

# Pathogen evolution and spillover events

Peter Fransson<sup>1</sup> and Henrik Sjödin<sup>2</sup>



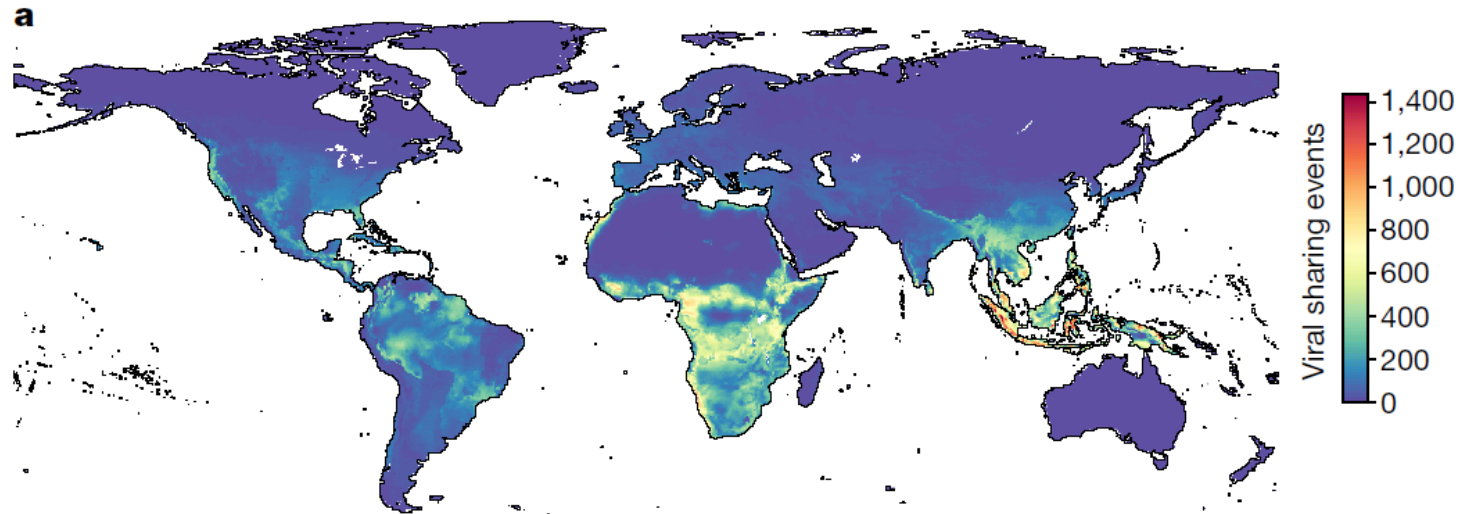
UNIVERSITÄT  
HEIDELBERG  
ZUKUNFT  
SEIT 1386

- How will interactions between species and biodiversity impact pathogen evolution?
- Contact network between species
- Epi-evolutionary model
- Niche expansion

1. Interdisciplinary center for scientific computing, University of Heidelberg, Germany

2. Department of Public Health and Clinical Medicine, Section of Sustainable Health, Umeå University, Sweden

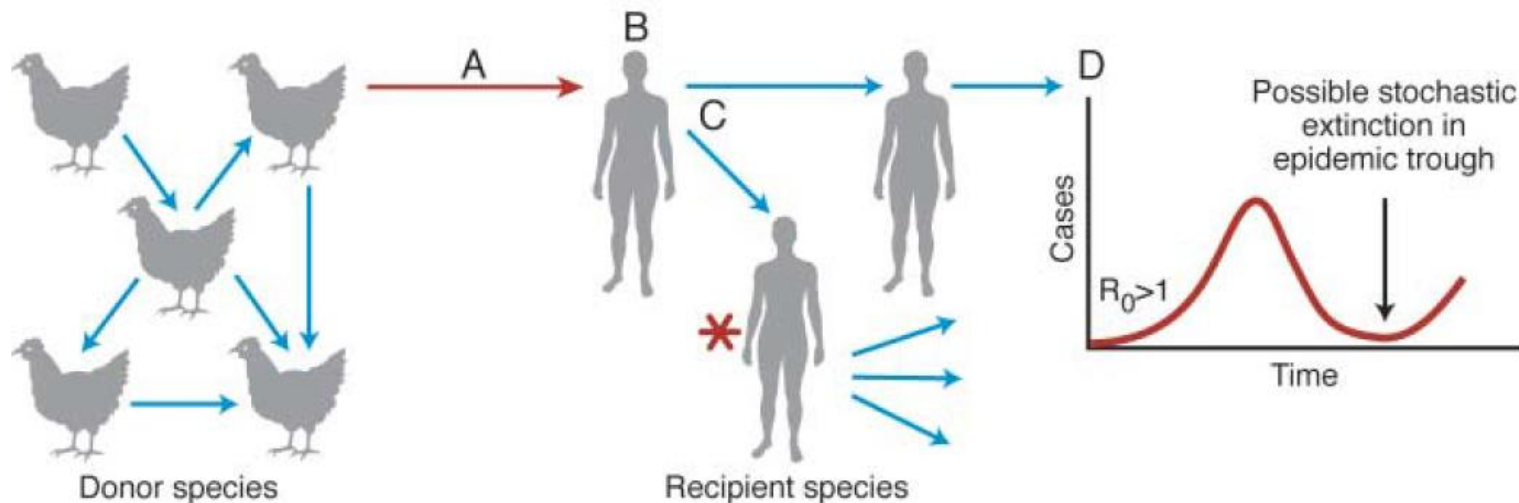
# Pathogen evolution and spillover events



The projected number of novel viral sharing events among mammal species in 2070. Adapted from [1]

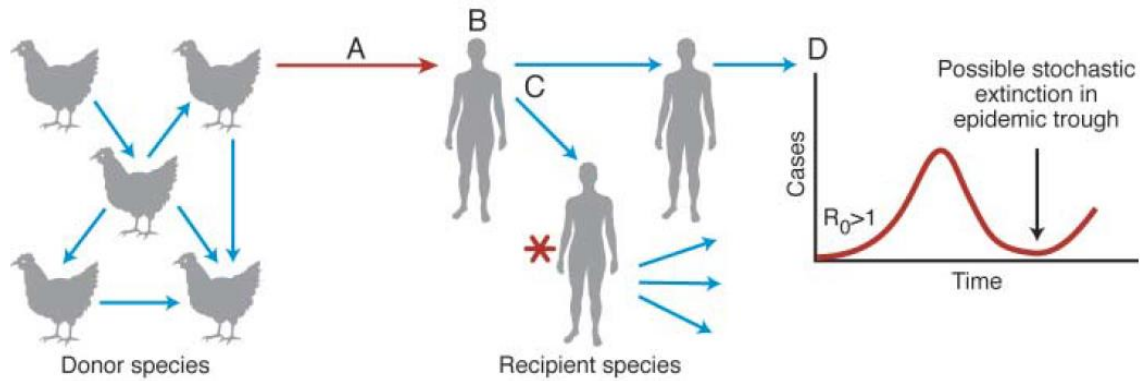
# Spillover barriers

- The between-species barrier (A)
- The within-host barrier (B)
- The within-species barrier (C)

