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RESEARCH ARTICLE

Random placement models explain species richness and dissimilarity of frog assemblages within Atlantic Forest fragments

Mauricio Almeida-Gomes[1] | **Nicholas J. Gotelli**[2] | **Carlos Frederico Duarte Rocha**[3] | **Marcus Vinícius Vieira**[4] | **Jayme Augusto Prevedello**[3]

[1]Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, Campo Grande, Brazil

[2]Department of Biology, University of Vermont, Burlington, VT, USA

[3]Departamento de Ecologia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil

[4]Laboratório de Vertebrados, Departamento de Ecologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil

Correspondence
Mauricio Almeida-Gomes
Email: almeida.gomes@yahoo.com.br

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Abstract

1. Understanding the effects of random versus niche-based processes on biodiversity patterns is a central theme in ecology, and an important tool for predicting effects of habitat loss and fragmentation on biodiversity. We investigated the predictive power of random processes to explain species richness and species dissimilarity of amphibian assemblages in a fragmented tropical landscape of the Atlantic Forest of South America.
2. We analyzed a large database of amphibian abundance and occupancy, sampled in 21 forest fragments ranging in size from 1.9 to 619 ha. We compared observed species richness and species dissimilarity with the outcomes of two null (random placement) models: 1- the traditional Coleman's area-based model and 2- an abundance-based model (based on the number of individuals observed in each fragment). We applied these models for all species combined, and separately for forest-dependent and habitat-generalist species.
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Ziv, 2016; Jacquemyn et al., 2021). In the absence of autocorrelated environmental variables, limited dispersal in a neutral model can also cause changes in species association and composition among sites (Ulrich, 2004).

In the absence of dispersal limitation or environmental gradients, purely random processes could potentially explain species dissimilarity in habitat patches, because most indices of species association (which reflect differences in species composition) are highly correlated with species richness (Ulrich et al., 2018). Species dissimilarity could reflect, at least partially, the number of individuals and species in patches randomly sampled from a larger regional source pool of species. For example, two large patches could receive a high and similar number of individuals from a regional pool, thus sampling higher number of species and potentially increasing their species richness and similarity in species composition (Chao et al., 2005), especially if the regional pool is small. Therefore, it remains an open question the degree to which random processes alone may explain patterns of species dissimilarity in patchy systems.

Here, we used area-based and abundance-based random placement models to test whether simple random processes explain species richness and species dissimilarity in tropical forest fragments. To do so, we used a large empirical dataset of frogs from the Brazilian Atlantic Forest, one of the most threatened world's biodiversity hotspots (Laurance, 2009). In a previous study using this dataset, we showed that larger forest fragments had more similar communities compared to continuous forest than smaller fragments (Almeida-Gomes, Vieira, et al., 2016). These patterns were previously attributed to the higher diversity of reproductive sites in larger fragments (Almeida-Gomes & Rocha, 2015; Almeida-Gomes, Vieira, et al., 2016). Here we tested a simpler hypothesis: that the variation in both species richness and species dissimilarity among patches is a simple consequence of variation in abundance per patch. To do so, we evaluated the outcomes of the area-based and abundance-based models. If both models were able to explain community structure (i.e. species richness and/or dissimilarity), it would suggest that the distribution of individuals and species across forest frallK ibr

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(Almeida-Gomes, Prevedello, et al., 2016). Therefore, we classified frog species as “forest-dependent” and “generalists”, according to their habThe ß “generIR in of the overall fragment areas (the sum of all sampled areas) would receive 10% of the total number of individuals from the sampled reas the observed SAR, we log-transformed fragment areas. We performed a Mantel correlation test (Mantel,

TABLE 1 Parameters of linear regression between observed (response variable) and predicted species richness (explanatory variable). If *t* tests for intercept = 0 and slope = 1 are significant ($p < 0.05$), they are considered different from 0 and 1, respectively

Model	**Intercept** – SE	**Slope** – SE	R^2	F **overall**	p	t **for intercept** = **0**	p	t **for slope** = **1**	p
(a) All species									
Area-based									
Species richness	4.19 ± 1.85	0.46 ± 0.12	0.42	14.00	<0.01	−2.26	0.04	4.27	<0.01
Abundance-based									
Species richness	−7.13 ± 2.49	0.98 ± 0.14	0.73	51.70	<0.01	2.86	<0.01	0.17	0.87
(b) Forest-dependent species									
Area-based									
Species richness	0.16 ± 1.06	0.60 ± 0.14	0.48	17.51	<0.01	−0.15	0.88	2.79	0.01
Abundance-based									
Species richness	−4.18 ± 1.57	0.97 ± 0.18	0.61	30.1	<0.01	2.66	0.01	0.16	0.88
(c) Habitat-generalist species									
Area-based									
Species richness	3.45 ± 1.32	0.36 ± 0.16	0.22	5.24	0.03	−2.62	0.02	3.98	<0.01
Abundance-based									
Species richness	−0.14 ± 1.09	0.70 ± 0.11	0.67	38.98	<0.01	0.14	0.90	2.62	0.01

FIGURE 3 Results from the two random placement models (area-based model and abundance-based model) for forest-dependent and habitat-generalist species, using sampling with replacement: (a, c, e and g) Observed and predicted species richness. (b, d, f and h) Observed (black dots) and predicted (white dots) species-area relationships. In all plots, predicted values represent the average values obtained for each forest fragment across 1,000 iterations of the model and the shaded polygons delimit 95% confidence intervals. In (b, d, f and h), the

Simpson, G. G. (1943). Mammals and the nature of continents. *American Journal of Science*, *241*, 1–31. https://doi.org/10.2475/ajs.241.1.1

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