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

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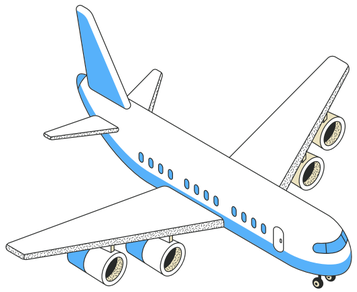
FEEDME project

Introduction

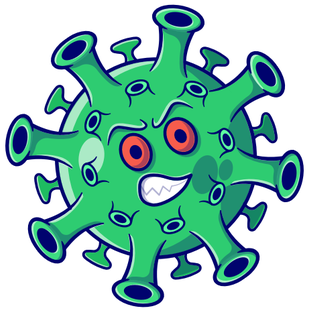
Dispersion of individuals

- Moving in space
- Contact with other individuals



Disease caused by a parasite

- Contact transmission
- Virulence = Mortality of pathogen



Introduction

Dispersion dependent on the epidemiological status of the individual

Good health

+++ Dispersion

Infected

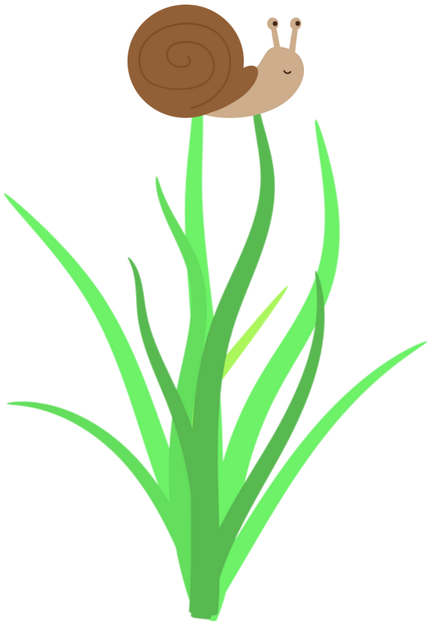
--- Dispersion

Introduction

Dispersion dependent on the epidemiological status of the individual

Snail + Leucochloridium paradoxum

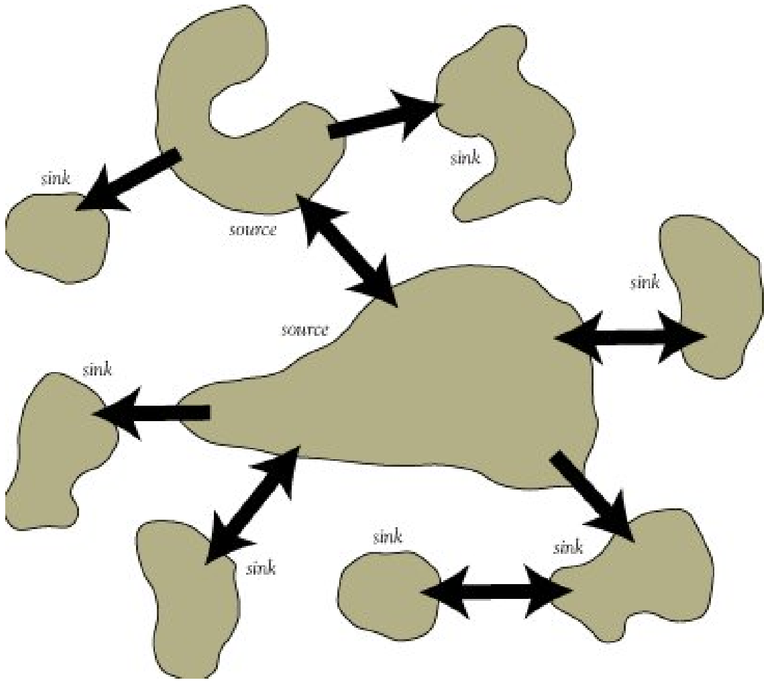
+++ Dispersion



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



Introduction

What effects can infection-dependent dispersal have on the evolution of virulence ?

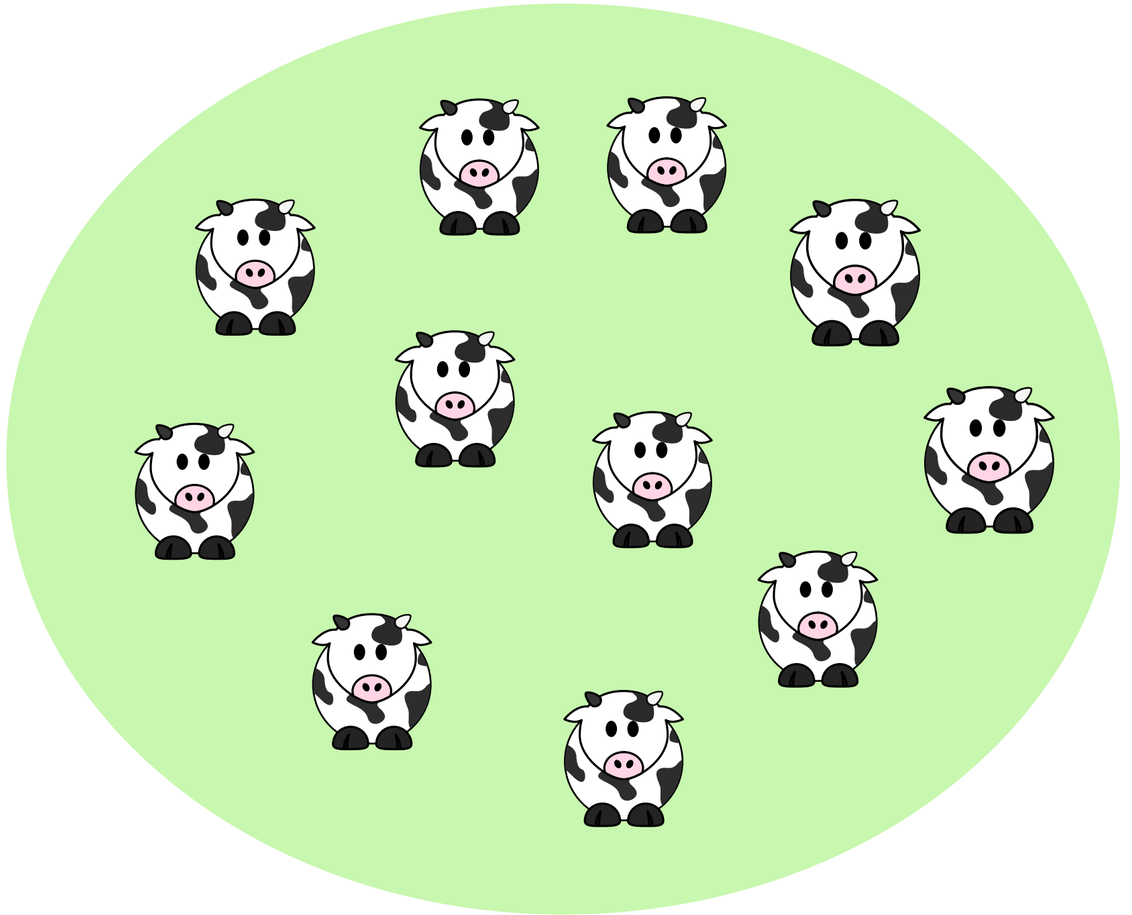
- Infected Dispersal > Susceptible Dispersal
- Infected Dispersal < Susceptible Dispersal

Model

Local Dynamics

Patch with one theoretical species of host

- Birth of individuals (b)
- Death of individuals (μ)
- Carrying Capacity (k)



 = Host

Model

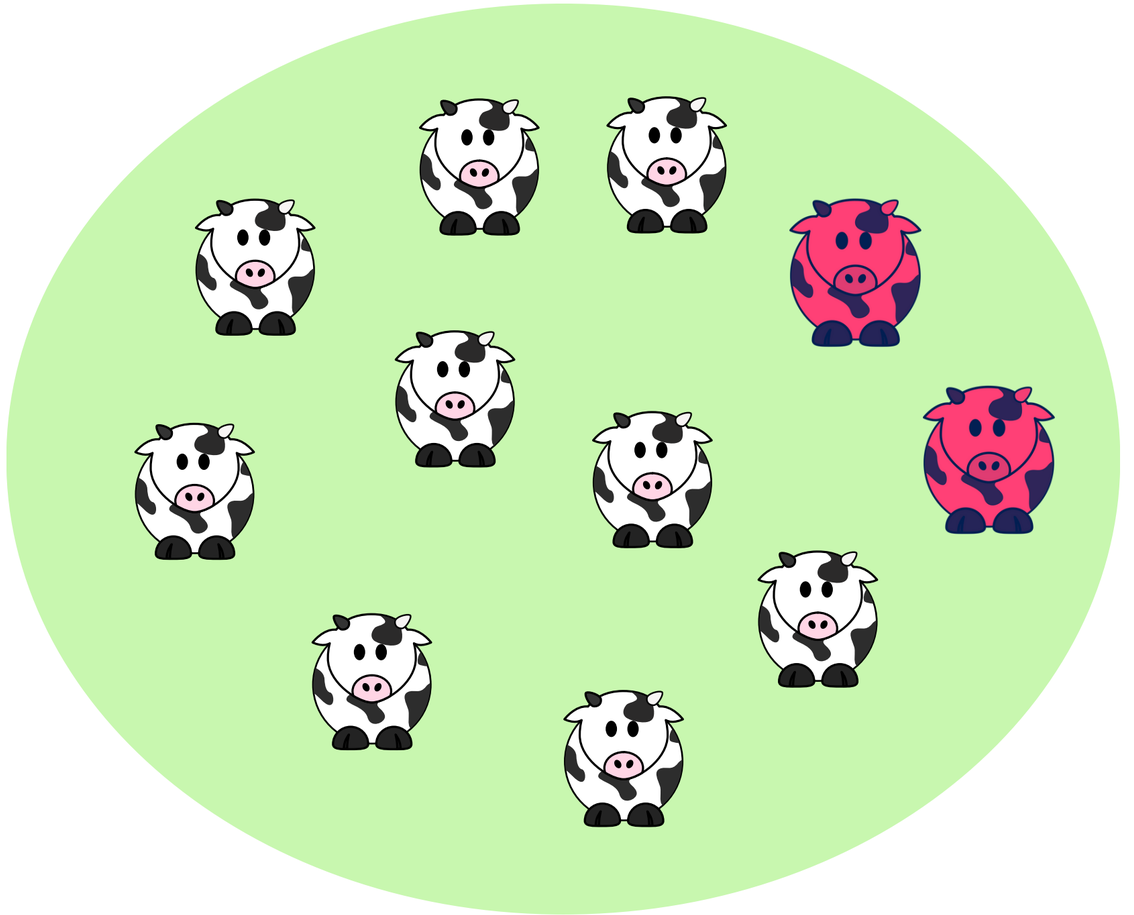
Local Dynamics

Patch with one theoretical species of host

- Birth of individuals (b)
- Death of individuals (μ)
- Carrying Capacity (k)

