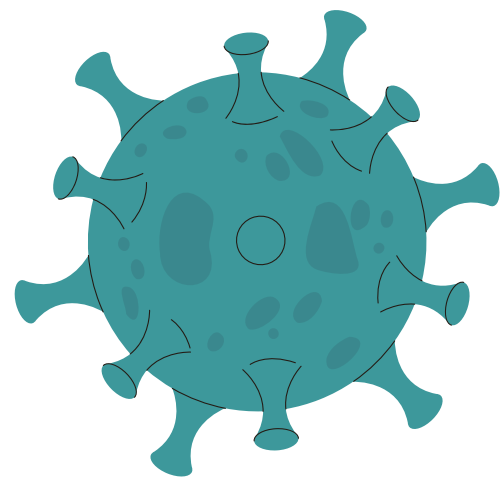


Effect of infection-dependent dispersal on the evolution of parasite virulence in metapopulation epidemiological models

Grégoire Azé
10/03/2023



CGIM Team & FEEDME project



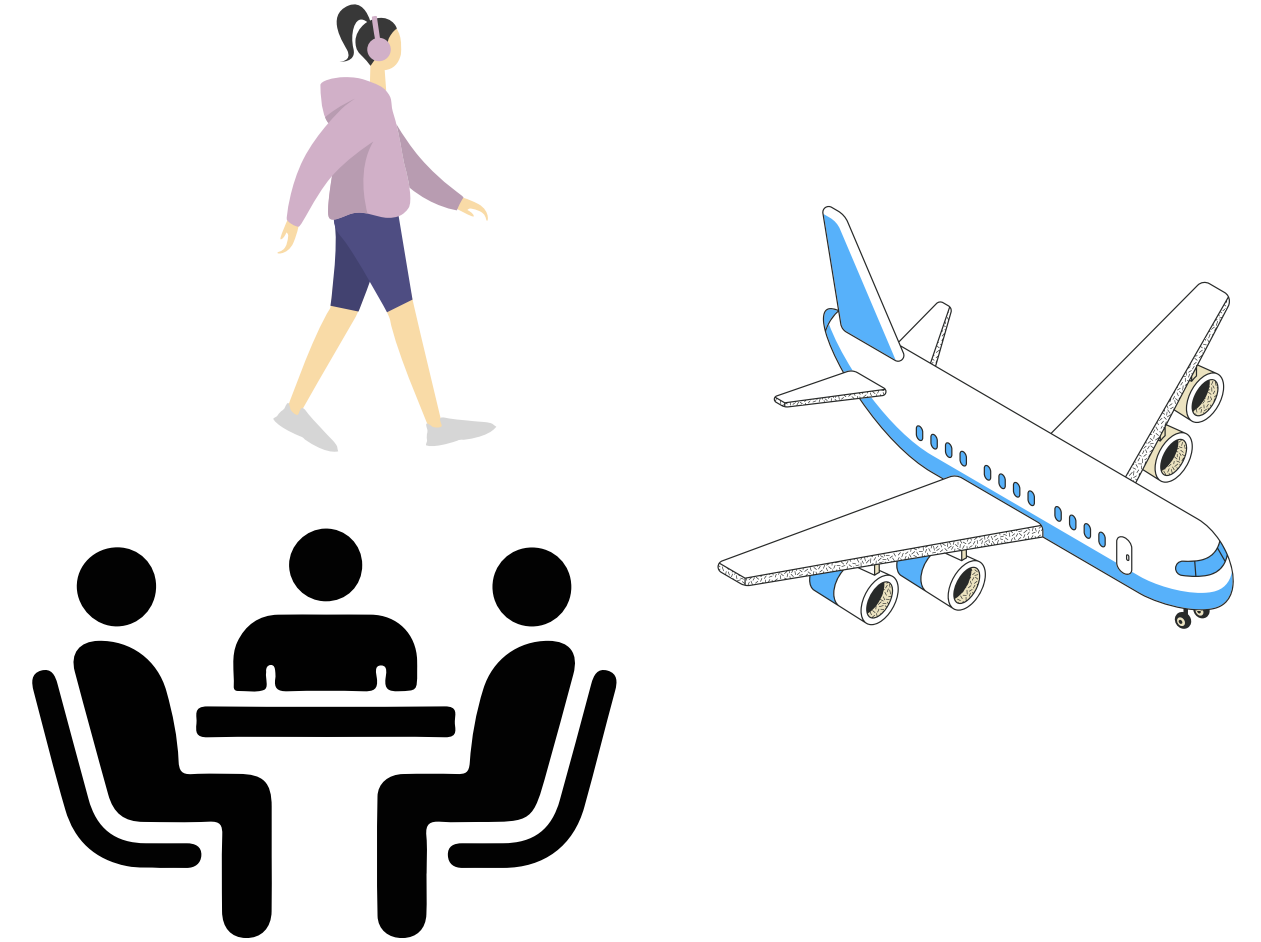
Université
de Rennes



Introduction

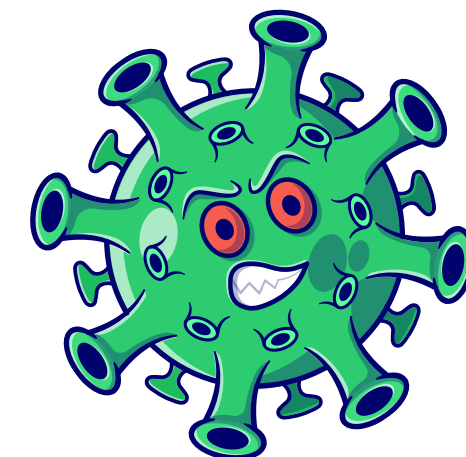
Dispersion of individuals

- Moving in space
- Contact with other individuals



Disease caused by a pathogen (Bacteria, parasite, ...)

