

Ecography

E7430

Giehl, E. L. H. and Jarenkow, J. A. 2012. Niche conservatism and the differences in species richness at the transition of tropical and subtropical climates in South America. – *Ecography* 35: xxx–xxx.

Supplementary material

Appendix 1

Table A1. Bioclimatic variables available in the WorldClim database (Hijmans, et al. 2005). We extracted main variations in the subsets of temperature (BIO1-BIO11) and precipitation (BIO12-BIO19) by principal components analysis (PCA). Symbols indicate Pearson linear correlations that are significantly different from zero among ordination axes and variables (***) = $P < 0.001$; ** = $P < 0.01$; * = $P < 0.05$).

	Bioclimatic Variables	Code	Axis 1	Axis 2
<i>Temperature</i>				
BIO1	Annual Mean Temperature [1]	AMT	0.954 ***	-0.286 *
BIO2	Mean Monthly Temperature Range [2]	MMTR	0.336 **	-0.091
BIO3	Isothermality (2/7) (* 100) [3]	ISOT	0.678 ***	0.521 ***
BIO4	Temperature Seasonality (STD * 100) [4]	TSEAS	-0.657 ***	-0.742 ***
BIO5	Max Temperature of Warmest Month [5]	MTWM	0.344 **	-0.929 ***
BIO6	Min Temperature of Coldest Month [6]	MTCM	0.905 ***	-0.13
BIO7	Temperature Annual Range (5-6) [7]	TAR	-0.489 ***	-0.766 ***
BIO8	Mean Temperature of Wettest Quarter [8]	MTWeQ	0.581 ***	-0.174
BIO9	Mean Temperature of Driest Quarter [9]	MTDQ	0.769 ***	0.047
BIO10	Mean Temperature of Warmest Quarter [10]	MTWaQ	0.567 ***	-0.808 ***
BIO11	Mean Temperature of Coldest Quarter [11]	MTCQ	0.995 ***	0.049
<i>Precipitation</i>				
BIO12	Annual Precipitation [12]	AP	0.195	-0.969 ***
BIO13	Precipitation of Wettest Month [13]	PWM	-0.862 ***	-0.484 ***
BIO14	Precipitation of Driest Month [14]	PDM	0.906 ***	-0.391 **
BIO15	Precipitation Seasonality (CV) [15]	PSEAS	-0.995 ***	0.007
BIO16	Precipitation of Wettest Quarter [16]	PWQ	-0.867 ***	-0.491 ***
BIO17	Precipitation of Driest Quarter [17]	PWeQ	0.926 ***	-0.368 **
BIO18	Precipitation of Warmest Quarter [18]	PWaQ	-0.853 ***	-0.462 ***
BIO19	Precipitation of Coldest Quarter [19]	PCQ	0.906 ***	-0.383 **

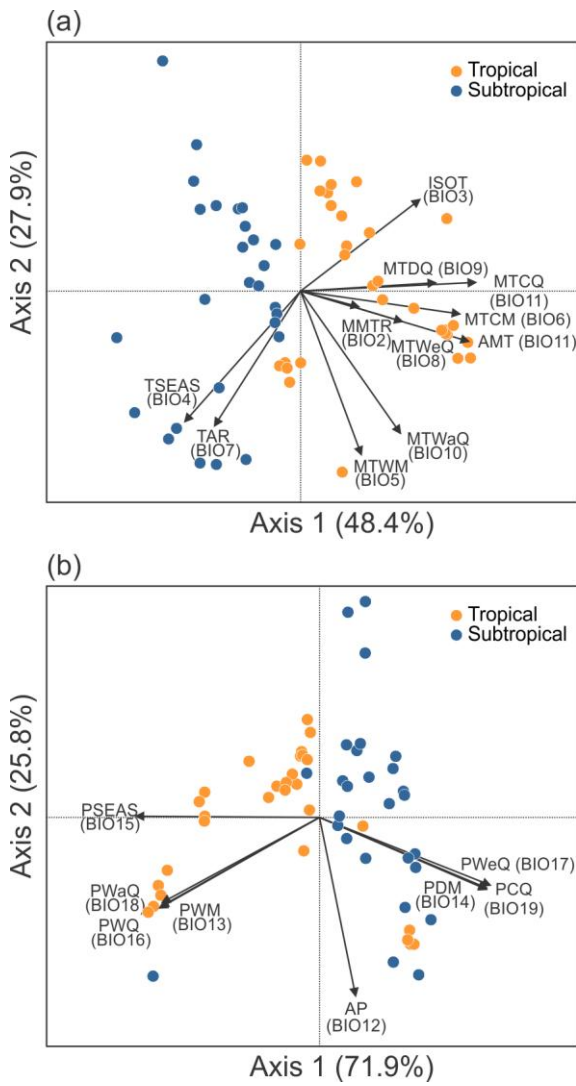


Figure A2. Ordination of temperature-related variables (a) and precipitation-related variables (b), extracted from WorldClim (Hijmans et al. 2005). The variance extracted for each axis is shown within parentheses. See Table S1 for variable codes. Previously to principal components analysis (PCA), we centered and normalized all variables by their means and standard deviations, respectively. The PCA for temperature-related variables extracted 48.4% and 27.9% of variation from data in the first and second components, respectively (a). The second PCA, for precipitation-related variables, extracted 71.9% and 25.8% of variation in the first and second components, respectively (b).

