9th international Meeting on Vegetation Databases: Vegetation Databases and Climate Change, Hamburg, 24–26 February 2010

Shapes of species richness curves depend on sampling design – Insights for richness extrapolations from a simulation study

Presented by:
Jürgen Dengler

Jürgen Dengler[1,2] & Jens Oldeland[1,3]

[1]Biodiversity, Evolution and Ecology of Plants, Biocentre Klein Flottbek and Botanical Garden, University of Hamburg, Ohnhorststr. 18, 22609 Hamburg, Germany
[2]dengler@botanik.uni-hamburg.de; [3]oldeland@botanik.uni-hamburg.de

Aim

In ecological research, it is often not feasible to sample all species of a larger area comprehensively. Thus, various extrapolation techniques are frequently used to estimate the total species richness on a larger plot based on compositional data of nested subplots:

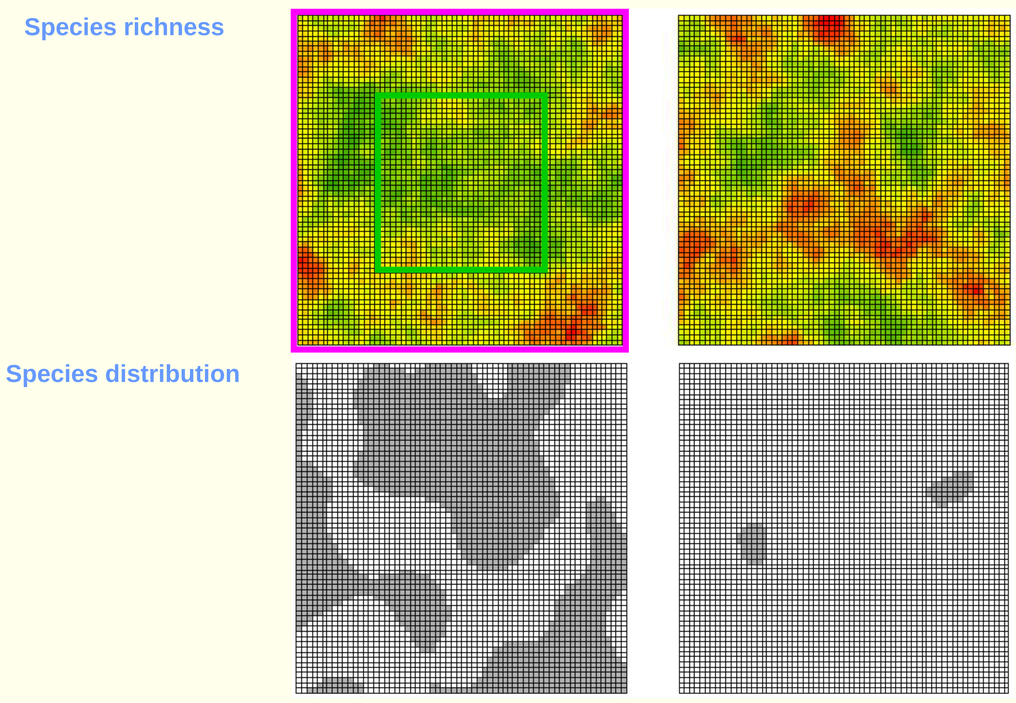
(i) species-area relationships (SARs)
(ii) species sampling relationships (SSRs)

(iii) **(non-parametric) richness estimators** based on SSRs.

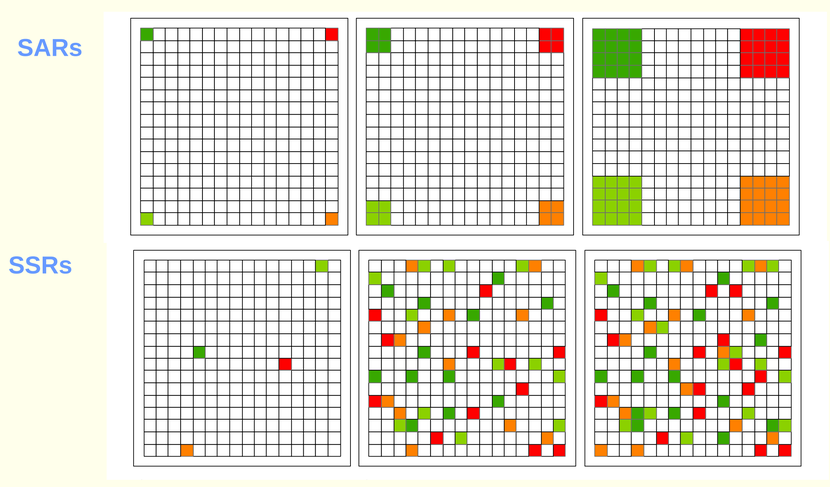
The suitability of these fundamentally different extrapolation approaches has hardly ever been tested in comparison. Here we use a simulation model of ecological communities to demonstrate the effects of different sampling schemes (SARs, SSRs) on shapes of species richness curves and their extrapolation capability.