- Contact transmission
- Virulence = Mortality of pathogen



Introduction

Dispersion dependent on the epidemiological status of the individual

Good health



+++ Dispersion

Infected



--- Dispersion

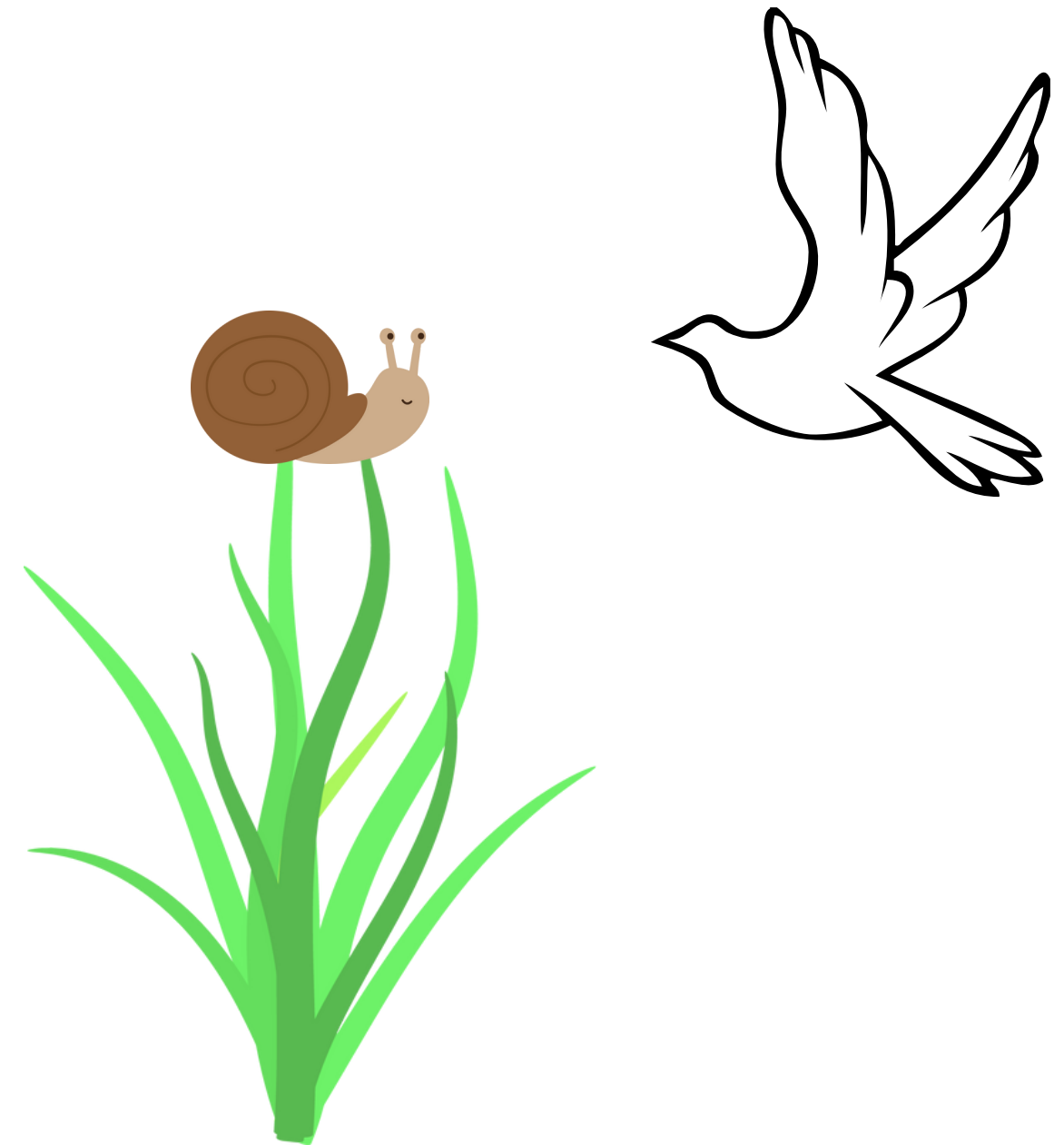
Introduction

Dispersion dependent on the epidemiological status of the individual



Snail + *Leucochloridium paradoxum*

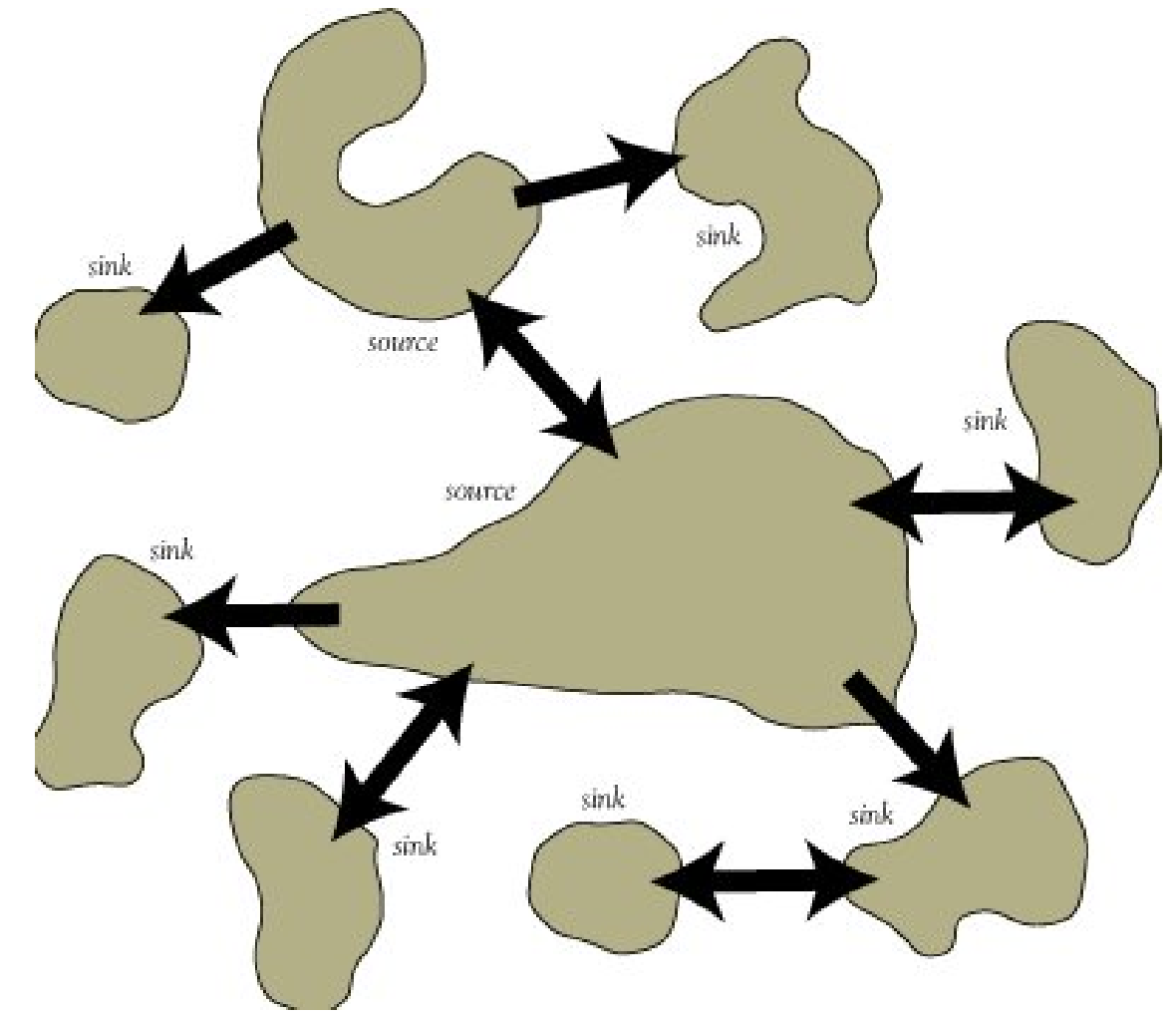
→
+++ Dispersion



Introduction

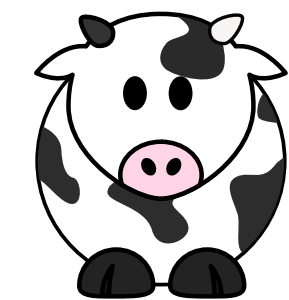
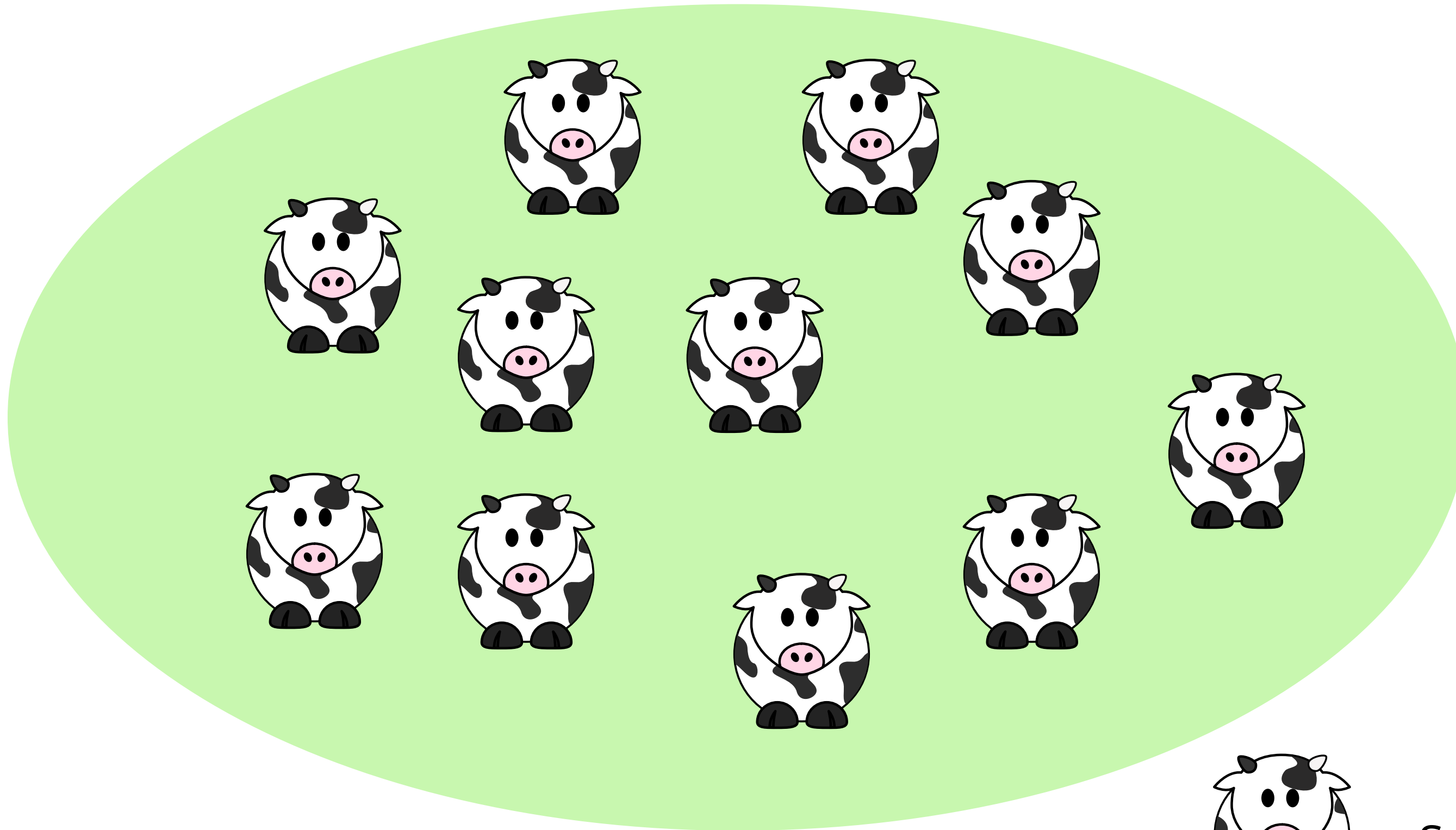
Metapopulation

- Set of populations of individuals
- Spatially separated
- Connected with dispersion / migration
- Local dynamics for each patch
- Global dynamics with all patches of the metapopulation



Model

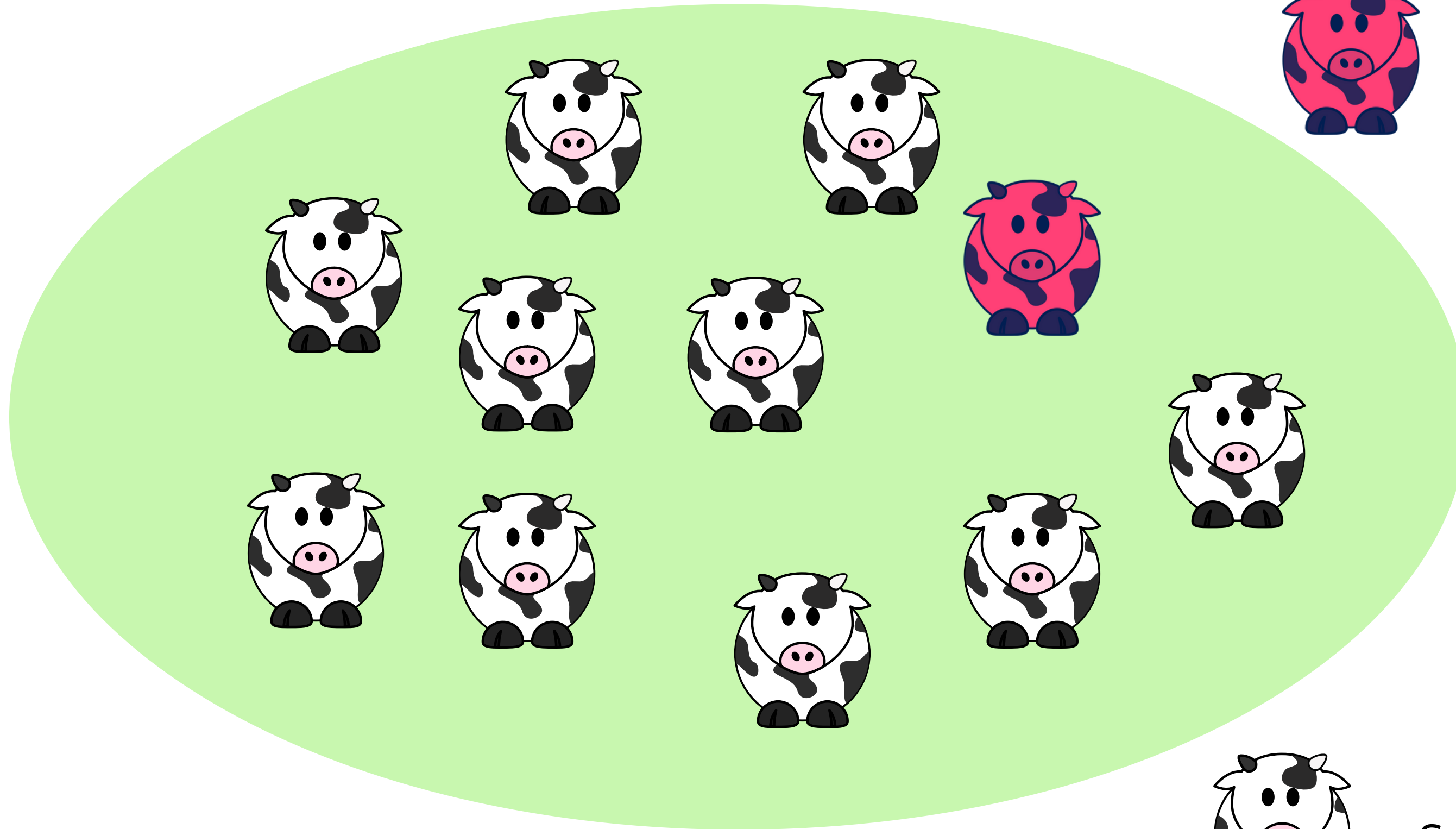
Local Dynamics



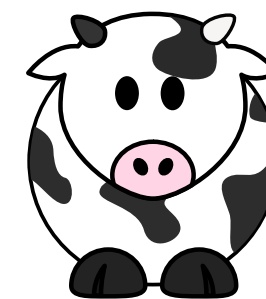
= Susceptible individuals

Model

Local Dynamics



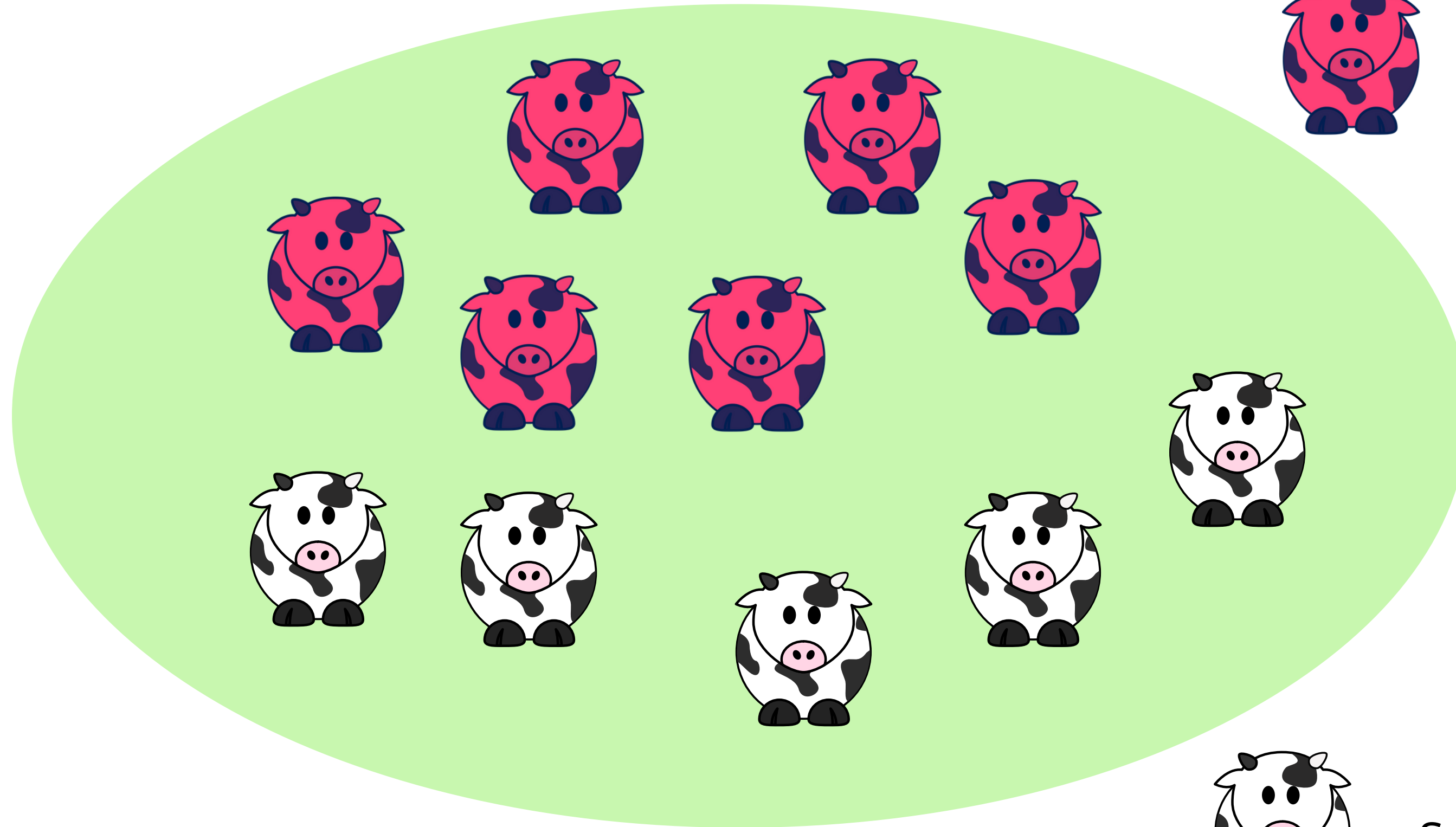
= Infected individuals



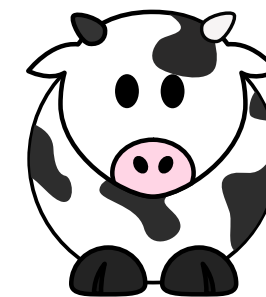
= Susceptible individuals

Model

Local Dynamics



= Infected individuals





= Susceptible individuals

Model

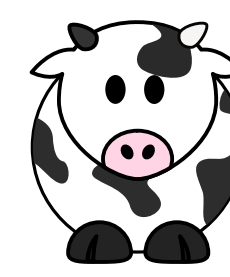

Local Dynamics Equilibrium

 = 0  = 0

- Empty patch

 = S^*  = 0

- Only susceptible individuals
- "Disease-free equilibrium"

 = S^o  = S^o

- Fraction of susceptible and infected hosts constant
- "Endemic equilibrium"

Model

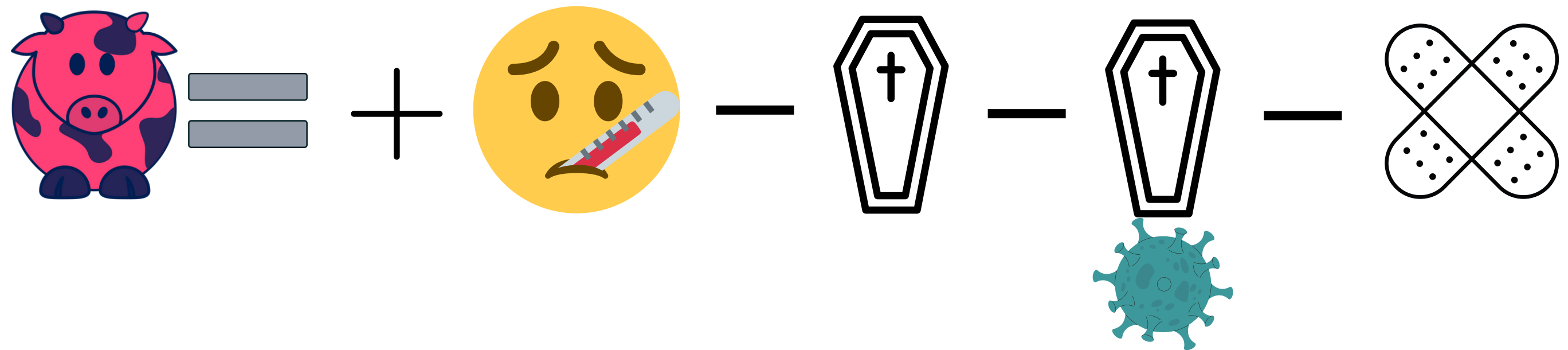
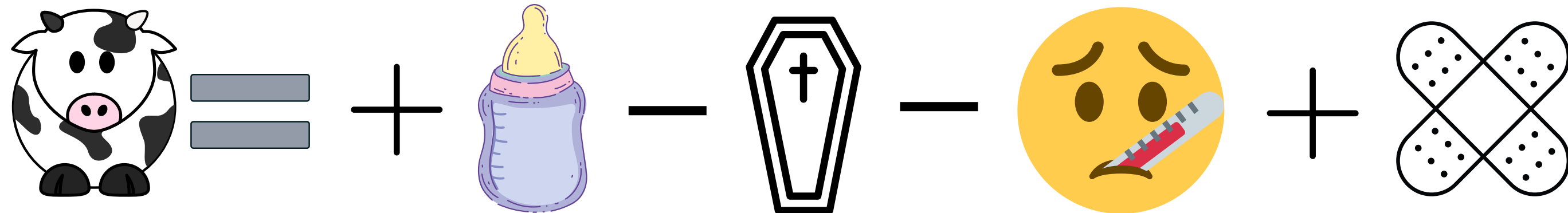
Local Dynamics

