Influence of environmental constraints, biotic interaction and evolution on geographical distribution of species

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UQAR/ISEM

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- To understand past, present and future distributions

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3. Biotic variables : interaction networks, depicted by community matrix **A**
4. Evolution : slight changes in species characteristics, $\mathbf{T} = (\tau_1, \tau_2, ..., \tau_m)$

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- Biogeography aims at enlightening g

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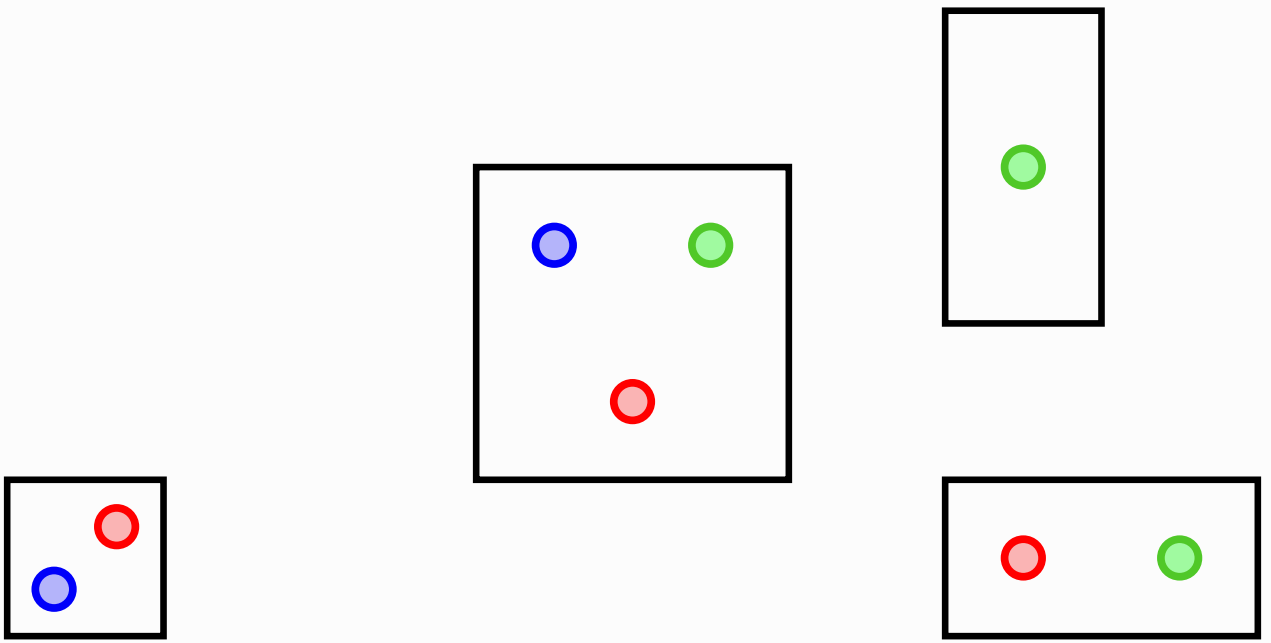

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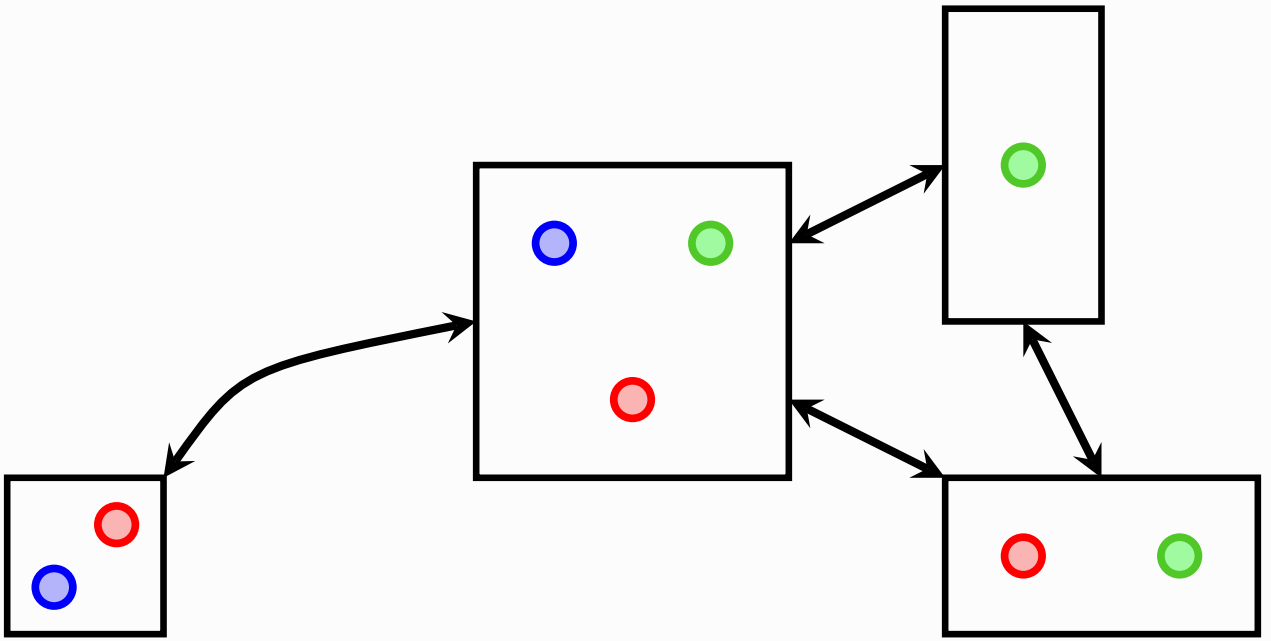
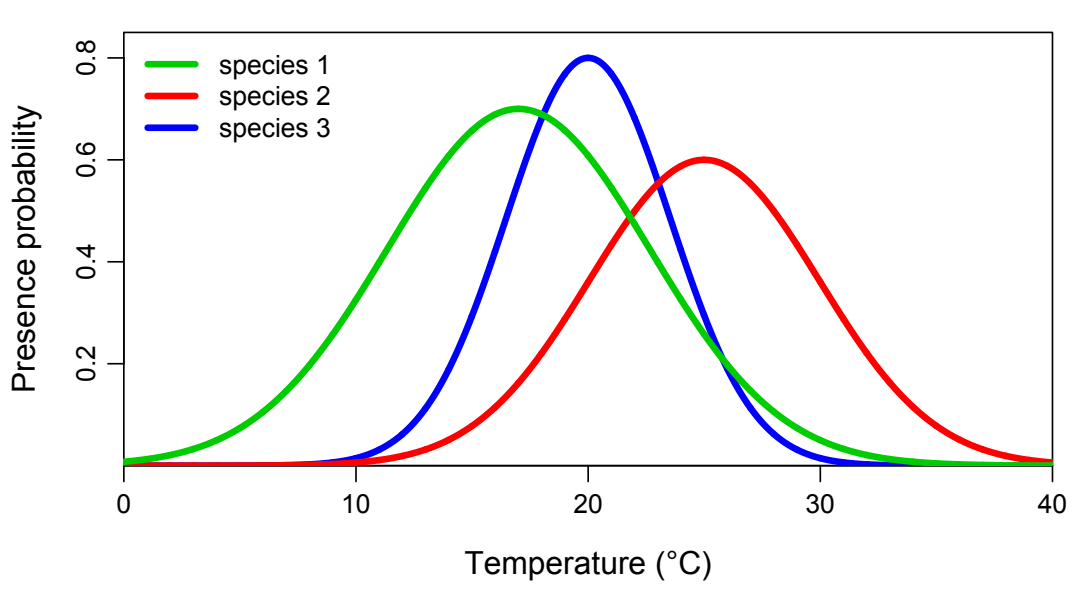


Ecological niche

Relationship between environmental variables (**W**) and species presence.



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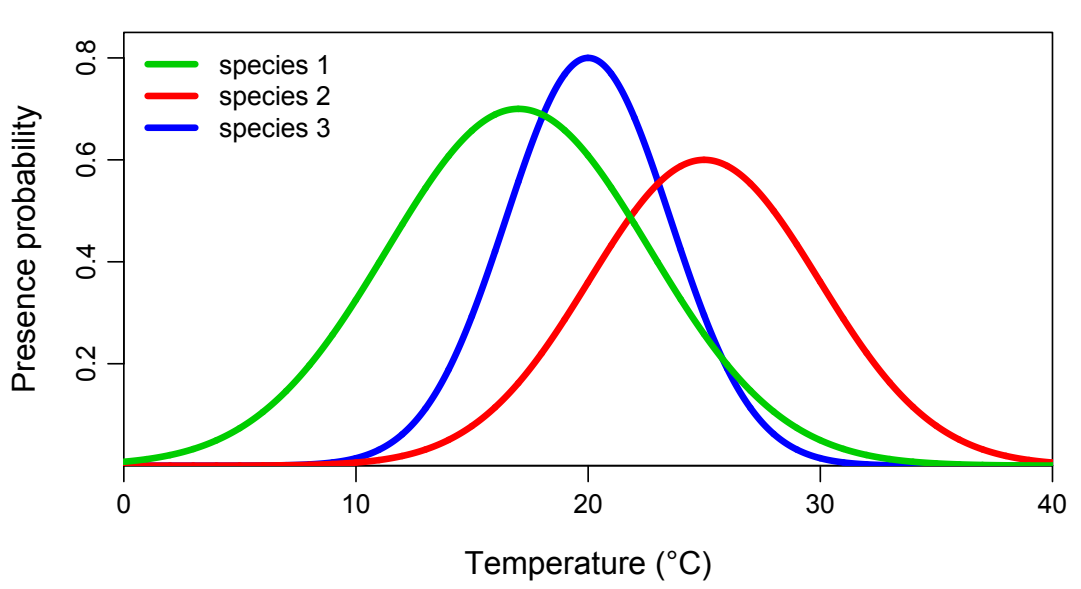

- Best set of environment variables for a given species ?
- At which scales ?