And one theoretical species of parasite

- 2 different states (S and I)
- Transmission rate (β)
- Remission rate (γ)
- Virulence of the parasite (α)



 = Infected individuals (I)

 = Susceptible individuals (S)

Model

Local Dynamics

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

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

Model

Local Dynamics

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

Birth and death of individuals :

- No reproduction for infected individuals
- Density-dependent effect of k on birth rate

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

Model

Local Dynamics

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Transmission of the parasite :

- No spatial structure in a patch

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Model

Local Dynamics

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

Remission of hosts :
- No immunity for susceptible individuals

Birth and death of individuals :
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- Density-dependent effect of k on birth rate

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Model

Local Dynamics

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Transmission of the parasite :
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$$\frac{dI}{dt} = \beta SI - \gamma I - \alpha I - \mu I$$

Virulence of the parasite
- Additional mortality due to the parasite

Model

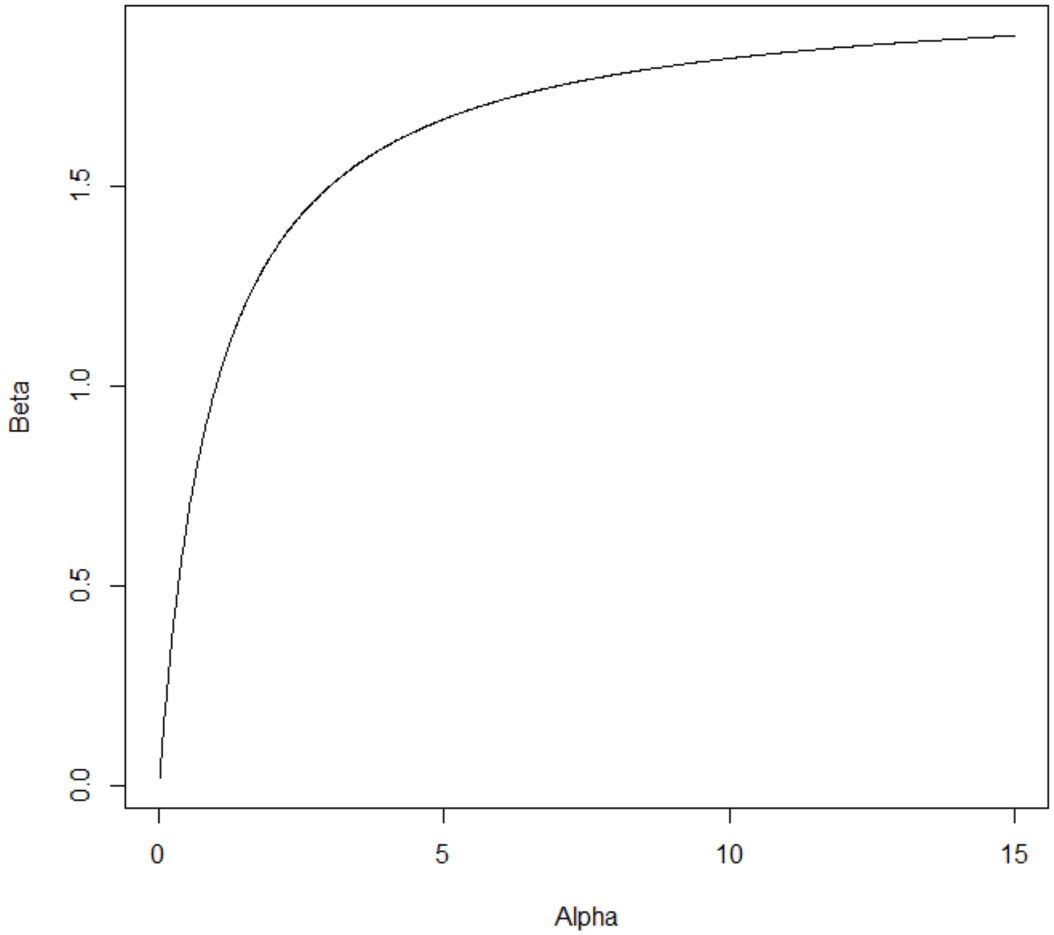
Local Dynamics

Trade-off between Transmission (β) and Virulence of the parasite (α)

$$\beta(\alpha) = \beta_0 * \alpha/(1+\alpha)$$

Value of β depends :

- β base value (β0)
- Virulence (α)



Model

Local Dynamics

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

Emigration of hosts = Dispersal of individuals

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

Model

Local Dynamics Equilibrium

 = 0  = 0

- Empty patch

 = S*  = 0

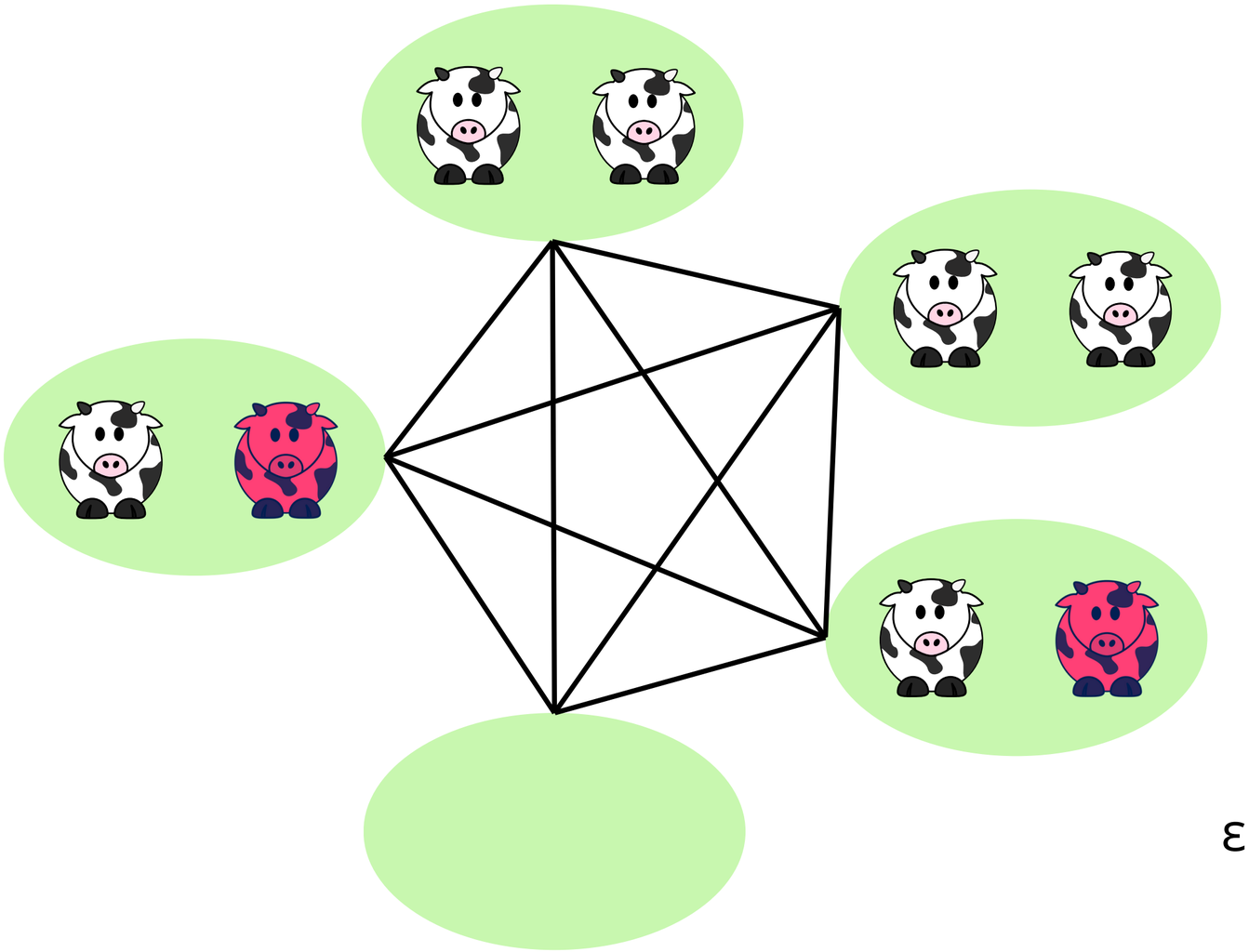
- Only susceptible individuals
- "Disease-free equilibrium" (DFE)

 = $\hat{S}$  = $\hat{I}$

- Constant fraction of susceptible and infected hosts
- "Endemic equilibrium"

Model

Metapopulation



Metapopulation :

- All neighbors
- Migration between patches

3 quasi-stationary equilibrium :

- Empty patch
- DFE
- Endemic Equilibrium

ε = Extinction of the population of a patch

Model

Local Dynamics in a metapopulation

$$\frac{dS_i}{dt} = (b(1-(S+I)/k) - \mu)S - \beta SI + \gamma I - m_S S + \sum_{i=1}^{z} m_S(1-\rho)S_j/z$$

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

Model

Local Dynamics in a metapopulation

$$-m_S S + \sum_{i=1}^{z} m_S(1-\rho)S_j/z$$

$$-m_I I + \sum_{j=1}^{z} m_I(1-\rho)I_j/z$$

Migration parameters :