Methods

Simulation study: 5 random communities with 100 species on a 64 x 64 grid



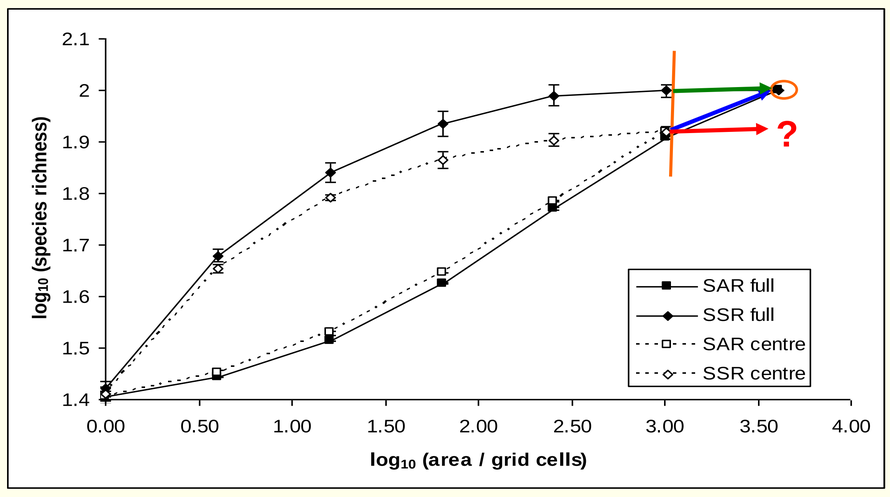
Two sampling approaches: SARs vs. SSRs



- nested-plots **SARs vs. SSRs** (= rarefaction curves)
- **full extent vs. central quarter**

Results

Shape of curves



Goodness of fit *(mean Akaike weights)*

Model	*k*	Saturation	SAR		SSR	
Power	2	no	92.8%	1.8%	0.0%	0.0%
Power, quadratic	3	no	5.0%	2.0%	3.9%	5.5%
Logarithm	2	no	0.1%	0.1%	0.0%	0.0%
Michaelis-Menten	2	yes	0.0%	0.0%	0.2%	0.1%
Lomolino	3	yes	2.1%	0.2%	95.9%	5.6%

Extrapolation capability

(predicted richness; true richness = 100)

	SAR		SSR	
Extent	**Full**	**Centre**	**Full**	**Centre**
Power	**103.3 ± 1.1**	**106.5 ± 4.9**	134.1 ± 0.3	**107.8 ± 3.7**
Power, quadr.	122.8 ± 1.8	122.3 ± 3.5	88.0 ± 8.5	72.7 ± 2.2
Logarithm	82.8 ± 1.6	85.8 ± 3.5	124.4 ± 6.2	**101.9 ± 3.2**
Michaelis-Menten	64.9 ± 4.8	67.5 ± 3.1	**95.7 ± 0.1**	79.2 ± 2.3
Lomolino	**102.2 ± 1.1**	**104.9 ± 3.4**	**102.7 ± 9.4**	84.0 ± 2.7

x = w_i > 90%
x = w_i > 50%
x = w_i > 10%
red = good extrapolation capability

Conclusions

- **2 types of species richness curves have fundamentally different shapes:**
  - SARs: power law
  - SSRs: saturation functions
- **Models that provide a good curve fit do not necessarily provide reliable extrapolations**

Suitability of function types should be measured with three parameters *(Dengler 2009, J. Biogeogr. 36: 728–744)*

- **AIC for *S***
- **AIC for log *S***
- **Log error or extrapolation (LEE):** "Leave one out approach"

- **Interpolations:**
  Can be done by any function that gives a good fit to the actual data (AIC, R^2)
- **Extrapolations** (to larger areas):
  - ***To "target" area:***
    - SARs (with power function)
    - SSRs (with saturation functions, e.g. Lomolino)
  - ***To areas larger than "target area":***
    - only possible with SARs!