



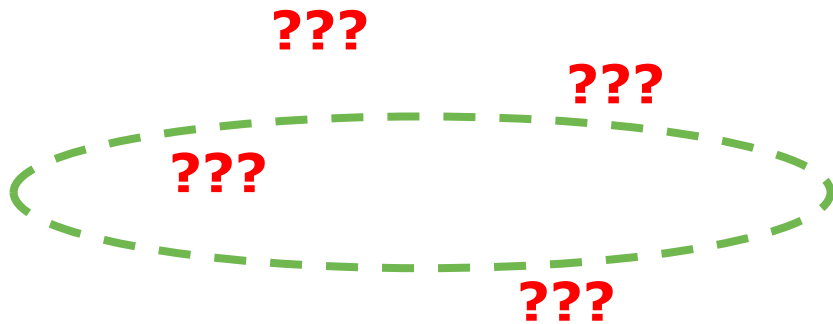
# Introduction to the R package `mobsim`

January 19th 2022

Alban Sagouis  
Original creator: Felix May

# Biodiversity science

Real world



# Biodiversity science

Real world

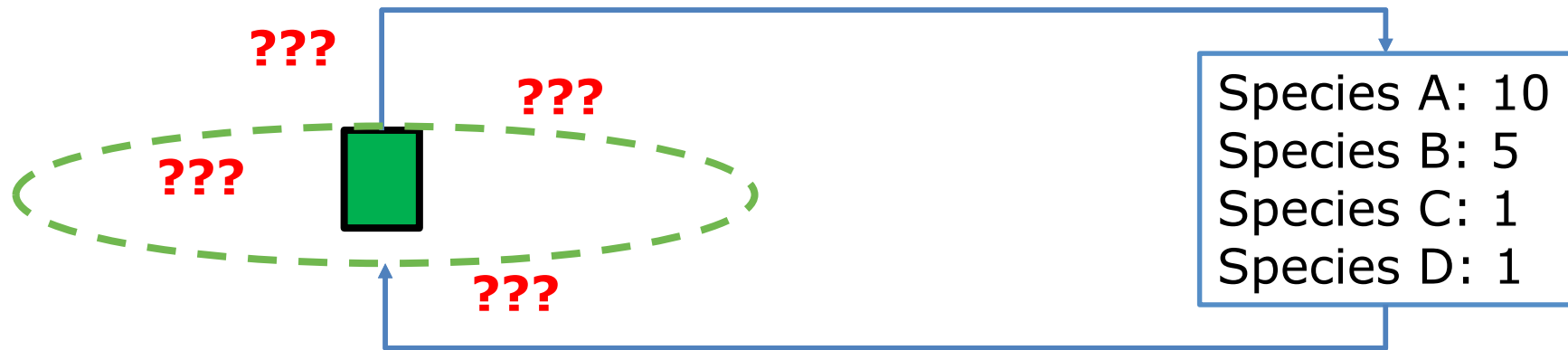
Sampling