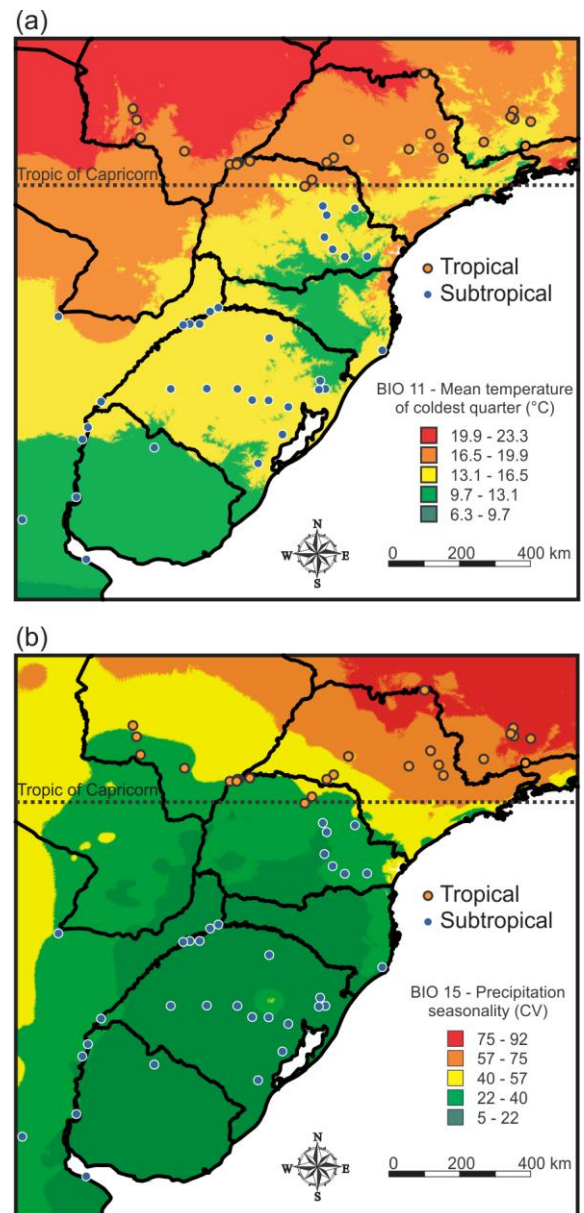


Figure A3. Variation in mean temperature of coldest quarter – BIO11 (a) and precipitation seasonality – BIO15 (b) along the sample area in southeastern South America. Circles indicate site locations.

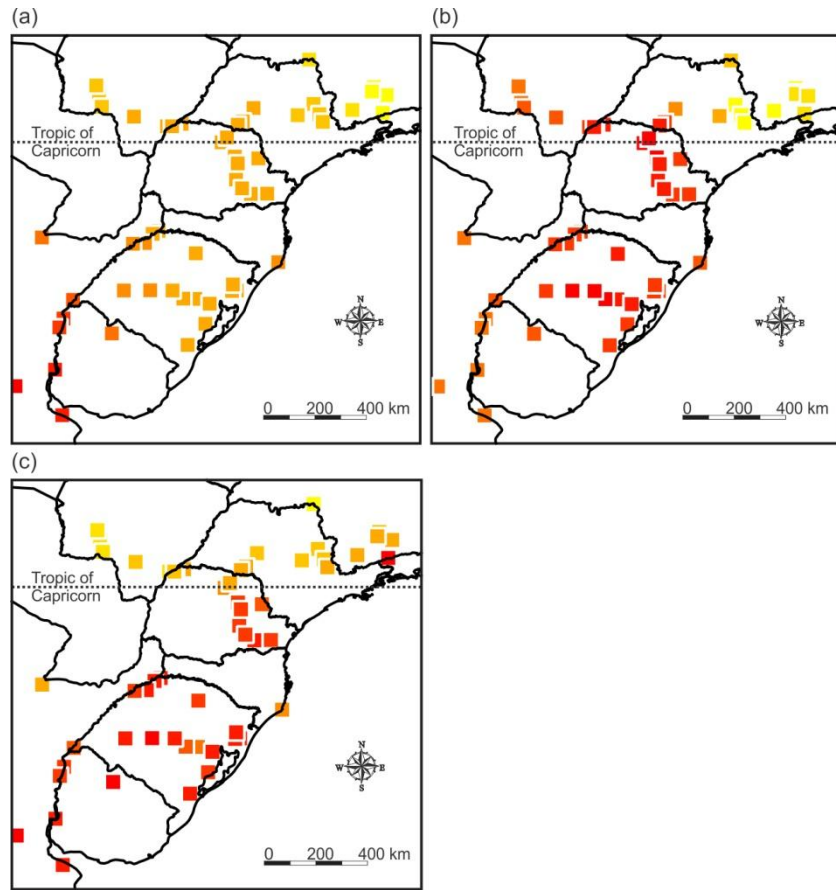


Figure A4. Squared longitude multiplied by latitude – $\text{Long}^2 \times \text{Lat}$ (a), second component derived from a principal component analysis on the spatial distance matrix among sites – PCNM2 (b), and interaction between Precipitation and squared Temperature – $\text{Prec} \times \text{Temp}^2$ (c). Values increase from yellow, to orange, to red.

Table A5. Spatial autocorrelation for the residuals of the OLS regression, with species richness (SR) as the response variable. Model 1 had Temperature, Precipitation, Phylogenetic Species Variability (PSV) and Phylogenetic Species Clustering (PSC) as predictors, while Model 2 had two additional spatial predictors ($\text{Long}^2 \times \text{Lat}$ and PCNM2). We assessed spatial autocorrelation with Moran's I coefficients and calculated *P*-values by applying Monte Carlo permutations. While Model 1 had six classes with significant autocorrelation, Model 2 had only one distance class with significant Moran's I coefficients; thus, it is much more reliable.

Model 1: SR ~ Temperature + Precipitation + PSV + PSC

Number of points	Class center (km)	Moran's I	<i>P</i> -value
330	115	0.16	0.019
328	291	< 0.001	0.985
328	419	-0.024	0.744
330	534	-0.241	0.004
328	637	-0.108	0.13
328	744	-0.07	0.335
330	860	0.008	0.892
328	991	0.236	0.004
328	1161	0.061	0.371
330	1647	-0.182	0.023

Model 2: $SR \sim \text{Temperature} + \text{Precipitation} + PSV + PSC + \text{Long}^2 \times \text{Lat} + PCNM2$

Number of points	Class center (km)	Moran's I	P
330	115	0.053	0.486
328	291	-0.087	0.236
328	419	-0.039	0.595
330	534	-0.149	0.043
328	637	0.051	0.449
328	744	-0.002	0.976
330	860	-0.022	0.724
328	991	0.097	0.156
328	1161	-0.019	0.781
330	1647	-0.051	0.312

Table A6. Taxa and divergence times in millions of years before present (MYBP), which were used to adjust phylogenetic branch lengths in Phylocom.

