Appendices

Appendix 1: Barro colorado Island forest plot discretization procedure

To analyze the patch distribution of BCI plot we first have to discretized the positions of the trees to fit them in a lattice. In each position only one individual of a particular species can be present, this is the same assumption that we made for the model that we use in the paper above.

We have to choose a length scale to make the discretization, if we intend to fit all the individuals of all species in a different site the scale should be around 0.10 m for this plot, as the plot has 1000m x 500 m, that would result in an big lattice of 10000x5000 sites with a great proportion of empty places. This will result in a majority of isolated sites with almost no patches. If we use a bigger scale e.g. of 0.5 m, more than 1 individual of possibly different species get in some of the sites, in these cases we have to decide which one will occupy the site. We establish that the one with greater dbh, no matter the species, will be the one that occupies the site, thus we are favoring the more mature individuals.

In this process we have to find the scale that give us the maximal occupation of the lattice without loosing the species structure of the community. Then the criteria to stop enlarging the scale is that the species abundance distribution (SAD) of the discretized lattice has not to be statistically different from the original SAD. To test this we use the Anderson-Darling statistic with a randomization procedure using the R package kSamples [1], this statistic has been proved powerful to detect different kinds of communities [2]. Using this procedure we obtained a scale of 1 m, thus we used a lattice of 1000x500 sites.

1. Scholz F, Zhu A (2015) kSamples: K-Sample Rank Tests and their Combinations. Available: http://cran.r-project.org/package=kSamples.

2. Saravia LA (2015) A new method to analyse species abundances in space using generalized dimensions. Methods Ecol Evol 6: 1298–1310. Available: http://doi.wiley.com/10.1111/2041-210X.12417.

Appendix Tables

Table S1: Equivalence of spatially explicit parameters m and α (Mean dispersal distance) with spatially implicit neutral parameters θ and I.

m	α (mean dist.)	θ	I
0.01	2.08 (13.3)	155.7	121.1
0.001	2.08 (13.3)	113.8	97.3
0.0001	2.08 (13.3)	83.2	78.2
0.01	2.04 (26.6)	561.2	342.5
0.001	2.04 (26.6)	410.3	275.2
0.0001	2.04 (26.6)	300.0	221.1
0.01	2.02 (53.3)	2026.0	969.7
0.001	2.02 (53.3)	1482.0	779.2
0.0001	2.02 (53.3)	1083.0	626.1

Table S2: Size of the largest patch relative to the total area S_{max} before the critical point $\rho < \rho_c$ and after the critical point $\rho > \rho_c$, and for the largest patch relative to the total species area RS_{max}. The parameters used were the specified in the first row of table 1.

Side	MetaType	before/after	S_{max}	RS_{max}
128	Logseries	$\rho > \rho_c$	0.938	0.973
128	Logseries	$\rho < \rho_c$	0.147	0.230
128	Uniform	$\rho > \rho_c$	0.951	0.985
128	Uniform	$\rho < \rho_c$	0.127	0.205
192	Logseries	$\rho > \rho_c$	0.934	0.972
192	Logseries	$\rho < \rho_c$	0.020	0.040
192	Uniform	$\rho > \rho_c$	0.942	0.978
192	Uniform	$\rho < \rho_c$	0.031	0.056
256	Logseries	$\rho > \rho_c$	0.928	0.967
256	Logseries	$\rho < \rho_c$	0.002	0.008
256	Uniform	$\rho > \rho_c$	0.940	0.974
256	Uniform	$\rho < \rho_c$	0.002	0.009

Table S3: Critical points ρ_c^∞ for infinite lattices. Where *Mean Distance* is the mean dispersal distance, m is the migration parameter, and SE p_c the standard error of the critical point.

Metacomm. species	Metacomm. type	Mean Distance	m	ρ_c^∞	SEρ_c
16	L	26.66	0.0001	0.00017	0.00003
16	U	26.66	0.0001	0.00026	0.00001
64	L	26.66	0.0001	0.00029	0.00001
64	U	26.66	0.0001	0.00026	0.00000
320	L	53.33	0.0001	0.00028	0.00002
320	U	53.33	0.0001	0.00026	0.00001
320	L	26.66	0.0001	0.00026	0.00002
320	U	26.66	0.0001	0.00024	0.00001
320	L	13.34	0.0001	0.00027	0.00000
320	U	13.34	0.0001	0.00026	0.00001
320	L	26.66	0.0010	0.00052	0.00008
320	U	26.66	0.0010	0.00062	0.00007
320	L	26.66	0.0100	0.00646	0.00000
320	U	26.66	0.0100	0.00640	0.00000