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- Demography ($g(\mathbf{A}X)$) pressure $=>$ Distribution
- Species or communities ?
- At which scales interactions are relevant ?

PNAS

Macroecological signals of species interactions in the Danish avifauna

Nicholas J. Gotelli[a,1], Gary R. Graves[b], and Carsten Rahbek[c]

[a]Department of Biology, University of Vermont, Burlington, VT 05405; [b]Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, DC 20013; and [c]Center for Macroecology, Evolution and Climate, Department of Biology, University of Copenhagen, DK-2100 Copenhagen Ø, Denmark

Communicated by Thomas W. Schoener, University of California, Davis, CA, December 21, 2009 (received for review August 6, 2009)

The role of intraspecific and interspecific interactions in structuring continental mainland regions (23). Inferences of community

Evolution and functional traits

Through time, evolutionary processes shape species :

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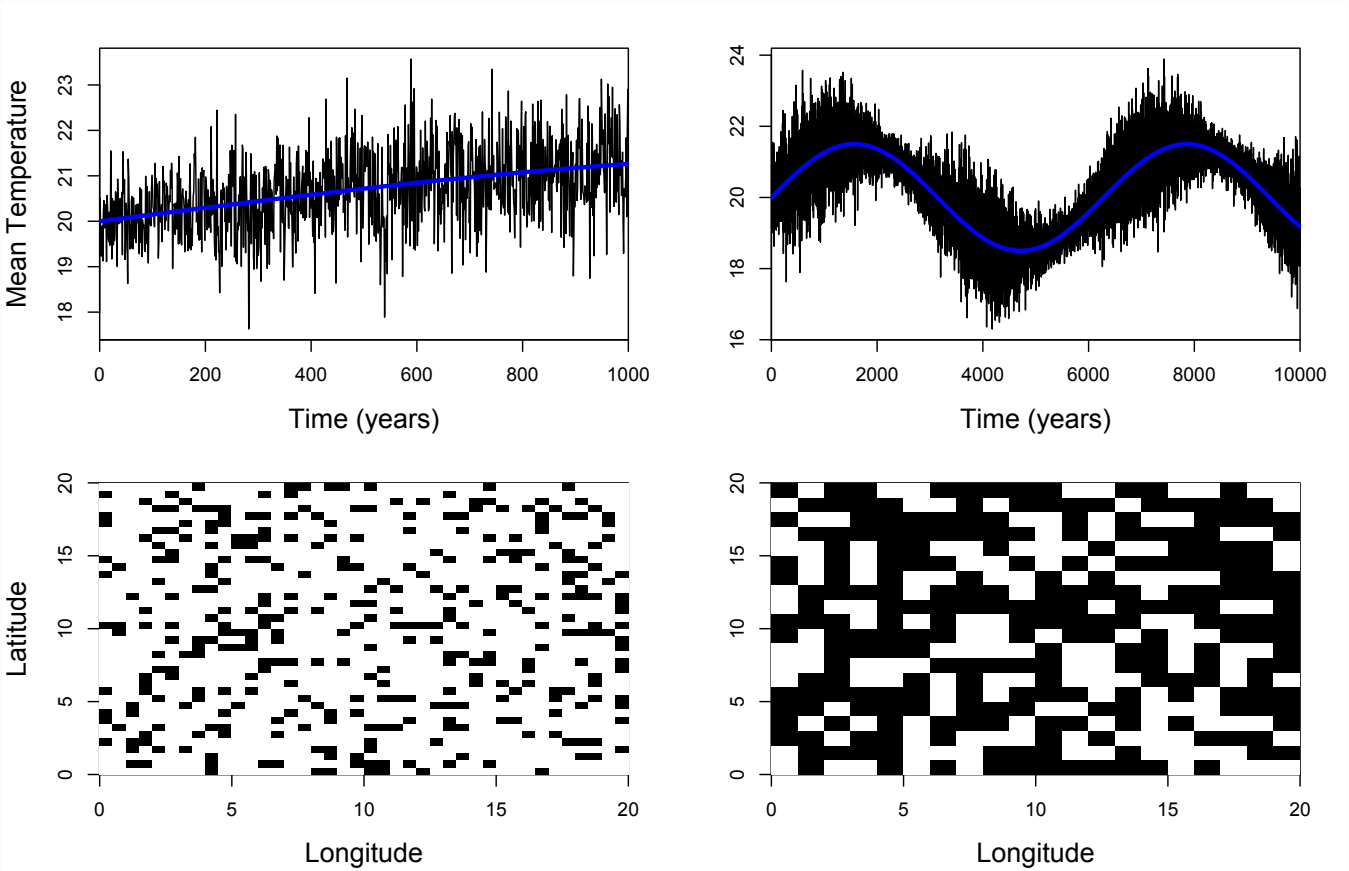
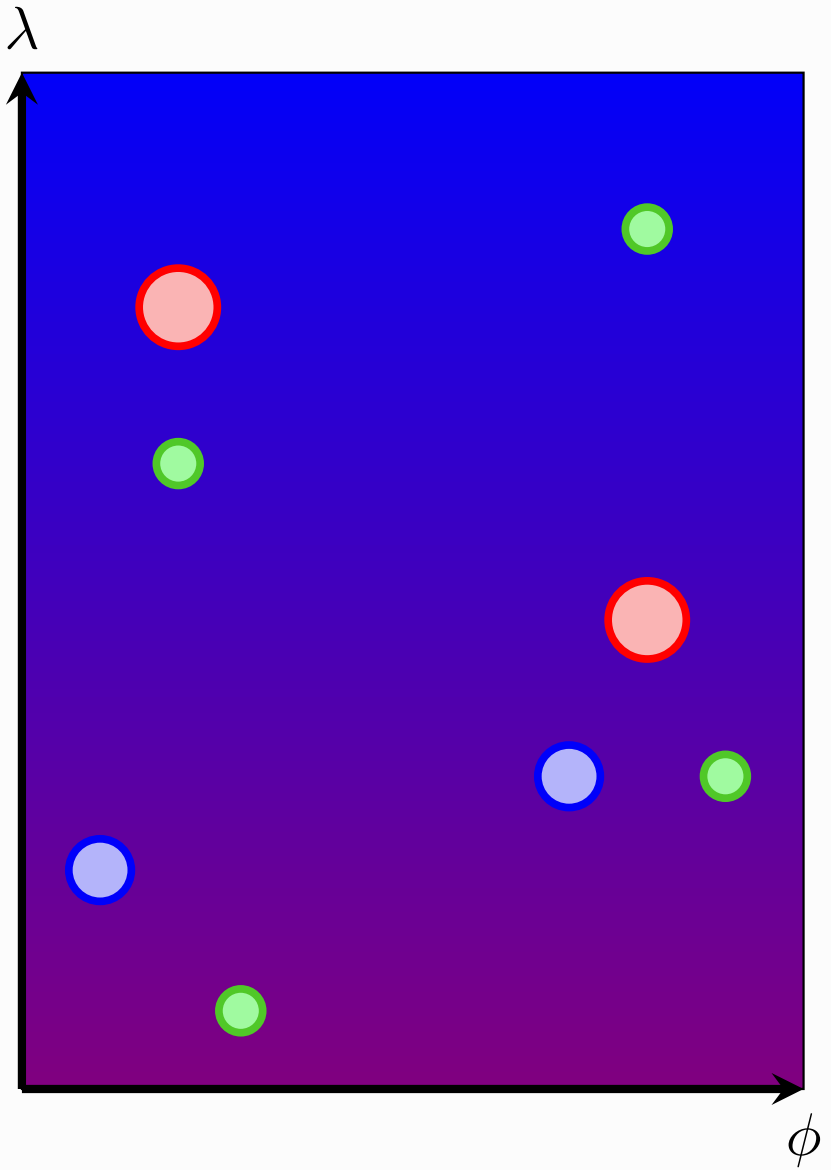
- Phenotypes ($\mathbf{T}$) are selected according to ($\mathbf{F}, \mathbf{A}, \mathbf{W}$)
- species identity or traits set series ?

Spatio-temporal Scale issues

- Range of variation are deeply linked to scale
- What is the adequate set of variables at a given scale
- How to scale up and down ?



Components interplay!



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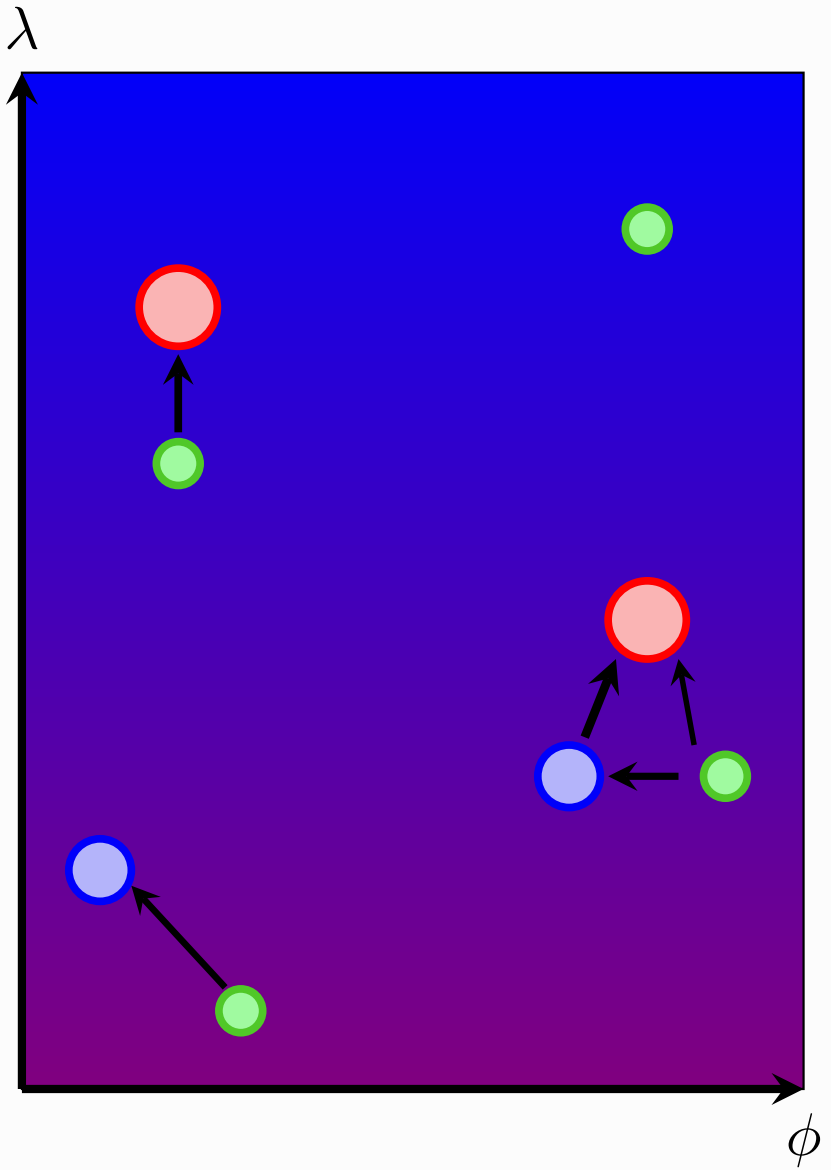