- ρ : Dispersal cost
- *z* : Number of neighboring patches

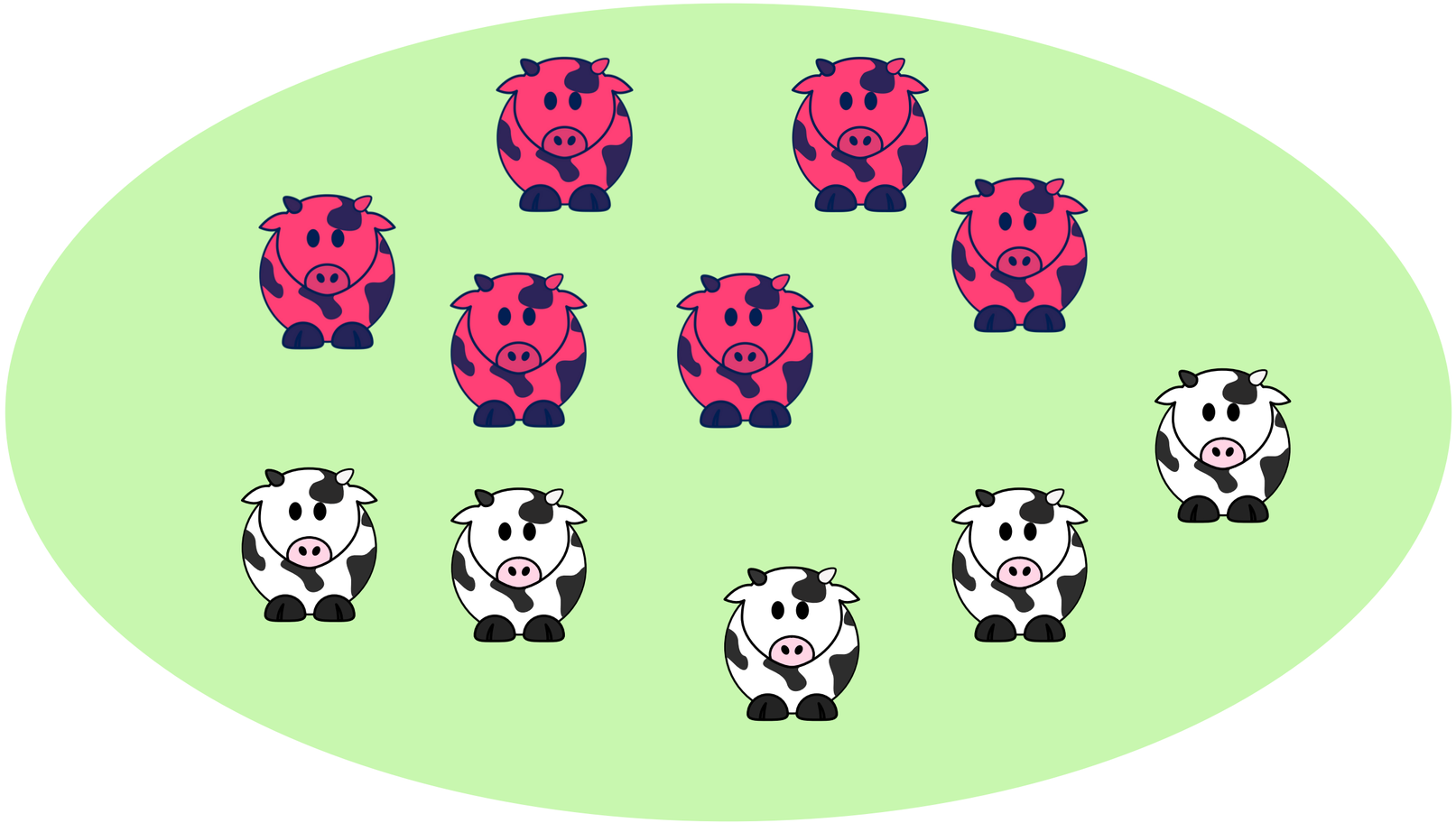
- m_S : Dispersal of susceptible individuals
- m_I : Dispersal of infected individuals

Model

Evolution of traits

Evolution of virulence :

- Mortality of the pathogen
- Noted α



Model

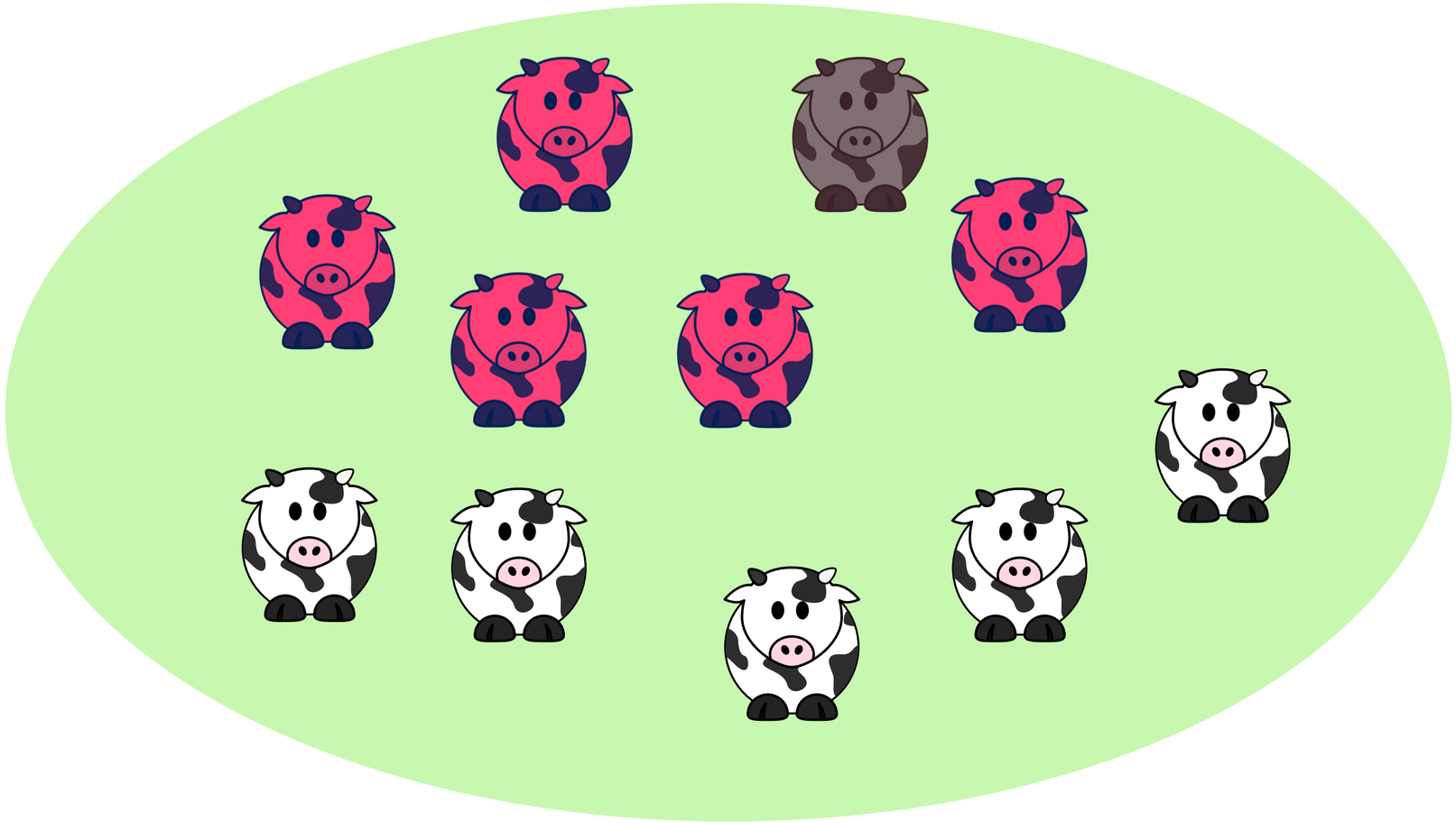
Evolution of traits

Evolution of virulence :

- Mortality of the pathogen
- Noted α

Mutation :

- Rare
- Low effect



Model

Evolution of traits

Evolution of virulence :

- Mortality of the pathogen
- Noted α

Mutation :

- Rare
- Low effect

Resident
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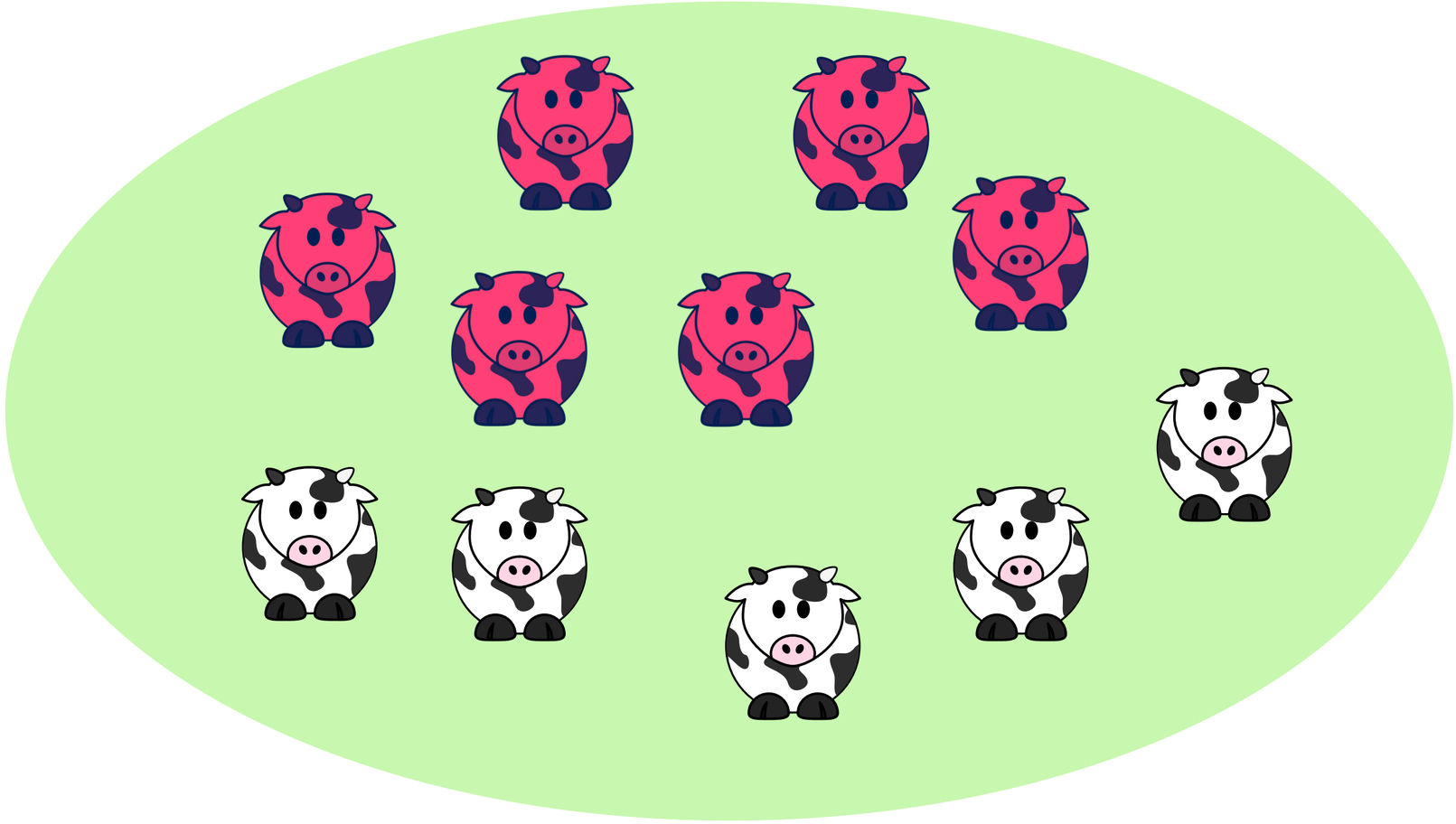
Mutant



Dominant phenotype :