# Biodiversity science

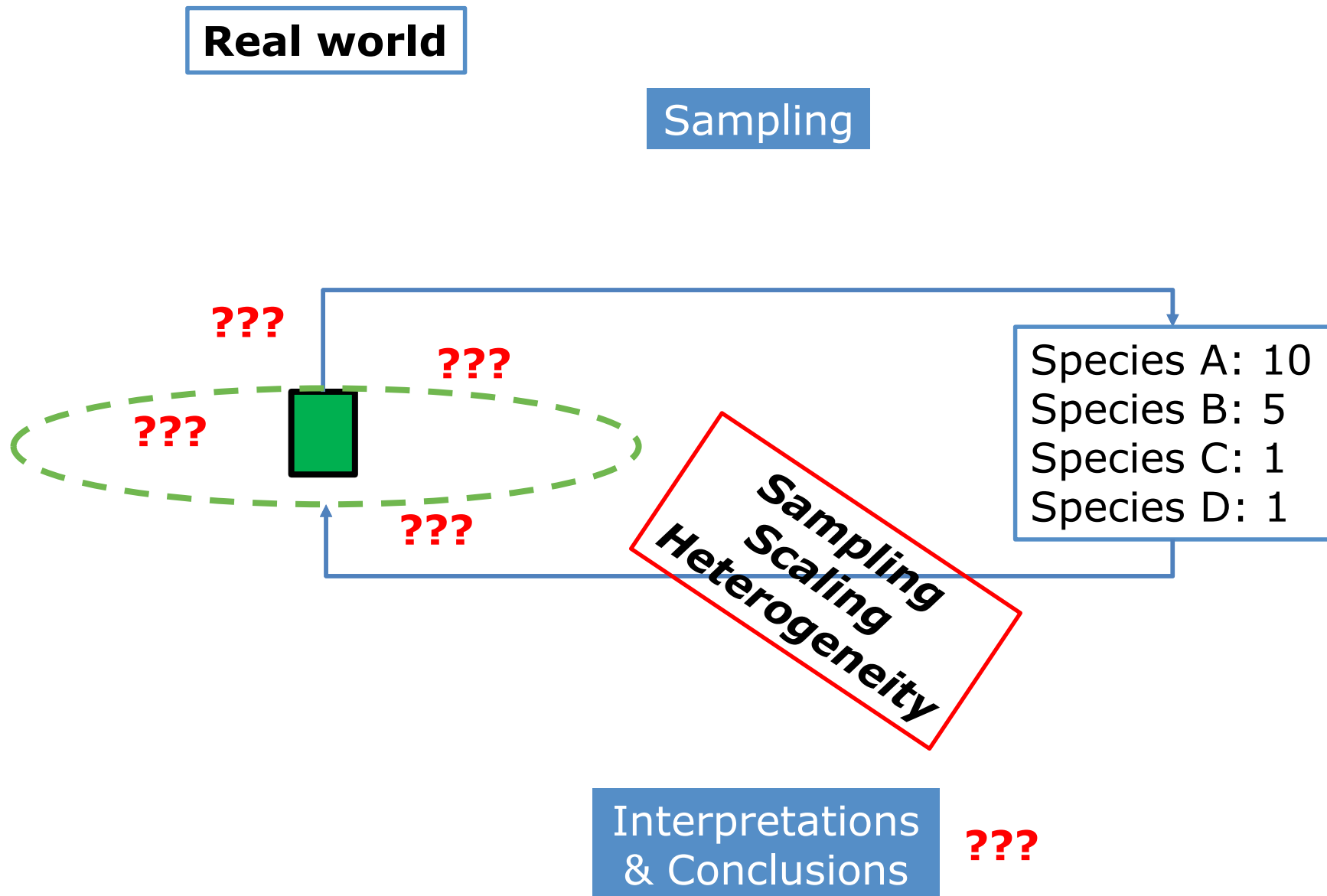
Real world

Sampling



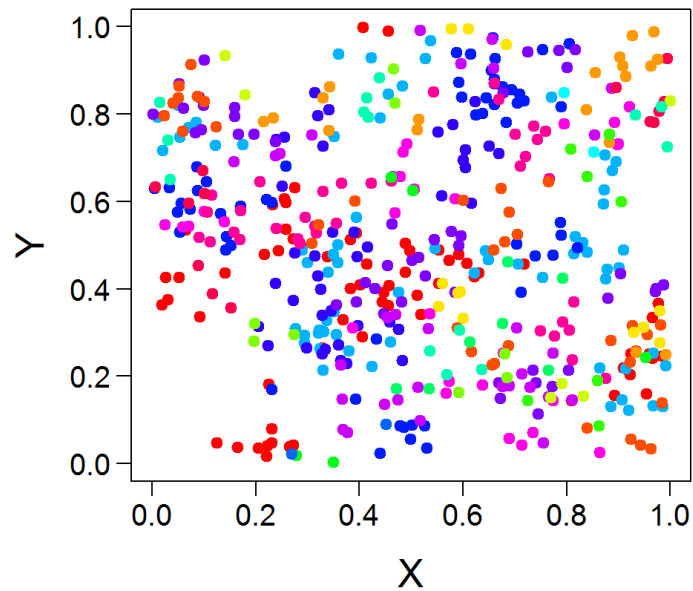
Interpretations  
& Conclusions

# Biodiversity science



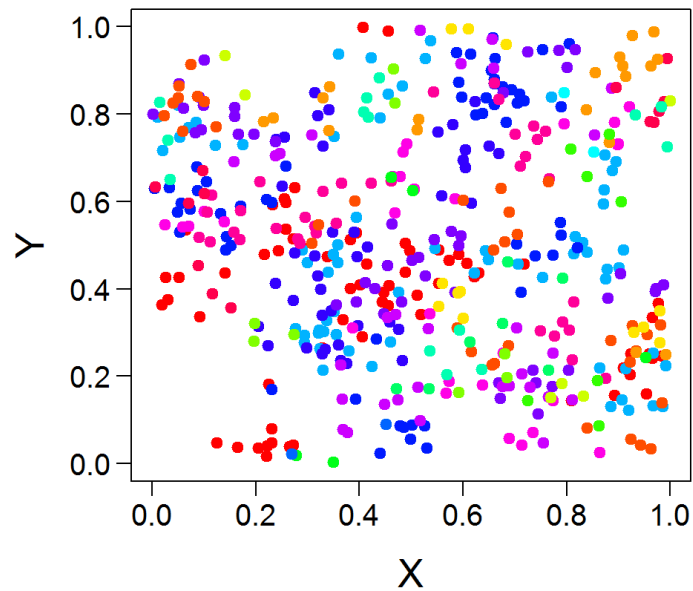
# Learning from simulated data

**Simulation:** complete control



# Learning from simulated