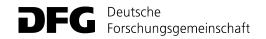


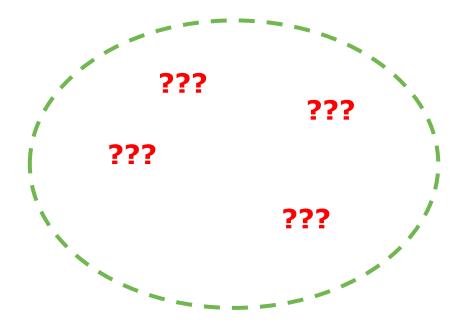
Introduction to the R package mobsim

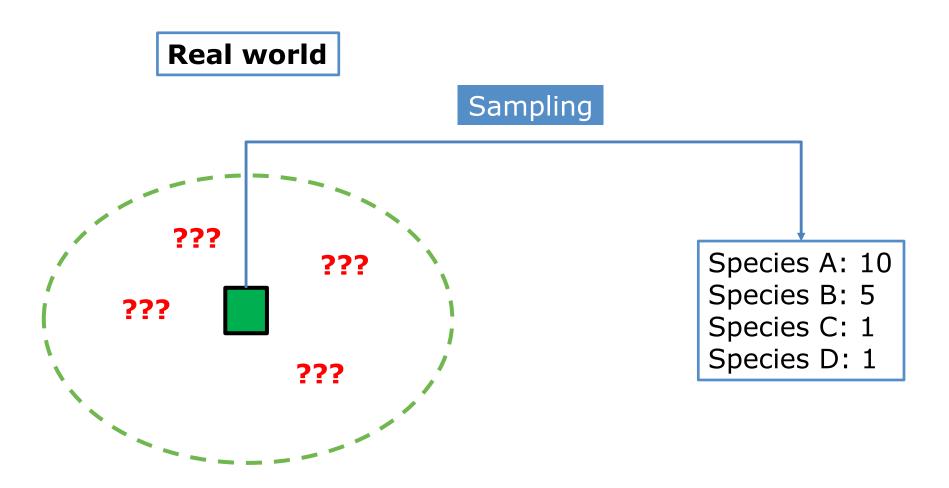
January 26th 2021

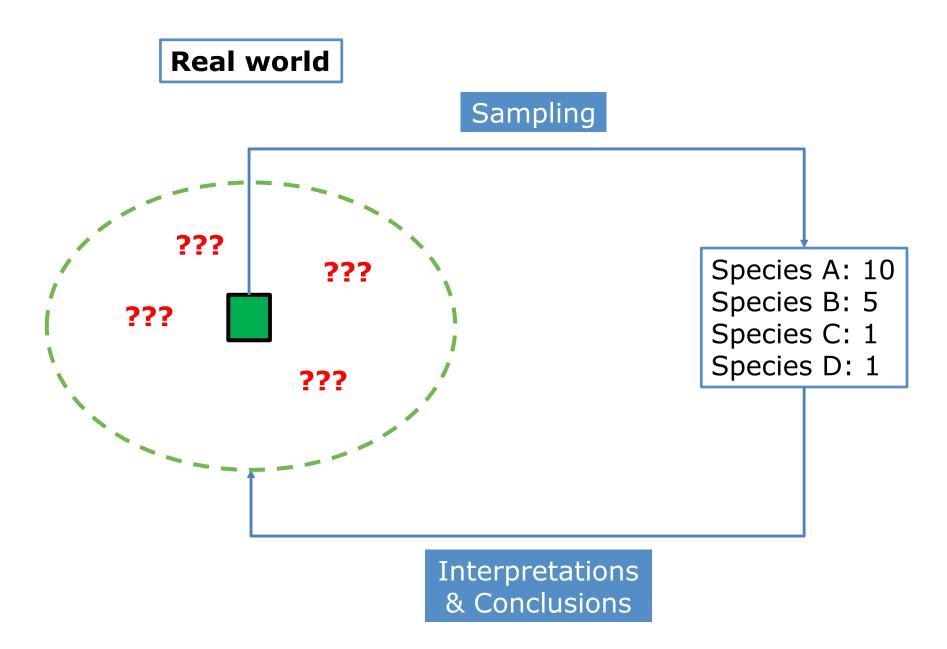
Alban Sagouis
Original creator: Felix May