Model

Evolution of traits

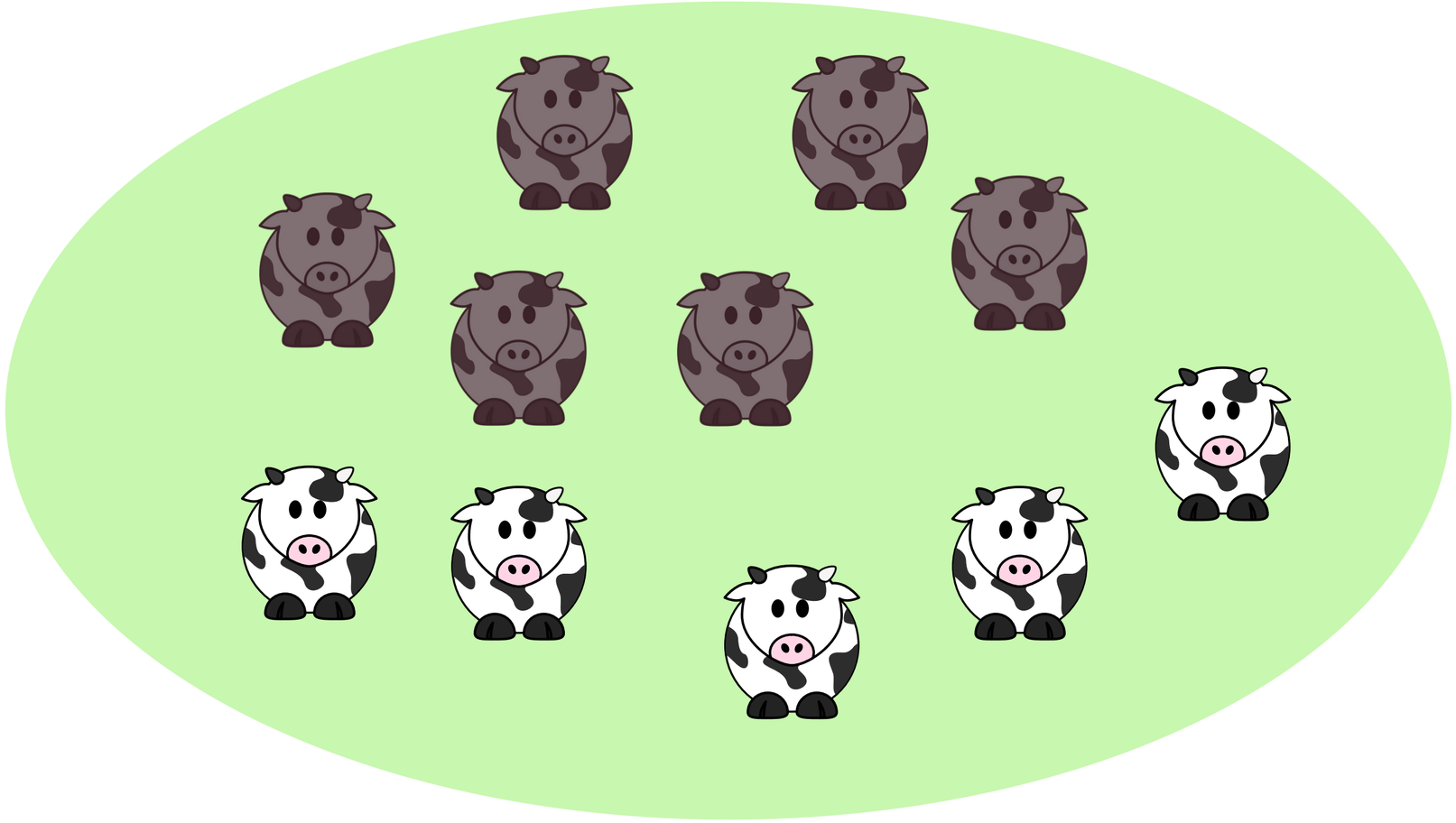
Evolution of virulence :

- Mortality of the pathogen
- Noted α

Mutation :

- Rare
- Low effect

Mutant
>
Resident



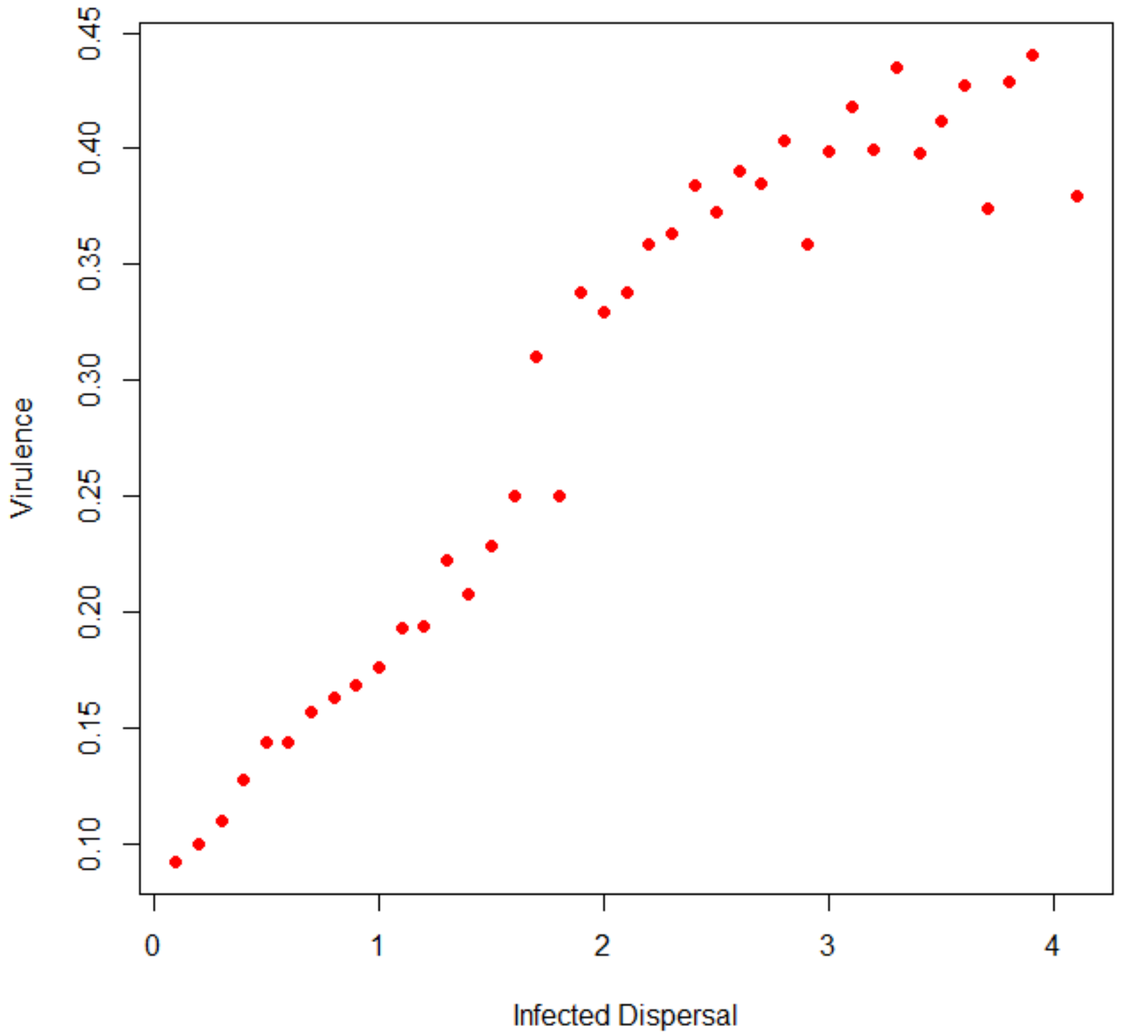
Dominant phenotype :

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 4.0



Results

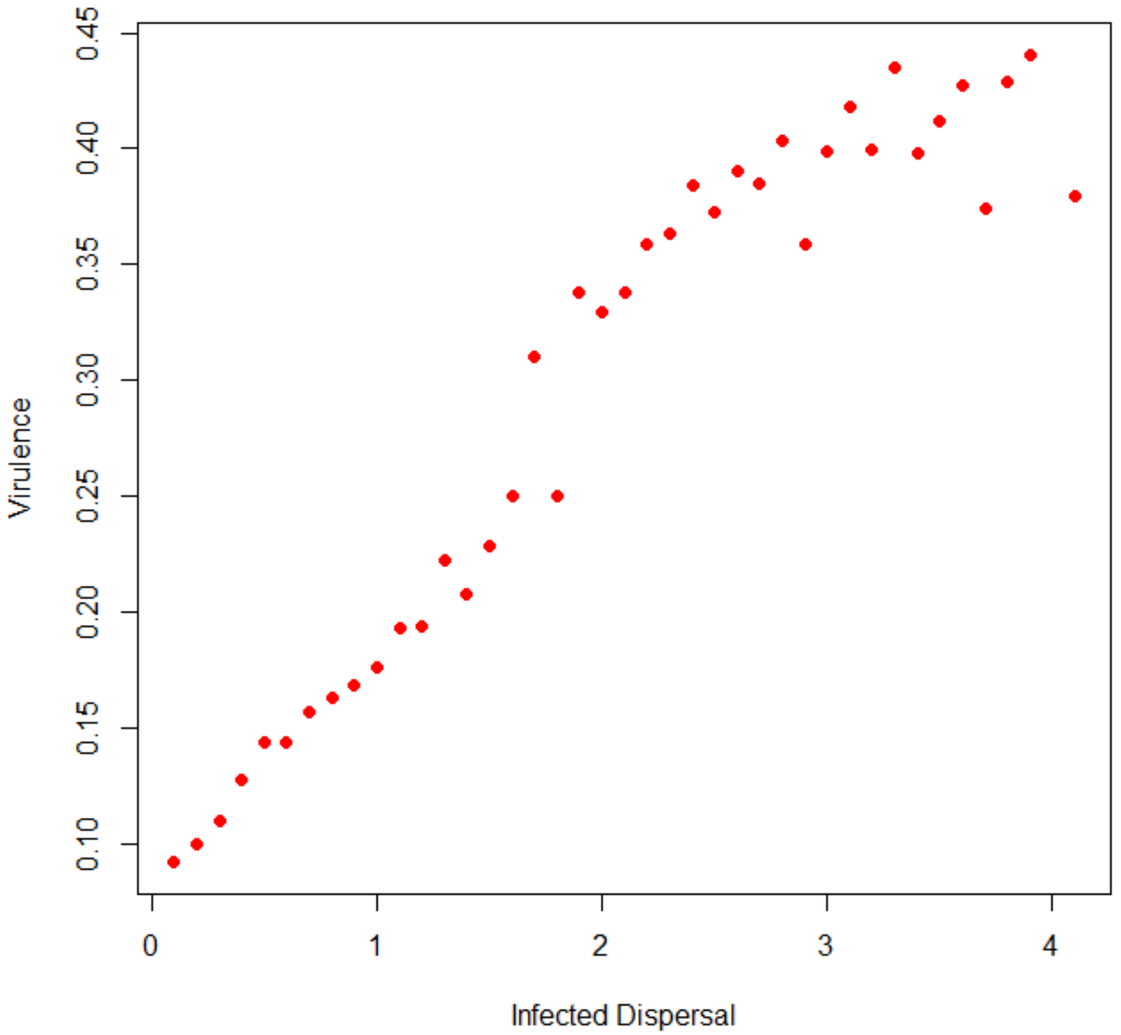
Evolution of virulence according to the infected dispersal