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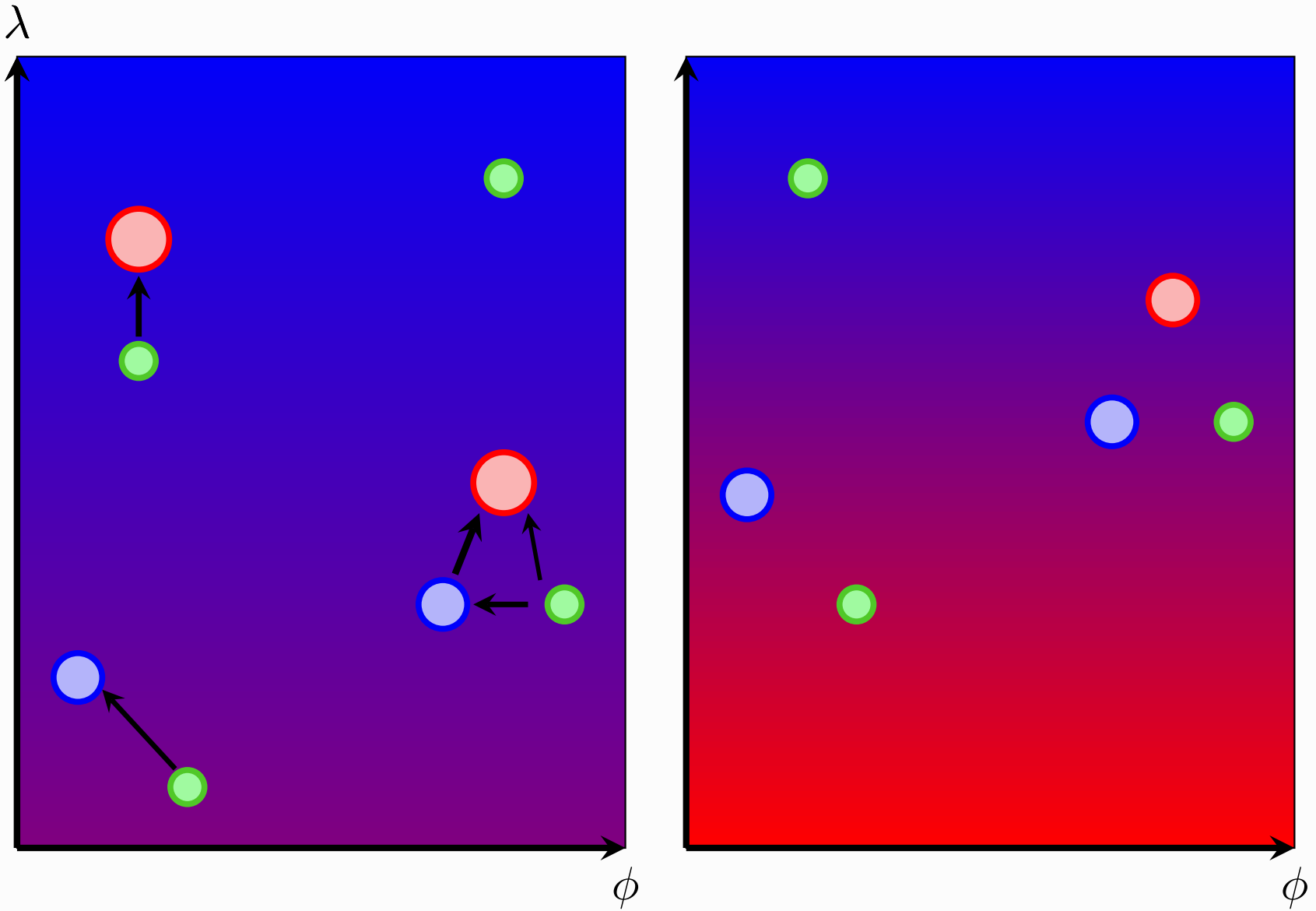

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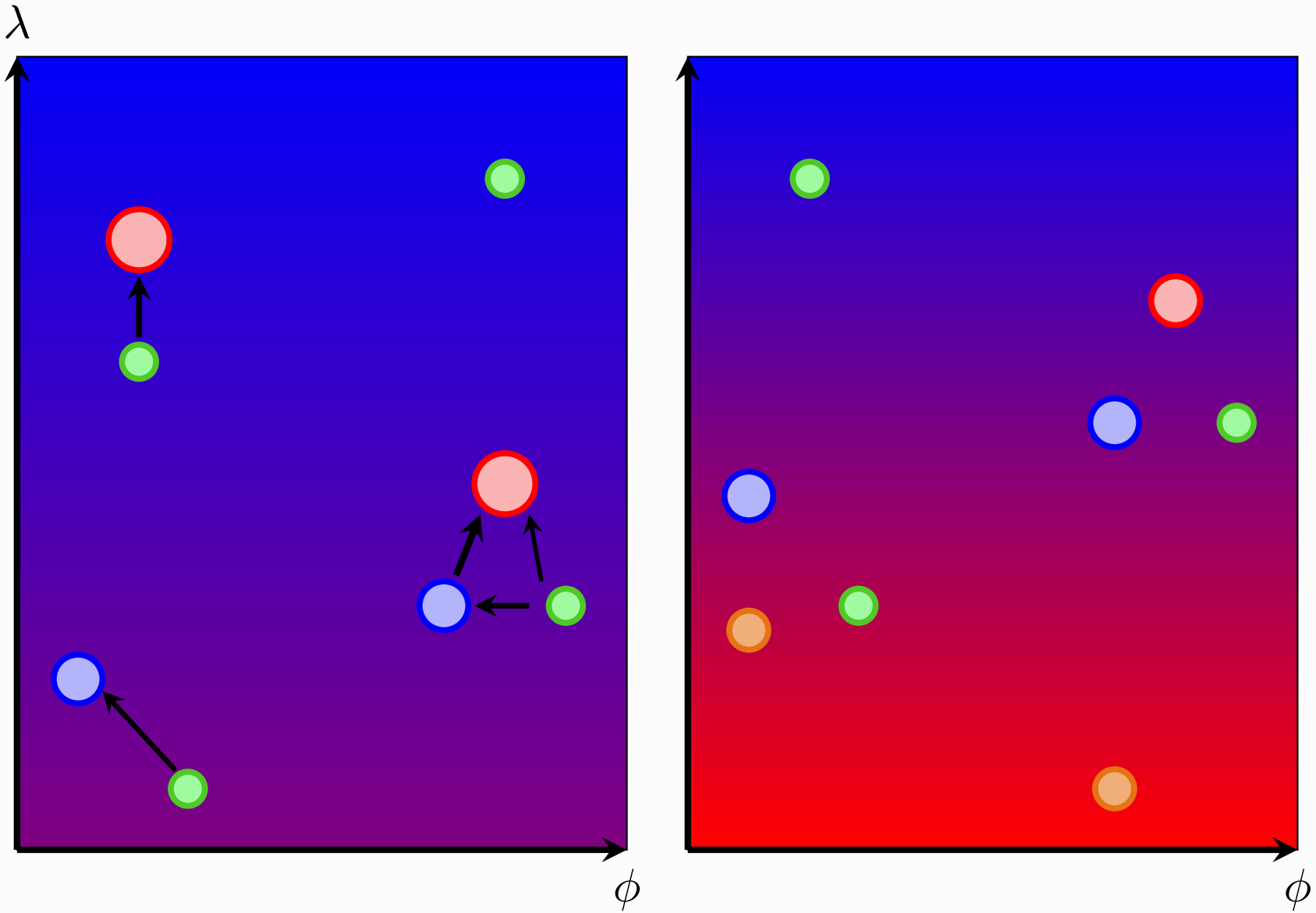

