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## ADDITIONAL TABLES AND FIGURES

**Table A1**

Detailed results of the two-way ANOVA and Tukey's post-hoc tests. Adjusted  $R^2$  values of stochastic species-environment relationships were compared among hypotheses and continents. Only adjusted  $R^2$ s of the primary variable in each simulation run were used. Primary adjusted  $R^2$  values were logit-transformed before analysis. Significant p-values are presented in bold letters. Not applicable values (NA) are generated because energy and heterogeneity were never the best predictors of simulated richness in Eurasia (Fig. 5).

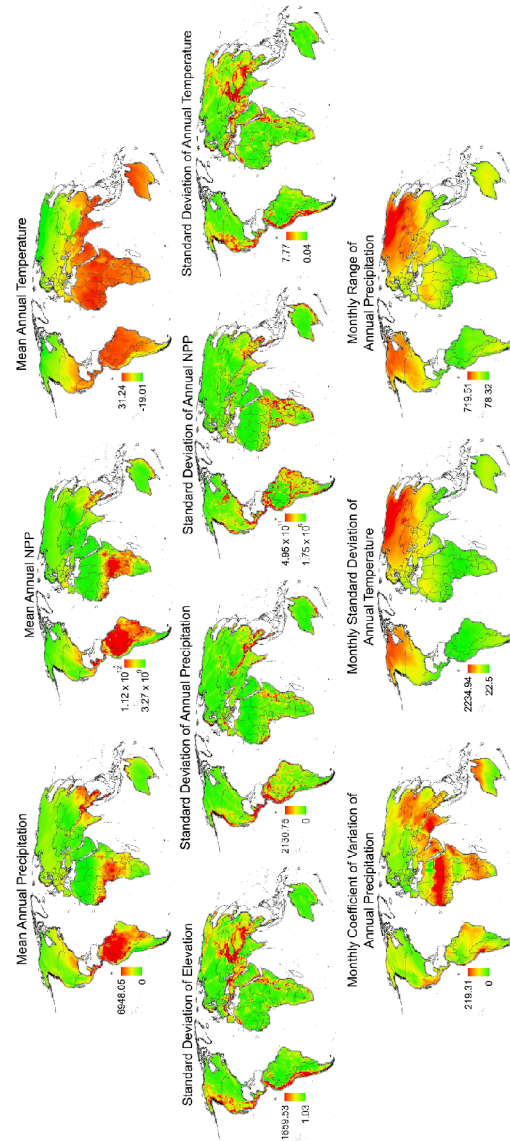
Two-way AVOVA test		Tukey's post hoc test			
F	p	Contrast		Difference	p
Hypothesis					
187.249	<0.001	Heterogeneity	Energy	-0.780	0.009
		Seasonality	Energy	0.559	<0.001
		Seasonality	Heterogeneity	1.339	<0.001
Continent					
458.849	<0.001	Australia	Africa	0.954	<0.001
		Eurasia	Africa	-0.016	0.973
		New World	Africa	-0.188	<0.001
		Eurasia	Australia	-0.970	<0.001
		New World	Australia	-1.142	<0.001
		New World	Eurasia	-0.172	<0.001
Hypothesis*Continent					
7.471	<0.001	Energy: Africa	Energy: Australia	0.492	0.271
		Energy: Africa	Energy: Eurasia	NA	NA
		Energy: Africa	Energy: New World	0.181	0.128
		Energy: Africa	Heterogeneity: Africa	-1.050	0.475
		Energy: Africa	Heterogeneity: Australia	0.109	1.000
		Energy: Africa	Heterogeneity: Eurasia	NA	NA
		Energy: Africa	Heterogeneity: New World	-1.252	0.205
		Energy: Africa	Seasonality: Africa	-0.191	0.173
		Energy: Africa	Seasonality: Australia	1.381	<0.001
		Energy: Africa	Seasonality: Eurasia	0.405	<0.001
		Energy: Africa	Seasonality: New World	0.077	0.790
		Energy: Australia	Energy: Eurasia	NA	NA
		Energy: Australia	Energy: New World	-0.311	0.907
		Energy: Australia	Heterogeneity: Australia	-0.383	1.000
		Energy: Australia	Heterogeneity: Eurasia	NA	NA
		Energy: Australia	Heterogeneity: New World	-1.745	0.020