data

**Simulation:** complete control

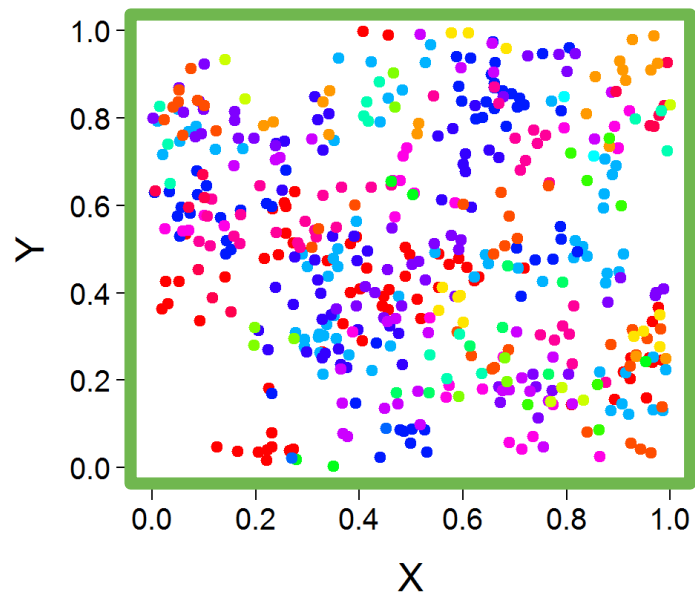


Change  
parameters

Test  
hypotheses

# Learning from simulated data

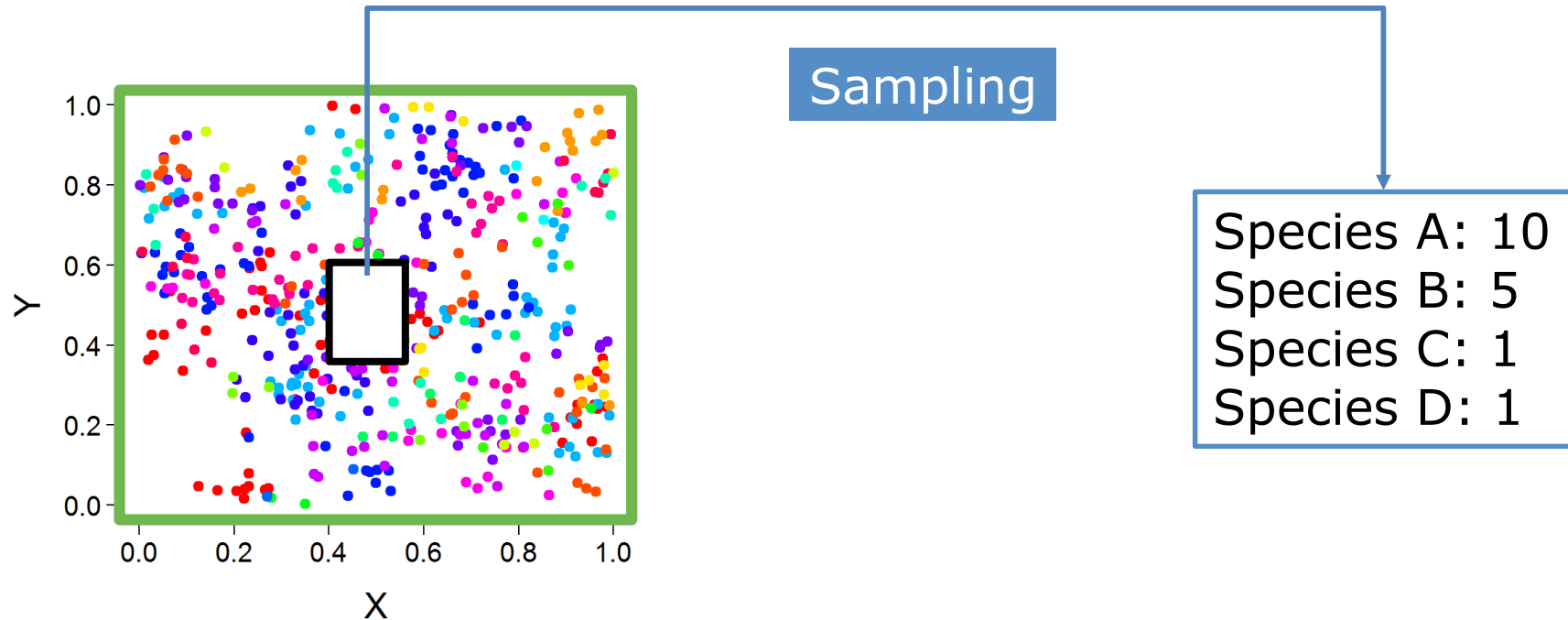
**Simulation:** complete knowledge





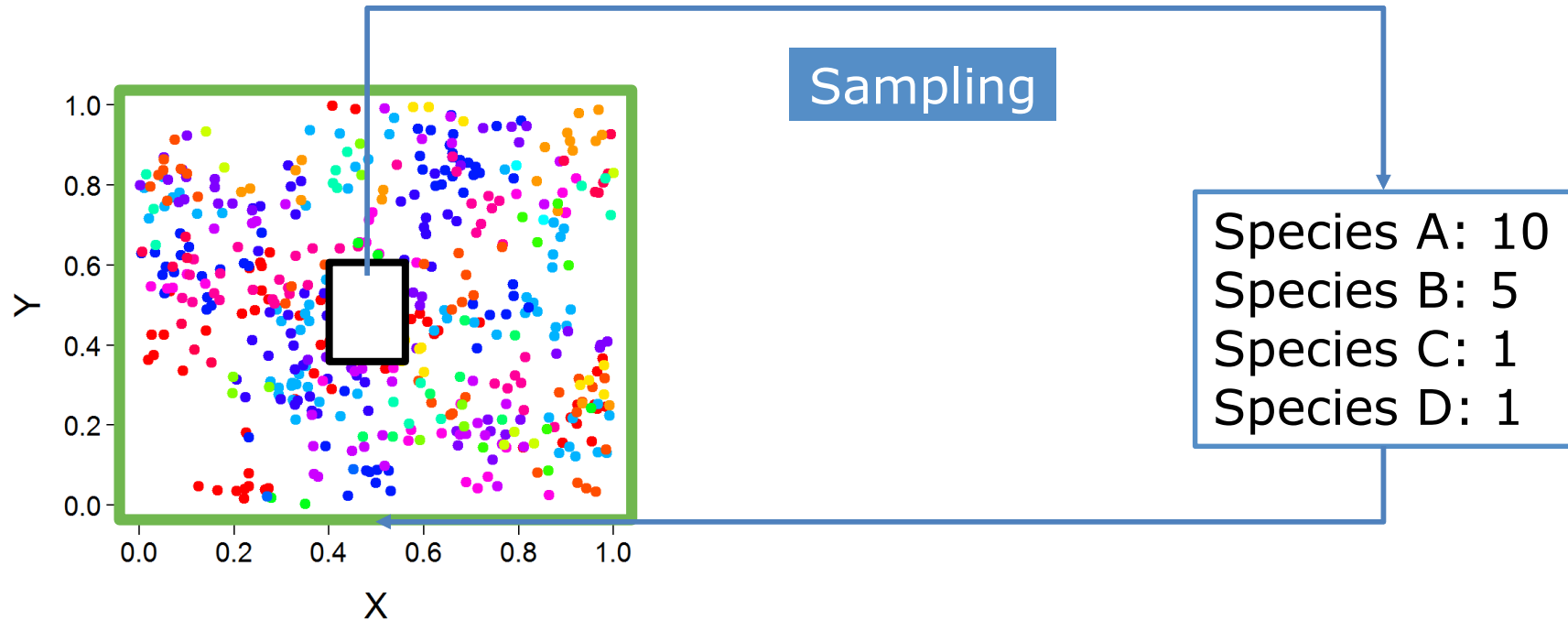
