minA: A minimum area indicator of alpha-diversity patterns

Biodiversity and Conservation

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Supplementary Information

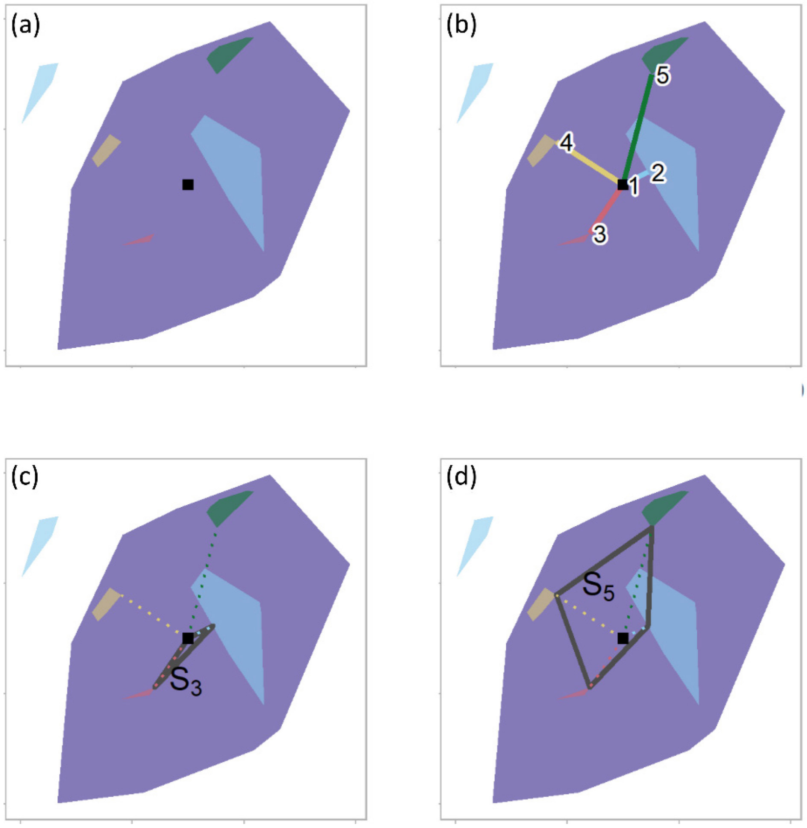

Fig. SI 1 The steps for estimating minA using simulated polygons as distribution data. (a) Polygons of different color correspond to different species, with the black square corresponding to the starting point of the sampling. (b) Estimation of the shortest distance between all polygon perimeters and the starting point. The numbers indicate the order in which new species are detected according to the distance from the starting point. (c) The minA for three species (polygon with grey outline) as defined by the starting point and the closest points in the distribution of two species. (d) The minA for five species (polygon with grey outline)

