

Modeling infectious diseases  
**Modeling infectious diseases using R:**  
**Practical Session**

**Transmission within multiple sub populations**

Prof. Dr. Ziv Shkedy,  
Hasselt University, Belgium

SUSAN-SSACAB 2019 Conference, 8 - 11 September  
2019, Cape Town, South Africa

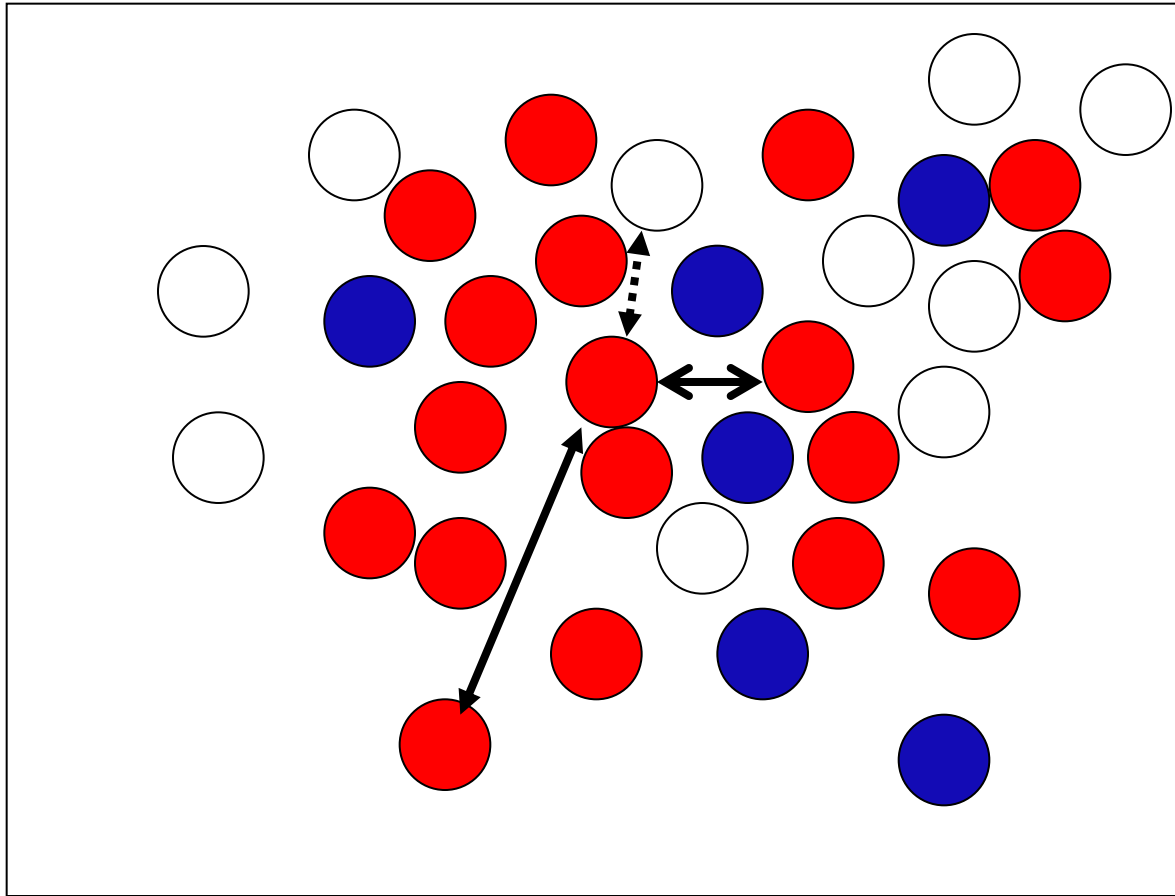
# What do we cover in this practical session ?

- More complicated transmission models in R.
- Models for multiple populations.
- Software: the deSolve package in R.

R program: ModelingIDinR3\_V1\_MultiPOP\_Sep2019.R

Transmission within sub populations

# The Mass-Action Principle and the force of infection



Contacts are made in random.

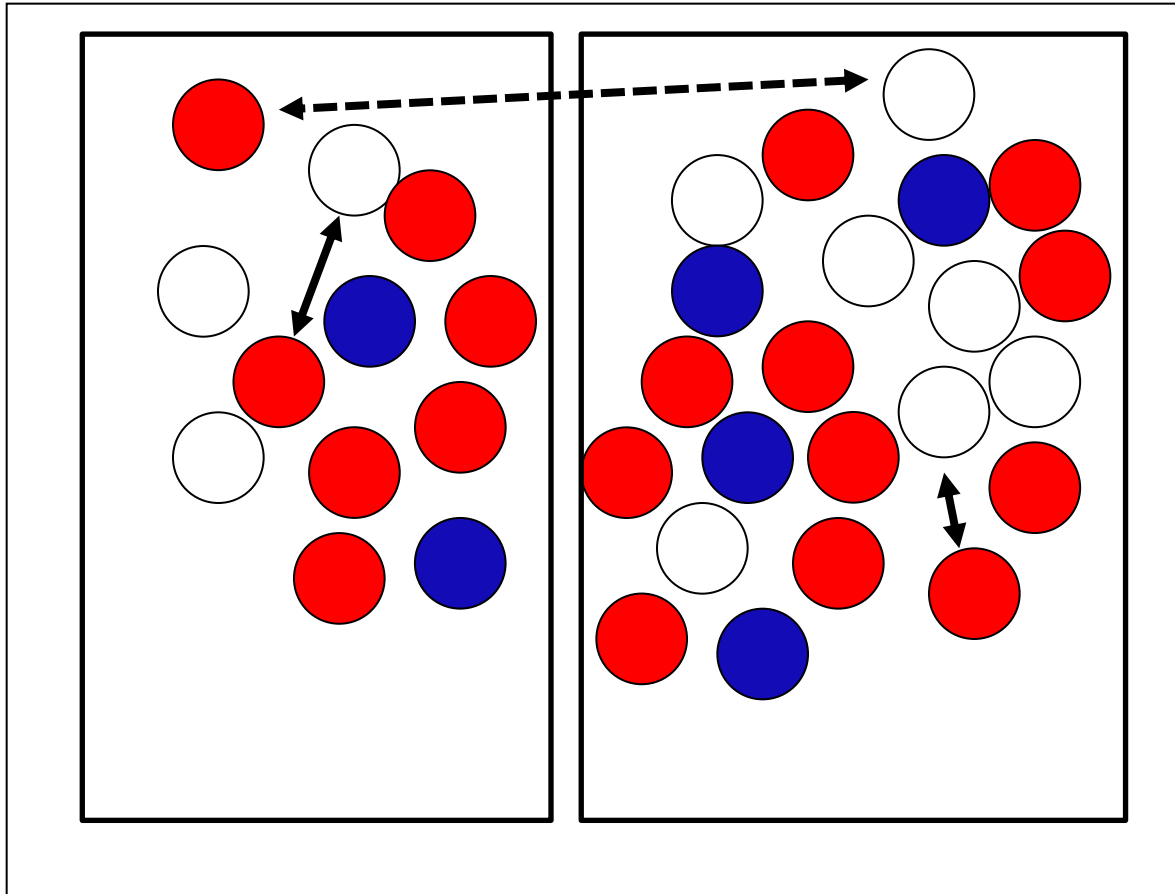
Number of new cases:

$$\beta \times I \times S$$

Transmission  
probability per  
contact

Number of new cases =  $P(\text{transmission}) \times \# \text{ of infectious} \times \# \text{ of susceptible}$

# Transmission within/between sub populations



Contacts are **NOT** made in random.

Transmission between and within the sub population

# Transmission revisited

- Until now, we assumed that transmission is **homogeneous** within the population → unique transmission coefficient  $\beta$

$$\text{Incidence rate (t)} = \beta \times I(t) \times S(t)$$

- It means that every individual has the same "chance" to be in contact with every other individual within the population
- In general, this is not very realistic!

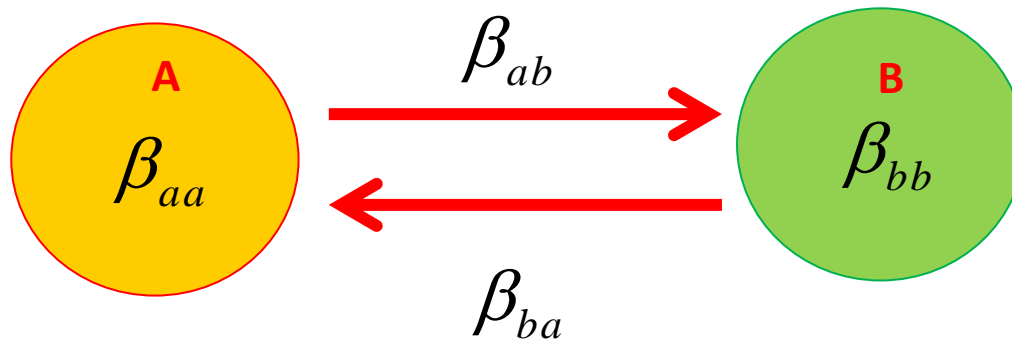
# Transmission and mixing pattern

- In general, the “mixing pattern” within the population will **NOT be homogeneous**.
- The population is structured with respect to contacts.
- Examples:
  - Childhood infections: measles, mumps, rotavirus, ...:  
greater risk between infants:  
in day care centre, school, ..
  - Sexually transmitted infections: contact only possible  
within a sexual partnership.