Taxon	Divergence time
Euphyllophyte	400
Seedplant	325
Araucariaceae	308
Angiosperm	179
Nym2ast	171
Aus2ast	165
Monocotneudicot	161
Eudicot	147
Cyatheaceae	145.5
Ranunculales	140
Bux2ast	137
Proteales	135
Piperales	132
Chloranthaceae	132
Nymphaeaceae	132
Sabiaceae	129
Coreeudicot	127
Alismatales	124
Subrosid	121
Asterid	117
Magnoliales	113
Papaveraceae	112
Saxifragales	111
Laurales	111
Aristolochiaceae	108
Euasterid2	107
Euasterid1	107

Taxon	Divergence time
Asparagales	107
Trochodendraceae	106
Hamamelidaceae	104
Cornales	101
Ericales	100
Canellales	99
Eurosid1	98
Araceae	98
Aquifoliales	97
Buxaceae	97
Liliales	96
Eurosid2	95
Dioscoreales	95
Garryales	93
Geraniales	92
Vitaceae	92
Asterales	90
Myrtales	88
Pandanaceae	88
Caryophyllales	84
Malpighiales	81
Dipsacales	81
Fabales	79
Brassicales	79
Solanales	78
Hydrangeaceae	78
Oxalidales	77
Lardizabalaceae	77
Rosales	76
Podocarpaceae	75

Taxon	Divergence time	Taxon	Divergence time
Saururaceae	75	Berberidaceae	44
Arecaceae	73	Oxalidaceae	43
Poales	72	Nyssaceae	43
Gentianales	71	Piperaceae	43
Monimiaceae	71	Cunoniaceae	42
Zygophyllales	70	Celastrales	42
Magnoliaceae	70	Winteraceae	42
Apiales	69	Crassulaceae	41
Santalales	69	Solanaceae	41
Malvales	68	Rutaceae	39
Commelinales	68	Picrodendraceae	38
Loasaceae	67	Geraniaceae	38
Cucurbitales	65	Bignoniaceae	38
Icacinaceae	65	Gesneriaceae	38
Lecythidaceae	65	Lythraceae	37
Ranunculaceae	65	Santalaceae	37
Cornaceae	64	Sapindaceae	36
Lamiales	63	Polemoniaceae	35
Crossosomatales	62	Celastraceae	34
Zingiberales	62	Fagaceae	34
Fagales	61	Malvaceae	34
Sapindales	61	Lauraceae	34
Elaeocarpaceae	59	Linaceae	33
Boraginaceae	59	Apiaceae	33
Adoxaceae	57	Campanulaceae	33
Fabaceae	56	Bromeliaceae	33
Altingiaceae	56	Malpighiaceae	32
Rubiaceae	56	Iridaceae	32
Rhamnaceae	55	Acaniaceae	31
Ternstroemiaceae	54	Acanthaceae	31
Circaeasteraceae	54	Meliaceae	30
Menispermaceae	53	Strelitziaceae	29
Dilleniaceae	52	Hyacinthaceae	29
Calycanthaceae	52	Polygalaceae	28
Bursa2anaca	51	Utriculariaceae	28
Saxifragaceae	51	Polygonaceae	28
Menyanthaceae	51	Amaryllidaceae	28
Musaceae	50	Combretaceae	27
Liliaceae	48	Plumbaginaceae	27
Rosaceae	47	Costaceae	27
Oleaceae	47	Convallariaceae	27
Proteaceae	47	Passifloraceae	26
Styracaceae	45	Thymelaeaceae	26
Cyclanthaceae	45	Araliaceae	26
Asteraceae	44	Loranthaceae	26

Taxon	Divergence time
Orchidaceae	26
Annonaceae	26
Brassicaceae	24
Flacourtiaceae	23
Moraceae	23
Lamiaceae	23
Marantaceae	23
Myristicaceae	23
Urticaceae	22
Salicaceae	20
Cucurbitaceae	20
Onagraceae	20
Verbenaceae	20
Convolvulaceae	20
Parnassiaceae	19
Betulaceae	19

Taxon	Divergence time
Amaranthaceae	19
Apocynaceae	18
Haloragaceae	17
Canellaceae	17
Cyperaceae	16
Pittosporaceae	14
Elaeagnaceae	13
Nyctaginaceae	13
Ericaceae	12
Poaceae	12
Dipsacaceae	10
Zingiberaceae	10
Rhizophoraceae	9
Limnanthaceae	9
Chrysobalanaceae	8

Table A7. Nodes in the phylogeny with significantly 'more' or 'less' daughter taxa for the pooled samples of tropical and subtropical climates when compared to random draws of species obtained from the whole phylogenetic tree.

Taxa	Tropics	Subtropics	P-value
<i>Albizia</i>		More	0.045
Anacardiaceae	Less		0.021
<i>Banara</i>	Less		0.049
Celastrales+Malpighiales	More		0.035
<i>Chrysophyllum</i>		More	0.045
Fabaceae		More	0.043
Fabales		More	0.035
Gentianales	More		0.032
<i>Guatteria</i>		Less	0.045
<i>Leandra</i>		Less	0.003
<i>Lonchocarpus</i>		More	0.008
Malpighiales	More		0.025
Malvales	More		0.033
Melastomataceae		Less	< 0.001
Melastomataceae	More		< 0.001
<i>Miconia</i>		Less	< 0.001
<i>Miconia</i>	More		0.008
<i>Myrceugenia</i>		More	0.017
<i>Myrceugenia</i>	Less		< 0.001
<i>Myrciaria</i>		More	0.024
Myrtaceae		More	0.003
Myrtaceae	Less		< 0.001
Myrtales	Less		0.047
N104 ¹		More	0.016
N104 ¹	Less		< 0.001
N147 ²	Less		0.021
N166 ³	More		0.013
N206 ⁴		More	0.009
Ochnaceae		Less	0.045
<i>Ruprechtia</i>	Less		0.047
Salicaceae		More	0.024
<i>Schinus</i>		More	0.041
<i>Schinus</i>	Less		0.009
Vochysiaceae		Less	0.018

¹ N104 (Myrtaceae + Vochysiaceae)

² N147 (Burseraceae + Anacardiaceae)

³ N166 (Elaeocarpaceae + Cunoniaceae + Connaraceae + Ochnaceae + Humiriaceae + Picrodendraceae + Phyllantaceae + Erythroxylaceae + Putranjivaceae + Chrysobalanaceae + Cariocaraceae + Clusiaceae + Hypericaceae + Calophyllaceae + Malpighiaceae + Lacistemataceae + Salicaceae + Euphorbiaceae)

⁴ N206 (Rosaceae + Rhamnaceae + Cannabaceae + Moraceae + Urticaceae + Fabaceae + Quillajaceae)

Table A8. Observed and mean of randomly generated statistics by solving polytomies and cross-validation for Welch one-tailed tests and correlation results in both climate types. In general, solving polytomies or cross-validation did not change the conclusions of the tests based on the original data set. Solving polytomies resulted in even higher mean differences and *P*-values in PSC between tropical and subtropical sites and a higher correlation of PSC with species richness. Changes in PSC statistics are expected because the index is more likely to be influenced by polytomies located on the tips of the phylogeny. Cross-validation resulted in no significant deviations of the observed statistics from those obtained from randomly reduced data sets. *P**: probability for H_0 : observed statistics is within confidence intervals.