# Learning from simulated data

**Simulation:** complete knowledge



# Learning from simulated data

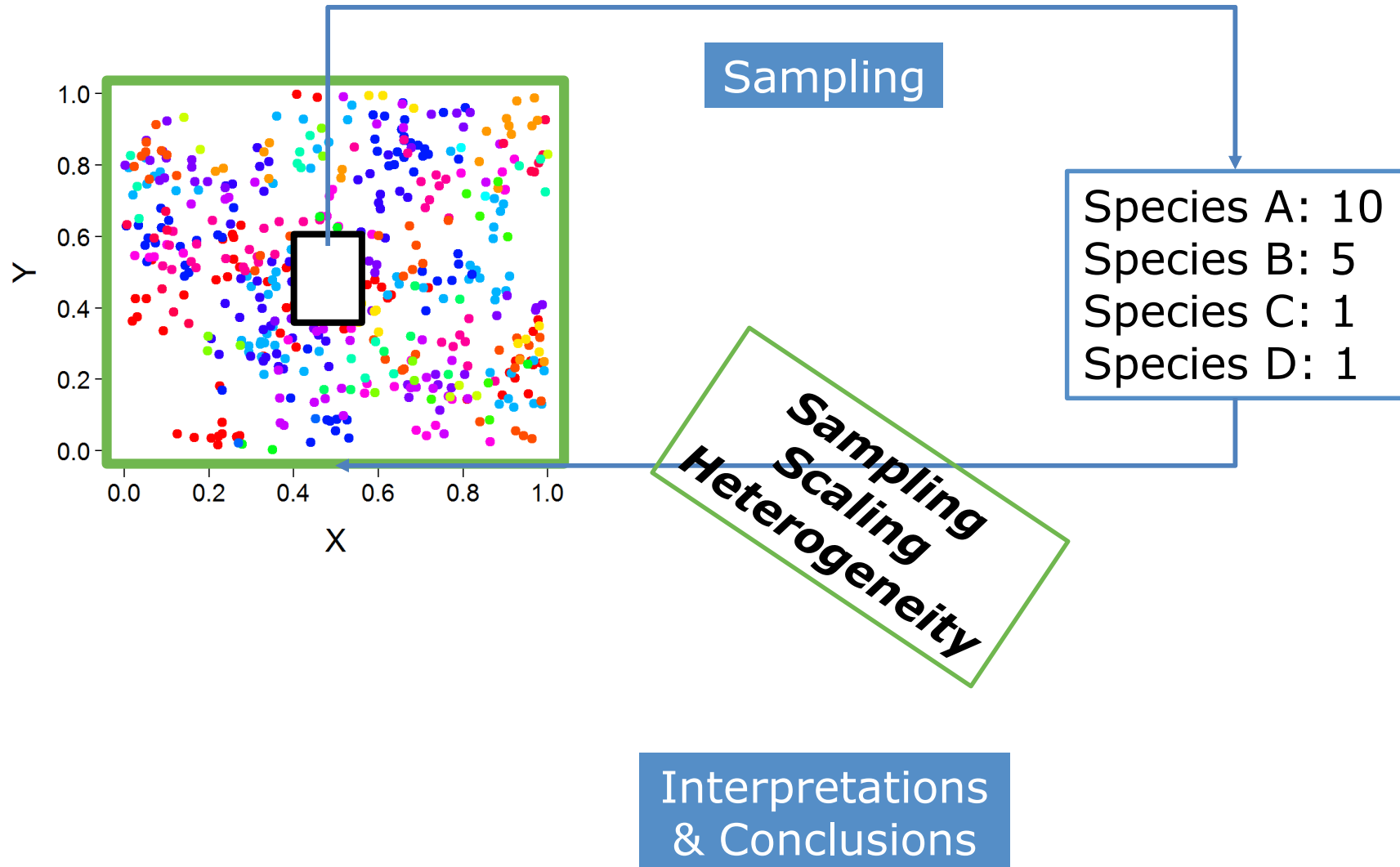
**Simulation:** complete knowledge



Interpretations  
& Conclusions

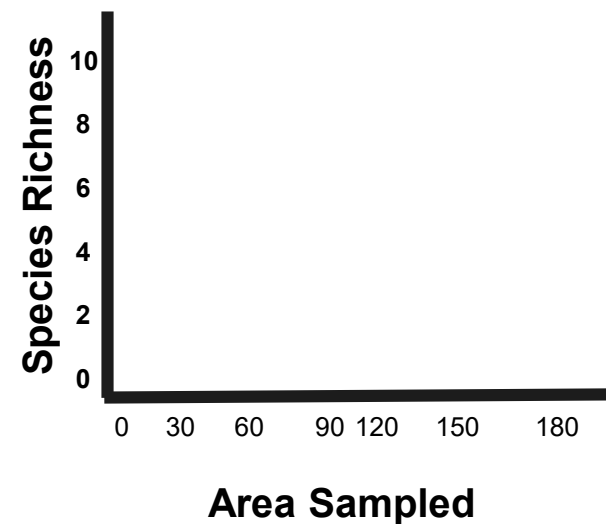
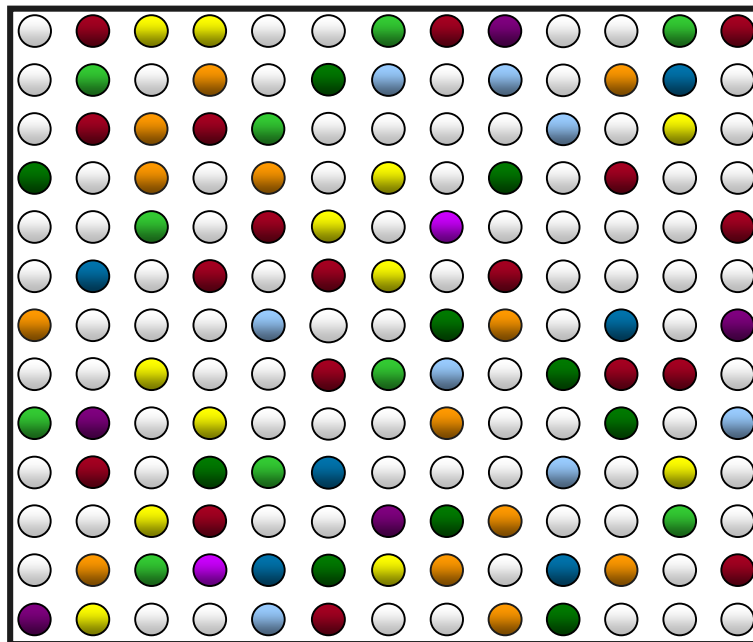
# Learning from simulated data