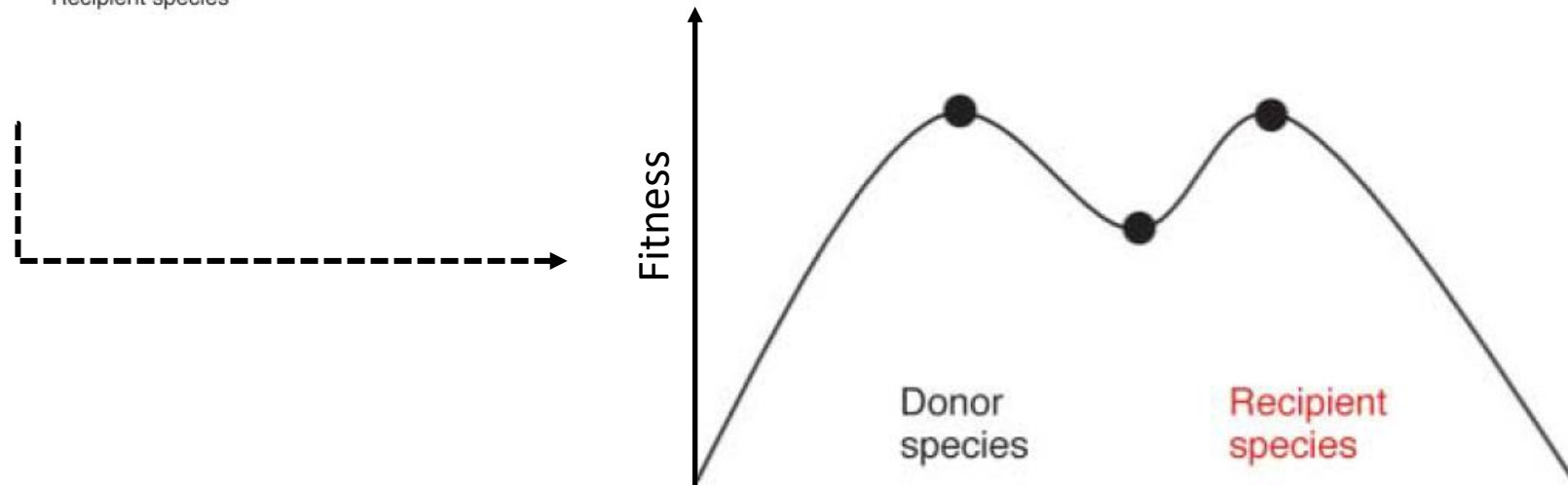


Adapted from [2]

# Spillover barriers



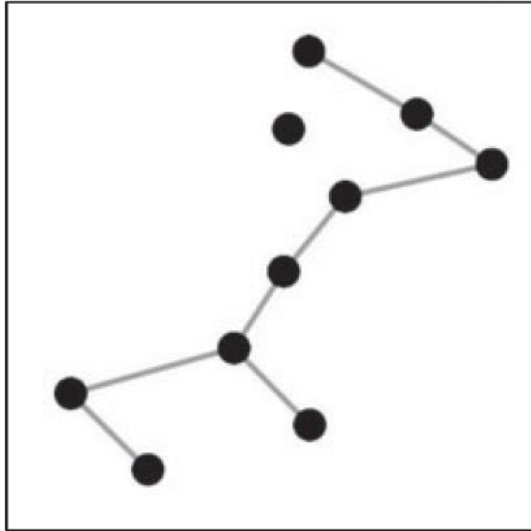
- The between-species barrier (A)
- The within-host barrier (B)
- The within-species barrier (C)



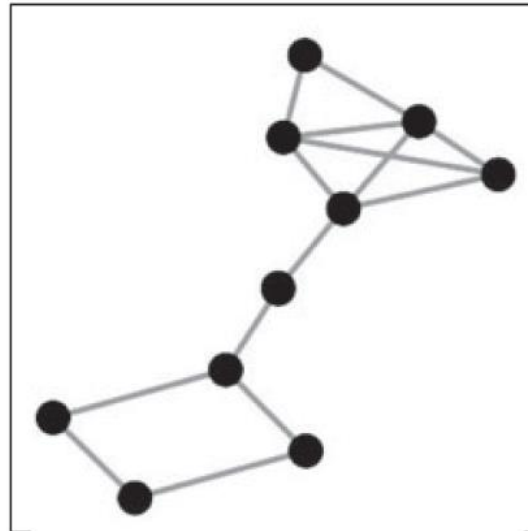
Adapted from [2]

# Contact network

(a) transmission network ( $\beta$ )



(b) contact network ( $c$ )



$= \tau *$

$\tau$  - Probability of pathogen transmission

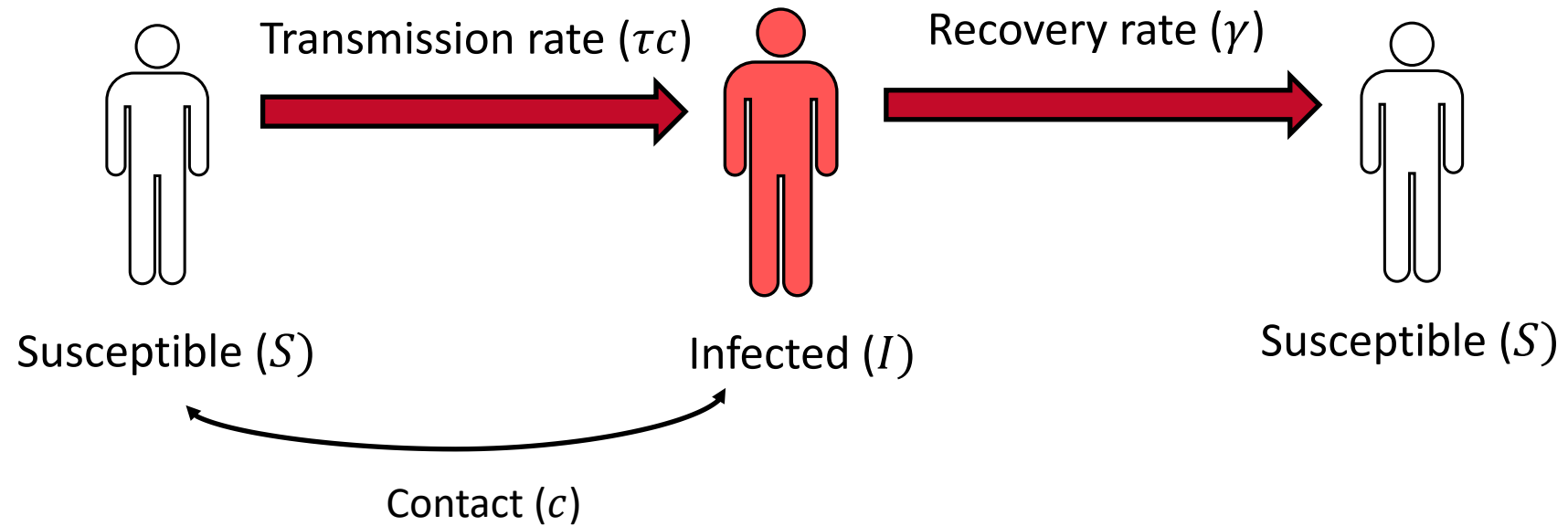
$c$  - Contact rate

$\beta = \tau c$  - Transmission rate

Adapted from [3]