Increase of infected hosts dispersal

→ Increase of virulence

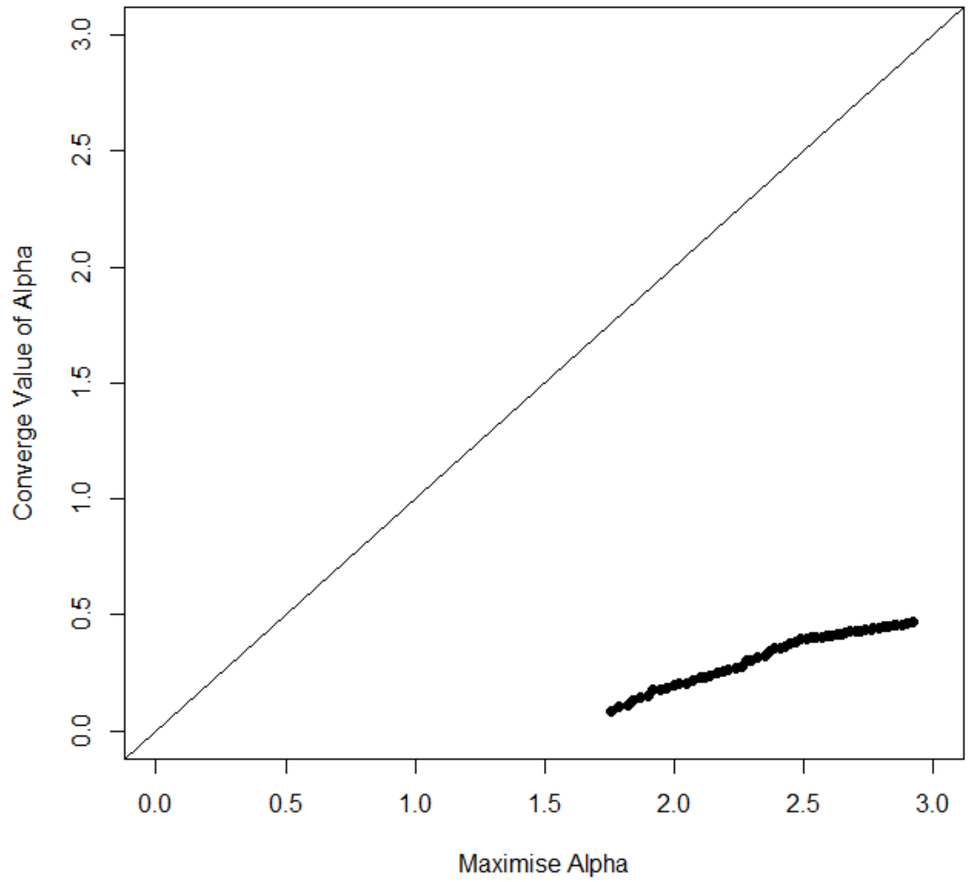
Increase of infected hosts dispersal

→ More chance of finding patches with many susceptible hosts



Results

Interest of the metapopulation



α obtained with metapopulation

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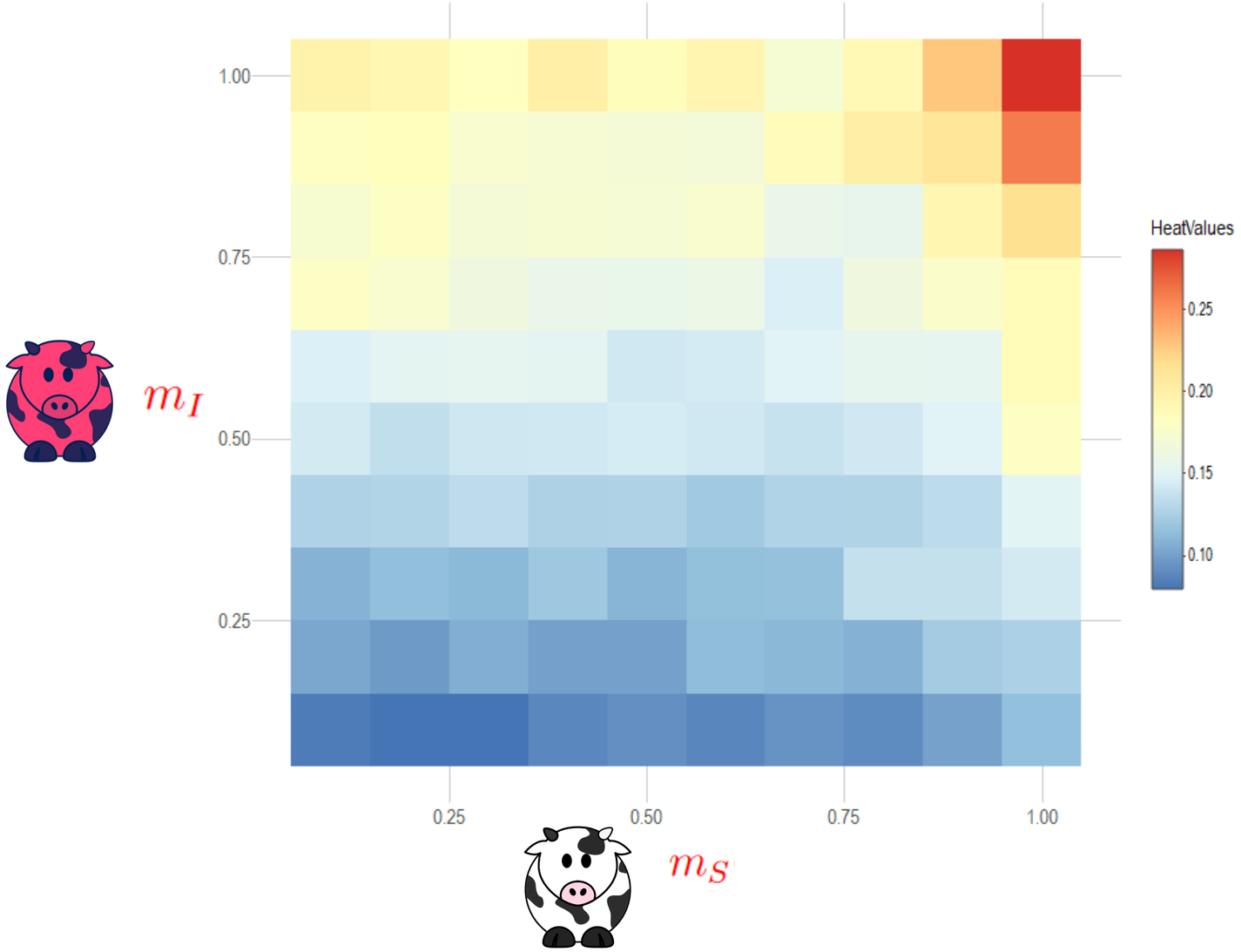
α maximise

Introduction of a spatial structure

- Alpha evolves towards lower values

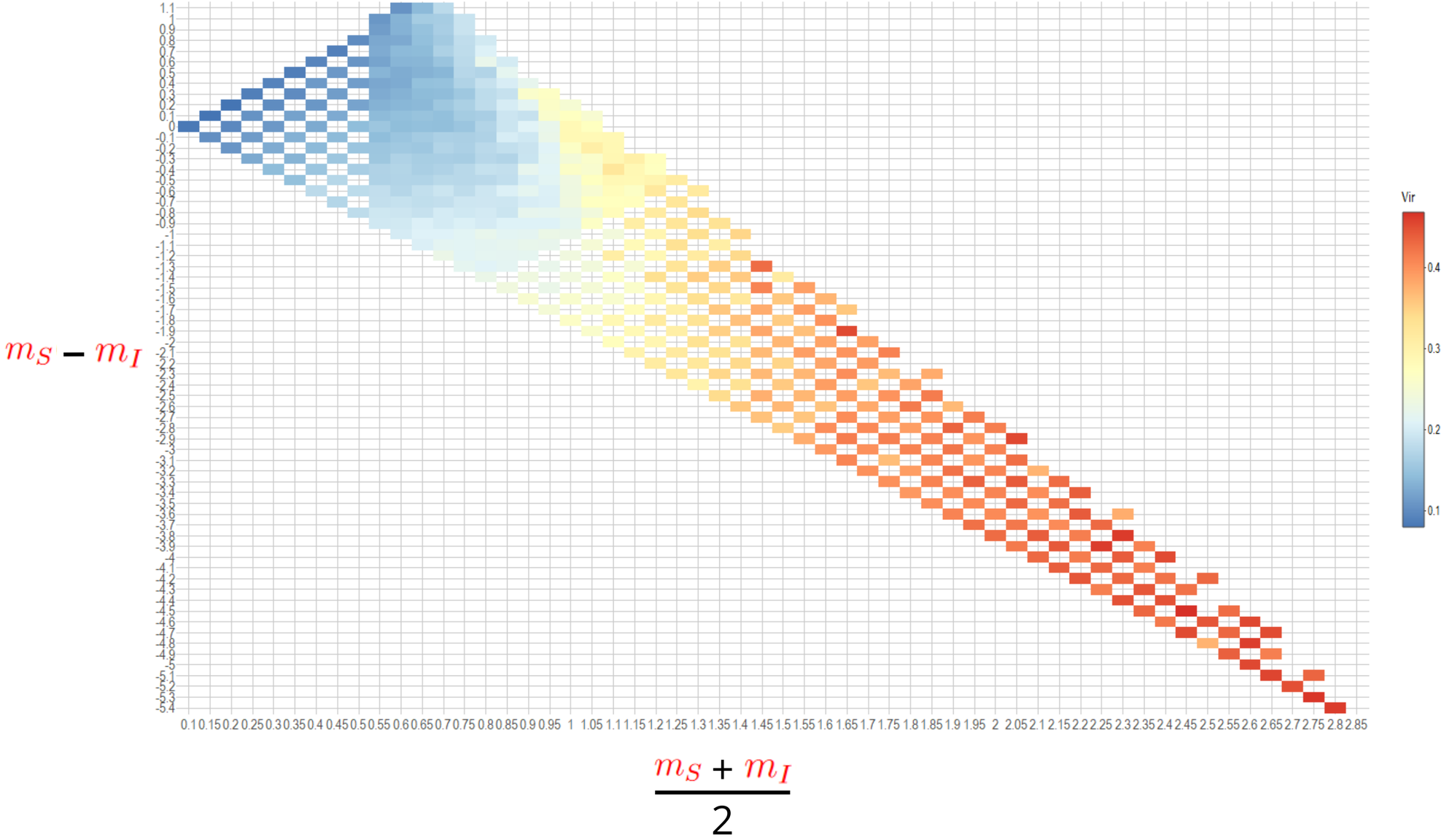
Results



- Increase in virulence with dispersion of the infected
- Effect of the difference between m_S and m_I ?

