

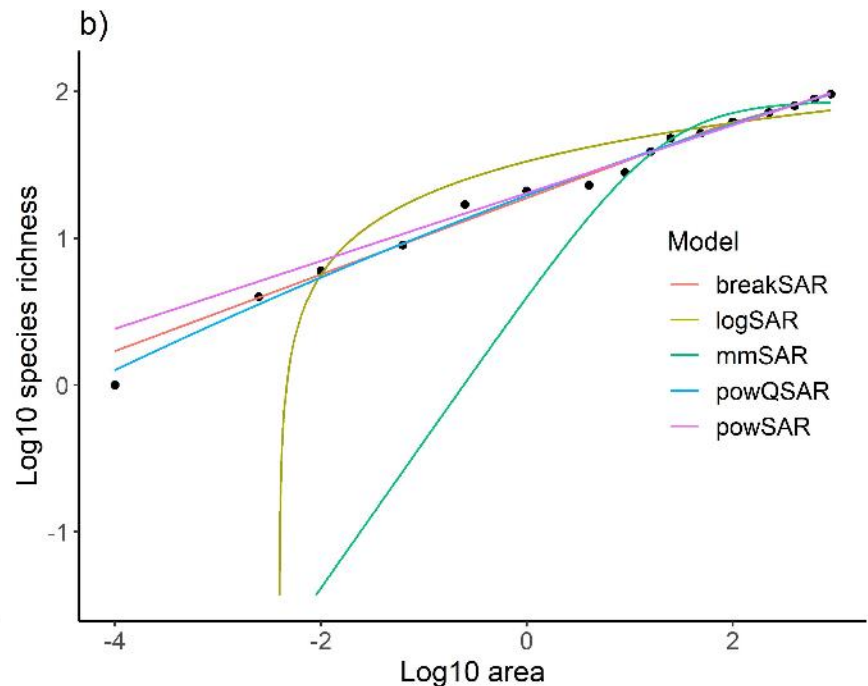
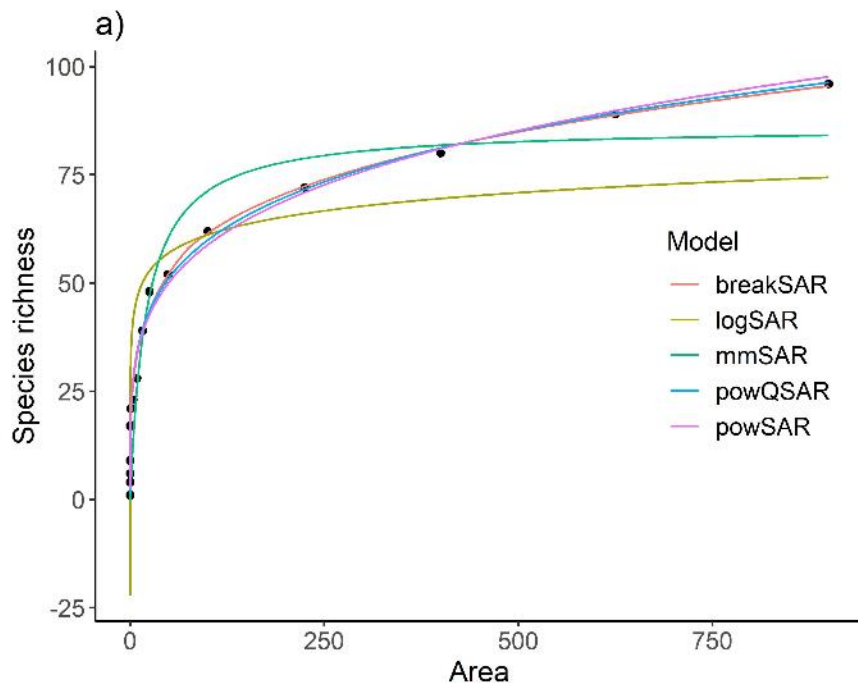
# Species-area relationships in continuous vegetation: evidence from Palearctic grasslands

Jürgen Dengler, Idoia Biurrun, Thomas J. Matthews, Manuel J. Steinbauer, Sebastian Wolfrum, Steffen Boch, Alessandro Chiarucci, Timo Conradi, Iwona Dembicz, Corrado Marcenò, Itziar García-Mijangos, Arkadiusz Nowak, David Storch, Werner Ulrich,  
& the GrassPlot Consortium



