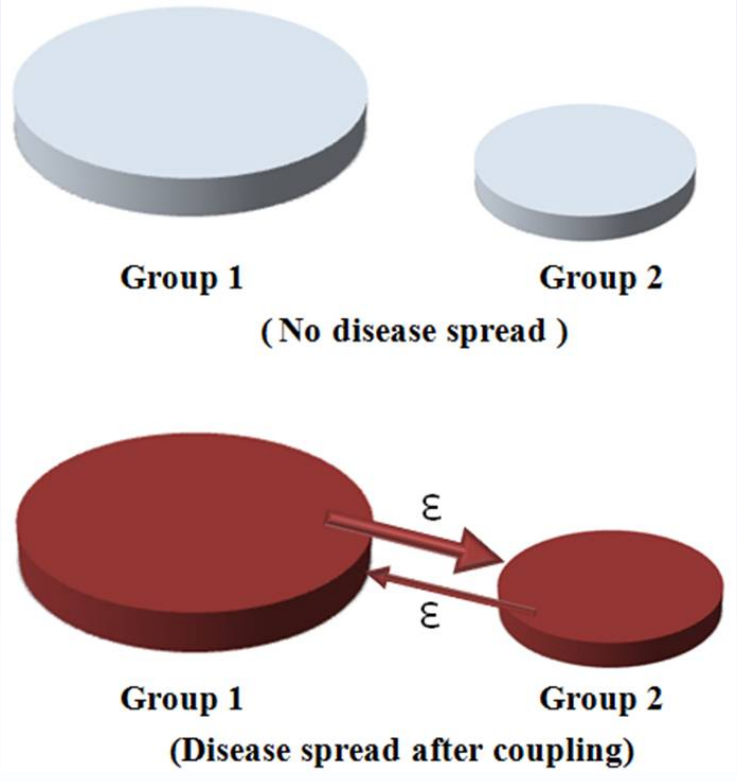

Figure: Coupling of groups causes $\mathcal{T}_{10} > 1$.

Reduction of the coupling strength

If the coupling between the two groups is reduced so that

$$\epsilon < \min\{\sqrt{\frac{B^2 - 4AC}{2A}}, \sqrt{\frac{1 - b_1 a_2}{a_1 b_2}}\} \tag{9}$$

provided that $1 - b_2 a_2 + a_1 b_2 \epsilon^2 > 0$, where $A = b_1 a_1 b_2 a_2$, $B = a_2 b_1 + 2 a_2 b_2 a_1 b_1 + a_1 b_2$, and $C = (1 - a_1 b_1)(1 - a_2 b_2)$,

then the disease dies out, i.e. $\mathcal{T}_c < 1$.

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$\Rightarrow$ showing the need of a border control when a disease can survive with sufficiently large coupling strength between groups but cannot survive in individual groups.

Case 1: Gonorrhea sustains in the core group, group 1

Group 1 is considered five times as active as the non-core group. In this case, $\mathcal{T}_{10} > 1$.