# Contact pattern

$$\begin{bmatrix} \beta_{aa} & \beta_{ab} \\ \beta_{ba} & \beta_{bb} \end{bmatrix}$$

Contact matrix



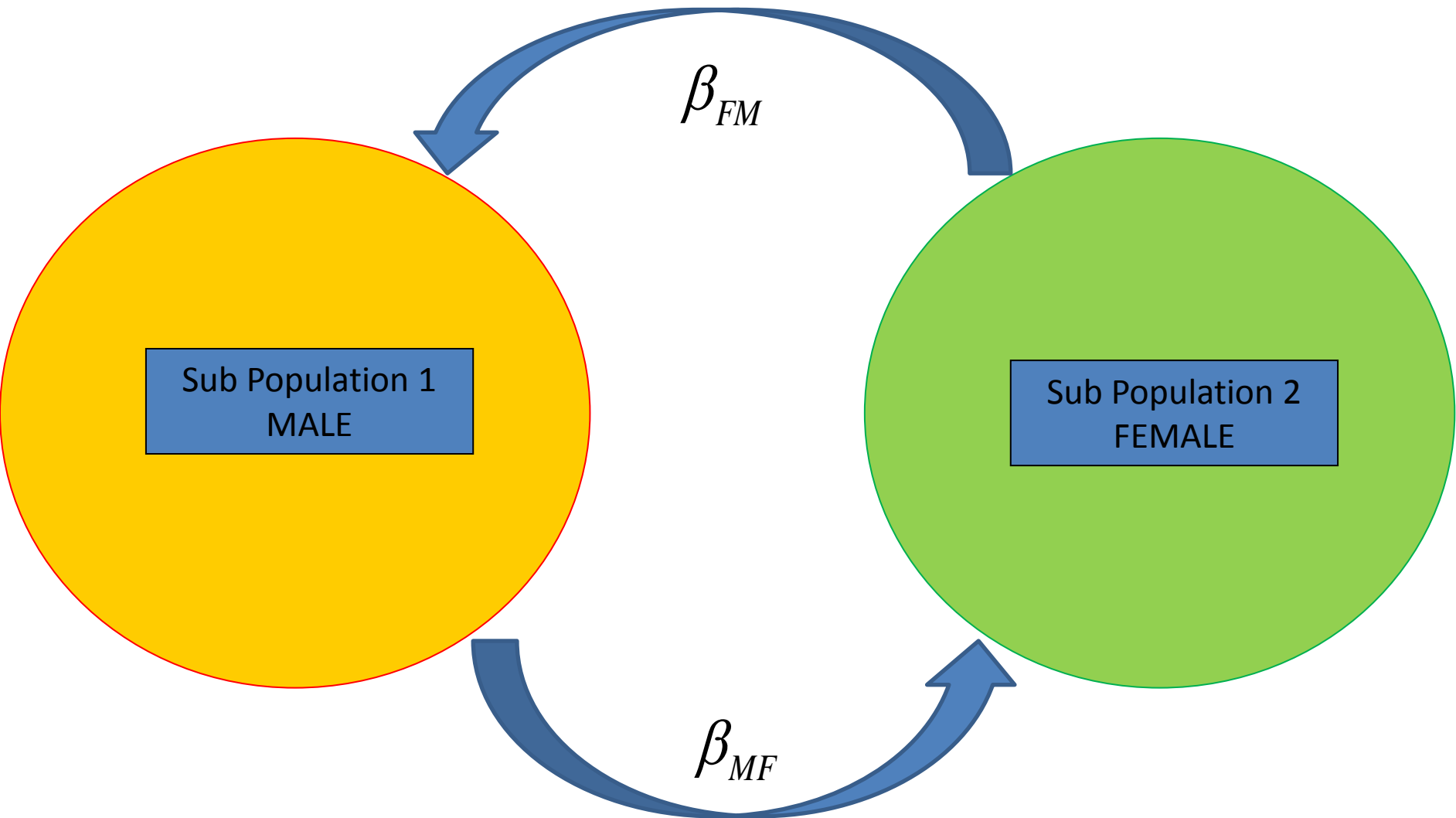
$\beta_{ab}$  contact between susceptible from sub population A and infected from subpopulation B

$\beta_{ba}$  contact between susceptible from sub population B and infected from subpopulation A

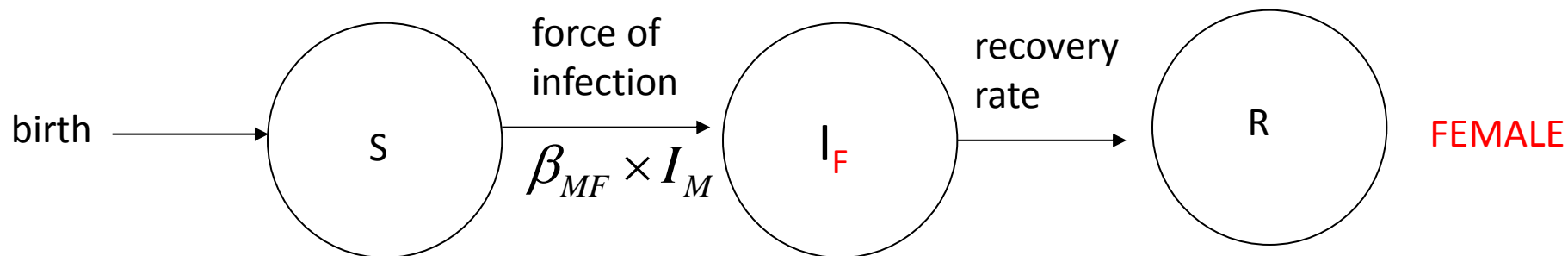
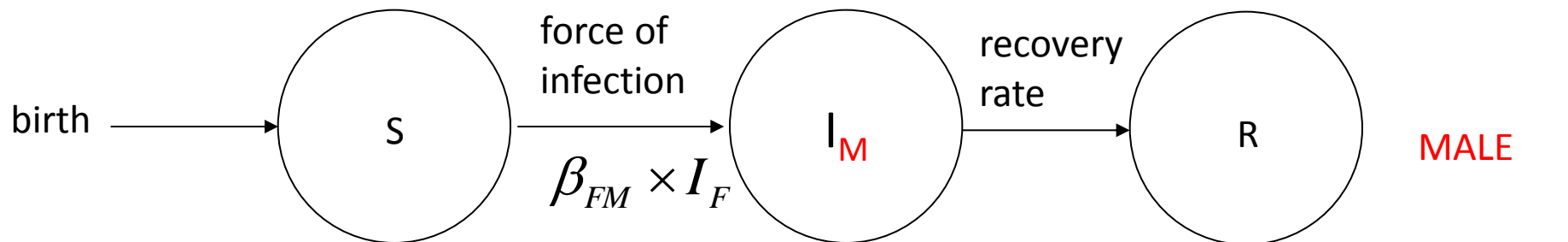


## Example 1: Gonorrhea

# Sexually transmission diseases: Gonorrhea

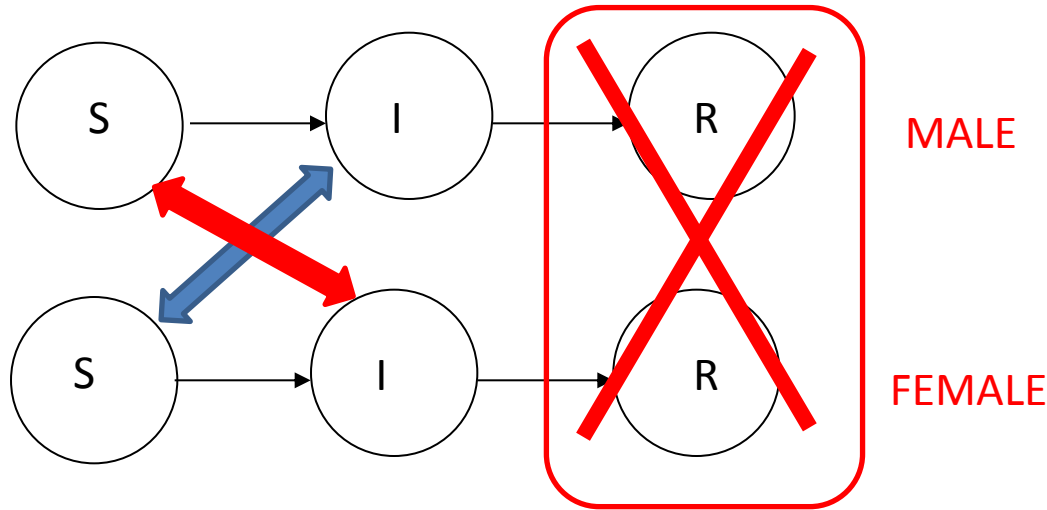


# Model structure



$$\begin{bmatrix} \beta_{FM} \\ \beta_{MF} \end{bmatrix} \text{ Contact patterns}$$