Energy: Australia	Seasonality: Australia	0.889	<b>&lt;0.001</b>
Energy: Australia	Seasonality: Eurasia	-0.088	1.000
Energy: Australia	Seasonality: New World	-0.415	0.547
Energy: Eurasia	Energy: New World	NA	NA
Energy: Eurasia	Heterogeneity: Eurasia	NA	NA
Energy: Eurasia	Heterogeneity: New World	NA	NA
Energy: Eurasia	Seasonality: Eurasia	NA	NA
Energy: Eurasia	Seasonality: New World	NA	NA
Energy: New World	Heterogeneity: New World	-1.434	0.08
Energy: New World	Seasonality: New World	-0.104	0.881
Heterogeneity: Africa	Energy: Australia	1.542	0.075
Heterogeneity: Africa	Energy: Eurasia	NA	NA
Heterogeneity: Africa	Energy: New World	1.231	0.234
Heterogeneity: Africa	Heterogeneity: Australia	1.158	0.818
Heterogeneity: Africa	Heterogeneity: Eurasia	NA	NA
Heterogeneity: Africa	Heterogeneity: New World	-0.203	1.000
Heterogeneity: Africa	Seasonality: Africa	0.858	0.778
Heterogeneity: Africa	Seasonality: Australia	2.430	<b>&lt;0.001</b>
Heterogeneity: Africa	Seasonality: Eurasia	1.454	0.064
Heterogeneity: Africa	Seasonality: New World	1.127	0.359
Heterogeneity: Australia	Energy: Eurasia	NA	NA
Heterogeneity: Australia	Energy: New World	0.073	1.000
Heterogeneity: Australia	Heterogeneity: Eurasia	NA	NA
Heterogeneity: Australia	Heterogeneity: New World	-1.361	0.612
Heterogeneity: Australia	Seasonality: Australia	1.272	0.185
Heterogeneity: Australia	Seasonality: Eurasia	0.296	1.000
Heterogeneity: Australia	Seasonality: New World	-0.031	1.000
Heterogeneity: Eurasia	Energy: New World	NA	NA
Heterogeneity: Eurasia	Heterogeneity: New World	NA	NA
Heterogeneity: Eurasia	Seasonality: Eurasia	NA	NA
Heterogeneity: Eurasia	Seasonality: New World	NA	NA
Heterogeneity: New World	Seasonality: New World	1.330	0.136
Seasonality: Africa	Energy: Australia	0.684	<b>0.025</b>
Seasonality: Africa	Energy: Eurasia	NA	NA
Seasonality: Africa	Energy: New World	0.373	<b>&lt;0.001</b>
Seasonality: Africa	Heterogeneity: Australia	0.300	1.000
Seasonality: Africa	Heterogeneity: Eurasia	NA	NA
Seasonality: Africa	Heterogeneity: New World	-1.061	0.469
Seasonality: Africa	Seasonality: Australia	1.572	<b>&lt;0.001</b>

Seasonality: Africa	Seasonality: Eurasia	0.596	<b>&lt;0.001</b>
Seasonality: Africa	Seasonality: New World	0.269	<b>0.005</b>
Seasonality: Australia	Energy: Eurasia	NA	NA
Seasonality: Australia	Energy: New World	-1.200	<b>&lt;0.001</b>
Seasonality: Australia	Heterogeneity: Eurasia	NA	<b>NA</b>
Seasonality: Australia	Heterogeneity: New World	-2.633	<b>&lt;0.001</b>
Seasonality: Australia	Seasonality: Eurasia	-0.976	<b>&lt;0.001</b>
Seasonality: Australia	Seasonality: New World	-1.303	<b>&lt;0.001</b>
Seasonality: Eurasia	Energy: New World	-0.223	<b>0.012</b>
Seasonality: Eurasia	Heterogeneity: New World	-1.657	<b>0.015</b>
Seasonality: Eurasia	Seasonality: New World	-0.327	<b>&lt;0.001</b>

## Figure A1

Spatial distribution of environmental characteristics used to predict simulated species richness. Values are estimated in each 100 by 100 km cell of the four domains used: Africa, Australia, Eurasia and the New World. First row are energy variables: mean annual net primary productivity (g of Carbon/yr), mean annual precipitation (mm), and mean average annual temperature (°C). Second row are heterogeneity variables: elevation standard deviation (masl), annual NPP standard deviation (g of Carbon/yr), annual precipitation standard deviation (mm), average annual temperature standard deviation (°C). Third row are seasonality variables: mean coefficient of variation of monthly precipitation, mean monthly standard deviation of temperature (°C), and mean range of monthly temperature (°C). White and gray areas were not considered in analyses. Maps use a Mollweide projection.



## COMPLETE DESCRIPTION OF DRD SIMULATION MODEL

The DRD model takes place in time steps. In the first time step, one cell from throughout the domain is randomly selected to be the point of origin for the diversifying clade; all cells in the domain have the same probability of being chosen. The first species in the simulation colonizes this starting cell, and its target range is selected at random from a pool of range sizes; this pool of range sizes follows a log-normal distribution (see variations to simulation parameters). Starting with the second time step, a number of events take place in the following sequence.

1. *Range shift.* Each species currently present in the domain is evaluated for range shift. Whether a species moves its distribution or not is determined by the parameter MP, which is the probability of range movement. MP is identical for all species and it is constant through time. If a species is selected to move its distribution, then it chooses at random one of eight directions (north, north-east, east, south-east, south, south-west or west), and moves its entire distribution one cell in such direction. This process, repeated through time, causes species distributions to follow random walks within the domain, and the rate of movement is given by MP.

During these random shifts, a species can move part of its distribution outside of the domain. In such case, that part of the distribution is lost and will need to be regained by stochastic spread of its range elsewhere (see below). However, no species was allowed to go extinct by moving its entire distribution outside the domain.

2. *Range spread.* Each species present in the domain is evaluated as to whether it has reached its target range size. Those species that have range sizes smaller than their target range size are tagged for stochastic range spread. In the spreading dye algorithm of Jetz & Rabhek (2001), stochastic spread of species occurs as each cell at the edge of the distribution “sends dispersers” and colonizes one of the immediately adjacent cells. In our algorithm, however, we allow for each of the already occupied cells to “send dispersers” to adjacent cells or to cells that are farther away (similar to Colwell *et al.*, 2009). Coordinates for the cell to “receive dispersers” from an already occupied cell are determined by: 1) sampling a dispersal distance at random from a log-normal distribution with mean of 0 and standard deviation of 0.4 on a log-scale; dispersal distance was then rounded to the nearest higher integer, 2) giving the dispersal distance a direction by multiplying it by either 1, 0 or -1 selected at random, and 3) summing the coordinates of the cell of origin plus the dispersal distance. This process is carried out independently for the x and y coordinates. If the cell “receiving dispersers” is empty, then the species colonizes it. If the species is already present in that cell, the cell is outside of the domain, or the cell of destination is the same as the cell of origin, then no change in the distribution of the species occurs. This process is conducted for all occupied cells.