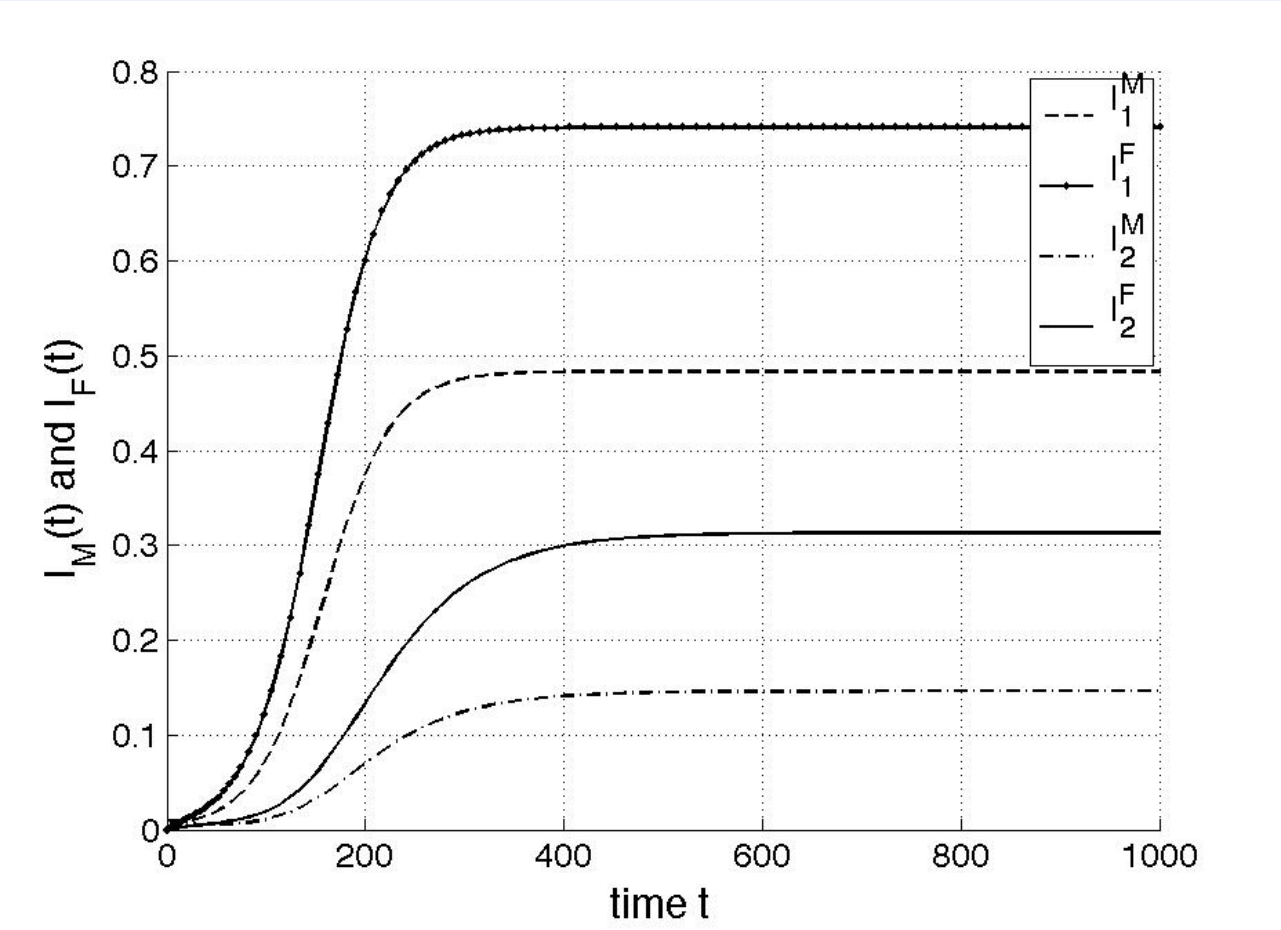
From Heghcote and Yorke (1984),

- $[d_M, d_F] = [40, 80]$: average infectious duration (days) of males and females
- $[\gamma_M, \gamma_F] = [1/40, 1/80]$; recovery rate of males and females
- contact rates:

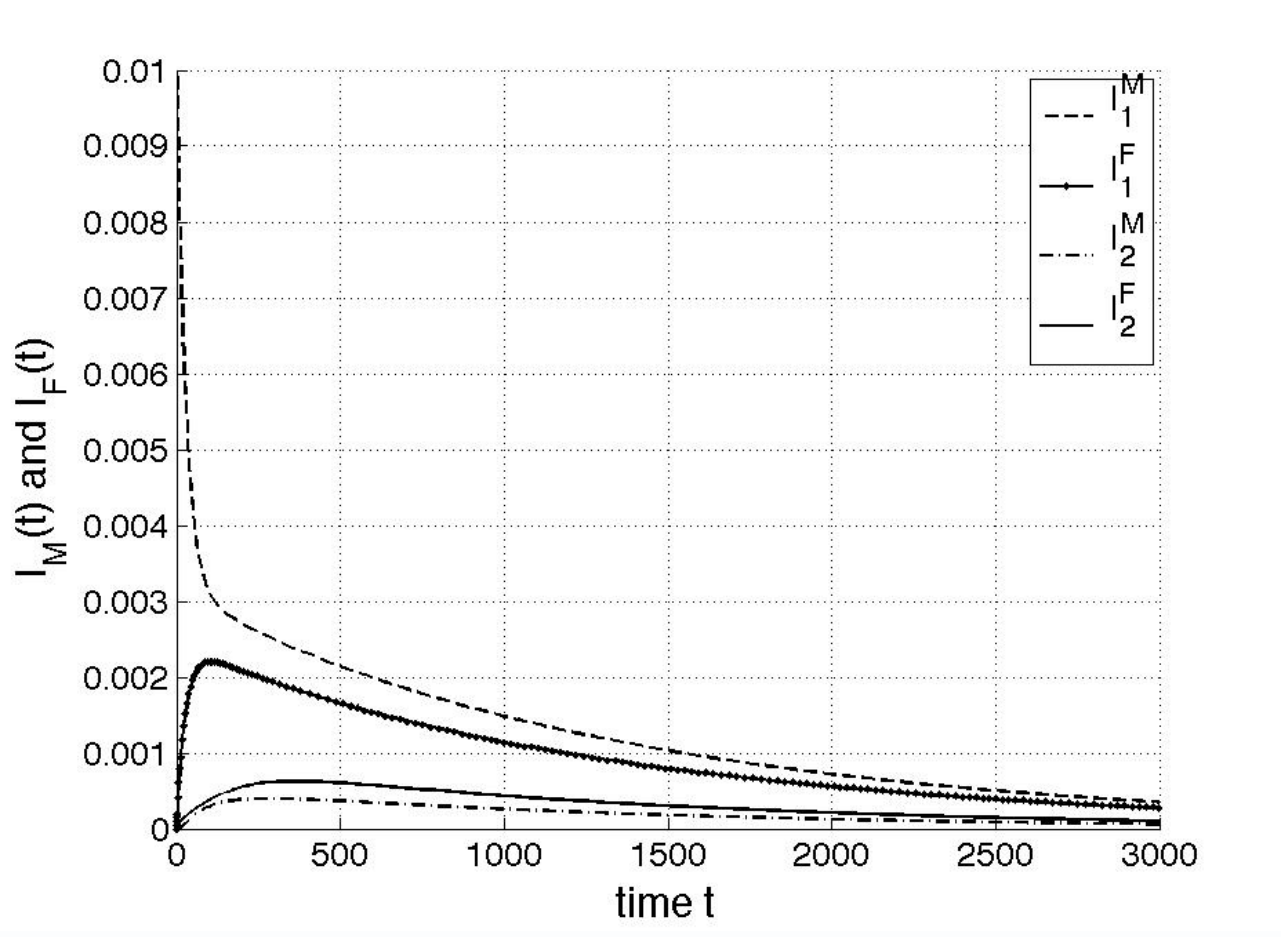
$$[\beta_1^M, \beta_1^F] = [0.0735, 0.0313] \text{ and } [\beta_2^M, \beta_2^F] = [0.0147, 0.0063] \tag{10}$$

- initial data
$[S_1^M, I_1^M, S_1^F, I_1^F, S_2^M, I_2^M, S_2^F, I_2^F] = [0.99, 0.01, 1, 0, 1, 0, 1, 0]$

For small $\epsilon = 0.1$, $\mathcal{T}_{10} = 7.61 > 1$ and gonorrhea sustains in the whole network:



By using (8), the control factor is $\sigma < 0.13$. For $\sigma = 0.12$, $\mathcal{T}_c = 0.912 < 1$ and hence gonorrhea dies out:



Effect of the control factor σ

- Increase of the male recovery rate of group 1 to $\gamma_M/\sigma = 0.1323$ from $\gamma_M = 0.0159$ by treating the infectious males of group 1;

- Reduction of the male contact rate of group 1 to $\sigma\beta_1^M = 0.0088$ from $\beta_1^M = 0.047$ via sex education, promotion of the use of condoms or temporal isolation of infectious male

Case 2: Gonorrhea does not persist in both groups

The contact rates are

$$[\beta_1^M, \beta_1^F] = [0.0176, 0.0075] \text{ and } [\beta_2^M, \beta_2^F] = [0.0147, 0.0063], \tag{11}$$

where $\mathcal{R}_o^{(1)} = 0.6571 < 1$ and $\mathcal{R}_o^{(2)} = 0.5431 < 1$.