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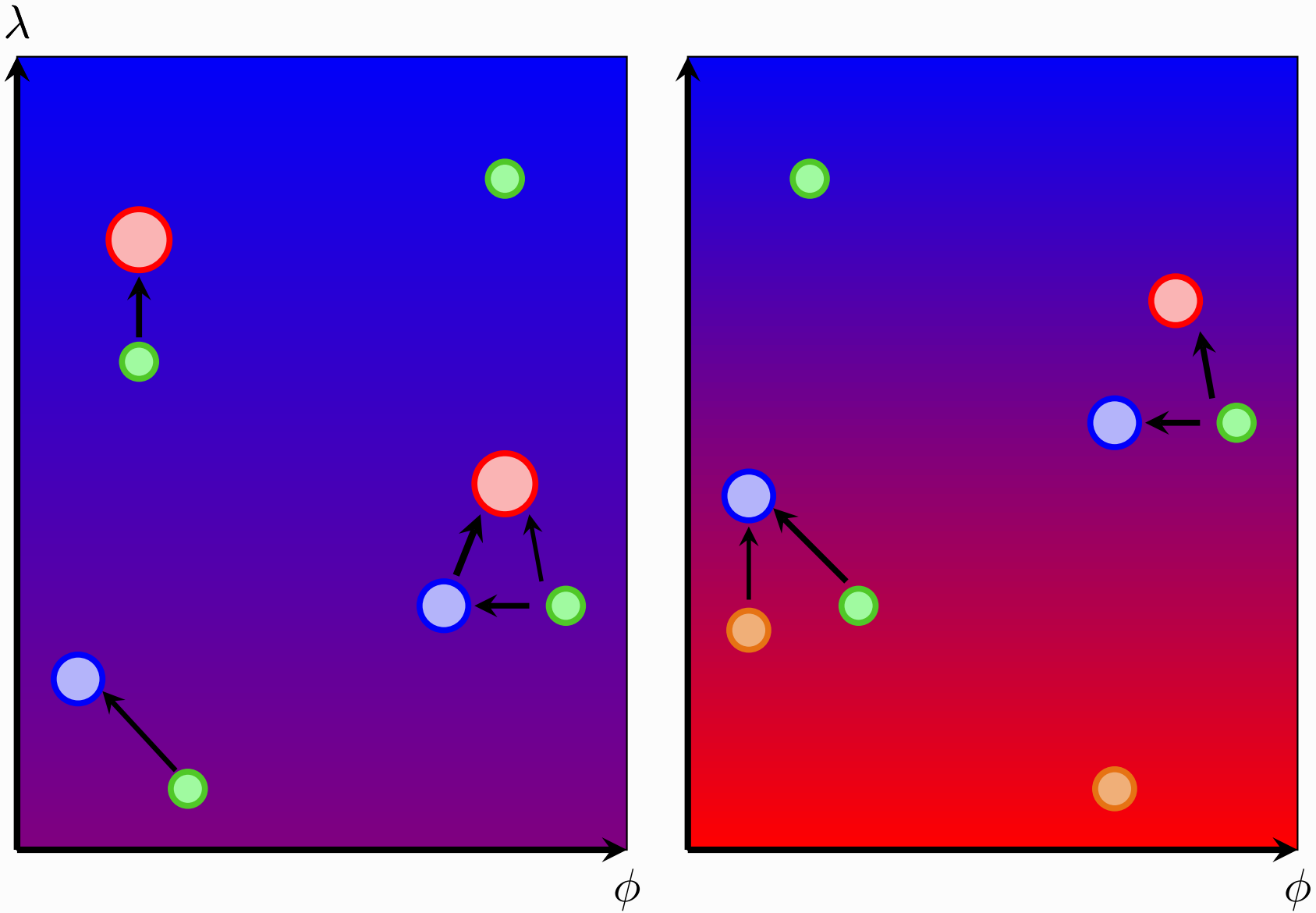

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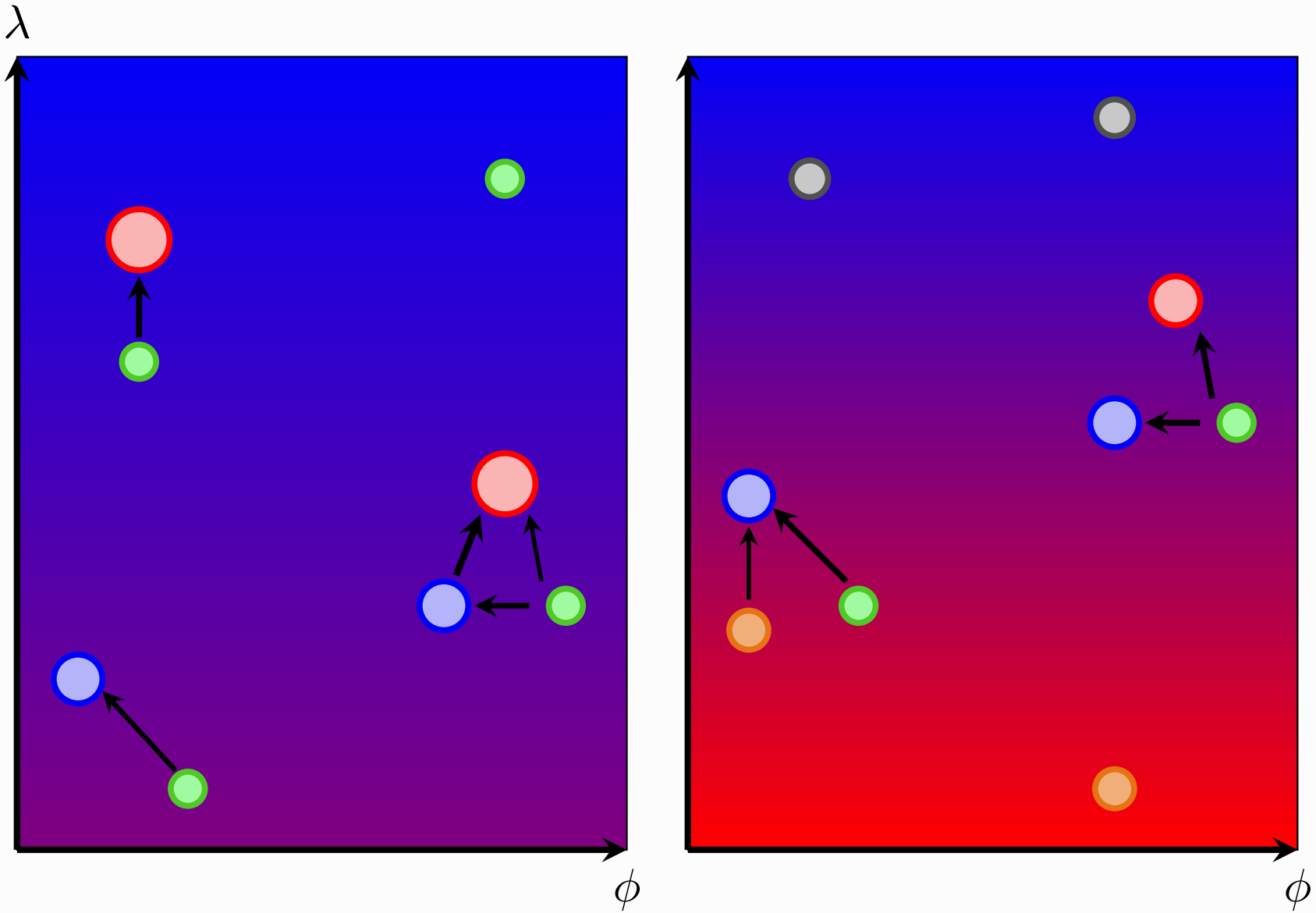

Globally

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- Aim 1 : Developing theoretical approaches to gather $\mathbf{F}, \mathbf{W}, \mathbf{A}, \mathbf{T}$
- Aim 2 : Developing new inference methods based on the theoretical work achieved

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- Aim 1-2 : Adding evolution through a population based approach
  - All processes well integrated provides a powerful model to address many questions
  - How traits of new emerging species are distributed regarding to their role in the network?

From theoretical to applied approach

- Aim 2-1 Can we find a general method to detect and quantify interactions in presence/absence data ?

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  - If species are dependent, their distributions must be related, which must be found in presence absence data (at large scale)

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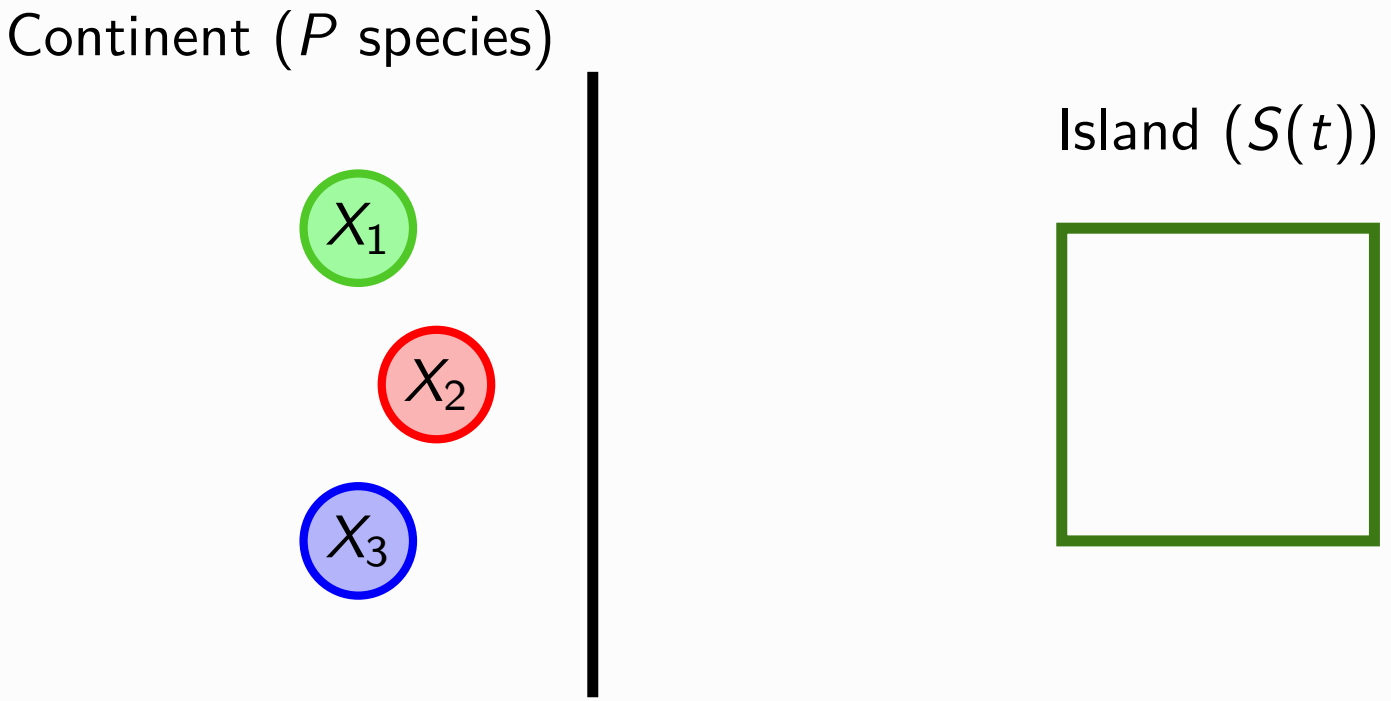
- Focusing on species diversity (S) in a given locality :
  - S can be increased by colonization c of species from a continental pool of species
  - Locally, species can die out e which decreases S