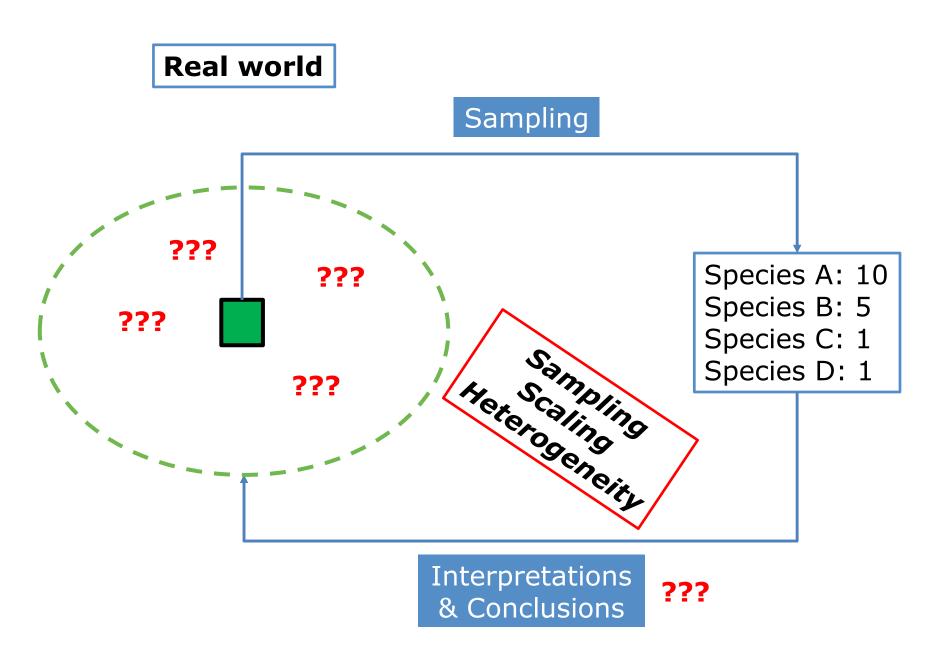


Real world

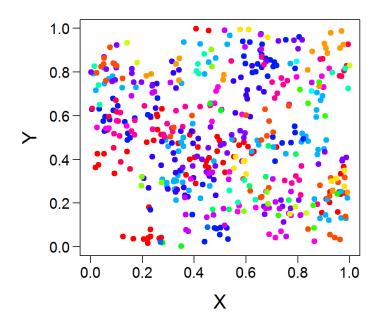




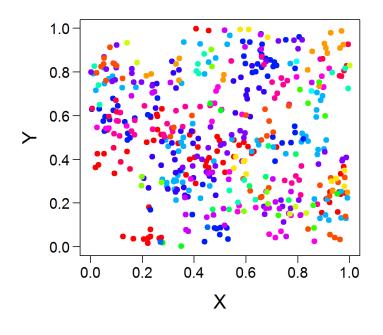




Simulation: complete control



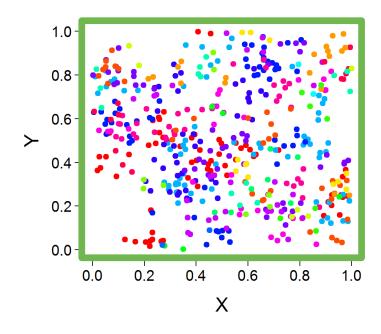
Simulation: complete control



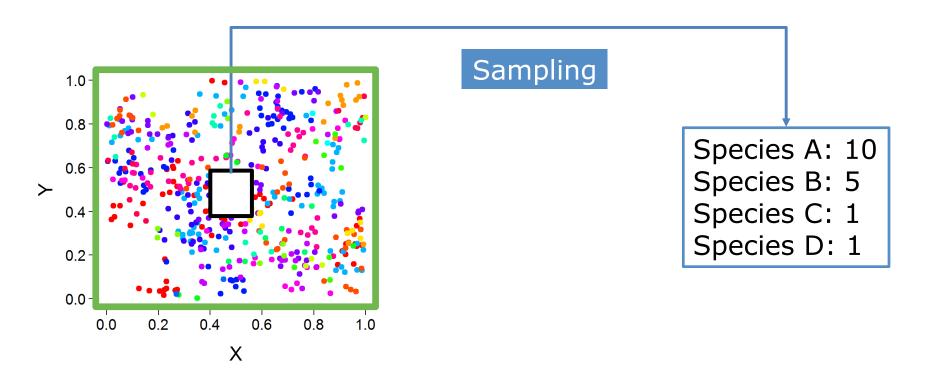
Change parameters

Test hypotheses

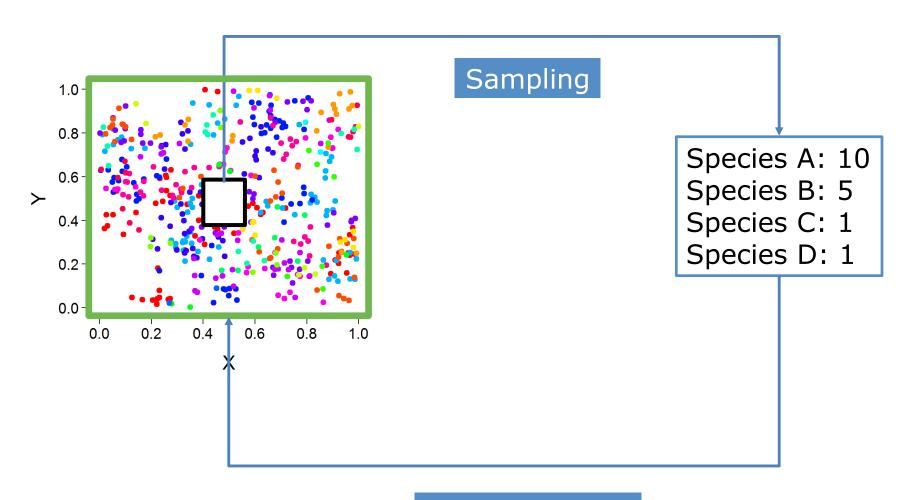
Simulation: complete knowledge