	Tropical	Subtropical	t	<i>P</i>	r_{SR}	<i>P</i>
All taxa:						
<i>Polytomy-solved PSV tests</i>						
Observed statistics	0.494	0.499	0.660	0.744	0.338	0.009
Random mean	0.494	0.498	0.670	0.747	0.336	0.010
<i>P</i> *	0.023	0.018	0.409	0.410	0.272	0.272
<i>Polytomy-solved PSC tests</i>						
Observed statistics	0.898	0.876	-2.691	0.006	0.589	< 0.001
Random mean	0.905	0.881	-2.789	0.004	0.621	< 0.001
<i>P</i> *	0.001	0.001	0.210	0.178	0.001	0.001
<i>Cross-validated species richness results</i>						
Observed statistics	126.000	78.000	-2.663	0.005		
Random mean	126.000	78.000	-2.507	0.010		
<i>P</i> *	0.989	1.000	0.592	0.418		
<i>Cross-validated PSV tests</i>						
Observed statistics	0.494	0.499	0.660	0.744	0.338	0.009
Random mean	0.494	0.499	0.610	0.717	0.336	0.024
<i>P</i> *	0.982	0.996	0.885	0.815	0.963	0.429
<i>Cross-validated PSC tests</i>						
Observed statistics	0.898	0.876	-2.691	0.006	0.589	< 0.001
Random mean	0.898	0.876	-2.534	0.010	0.593	< 0.001
<i>P</i> *	0.990	0.965	0.540	0.427	0.764	0.143
Angiosperms:						
<i>Polytomy-solved PSV tests</i>						
Observed statistics	0.494	0.499	0.660	0.744	0.338	0.009
Random mean	0.172	0.224	0.420	0.421	0.260	0.250
<i>P</i> *						
<i>Polytomy-solved PSC tests</i>						
Observed statistics	0.898	0.876	-2.691	0.006	0.589	< 0.001
Random mean	0.905	0.881	-2.789	0.004	0.621	< 0.001
<i>P</i> *	0.002	0.002	0.212	0.180	0.001	0.001
<i>Cross-validated species richness results</i>						
Observed statistics	125.000	77.000	-2.725	0.004		
Random mean	125.000	77.000	-2.567	0.009		
<i>P</i> *	0.999	0.978	0.572	0.416		
<i>Cross-validated PSV tests</i>						
Observed statistics	0.646	0.648	0.324	0.626	0.258	0.051

	Tropical	Subtropical	t	P	r _{SR}	P
Random mean	0.646	0.648	0.289	0.606	0.259	0.082
P*	1.000	0.955	0.924	0.881	0.981	0.522
<i>Cross-validated PSC tests</i>						
Observed statistics	0.867	0.841	-2.334	0.013	0.608	< 0.001
Random mean	0.867	0.841	-2.189	0.021	0.611	< 0.001
P*	0.995	0.986	0.581	0.476	0.798	0.158

Table A9. Estimates, standardized error, Z-values, parametric pathway probabilities, standardized path coefficients and bootstrap based probabilities for the structural equation models relating climatic, spatial and phylogenetic structure predictors of tree species richness variation. Temperature, mean temperature of coldest quarter (BIO11); Precipitation, precipitation seasonality (BIO15); Long² × Lat, squared longitude multiplied by latitude; PCNM2, second axis of a principal components analysis on the spatial distance matrix; PSV, phylogenetic species variability; PSC, phylogenetic species clustering; and Prec × Temp², Precipitation (BIO15) multiplied by squared Temperature (BIO11). When evaluating angiosperms only (models c and d), the models received more support from data and corroborated the predictions of the TCH.

Model a

	Estimates	Std. Errors	Z-values	P-values	Path coefficients	Bootstrap P-values
Regressions:						
<i>Effects on species richness</i>						
Temperature	-0.266	0.174	-1.529	0.126	-0.092	0.104
PSV	2.136	1.361	1.57	0.116	0.086	0.144
PSC	13.317	1.322	10.076	< 0.001	0.666	< 0.001
Precipitation	-0.013	0.062	-0.217	0.828	-0.015	0.851
PCNM2	1.057	0.364	2.903	0.004	0.217	0.016
Long ² × Lat	0.076	0.026	2.946	0.003	0.234	0.001
<i>Effects on PSV</i>						
Temperature	-0.045	0.016	-2.904	0.004	-0.388	0.018
PCNM2	-0.008	0.035	-0.228	0.819	-0.041	0.857
Long ² × Lat	0.005	0.002	2.455	0.014	0.367	0.038
Precipitation	0.006	0.006	1.004	0.316	0.167	0.415
<i>Effects on PSC</i>						
Temperature	0.012	0.016	0.733	0.463	0.081	0.467
PCNM2	-0.021	0.036	-0.594	0.553	-0.088	0.531
Long ² × Lat	0.011	0.002	5.468	< 0.001	0.679	< 0.001
Precipitation	0	0.006	0.056	0.956	0.008	0.949
Variances:						
Species richness	0.056	0.01	5.385	< 0.001	0.136	< 0.001
PSV	0.001	0	5.385	< 0.001	0.778	< 0.001
PSC	0.001	0	5.385	< 0.001	0.536	< 0.001

Model b

	Estimates	Std. Errors	Z-values	P-values	Path coefficients	Bootstrap P-values
Regressions:						
<i>Effects on species richness</i>						
Prec × Temp ²	-0.002	0.006	-0.394	0.694	-0.026	0.699

PSC	15.571	1.105	14.096	< 0.001	0.779	< 0.001
PSV	3.753	1.335	2.811	0.005	0.151	0.006
PCNM2	1.445	0.32	4.511	< 0.001	0.296	< 0.001
<i>Effects on PSV</i>						
Prec x Temp ²	0	0.001	-0.032	0.975	-0.005	0.98
PCNM2	0.056	0.031	1.823	0.068	0.284	0.062
<i>Effects on PSC</i>						
Prec x Temp ²	0.001	0.001	2.148	0.032	0.326	0.01
PCNM2	0.011	0.037	0.309	0.757	0.047	0.737
Variances:						
Species richness	0.064	0.012	5.385	< 0.001	0.155	< 0.001
PSV	0.001	0	5.385	< 0.001	0.921	< 0.001
PSC	0.001	0	5.385	< 0.001	0.874	< 0.001