**Simulation:** complete knowledge



# Scale and Sampling effect on Species Area Relationships

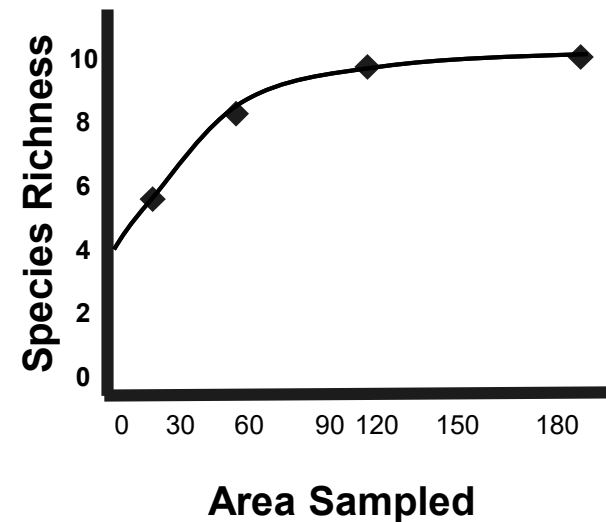
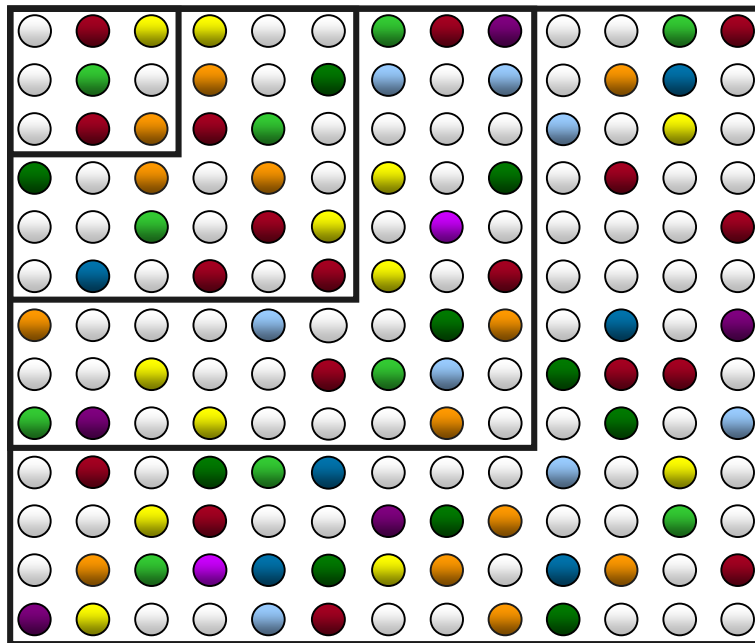
Pristine Community



*Chase and Knight 2013 Ecology Letters*

# Scale and Sampling effect on Species Area Relationships

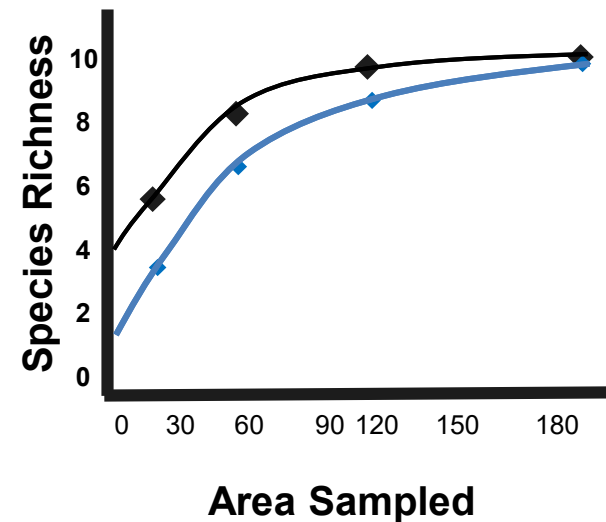
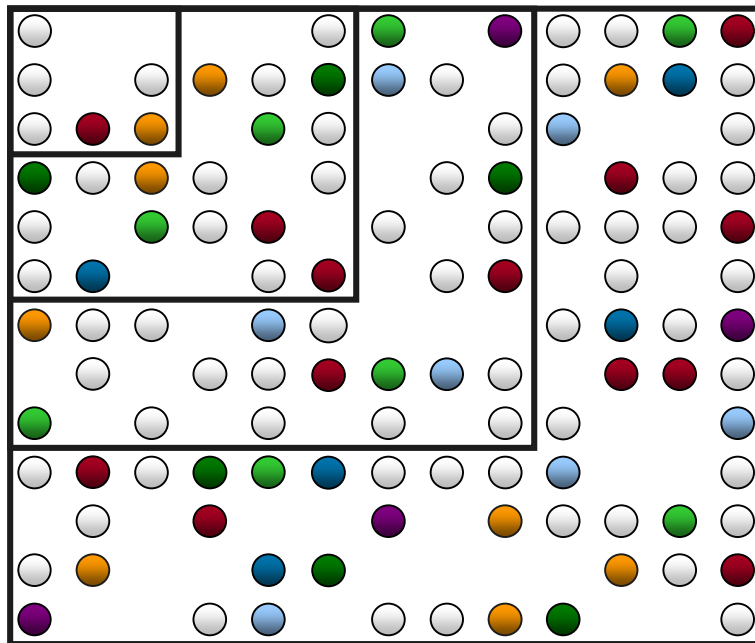
Pristine Community



*Chase and Knight 2013 Ecology Letters*

# Scale and Sampling effect on Species Area Relationships

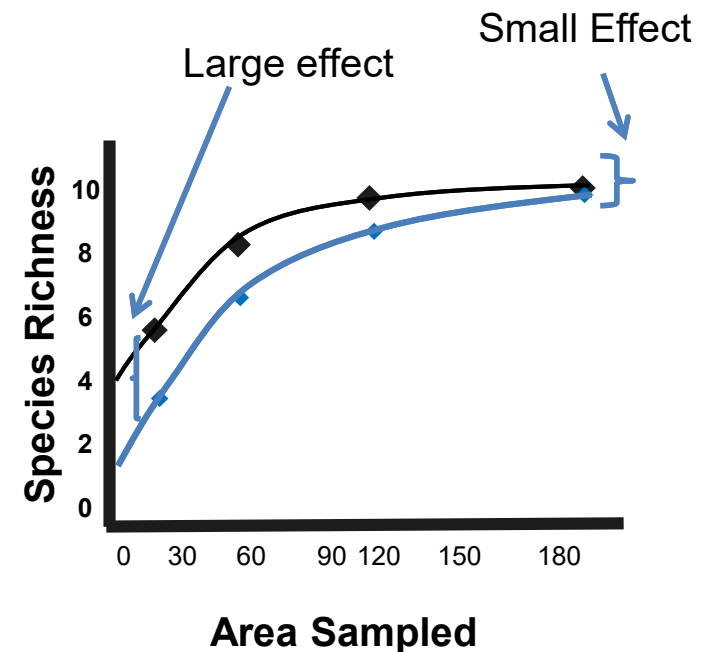
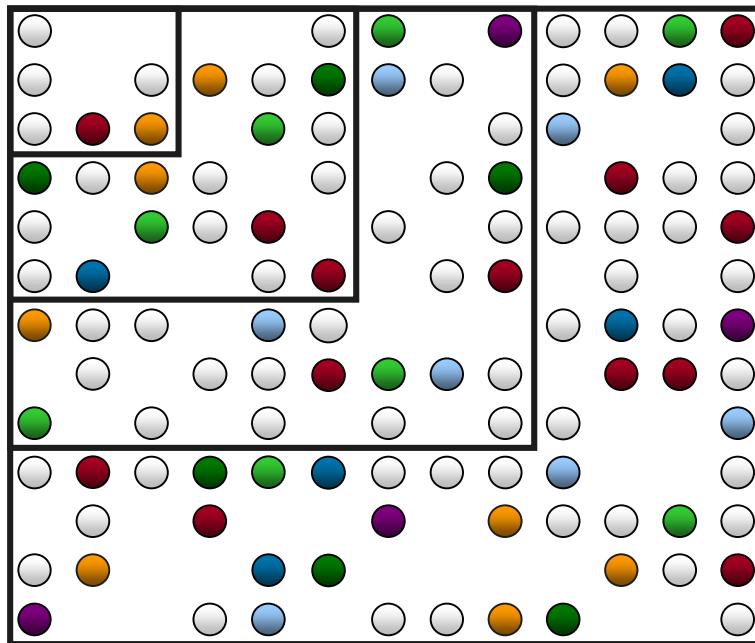
Degraded Community