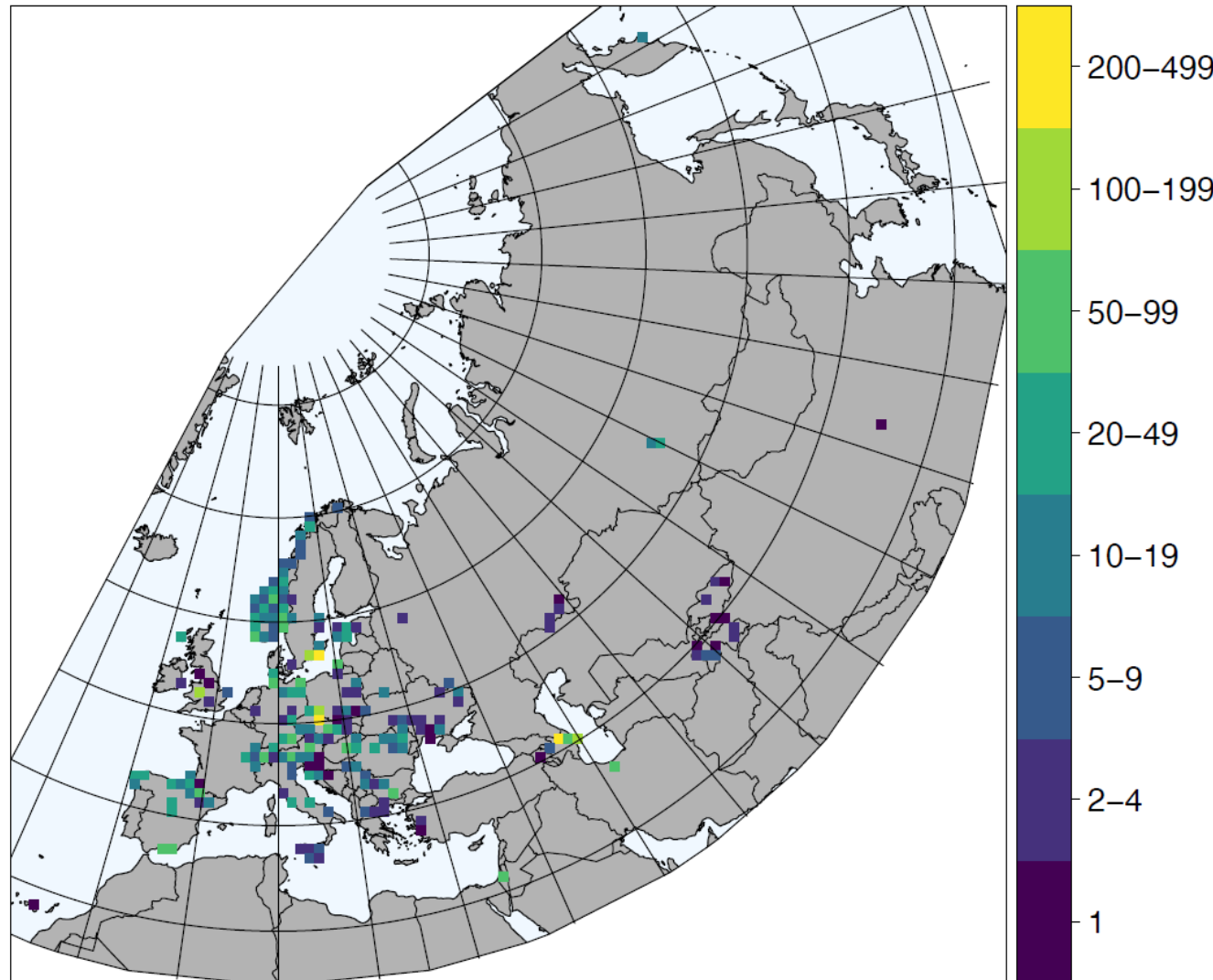
# Species-area relationships (SARs)

- Numerous function types proposed for SARs  
(e.g. Tjørve 2003, *J. Biogeogr.* 30: 827-835; Dengler 2009, *J. Biogeogr.* 36: 728-744)
- At coarse grain sizes the power function overall performs best  
(e.g. Triantis et al. 2012, *J. Biogeogr.* 39: 215-239)
- For fine grain sizes, the situation, however, was disputed



# Data

- GrassPlot database  
[Dengler et al. 2018, \*Phytocoenologia\* 48, 331-347.](#)
- 2057 nested-plot series with  $\geq 7$  grain sizes
- Many series also with bryophyte and lichen records
- Extensive environmental and structural data from the plots



# Annual EDGG Field Workshops



Dengler et al. 2016, *Bull. Eurasian Dry Grassland Group* 31: 12-26.

# Analyses

- Five representative functions in comparison

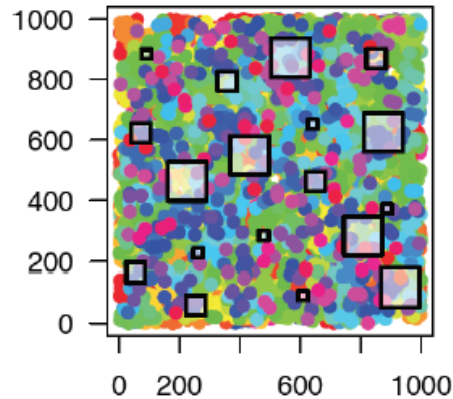
Function name	Akronym	$k$	Formula in $S$ -space
Power	powSAR	2	$S = c A^z$
Power quadratic	powQSAR	3	$S = 10^{(\log c + z_1 \log A + z_2 (\log A)^2)}$
Power breakpoint	breakSAR	4	$S = 10^{[\log c + (\log A < \log T) (z_1 \log A) + (\log A \geq \log T) (z_1 \log T + z_2 (\log A - \log T))]}$
Logarithmic	logSAR	2	$S = b_0 + b_1 \log A$
Michaelis-Menten	mmSAR	2	$S = b_0 A / (b_1 + A)$

- Fitting in  $S$ -space and in  $\log S$ -space
- Non-linear regression with a wide range of starting values to assure convergence
- Model comparison via AICc (mean Akaike weights, fraction of best fits), BIC and  $R^2_{adj}$ .