Table S4: Proportion of best models for patch size distributions from simulated neutral/niche model communities. We fitted the distribution of patches of the species with the largest patch (MaxPatch) or the spanning patch (Spanning). We used 3 models: exponential (Exp), power law (Pow) and power law with exponential cutoff (PowExp), when there is not enough number of patches we did not fit any model (NoModel). The best model was selected using the Akaike information criteria. We made 30 simulations in a range of ρ (see methods) and we used the following parameters: metacommunities have 64 species and two different species abundance distributions: logseries and uniform SAD. The size of the grid was 512*512 sites, migration=0.0001, and dispersal distance=26.66.

model	type	n	Frequency
NoModel	Spanning	121	0.25
Pow	Spanning	40	0.08
Pow	MaxPatch	65	0.13
PowExp	Spanning	42	0.08
PowExp	MaxPatch	221	0.46
Exp	Spanning	0	0.00
Exp	MaxPatch	0	0.00

Appendix Figures
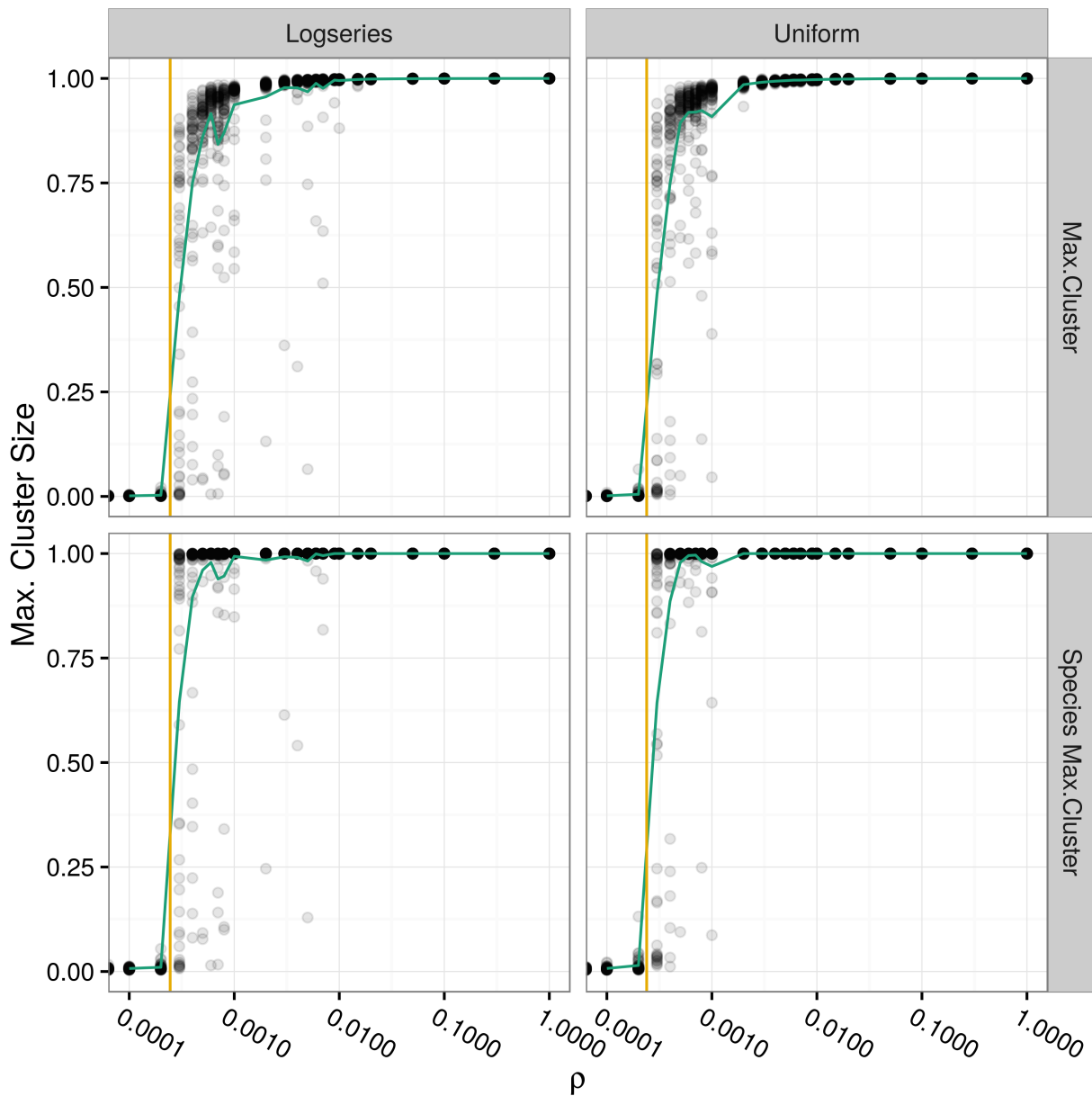