# Epi-evolutionary model

## SIS model:



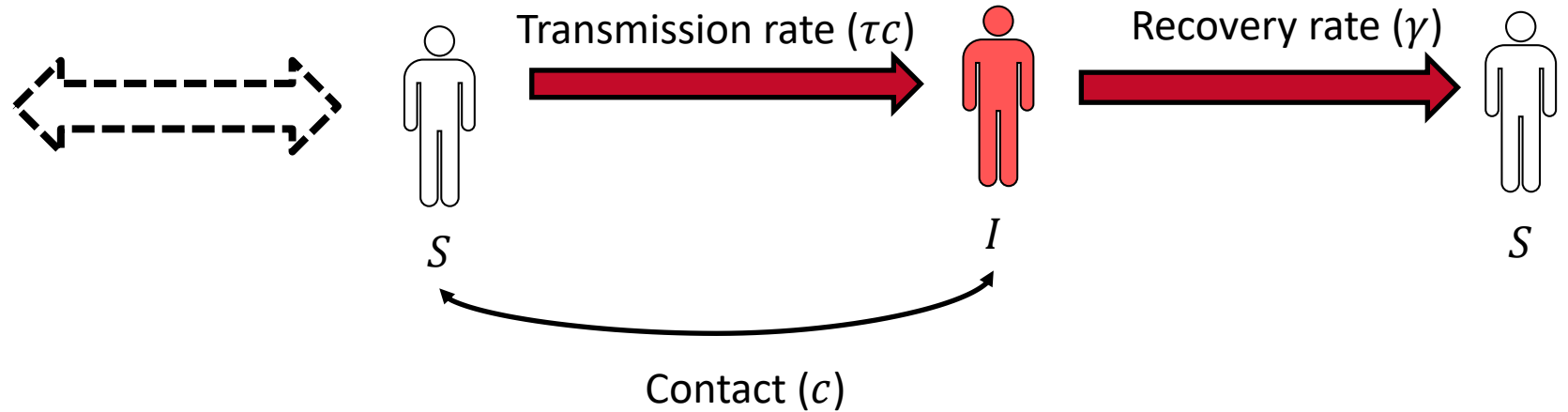
# Epi-evolutionary model

## SIS model:

$$\frac{dS}{dt} = \gamma I - \tau c S \frac{I}{N}$$

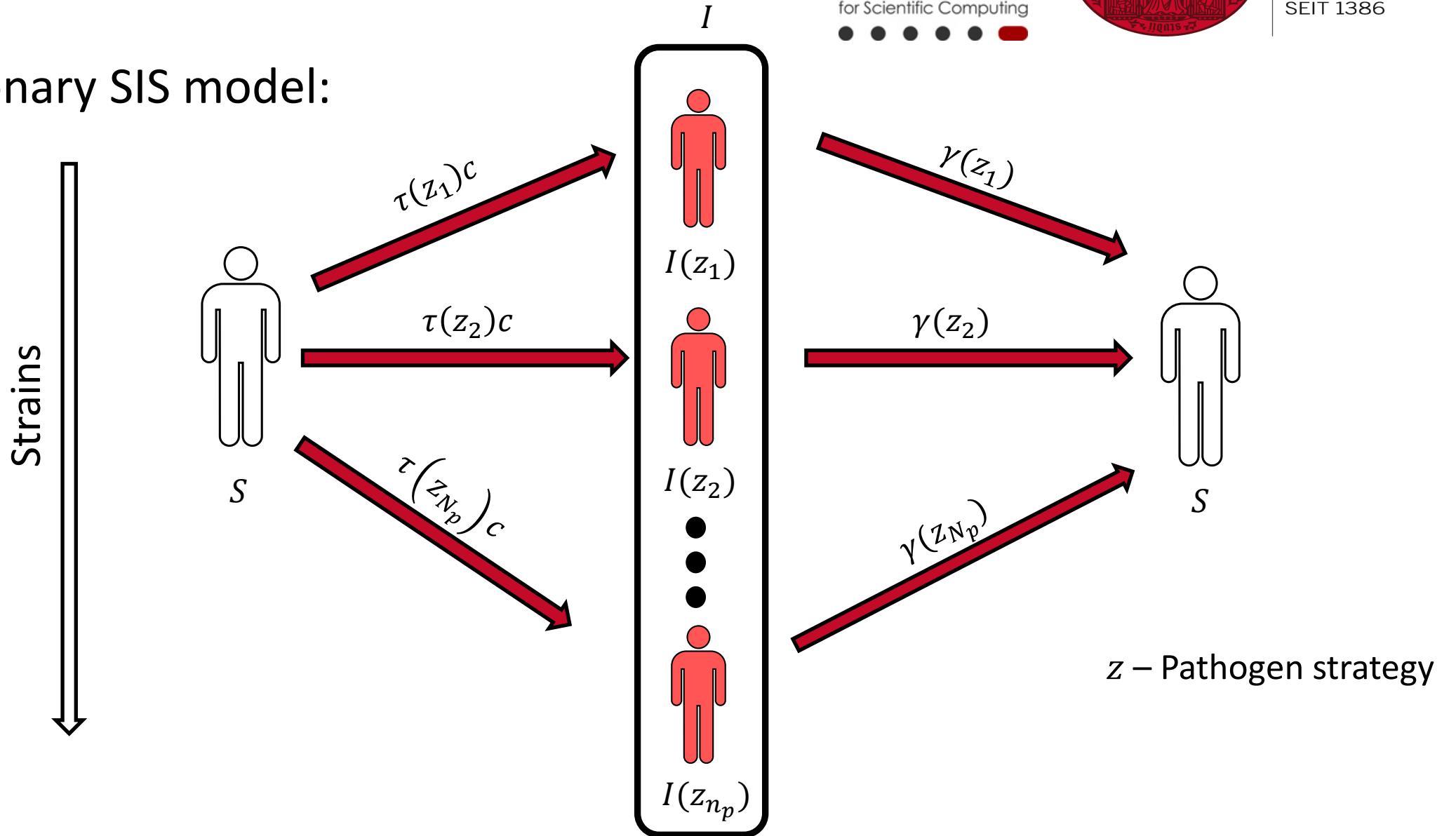
$$\frac{dI}{dt} = \tau c S \frac{I}{N} - \gamma I$$

$$N = S + I \text{ Population size}$$



# Epi-evolutionary model

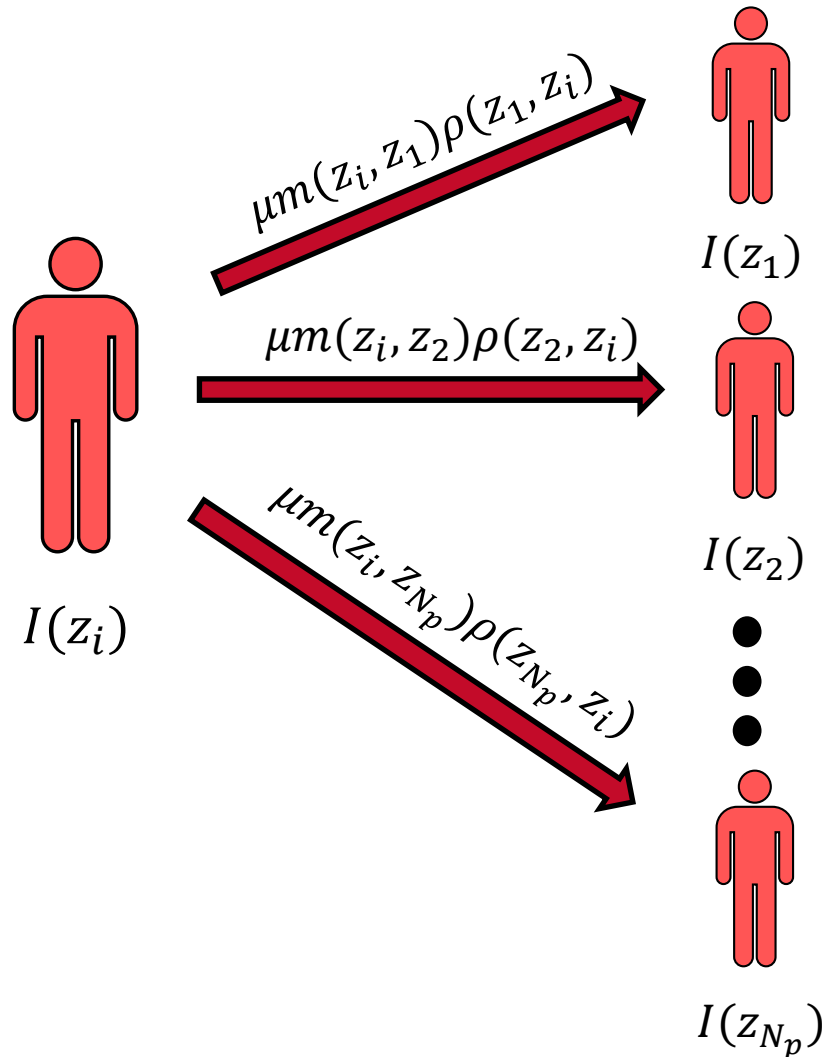
## Epi-evolutionary SIS model:





# Epi-evolutionary model

## Mutations:



$\mu$  - Mutation rate

$m(z_r, z_m)$  - probability of a resident type  $z_r$  giving rise to a mutant type  $z_m$

$\rho(z_m, z_r)$  - Fitness of mutant type  $z_m$  within infected host type  $z_r$

# Epi-evolutionary model

Change of infected with pathogen strategy  $z_i$

$$\frac{dI(z_i)}{dt} = I(z_i) \left[ \tau(z_i)c \frac{S}{N} - \gamma(z_i) \right] - \mu \left[ \sum_{j \in N_p} I(z_j)m(z_j, z_i)\rho(z_i, z_j) - \sum_{j \in N_p} I(z_i)m(z_i, z_j)\rho(z_j, z_i) \right]$$