# Contact pattern: positive feedback

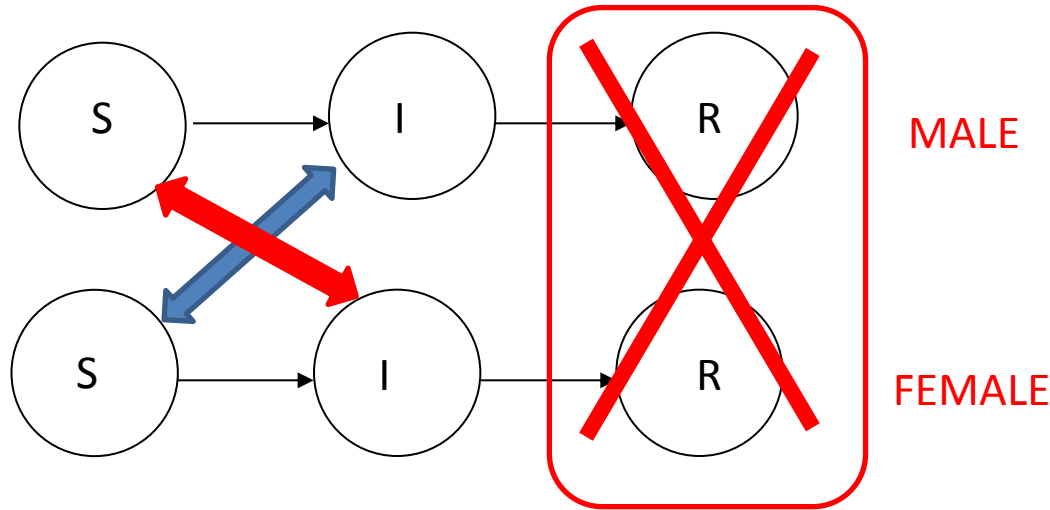


$$\begin{bmatrix} \beta_{MF} & \beta_{FM} \end{bmatrix}$$

The contact matrix represent the interaction between the population of MALE and FEMALE.

Positive feedback: one population influence the transmission of the other population

# Transmission model for gonorrhea in R



THE ODE system

$$\frac{dI_F(t)}{dt} = \beta_{MF}(N_F - I_F)I_M - \nu_1 I_F$$
$$\frac{dI_M(t)}{dt} = \beta_{MF}(N_M - I_M)I_F - \nu_2 I_M$$

# Contact matrix

```
parameters <- c(beta1=0.000003,beta2=0.000006,  
                v1=0.007,v2=0.05,N1=10000,N2=15000)
```

$$\begin{bmatrix} & \beta_{FM} \\ \beta_{MF} & \end{bmatrix} = \begin{bmatrix} & 0.000003 \\ 0.000006 & \end{bmatrix}$$

# Transmission model for gonorrhea in R

```
Gonorrhea<-function(t,state,parameters)
{
  with(as.list(c(state, parameters)),
  {
    dY1 <- beta1*(N1-Y1)*Y2-v1*Y1
    dY2 <- beta2*(N2-Y2)*Y1-v2*Y2
    list(c(dY1,dY2))
  })
}
```

$$\frac{dI_F(t)}{dt} = \beta_{MF}(N_F - I_F)I_M - \nu_1 I_F$$
$$\frac{dI_M(t)}{dt} = \beta_{MF}(N_M - I_M)I_F - \nu_2 I_M$$

# State variables

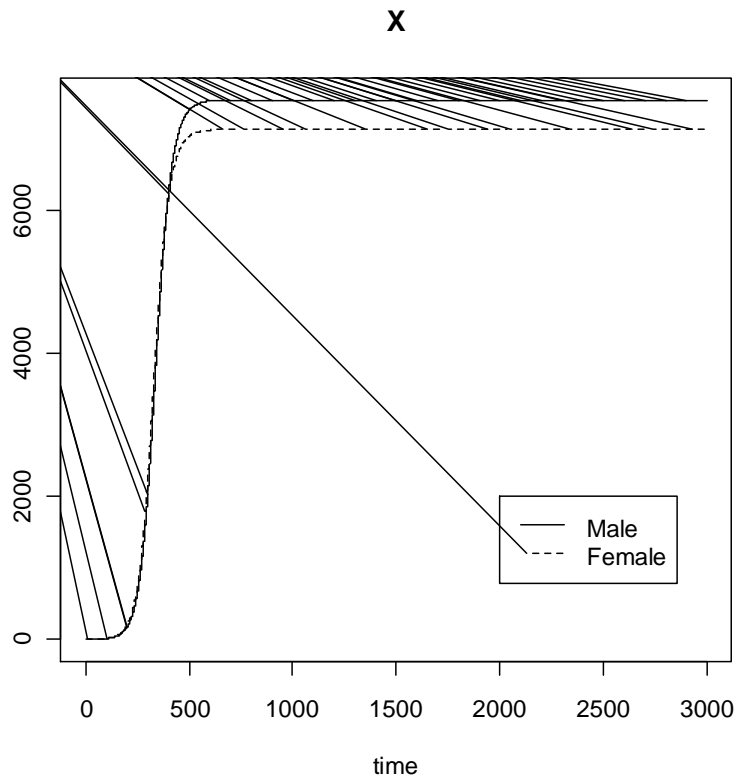
Population sizes are 10000 & 15000.

At t=one infected in population 1 and zero in population 2.

```
> state <- c(Y1=1,Y2=0)
> state
Y1 Y2
1  0
```



# Parameter setting



## Parameter setting

$$\beta_{FM} = 0.000003$$

$$\beta_{MF} = 0.000006$$

$$N_M = 10000$$

$$N_F = 15000$$

$$\nu_1 = 0.007$$

$$\nu_5 = 0.05$$

} Different recovery rate

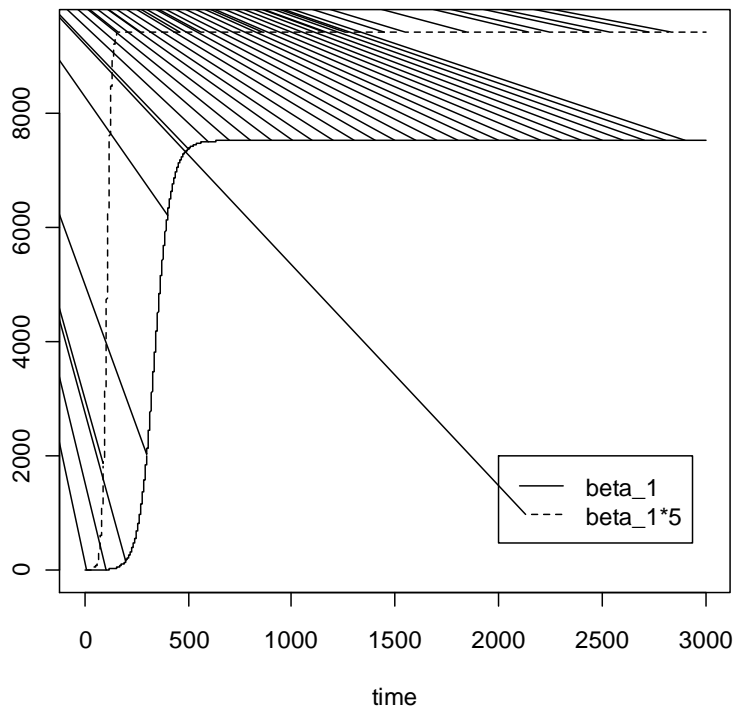
```
parameters <- c(beta1=0.000003,beta2=0.000006,  
                v1=0.007,v2=0.05,N1=10000,N2=15000)
```

# Change in the parameter setting

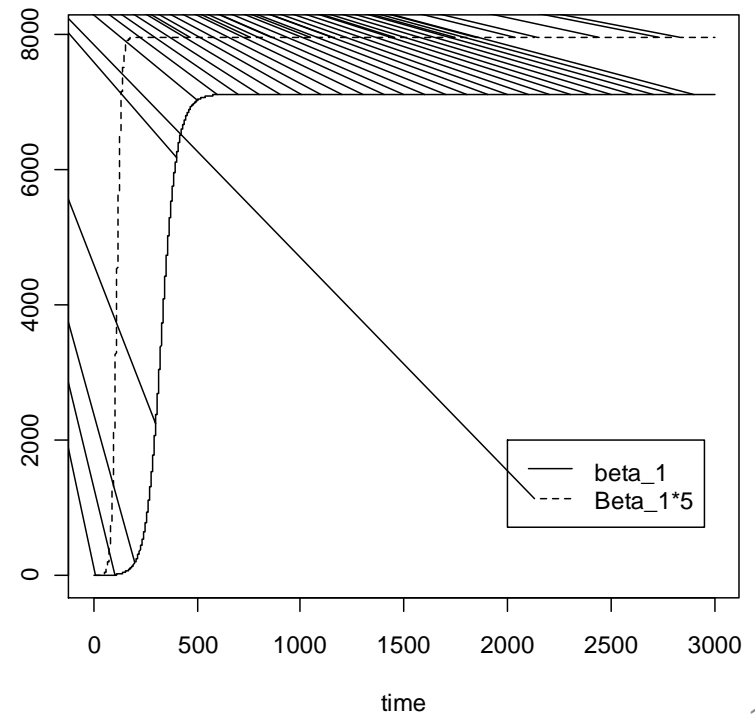
$$\beta_{FM} = \beta_{FM} \times 5$$

```
parameters <- c(beta1=0.000003*5,beta2=0.000006,  
                v1=0.007,v2=0.05,N1=10000,N2=15000)
```