Taking group 1 as a core group, by using (9), the necessary coupling range is

$$\epsilon \in (0, 0.6715) \tag{12}$$

So for $\epsilon = 0.67$ $\mathcal{T}_{10} = 0.99$ and

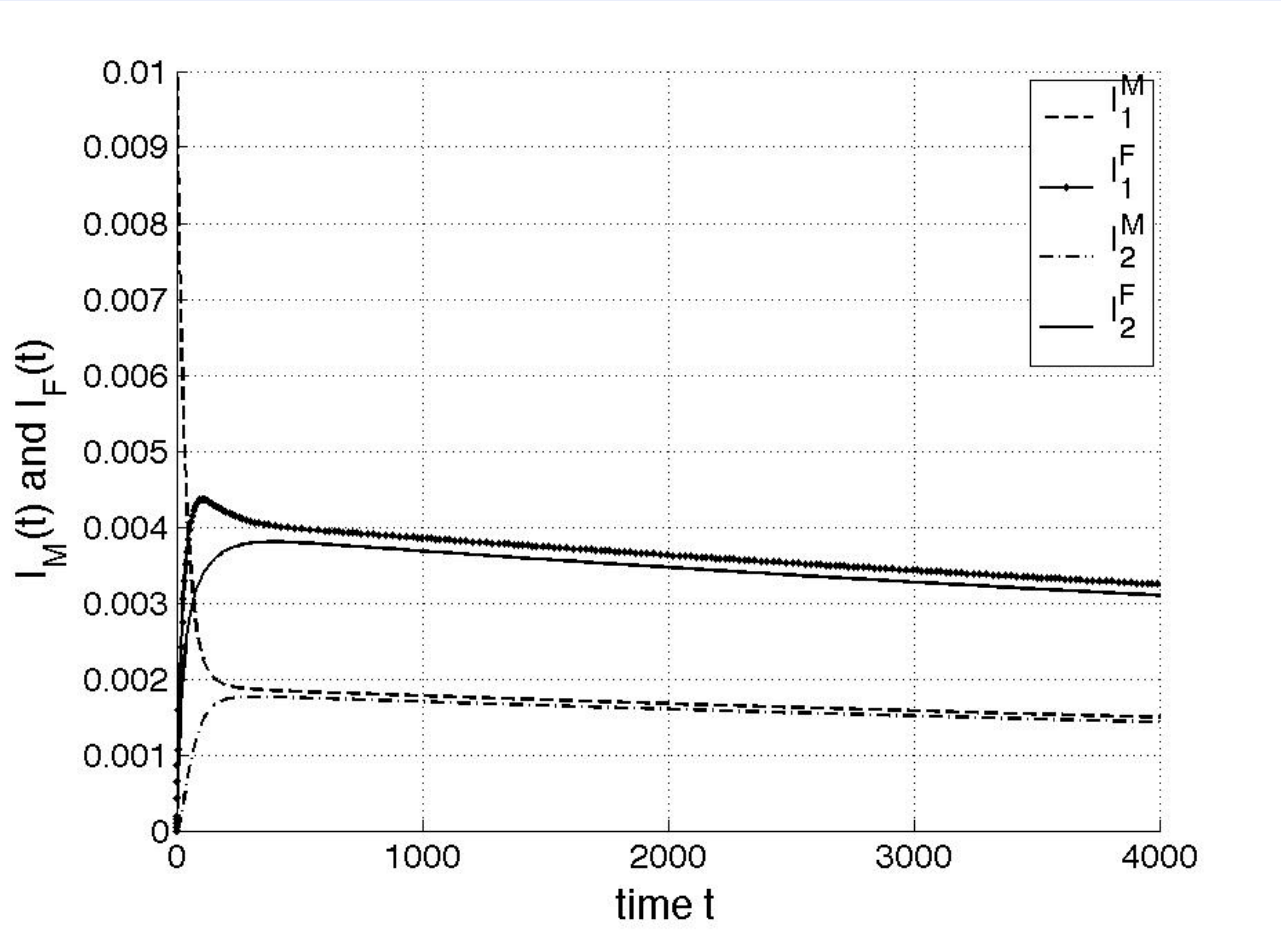


Figure: Gonorrhea dies out with the coupling strength $\epsilon = 0.67$.