Simulation: complete knowledge

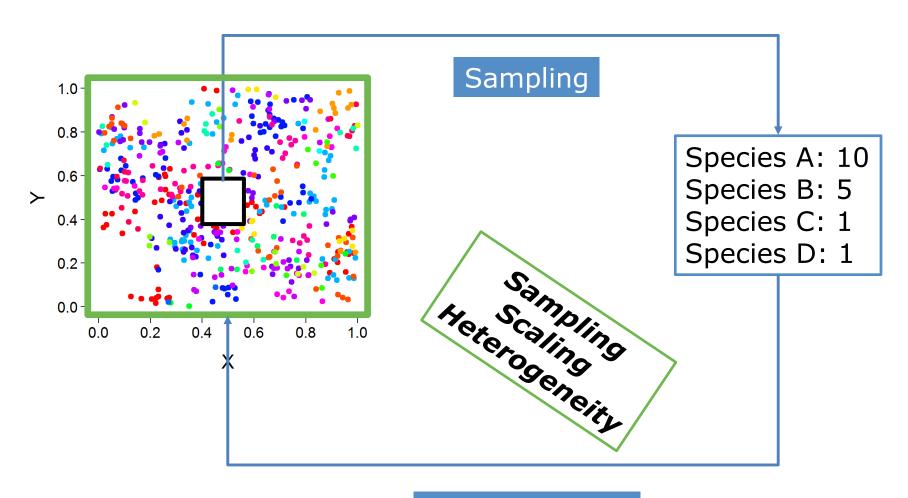


Simulation: complete knowledge



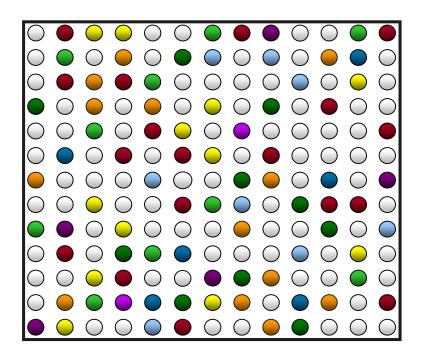
Interpretations & Conclusions

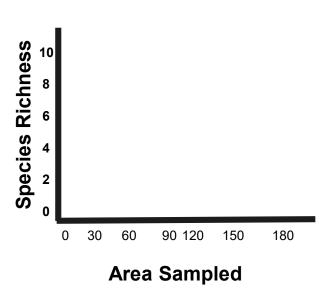
Simulation: complete knowledge



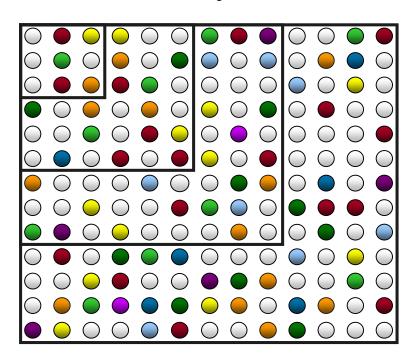
Interpretations & Conclusions

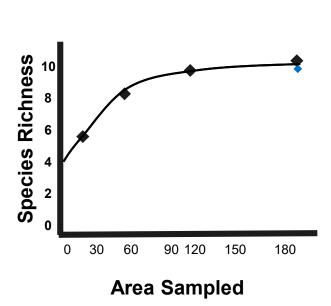