$$\frac{dS_i}{dt} = rS(1 - (S + I)/k) - \beta SI - dS + \gamma I$$

$$\frac{dI_i}{dt} = \beta SI - dI - \gamma I - \alpha I - \mu I$$

Model

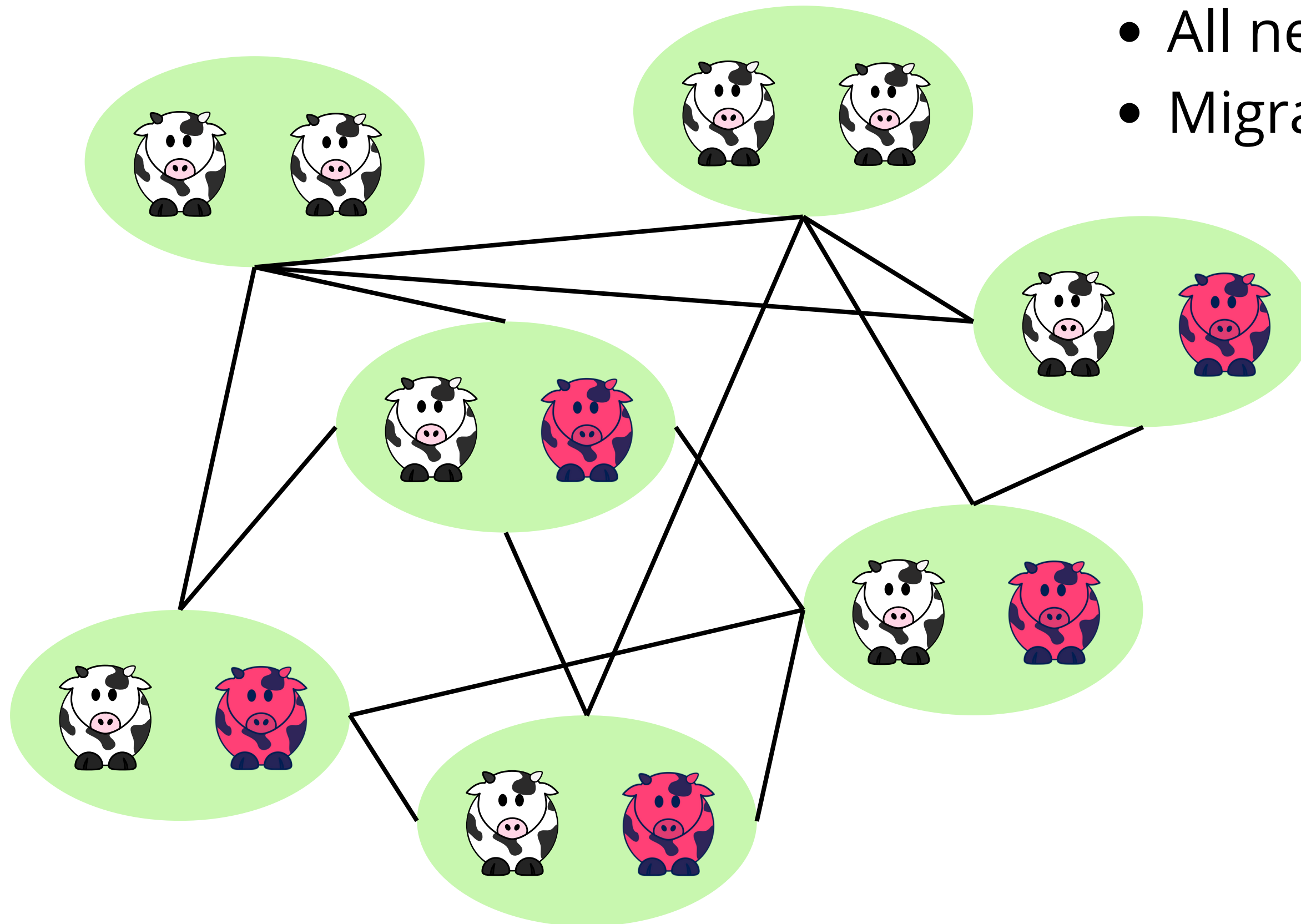
Local Dynamics



Model

Metapopulation :

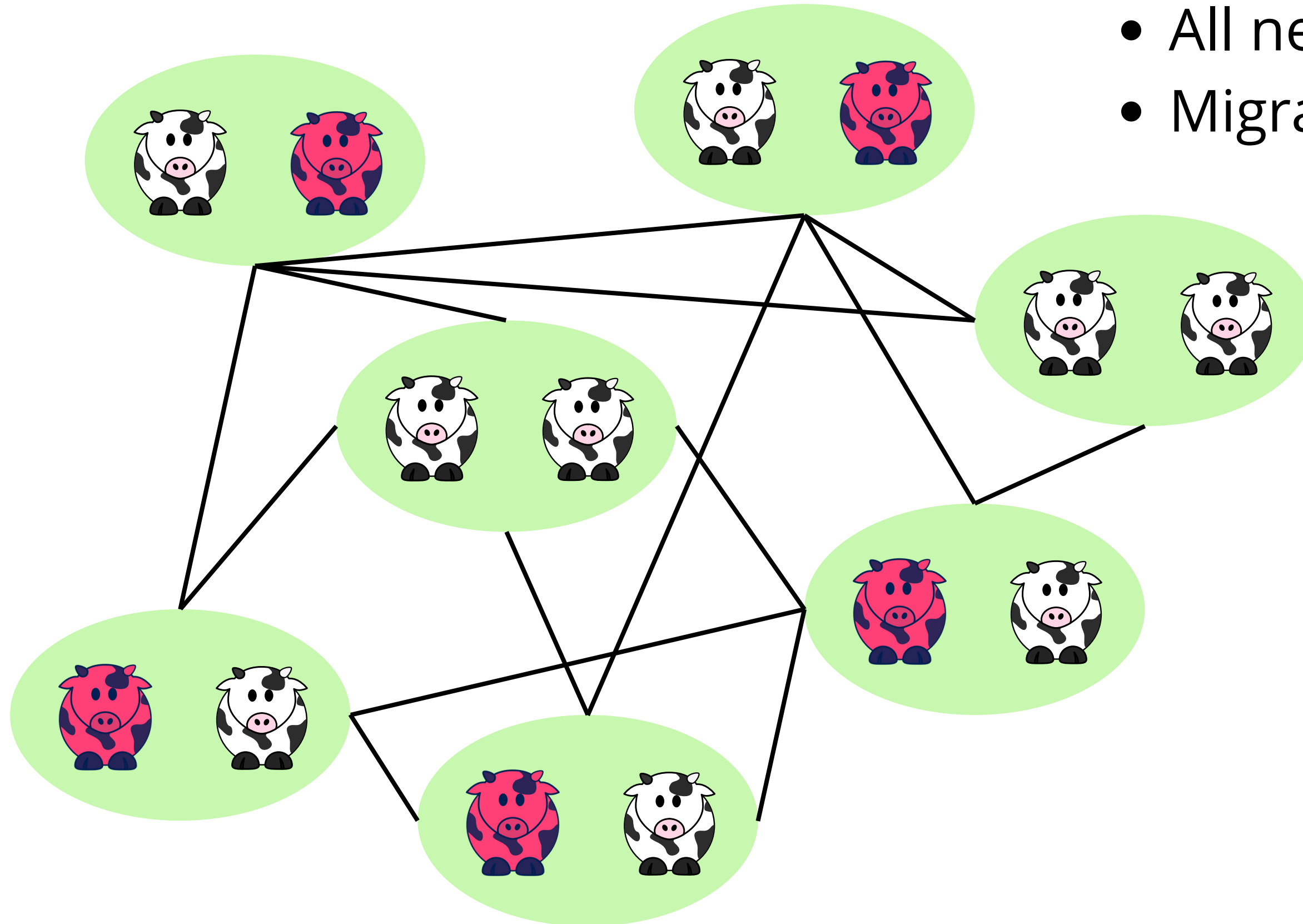
- All neighbors
- Migration between patches



Model

Metapopulation :

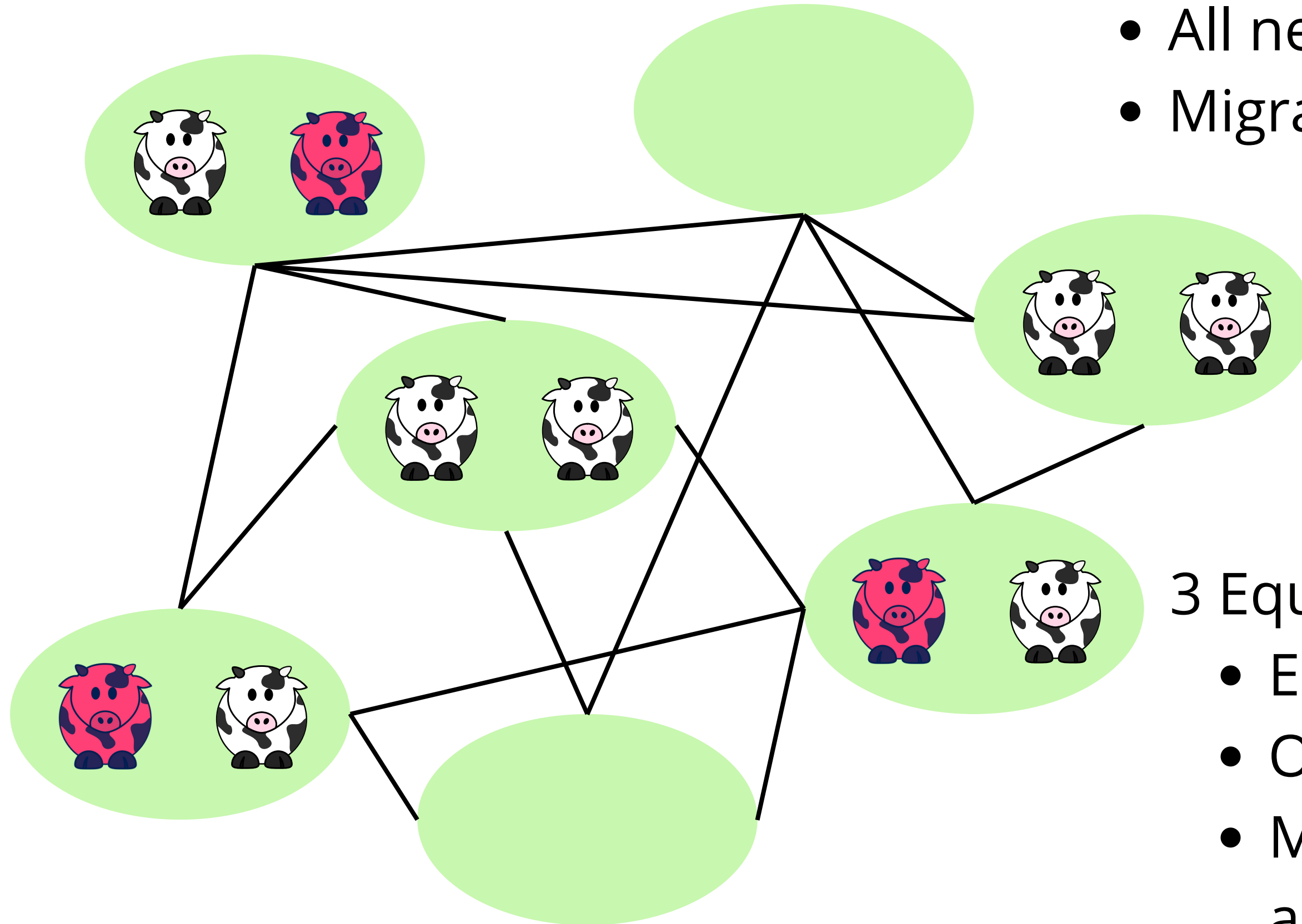
- All neighbors
- Migration between patches



Model

Metapopulation :

- All neighbors
- Migration between patches



3 Equilibrium :

- Empty patch
- Only susceptibles
- Mix between susceptible and infected

Model

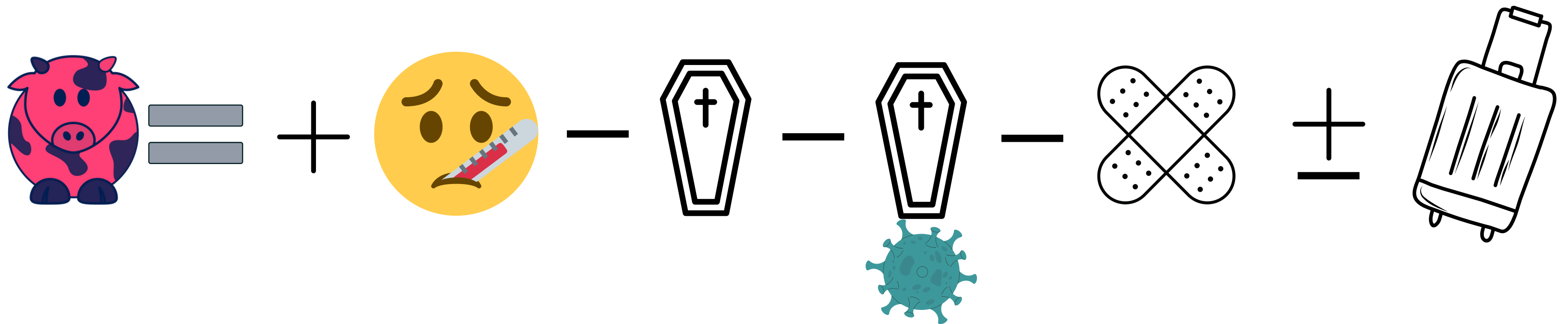
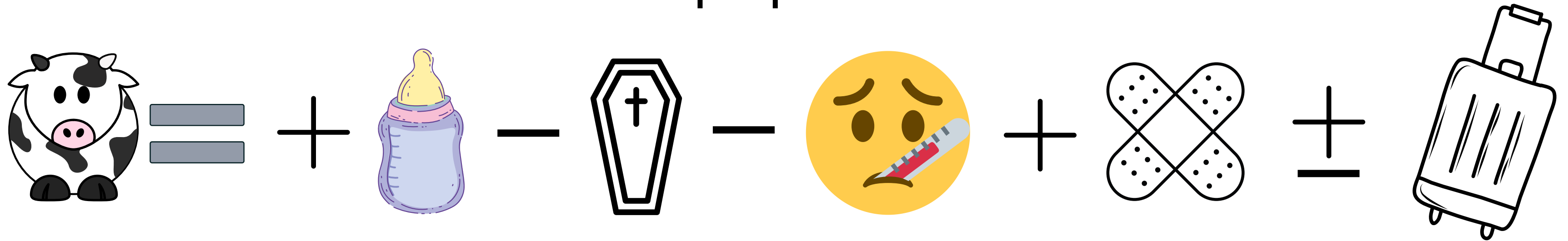
Local Dynamics in a metapopulation

$$\frac{dS_i}{dt} = r S (1 - (S + I)/k) - \beta S I - d S + \gamma I + \sum_{j=1}^z d (1 - \rho) S_j / k$$

$$\frac{dI_i}{dt} = + \beta S I - d I - \gamma I + \sum_{j=1}^z d (1 - \rho) I_j / k - \alpha I$$