$r(z_i)$  - per capita growth rate

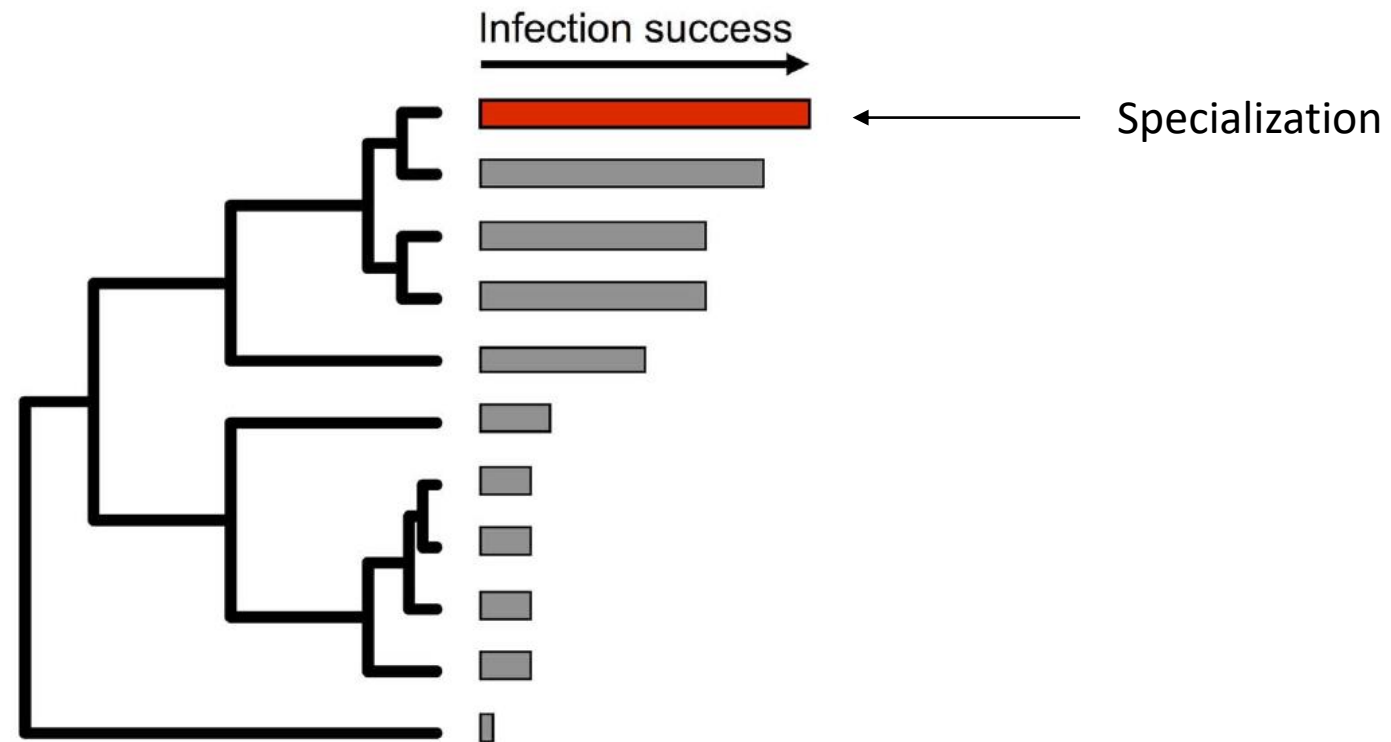
Mutation

$N_p$  - Pathogen  
strategy index set

# Multispecies

Host phylogenetic tree:

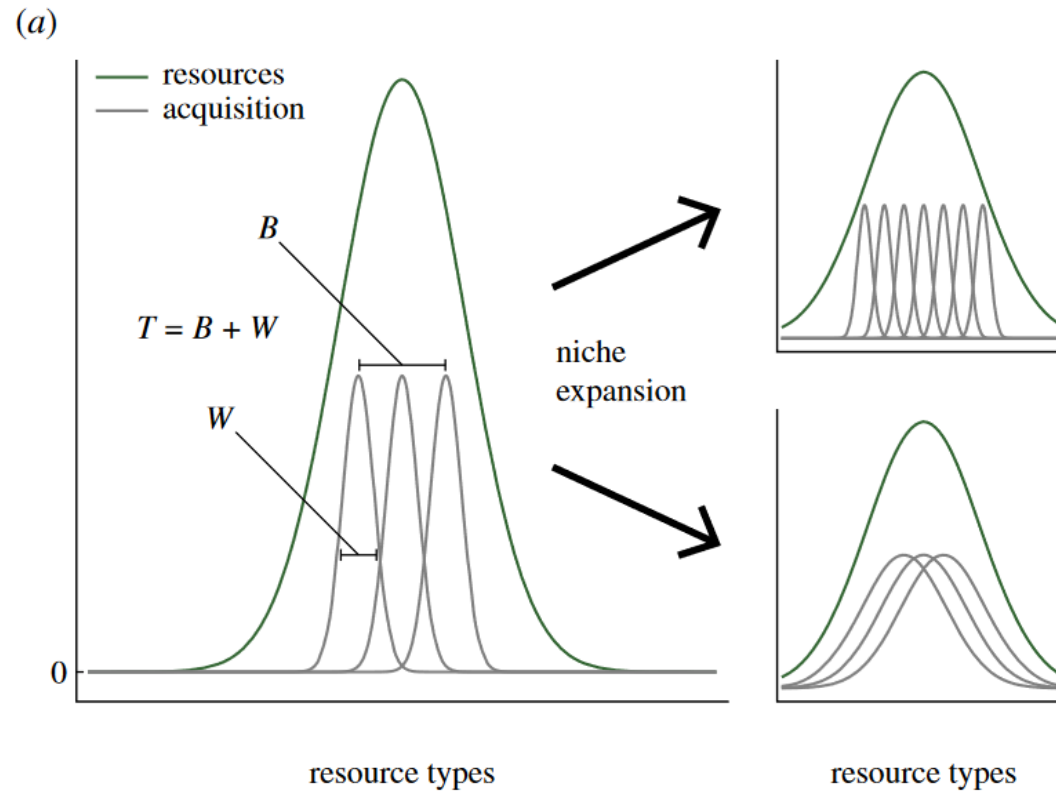
**A** Parasite infection success declines with genetic distance from the natural host



Adapted from [4]

# Multispecies

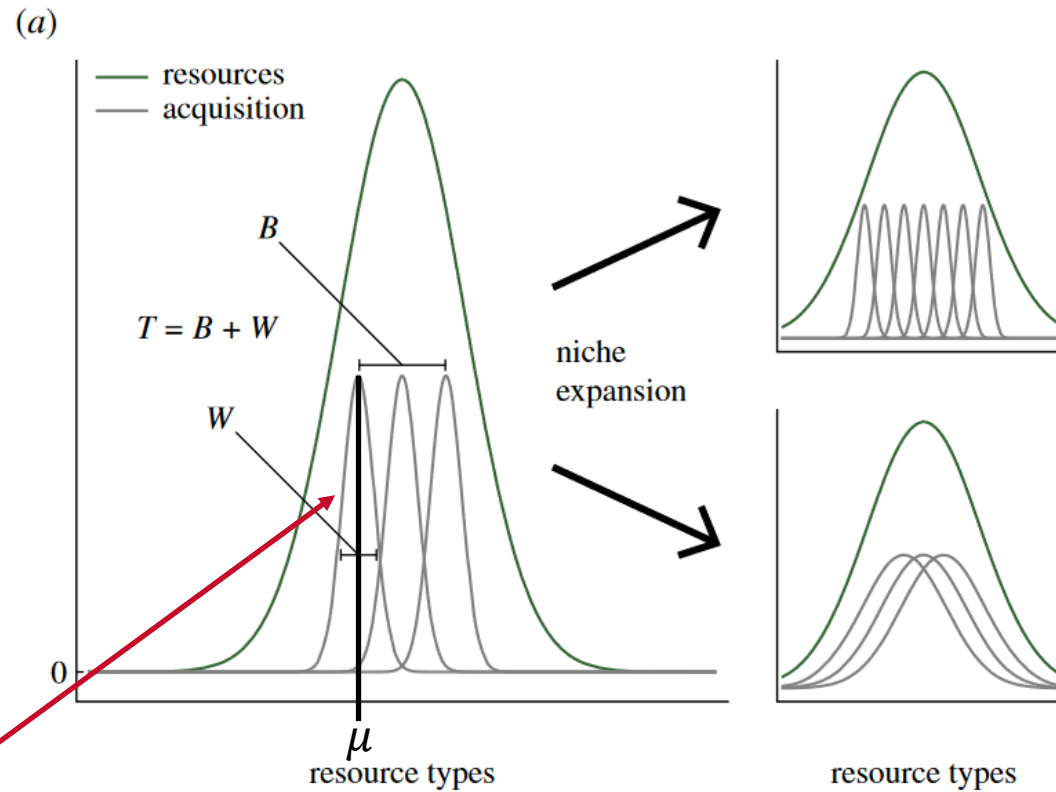
Niche expansion:



Adapted from [5]

# Multispecies

Niche expansion:



$W$  - Niche width  
 $\mu$  - Niche position

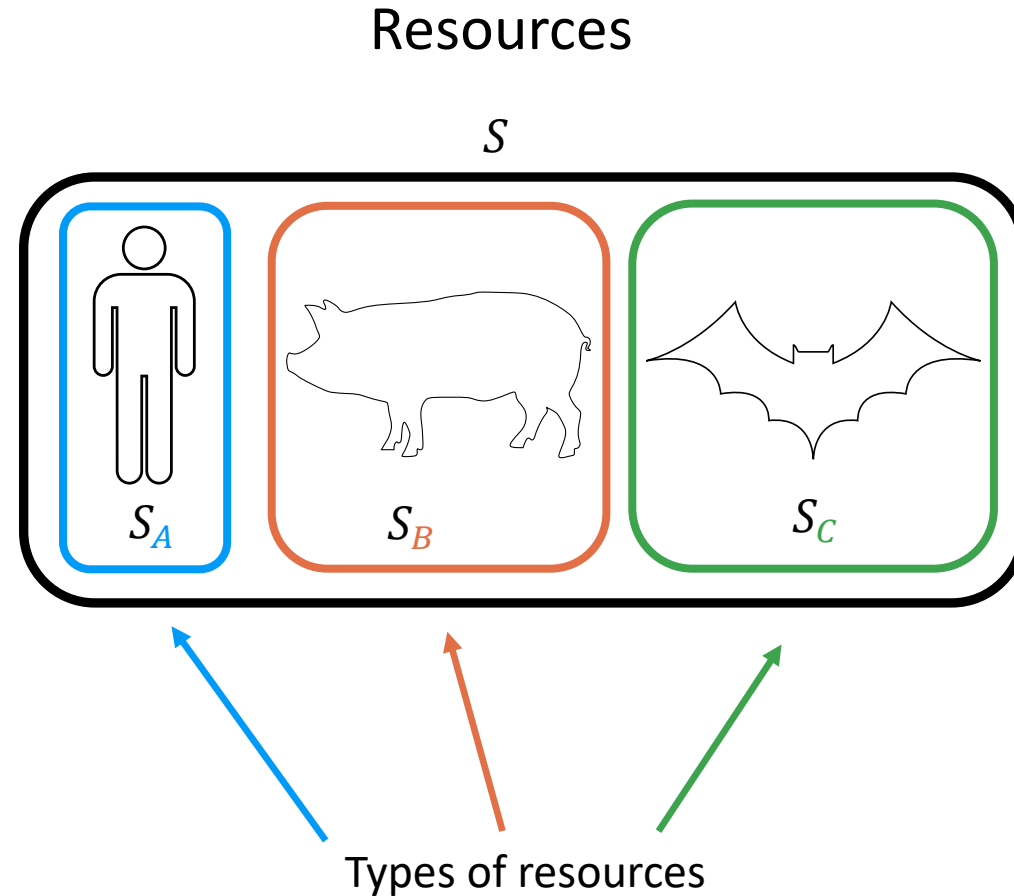
Consumer strategy  $(W, \mu)$

Adapted from [5]

# Multispecies

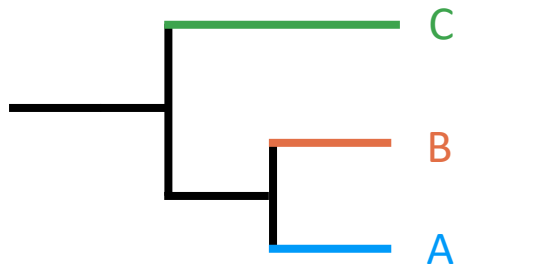
From the perspective of the pathogen

- Resource = susceptible cells in individuals
- Resource type = susceptible cells of a species
- Niche position = pathogen strategy  $z$