The standard deviation for the log-normal distribution was set to 0.4 because this value was found to produce rare dispersal events larger than one or two cells away from the cell of origin; this has the consequence of producing distributions with few or no internal empty cells (Colwell *et al.*, 2009). This was important because most current studies of diversity at broad scales have used range map overlaps to estimate diversity (McPherson & Jetz, 2007). These are typically maps of extent

of occurrence, which contain little or no unoccupied areas within the distribution of a species. At the same time, the value of 0.4 also speeds the spread of species distributions by producing rare long dispersal events.

3. *Speciation*. Each species in the domain is evaluated for speciation. Probability of a species giving rise to a new one is provided by the parameter SP, the speciation probability. Per-species probability of speciation is identical for all species and constant through time. Speciation in our simulations is modeled as a punctuated event. For each speciation event, a cell is selected at random from throughout the distribution of the parental species. These cells represent the points of origin for the distribution of the new species. This is equivalent to saying that a population or an individual has speciated and given rise to a new species. Then, new target range sizes are sampled at random and with replacement from the pool of range sizes; these range sizes are then assigned to each of the new species.
4. *Extinction*. All species currently present in the domain are evaluated for survival. Probability of a species going extinct is given by the parameter EP, the extinction probability. If a species is selected for extinction, then the distribution of such species disappears from the domain. EP is identical among all species, but it can either remain constant through time or change as a function of diversity. This produces two patterns of clade diversification: exponential and logistic (see variations to simulation parameters).

After these steps have taken place, the simulation moves to the next time step to start another cycle of range movements, range growths, speciations and extinctions. The simulation stops when the surviving number of species in the clade matches the predetermined number of species plus one. This time between the origin of the last required species and the origin of the additional species allows the distribution of the last species to develop. The additional species is then eliminated from the output. At this point, a species richness gradient is estimated by counting the number of range overlaps in each cell of the domain. For additional details see annotated R code.

### Variations to simulation parameters

Each repetition of the simulation models varied its parameterization. In this way, we tried to emulate some of the variation observed among empirical clades in the evolutionary and biogeographic processes that lead to the construction of richness gradients and richness-environment relationships. This variation can also be used to investigate the potential effects that simulation parameters have on the strength of richness-environment relationships produced by our simulations. Simulation runs varied in: 1) total number of species produced during the diversification of the clade, 2) mean of the pool frequency distribution of range sizes, 3) place of origin for the clade, 4) probability of species shifting their ranges, 5) probability of speciation, 6) initial probability of extinction, and 7) whether accumulation of species in a clade was logistic or exponential.

1. *Clade diversity (Div)*: For each simulation, the target clade diversity was selected at random from a uniform distribution of richness values ranging from 100 to 300 species. Many studies of species richness gradients use groups of species that contain more than our maximum number of species (e.g., Bokma *et al.*, 2001; Storch *et al.*, 2006; Rangel *et al.*, 2007); but, these studies typically use polyphyletic species groups. In our study, artificial clades with much larger

- numbers of species would have slowed down our simulations significantly, making it difficult to replicate extensively. However, we believe that much higher number of species would not strongly modify our conclusions.
2. *Proportional range size (PRS)*: During simulations, each species selects at random its target range size from a frequency distribution of ranges. It is well documented that range sizes in real species groups are skewed: more species have smaller distributions than large distributions (Gaston, 2003). Many of these empirical range-size frequency distributions approximate a log-normal distribution (although many times they are not perfectly described by this distribution; Gaston, 2003). Thus, for each of our simulation runs, the frequency distribution of range sizes was modeled as:  $F = \exp\left[N\left(\mu, \sigma^2\right)\right]$ . Where  $\mu = \ln(\text{domain size} * p)$ ;  $p$  is a variate from a uniform distribution ranging from 0.05 to 0.7. The value of  $p$  determines the proportional average range size, and was varied randomly among simulation runs. This caused the mean of the pool frequency distribution to vary approximately from 5% to 70% of the domain size. Many empirical studies of richness gradients at broad extents have used species groups where their average range size is within this range (Dunn *et al.*, 2007). The variance is determined as:  $\sigma^2 = (0.8 - p)^2$ . This ensured that as the average range size increased, the species with ranges larger than the domain did not dominate the frequency distribution. Any species with a range size larger than the domain was shortened to match the total domain size.
  3. *Place of clade origin*: The cell colonized by the first species represents the place of origin for the clade. For each simulation, a cell was selected at random for the initial colonization of the domain. All cells had identical probabilities of being selected. We then recorded the latitude (*Lat*) and longitude (*Lon*) of the place of origin for the clade in each simulation run.
  4. *Range movement probability (MP)*: the per-species/per-time step probability of range movement for each simulation was drawn at random from a uniform distribution varying from 0 to 1. MP of 0 produces species with static ranges, while MP of 1 causes every species to move its range at every time step.
  5. *Diversification type (DT)*: For each simulation, one of two modes of increase in species richness is possible: logistic or exponential (Lane & Benton, 2003; Benton & Harper, 2009). For exponential richness growth, per-species/per-time step probabilities of speciation and extinction remain constant through time. However, in the case of logistic richness growth, the speciation probability remains constant and the extinction probability changes positively as a function of the number of species in the domain (see below). In each continent, half the simulations used an exponential model of diversification, and the other half used a logistic model.
  6. *Speciation probability (SP)*: At each time step, there is a probability for each species to speciate. For each simulation, speciation probability was drawn at random from a uniform distribution varying from 0.0005 to 0.005. This typically puts the speciation events in a much longer time scale than either range growth or range movement.
  7. *Extinction probability (EP)*: For each simulation run, extinction probability was drawn at random from a uniform distribution of values ranging from 0 to (SP x 0.75). This ensures that in each simulation the extinction rate is at most 75% of the speciation rate, leading to diversifying clades with positive richness growth.