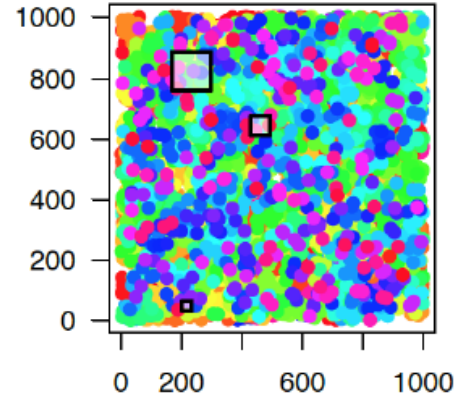
# Are nested plots a methodological problem?

## Accuracy of model selection based on simulation (with R package mobsim)

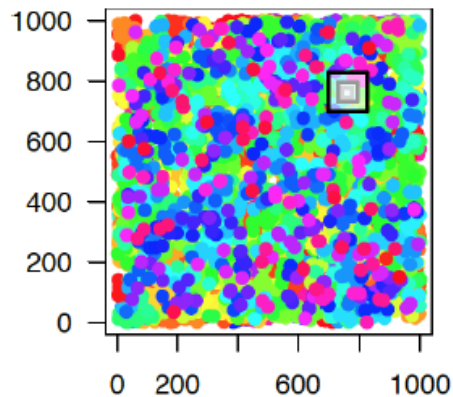
a) Sampling design for "true pattern":



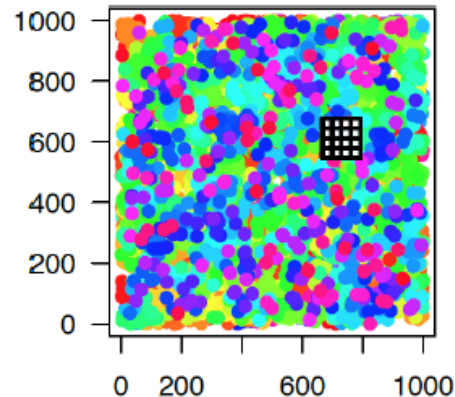
b) Sampling design (i):



c) Sampling design (ii):



d) Sampling design (iii):