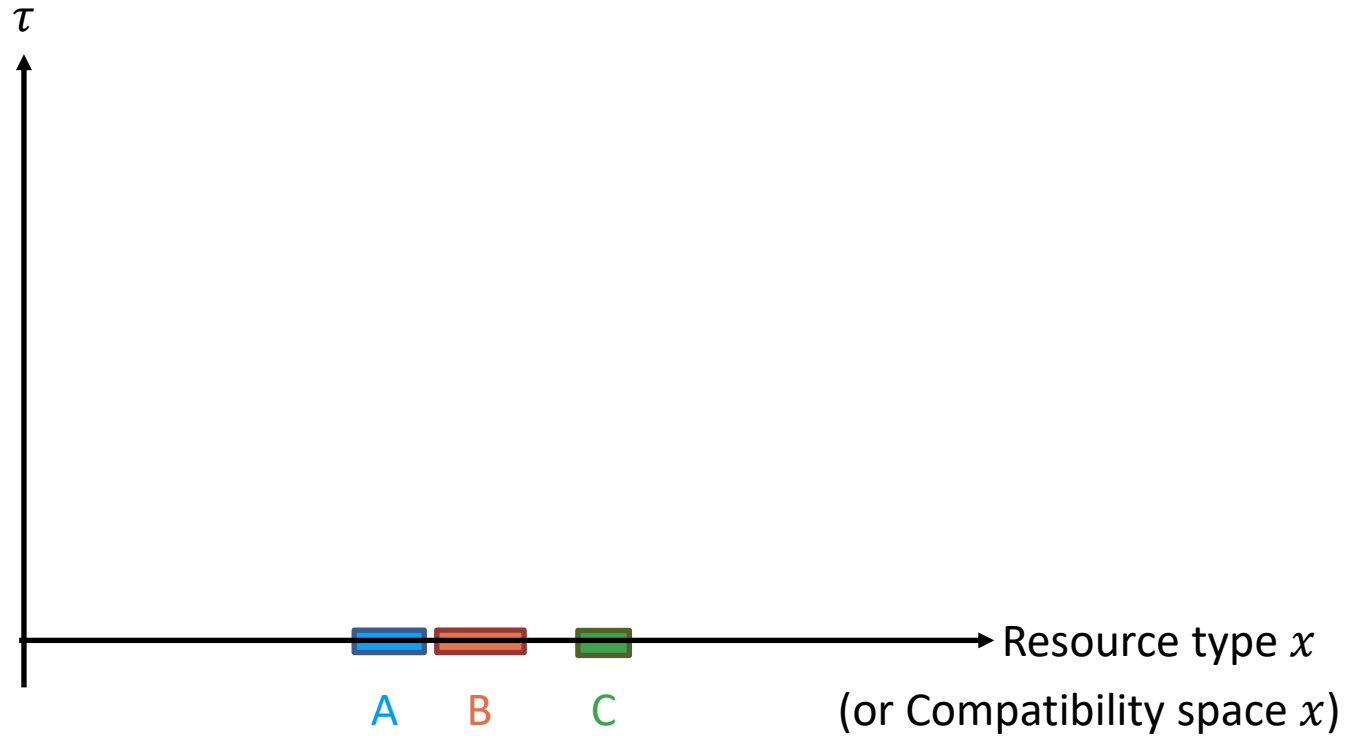


# Multispecies

## Pathogen Strategy ( $z$ )

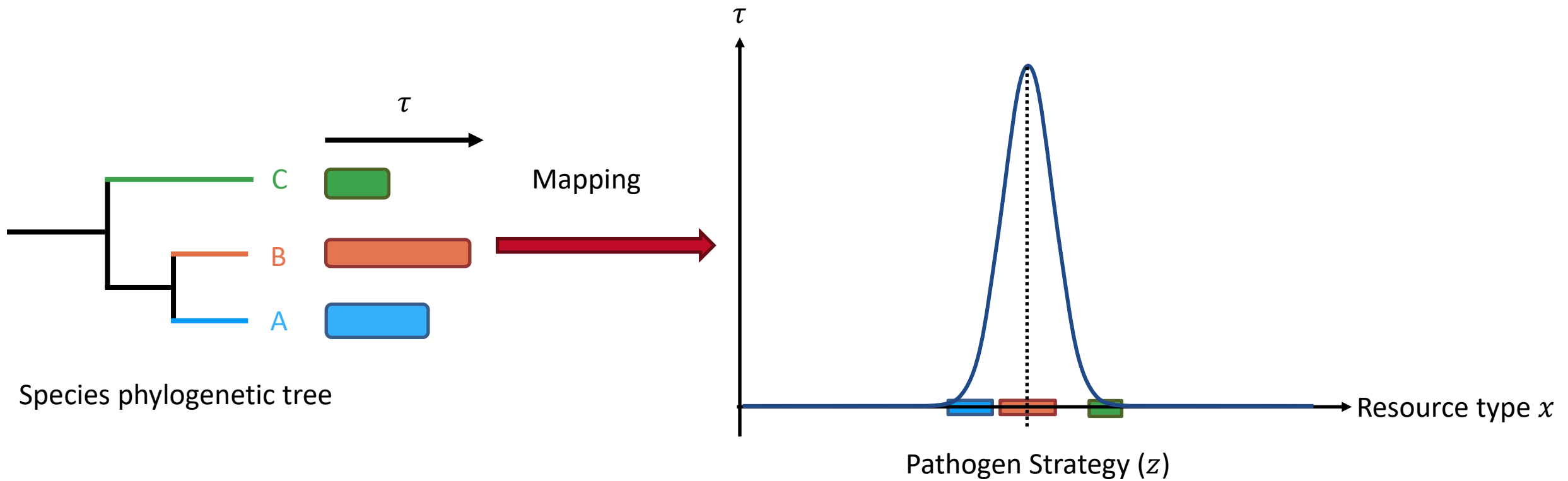


Species phylogenetic tree



# Multispecies

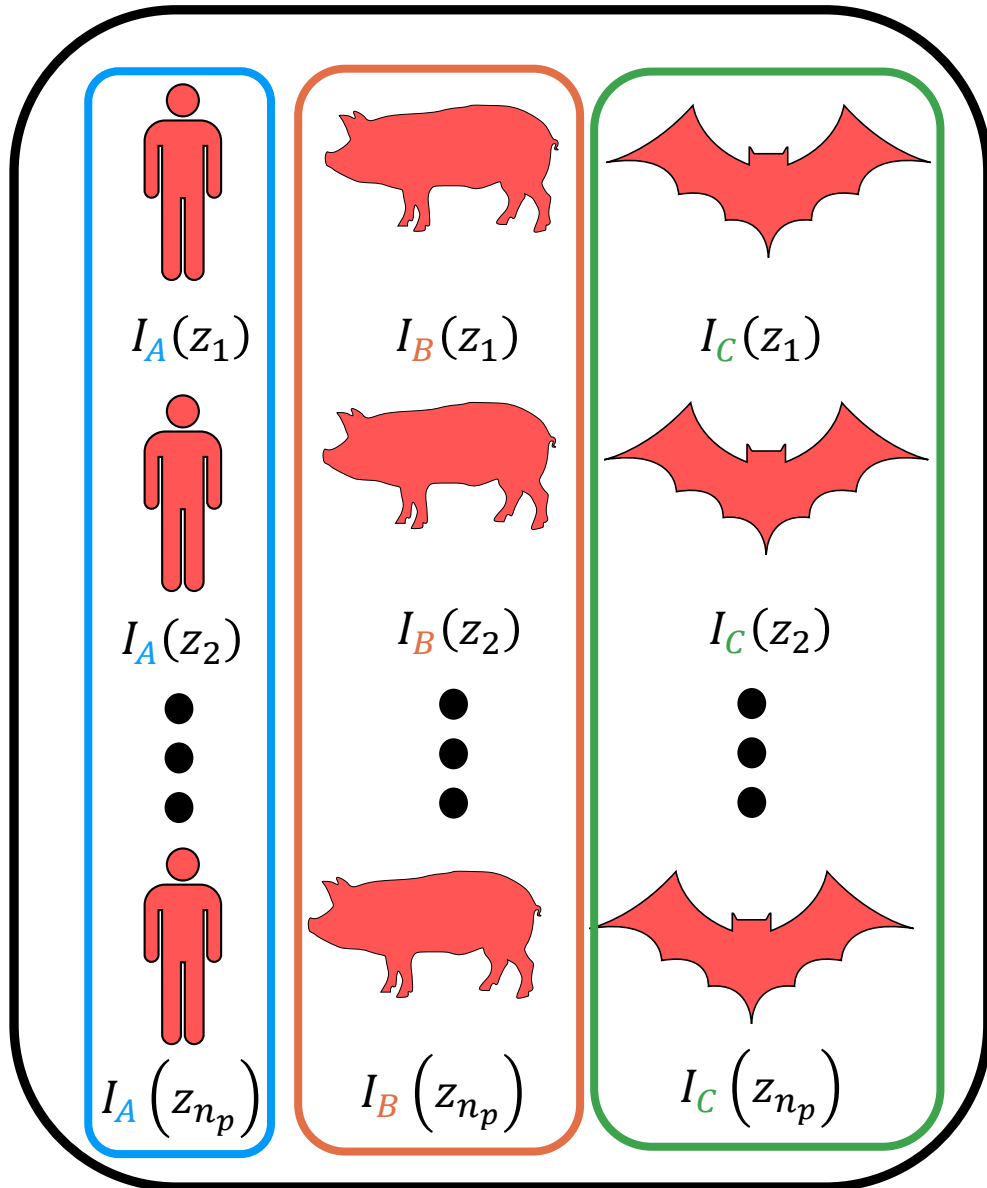
## Pathogen Strategy ( $z$ )