Results

Convergent values of parasite virulence



Results

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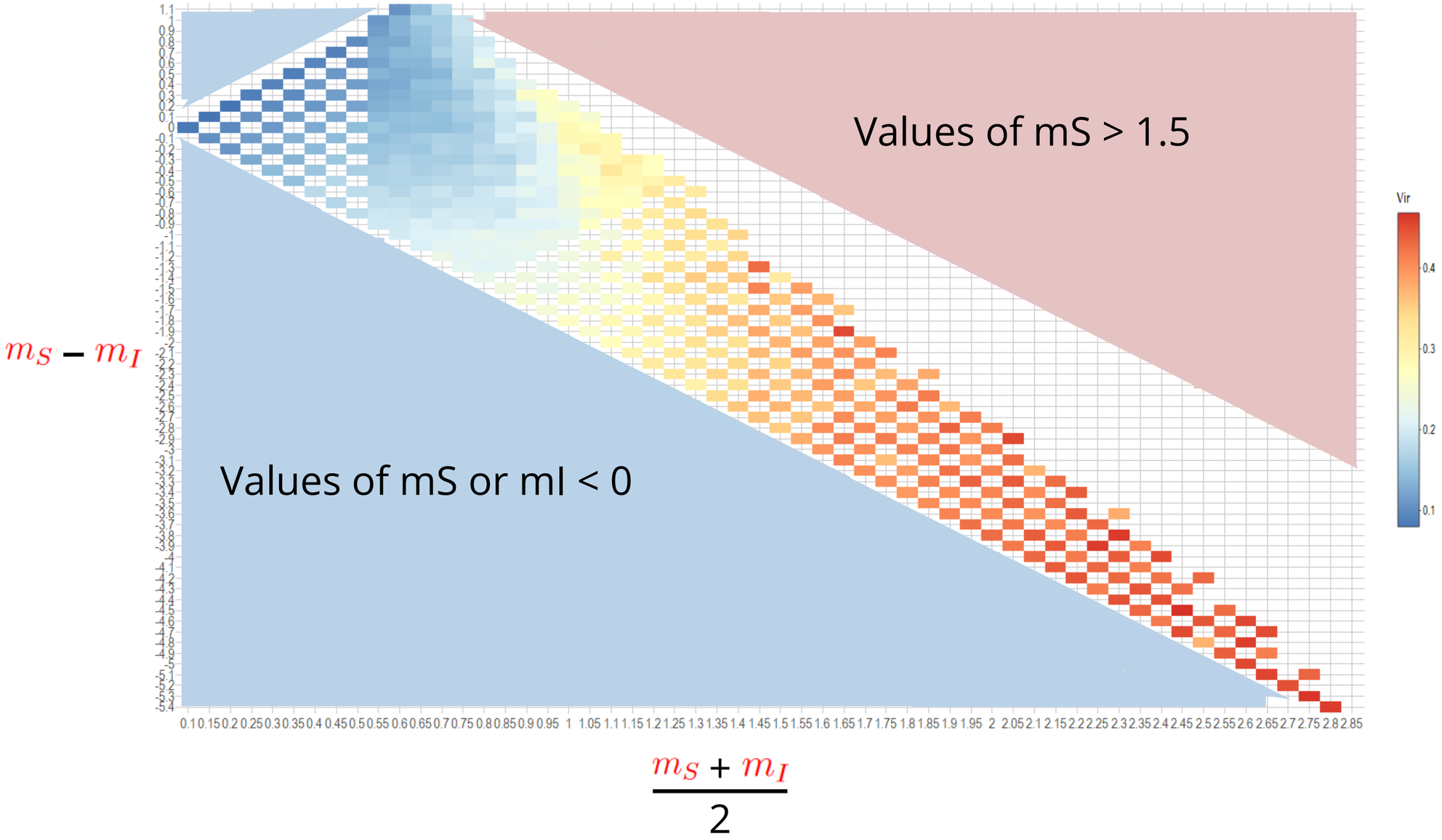
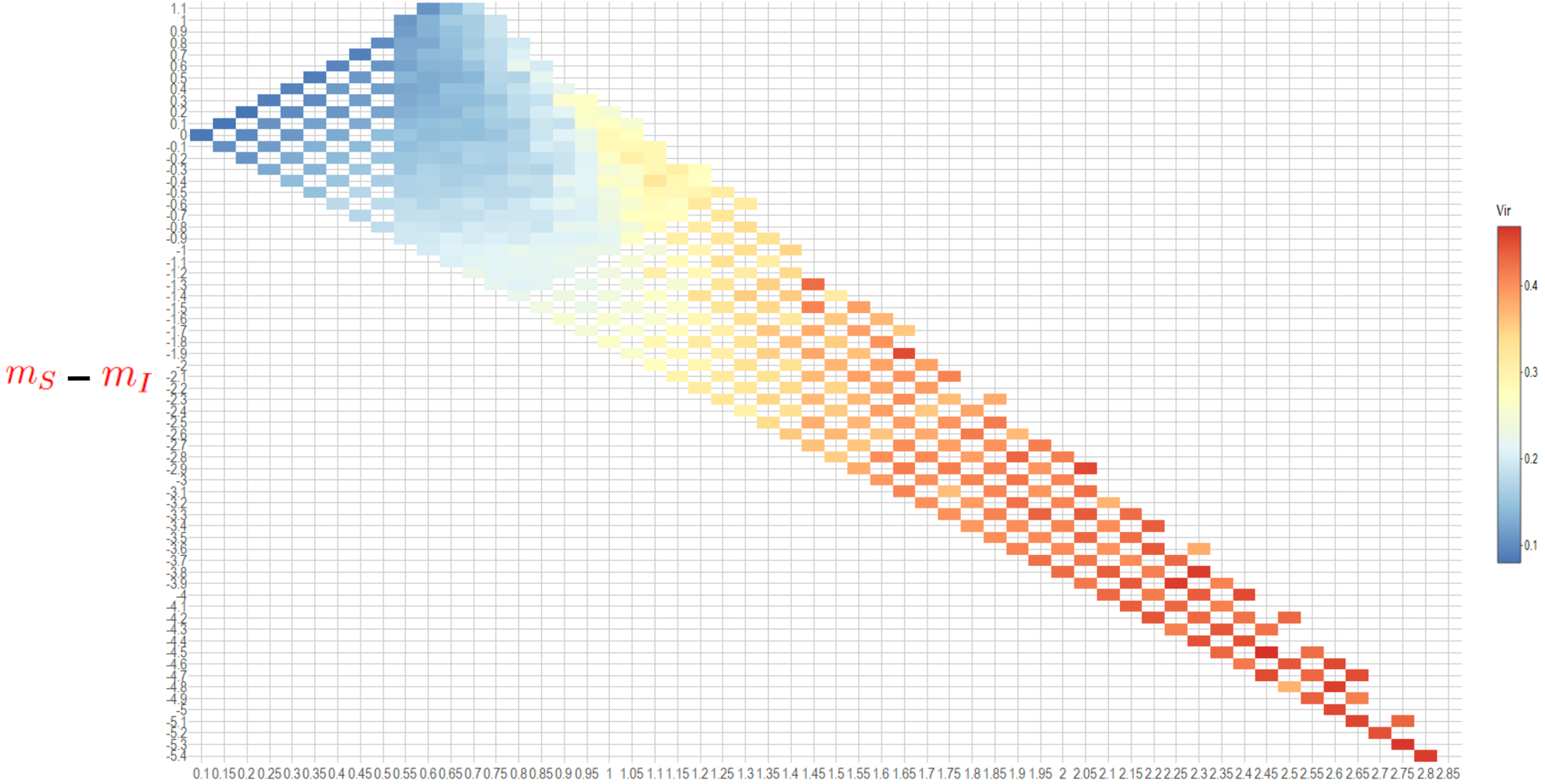


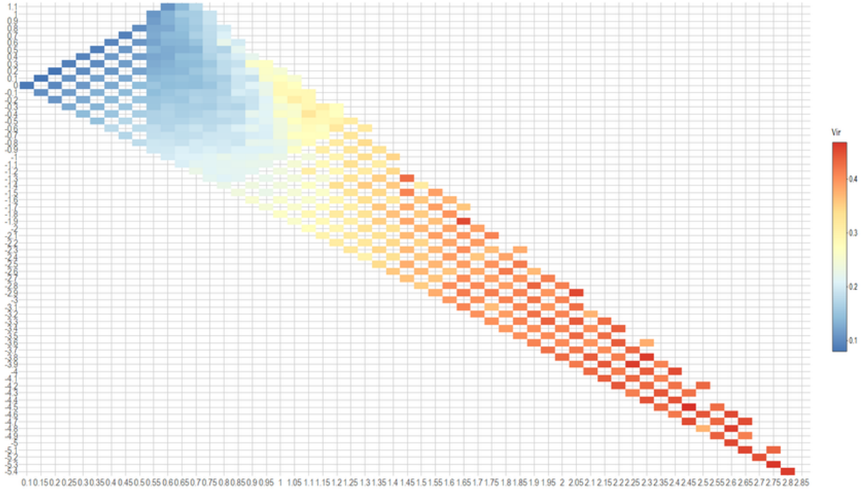
Results

Convergent values of parasite virulence



Results

Convergent values of parasite virulence



$m_S - m_I$ ↘

- Virulence of the parasite increases
  - More chance of finding patches with many susceptible hosts