Figure S1: Largest patch for a spatial neutral/niche model as a function of the intensity of competition ρ. The columns represent two different metacommunity types: Logseries, a metacommunity with logseries species abundance distribution (SAD); Uniform, a metacommunity with a uniform SAD. The rows represent the largest patch relative to total area S_{max} and the largest patch relative to the species area RS_{max}. The vertical line is the critical point, which is the value for parameter ρ where a phase transition between neutral and niche phases occurs. The parameters used were: side of the simulation lattice was 256 sites, the number of species in the metacomunity was 320, the metacommunity migration $m=0.0001$ and the dispersal distance $= 26.66$.
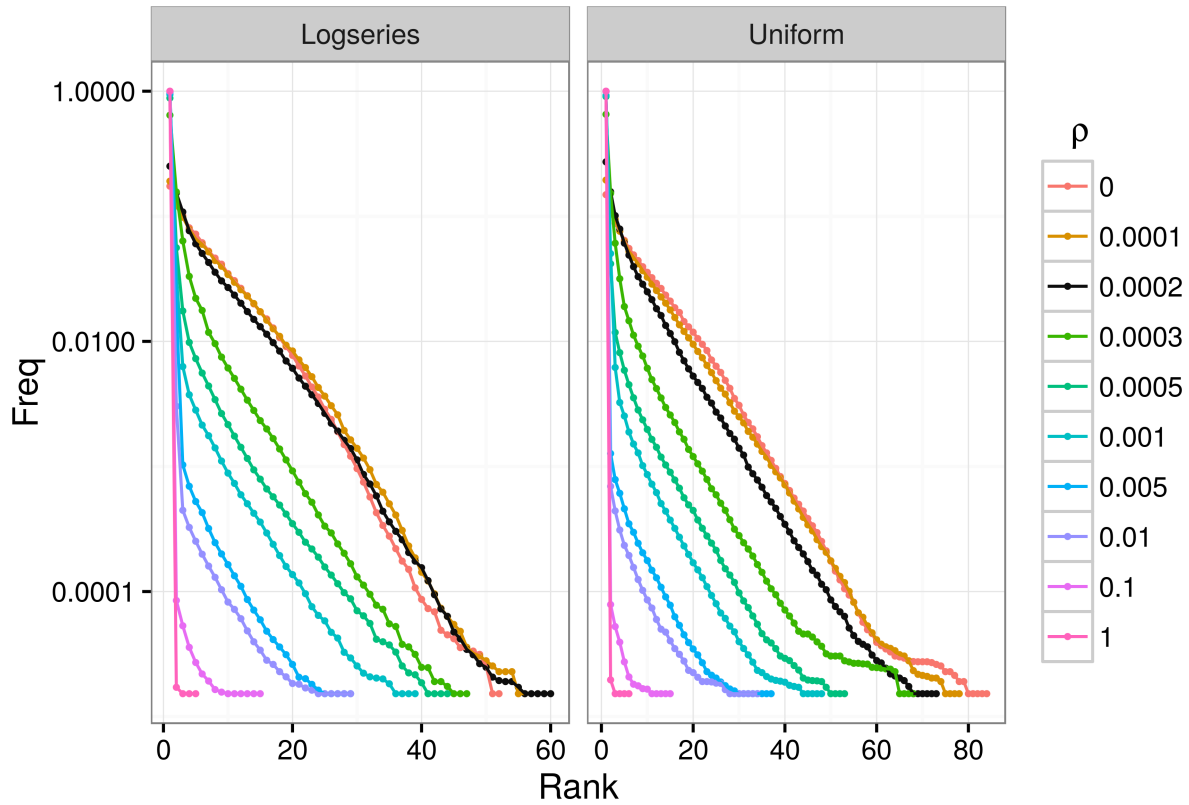
Figure S2: Rank abundance diagrams (RADs) for simulated neutral/niche model communities as a function of the intensity of competition ρ. Except for $\rho = 0$ the values in the legend are upper limits. The RADs are averages of 50 simulations. Metacommunities have 320 species and two different species abundance distributions (SAD): logseries SAD (L); and