Model c

	Estimates	Std. Errors	Z-values	P-values	Path coefficients	Bootstrap P-values
Regressions:						
<i>Effects on species richness</i>						
Temperature	-0.135	0.164	-0.824	0.41	-0.047	0.457
PSV	0.645	1.18	0.547	0.585	0.028	0.606
PSC	10.397	1.034	10.053	< 0.001	0.688	< 0.001
Precipitation	-0.039	0.061	-0.646	0.518	-0.045	0.561
PCNM2	1.349	0.365	3.697	< 0.001	0.28	0.001
Long ² x Lat	0.061	0.026	2.339	0.019	0.192	0.036
<i>Effects on PSV</i>						
Temperature	-0.028	0.018	-1.595	0.111	-0.227	0.228
PCNM2	0.02	0.04	0.508	0.611	0.096	0.663
Long ² x Lat	0.003	0.002	1.241	0.214	0.198	0.32
Precipitation	0.003	0.007	0.452	0.651	0.08	0.714
<i>Effects on PSC</i>						
Temperature	-0.002	0.02	-0.109	0.913	-0.012	0.915
PCNM2	-0.055	0.046	-1.215	0.224	-0.174	0.201
Long ² x Lat	0.016	0.003	6.286	< 0.001	0.755	< 0.001
Precipitation	0.004	0.008	0.458	0.647	0.061	0.682
Variances:						
Species richness	0.055	0.01	5.385	< 0.001	0.136	< 0.001
PSV	0.001	0	5.385	< 0.001	0.885	< 0.001
PSC	0.001	0	5.385	< 0.001	0.502	< 0.001

Model d

	Estimates	Std. Errors	Z-values	P-values	Path coefficients	Bootstrap P-values
Regressions:						
<i>Effects on species richness</i>						
Prec x Temp ²	-0.002	0.006	-0.441	0.659	-0.029	0.692
PSC	11.984	0.819	14.631	< 0.001	0.793	< 0.001
PSV	1.217	1.204	1.011	0.312	0.053	0.304

PCNM2	1.592	0.31	5.128	< 0.001	0.33	< 0.001
<i>Effects on PSV</i>						
Prec x Temp ²	0	0.001	-0.145	0.885	-0.023	0.888
PCNM2	0.059	0.033	1.776	0.076	0.278	0.057
<i>Effects on PSC</i>						
Prec x Temp ²	0.002	0.001	2.152	0.031	0.327	0.05
PCNM2	0.013	0.048	0.27	0.787	0.041	0.76
Variances:						
Species richness	0.06	0.011	5.385	< 0.001	0.149	< 0.001
PSV	0.001	0	5.385	< 0.001	0.93	< 0.001
PSC	0.002	0	5.385	< 0.001	0.876	< 0.001

Table A10. Observed and mean randomly generated estimates after solving polytomies in the phylogenetic tree for the four tested structural equation models. We repeated the solving polytomies procedure 1000 times for each model. For each statistics we provide the probability for null hypothesis that the observed value is within randomly generated ones. In general, the results were robust even when polytomies had been randomly solved with little changes in path strengths, which were mainly related to stronger connections of predictors with PSC and increased explanation power for species richness. In summary, the reported results of structural equation models are unlikely to be changed because of polytomies.

Model a						
	<i>Effects on species richness</i>					
	Temperature	PSV	PSC	Precipitation	PCNM2	Long ² × Lat
Observed statistics	-0.266	2.136	13.317	-0.013	1.057	0.076
Mean of random statistics	-0.268	2.009	13.261	-0.016	1.011	0.069
H ₀ : observed statistics is within random values	0.923	0.398	0.811	0.695	0.234	0.154
	<i>Effects on PSV</i>					
	Temperature	PCNM2	Long ² × Lat	Precipitation		
Observed statistics	-0.045	-0.008	0.005	0.006		
Mean of random statistics	-0.045	-0.007	0.005	0.006		
H ₀ : observed statistics is within random values	0.608	0.013	0.443	0.630		
	<i>Effects on PSC</i>					
	Temperature	PCNM2	Long ² × Lat	Precipitation		
Observed statistics	0.012	-0.021	0.011	0.000		
Mean of random statistics	0.012	-0.018	0.012	0.001		
H ₀ : observed statistics is within random values	0.842	0.276	0.020	0.626		
	Variances:			Model fit		
	Species richness	PSV	PSC	χ ²	P	
Observed statistics	0.056	0.001	0.001	3.473	0.062	
Mean of random statistics	0.051	0.001	0.001	3.125	0.078	
H ₀ : observed statistics is within random values	0.004	0.676	0.111	0.210	0.230	
Model b						
	<i>Effects on species richness</i>					

	Prec × Temp ²	PSC	PSV	PCNM2		
Observed statistics	−0.002	15.571	3.753	1.445		
Mean of random statistics	−0.003	15.246	3.491	1.371		
H ₀ : observed statistics is within random values	0.447	0.127	0.123	0.075		
	<i>Effects on PSV</i>					
	Prec × Temp ²	PCNM2				
Observed statistics	0.000	0.056				
Mean of random statistics	0.000	0.056				
H ₀ : observed statistics is within random values	0.607	0.113				
	<i>Effects on PSC</i>					
	Prec × Temp ²	PCNM2				
Observed statistics	0.001	0.011				
Mean of random statistics	0.002	0.017				
H ₀ : observed statistics is within random values	0.224	0.029				
	Variances:			Model fit		
	Species richness	PSV	PSC	χ ²	P	
Observed statistics	0.064	0.001	0.001	0.391	0.532	
Mean of random statistics	0.058	0.001	0.001	0.284	0.598	
H ₀ : observed statistics is within random values	0.005	0.977	0.021	0.147	0.177	

Model c

	<i>Effects on species richness</i>					
	Temperature	PSV	PSC	Precipitation	PCNM2	Long ² × Lat
Observed statistics	−0.135	0.645	10.397	−0.039	1.349	0.061
Mean of random statistics	0.013	151.847	11.645	−0.054	1.547	−150.467
H ₀ : observed statistics is within random values	0.016	0.374	0.015	0.531	0.026	0.376