Smaller differences between speciation and extinction rates would slow down simulations too much to be able to obtain enough replications.

For the cases where diversification model is exponential, the per-species/per-time step extinction probability is diversity-independent and constant through time. On the other hand, if richness growth is logistic, extinction probability increases as the clade diversifies. This increase is adjusted so that the equilibrium diversity produced by speciation and extinction probabilities equals the required clade diversity (*Div*). Thus, extinction varies with the number of species according to the following function:

$$EP_t = EP_0 + \frac{SP - EP_0}{Div} div_t$$

where  $EP_t$  is the probability of extinction at time  $t$ ,  $EP_0$  is initial probability of extinction,  $SP$  is the probability of speciation,  $Div$  is the target clade diversity, and  $div_t$  is the clade diversity at time  $t$ .

## EFFECTS OF SIMULATION PARAMETERS ON SIMULATED RICHNESS-ENVIRONMENT RELATIONSHIPS

Simulation runs for our DRD model varied in simulation parameters (see detailed description of DRD simulation model for more information). We included this variation with the objective of emulating variability observed in diversification of empirical clades. However, this random variation can also be used to investigate the influence that simulation parameters have on strength of species-environment relationships produced by our model.

### Methods

To determine which parameters had a significant effect on strength of stochastic species-environment relationships, we ran multiple regressions in which logit-transformed adjusted  $R^2$ s (not primary adjusted  $R^2$ s) of stochastic richness-environment relationships were the dependent variable and the different simulation parameters were the predictors: 1) final clade diversity, 2) proportional range size, 3) latitude of clade origin, 4) longitude of clade origin, 5) probability of range movement, 6) probability of speciation 7) initial probability of extinction, and 8) diversity growth type. We ran one of these regressions for each combination of hypothesis and domain. We used regression coefficients to estimate the effects of parameters on simulation outcomes. To make coefficients comparable, both dependent and independent variables were centered and standardized.

### Results and Discussion

Our results indicate that simulation parameters can explain a significant proportion of variation in stochastic species-environment relationships (from 2.1% to 60.1%; mean=24.1%; Fig. A2). But in the majority of cases, most variation cannot be accounted for (Fig. A2). This suggests that influence of simulation parameters is overridden by stochasticity in our model, so that frequently most variation in strength of species-environment relationships is not produced by variation in simulation parameters.