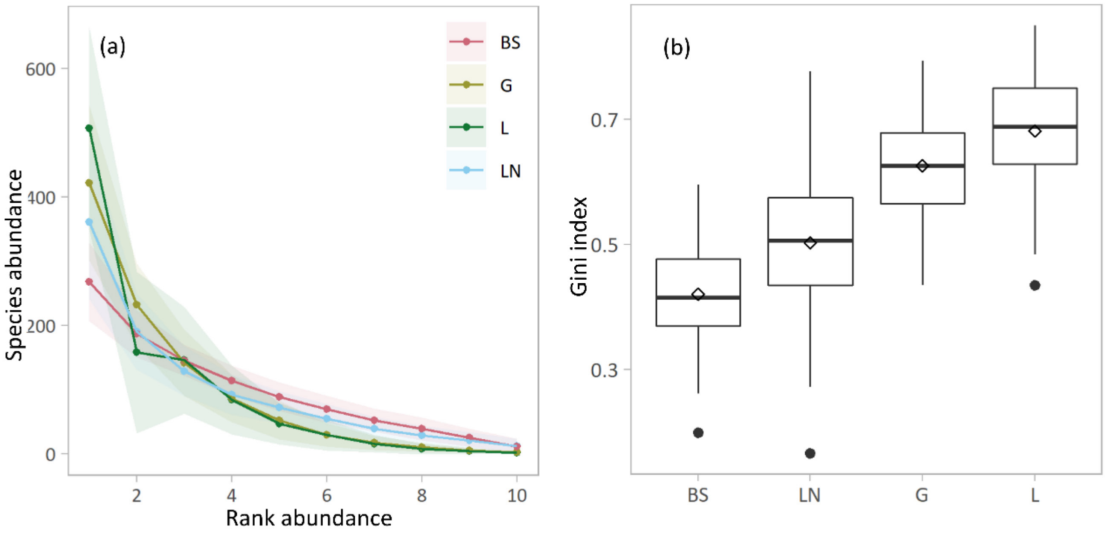

Fig. SI 2 The abundance distribution models used in the study. (a) Average species abundance rankings for the simulated communities by abundance distribution model. Shaded polygons correspond to the standard deviation. (b) Observed values of the Gini index for each abundance distribution model. The median in each boxplot is indicated by a horizontal line and the average by a diamond. Abbreviations for abundance distribution models: BS = Broken-stick, LN = Lognormal series, G = Geometric series, L = Logarithmic series