<i>Effects on PSV</i>					
	Temperature	PCNM2	Long ² × Lat	Precipitation	
Observed statistics	-0.028	0.020	0.003	0.003	
Mean of random statistics	0.000	0.000	0.997	0.000	
H ₀ : observed statistics is within random values	0.001	0.001	0.001	0.001	
<i>Effects on PSC</i>					
	Temperature	PCNM2	Long ² × Lat	Precipitation	
Observed statistics	-0.002	-0.055	0.016	0.004	
Mean of random statistics	0.056	0.064	-0.016	0.008	
H ₀ : observed statistics is within random values	0.001	0.001	0.024	0.001	
Variances:					
	Species richness	PSV	PSC	Model fit	
				χ ²	P
Observed statistics	0.055	0.001	0.001	1.487	0.223
Mean of random statistics	0.051	0.000	0.002	4.698	0.223
H ₀ : observed statistics is within random values	0.233	0.001	0.001	0.533	0.999

Model d

<i>Effects on species richness</i>					
	Prec × Temp ²	PSC	PSV	PCNM2	
Observed statistics	-0.002	11.984	1.217	1.592	
Mean of random statistics	-0.003	11.767	1.077	1.512	
H ₀ : observed statistics is within random values	0.542	0.194	0.361	0.062	
<i>Effects on PSV</i>					
	Prec × Temp ²	PCNM2			
Observed statistics	0.000	0.059			
Mean of random statistics	0.000	0.059			

H ₀ : observed statistics is within random values	0.058	0.299			
	<i>Effects on PSC</i>				
	Prec x Temp ²	PCNM2			
Observed statistics	0.002	0.013			
Mean of random statistics	0.002	0.021			
H ₀ : observed statistics is within random values	0.326	0.041			
	Variances:			Model fit	
	Species richness	PSV	PSC	χ ²	P
Observed statistics	0.060	0.001	0.002	0.152	0.697
Mean of random statistics	0.053	0.001	0.002	0.110	0.746
H ₀ : observed statistics is within random values	0.001	0.713	0.020	0.316	0.315

Table A11. Observed and mean generated estimates by dropping 10% of the sampling units at random (cross-validation) for the four structural equation models tested. We repeated cross-validation procedure 1000 times for each model. For each statistics we provide the probability for null hypothesis that the observed value is within randomly generated ones. All results were robust to different subsets of sampling units.

Model a						
<i>Effects on species richness</i>						
	Temperature	PSV	PSC	Precipitation	PCNM2	Long ² x Lat
Observed statistics	-0.266	2.136	13.317	-0.013	1.057	0.076
Mean of random statistics	-0.264	2.147	13.354	-0.015	1.054	0.077
H ₀ : observed statistics is within random values	0.982	0.987	0.945	0.950	0.987	0.885
<i>Effects on PSV</i>						
	Temperature	PCNM2	Long ² x Lat	Precipitation		
Observed statistics	-0.045	-0.008	0.005	0.006		
Mean of random statistics	-0.045	-0.008	0.005	0.006		
H ₀ : observed statistics is within random values	0.992	0.986	0.998	1.000		

	<i>Effects on PSC</i>					
	Temperature	PCNM2	Long ² × Lat	Precipitation		
Observed statistics	0.012	-0.021	0.011	0.000		
Mean of random statistics	0.012	-0.020	0.011	0.000		
H ₀ : observed statistics is within random values	0.997	0.918	0.798	0.972		
	<i>Variances:</i>				<i>Model fit</i>	
	Species richness	PSV	PSC		χ ²	P
Observed statistics	0.056	0.001	0.001		3.473	0.062
Mean of random statistics	0.054	0.001	0.001		3.351	0.149
H ₀ : observed statistics is within random values	0.837	0.914	0.921		0.897	0.566

Model b

	<i>Effects on species richness</i>			
	Prec × Temp ²	PSC	PSV	PCNM2
Observed statistics	-0.002	15.571	3.753	1.445
Mean of random statistics	-0.002	15.635	3.717	1.444
H ₀ : observed statistics is within random values	0.978	0.876	0.926	0.993
	<i>Effects on PSV</i>			
	Prec × Temp ²	PCNM2		
Observed statistics	0.000	0.056		
Mean of random statistics	0.000	0.055		
H ₀ : observed statistics is within random values	0.927	0.930		
	<i>Effects on PSC</i>			
	Prec × Temp ²	PCNM2		
Observed statistics	0.001	0.011		
Mean of random statistics	0.001	0.011		
H ₀ : observed statistics is within random values	0.971	0.997		

	Variances:			Model fit	
	Species richness	PSV	PSC	χ^2	P
Observed statistics	0.064	0.001	0.001	0.391	0.532
Mean of random statistics	0.063	0.001	0.001	0.530	0.529
H ₀ : observed statistics is within random values	0.881	0.972	0.973	0.759	0.987

Model c

Effects on species richness

	Temperature	PSV	PSC	Precipitation	PCNM2	Long ² × Lat
Observed statistics	-0.135	0.645	10.397	-0.039	1.349	0.061
Mean of random statistics	-0.131	0.663	10.530	-0.039	1.337	0.060
H ₀ : observed statistics is within random values	0.937	0.974	0.789	0.990	0.933	0.950

Effects on PSV

	Temperature	PCNM2	Long ² × Lat	Precipitation
Observed statistics	-0.028	0.020	0.003	0.003
Mean of random statistics	-0.028	0.020	0.003	0.003
H ₀ : observed statistics is within random values	0.942	0.998	0.886	0.959

Effects on PSC

	Temperature	PCNM2	Long ² × Lat	Precipitation
Observed statistics	-0.002	-0.055	0.016	0.004
Mean of random statistics	-0.002	-0.054	0.016	0.003
H ₀ : observed statistics is within random values	0.995	0.922	0.837	0.952

Variances:

	Variances:			Model fit	
	Species richness	PSV	PSC	χ^2	P
Observed statistics	0.055	0.001	0.001	1.487	0.223

Mean of random statistics	0.054	0.001	0.001	1.922	0.195
H ₀ : observed statistics is within random values	0.847	0.895	0.897	0.565	0.743

Model d

Effects on species richness

	Prec × Temp ²	PSC	PSV	PCNM2
Observed statistics	-0.002	11.984	1.217	1.592
Mean of random statistics	-0.002	12.037	1.187	1.577
H ₀ : observed statistics is within random values	0.963	0.913	0.935	0.907

Effects on PSV

	Prec × Temp ²	PCNM2
Observed statistics	0.000	0.059
Mean of random statistics	0.000	0.058
H ₀ : observed statistics is within random values	0.999	0.962

Effects on PSC

	Prec × Temp ²	PCNM2
Observed statistics	0.002	0.013
Mean of random statistics	0.002	0.012
H ₀ : observed statistics is within random values	0.995	0.942

Variances:

	Species richness	PSV	PSC	Model fit	P
				χ ²	
Observed statistics	0.060	0.001	0.002	0.152	0.697
Mean of random statistics	0.059	0.001	0.002	0.408	0.584
H ₀ : observed statistics is within random values	0.851	0.928	0.983	0.494	0.573

Appendix 2

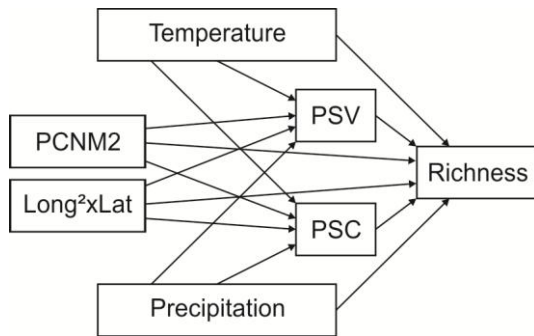


Figure A12. Hypothetical relationships among climatic, spatial and phylogenetic structure predictors of tree species richness. Phylogenetic niche conservatism is expected when ‘environmental’ predictors shape phylogenetic structure, which is then associated with richness patterns. $\text{Long}^2 \times \text{Lat}$, squared longitude multiplied by latitude; PCNM2, second axis of a principal components analysis on the spatial distance matrix; PSV, phylogenetic species variability; and PSC, phylogenetic species clustering.

Niche conservatism and structural equation modeling

Wiens et al. (2010) proposed a formal distinction between niche conservatism and phylogenetic niche conservatism. Niche conservatism is the retention of niche-related ecological traits over time. Phylogenetic niche conservatism is nested within the broader concept of niche conservatism, being the retention of niche-related ecological traits over time by related taxa. In short, tests for phylogenetic niche conservatism normally involve the evaluation of phylogenetic signal in ecological traits. Nevertheless, phylogenetic signals per se seem to provide insufficient information for the occurrence of niche conservatism (Losos 2008, Wiens et al.

2010). In order to effectively estimate niche conservatism, which is necessary to test the tropical niche conservatism hypothesis (TCH; Wiens and Donoghue 2004), a more complex approach is needed. It requires the evaluation of two potential explanations for ecological parameters, such as species richness (Algar et al. 2009, Pillar et al. 2010). First, when niche conservatism occurs, environmental conditions should impose constraints on phylogenetic structure, which mediates the output on the ecological parameters (Environment \rightarrow Phylogenetic structure \rightarrow Ecological structure). Conversely, when such a relationship is unlikely to occur and environment and phylogenetic structure influence the ecological structure independently, the occurrence of niche conservatism can be rejected (Environment \rightarrow Ecological structure \leftarrow Phylogenetic structure). The main way to evaluate the likelihood of such relationships is by means of pathway analyses, of which the most prominent is structural equation modeling (Shipley 2002). Furthermore, it allows the evaluation of these two concurrent hypotheses at the same time, within a single analysis.

More specifically, to test the TCH we evaluated a model that contained direct effects of precipitation seasonality on species richness and indirect effects, which linked precipitation seasonality with phylogenetic clustering and then species richness. Following this structure, we included

temperature-related and spatial predictors in the model, as long as the latter may stand for missing environmental variables. We log-transformed temperature, precipitation and species richness because of large variances (Table S9). Afterwards, we estimated the model parameters employing the maximum likelihood algorithm and based on the variance-covariance matrix obtained from the raw data. To generate estimates for model fit and pathway coefficients, we employed parametric and bootstrap statistics. Model fit can be evaluated by a chi-square statistics, but it requires multivariate normality. Because our data sets failed the Mardia's test for multivariate normality, we assessed model fit also by bootstrapping. This is done by creating a new data matrix with a similar variance-covariance to that of raw data. This new matrix is then sampled with reposition several times, after which the original model parameters are compared with randomly generated ones (p. 188, Shipley 2002).

When fitting our initial hypothetical model, we found a significant correlation of a spatial predictor, $\text{Long}^2 \times \text{Lat}$, with species richness, which was mediated via phylogenetic structure. We interpreted this significant relationship as an evidence for an interaction between climatic predictors (precipitation seasonality and squared mean temperature of coldest quarter; $\text{Prec} \times \text{Temp}^2$). There was a significant correlation between $\text{Long}^2 \times \text{Lat}$ and $\text{Prec} \times \text{Temp}^2$ ($r = 0,556$; $P < 0,001$); thus, we tested a new model without Temperature and Precipitation, but with Prec

$\times \text{Temp}^2$ replacing $\text{Long}^2 \times \text{Lat}$. This new model supports TCH because $\text{Prec} \times \text{Temp}^2$ is indirectly related to species richness, without residual direct correlation (Environment \rightarrow Phylogenetic structure \rightarrow Ecological structure).

References for Appendix 2

- Algar, A. C. et al. 2009. Evolutionary constraints on regional faunas: whom, but not how many. — *Ecology Letters* 12: 57–65.
- Losos, J. B. 2008. Phylogenetic niche conservatism, phylogenetic signal, and the relationship between phylogenetic relatedness and ecological similarity among species. — *Ecology Letters* 11: 995–1007.
- Pillar, V. D. and Duarte, L. d. S. 2010. A framework for metacommunity analysis of phylogenetic structure. — *Ecology Letters* 13: 587–596.
- Shipley, B. 2002. Cause and correlation in biology: a user's guide to path analysis, structural equations and causal inference. — Cambridge University Press.
- Wiens, J. J. and Donoghue, M. J. 2004. Historical biogeography, ecology and species richness. — *Trends in Ecology & Evolution* 19: 639–644.
- Wiens, J. J. et al. 2010. Niche conservatism as an emerging principle in ecology and conservation biology. — *Ecology Letters* 13: 1310–132.

Table A13. Variance-covariance matrices used to perform structural equation modeling. To represent the major climatic constraints on tree species richness, we used the mean temperature of coldest quarter (Temperature) and precipitation seasonality (Precipitation). Long² × Lat and PCNM2 are spatial descriptors, which aimed to control for the effects of spatial dependence between sites and unmeasured environmental variables. PSV and PSC are the phylogenetic species variability and phylogenetic species clustering, respectively (Helmus et al. 2007). Temperature, Precipitation and species richness were log-transformed. In models b and d, we replaced Long² × Lat by an interaction between Precipitation and squared Temperature (Prec × Temp²). Models a and b are for all taxa and models c and d for angiosperms only.