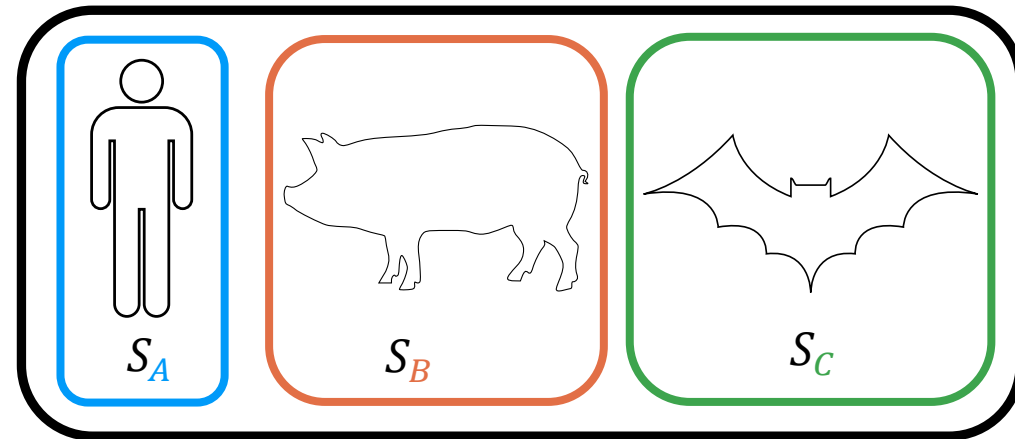


# Multispecies

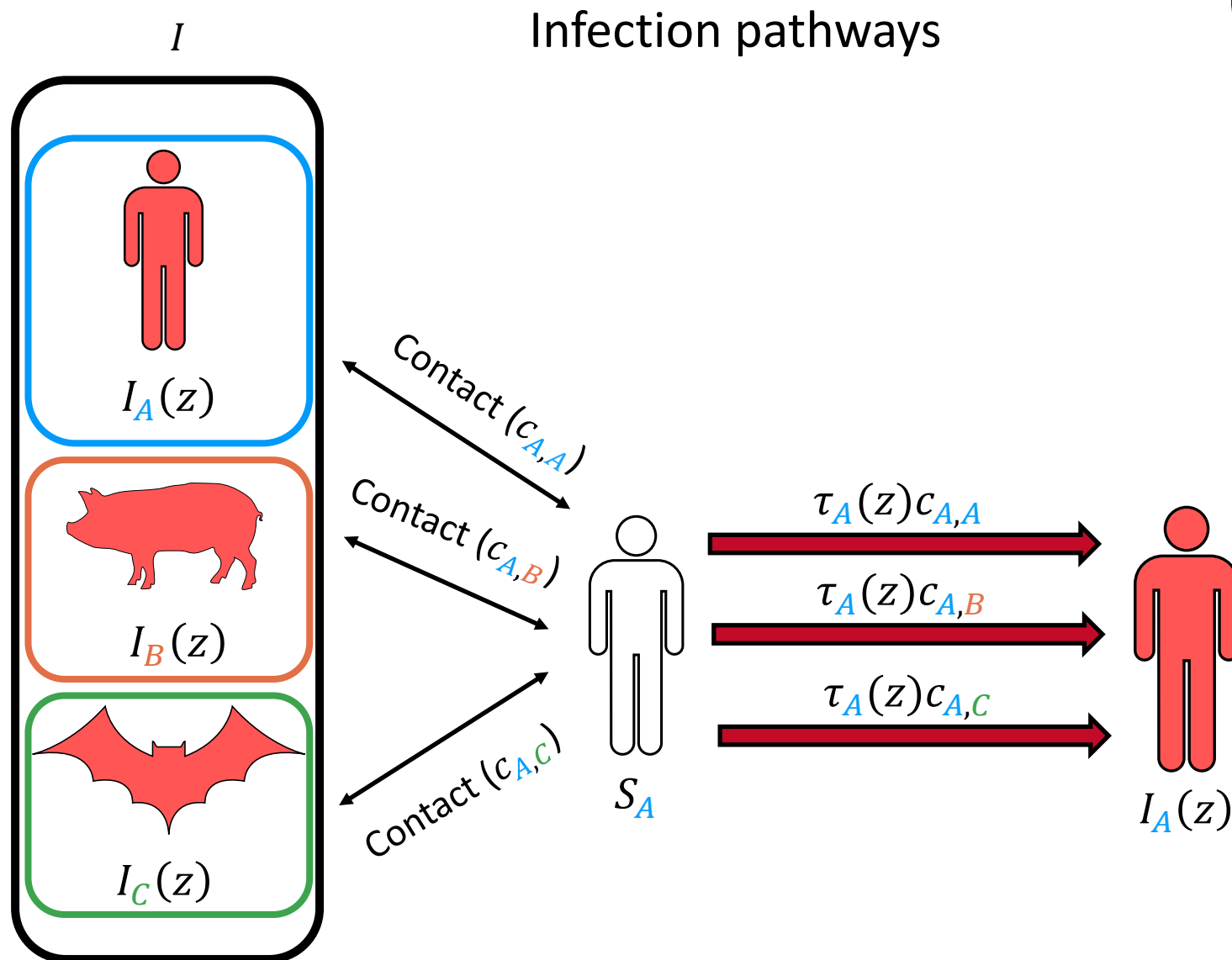
$I$



$S$



# Multispecies



# Multispecies



Change of infected with pathogen strategy  $z$  in focal species  $i$

$$\frac{dI_i(z)}{dt} = S_i \tau_i(z) \underbrace{\sum_{j \in N_s} \left( c_{j,i} \frac{I_j(z)}{N_j} \right)}_{\text{Infection pathways}} - \gamma_i(z) I_i(z) + \text{mutation terms}$$

$i$  - Focal species

$N_s$  - Species index set

$c_{j,i}$  - Contact rate between species  $i$  and  $j$

Change of infected with pathogen strategy  $z$

$$\frac{dI(z)}{dt} = \sum_{i \in N_s} \frac{dI_i(z)}{dt} = I(z) \underbrace{\left[ \sum_{i \in N_s} S_i \tau_i(z) \frac{\bar{c}_{*,i}}{N_*} - \bar{\gamma}_*(z) \right]}_{r(z) \text{ - per capita growth rate}} + \sum_{i \in N_s} \text{mutation terms}$$

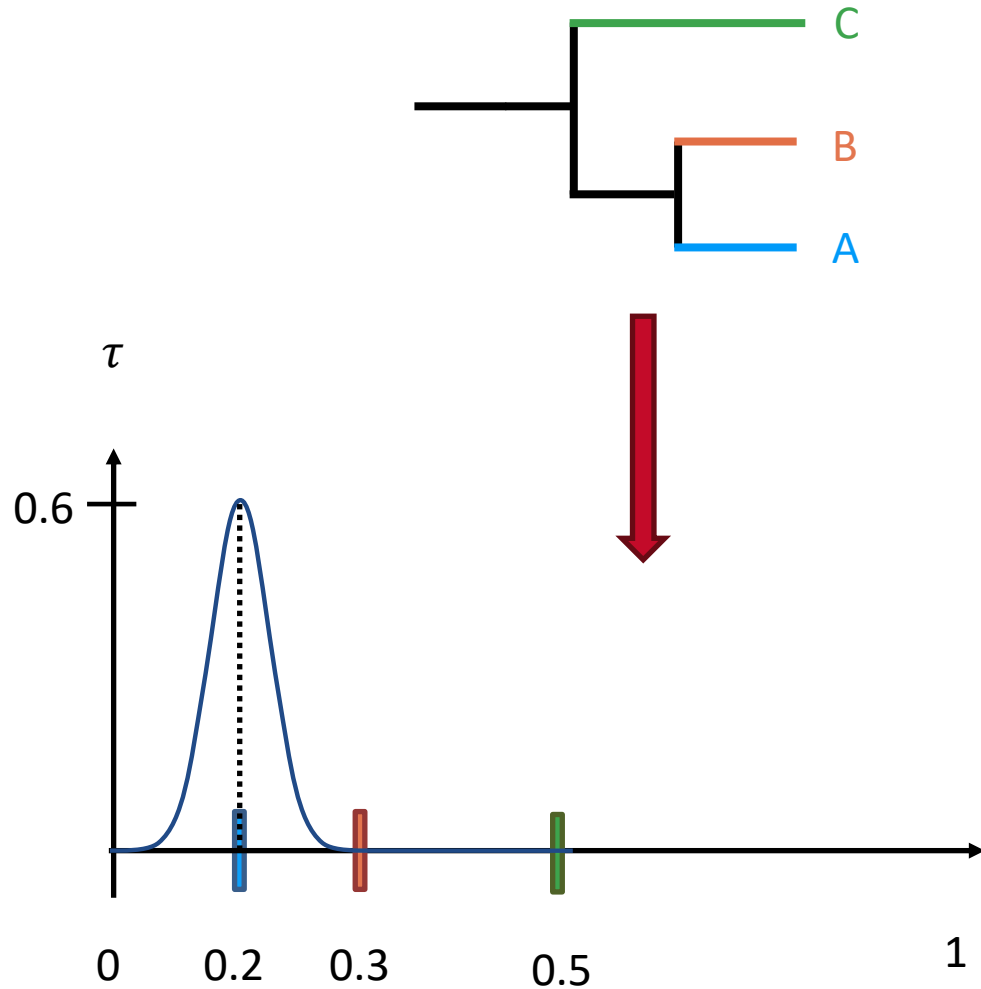
# Stochastic simulation

Gillespie algorithm:

| Description | Reaction   | Reaction propensity ( $\alpha_\mu$ )                             | Depends on ( $\alpha_\mu$ ) | Affects ( $\mu$ )    |
|-------------|--|--|-----------------------------|----------------------|
| Infection   | $S_i + I_j(z) \xrightarrow{\tau_i(z) \frac{c_{j,i}}{N_j}} I_i(z) + I_j(z)$ | $c_{j,i} \frac{\tau_i(z)}{N_j} \times (\#S_i) \times (\#I_j(z))$ | $S_i, I_j(z)$               | $S_i, I_i(z)$        |
| Recovery    | $I_i(z) \xrightarrow{\gamma_i(z)} S_i$                                     | $\gamma_i(z) \times (\#I_i(z))$                                  | $I_i(z)$                    | $S_i, I_i(z)$        |
| Mutation    | $I_i(z_r) \xrightarrow{\mu m(z_r, z_m) \rho_i(z_m, z_r)} I_i(z_m)$         | $\mu m(z_r, z_m) \rho_i(z_m, z_r) \times (\#I_i(z_r))$           | $I_i(z_r)$                  | $I_i(z_r), I_i(z_m)$ |