uniform SAD (U); the black line with $\rho = 0.0002$ is the closest SAD previous to the critical point. The size of the grid was 256*256 sites and the other parameters used are the migration rate m=0.0001, and dispersal distance=26.66.
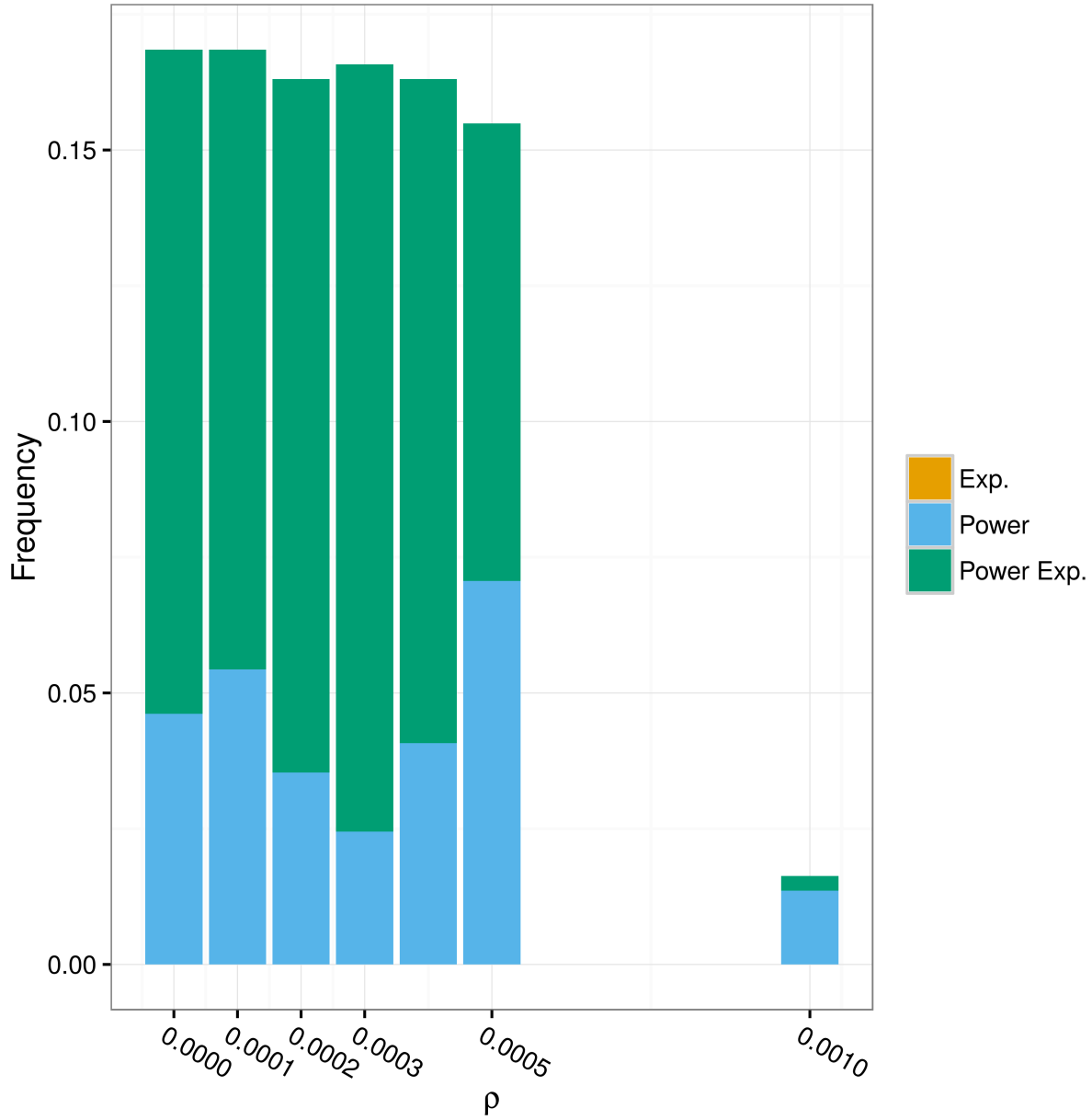
Figure S3: Proportion of best models as function of the competition intensity (ρ) for patch size distributions of the species with the largest patch or the spanning patch. We fitted fitted a power law (Pow), a power law with exponential cutoff, and an exponential models to distribution of patch sizes and selected the best model using the Akaike criterion. We made 30 simulations for each ρ and metacommunity type. Metacommunities have 64 species and two different species abundance distributions (SAD): *L*, logseries SAD; and *U*, uniform SAD. The size of the grid was 512*512 sites and the other parameters used were migration=0.0001, dispersal distance=26.66. The critical point ρ_c is 0.00029 for Logseries and 0.00026 for uniform metacommunities.
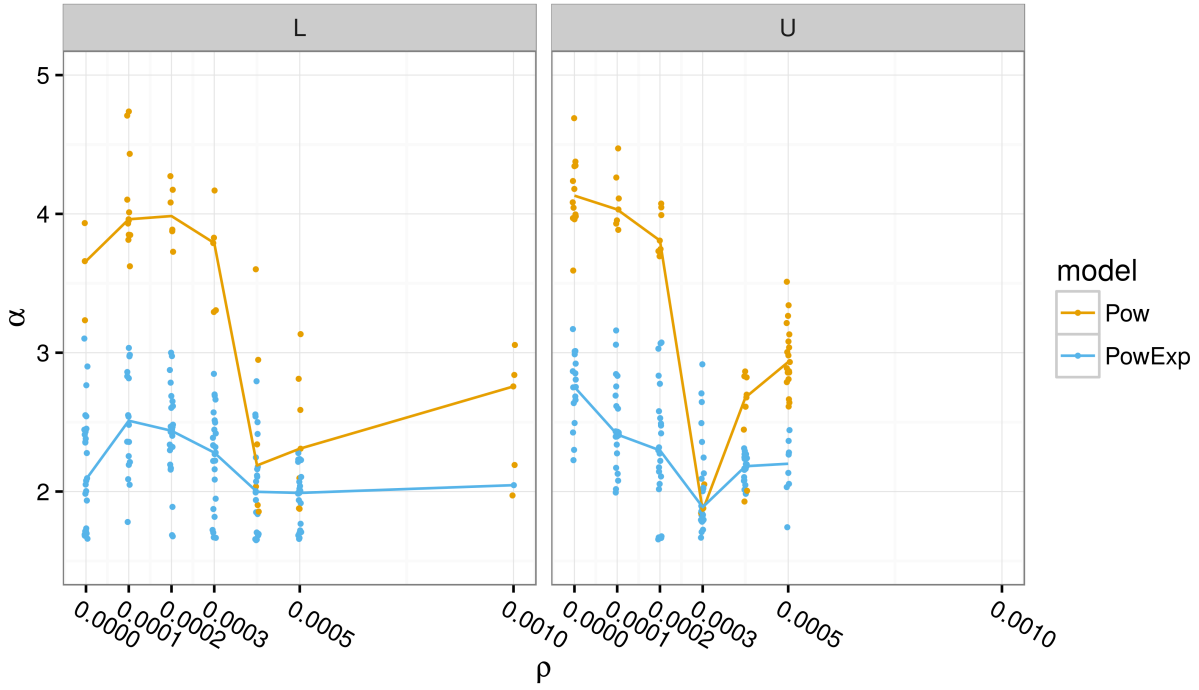
