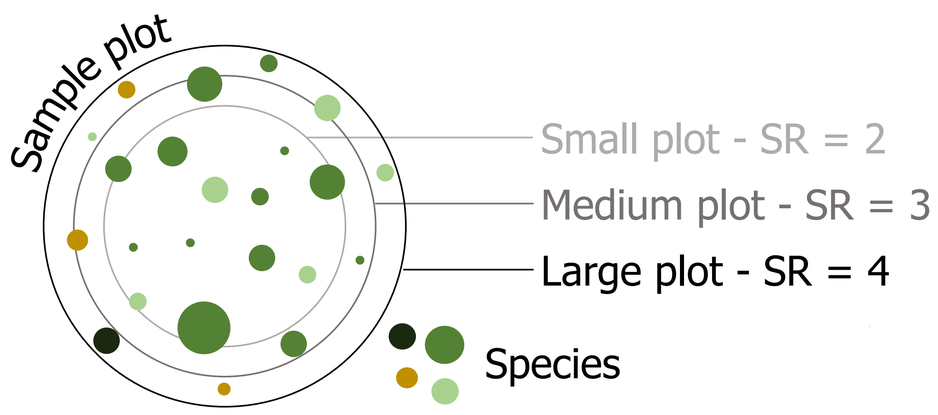
Scaling species richness data to enable comparisons between inventories with different plot sizes

Jeanne Portier, Florian Zellweger, Jürgen Zell, Rafael O. Wüest, Iciar Alberdi Asensio, Michal Bosela, Johannes Breidenbach, Vladimír Šebeň, Brigitte Rohner

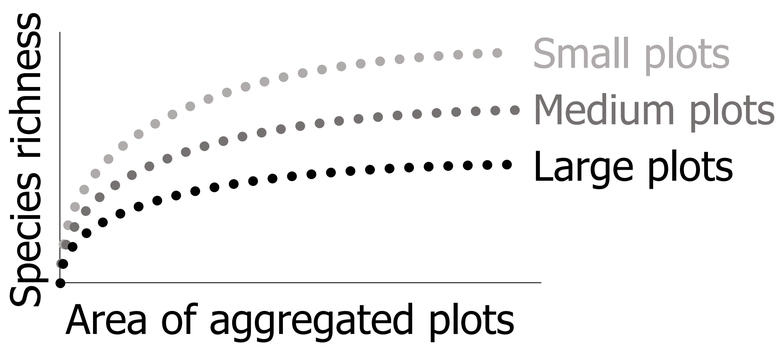
The issue

For a more comprehensive picture of biodiversity, how can we compare species richness between inventories using different plot sizes?

Species richness (SR) is affected by plot size:



Sample-based rarefaction curves are not comparable between inventories with different plot sizes:

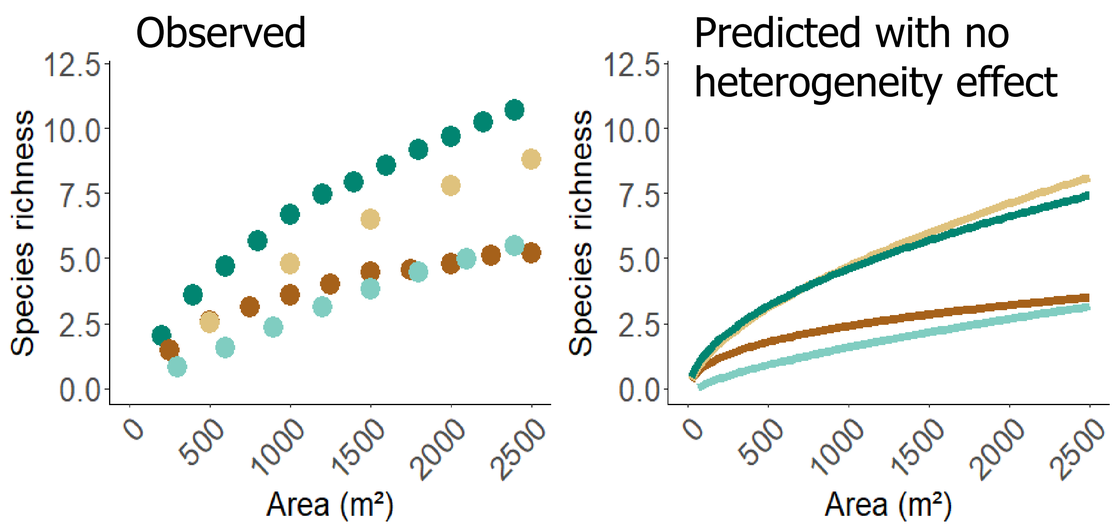


The solution

By using sample-based rarefaction curves accounting for environmental heterogeneity effects!