Model a							
	Temperature	Precipitation	PCNM2	Long ² × Lat	PSV	PSC	Species richness
Temperature	0.049803	0.021013	-0.002269	0.165306	-0.001326	0.002454	0.026417
Precipitation	0.021013	0.532543	0.066702	0.653086	0.004798	0.006155	0.199347
PCNM2	-0.002269	0.066702	0.017540	0.127651	0.000969	0.001019	0.043535
Long ² × Lat	0.165306	0.653086	0.127651	4.015420	0.014544	0.043428	0.995130
PSV	-0.001326	0.004798	0.000969	0.014544	0.000679	-0.000007	0.003774
PSC	0.002454	0.006155	0.001019	0.043428	-0.000007	0.001045	0.017526
Species richness	0.026417	0.199347	0.043535	0.995130	0.003774	0.017526	0.409729

Model b					
	Prec × Temp ²	PCNM2	PSV	PSC	Species richness
Prec × Temp ²	5.287258	0.195506	0.012254	0.024007	0.665289
PCNM2	0.195506	0.017540	0.000969	0.001019	0.043535

PSV	0.012254	0.000969	0.000679	-0.000007	0.003774
PSC	0.024007	0.001019	-0.000007	0.001045	0.017526
Species richness	0.665289	0.043535	0.003774	0.017526	0.409729

Model c

	Temperature	Precipitation	PCNM2	Long ² × Lat	PSC	PSV	Species richness
Temperature	0.049793	0.020986	-0.002275	0.165206	0.002722	-0.000943	0.027167
Precipitation	0.020986	0.532644	0.066716	0.653297	0.008547	0.004190	0.197604
PCNM2	-0.002275	0.066716	0.017540	0.127659	0.001303	0.000977	0.043299
Long ² × Lat	0.165206	0.653297	0.127659	4.015835	0.058857	0.010971	0.988258
PSC	0.002722	0.008547	0.001303	0.058857	0.001787	0.000012	0.023229
PSV	-0.000943	0.004190	0.000977	0.010971	0.000012	0.000779	0.002582
Species richness	0.027167	0.197604	0.043299	0.988258	0.023229	0.002582	0.406086

Model d

	Prec × Temp ²	PCNM2	PSV	PSC	Species richness
Prec × Temp ²	54.084368	0.571653	0.028809	0.109005	2.116573
PCNM2	0.571653	0.017540	0.000977	0.001303	0.043299

PSV	0.028809	0.000977	0.000779	0.000012	0.002582
PSC	0.109005	0.001303	0.000012	0.001787	0.023229
Species richness	2.116573	0.043299	0.002582	0.023229	0.406086

Appendix 3

Code A14. Function to randomly solve polytomies in phylogenetic trees. We used the function to generate confidence intervals for test statistics derived from trees with polytomies. It requests the use of the ‘picante’ package in R, and a ‘phylo’ class object.

```
adj.poly = function(phy) {  
  require(picante) # Requested package dependence to run "adj.poly()"  
  if(class(phy)!="phylo"){ print("You must provide an object of class 'phylo'."); } else {  
    if(!is.binary.tree(phy)){  
      # This step evaluates if the tree is dichotomic/binary.  
      phy = multi2di(phy)  
      # If it is not, random "dichotomization" is performed.  
      # Nevertheless, multi2dist does not generate branch lengths.  
      # Thus, next steps perform random assignment of branch  
      # lengths.  
      phy = reorder(phy, "pruningwise")  
      # This reorders the nodes to facilitate further calculations.  
    }  
    while(min(phy$edge.length) <= 0) {  
      # This loop only finishes when all nodes have  
      # branch lengths > 0.  
      handle = data.frame(phy$edge,phy$edge.length)  
      colnames(handle) = c("ancestor","daughter","age")  
      # Next steps generate random branch lengths.  
      handle = handle[order(handle$daughter, handle$ancestor),]  
      for (i in which(handle$age == 0)) {  
        nodes = which(handle$ancestor == handle$daughter[i])  
        val = runif(n=1,min=0,max=min(handle$age[nodes]))  
        handle$age[i]=val  
        handle$age[nodes] = handle$age[nodes]-val  
      }  
      handle = handle[order(as.numeric(rownames(handle))),]  
      phy$edge.length = handle[,3]  
    }  
    phy = reorder(phy, "cladewise")  
    return(phy)  
  }  
}
```

```
# Usage (picante package, a community object, here called comm, and a phylo object, here called phy, are required):
```

```
library(picante)
```

```
data(phylocom)
```

```
comm <- phylocom$sample
```

```
phy <- phylocom$phylo
```

```
pscs <- matrix(nrow=dim(comm)[1], ncol=10)
```

```
phy <- prune.sample(comm, phy)
```

```
for (i in 1:10){
```

```
  new.phy <- adj.poly(phy)
```

```
  comm <- comm[,order(new.phy$tip.label)]
```

```
  pscs[,i] <- t(psc(comm, new.phy)$PSCs)
```

```
}
```

```
# In this case, the output, pscs, is a matrix with 100  
# PSC values for each of m communities (row-wise) in the  
# comm object.  
# Note that in this example all outputted PSC-values are equal  
# within communities. This is because there are no polytomies  
# in the phylocom dataset. Compare the results with the example  
# below.
```

```
library(picante)
```

```
data(phylocom)
```

```
comm <- phylocom$sample
```

```
phy <-
```

```
read.tree(text="((sp1:3,sp2:3,(sp3:1,sp4:1)F:2,((sp5:1,sp6:1)H:1,(sp7:1,sp8:1)I:1)G:1)C  
:1,(((sp9:1,sp10:1)L:1,(sp11:1,sp12:1)M:1)K:1,((sp13:1,sp14:1)O:1,sp15:2)N:1)J:1)B:1,(((  
(sp17:1,sp18:1)T:1,(sp19:1,sp20:1)U:1)S:1,((sp21:1,sp22:1)W:1,sp24:2)V:1)R:1,((sp25:1,sp  
26:1)AA:2,sp29:3)Y:1)Q:1)A;")
```

```
pscs <- matrix(nrow=dim(comm)[1], ncol=10)
```

```
phy <- prune.sample(comm, phy)
```

```
for (i in 1:10){
```

```
  new.phy <- adj.poly(phy)
```

```
  comm <- comm[,order(new.phy$tip.label)]
```

```
  pscs[,i] <- t(psc(comm, new.phy)$PSCs)
```

```
}
```

```
# Try it with another dataset and  
# send me feedback for bugs or even a successful  
# attempt. A citation to this article will be appreciated  
# wherever possible if you have employed the adj.poly() function  
# with your own data in publications.
```