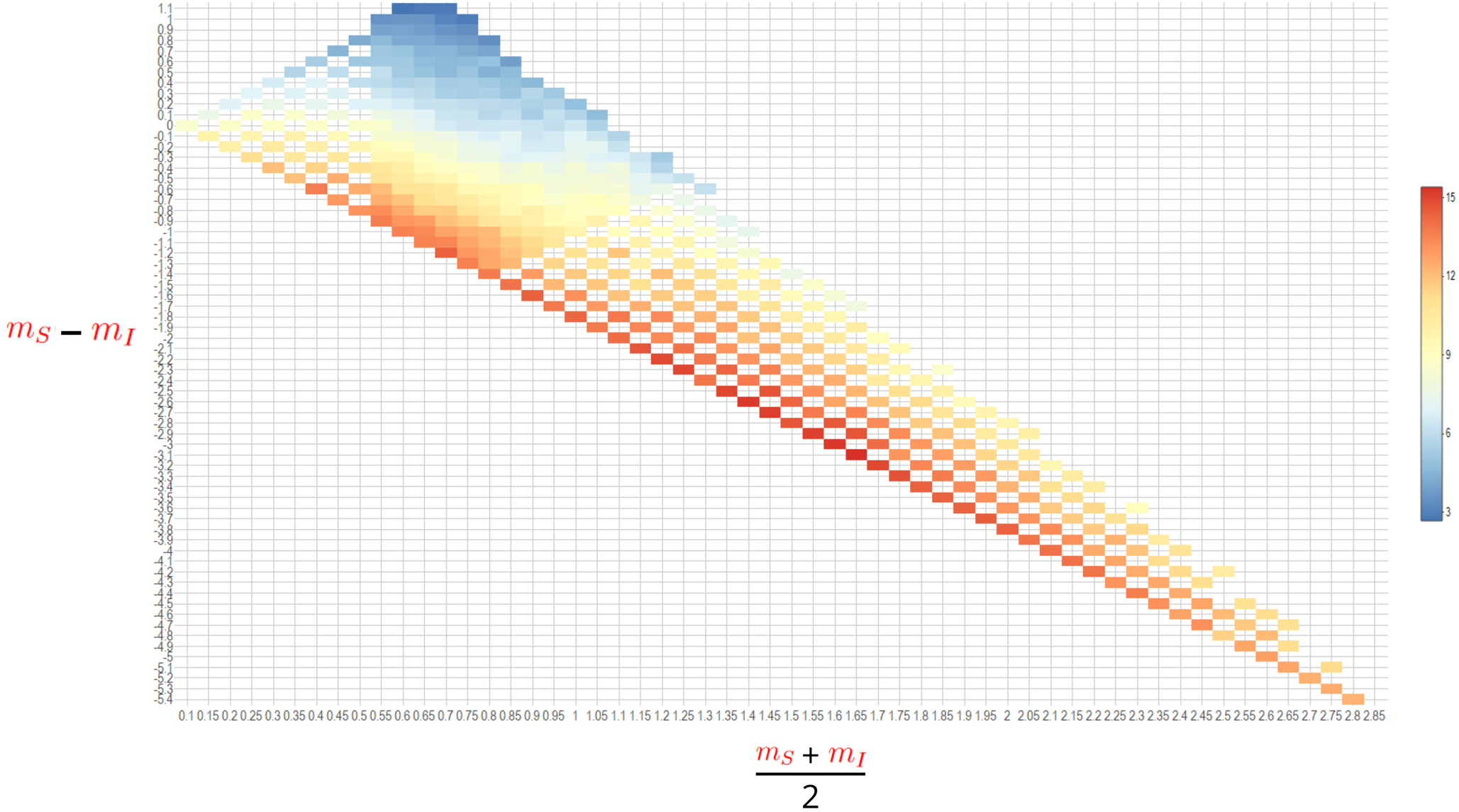
$\frac{m_S + m_I}{2}$ ↗

- Virulence of the parasite increases
  - More chance of finding empty patches for susceptible individuals

- High values of infected dispersal = Values of virulence reach a limit ?
  - Not enough benefit from the trade off with transmission rate

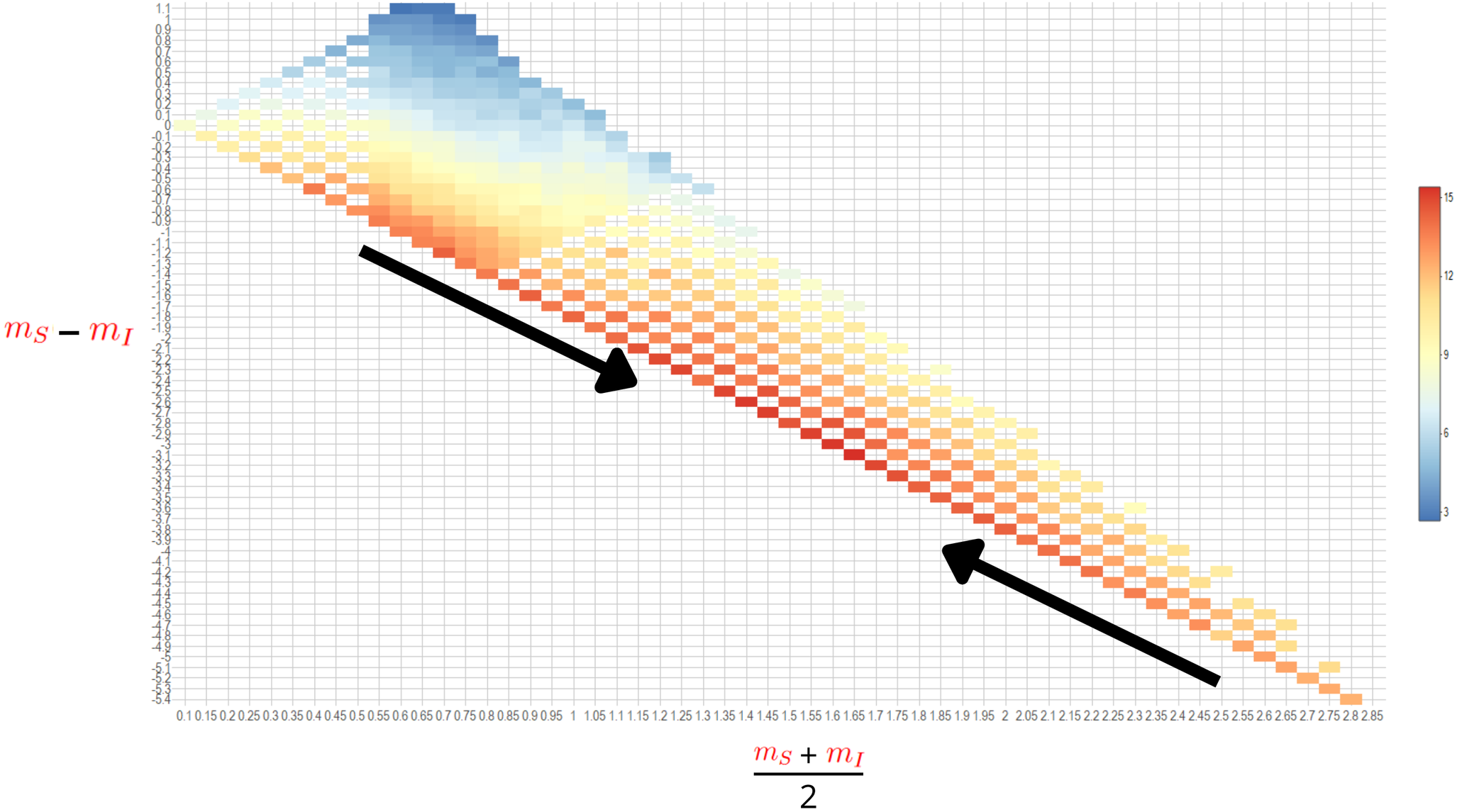
Results

R0 Value



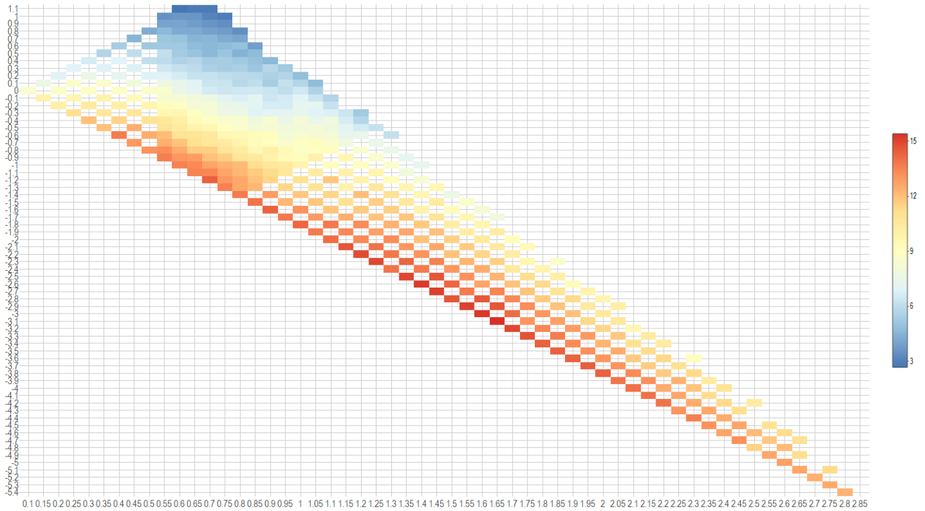
Results

R0 Value



Results

R0 Value



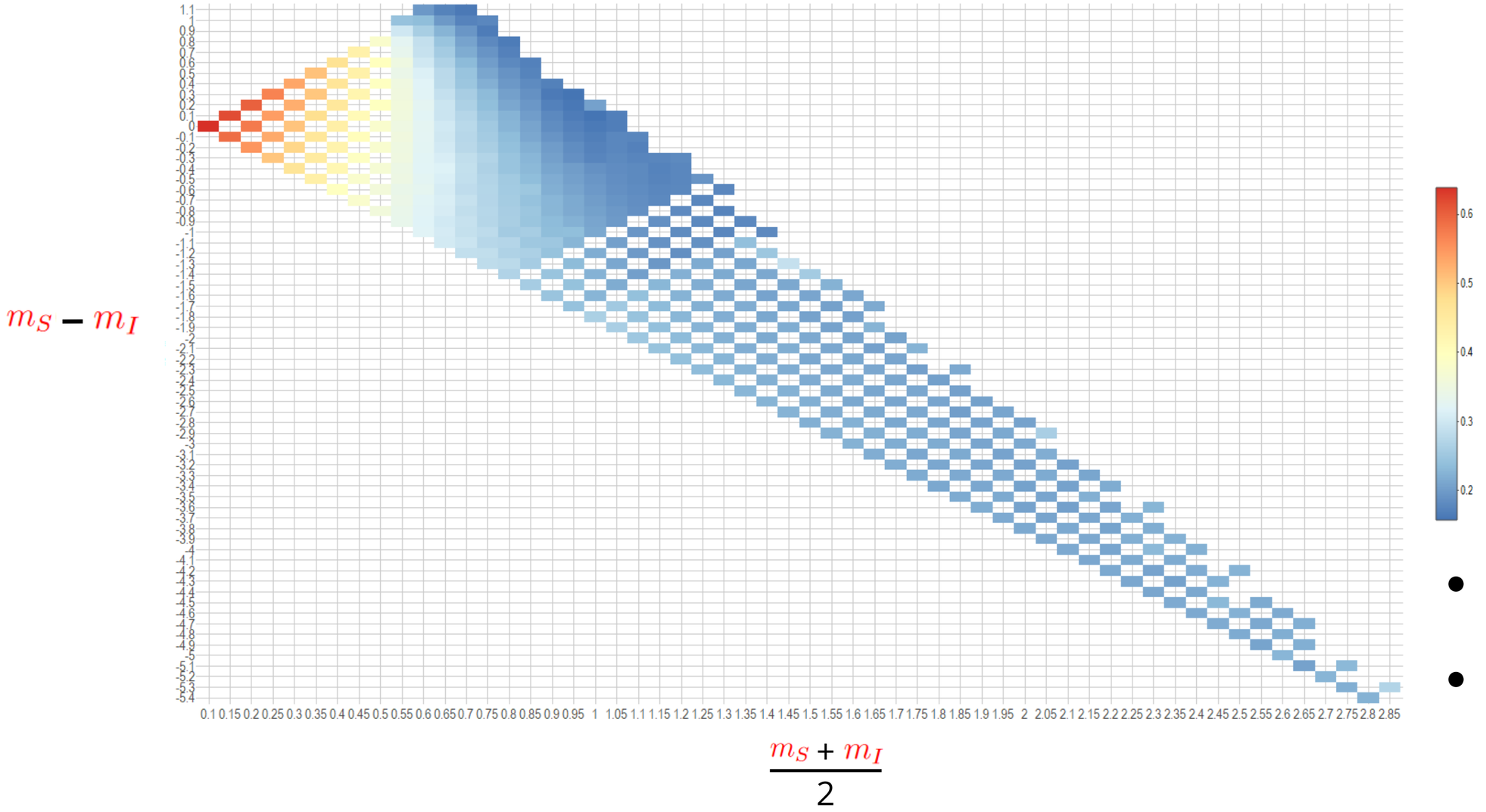
$m_S - m_I$ ↘

- Value of R0 increase

- With small Suceptible dispersal, R0 value has a bell-shaped structure
  - Small Infected dispersal, less transmission for infected
  - High Infected dispersal, Not enough S in patches, less transmission