Model

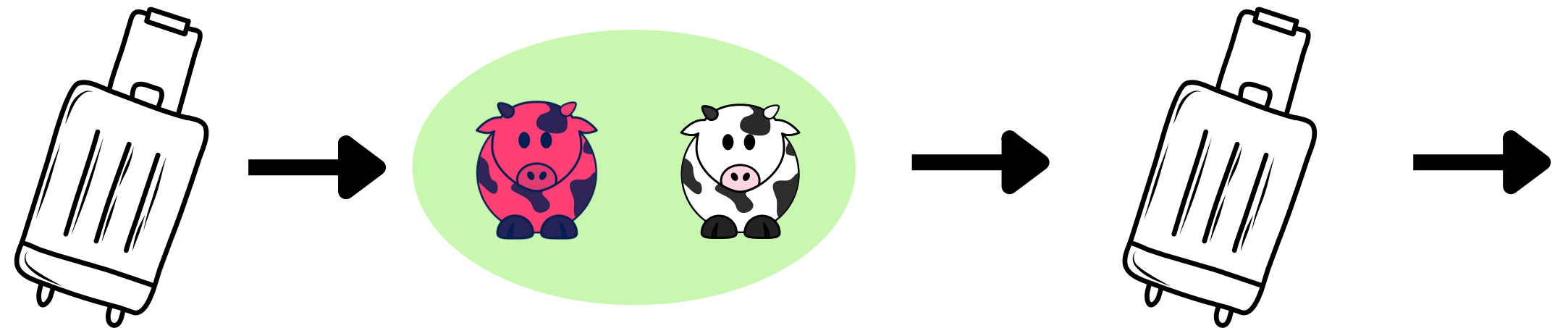
Local Dynamics in a metapopulation



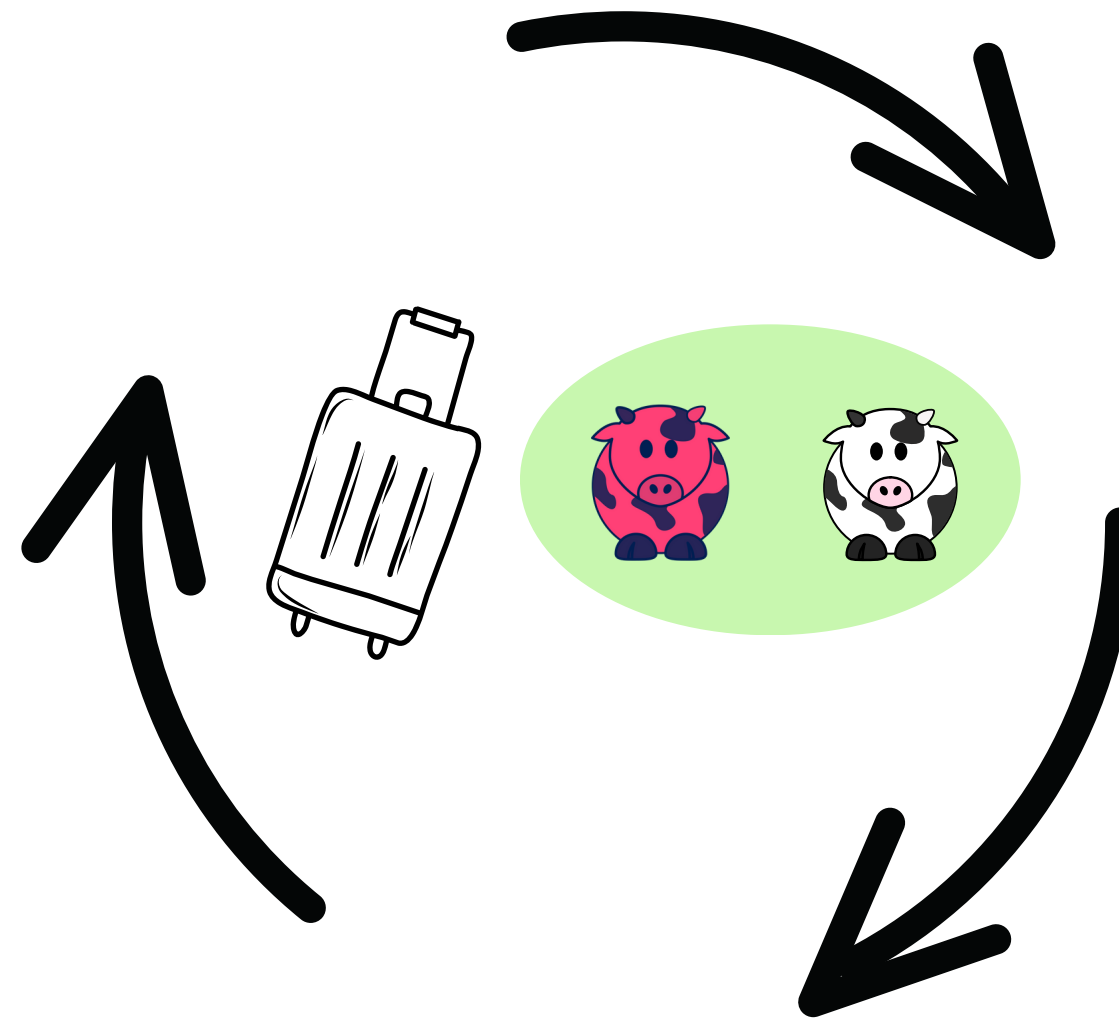
Model

Separation of time scales

Mathematical model



Simulation



Model

Distinction between dispersion of susceptibles and infected

$$\frac{dS_i}{dt} = rS(1 - (S + I)/k) - \beta SI - d_S S + \gamma I + \sum_{j=1}^k d(1 - \rho)S_j/k$$

$$\frac{dI_i}{dt} = \beta SI - d_I I - \gamma I + \sum_{j=1}^k d(1 - \rho)I_j/k - \alpha I - \mu I$$

$$d_S \neq d_I$$



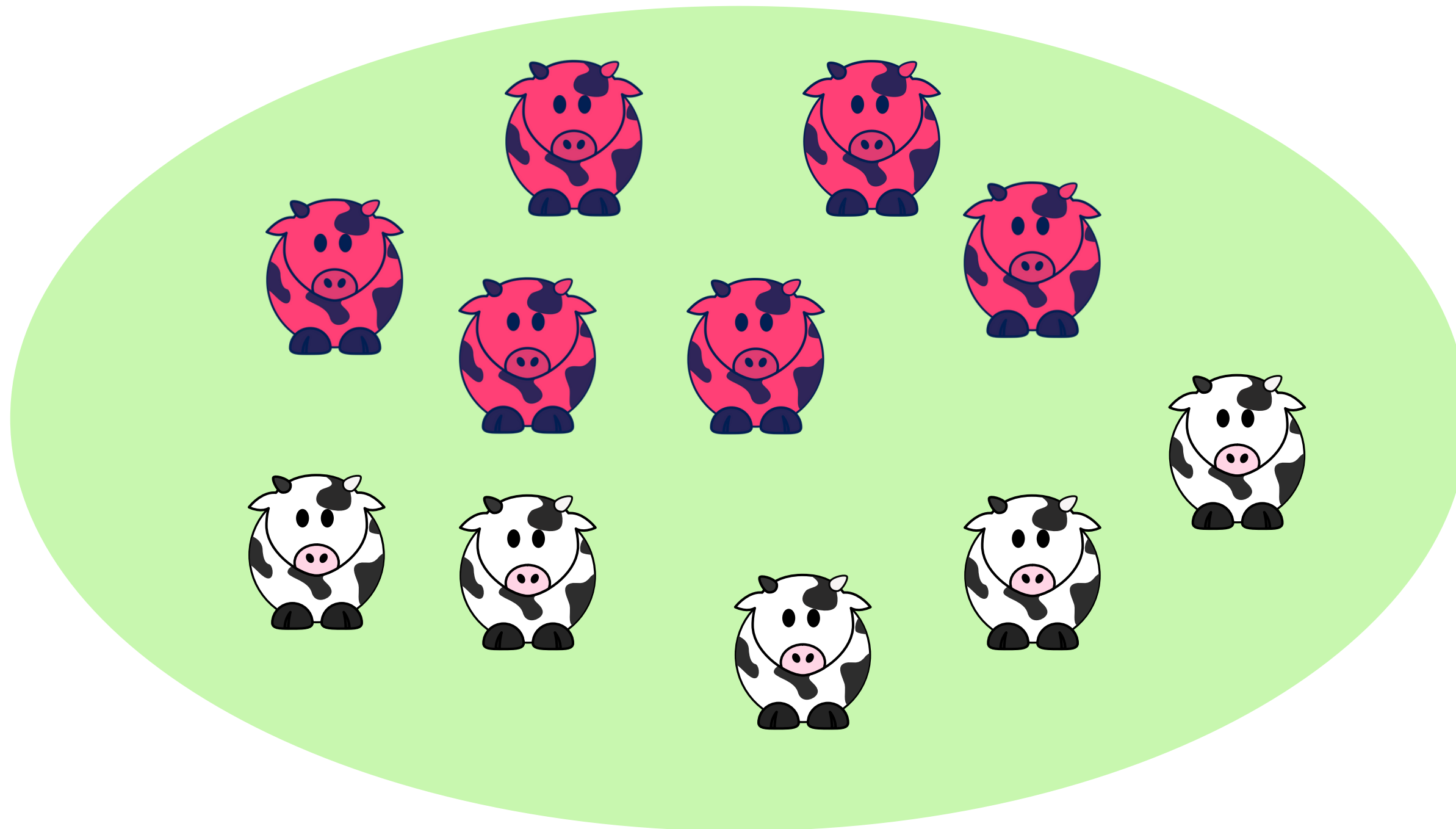
\neq



Model

Evolution of virulence :

- Mortality of the pathogen
- Noté α



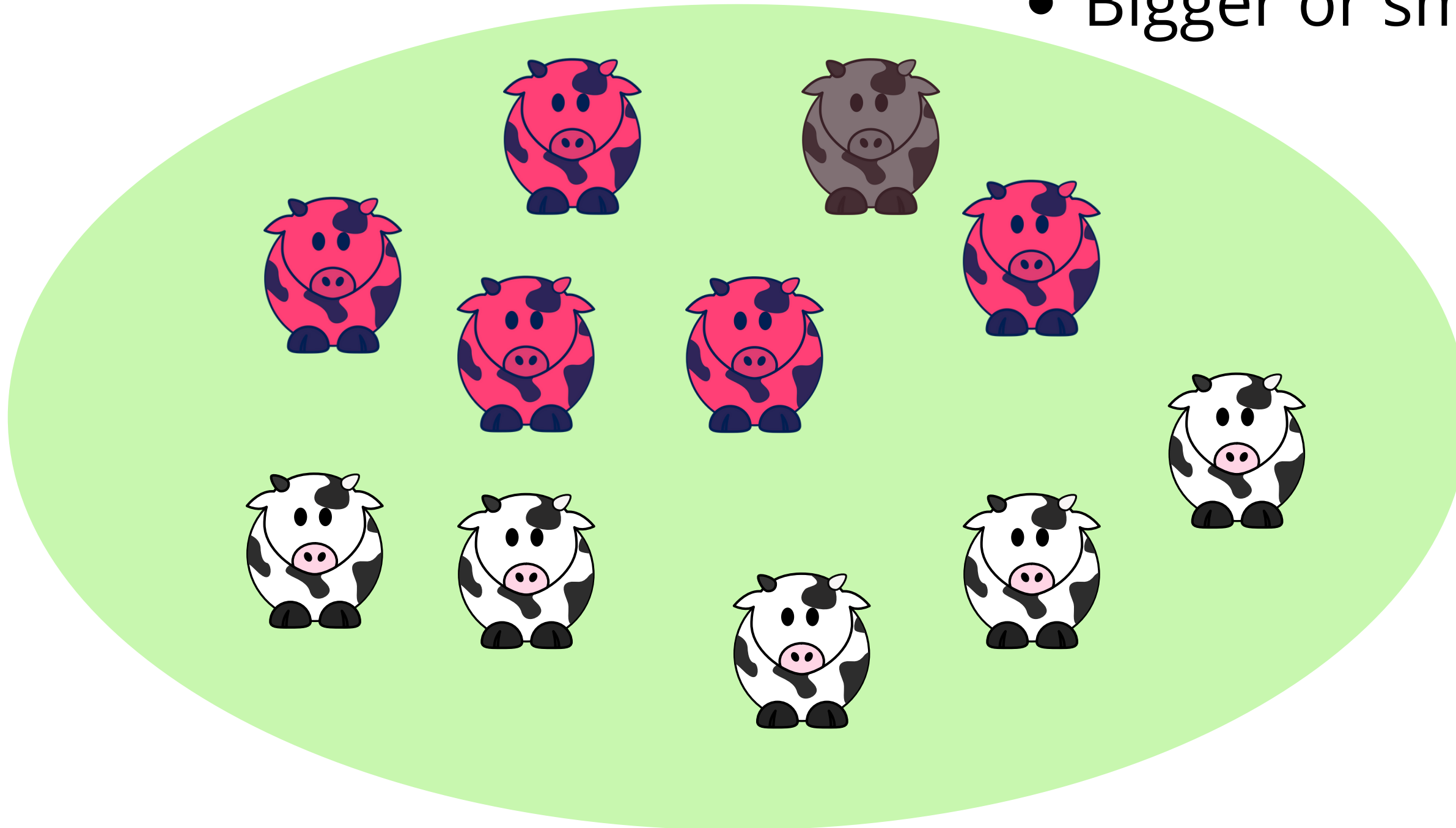
Model

Evolution of virulence :

- Mortality of the pathogen
- Noté α

Mutant :

- Small difference in the virulence value
- Bigger or smaller



Model

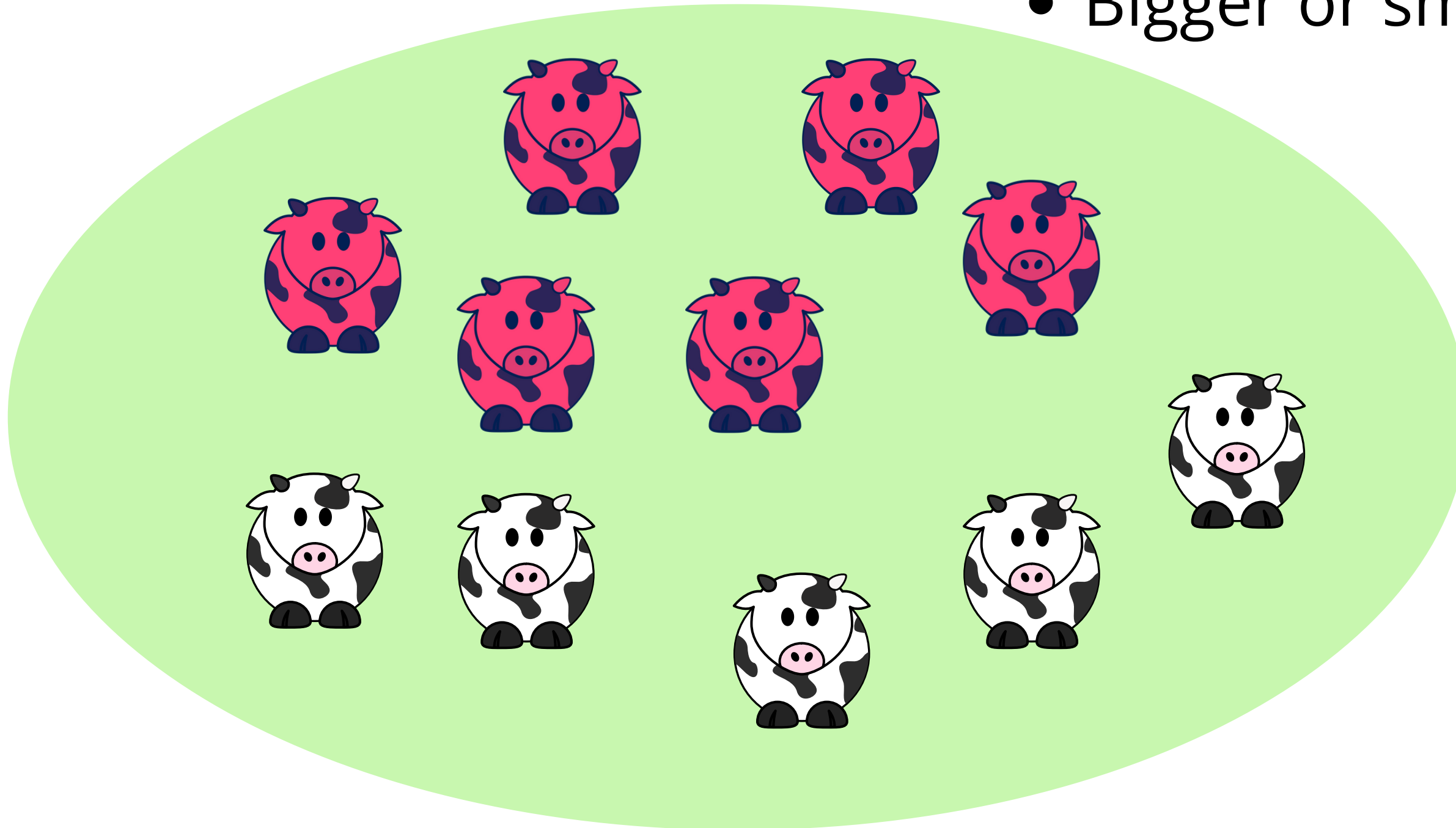
Evolution of virulence :