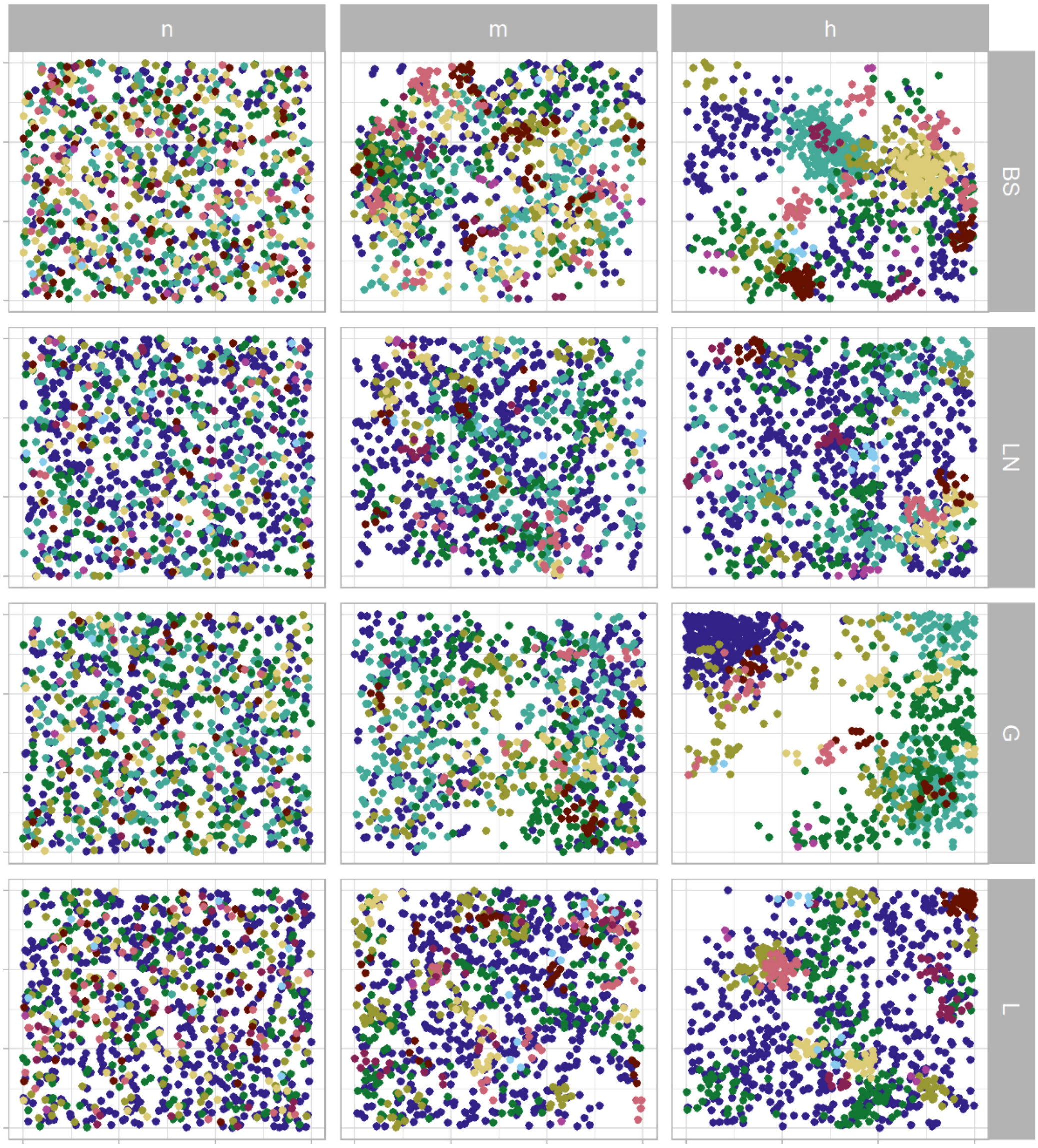

Fig. SI 3 Indicative spatial distribution of species' individuals for 12 simulated communities across the combination of four abundance distribution models and three degrees of spatial aggregation. Abbreviations of abundance distribution models: BS = Broken-stick, LN = Lognormal series, G = Geometric series, L = Logarithmic series and spatial aggregation degrees (SPAD): n = zero, m = moderate, h = high

Table SI 1 Mixed-effects model statistics for the effect of Gini index and the spatial degree of aggregation (SPAD) on log minimum area (minA) per species number. For each model, the estimates per predictor variable with 95% confidence interval (CI) and overall model statistics are given. Asterisks indicate the significance of each variable. Abbreviations for SPAD: n = zero, m = moderate, h = high

	S = 2	**S = 3**	**S = 4**	**S = 5**	**S = 6**	**S = 7**	**S = 8**	**S = 9**	**S = 10**
Predictor									
Intercept	6.82***	7.65***	7.99***	8.46***	8.88***	9.27***	9.87***	10.50***	11.40***
Gini index	-0.02	1.22***	2.34***	2.78***	3.16***	3.46***	3.35***	3.27***	2.86***
SPAD									
m	-0.05	0.22**	0.37**	0.56***	0.73***	0.81***	0.83***	0.81***	0.69***
h	0.34***	0.69***	1.00***	1.32***	1.50***	1.59***	1.59***	1.52***	1.31***
RI SD	0.00	0.00	0.08	0.08	0.08	0.08	0.14	0.20	0.25
Residual SD	1.37	1.01	0.90	0.80	0.71	0.63	0.56	0.53	0.49
AIC	4,183	3,456	3,182	2,911	2,613	2,346	2,052	1,917	1,763
BIC	4,214	3,486	3,213	2,942	2,643	2,377	2,082	1,947	1,794
REML	4,171	3,444	3,170	2,899	2,601	2,334	2,040	1,905	1,751
Residual df	1,194	1,194	1,194	1,194	1,194	1,194	1,194	1,194	1,194

*p<0.05; **p<0.01; ***p<0.001

Table SI 2 Mixed-effects model statistics for the effect of Gini index, spatial degree of aggregation (SPAD) and distance of the starting point from the center of the study area on log minimum area (minA) per species number. For each model, the estimates per predictor variable with 95% confidence interval (CI) and overall model statistics are given. Asterisks indicate the significance of each variable. Abbreviations for SPAD: n = zero, m = moderate, h = high and distance from center: n = zero, m = moderate, l = high

	S = 2	**S = 3**	**S = 4**	**S = 5**	**S = 6**	**S = 7**	**S = 8**	**S = 9**	**S = 10**
Predictor									
Intercept	6.51***	7.44***	7.95***	8.42***	8.90***	9.36***	9.93***	10.5***	11.4***
Gini index	0.12	1.27***	2.07***	2.57***	2.90***	3.10***	3.09***	3.02***	2.68***
SPAD									
m	0.25***	0.44***	0.62***	0.79***	0.91***	0.98***	0.99***	0.92***	0.78***
h	0.59***	0.96***	1.29***	1.54***	1.68***	1.73***	1.71***	1.62***	1.40***
Distance from center									
m	0.03	0.05	0.06	0.06	0.03	0.03	0.04	0.07	0.10
l	0.72***	0.70***	0.66***	0.58***	0.49***	0.45***	0.41***	0.40***	0.42***
RI SD	0.19	0.18	0.16	0.14	0.13	0.13	0.17	0.21	0.26
Residual SD	1.43	1.04	0.91	0.80	0.70	0.63	0.58	0.54	0.52
AIC	51,341	42,299	38,243	34,564	31,012	27,985	25,367	23,773	22,308
BIC	51,402	42,360	38,303	34,624	31,073	28,045	25,428	23,834	22,369
REML	51,325	42,283	38,227	34,548	30,996	27,969	25,351	23,757	22,292
Residual df	14,392	14,392	14,392	14,392	14,392	14,392	14,392	14,392	14,392