Figure S4: Power law exponent α for patch size distributions as a function of the intensity of competition ρ. We show the exponents of the two models selected by the Akaike criterion: the power law (Pow) and a power law with exponential cutoff. The continuous lines unite the medians for each ρ. The patch size distribution corresponds to the species that has the largest patch or the species that percolate and form a spanning cluster. We made 30 simulations for each ρ and metacommunity type. Metacommunities have 64 species and two different species abundance distributions (SAD): *L*, logseries SAD; and *U*, uniform SAD. The size of the grid was 512*512 sites and the other parameters used were migration=0.0001, dispersal distance=26.66. The critical point ρ_c is 0.00029 for Logseries and 0.00026 for uniform metacommunities.
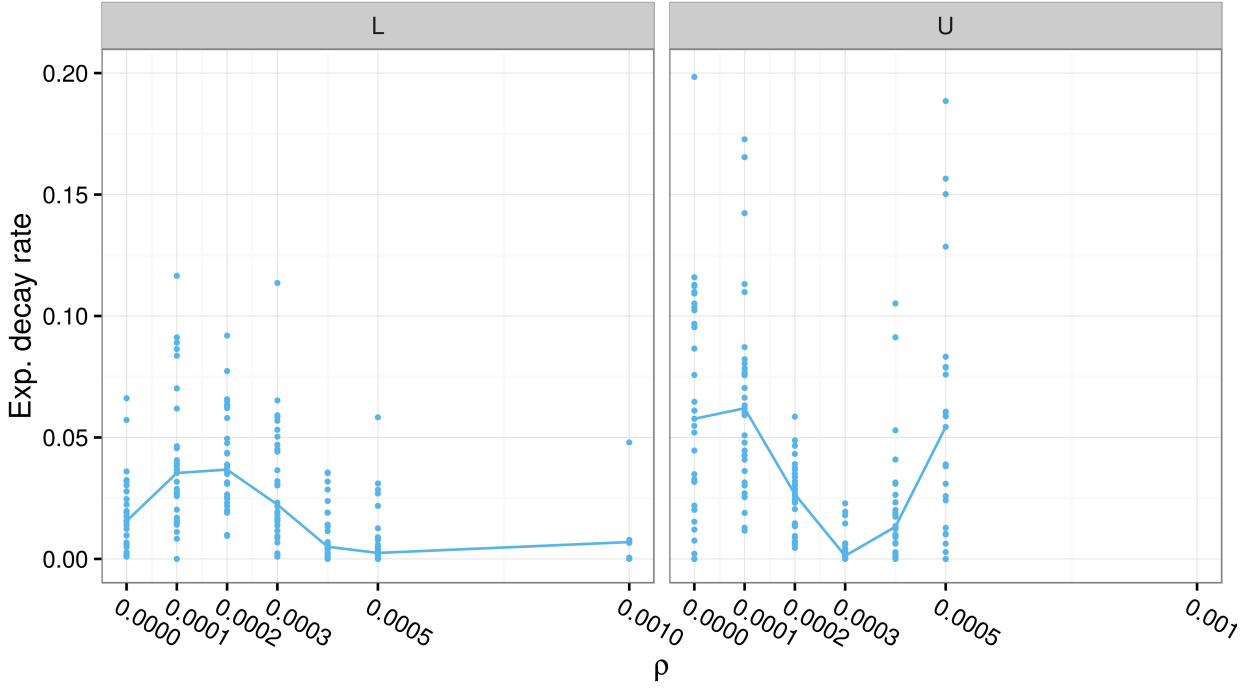
Figure S5: Exponential decay rate of the Power law with exponential cutoff model for patch size distributions as a function of the intensity of competition ρ. The continuous line unites the medians for each ρ. We fitted