Model of MacArthur and Wilson (1963,1967)

The model is summarized as follows :

$$\frac{dS}{dt} = c(P - S) - eS \tag{2}$$

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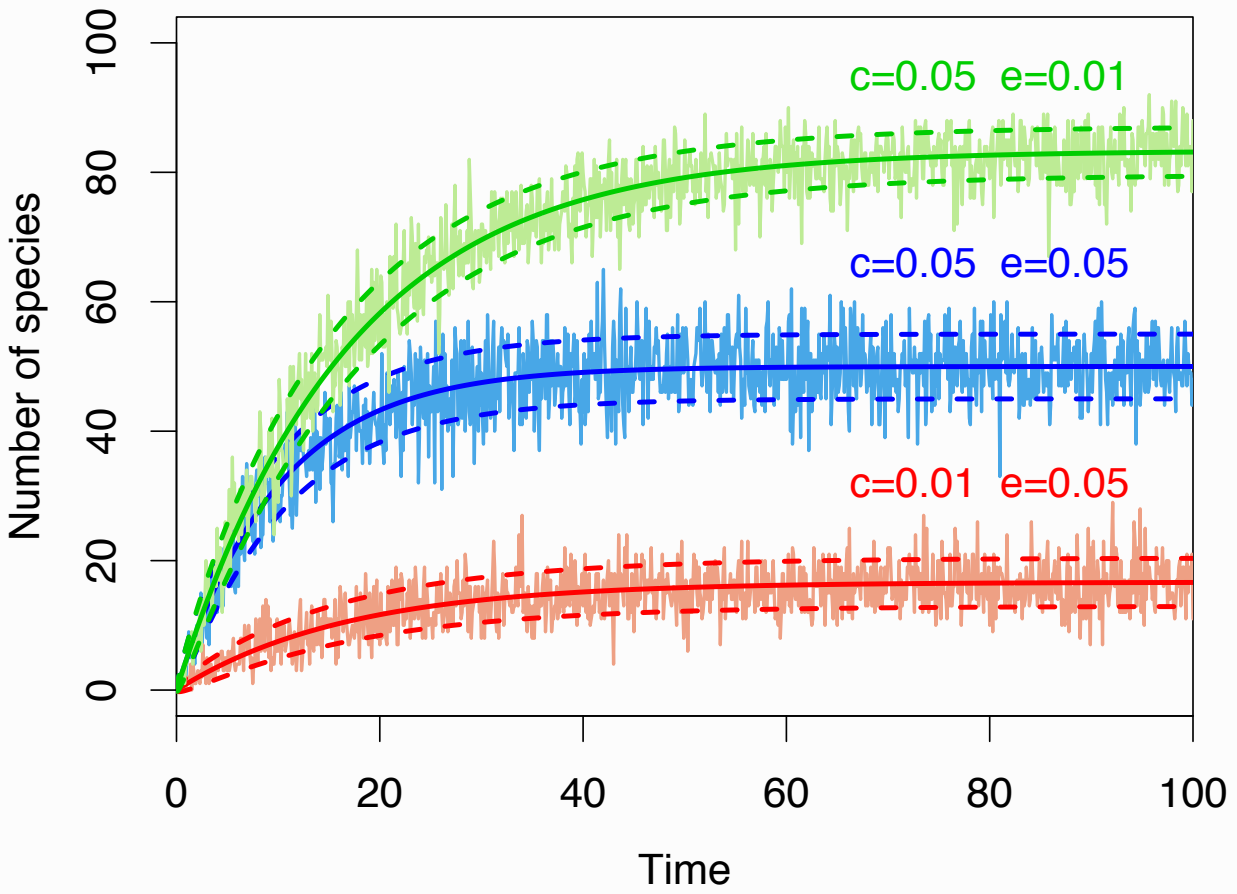
Which we can get from probabilities :

$$\begin{aligned}\mathbb{P}(S_{t+dt} = k) \quad = \quad & \mathbb{P}(S_{t+dt} = k | S_t = k)\mathbb{P}(S_t = k) \\ & + \mathbb{P}(S_{t+dt} = k | S_t = k-1)\mathbb{P}(S_t = k-1) \\ & + \mathbb{P}(S_{t+dt} = k | S_t = k+1)\mathbb{P}(S_t = k+1) \end{aligned} \tag{3}$$

Model of MacArthur and Wilson (1963,1967)

Two temporal dynamics :



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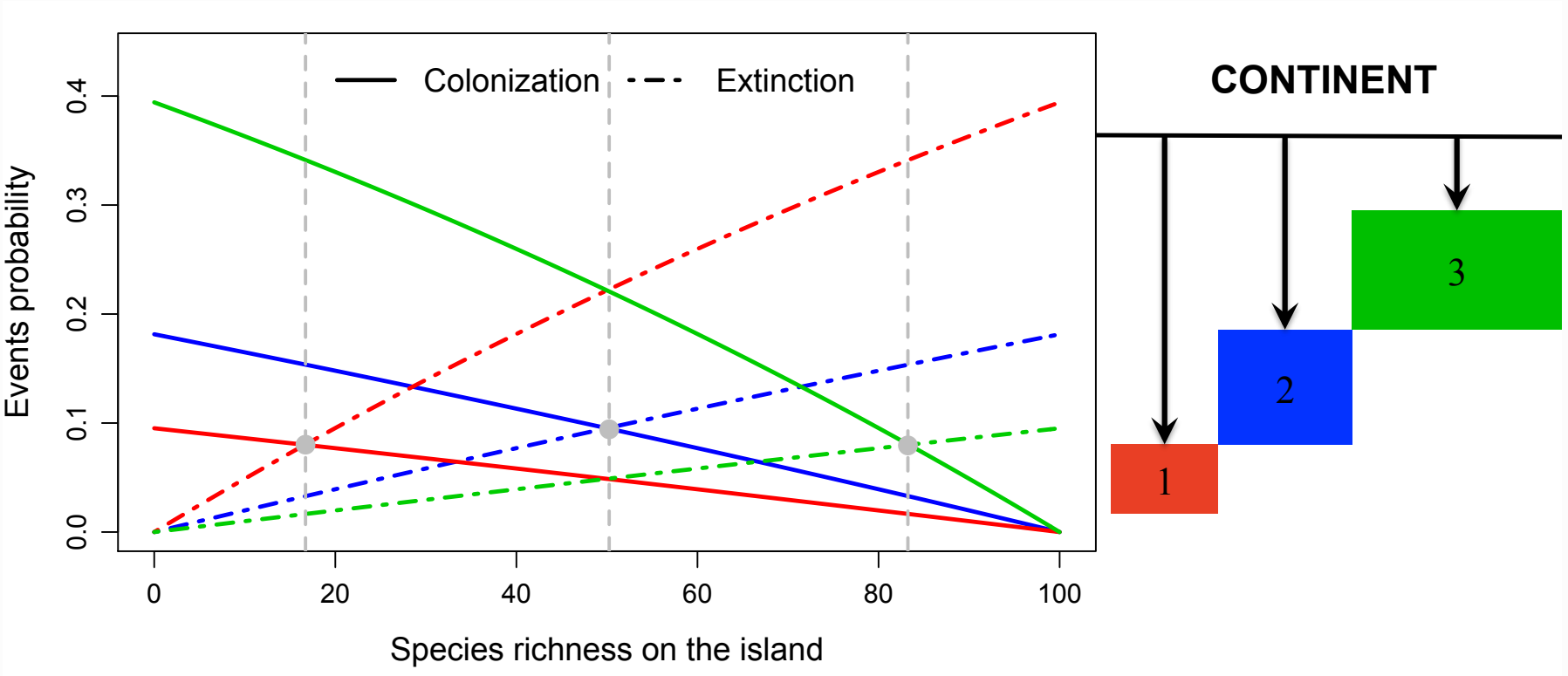
$$\text{Equilibrium reached for : } S_{eq} = P\frac{c}{c+e} \quad (4)$$



Chapter 1 :