However, for $\epsilon = 0.68$ $\mathcal{T}_{10} = 1.02 > 1$ and

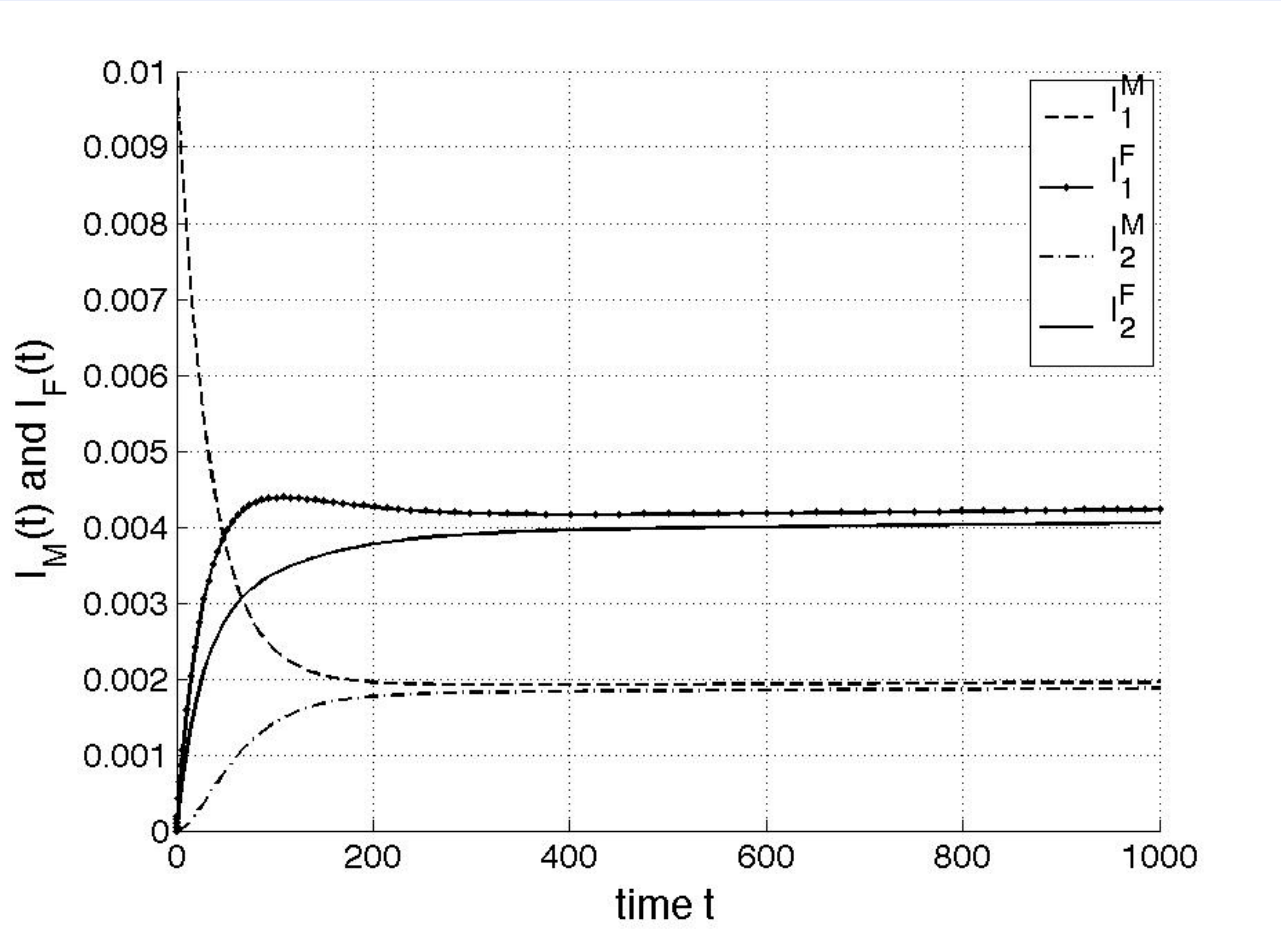


Figure: Gonorrhea persists in the network with the coupling strength $\epsilon = 0.68$.

Conclusions and Future Work

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For a multigroup model of a sexually transmitted disease in the presence of a **core group**,

Type reproduction number

- can determine the course of the disease by the number of secondary infection cases **only of the core group**
- can implement a **targeted control** on the core group or the coupling strength

Conclusions (Con't)

In the two group model,

- **Case 1**: The disease persists in the core group in isolation
  (i) Male contact rate reduction, or

  (ii) Infectious male treatment increase **in the core group**

- **Case 2**: The disease does not sustain in both groups in isolation,

  Reduction of the coupling strength between the two groups $\Rightarrow$ **border control**

Future Work

- Spatial movement in the model;
- Network structure to determine a core group
  - (i) A high traffic hub (could be $\mathcal{R}_o > 1$)
  - (ii) Time-varying coupling strength ($\epsilon(t)$)
- Social context like incomes, districts, etc.

- Thank you!
- Questions