# Stochastic simulation

## Example



Initial state

$$S_A = 998$$

$$I_A = 2 \quad \longleftarrow \quad z = 0.2$$

$$S_B = 1000$$

$$I_B = 0$$

$$S_C = 1000$$

$$I_C = 0$$

$$c_{A,A} = c_{B,B} = c_{C,C} = 0.43$$

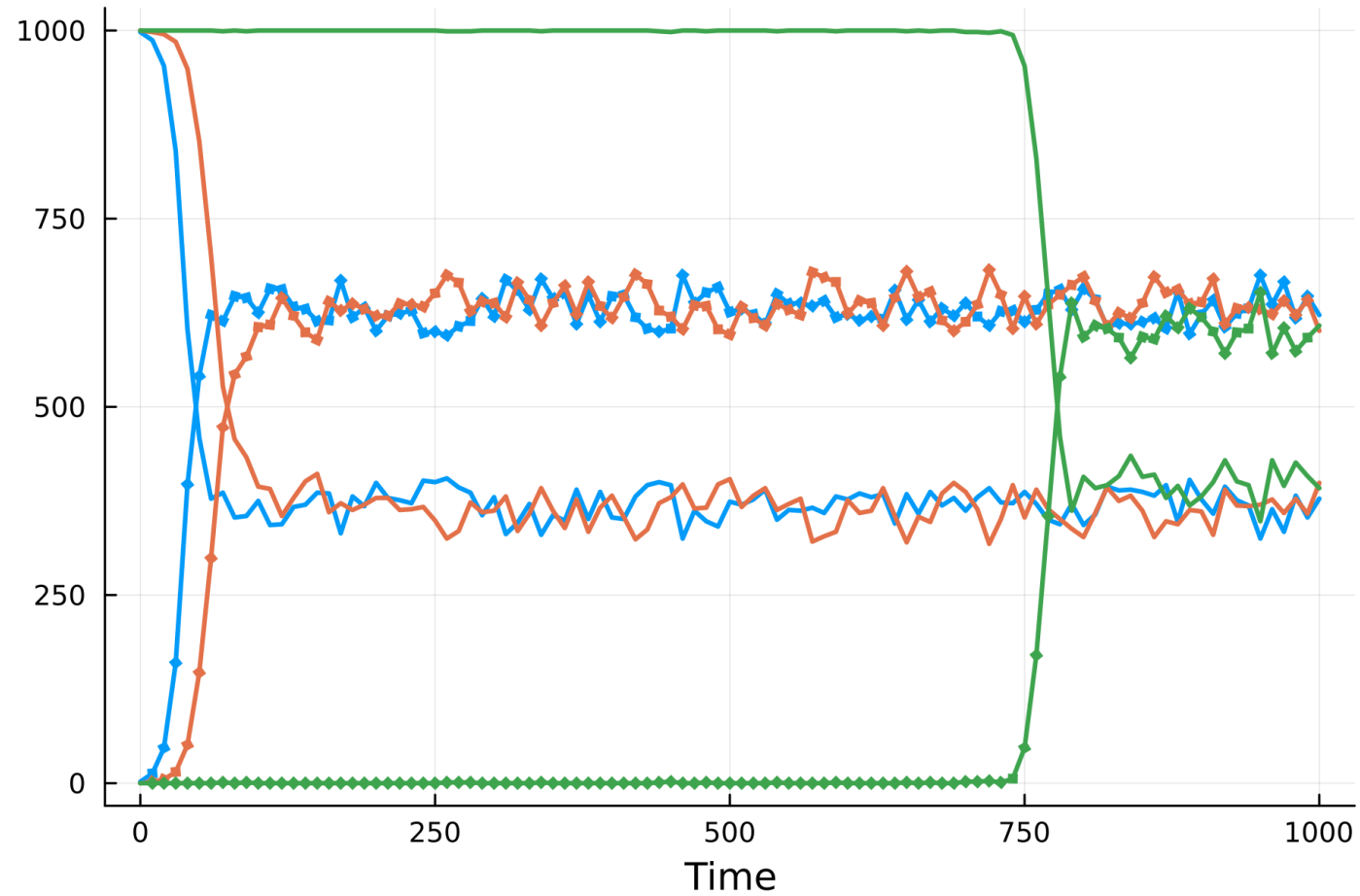
$$c_{A,B} = c_{A,C} = c_{B,C} = 0.3$$

$$\gamma_A = \gamma_B = \gamma_C = 0.1$$

Resource type  $x$

# Stochastic simulation

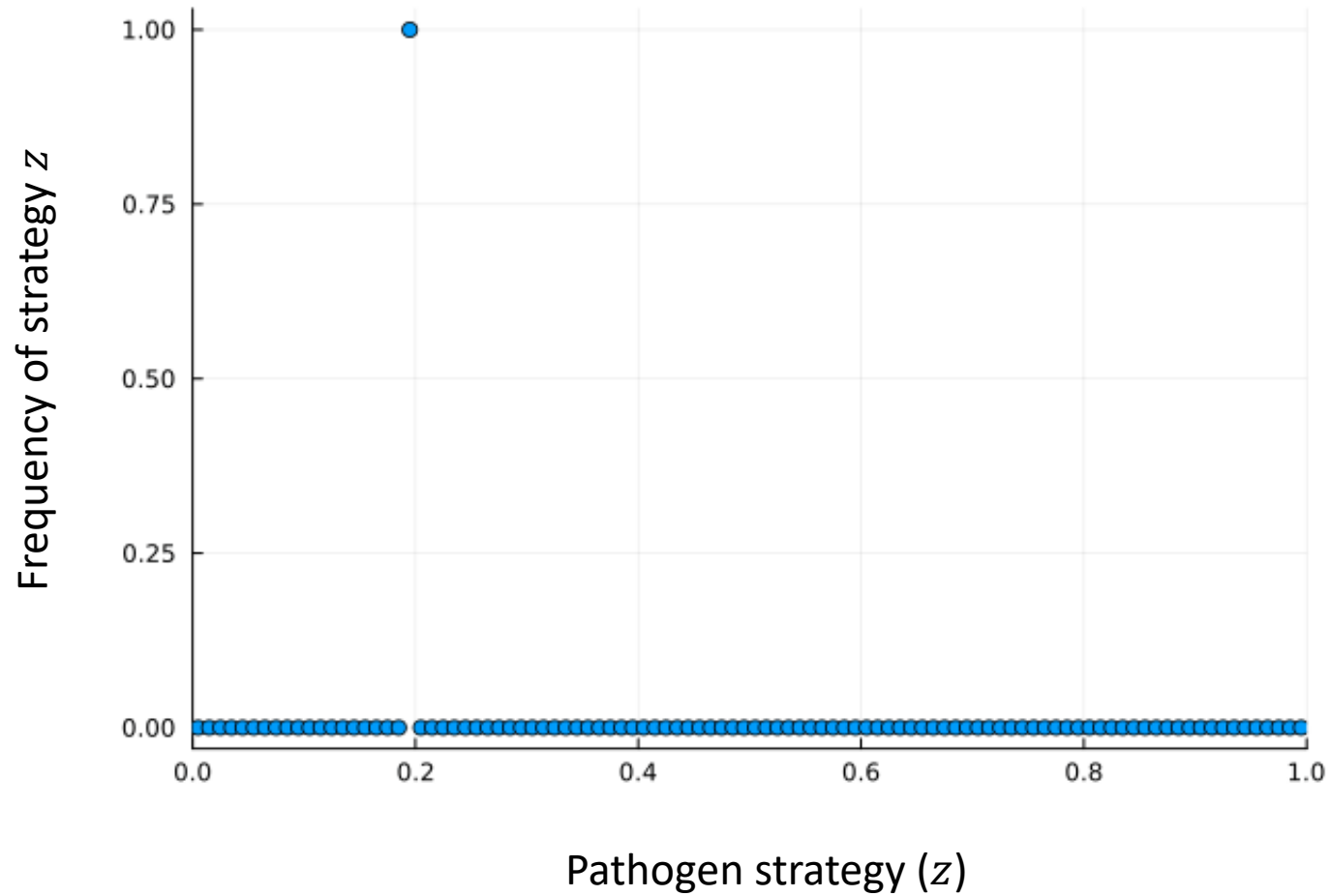
## Example



$S_A$  ———  
 $I_A$  —◆—  
 $S_B$  ———  
 $I_B$  —◆—  
 $S_C$  ———  
 $I_C$  —◆—

# Stochastic simulation

## Example



# Future work



**UNIVERSITÄT  
HEIDELBERG**  
ZUKUNFT  
SEIT 1386

- Phylogenetic tree mapping
- Analyze and simulate how contact network structure and change influence pathogen evolution
- How will biodiversity influence evolution?