Pristine Community



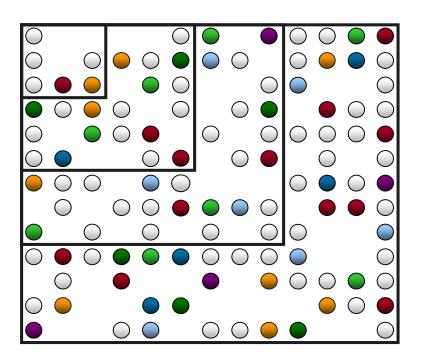


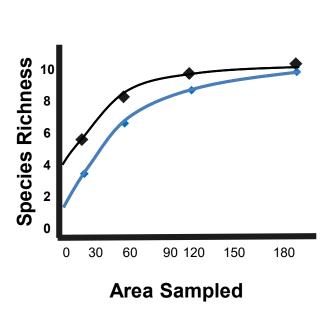
Pristine Community



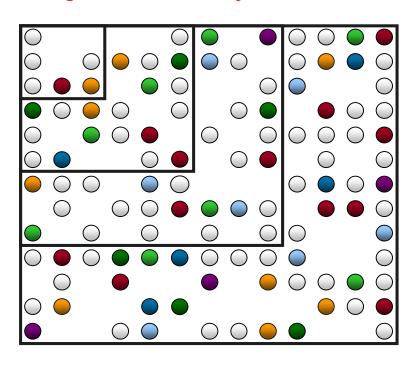


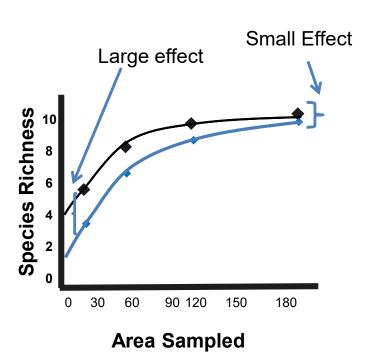
Degraded Community



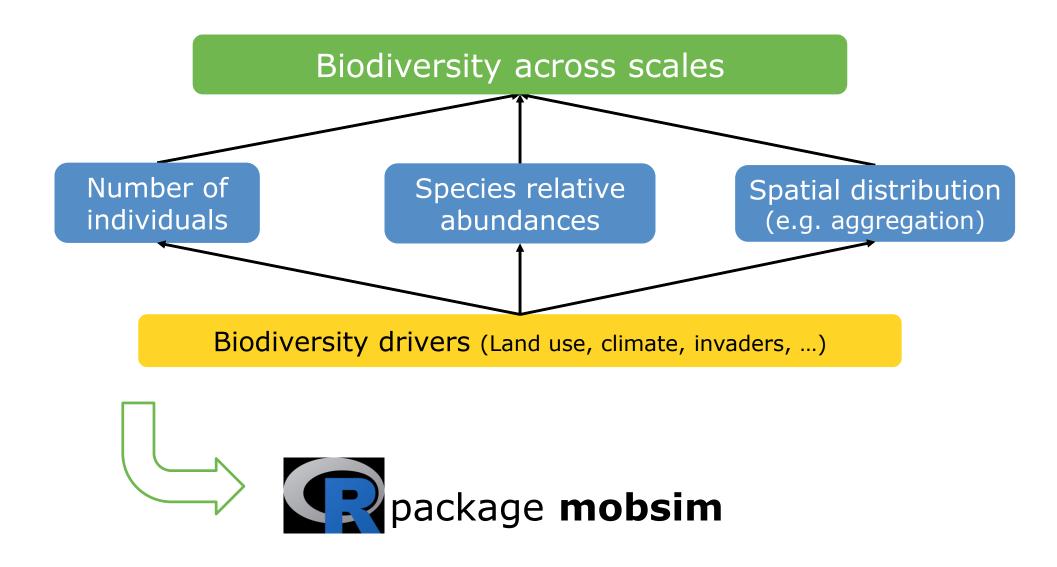


Degraded Community





Spatial analysis of scale-dependent biodiversity changes



Species Abundance Distribution (SAD)