Female

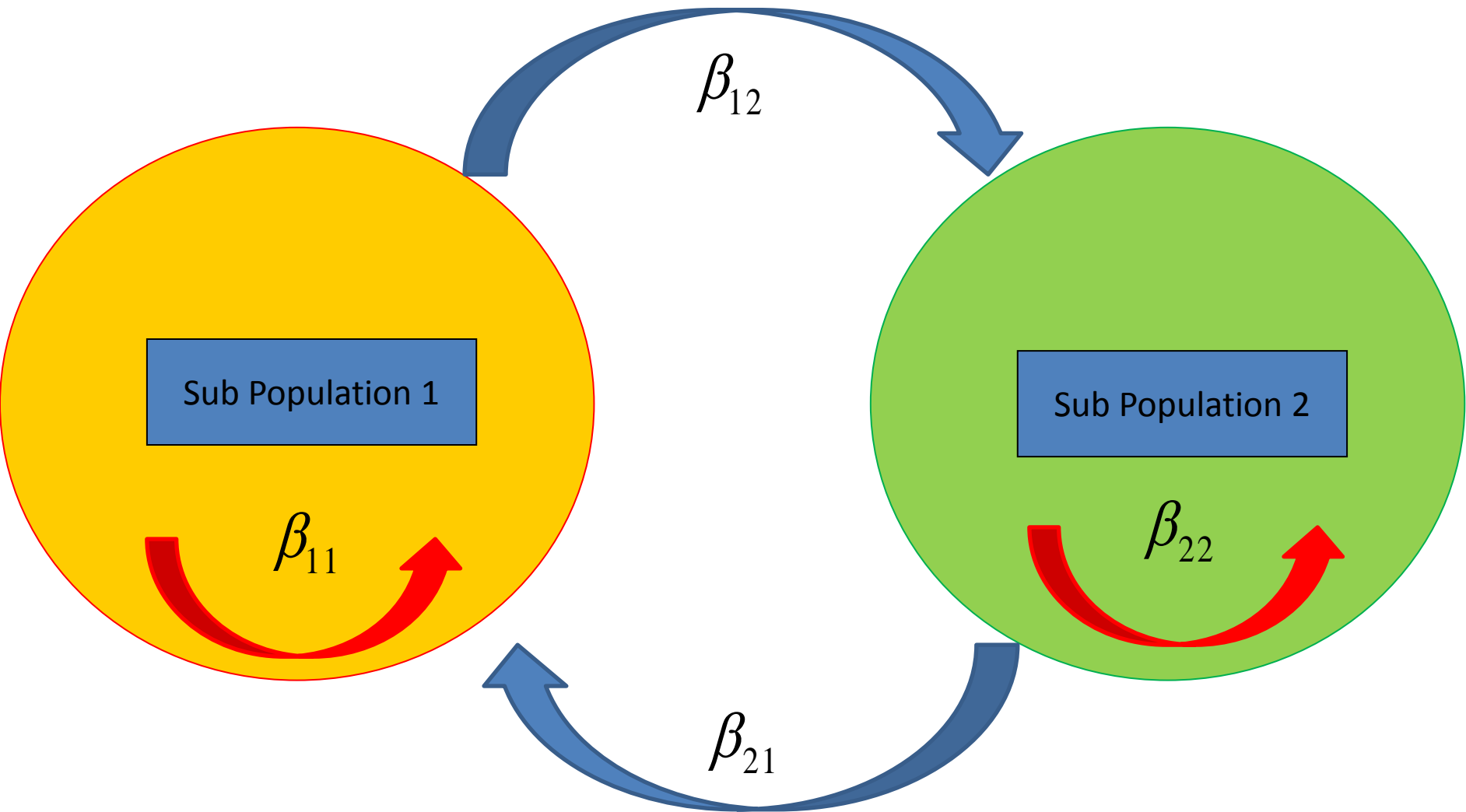


Male



## Example 2: two interacting populations

# Two interacting sub population



# Contact pattern

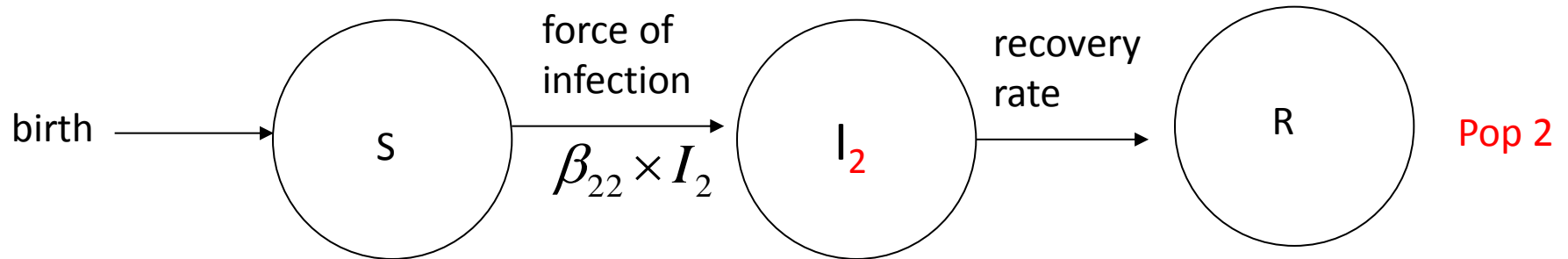
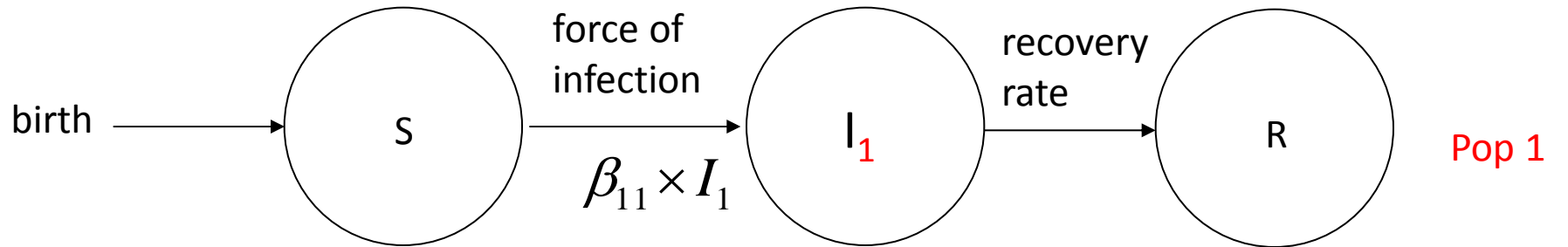
$$\begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{12} & \beta_{22} \end{bmatrix}$$

The contact matrix represent the interaction between the two sub populations.

Within population and within and between transmission.

```
parameters <-  
c(beta11=0.00,beta12=0.075,beta21=0.075,beta22=0.05,  
  v1=1/13,v2=1/30,mu=0.001)
```

# Model structure 1

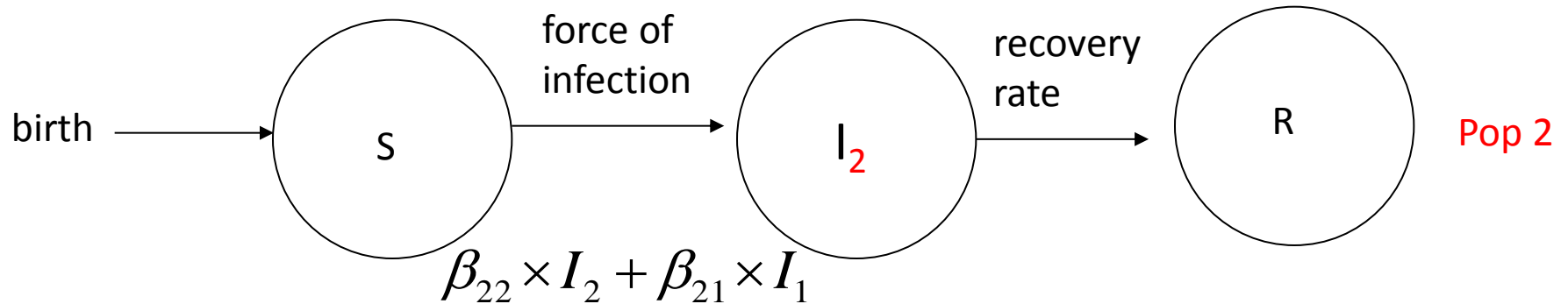
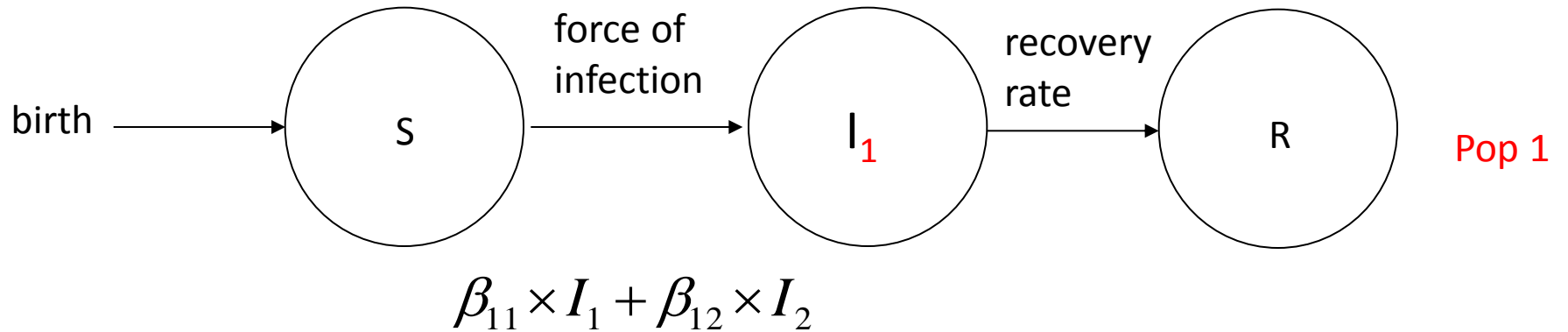


$$\begin{bmatrix} \beta_{11} & 0 \\ 0 & \beta_{22} \end{bmatrix}$$

Contact patterns: only within group transmission

```
parameters <-  
c(beta11=0.05,beta12=0.000,beta21=0.000,beta22=0.05,  
  v1=1/13,v2=1/30,mu=0.001)
```