Results

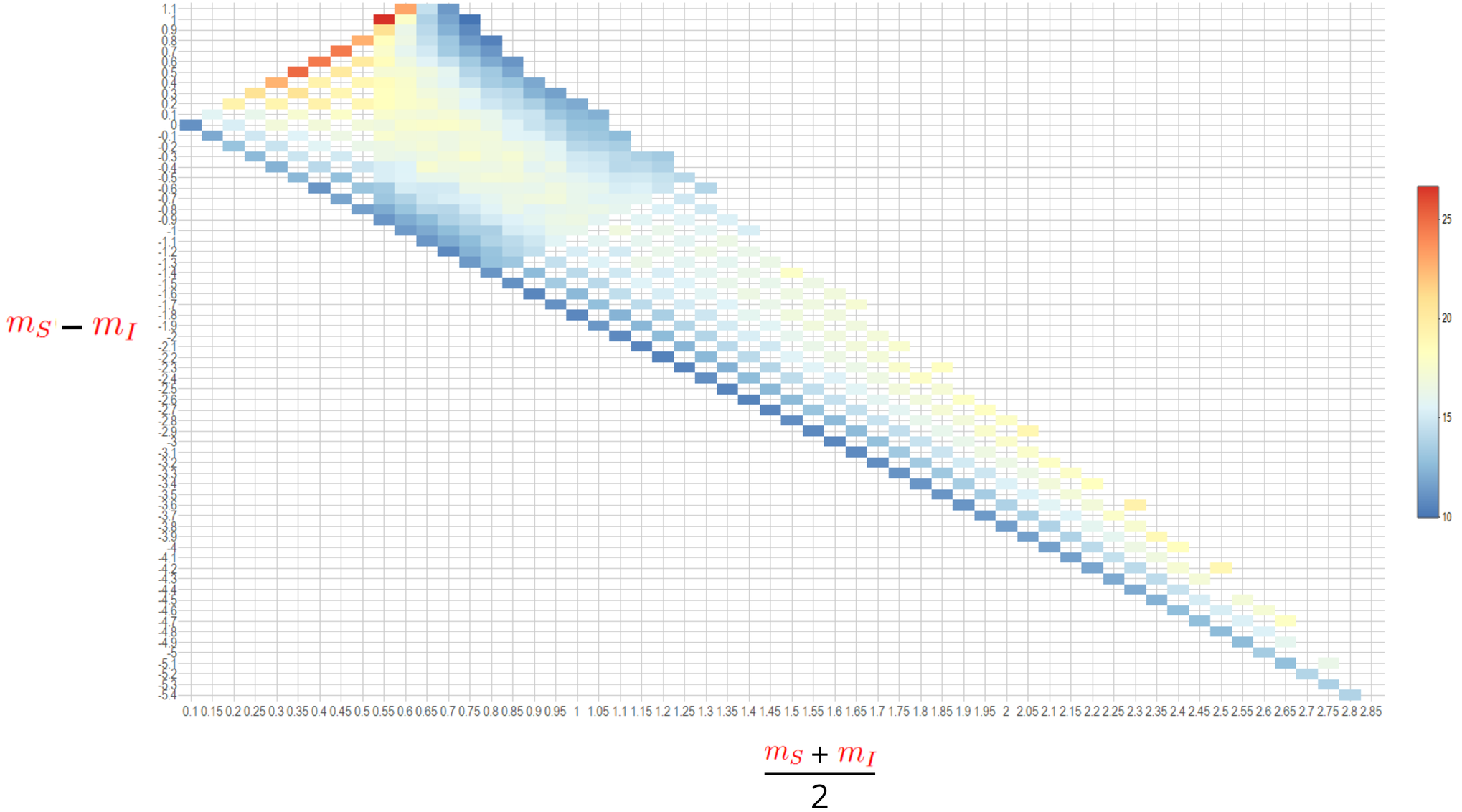
Local prevalence of infected individuals



- Impact of ρ
- Can explain high R0 and high virulence

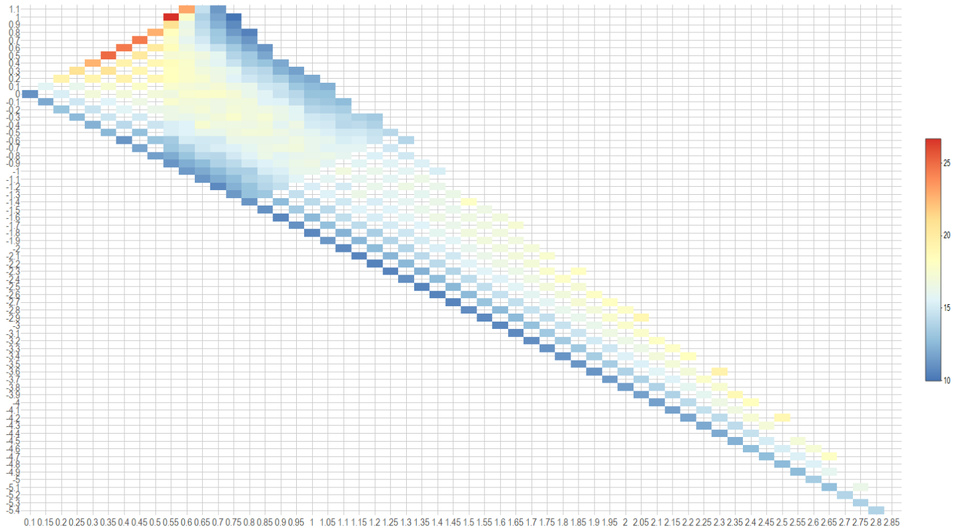
Results

Susceptible individuals colonization



Results

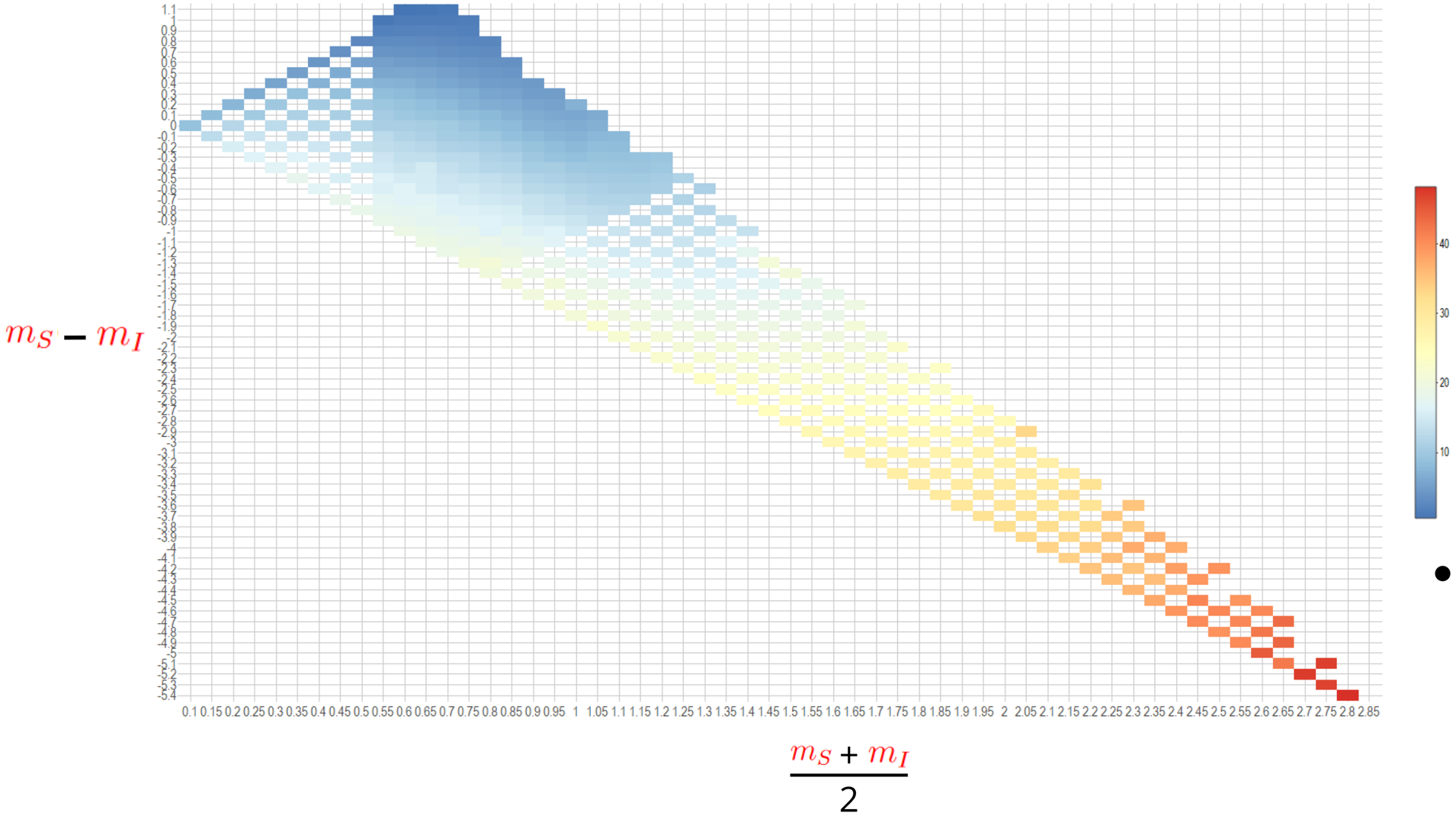
Susceptible individuals colonization



- Optimum of colonization influenced by Susceptible dispersal
- m_S ↘ = Less dispersal for individuals, Fewer colonised patches
- m_S ↗ = All patches occupied with a large population of susceptibles, Less colonisation

Results

Infected individuals colonization



- Better colonization when high infected dispersal

Conclusion

- High Infected dispersal = High values of evolved virulence
- $m_S - m_I$ ↘ = High values of evolved virulence
- Higher infected dispersal not the optimum

Perspectives

Evolution of virulence and Infected dispersal

- Evolution of α and m_I
- Same probabilty of mutation
- No trade-off between for infected dispersal, like α and β
- What values of infected dispersal will be selected ?

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Evolution of virulence and Infected dispersal

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Thank you for
your attention