- Mortality of the pathogen
- Noté α

Mutant :

- Small difference in the virulence value
- Bigger or smaller

Resident
>
Mutant



Dominant
phenotype :



Model

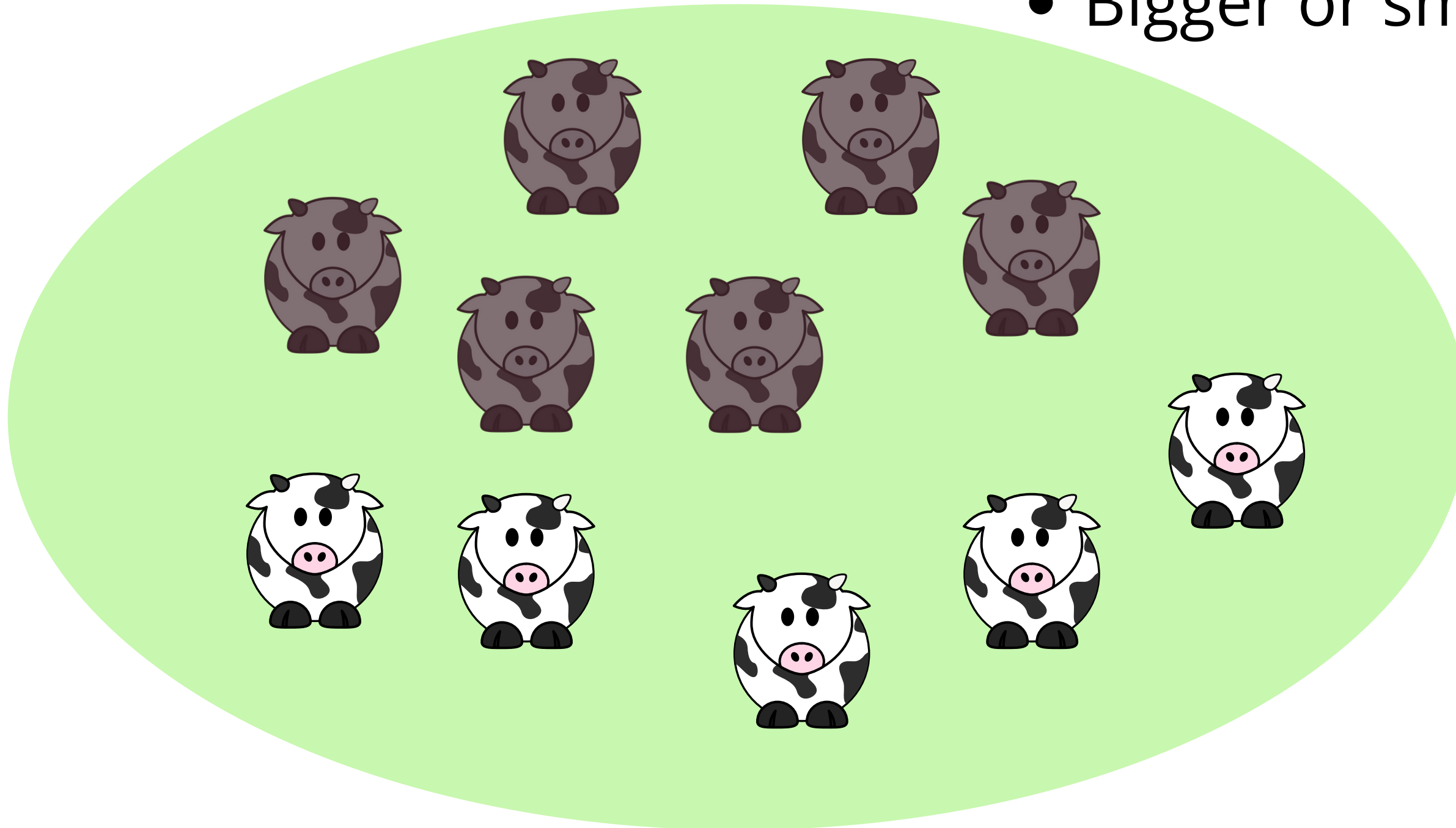
Evolution of virulence :

- Mortality of the pathogen
- Noté α

Mutant :

- Small difference in the virulence value
- Bigger or smaller

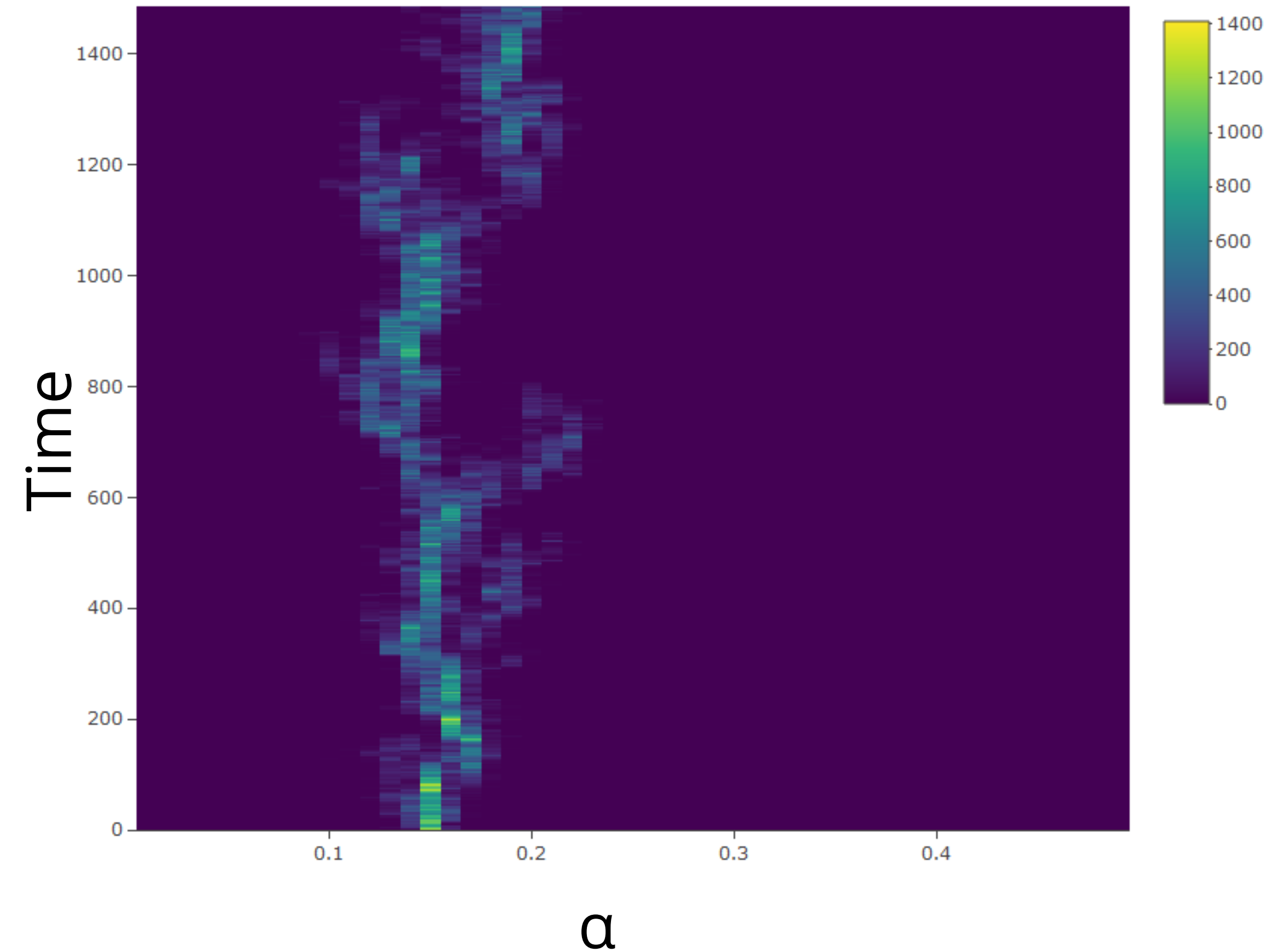
Mutant
>
Resident



Dominant
phenotype :



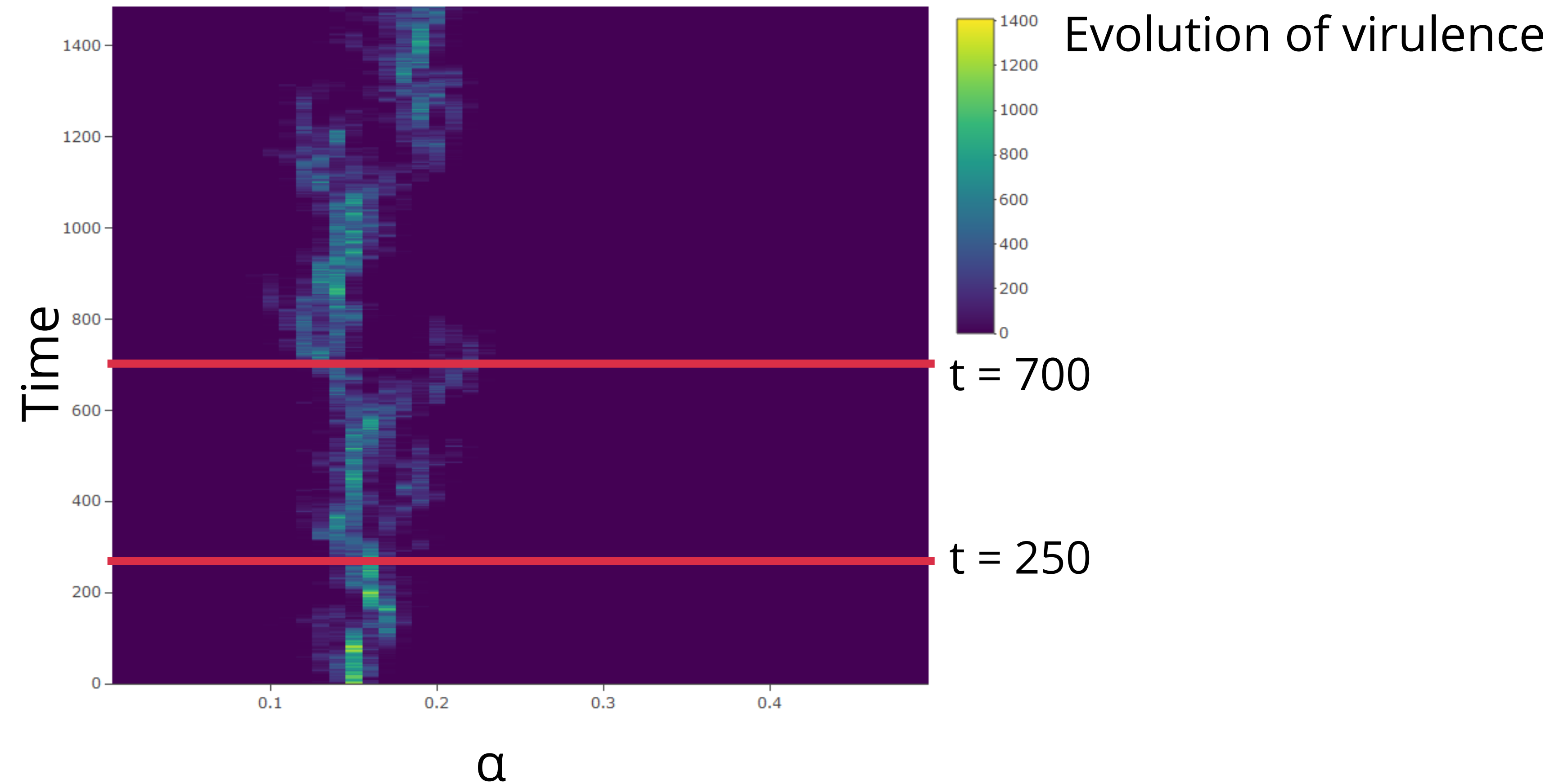
Results



Evolution of virulence :