# Model structure 2



$$\begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \end{bmatrix}$$

Contact patterns: within/between transmission

```
parameters <-  
c(beta11=0.00,beta12=0.075,beta21=0.075,beta22=0.05,  
  v1=1/13,v2=1/30,mu=0.001)
```

# Model Structure

$$\begin{aligned}\frac{dS_1(t)}{dt} &= \mu - (\beta_{11}I_1 + \beta_{12}I_2)S_1 - \mu S_1 \\ \frac{dI_1(t)}{dt} &= (\beta_{11}I_1 + \beta_{12}I_2)S_1 - \nu_1 I_1 - \mu I_1 \\ \frac{dR_1(t)}{dt} &= \nu_1 I_1 - \mu R_1 \\ \frac{dS_2(t)}{dt} &= \mu - (\beta_{21}I_1 + \beta_{22}I_2)S_2 - \mu S_2 \\ \frac{dI_2(t)}{dt} &= (\beta_{21}I_1 + \beta_{22}I_2)S_2 - \nu_2 I_2 - \mu I_2 \\ \frac{dR_2(t)}{dt} &= \nu_2 I_2 - \mu R_2\end{aligned}$$

## Structure in R

```
SIRtwo<-function(t,state,parameters)
{
  with(as.list(c(state, parameters)),
  {
    dY1 <- - (beta11*Y2+beta12*Y5)*Y1+mu-mu*Y1
    dY2 <- (beta11*Y2+beta12*Y5)*Y1-v1*Y2-mu*Y2
    dY3 <- v1*Y2 - mu*Y3
    dY4 <- - (beta21*Y2+beta22*Y5)*Y4+mu-mu*Y4
    dY5 <- (beta21*Y2+beta22*Y5)*Y4-v2*Y5-mu*Y5
    dY6 <- v2*Y5-mu*Y6
    list(c(dY1,dY2,dY3,dY4,dY5,dY6))
  })
}
```



# State variables

We run the model in a “proportion” setting (population size=1).

At  $t = 0$ , 80% are susceptible and 20% are infected (at each sub population)

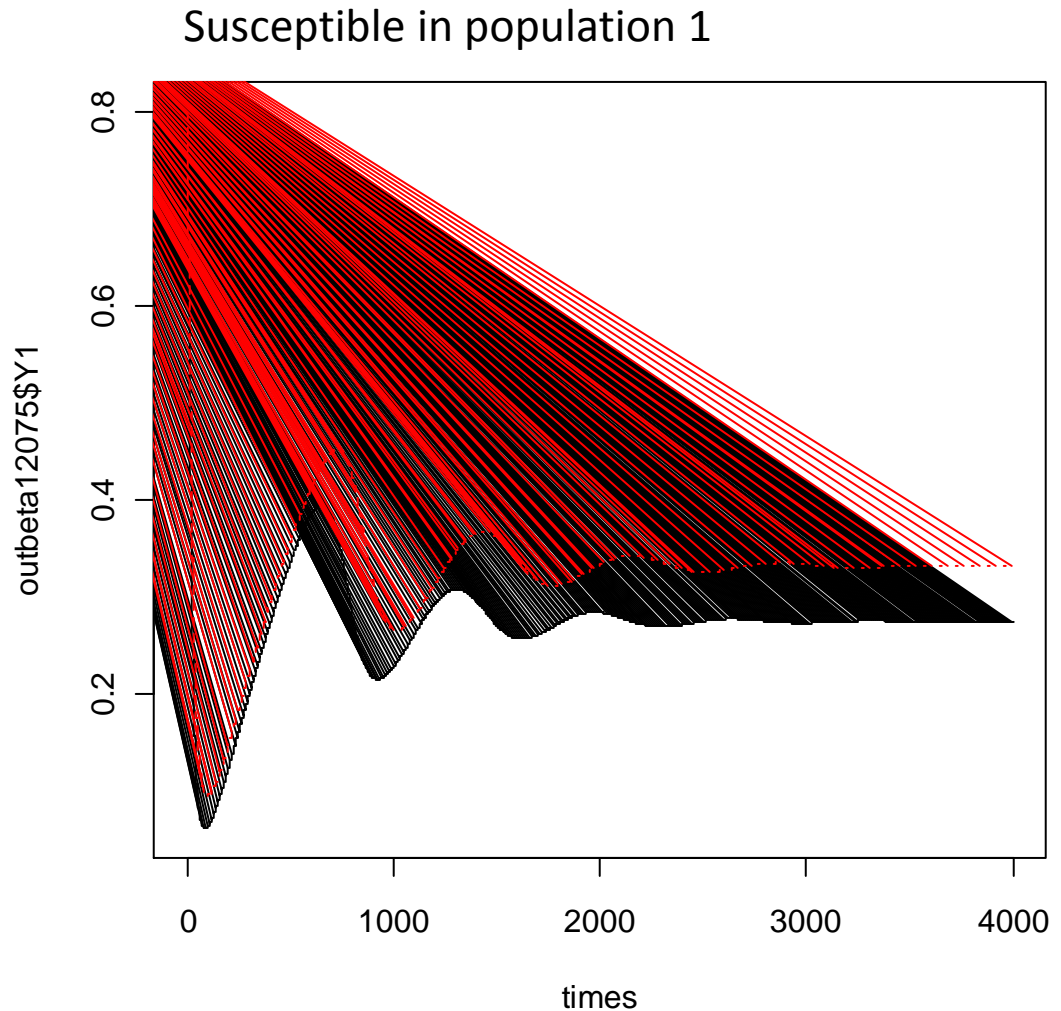
```
> state <- c(Y1=0.8,Y2=0.2,Y3=0,Y4=0.8,Y5=0.2,Y6=0)
> state
  Y1  Y2  Y3  Y4  Y5  Y6
0.8 0.2 0.0 0.8 0.2 0.0
```

# Example

## Parameter setting

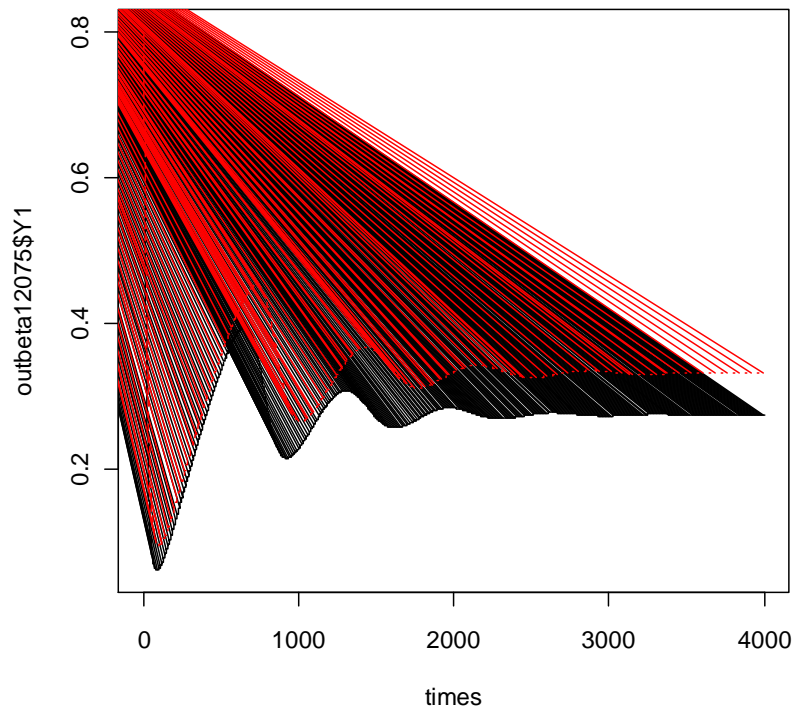
$$\begin{bmatrix} \beta_{11} = 0.05 & \beta_{12} = 0.075 \\ \beta_{12} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

$$\begin{bmatrix} \beta_{11} = 0.05 & \beta_{12} = 0.05 \\ \beta_{12} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