a power law with exponential cutoff to patch size distribution of the species that has the biggest patch or the species that percolate and form a spanning cluster. We made 30 simulations for each ρ and metacommunity type. Metacommunities have 64 species and two different species abundance distributions (SAD): *L*, logseries SAD; and *U*, uniform SAD. The size of the grid was 512*512 sites and the other parameters used were migration=0.0001, dispersal distance=26.66. The critical point ρ_c is 0.00029 for Logseries and 0.00026 for uniform metacommunities.
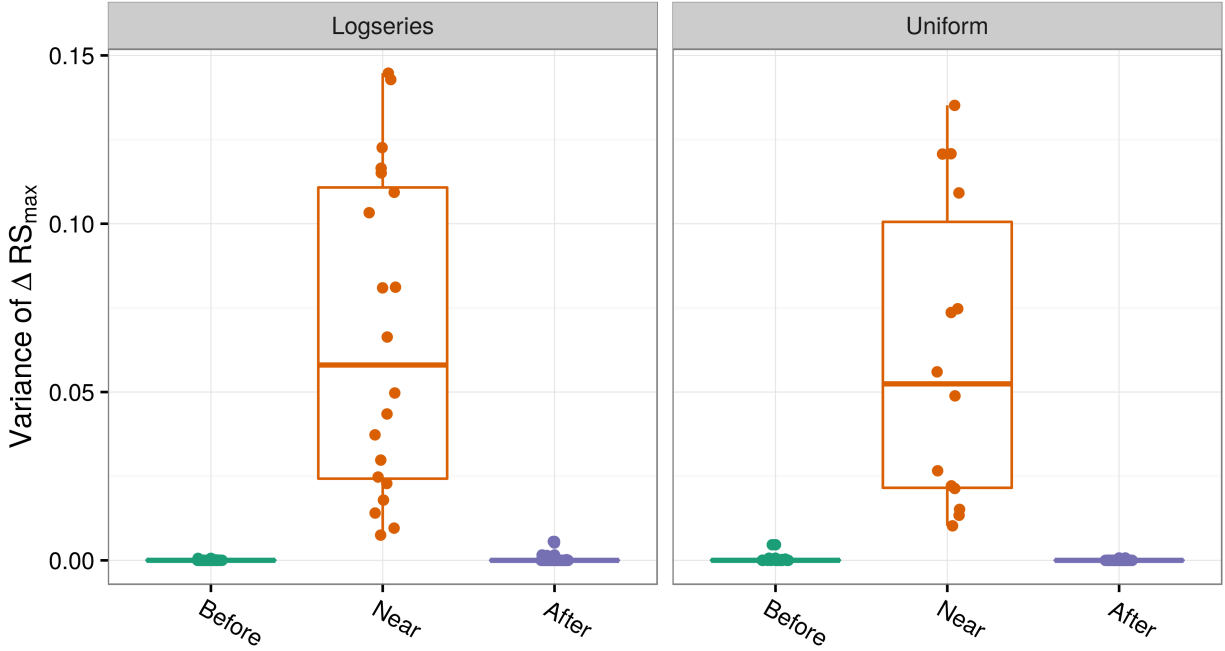
Figure S6: Variance of temporal fluctuations of the largest patch species relative to the total abundance of the same species ΔRS_{max}. We simulated communities in the same time span than the simulations to determine the critical point—typically around 20000 time steps—we take the last 5000 and measure the patch sizes each 100 time steps. The communities that did not have a spanning patch were classified as "Before" the critical point, with a range of $\rho : 0 - 0.0004$. The