*p<0.05; **p<0.01; ***p<0.001

Table SI 3 The mean and standard deviation (in parenthesis) of minA (in km^2) for specific numbers of species and for all starting points by taxonomic group

Number of species requested	Sauria	Serpentes	Amphisbaenia	Testudines

Maximum number of species with overlapping distributions	860,107 (± 947,744)	1,674,165 (± 2,027,158)	1,182,598 (± 1,618,090)	900,711 (± 1,130,856)
10 species	269 (± 4,124)	3,126 (± 11,423)	1,652,021 (± 1,982,925)	555,263 (± 809,268)
20 species	17,708 (± 53,983)	71,359 (± 156,067)	3,952,425 (± 2,996,725)	2,947,278 (± 2,316,043)
10% of γ-diversity	2,111,269 (± 2,077,412)	747,727 (± 1,278,728)	982,011 (± 1,445,289)	127,083 (± 266,794)
25% of γ-diversity	8,293,761 (± 4,732,078)	2,688,125 (± 2,547,324)	3,519,868 (± 2,841,499)	900,711 (± 1,130,856)
50% of γ-diversity	18,025,649 (± 5,326,788)	9,742,872 (± 5,151,789)	8,459,939 (± 4,410,531)	4,700,559 (± 2,851,111)
75% of γ-diversity	25,668,078 (± 4,604,583)	17,996,042 (± 6,091,182)	14,315,216 (± 5,219,619)	10,811,334 (± 4,316,324)
100% of γ-diversity	35,988,755 (± 372,597)	34,395,719 (± 368,218)	24,192,118 (± 884,843)	18,122,353 (± 3,262,858)