- Evolutionary branching
- 2 phenotypes can evolve at the same time

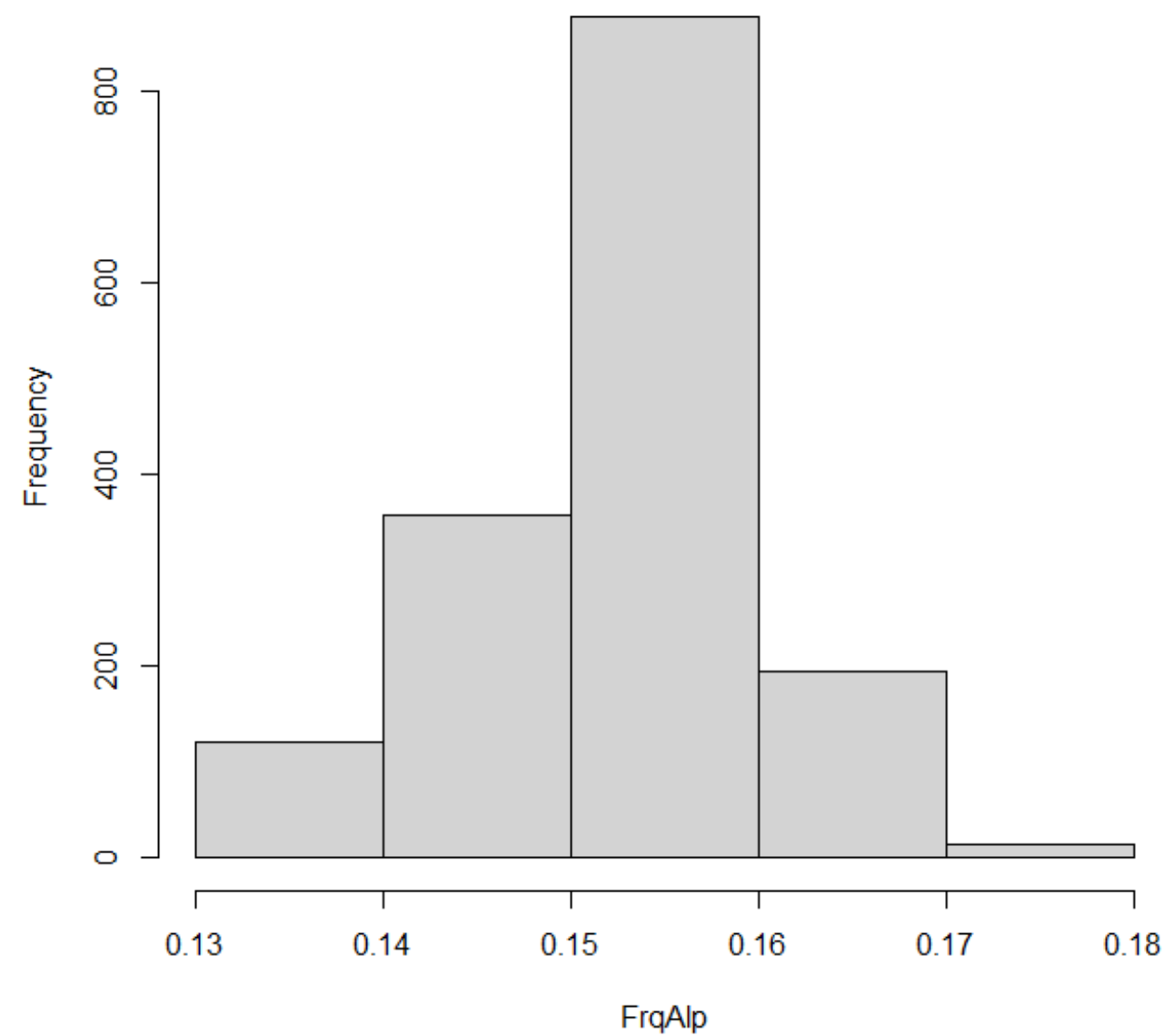
Results



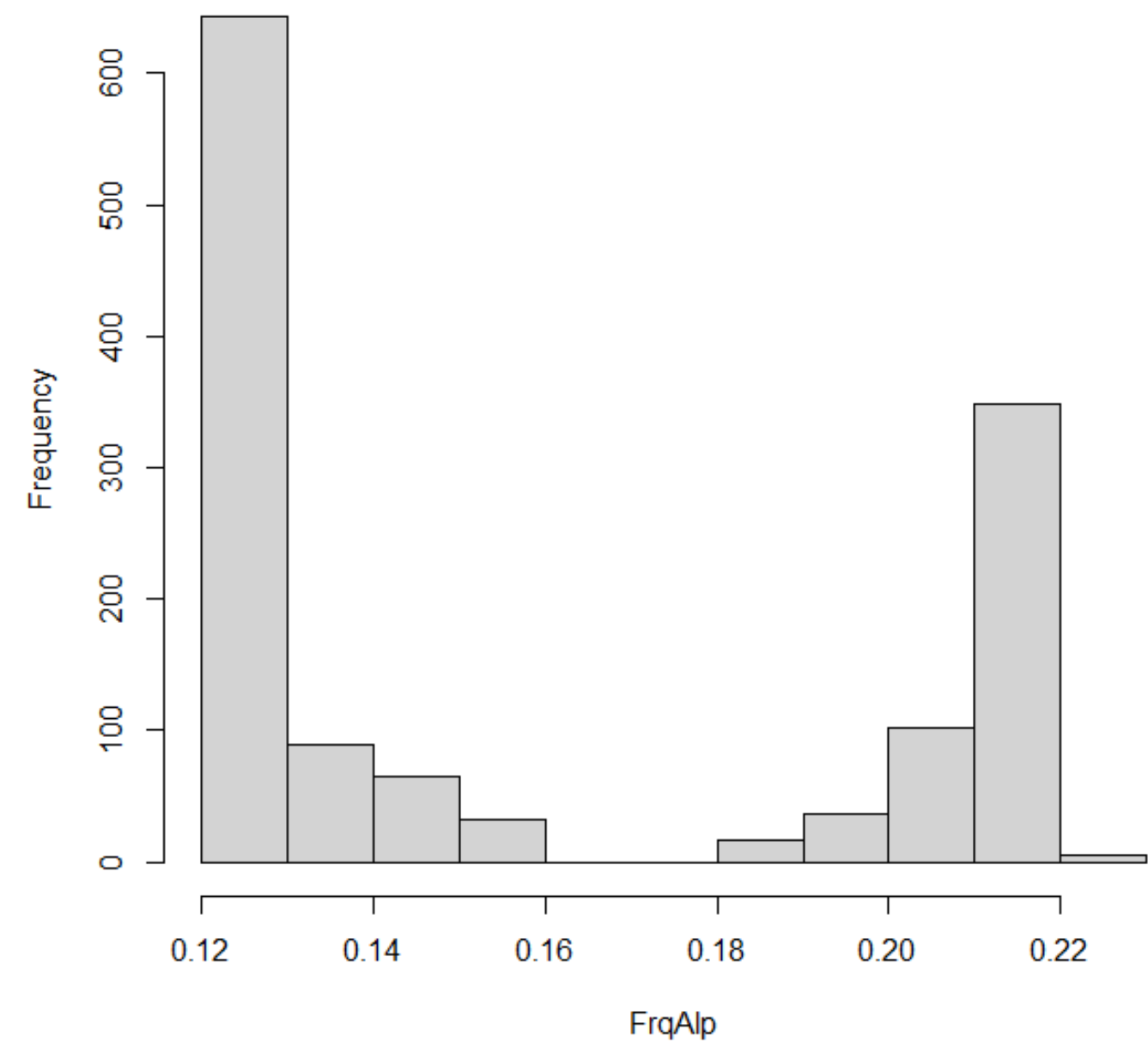
Results

Evolutionnary branching

t = 250



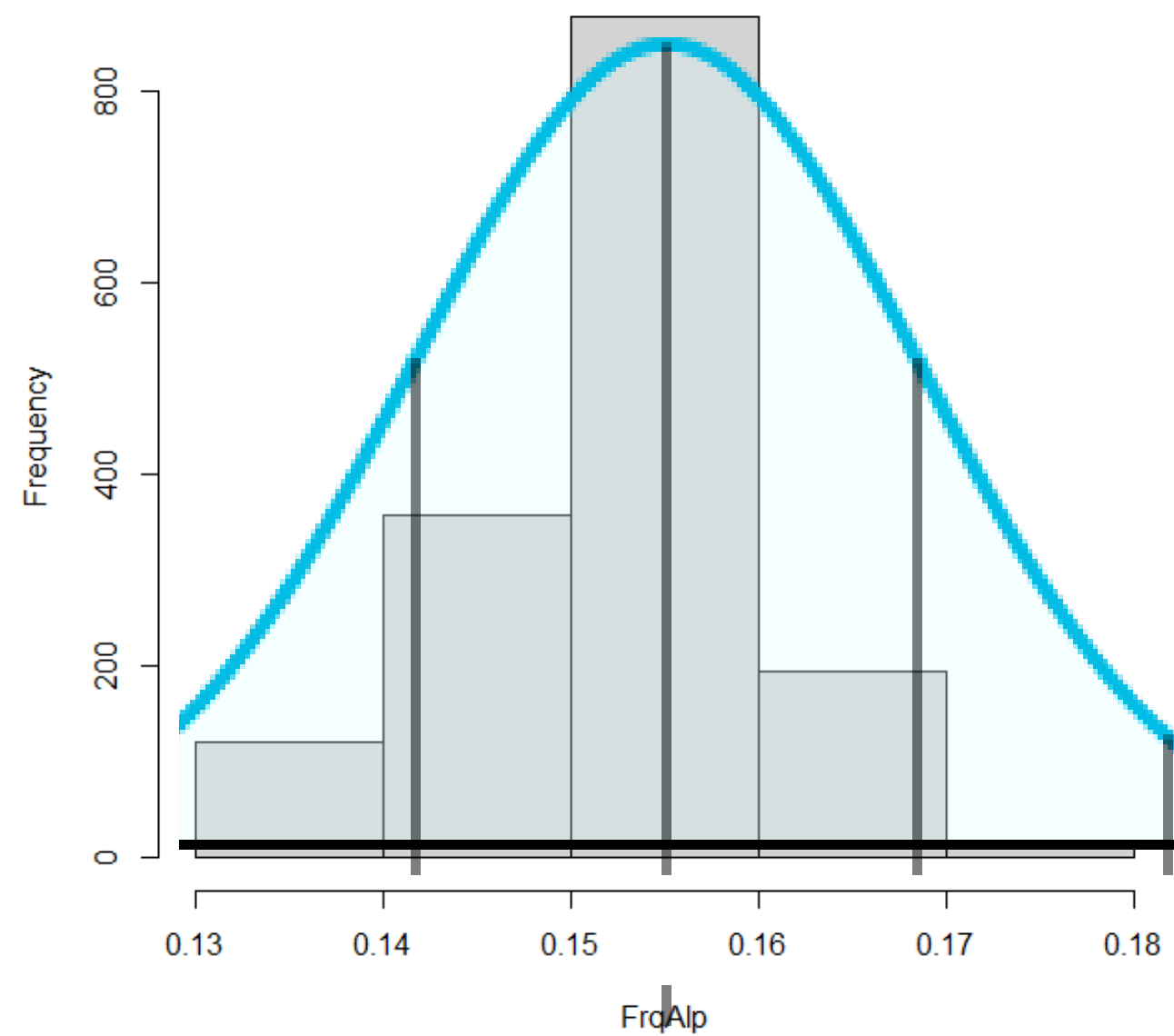
t = 700



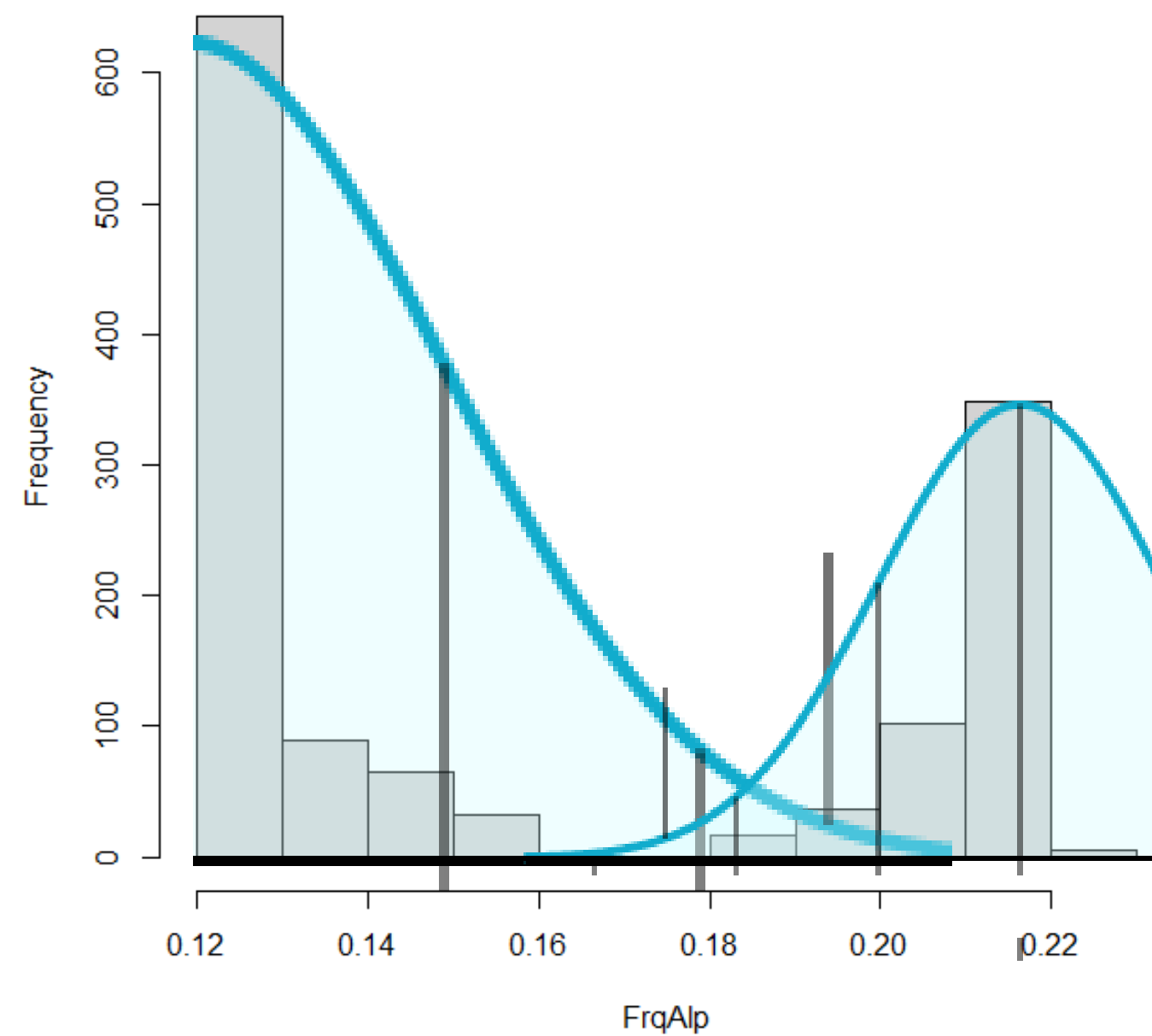
Results

Evolutionary branching

$t = 250$

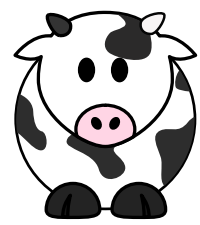


$t = 700$



Results

Evolution of virulence according to the infected dispersal



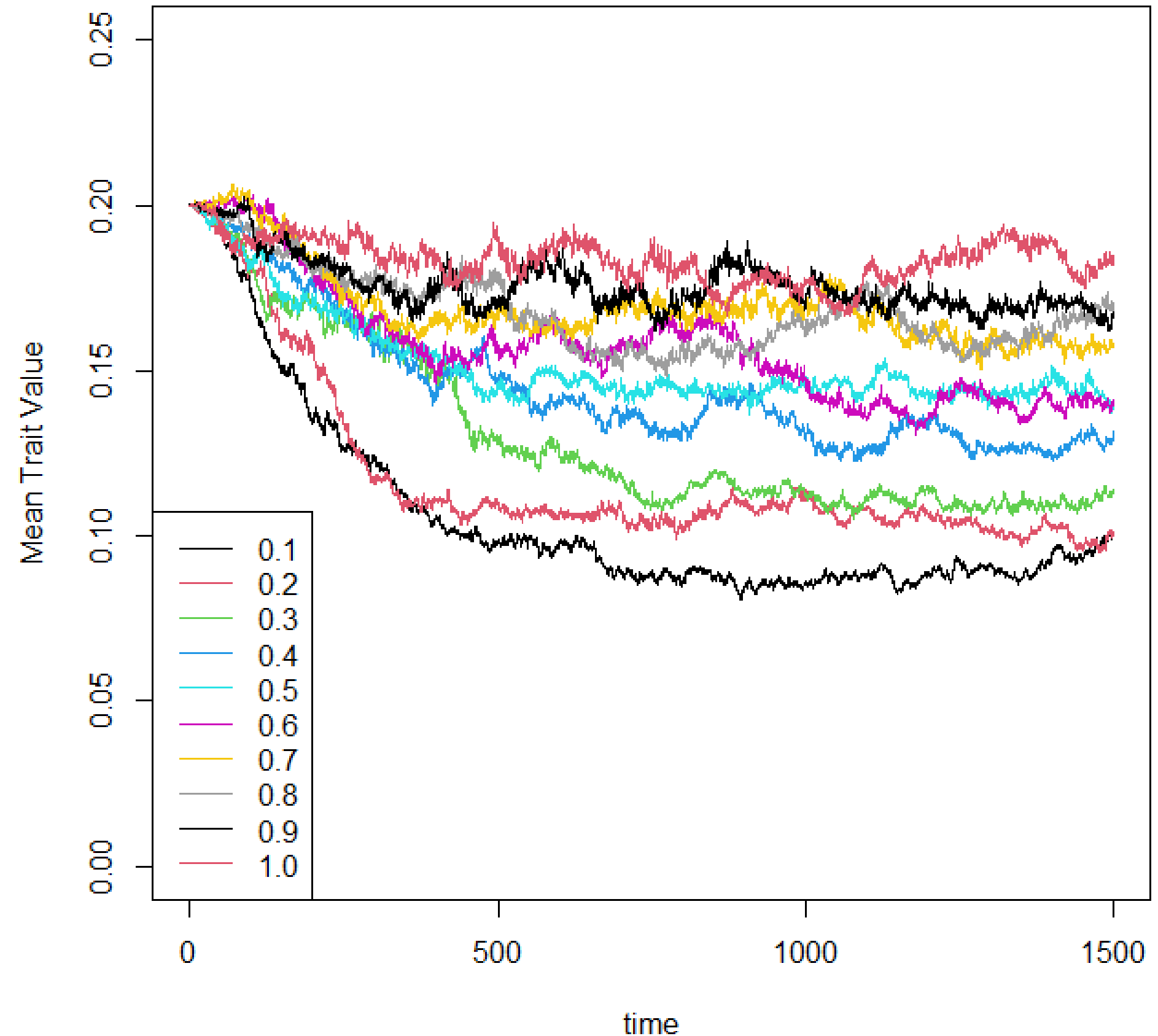
Dispersal value of susceptible hosts

- Fixed at 0.5