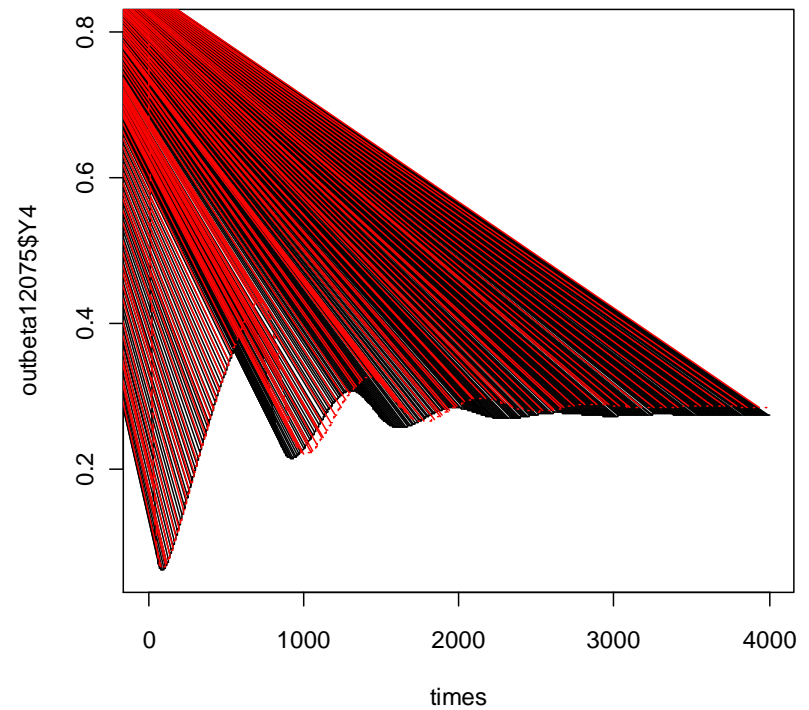


# Susceptible in the two sub population

Susceptible in population 1



Susceptible in population 2



# Example

## Parameter setting

$$\begin{bmatrix} \beta_{11} = 0.05 & \beta_{12} = 0.075 \\ \beta_{21} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

```
parameters <-  
c(beta11=0.05,beta12=0.075,beta21=0.075,beta22=0.05,  
  v1=1/13,v2=1/30,mu=0.001)
```

$$\begin{bmatrix} \beta_{11} = 0.05 & \beta_{12} = 0.00 \\ \beta_{21} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

```
parameters <-  
c(beta11=0.05,beta12=0.00,beta21=0.075,beta22=0.05,  
  v1=1/13,v2=1/30,mu=0.001)
```

In the second setting:

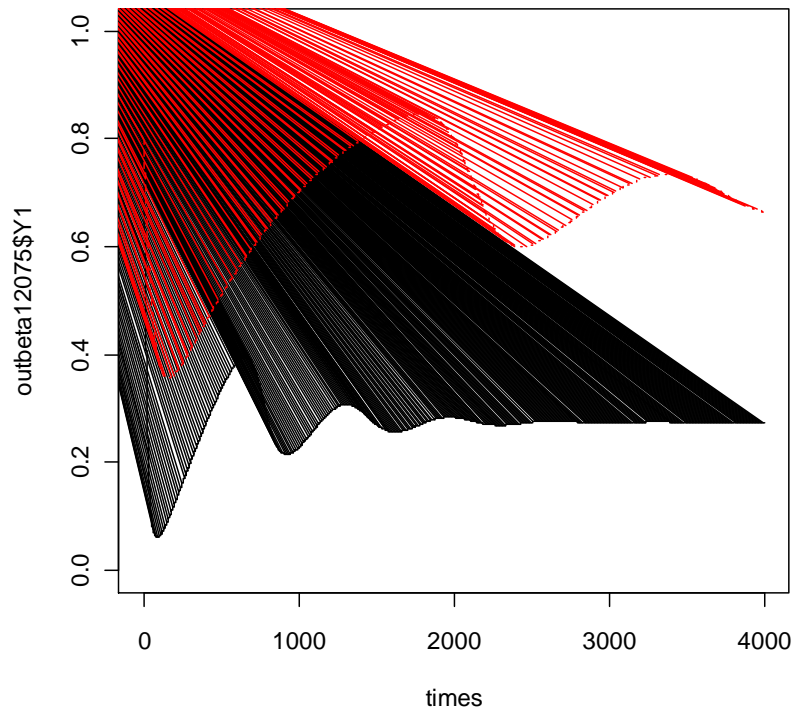
Per contact:

Susceptible from pop. 1 with infected pop. 2: no transmission.

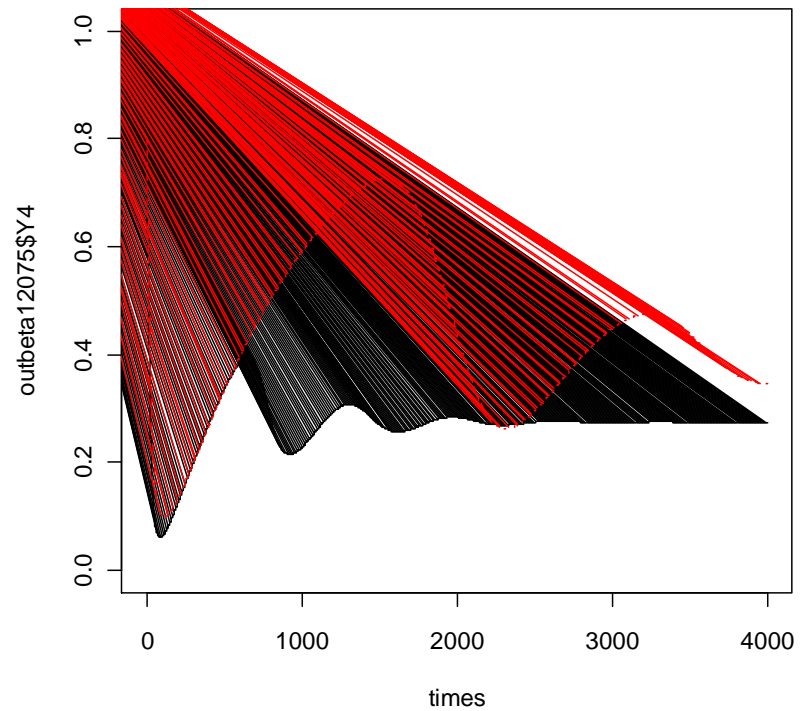
Susceptible from pop. 2 with infected pop. 1: transmission is possible.

# Susceptible in the two sub population

Susceptible in population 1



Susceptible in population 2



# Example: positive feedback

## Parameter setting

$$\begin{bmatrix} \beta_{11} = 0.05 & \beta_{12} = 0.075 \\ \beta_{21} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

$$\begin{bmatrix} \beta_{11} = 0.0 & \beta_{12} = 0.075 \\ \beta_{21} = 0.075 & \beta_{22} = 0.05 \end{bmatrix}$$

## In the second setting:

First population:

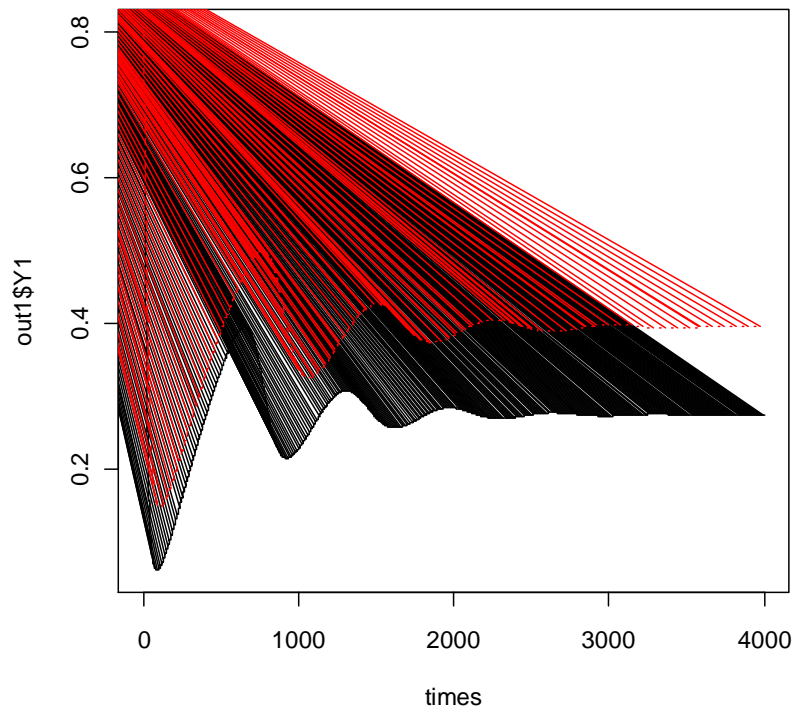
All transmission via contact  
between the population

Second population:

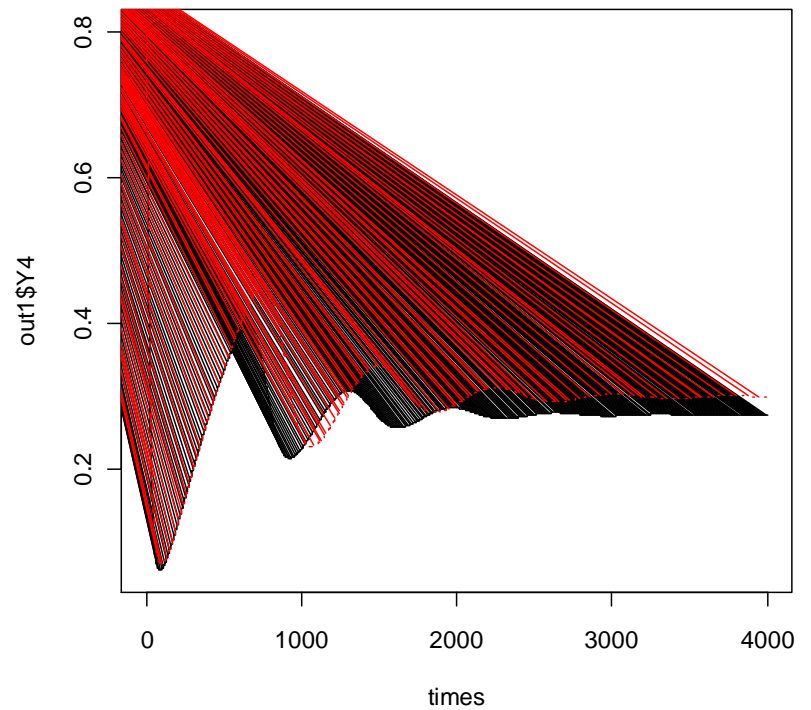
Transmission within / between the  
populations.