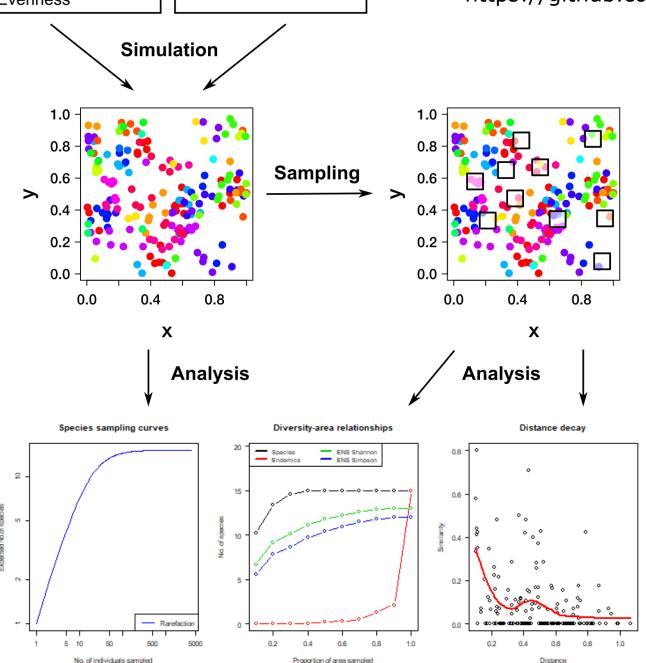
- No. of individuals
- No. of species
- Evenness

Species clumping

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



https://github.com/MoBiodiv/mobsim



Proportion of area sampled

Aims

Distance

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

Exercise #1: Biodiversity components 5 minutes

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

Exercise #1: Biodiversity components5 minutes

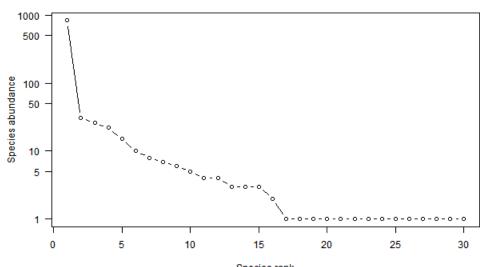
- Imagine a realistic community
 - Forest, bushes, prairie, (ants and termites, small mammals), etc
- Using biodiversity components
 - Species richness (S)
 - Total abundance (N)
 - Species abundance distribution (SAD)

Exercise #1: Biodiversity components 5 minutes

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

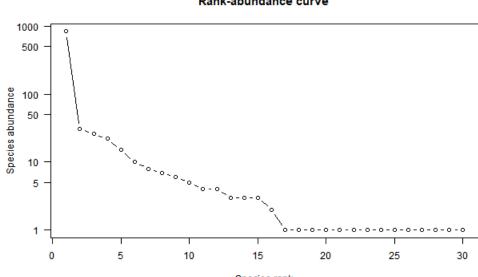
Rank-abundance curve



Exercise #1: Biodiversity components 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

 Rank-abundance curve
- 2. Use mobsim: 1 SAD Popsimulate this community
- 3. Get familiar with the differ parameters
- 4. Verify your expectation



Exercise #2: Biodiversity spatial distribution 5 minutes

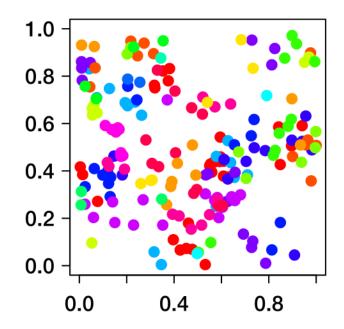
- Imagine a realistic spatial distribution for your community
 - Intraspecific aggregation (clumping)
 - Number of mother points
 - Mean distance to mother points

Exercise #2: Biodiversity spatial distribution 5 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)



Exercise #2: Biodiversity spatial distribution 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
- Get familiar with the different cluster types and their parameters. Try giving different parameter values to the species.
- 4. Verify your expectations

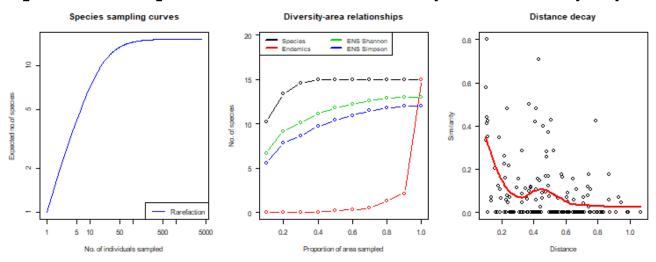
Exercise #3: Biodiversity components15 minutes

- 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 components15 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())

1. Draw your expectations with pen and paper



Exercise #3: Biodiversity components15 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())
- 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
 - 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 $(D_{ref}/D_{change} 1)$
 - 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?