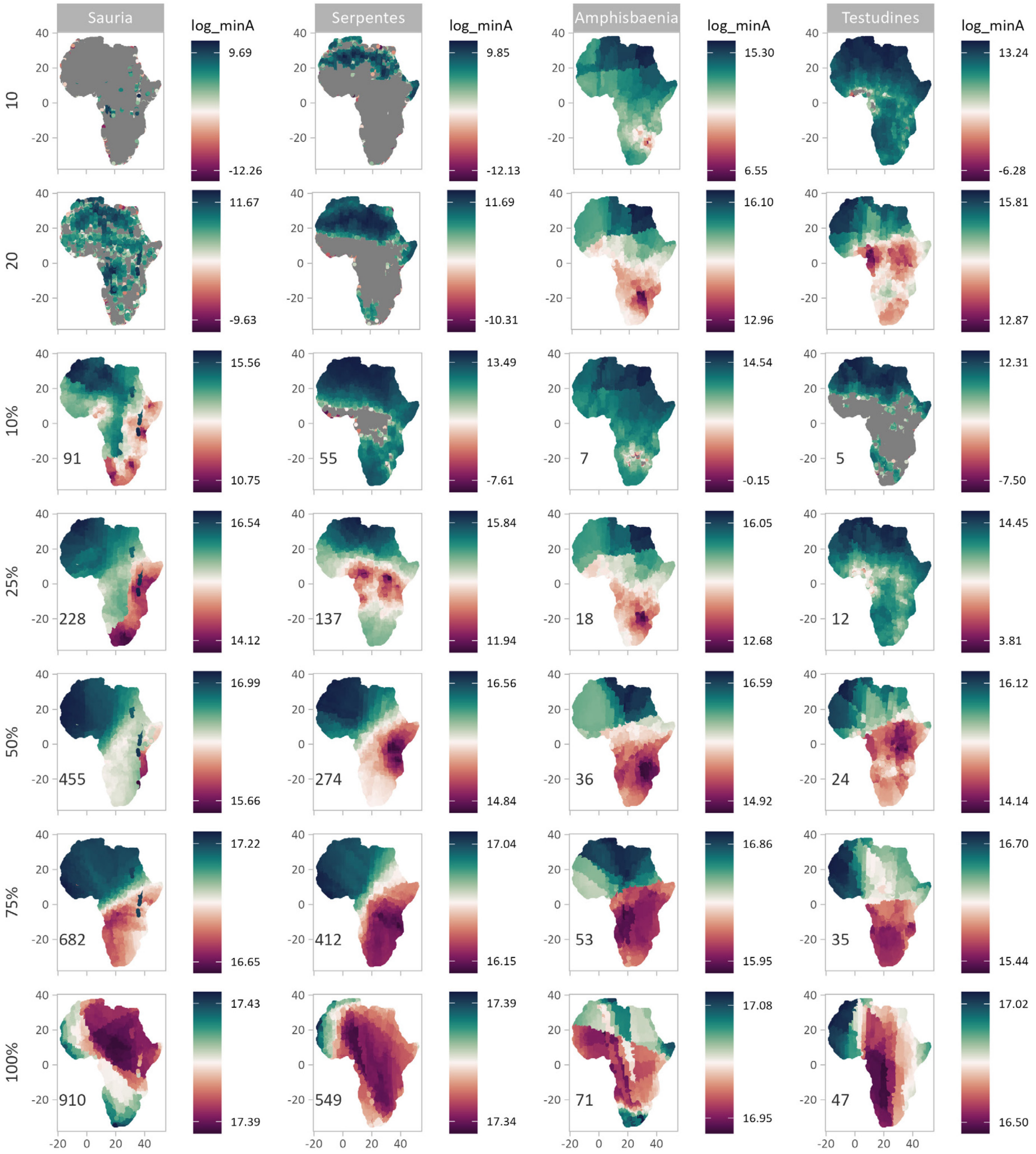

Fig. SI 4 The minA size per sampling point for different numbers of species as diverging color. In the first and second rows, minA is estimated for 10 and 20 species respectively. In the rest, the required number of species is expressed as a percentage of γ-diversity of the taxonomic group. The number of species in these cases is given within the map (bottom left of each plot). Areas in grey indicate that the requested number of species exists at the sampling point and minA cannot be defined

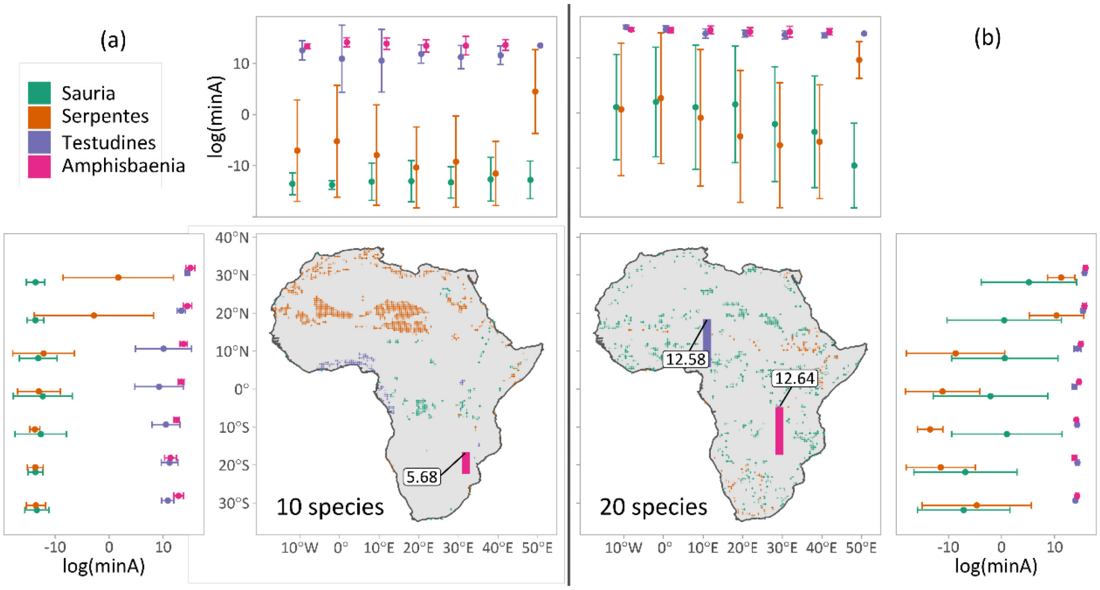

Fig. SI 5 The location and size of the minimum minA for (a) 10, (b) 20 species for each taxonomic group is shown within the maps. The size of the bars within the maps corresponds to the value of the minimum minA (the logarithmic value is given in the label). In case of inability to define the minA due to co-occurrence of the selected number of species, points with a number of species equal to the selected number are depicted. The plots next to the map show the average (circle) and standard deviation (whiskers) of minA for the starting points divided into zones of 10 degrees longitude (to the right and left of the maps) and latitude (above and below the maps). Each taxonomic group is highlighted in a different color