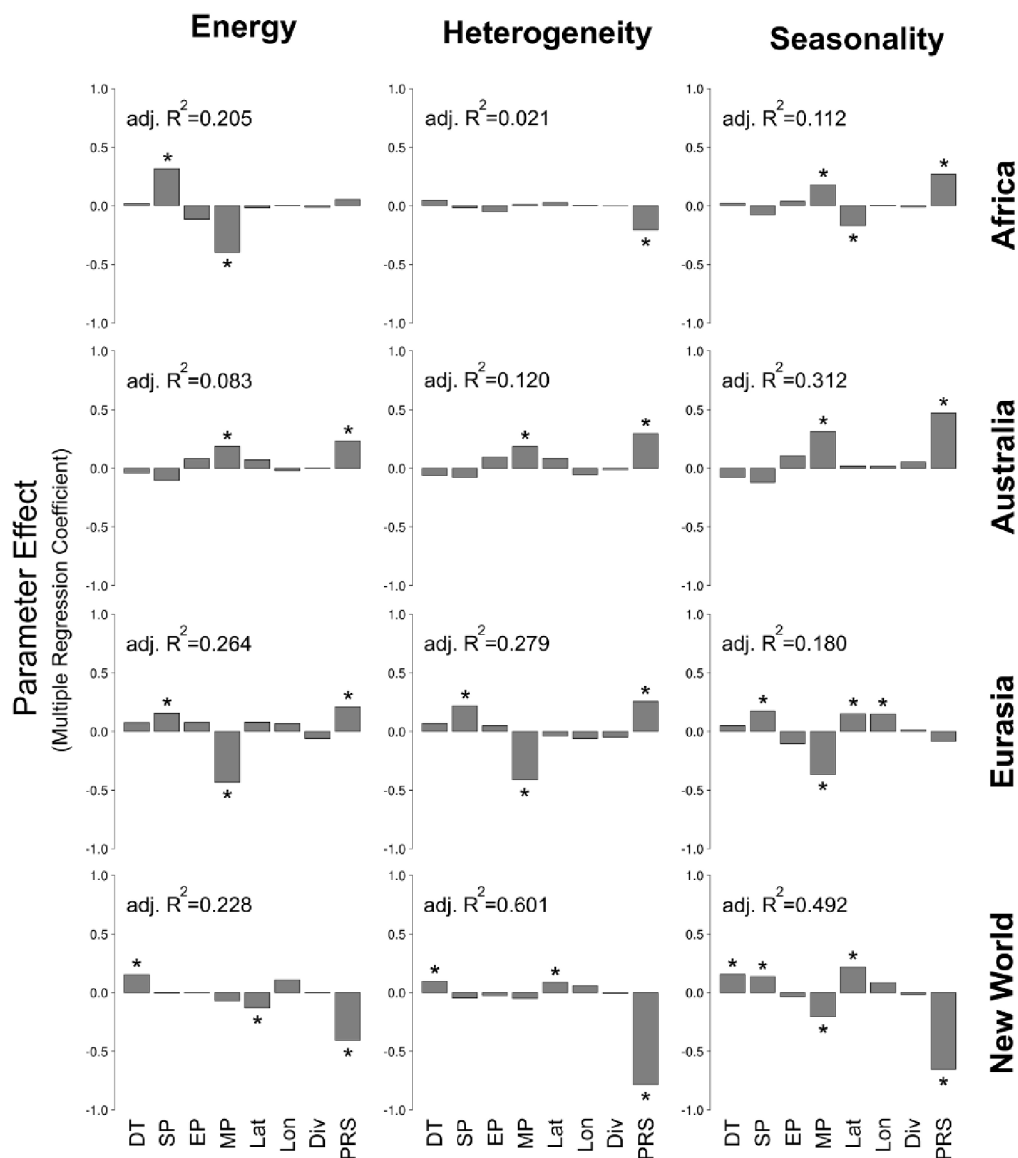
Moreover, effects of simulation parameters change much among continents and hypotheses, and no simulation parameter had a consistently strong effect on species-environment relationships (Fig. A2). For example, even though proportional range size was significant in 10 of 12 cases, its effects were variable and usually small. The only exception was the effect of this parameter on the species-heterogeneity and species-seasonality relationships in the New World. According to our results, as range size increases, the strength of species-environment relationships in the New World tend to significantly decrease. The causes for this effect are unclear, and would require further investigation, which is outside the objectives of the current analyses. Movement probability was also frequent predictor of species-environment relationships: it was significant in 9 out of 12 cases. However, the direction of its effect changes considerably: in 4 cases it had a positive effect, and in 5 its effect was negative. Moreover, its effects were typically small. Speciation probability and latitude of clade origin were significant predictors in 5 out of 12 cases, but once again effects were typically very small. All other simulation parameters were rarely significant predictors of stochastic species-

environment correlations (Fig. A2).

In general, no simulation parameter had a consistently strong effect on species-environment relationships simulated by our DRD model. Moreover, significant parameters frequently changed in the direction of their effect and in their strength among domains and among environmental characteristics. This suggests that, when the distribution and diversification of clades occur independently of environmental gradients and at random, clade diversity, rates at which distributions have moved, and rates at which clades have diversified might not always be dominant determinants of the relationship between richness and environment gradients. These results, however, might be contingent on the particularities of the simulation model used, and are not necessarily applicable to other models of geographic clade diversification (see Gotelli *et al.*, 2009 for a review).

**Figure A2**

Effects of simulation parameters on strength of species-environment relationships produced by the DRD model. For each combination of hypothesis and continent, bars corresponds to standardized multiple regression coefficients representing effect of each particular parameter. Bars with asterisks represent parameters that were statistically significant ( $p \leq 0.05$ ). We also report the total amount of variation in simulated species-environment relationships that is explained by all parameters together. **DT**: diversification type (dummy variable: 0=logistic, 1=exponential), **SP**: speciation probability, **EP**: initial extinction probability, **MP**: movement probability, **Lat**: latitude of clade origin, **Lon**: longitude of clade origin, **Div**: final clade diversity, and **PRS**: average range size proportional to domain size.



## COMPARISON OF RESULTS BASED ON OLS AND SPATIAL REGRESSIONS

Most analyses of environmental correlates of species richness at broad scales have made use of ordinary least squares (OLS) to fit models to data (Wright *et al.*, 1993; Field *et al.*, 2009). Even though the OLS approach has been widely used, this type of analysis has been criticized recently because data frequently violate some of its most fundamental assumptions, particularly due to the autocorrelation that is frequently inherent in spatial data (Dormann *et al.*, 2007; Beale *et al.*, 2010). The two most important consequences of spatial autocorrelation are: 1) undesired changes in type I error rates of statistical tests, and 2) biases or uncertainties in the estimation of model parameters. Thus, macroecological studies are increasingly using regression models that are capable of handling better spatial autocorrelation in data. Advantages and drawbacks of these spatial regression models have been discussed in many recent publications, and their use and correct interpretation continue to be a source of discussion (e.g., Diniz-Filho *et al.*, 2007; Dormann *et al.*, 2007; Bini *et al.*, 2009; Peres-Neto & Legendre, 2009; Beale *et al.*, 2010). Here, we investigate whether the spurious species-environment relationships we identified in our main analyses based on OLS regressions remain when analyses are repeated when using analyses that control for spatial autocorrelation.