communities that present a spanning patch in all the times are measured as "After" the critical point, with $\rho : 0.0004 - 1$. The communities where the spanning patch appears and disappears were classified as "Near" the critical point, with $\rho : 0.0002 - 0.0004$. We made 10 simulations for each ρ and two metacommunity types: "Logseries" species abundance distribution (SAD) and "Uniform" SAD. Metacommunities have 320 species, the size of the grid was 256*256 sites, migration from metacommunity was 0.0001, dispersal distance=26.66.
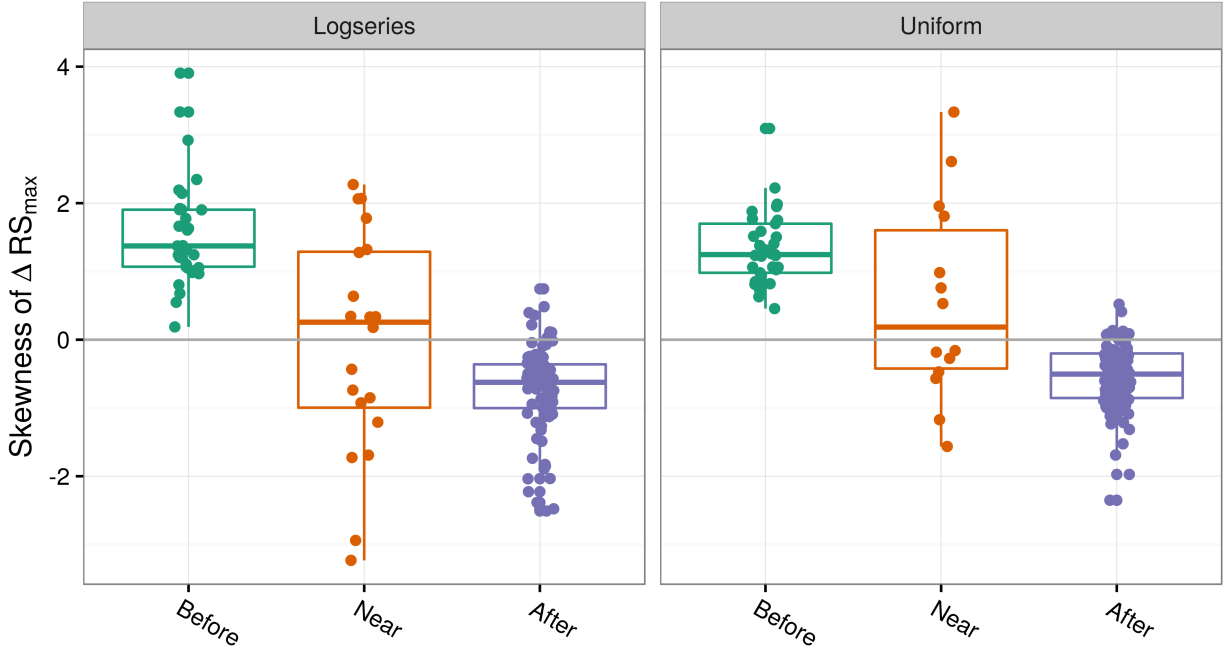
Figure S7: Skewness of the temporal fluctuations of the largest patch species relative to the total abundance of the same species. We simulated communities in the same time span than the simulations to determine the critical point—typically around 20000 time steps—we take the last 5000 and measure the patch sizes each 100 time steps. The communities that did not have a spanning patch were classified as "Before" the critical point, whit a range of $\rho : 0 - 0.0004$. The communities that present