Environmental constraints, interaction in the Theory of Island Biogeography

Adding environmental constraints

- one species (X_i) => one couple (c_i, e_i)
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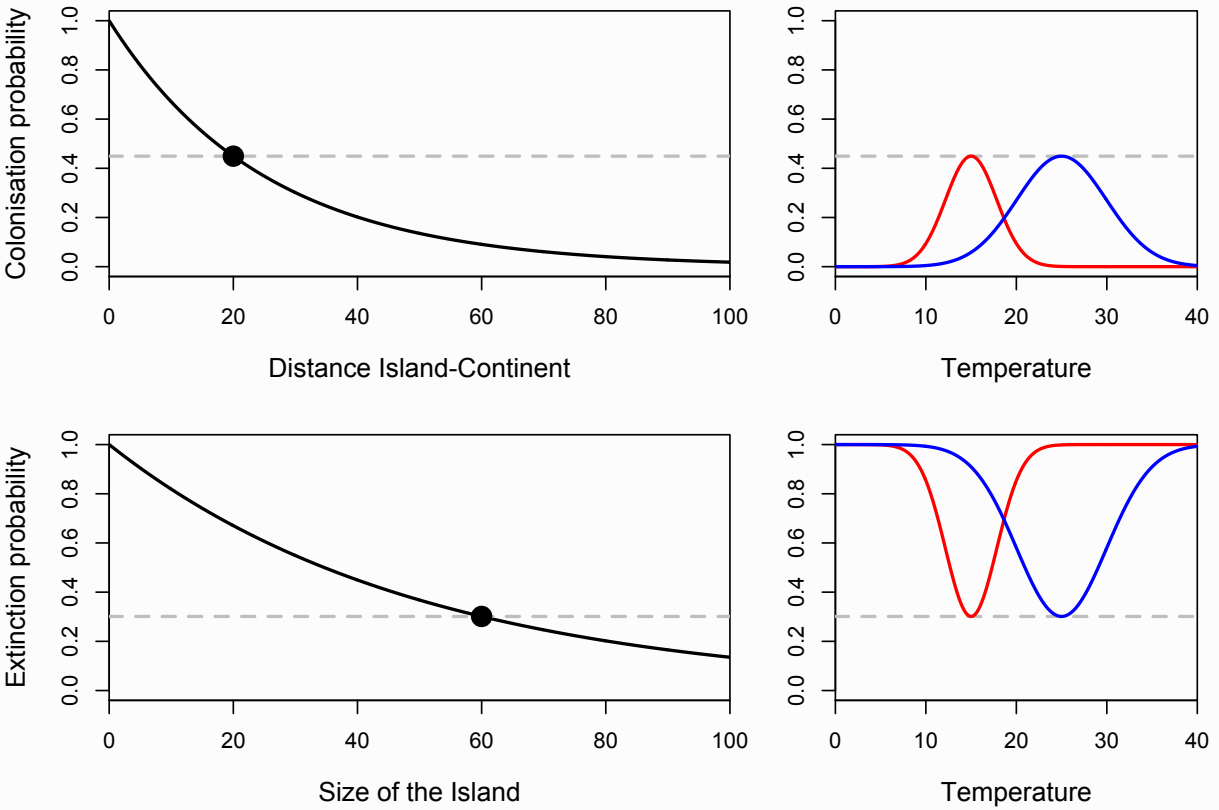

Adding environmental constraints

$$S_{eq} = P\frac{c}{c+e}$$

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then becomes :

$$S_{eq} = \sum_{k=1}^{P} \frac{c_k(w)}{c_k(w) + e_k(w)} \tag{5}$$

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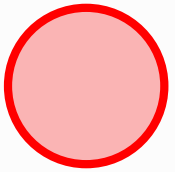

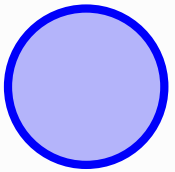

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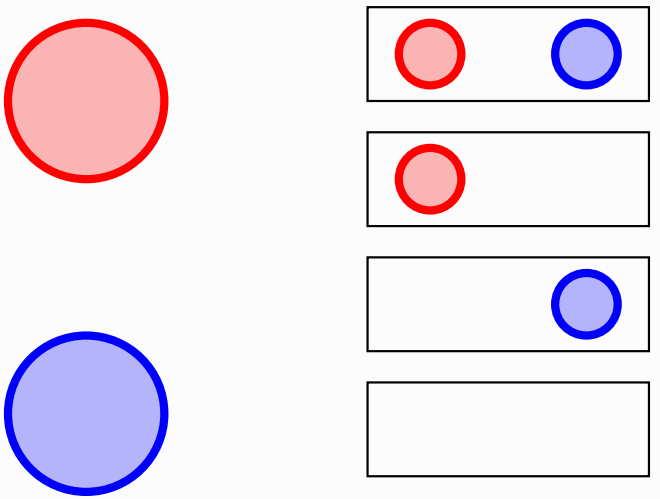

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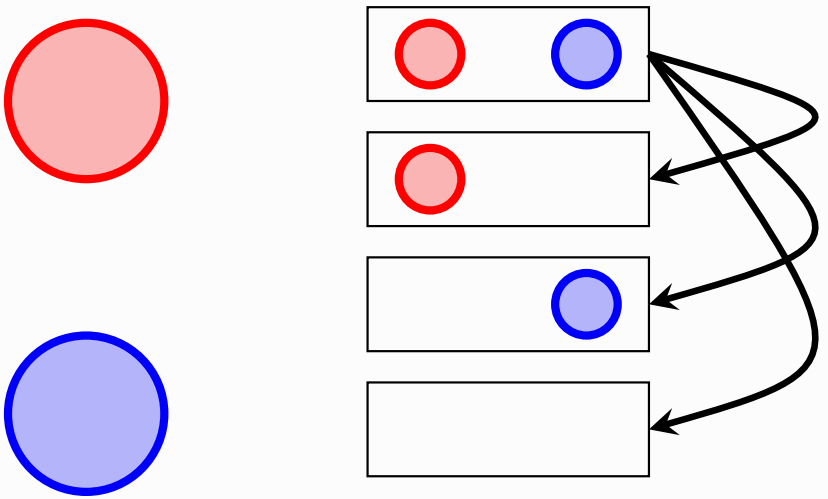

Transition Matrix of the Markov Chains

- By definition :

$$\begin{aligned} m_{i,j} &= \mathbb{P}((X_{1,t+dt}, X_{2,t+dt})_j | (X_{1,t}, X_{2,t})_i) \\ &= \mathbb{P}(Y_{j,t+dt} | Y_{i,t}) \end{aligned} \tag{6}$$

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- $e_i \Rightarrow e_i(w) \Rightarrow e_i(w, \mathbf{A})$?
- $c_i \Rightarrow c_i(w) \Rightarrow c_i(w, \mathbf{A})$?

Interactions change extinction and colonization rates

- Include A as a amount of interaction
- $\mathbf{A}(X_{1,t}, ..., X_{P,t})^T$

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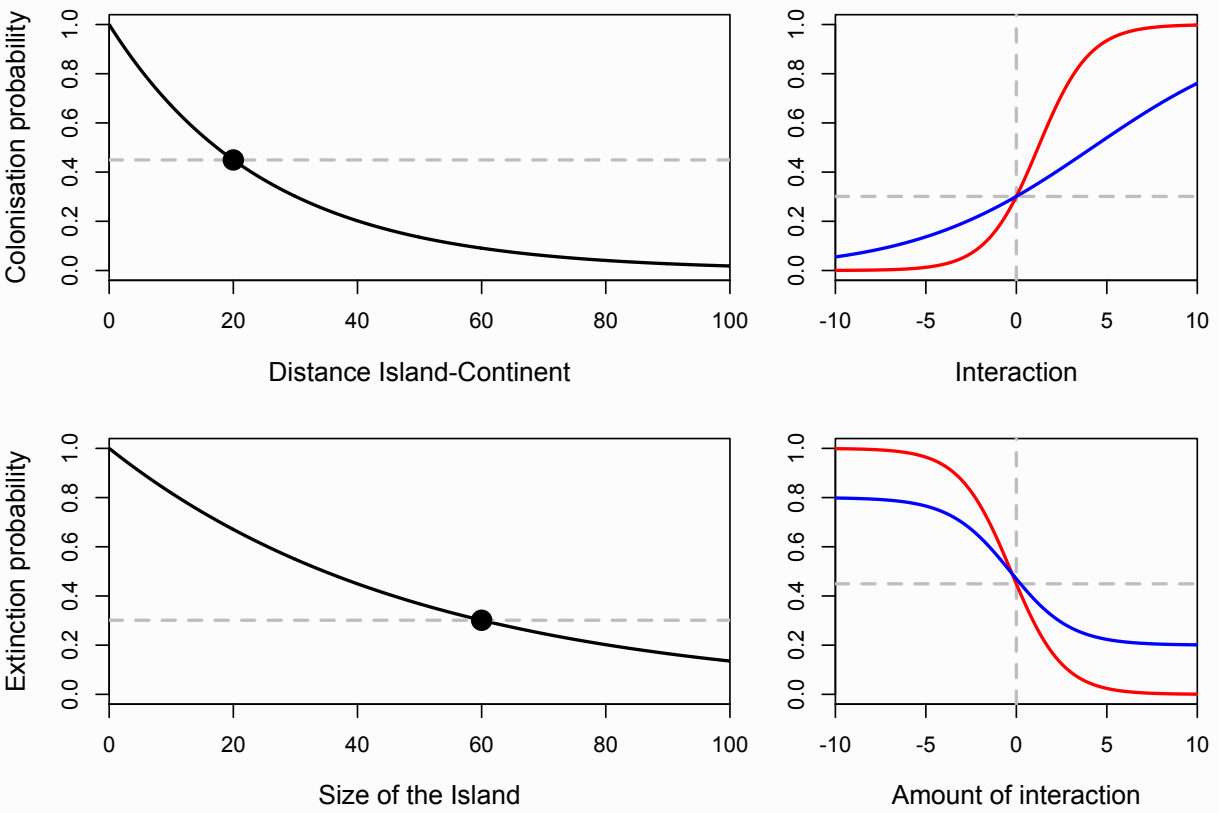

Equilibrium :

$$(\mathbb{P}(Y_{1,t+dt}), ..., \mathbb{P}(Y_{2^P,t+dt})) = (\mathbb{P}(Y_{1,t}), ..., \mathbb{P}(Y_{2^P,t+dt}))\mathbf{M} \quad (7)$$

- Under some assumptions, we can get S_{eq}
- Actually, we get more : $(\mathbb{P}(Y_{1,eq}), ..., \mathbb{P}(Y_{2^P,eq}))$:
  - S_{eq}
  - $\mathbb{P}(X_k = 1)_{eq}$
  - $\mathbb{P}(\bigcap_k X_k = 1)_{eq}$

Chapter 2 :

Environmental constraints, Interaction and Evolution in the Theory of Island Biogeography

How to integrate Evolution ?