*Chase and Knight 2013 Ecology Letters*

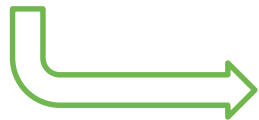
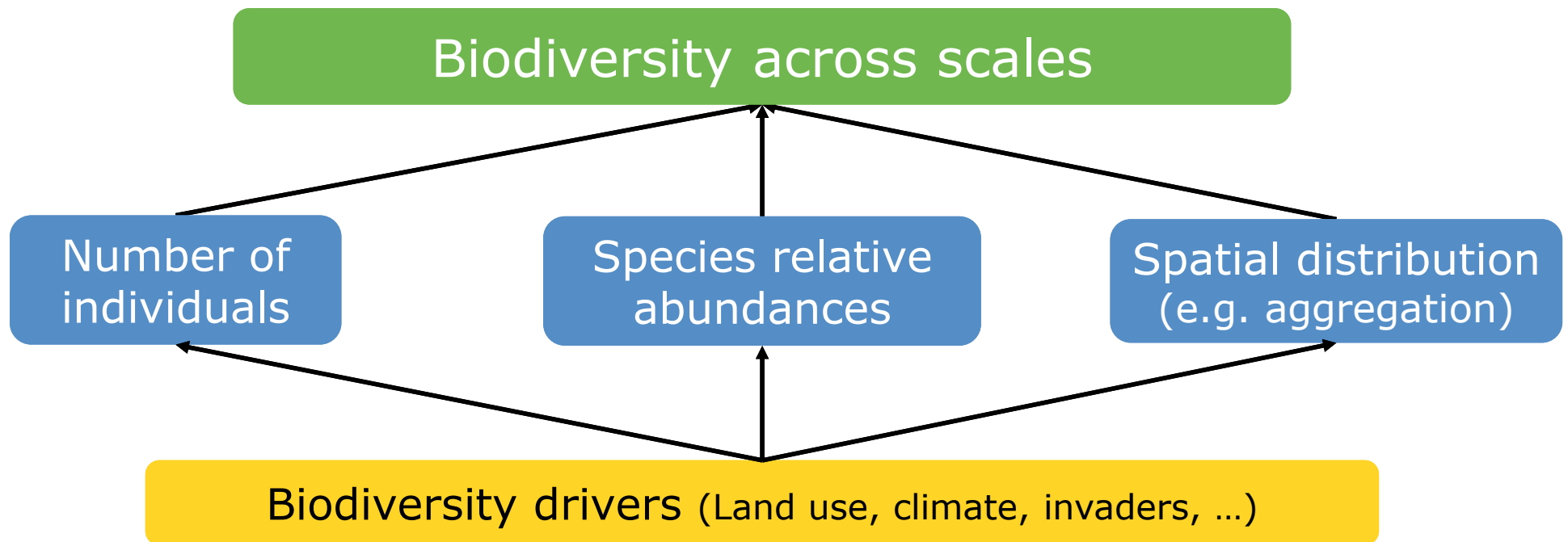
# Scale and Sampling effect on Species Area Relationships

Degraded Community



*Chase and Knight 2013 Ecology Letters*

# Spatial analysis of scale-dependent biodiversity changes



package **mobsim**



## Species Abundance Distribution (SAD)

- No. of individuals
- No. of species
- Evenness

## Species clumping

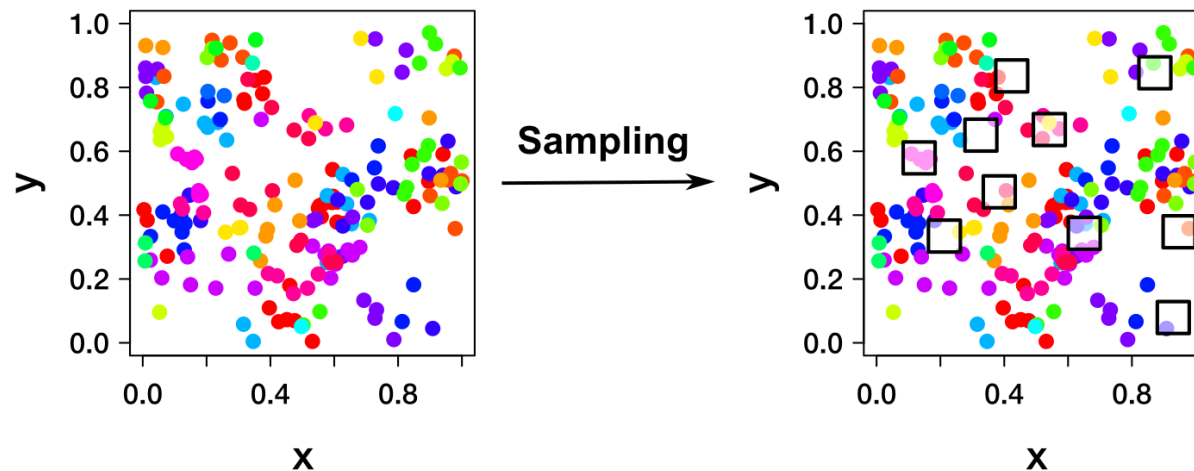
- Cluster extent
- No. of clusters
- Individuals per cluster