# Susceptible in the two sub population

Susceptible in population 1



Susceptible in population 2



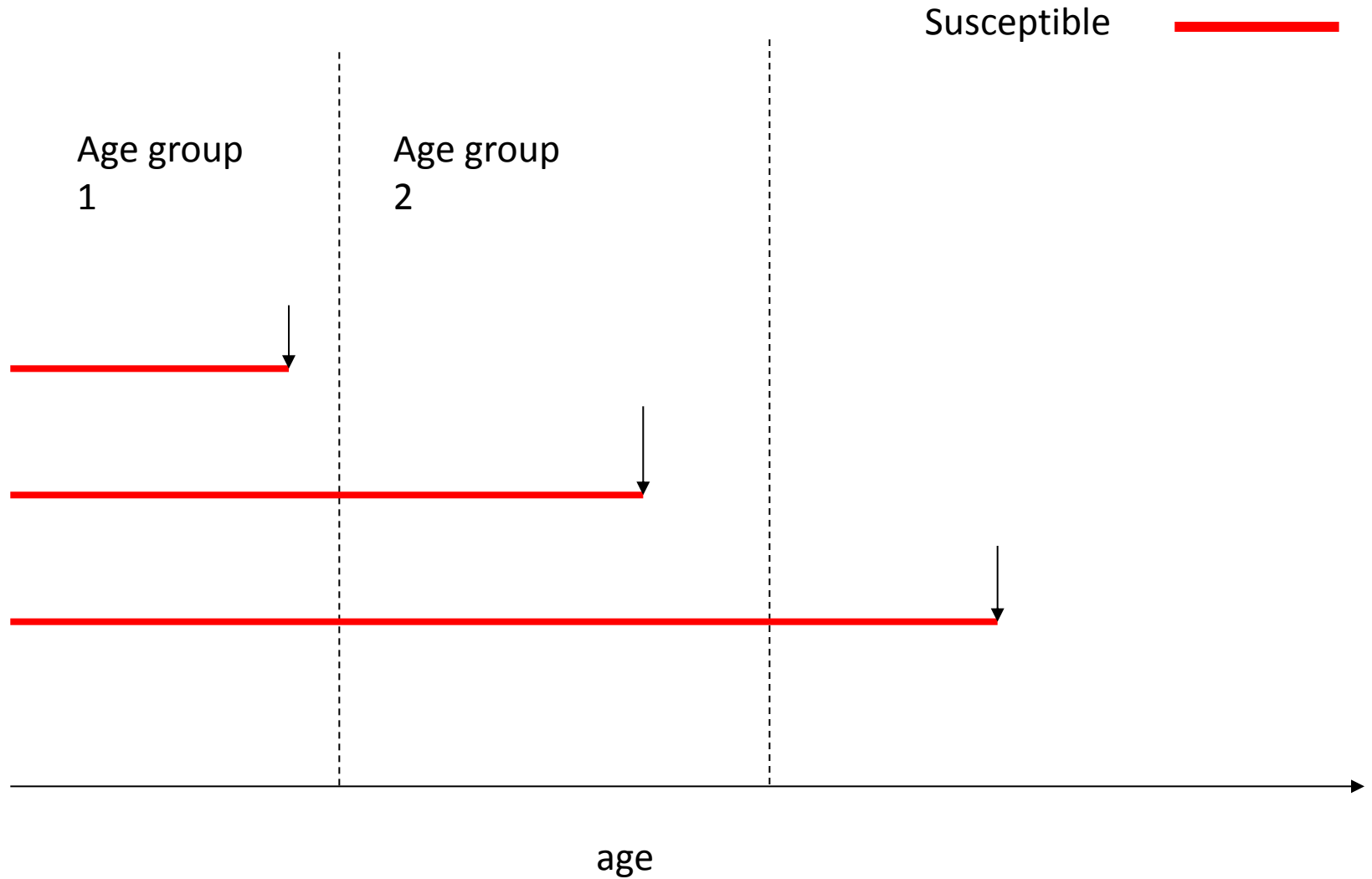
## Example 3: age structured



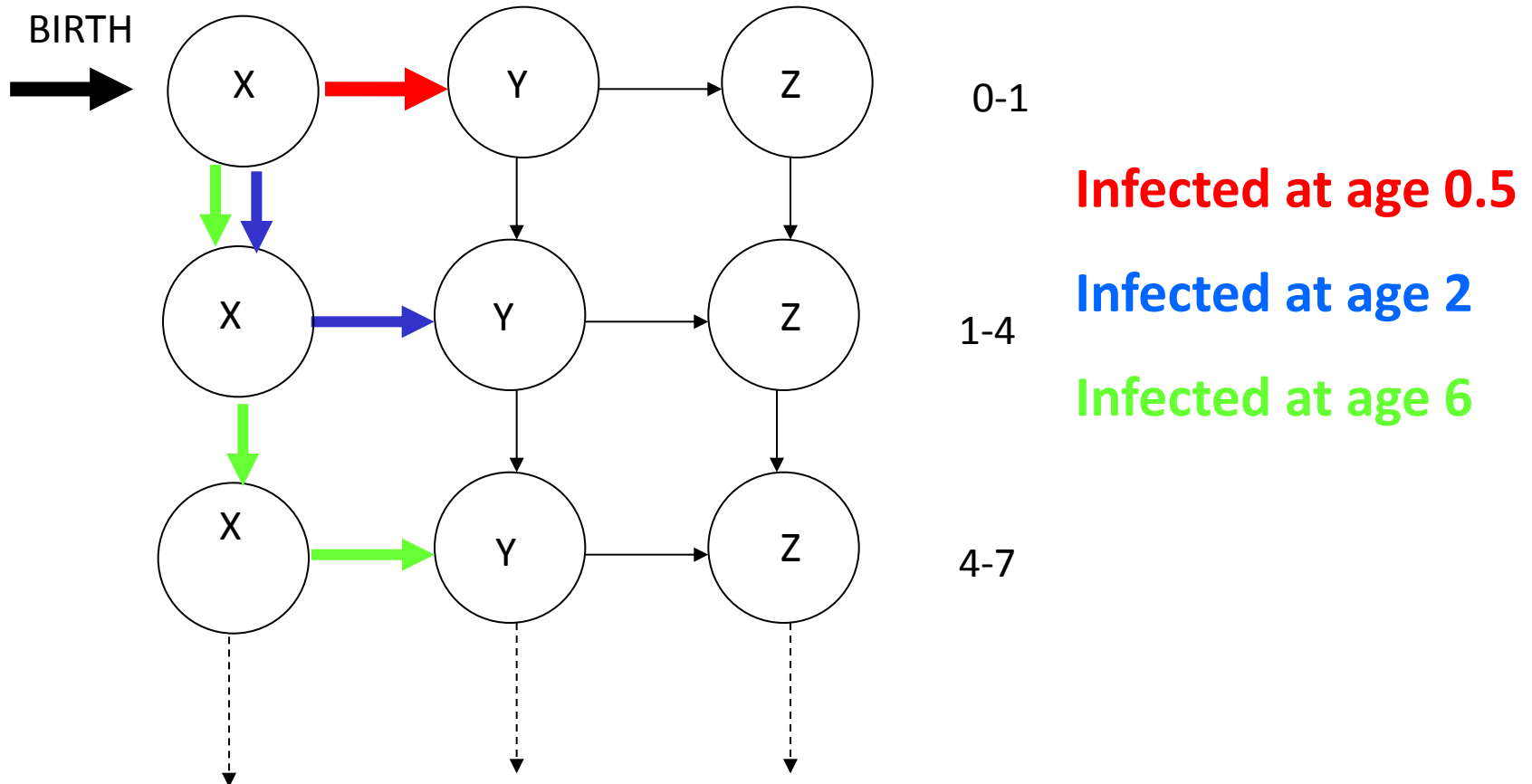
# Age Structured population

- The population is divided by age groups.
- Examples:
- People has a tendency to mix with their own age group (children in the same class at school, students in the university).
- Children and parents (between groups transmission).