### Methods

In these analyses, instead of fitting only OLS regressions to each of the 1200 stochastic richness gradients, we also used spatial autoregressive error models (SARe). SARe models have been frequently used, and a recent study by Beale *et al.* (2010) showed that SARe is among the spatial regression models with best statistical behavior. Unlike OLS regressions, SARe models are fitted by maximum likelihood. Under this approach, it is not possible to calculate a measure of effect size that is equivalent to the  $R^2$  values used in OLS regressions. Thus, we compared species-environment relationships among environmental characteristics and continents using regression coefficients. For each simulation run, we fitted two full models (where all environmental predictors were included simultaneously), one for OLS regression and one for SARe model. For each regression, both simulated species richness and environmental predictors were centered and standardized. Regression coefficients and their p-values were retained from these analyses.

For each environmental predictor, we built a frequency distribution of the coefficient values produced by our DRD model in each continent. If spatial analyses correctly identify the fact that species richness gradients and environmental characteristics are causally unrelated in our simulations, then these distributions should be tightly distributed with a mean of zero. Thus, the means of frequency distributions of coefficients were compared with the expected value of zero using a one sample t-tests (using a non-parametric tests leads to identical conclusions; results not shown).

Additionally, we tested whether absolute values of SARe coefficients were different among the different hypotheses that each variable represented, and for the different continents where simulations were run. We used absolute values because we were only interested in the degree of difference from zero for each coefficient (the “explanatory power” of each predictor), and not in its direction. For this analysis, we used

a linear mixed effects model. Coefficient absolute values were compared among hypotheses and continents, while simulation runs and variables were included as random effects. This was done in R using the function `lme` in the package `nlme` (Pinheiro, et al., 2009).

Finally, we used p-values calculated for each coefficient in each simulation to estimate type I error rates (the probability of rejecting a null hypothesis, given that the null hypothesis is true). These type I error rates were then compared to the expected value of 0.05.

One of the main drawbacks of spatial regression models is that they frequently are much more computer intensive than OLS regressions. Because of limits in computer capacity, we were not able to use every cell in each continent to fit these models. To make sure that we could run the analyses, we randomly subsampled and used 75% of the cells in each continent (Beale *et al.*, 2010). All analyses (OLS and SARE) were run using the same subsample of cells from each continent. To define the best neighborhood distance parameter, we randomly selected ten simulated gradients from each continent. For these, we investigated what distance to define neighborhoods produced the best model (i.e., minimized the Akaike Information Criterion) by fitting 15 models ranging in values from 100 to 600 km. Based on these sample cases, we found that a distance of 210 km was the best choice; thus, we used this neighborhood distance to build SARE models for all simulations. SARE models were fit using the function `errorsarm` in the R package `spdep` (Bivand *et al.*, 2010).

## Results

According to one-sample t-tests, coefficient values from spatial analyses were statistically different from zero in all continents and for variables representing all hypotheses. The degree to which a particular coefficient was different from zero, however, was reduced in comparison to coefficients calculated using OLS regressions (Fig. A3).

Despite this reduction in the value of coefficients from OLS to SARE, the magnitude of coefficients seem to follow a similar pattern to the one we established using OLS regression (Fig. A4). Our linear mixed effects model showed that there were statistically significant differences in the magnitude of SARE coefficient values among environmental hypotheses and among continents (Table A2). Moreover, a significant hypothesis-by-continent interaction term was identified (Table A2).

It is clear that random correlations of richness with seasonality are typically stronger than richness-energy correlations, and that random richness-energy relationships are stronger than richness-heterogeneity relationships (Fig. A4). Additionally, average species-seasonality relationships are typically strongest in the New World, followed by Africa. However, species-energy relationships are strongest in Eurasia, closely followed by Africa. Differences among continents seem to be strong for seasonality and energy; but, continents differ only slightly in terms of random richness-heterogeneity relationships. These conclusions seem to be independent of the type of analysis used (Fig. A4).

The fact that most coefficient values are on average different from zero (Fig. A3) also translate into high type I error rates. In all continents and for at least one variable of each hypothesis, there were coefficients that had type I error rates ranging from moderate to extremely large (Fig. A5).

## Discussion

As has been previously demonstrated (e.g., Dormann *et al.*, 2007; Beale *et al.*, 2010), when spatial autocorrelation is present in data, spatial analyses can typically produce better estimates of true coefficient values than the OLS approach can. In our case, spatial analyses typically produced coefficient values smaller than OLS regressions, approaching the true value of zero. Despite this improvement, however, spatial analyses did not solve the problem we identified with our OLS analyses: even if a clade has diversified independently of the influence of the environment, this clade can produce a richness gradient that is statistically correlated with environmental characteristics.

Likewise, spatial analyses and OLS analyses agree that the expected-by-chance correlations between richness and environment are not homogeneous, but change significantly among environmental characteristics and among domains of distribution (i.e., continents). Our evaluation of type I error rates stresses the idea that even the use of spatial regression coefficients will lead to consistently identifying significant species-environment relationships, even when these relationships are spurious.

Many other types of statistical analyses have been used to account for spatial autocorrelation (Dormann *et al.*, 2007). Among them, SARE has been identified as one of the models with best statistical behavior (Dormann *et al.*, 2007, Beale *et al.*, 2010). Other models, like generalized least squares (GLS), generalized additive mixed models (GAMM) and Bayesian conditional autoregressive models (BCA) were also identified by Beale *et al.* (2010) as good performing models. It is beyond the scope of this work to compare these different models in their performance with base on our simulated data. Nevertheless, GLS, GAMM and BCA, despite being more computer intensive, seem to lead to only marginally different models in most situations (Beale *et al.*, 2010). Thus, we do not expect other spatial models to be able to fully correct for the problem of spurious richness-environment correlations that are expected by the random geographical diversification of clades. However, a more in-depth evaluation of the performance of spatial models, null models or their integration is required, and will be presented elsewhere.