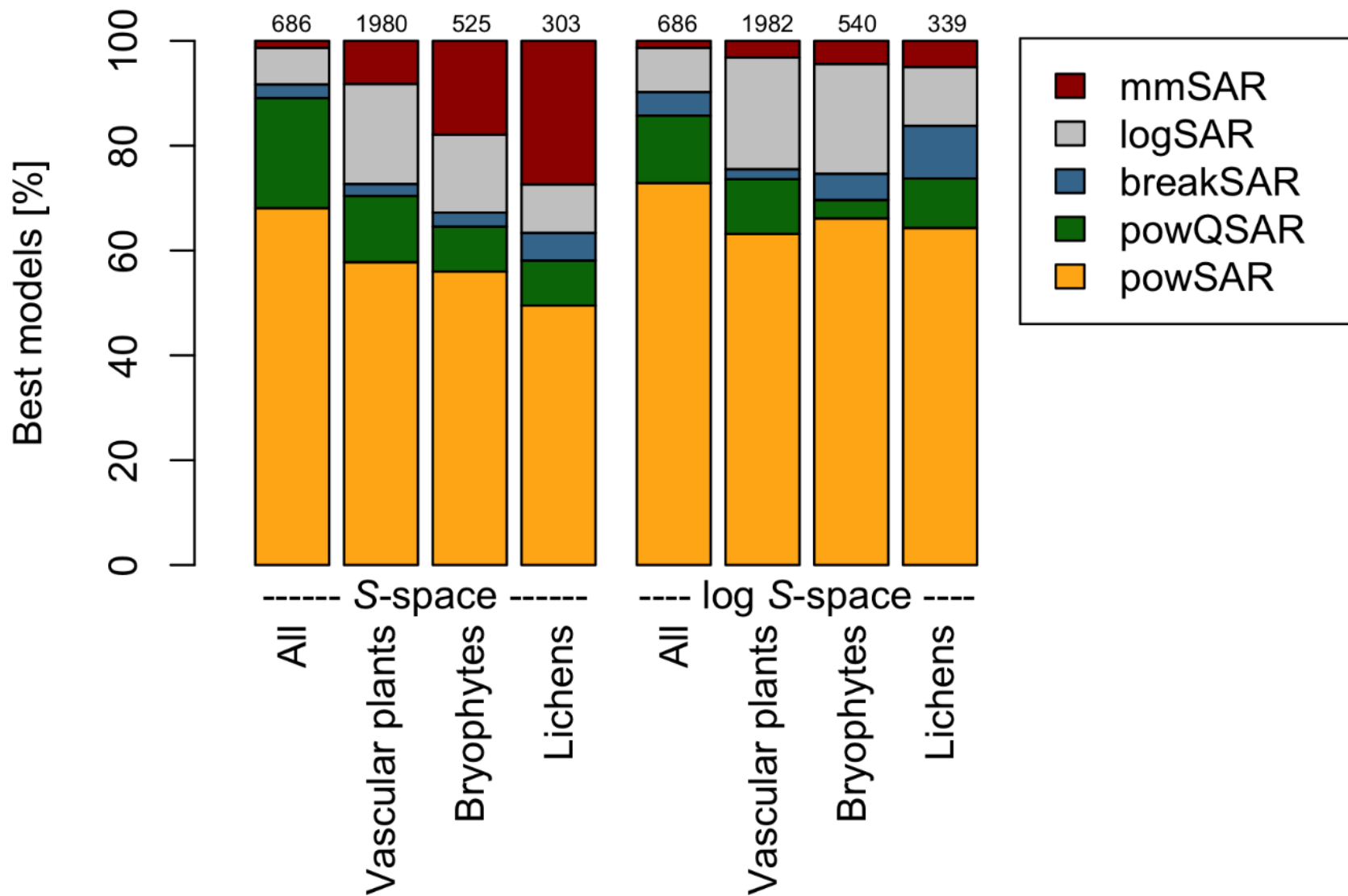


# Accuracy of model selection based on simulation

(true pattern = non-nested, averaged)

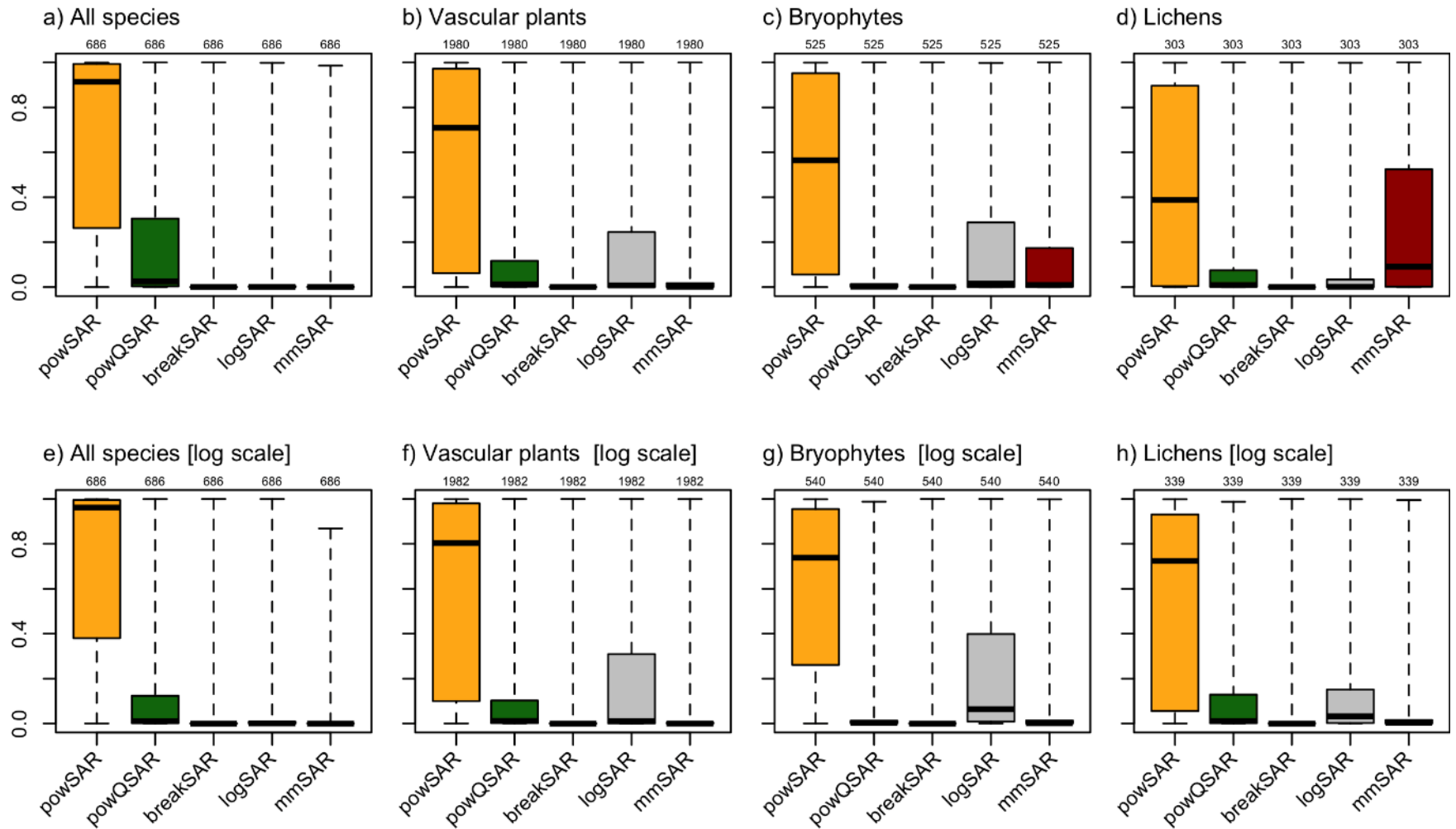
Sampling design	S-space		log S-space	
	AICc	BIC	AICc	BIC
Non-nested, single plots	42%	38%	38%	36%
Nested, single plots	54%	52%	48%	54%
Nested, averaged	50%	66%	70%	80%