a spanning patch in all the times are measured as "After" the critical point, with $\rho : 0.0004 - 1$. The communities where the spanning patch appears and disappears were classified as "Near" the critical point, with $\rho : 0.0002 - 0.0004$. We made 10 simulations for each ρ and two metacommunity types: "Logseries" species abundance distribution (SAD) and "Uniform" SAD. Metacommunities have 320 species, the size of the grid was 256*256 sites, migration from metacommunity was 0.0001, dispersal distance=26.66.
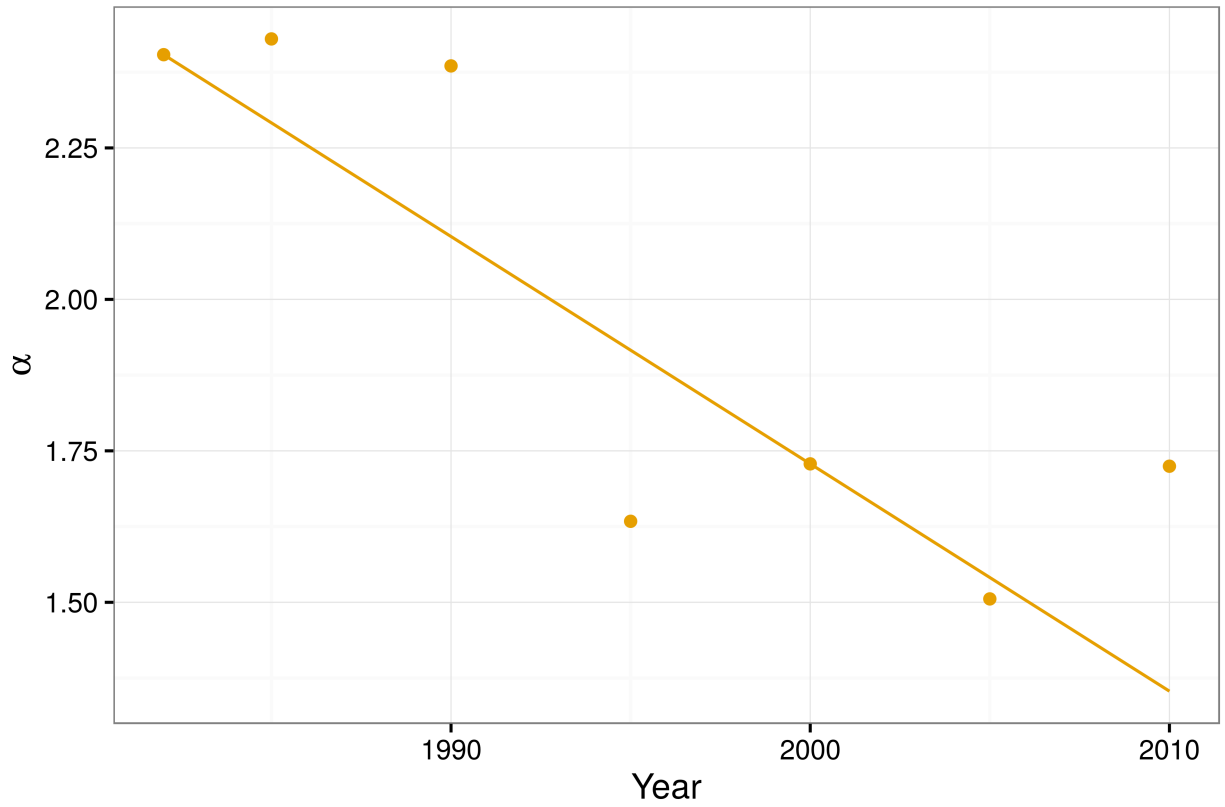
Figure S8: Power law exponent α for patch size distributions of the Barro Colorado Island forest plot as a function of the census year. The continuous line is a median regression (Slope: -0.0375, SE: 0.0145, t-value: -2.583, p-value: 0.049)
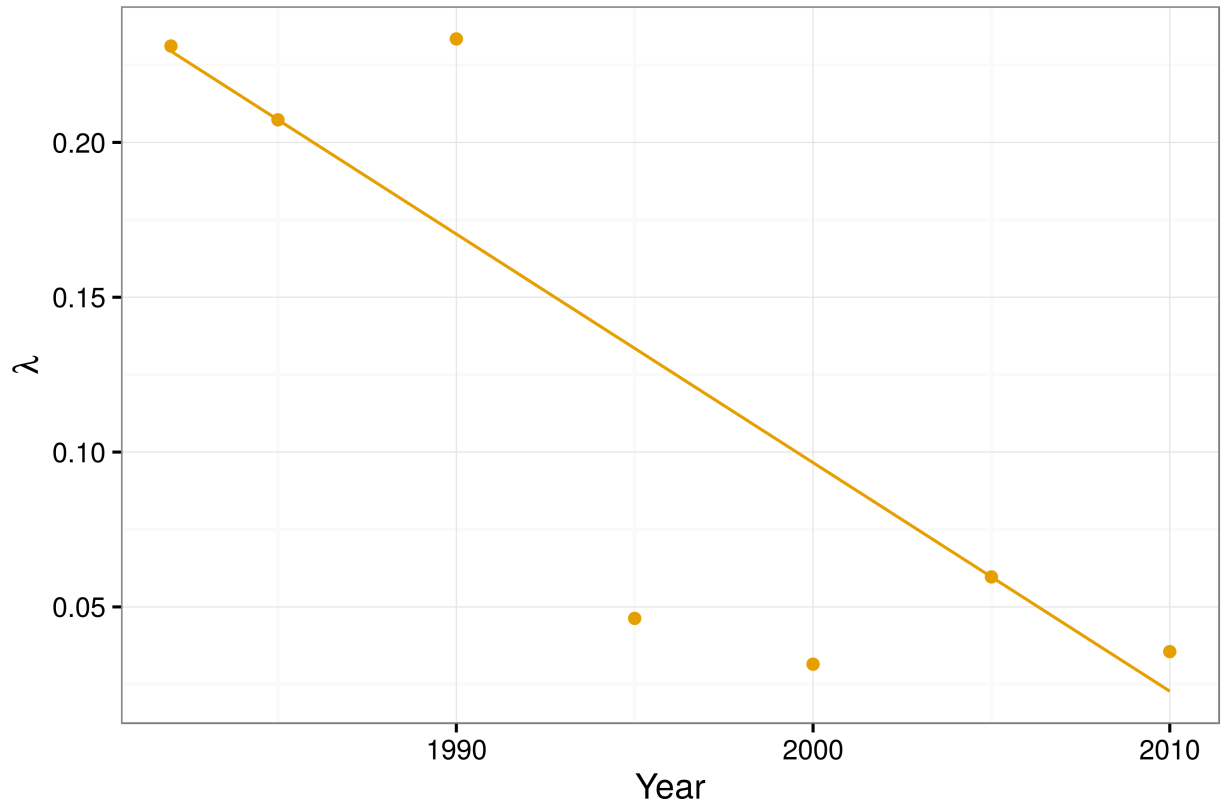
Figure S9: Power law exponent α for patch size distributions of the Barro Colorado Island forest plot as a function of the census year. The continuous line is a median regression (Slope: -0.0074, SE: 0.0033, t-value: -2.216, p-value: 0.078)