Overall our results indicate that, even if a clade diversifies and its species distribute independently of any environmental effect, some level of species-environment correlations should be expected by chance alone. The use of spatial analyses is a good way to correct for the value of species-environment relationships as estimated by regression coefficients. We see the use of these models as an improvement over the more traditional OLS approach. However, our preliminary analyses suggest that spatial regressions seem insufficient to solve the problem we have identified. This potential for spurious species-environment correlations that change among environmental characteristics and among domains of distribution should be considered in future studies.

**Table A2**

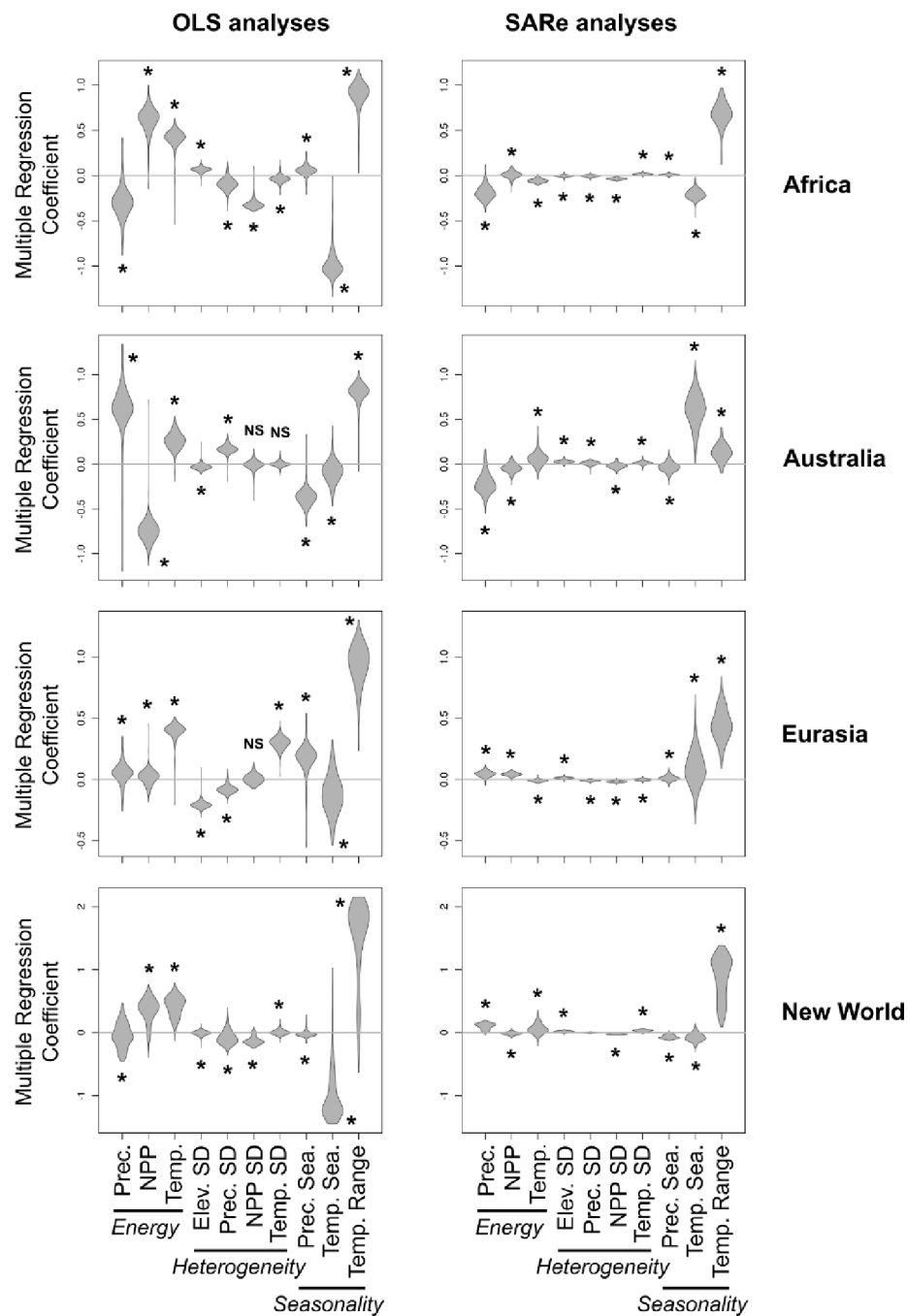
Results of the linear mixed effects model run on absolute values of regression coefficients calculated using SARE models. Absolute regression coefficients were compared among hypotheses and continents; simulation runs and variables were used as random effects. Significant p-values are presented in bold numbers.