package **mobsim**

<https://github.com/MoBiodiv/mobsim>

**Simulation**

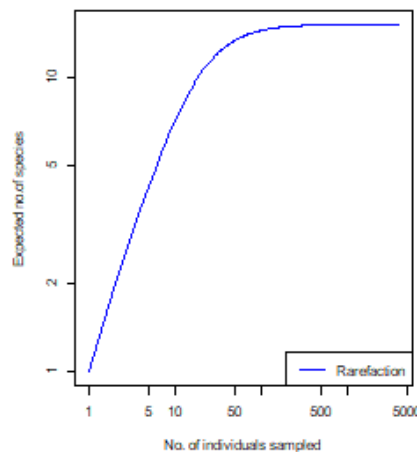


**Sampling**

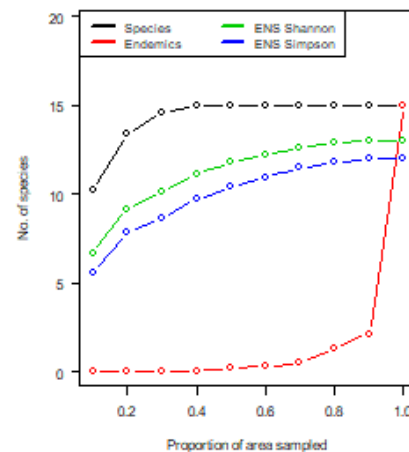
**Analysis**

**Analysis**

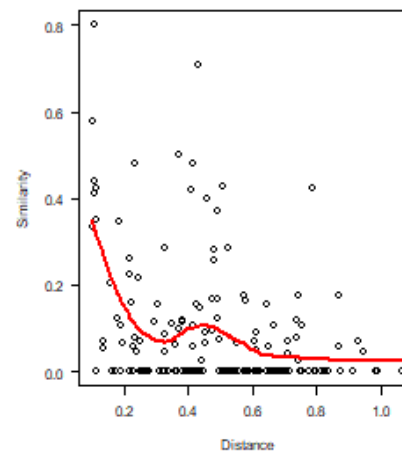
Species sampling curves



Diversity-area relationships



Distance decay



## Aims

- Interactive illustration of Measures of Biodiversity
- Sensibilization to their sensitivity to sampling
- Showing the shiny MOBSim and feedback

# **Exercise #1: Biodiversity components**

**5+5 minutes**

- Imagine a realistic community
  - Forest, bushes, prairie, (ants and termites, small mammals), etc

# **Exercise #1: Biodiversity components**

**5+5 minutes**

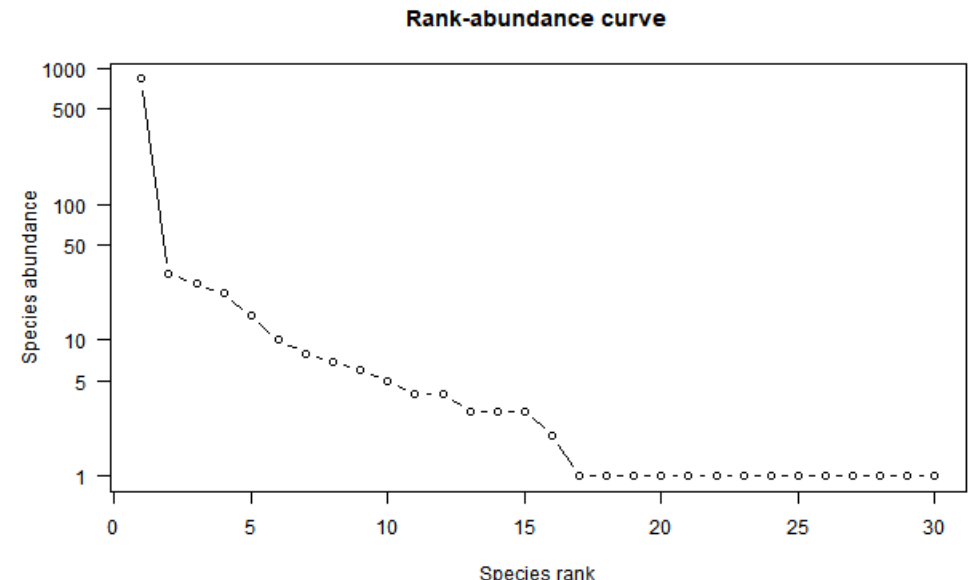
- Imagine a realistic community
  - Forest, bushes, prairie, (ants and termites, small mammals), etc
- Using biodiversity components
  - Species richness ( $S$ )
  - Total abundance ( $N$ )
  - Species abundance distribution (SAD)

# Exercise #1: Biodiversity components

5+5 minutes

- Imagine a realistic community
  - Forest, bushes, prairie, (ants and termites, small mammals), etc
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  - Species richness (S)
  - Total abundance (N)
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**1. Draw your expectations** for the rank abundance curve with pen and paper



# Exercise #1: Biodiversity components

5+5 minutes

- Imagine a realistic community
  - Forest, bushes, prairie, (ants and termites, small mammals), etc
- Using biodiversity components
  - Species richness ( $S$ )
  - Total abundance ( $N$ )
  - Species abundance distribution (SAD)

1. **Draw your expectations** for the rank abundance curve with pen and paper
2. Use `mobsim`: 1 SAD – Population simulation to simulate this community
3. Get familiar with the different SAD types and their parameters
4. **Verify your expectations**

# **Exercise #2: Biodiversity spatial distribution**

**5+5 minutes**

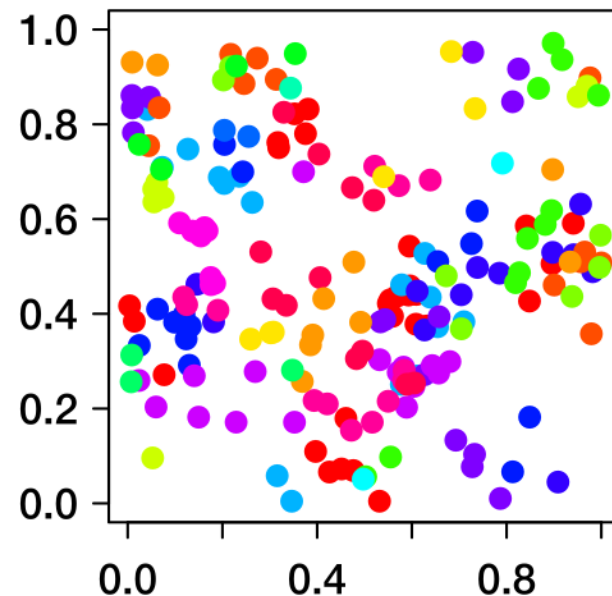
- Imagine a realistic spatial distribution for your community
  - Intraspecific aggregation (clumping)
    - Number of mother points
    - Mean distance to mother points