Dispersal value of infected hosts

- 0.1 to 1.0

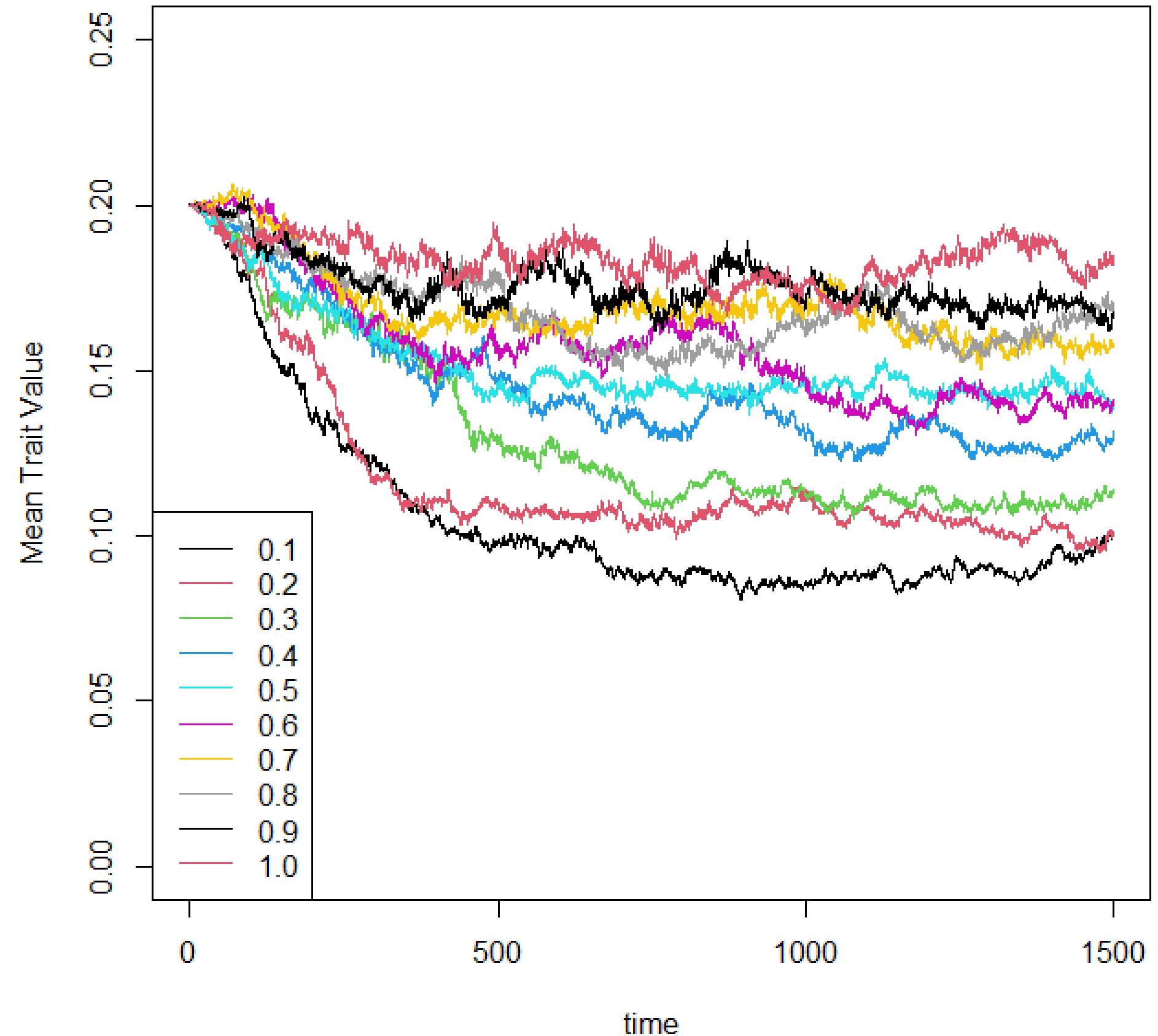


Results

Evolution of virulence according to the infected dispersal

Increase of infected hosts dispersal
➡ Increase of virulence

Increase of infected hosts dispersal
➡ More chance of finding patches with many susceptible hosts

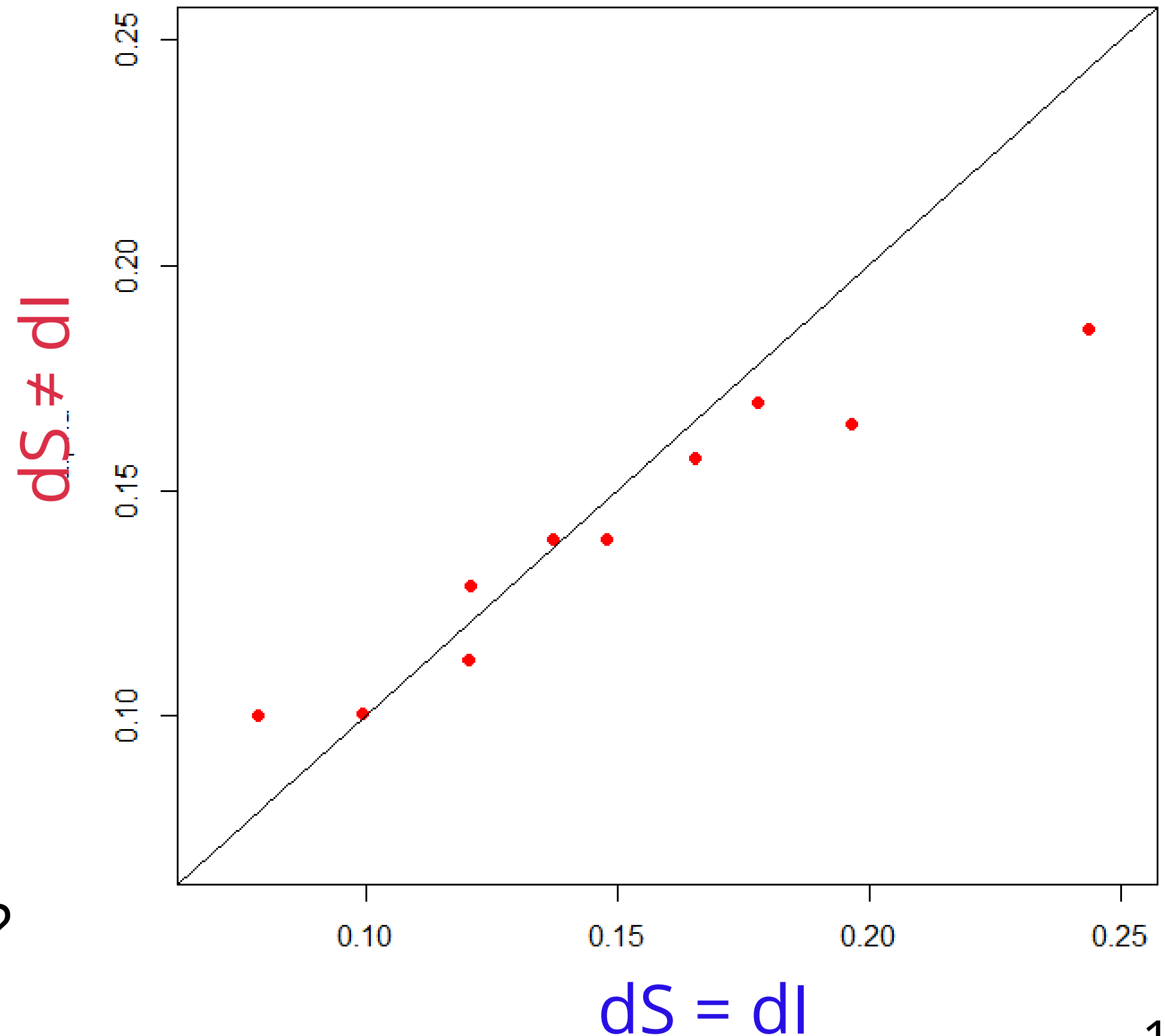


Results

Distinguishing dispersions :
Is it worth it ?

Virulence values compare
between :

- Model with $d = dS = dI$
- Model with $dS \neq dI$



➔ Does it affect the virulence ?

Results

Distinguishing dispersions :
Is it worth it ?