	<b>df</b>	<b>F</b>	<b>p</b>
<i>Hypothesis</i>	2, 2698	1163.45	<b>&lt;0.001</b>
<i>Continent</i>	3, 8991	101.06	<b>&lt;0.001</b>
<i>Hypothesis*Continent</i>	6, 8991	56.27	<b>&lt;0.001</b>



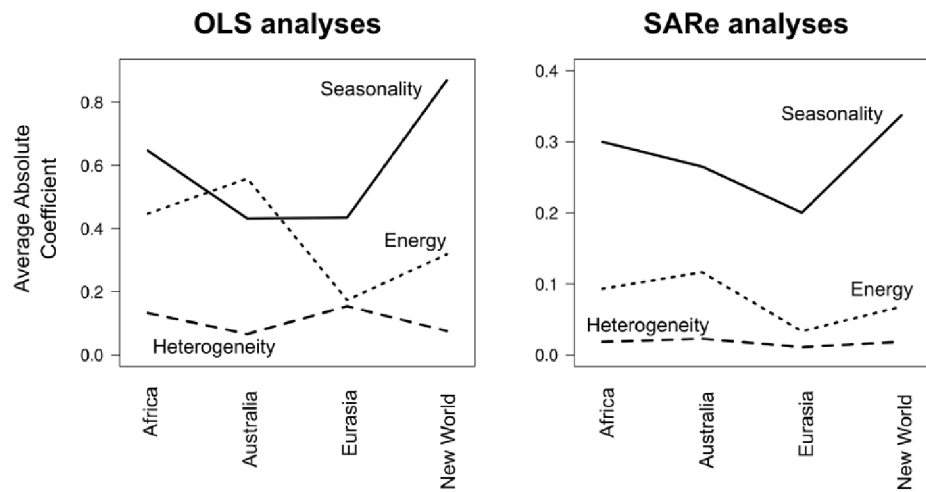
**Figure A3**

Violin plots comparing distributions of standardized regression coefficients between OLS and SARE analyses by continent. Variation in width is proportional to variation in number of simulations. Stars identify coefficients that were significantly biased ( $p \leq 0.05$ ) based on one-sample t-tests. NS identify non-biased coefficients. T-tests compared the mean of the distribution of each coefficient with the expected value of zero. These are regression coefficients from a multiple regression where all predictors were included simultaneously. This is different from the univariate regression coefficients shown in Fig. 3. Note that scaling is identical for OLS and SARE panels in each continent.



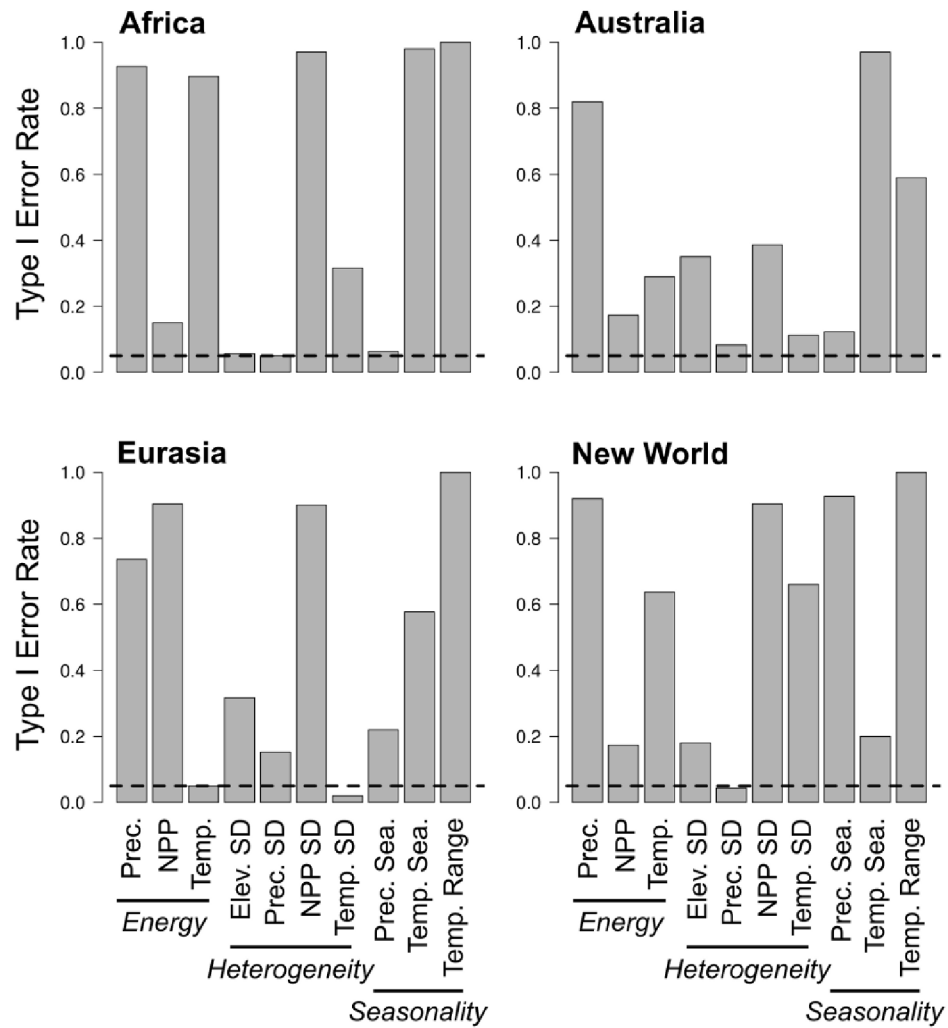
**Figure A4**

Interaction plot presenting the changes across hypotheses and continents in average absolute value of regression coefficients for OLS and spatial analyses.



**Figure A5**

Type I error rates for SARE coefficients in each continent. Horizontal dashed line represents the expected value of 0.05.



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