- Through time, mutations affect $\mathbf{T} = (\tau_1, \tau_2, ..., \tau_m)$

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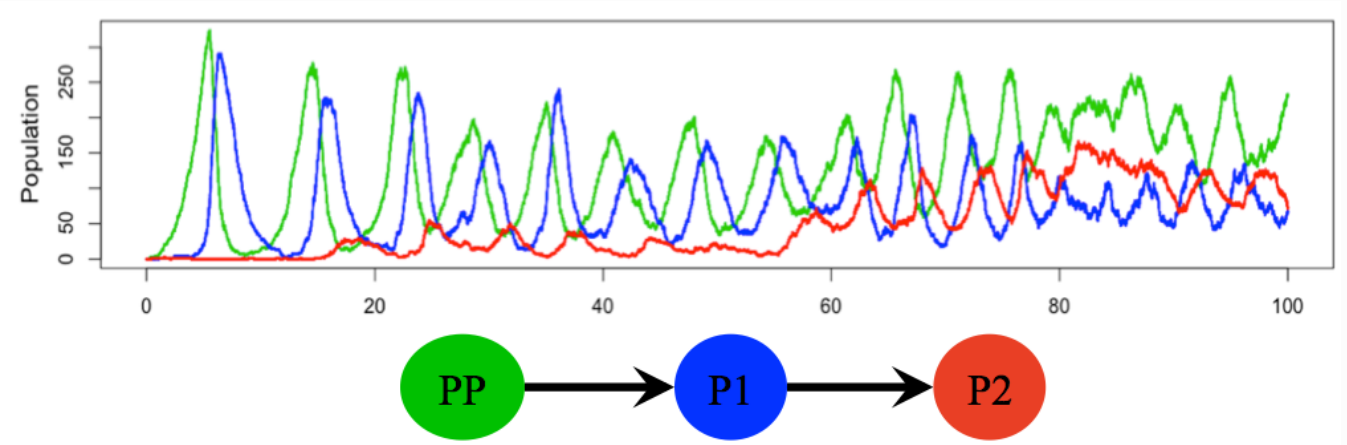
- Through time, mutations affect $\mathbf{T} = (\tau_1, \tau_2, ..., \tau_m)$
- Speciation can occur $=>$ P is no longer a constant
- To successfully integrate speciation, we use a stochastic population dynamics

Our model

- Generalized Lotka-Volterra formulated in birth dead processes
- Colonisation events



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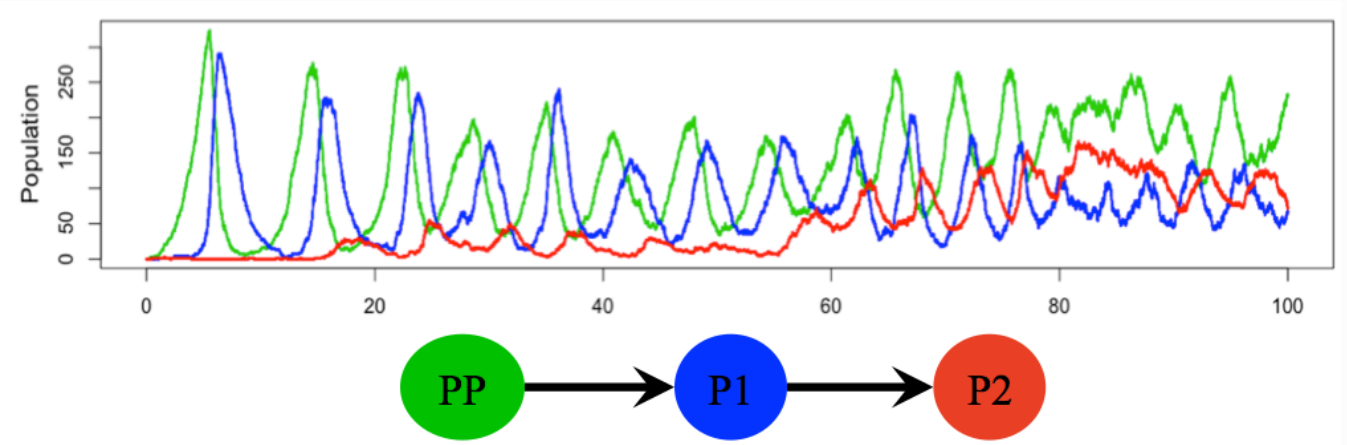

- Explicit environmental gradient
- At each time, possible mutation, traits change so

Functional traits as a key !

1. **T** defines responses to the environment $=>$ **W**

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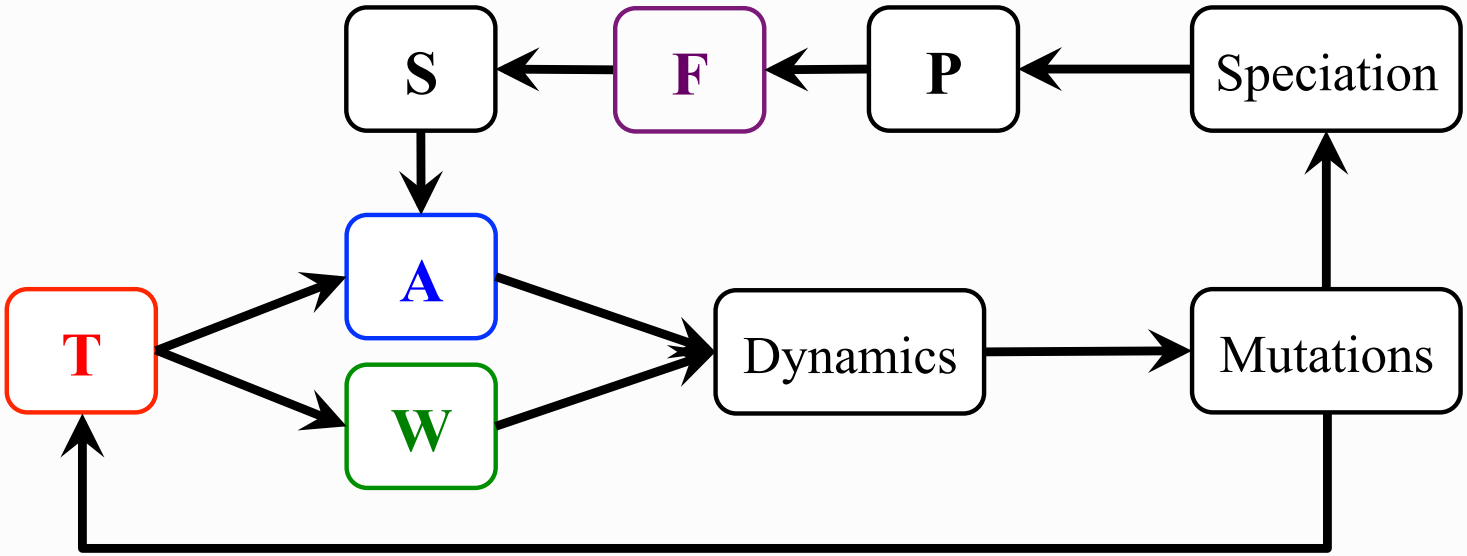
3. **T** defines species and speciation $=>$ P change

Functional traits as a key !



Again, this is a rich model, we will focus on traits distribution of new emerging species.

Species interactions in data

Chapter 3 :

Species interaction in presence/absence data

Species interactions in data

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- $\mathbb{P}(X_1|\mathbf{W})$
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How can we detect interactions in information we have ?

Species interactions in data

- Species independent : $\mathbb{P}(X_1, X_2|\mathbf{W}) = \mathbb{P}(X_1|\mathbf{W})\mathbb{P}(X_2|\mathbf{W})$