# Age Structured population



# Age Structured population



# Contact patterns

Population with two age groups:

Case 1: transmission only  
within the age groups

$$\begin{bmatrix} \beta_{11} & 0 \\ 0 & \beta_{22} \end{bmatrix}$$

Case 2: transmission  
within and between the  
age groups

$$\begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{12} & \beta_{22} \end{bmatrix}$$

# Contact patterns

Population with two age groups:

Case 1: transmission only  
within the age groups

$$\begin{bmatrix} \beta_{11} & 0 \\ 0 & \beta_{22} \end{bmatrix}$$

```
parameters <- ,  
c(beta11=0.0001,beta12=0.00000,beta21=0.00000,  
  beta22=0.0001,  
  v1=4,v2=4,mu=1/75,mu2=1/20,N=1000000)
```

# Contact patterns

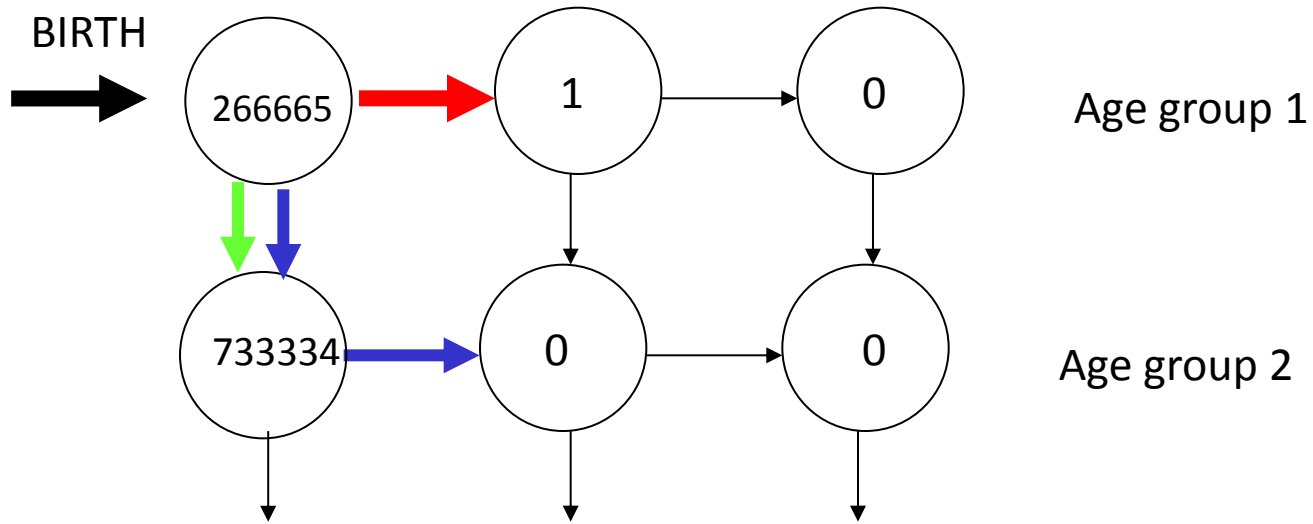
Population with two age groups:

Case 2: transmission within and between the age groups

$$\begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{12} & \beta_{22} \end{bmatrix}$$

```
parameters <-  
c(beta11=0.0001, beta12=0.0000075, beta21=0.0000075, beta22=0.0001,  
  v1=4, v2=4, mu=1/75, mu2=1/20, N=1000000)
```

# State variables



```
state <- c(Y1=266665,Y2=1,Y3=0,Y4=733334,Y5=0.0,Y6=0)
```

# Model Structure: two age groups

$$\begin{aligned}\frac{dS_1(t)}{dt} &= N\mu - (\beta_{11}I_1 + \beta_{12}I_2)S_1 - \mu S_1 - \eta S_1 \\ \frac{dI_1(t)}{dt} &= (\beta_{11}I_1 + \beta_{12}I_2)S_1 - \nu_1 I_1 - \mu I_1 - \eta I_1 \\ \frac{dR_1(t)}{dt} &= \nu_1 I_1 - \mu R_1 - \eta R_1 \\ \frac{dS_2(t)}{dt} &= \eta S_1 - (\beta_{21}I_1 + \beta_{22}I_2)S_2 - \mu S_2 \\ \frac{dI_2(t)}{dt} &= \eta I_1 + (\beta_{21}I_1 + \beta_{22}I_2)S_2 - \nu_2 I_2 - \mu I_2 \\ \frac{dR_2(t)}{dt} &= \eta R_1 + \nu_2 I_2 - \mu R_2\end{aligned}$$

```
SIRtwo<-function(t,state,parameters)
{
  with(as.list(c(state, parameters)),
  {
    dY1 <- - (beta11*Y2+beta12*Y5)*Y1+N*mu-mu*Y1-mu2*Y1
    dY2 <- (beta11*Y2+beta12*Y5)*Y1-v1*Y2-mu*Y2-mu2*Y2
    dY3 <- v1*Y2 - mu*Y3-mu2*Y3
    dY4 <- - (beta21*Y2+beta22*Y5)*Y4-mu*Y4+mu2*Y1
    dY5 <- (beta21*Y2+beta22*Y5)*Y4-v2*Y5-mu*Y5+mu2*Y2
    dY6 <- v2*Y5-mu*Y6+mu2*Y3
    list(c(dY1,dY2,dY3,dY4,dY5,dY6))
  })
}
```

$$\begin{bmatrix} \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \end{bmatrix}$$

Move from the first age group to the second age group.



# Parameter setting

$$N = 1000000$$

$$\mu_2 = \frac{1}{20} \quad \text{Age group: 0-20, 20-75}$$

$$\mu = \frac{1}{75} \quad \text{Life expectancy: 75 years}$$

$$v_1 = v_2 = 4$$

```
> parameters <- c(beta11=0.0001,beta12=0.0000075,beta21=0.0000075,beta22=0.0001,  
+                 v1=4,v2=4,mu=1/75,mu2=1/20,N=1000000)
```

```
>Parameters
```

beta11	beta12	beta21	beta22	v1	v2
1.000000e-04	7.500000e-06	7.500000e-06	1.000000e-04	4.000000e+00	4.000000e+00
mu	mu2	N			
1.333333e-02	5.000000e-02	1.000000e+06			

# State variables

$$S_1(0) = 266665$$

$$I_1(0) = 1$$

$$R_1(0) = 0$$

$$S_2(0) = 733334$$

$$I_2(0) = 0$$

$$R_2(0) = 0$$

```
> state <- c(Y1=266665,Y2=1,Y3=0,Y4=733334,Y5=0.0,Y6=0)
```

```
> state
```

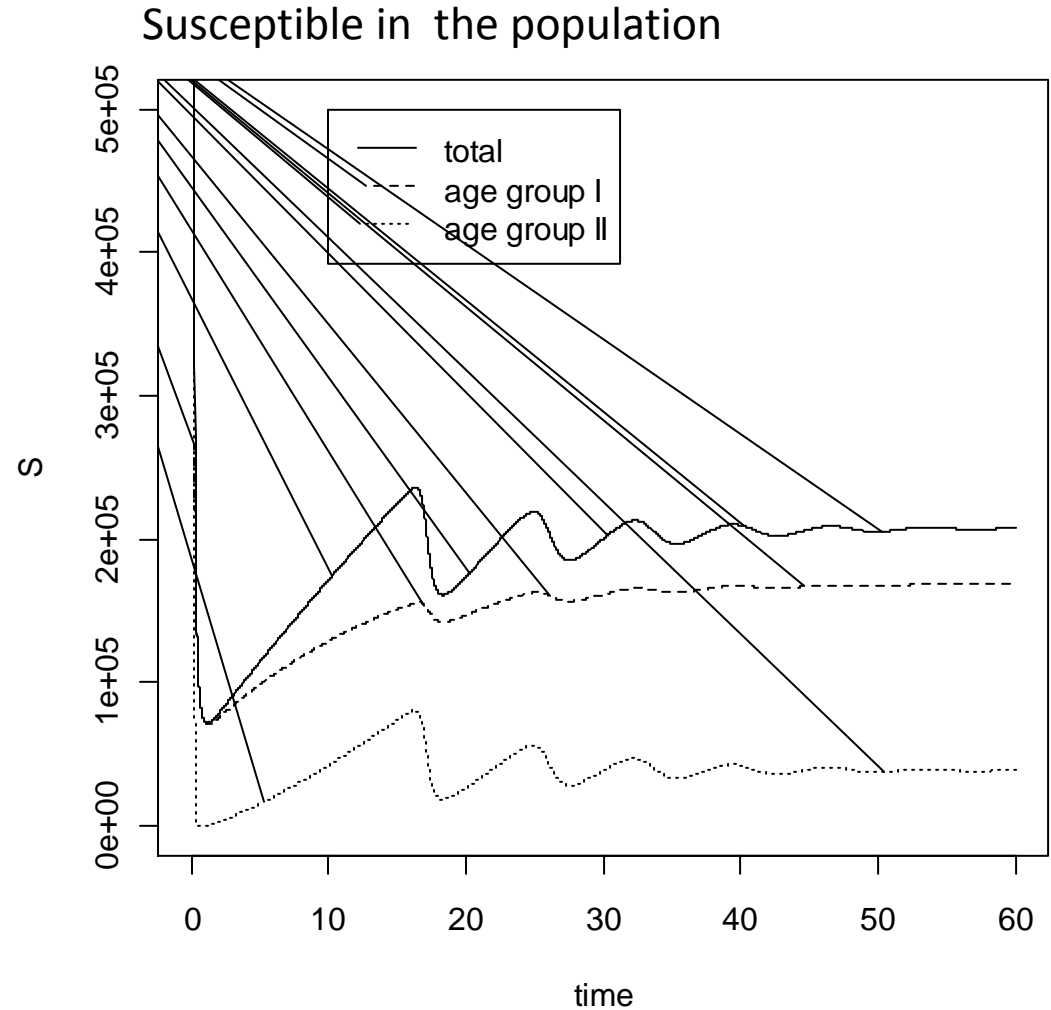
Y1	Y2	Y3	Y4	Y5	Y6
266665	1	0	733334	0	0

# Example

New parameter  
setting

$$\begin{bmatrix} \beta_{11} = 0.000001 & \beta_{12} = 0.000075 \\ \beta_{12} = 0.000075 & \beta_{22} = 0.0001 \end{bmatrix}$$

Less within group  
transmission in pop. 1



# Example

Infected in the population