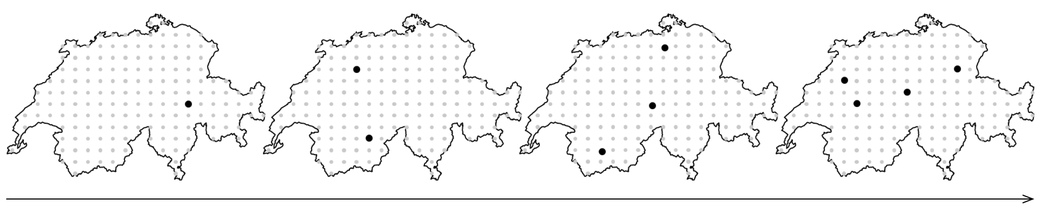
National Forest Inventory data from Norway, Slovakia, Spain and Switzerland

- Norway (plot size = 250m²)
- Slovakia (plot size = 500m²)
- Spain (plot size = 300m²)
- Switzerland (plot size = 200m²)

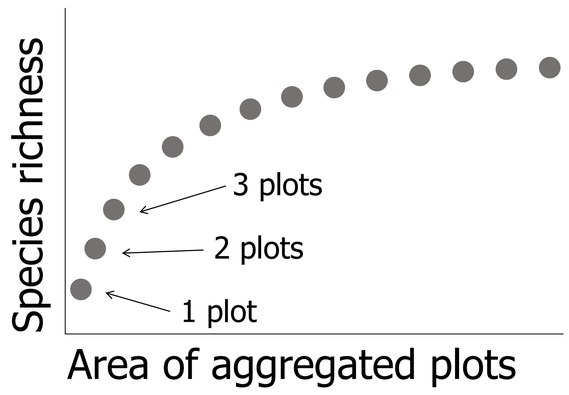


What is a sample-based rarefaction curve?

Aggregating sample plots to increase area and calculate species richness at each aggregation step.



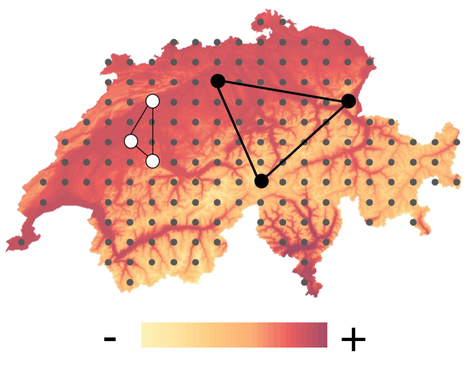
↗ Number of plots and aggregated area (A)
↗ Species richness (SR)
↗ Environmental heterogeneity (H)



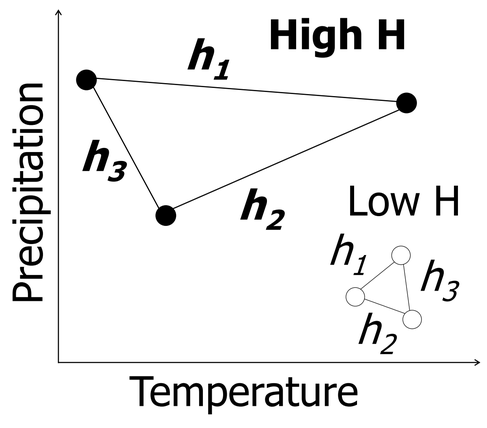
Methodological framework

Quantifying environmental heterogeneity (H) introduced when aggregating plots in terms of climate, topo, soil, basal area

e.g. H_{clim} for 3 plots



$$H = (h_1 + h_2 + h_3)/3$$



Modelling $SR = f(A, H)$