Species interactions in data

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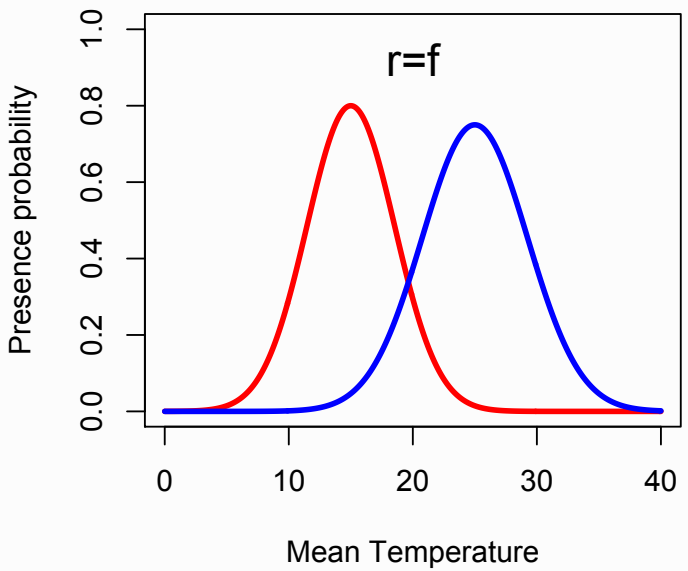
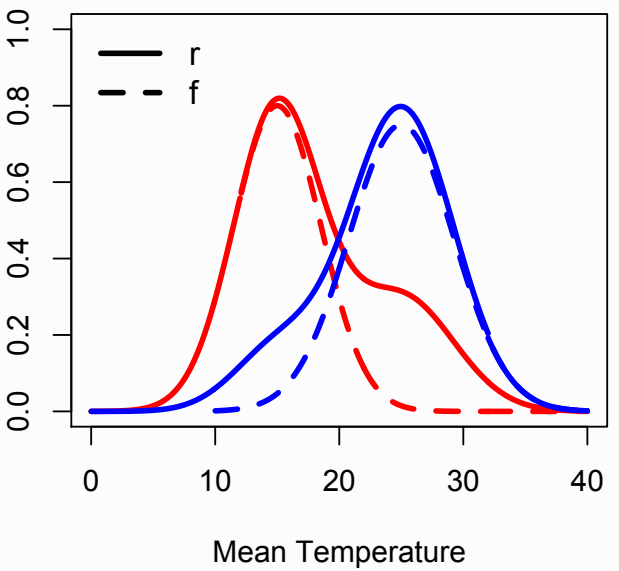
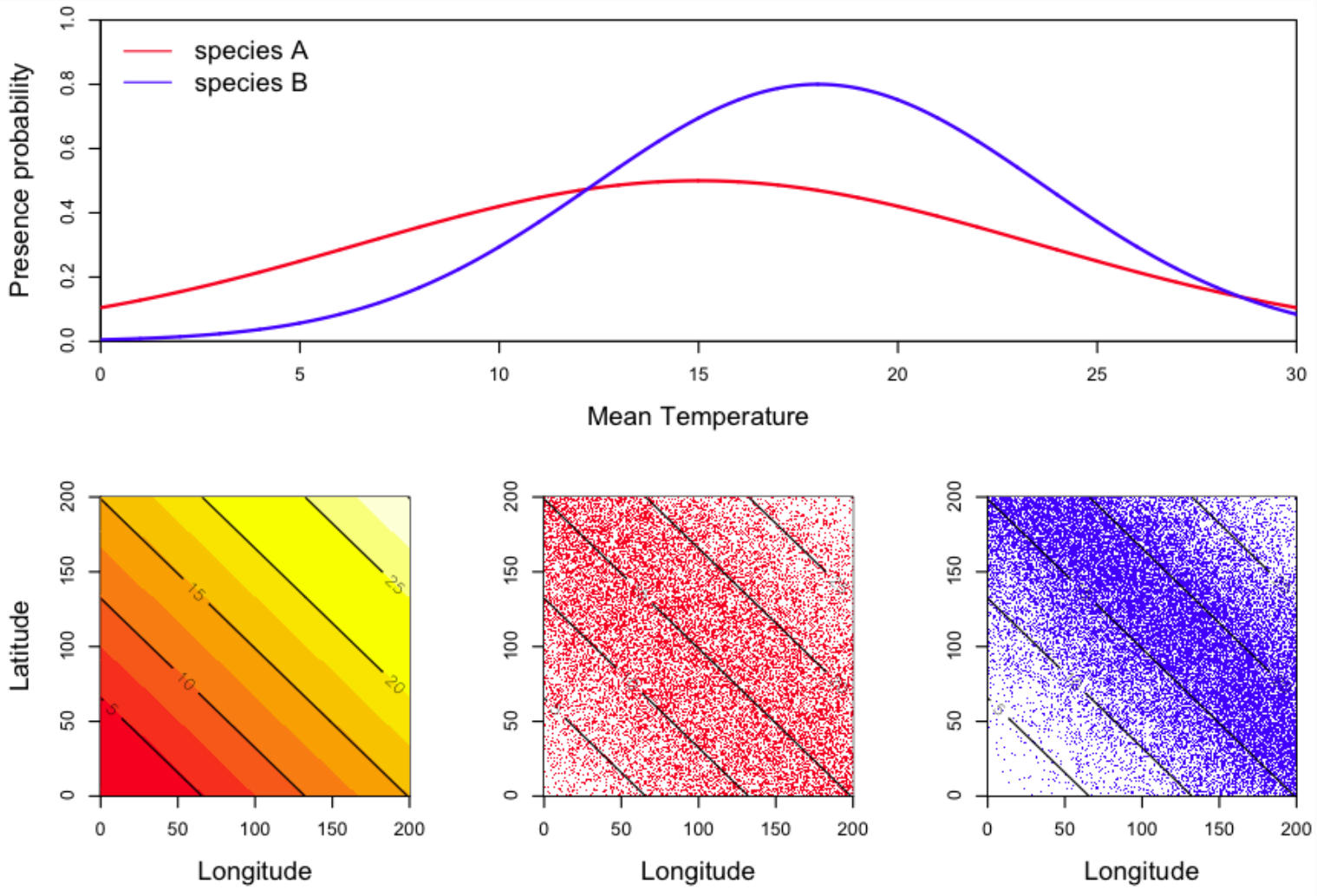
- Idea behind : $\epsilon_{1,2} = r_{X_1}(\mathbf{W}) - f_{X_1}(\mathbf{W})$

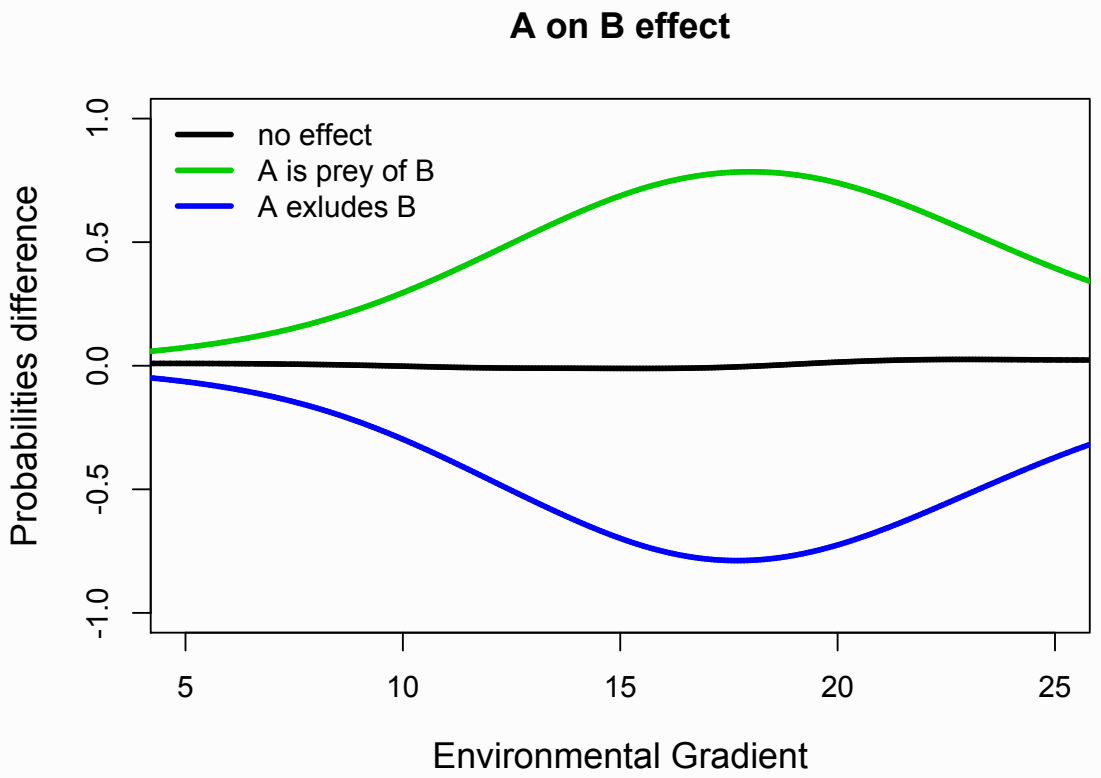




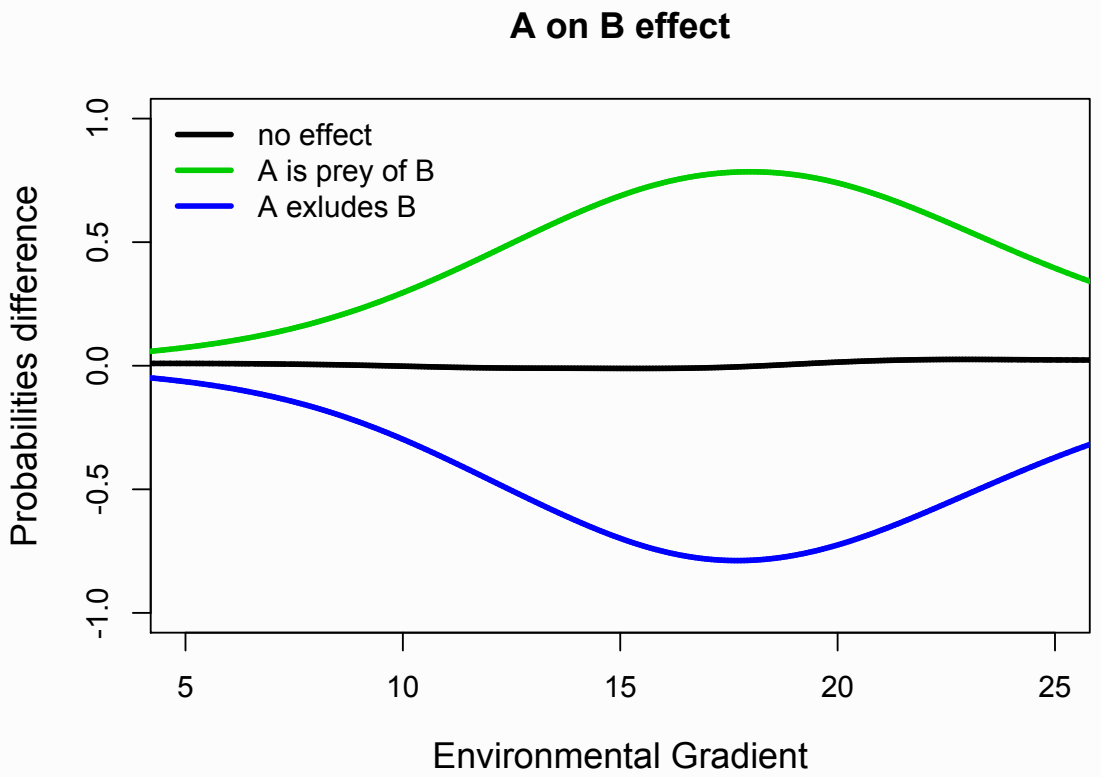
Species interactions in data



Species interactions in data



Species interactions in data



- Expanding the method for many species
- Using the method with large datasets

Merci