# Exercise #2: Biodiversity spatial distribution

5+5 minutes

- Imagine a realistic spatial distribution for your community
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    - Number of mother points
    - Mean distance to mother points

**1. Draw or describe your expectations** as a map (one dot = one individual)



# Exercise #2: Biodiversity spatial distribution

5+5 minutes

- Imagine a realistic spatial distribution for your community
    - Intraspecific aggregation (clumping)
      - Number of mother points
      - Mean distance to mother points
1. **Draw or describe your expectations** as a map (one dot = one individual)
  2. Use `mobsim: 2 Space - Distribution simulation` to simulate this community
  3. Get familiar with the different cluster types and their parameters. Try giving different parameter values to the species.
  4. **Verify your expectations**



# Exercise #3: Biodiversity components

15 minutes

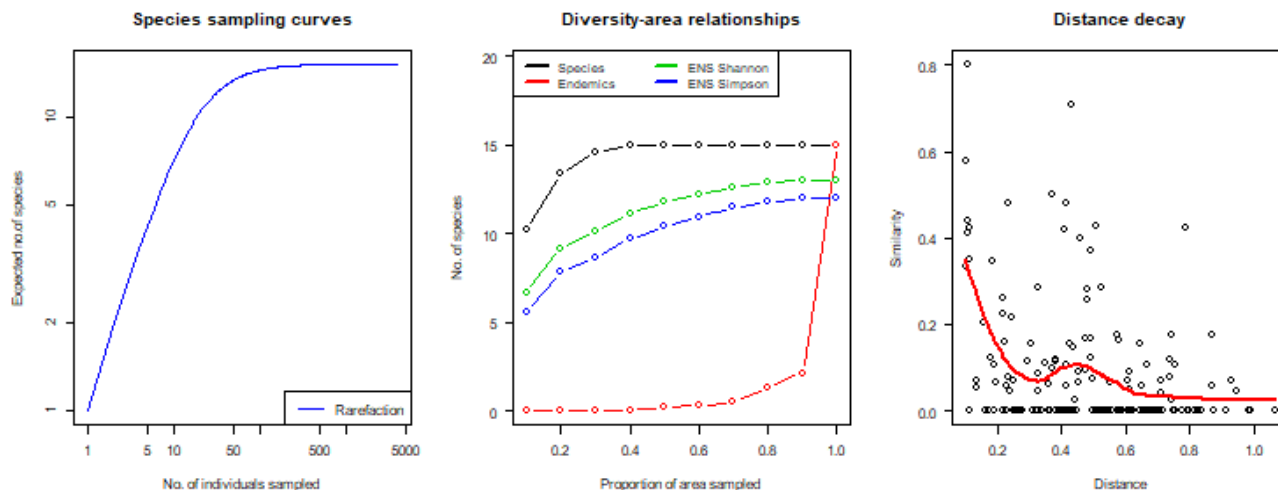
- How do biodiversity components
  - Total abundance (N)
  - Species abundance distribution (SAD)
  - Intraspecific aggregation (clumping)
- Influence the measured biodiversity
  - Rarefaction curve (`mobsim::spec_sample_curve()`)
  - Species-area relationship (`mobsim::divar()`)

# Exercise #3: Biodiversity components

15 minutes

- How do biodiversity components
  - Total abundance (N)
  - Species abundance distribution (SAD)
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- Influence the measured biodiversity
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## 1. Draw your expectations with pen and paper



# Exercise #3: Biodiversity components

15 minutes

- How do biodiversity components
  - Total abundance (N)
  - Species abundance distribution (SAD)
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  - Rarefaction curve (`mobsim::spec_sample_curve()`)
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**1. Draw your expectations** with pen and paper

**2. Use** `mobsim: 2 Space - Distribution simulation` [Exercise 3] to familiarize with these graphical representations of biodiversity sampling tools

**3. Verify your expectations + ecological interpretation**

# Exercise #3 part 2: Biodiversity components & Biodiversity scaling-relationships 15 minutes

- How do biodiversity components
    - Total abundance (N)
    - Species abundance distribution (SAD)
    - Intraspecific aggregation (clumping)
  - **And sampling**
  - Influence the measured biodiversity
    - Rarefaction curve (`mobsim::spec_sample_curve()`)
    - Species-area relationship (`mobsim::divar()`)
1. **Draw your expectations** with pen and paper
  2. Use `mobsim: 3 Basic Sampling` to familiarize with the sampling tools
  3. **Verify your expectations + ecological interpretation**
  4. **What is the best sampling design? Why?**
  5. Briefly present your results to the group

# Exercise #4: Detection of biodiversity changes across scales

- How is the detection of biodiversity changes influenced by the choice of sampling scale and biodiversity index?
1. Simulate two different communities
    - a) Forest vs. Prairie. Forest (species poor, low densities (trees) mixed with clumped and abundant species (bushes and understory), etc) Vs. Prairie (species rich, high densities, low aggregation)
    - b) Reference / control
    - c) Biodiversity change
    - d) Before vs. after a perturbation ; just after a perturbation vs. long after perturbation
  2. Sample both communities in the same way (`mobsim::sample_quadrats()`)
    - a) Apply different sampling designs: vary sample plot size, area and total sampling effort
  3. Calculate relative biodiversity changes ( $D_{\text{ref}}/D_{\text{change}} - 1$ )
    - a) Species richness (`vegan::specnumber`)
    - b) Shannon diversity (`vegan::diversity`)
    - c) Simpson diversity / PIE (`vegan::diversity`)

## **Exercise #4: Detection of biodiversity changes across scales**

4. How do your conclusions on biodiversity change with sampling and index used?
5. What does that mean for biodiversity research?