- $d = dS = dI = 1.0$

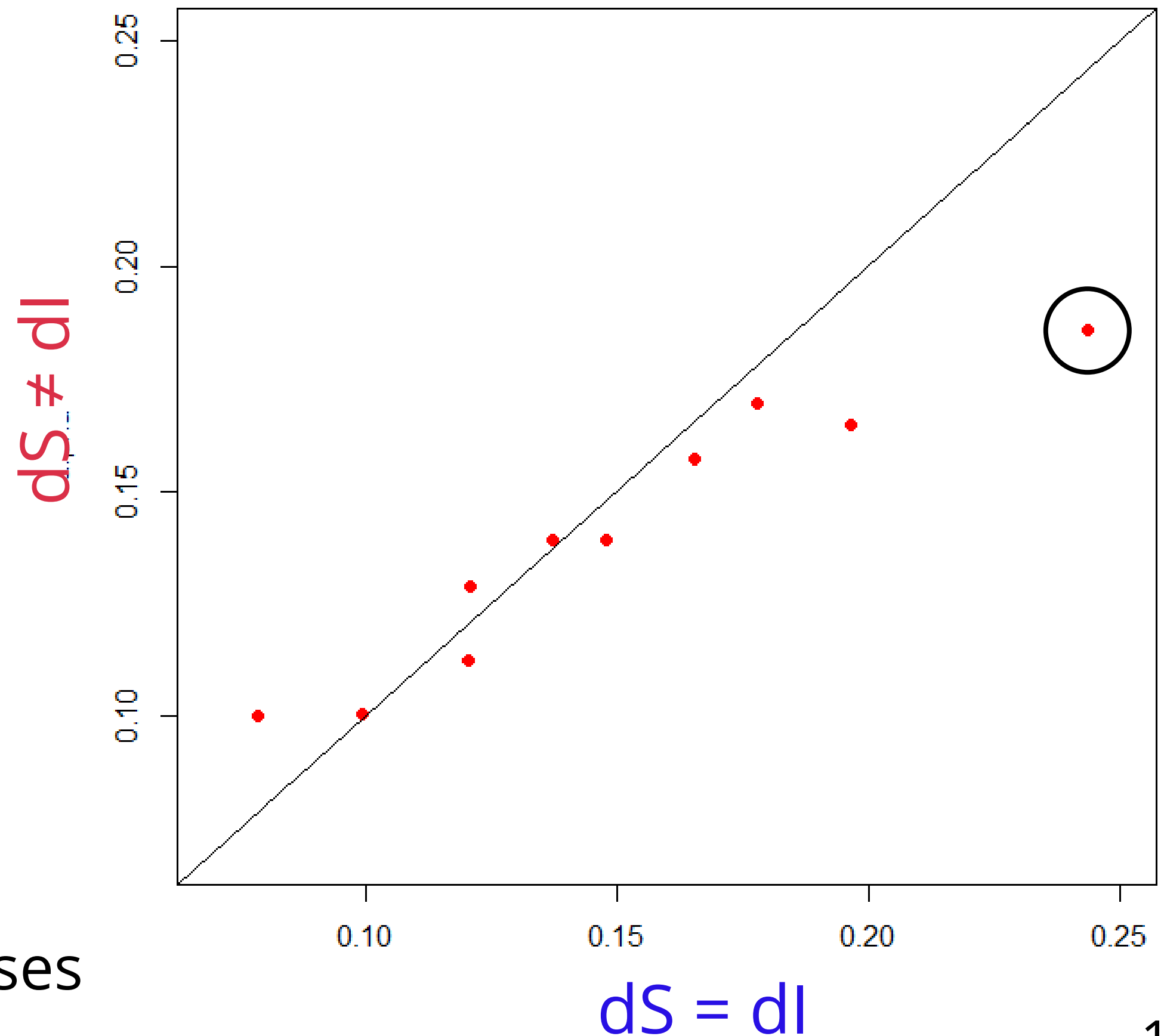
→ $\alpha = 0.25$

- $dS = 0.5$ et $dI = 1.0$

→ $\alpha = 0.18$

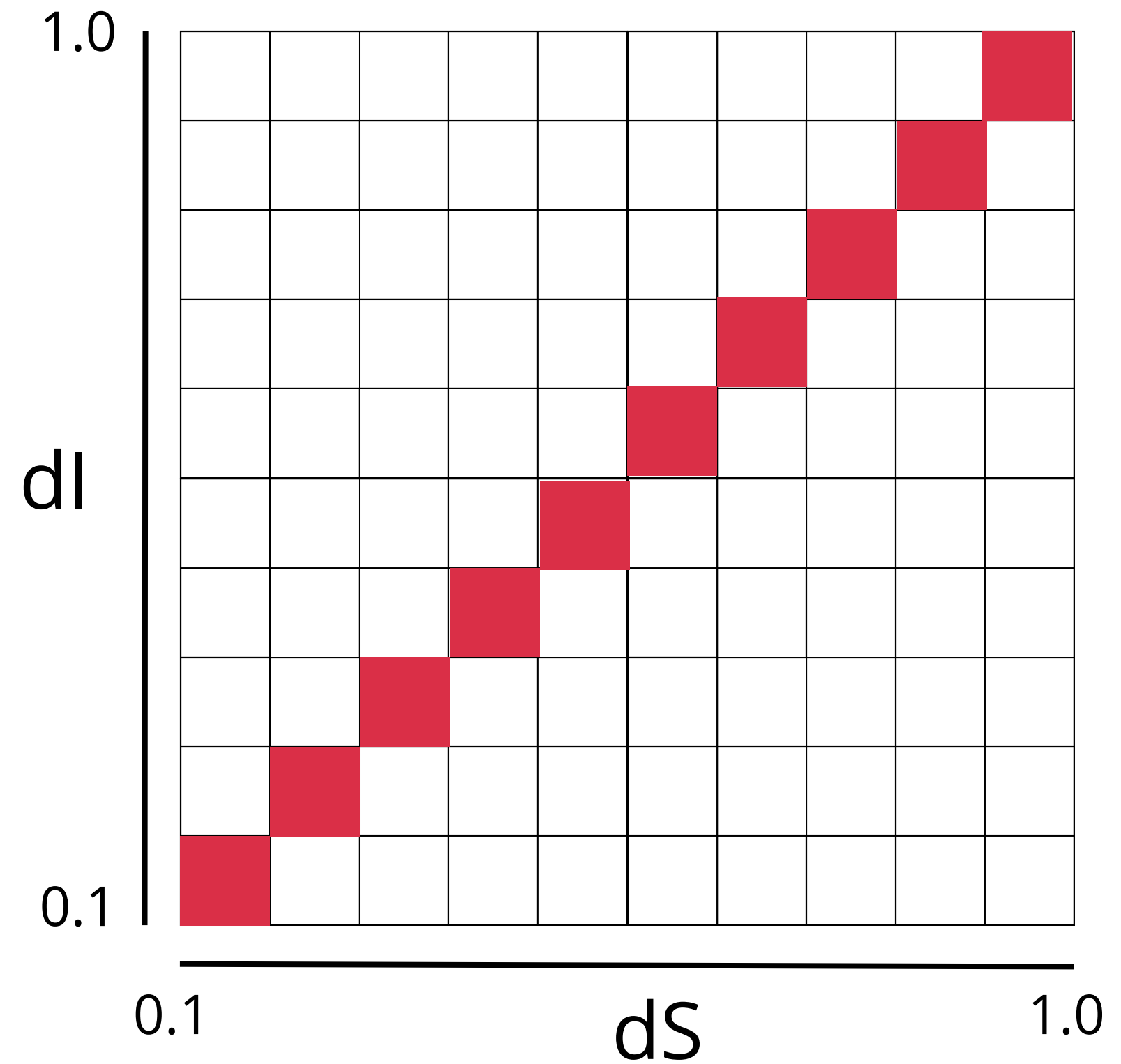
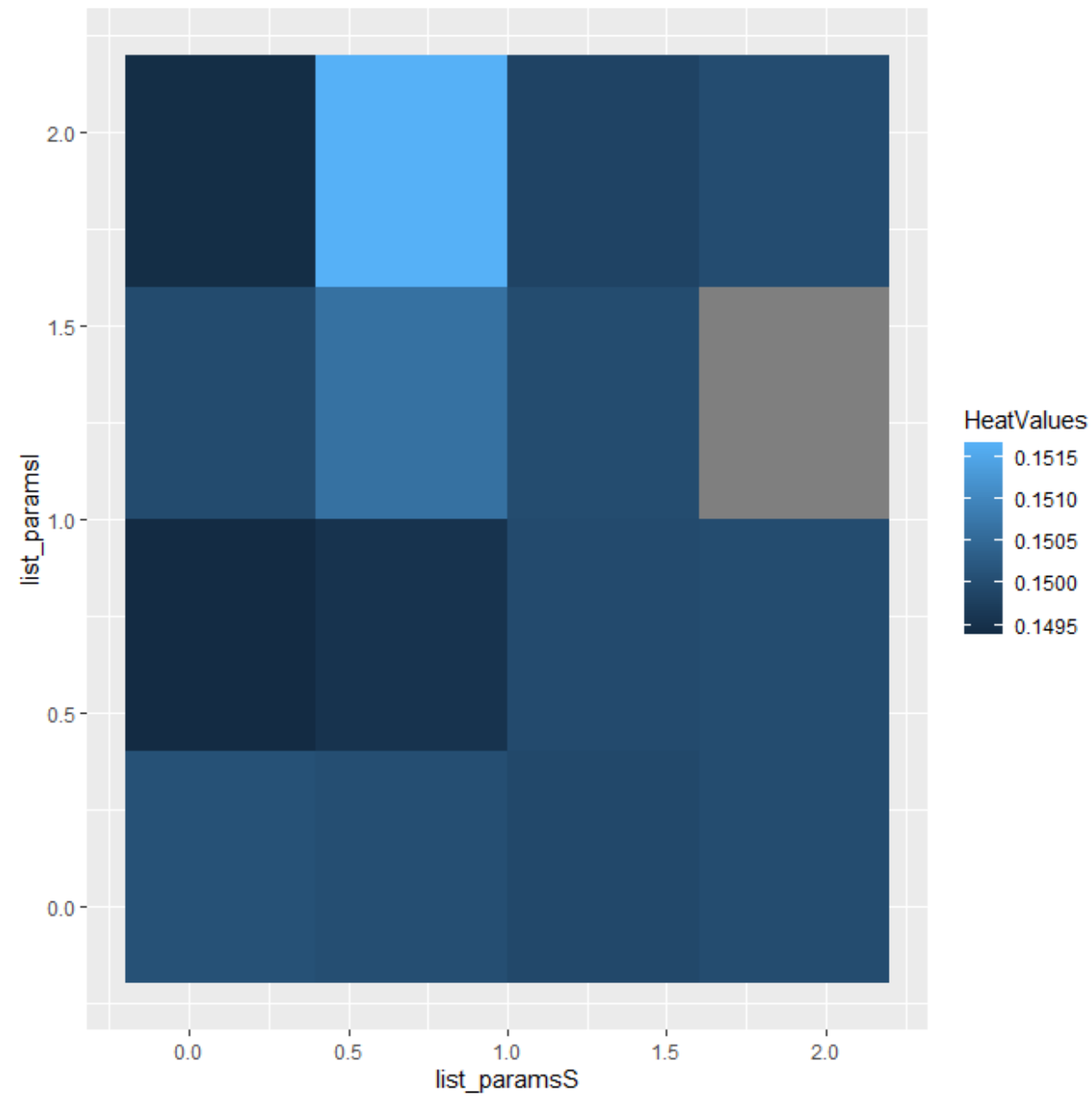
Greater infected dispersion

→ Fewer patches without diseases



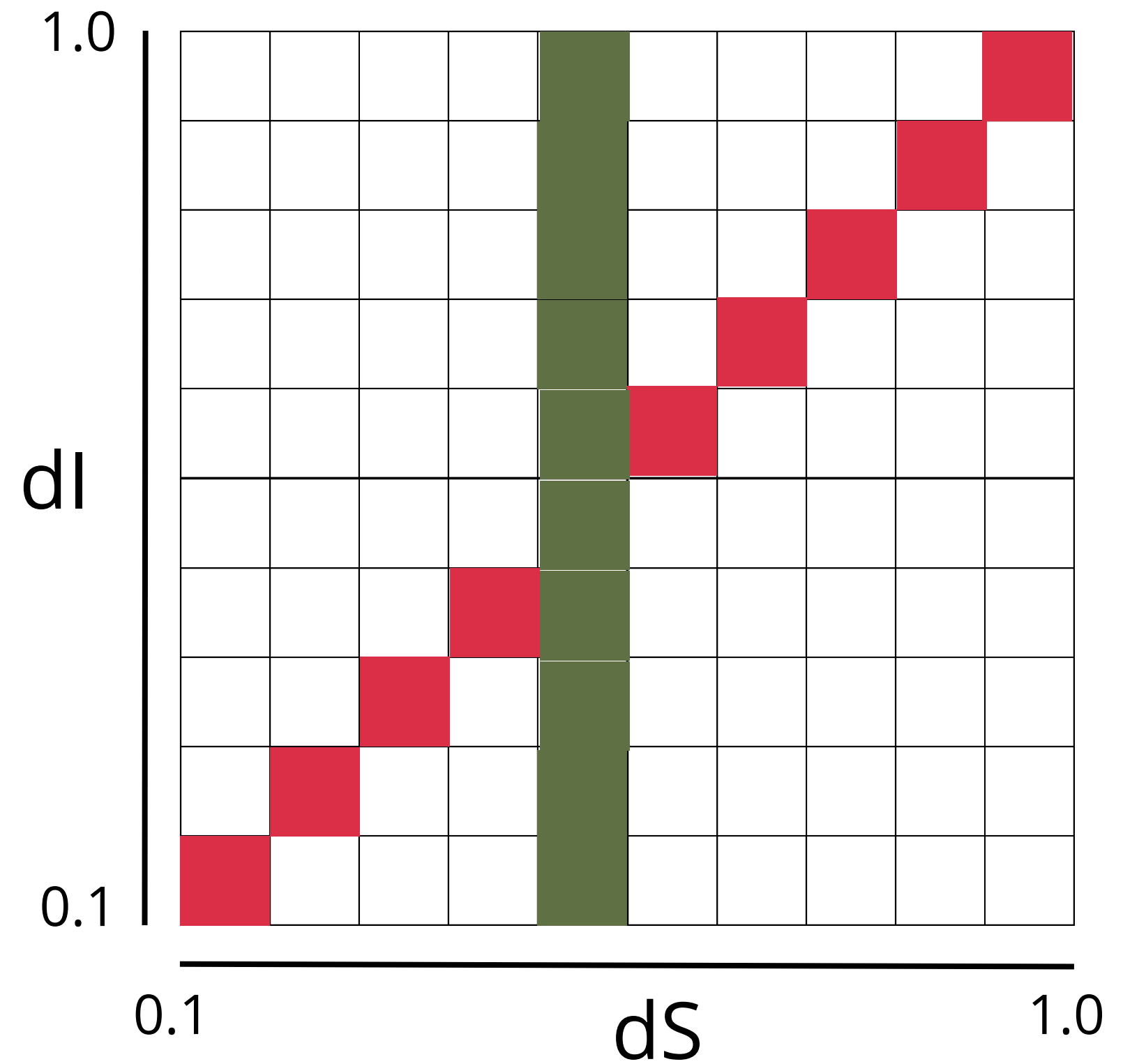
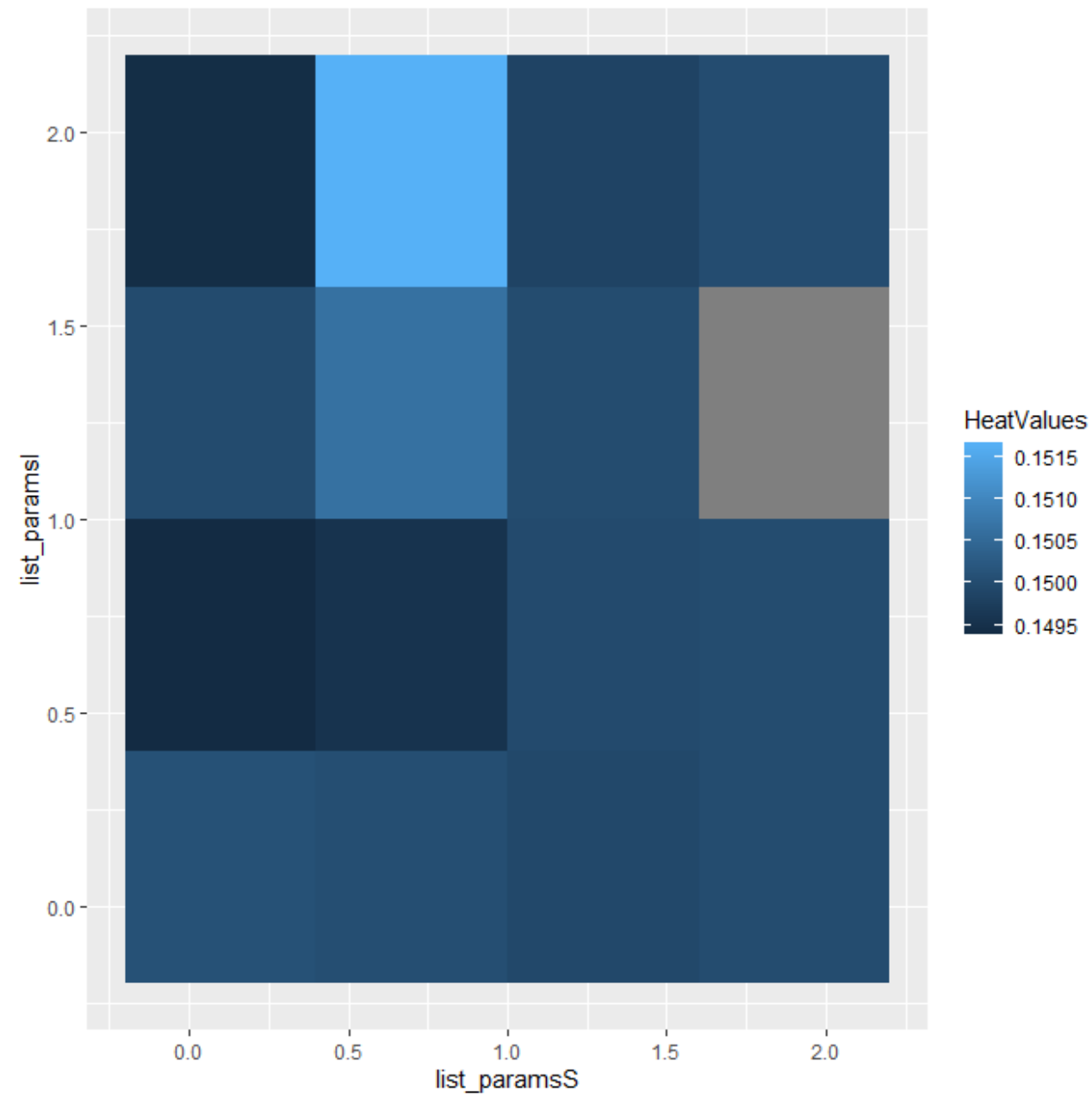
Perspectives

Simulation plan



Perspectives

Simulation plan



Perspectives

2 different ways :

- Continue in the simulations, introduce new spatial configurations
- Analysis of the model at the mathematical level

Perspectives

2 different ways :

- Continue in the simulations, introduce new spatial configurations
- Analysis of the model at the mathematical level



Thank you for
your attention