# Comparison of the five functions (AICc)

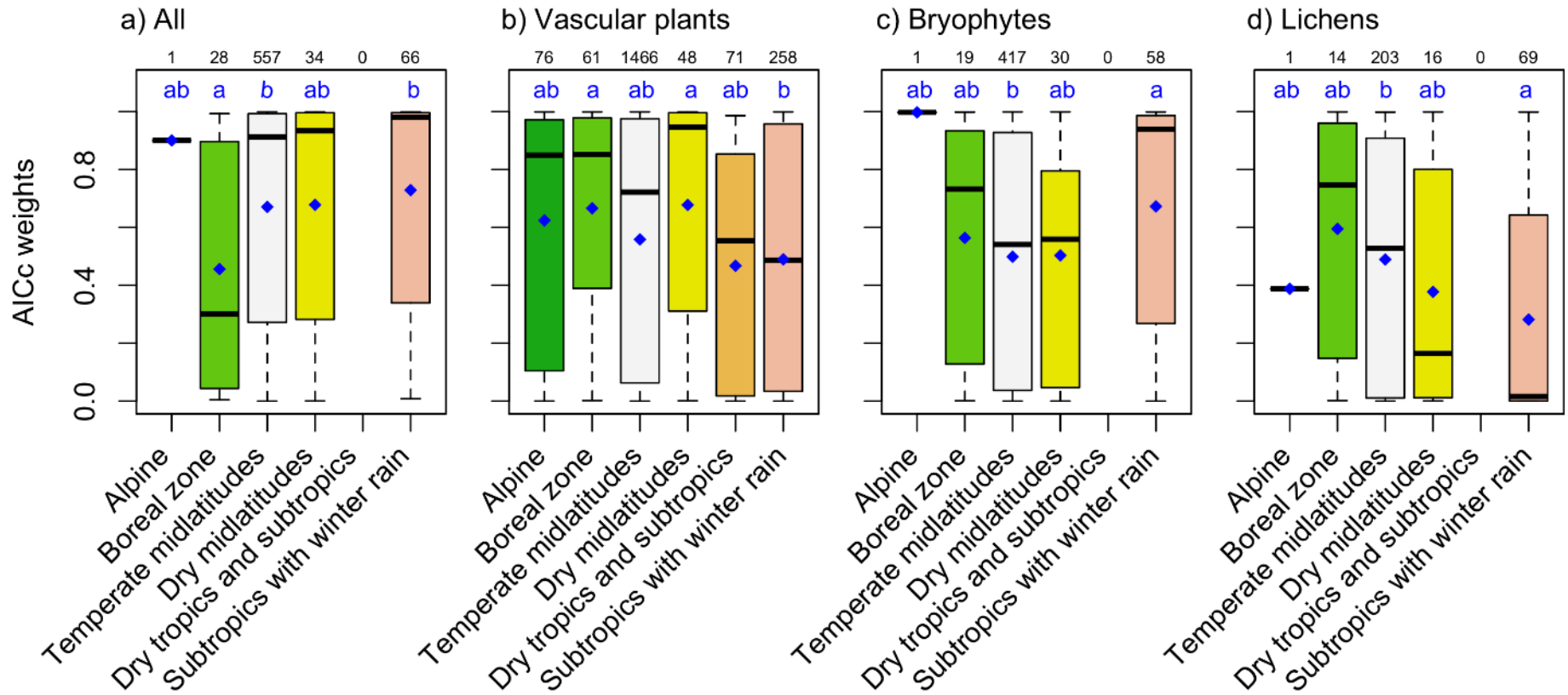




# Comparison of the five functions

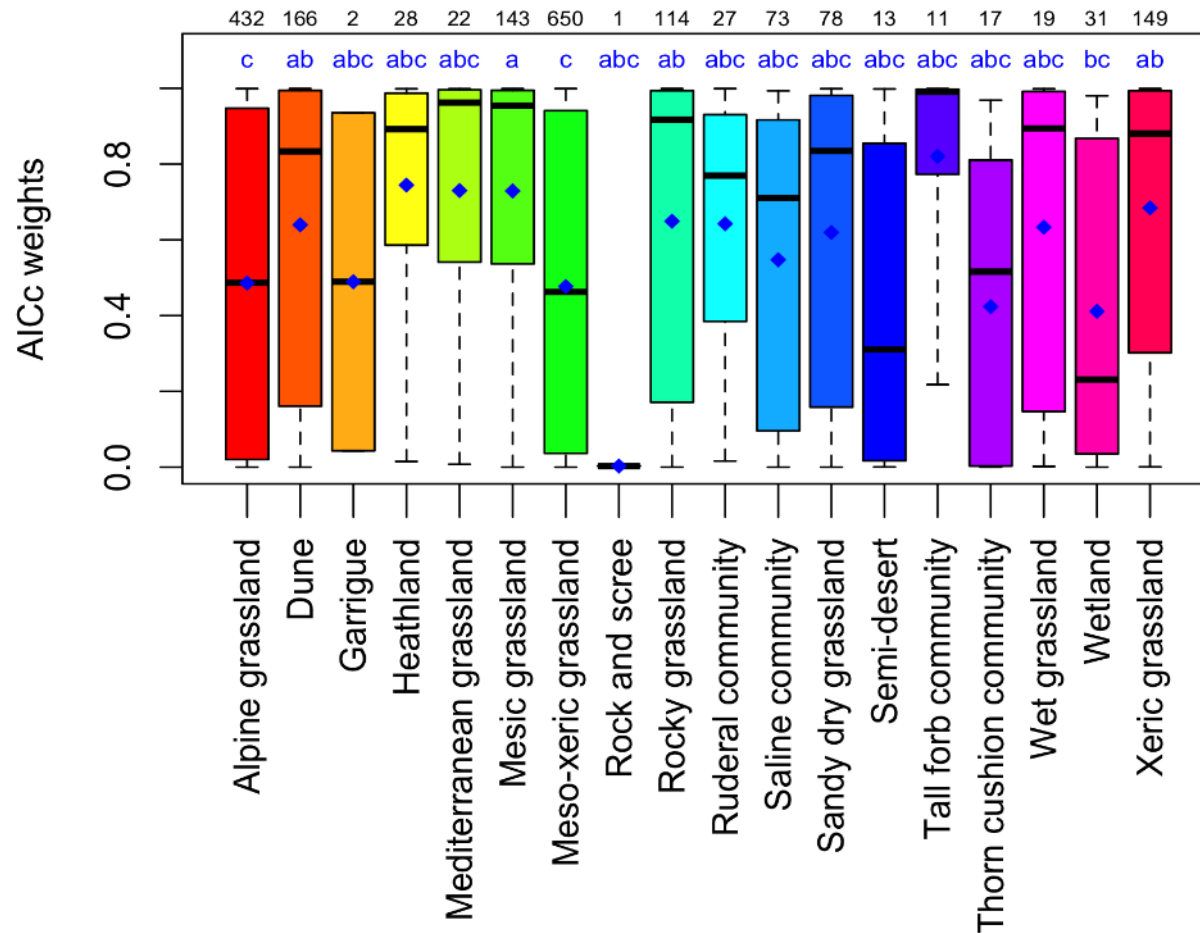


# Prevalence of power function vs. biome

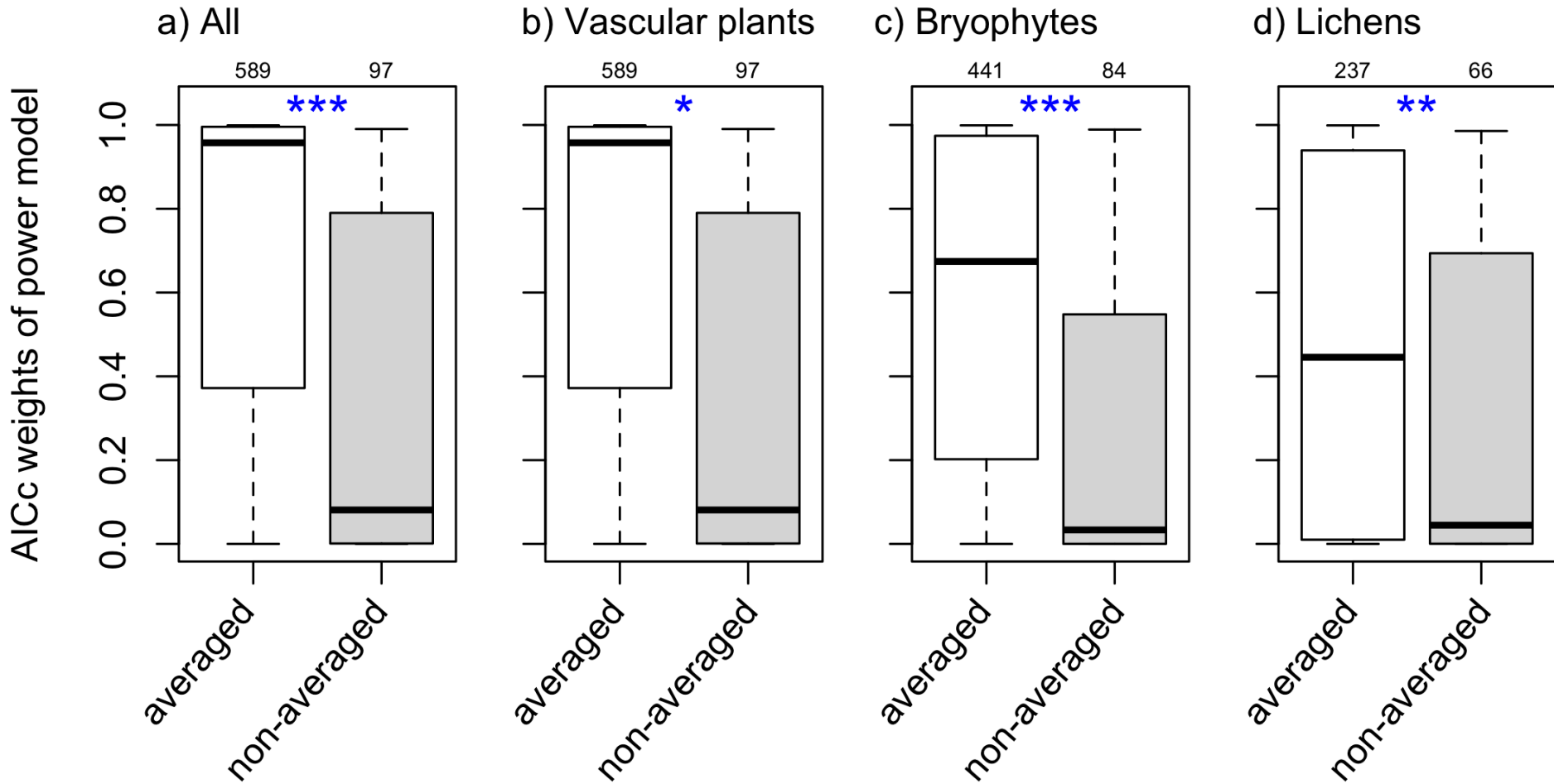


# Prevalence of power function vs. vegetation type

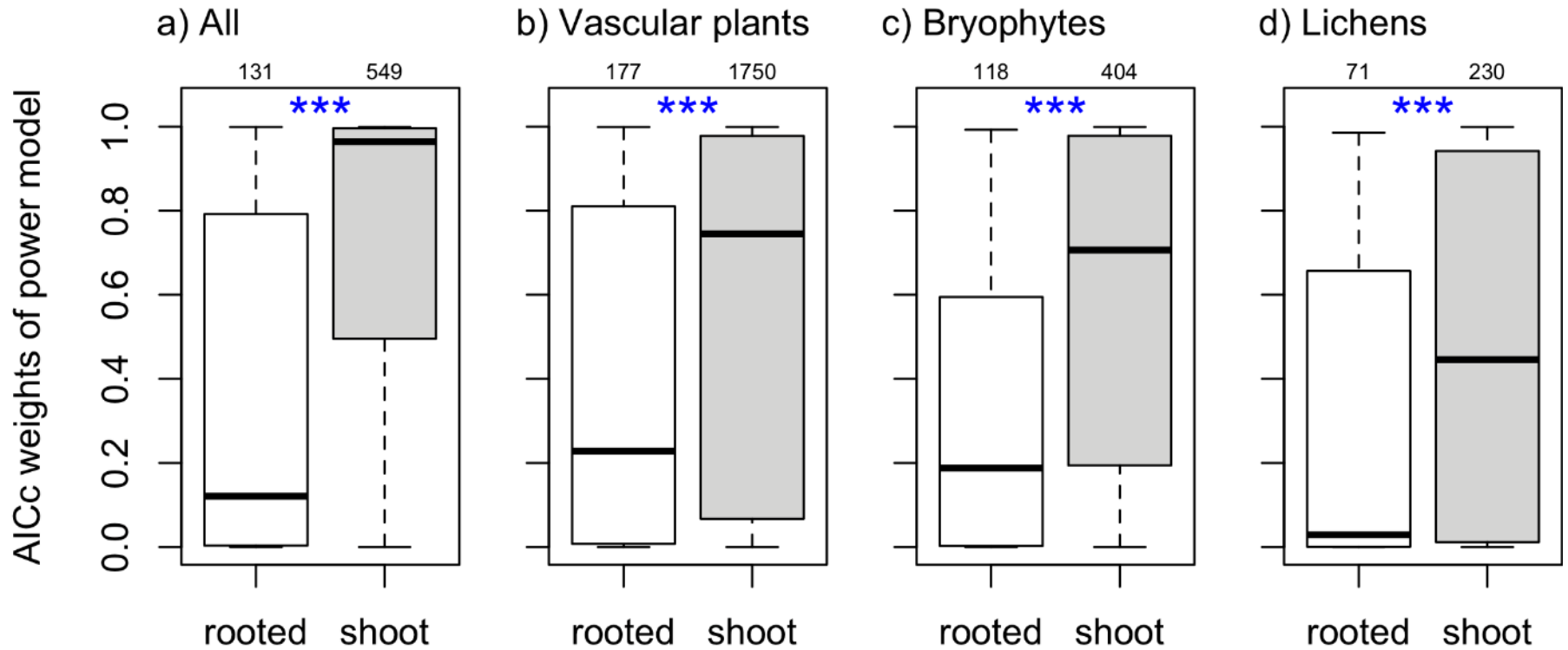
b) Vascular plants



# Prevalence of power function vs. methodology I: averaging



# Prevalence of power function vs. methodology II: rooted vs. shoot

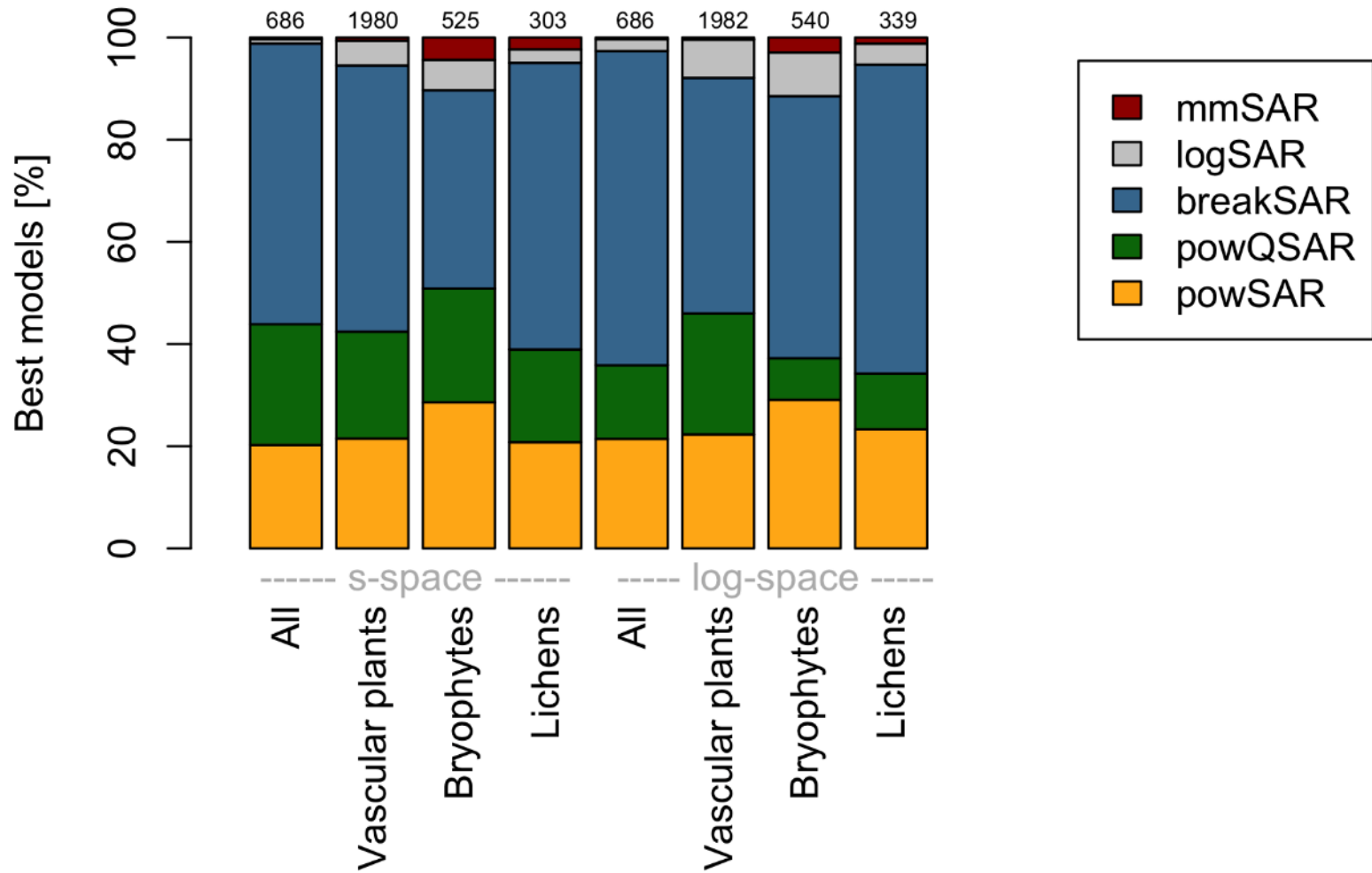


# Conclusions

- ✓ The **power function** also at small spatial scales is the prevalent model
- ✓ **No support** for logarithmic or saturated functions
- ✓ Relative performance of the **power function** is hardly affected by ecological context, but strongly by methodological issues (e.g. averaged vs. single values)
- ✓ Strong support to use **power function as generic model** and **z-values** as good measures for beta-diversity



# Comparison of the five functions (BIC)





### Species-area relationships (SARs)

### Species sampling relationships (SSRs)

Species-area relationships (SARs)			Species sampling relationships (SSRs)	
A.a	A.b	B	C	Species accumulation curves (A.a/b), Rarefaction curves (B.a/b)
I	IIA	IV	IV	II B, IIIA and IIIB (Species-area), Species accumulation, Rarefaction
contiguous plots			non-contiguous plots (samples)	
continuous ecosystems		islands (habitat/true)	continuous ecosystems	
single values	average values	single values		single/average values
nested		non-nested		nested

