

The author presents an interesting piece of work that aimed to prove that the kinetic hypothesis of biodiversity may not satisfactorily explain the central tendency in species richness (as it has been previously stated with empirical evidence for and against), but the upper bound (i.e. maximum richness) of the relationship (which according to the author's claims, it has been hypothesized but empirical evidence remains obscure). To do so, he used either linear or segmented quantile regressions, a statistical tool that has been proved useful to provide comprehensive descriptions of biological response patterns in observational studies of limiting factors. Overall, the manuscript is well written, including clearly stated hypotheses/results and fairly transparent descriptions of the methods. I think there is potential for an interesting publication in this draft. Yet, I would like the author to address few comments and suggestions before recommending the article, specially those concerning the hypotheses.

Firstly, a formal comment on the authorship. While the draft is signed by one single author, the text is written in plural tense (we). Please, fix the text to first person singular, otherwise add the omitted authors.

Title: I think the title is too general given that the study focuses just on tree species. I would suggest something like "Mean annual temperature drives the variation in maximum potential tree species richness and frost organizes the residual variation". I would also avoid the use of acronyms (i.e. MAT) in the title.

The author state that the model derived from the exponential Boltzmann temperature relationship predicts a negative slope of -0.65 between the inverse of temperature (1.000/kK) and the natural logarithm of species richness, and then cites Allen et al. (2002). These authors fitted linear regressions between the inverse of ambient temperature and the natural logarithm of species richness for multiple taxonomic groups (including North American tree species), and they presented both the slope of each relationship and the averaged slope across all groups. The only numerical difference between the models of Allen et al. (2002) and the ones presented by the author is that the former used 1000/K instead of 1000/kK, and thus the slopes reported by Allen et al. (2002) are fully comparable to the ones shown by the author if divided by 10. Given the data provided by Allen et al. (2002) (see Figure 1 and Table 1 below), I cannot see where the -0.65 slope is coming from (for example, in the case of North American trees, the slope provided by these authors is -1.005 if temperature is scaled at 1000/kK).

The text reads "Currie (2007) hypothesized that the model proposed by Allen et al. (2002) only fits the upper bound of the relationship between species richness and MAT in plants, but cannot explain the species richness variation in general". I wish I could have checked such statement in Currie (2007), but unfortunately the citation is a book chapter to which I have no access.

In line 33, the author introduces the case study. I would suggest expanding a bit the description of the data, given that "the Americas" is a rather vague term. Also, I think the manuscript will much benefit from a figure showing a map of the study area including the plots.

In line 48, the text reads "segmented models are more robust in all of the quantiles analyzed", and Figure 1 caption reads "The red lines represents the stronger models [...]". I would suggest using more specific descriptions of the results, because while "robust"

and “strong” are rather synonyms, they refer to completely different things in the article (i.e. the most supported models by the AIC criterion and the t-test on the two slopes of segmented models, respectively).

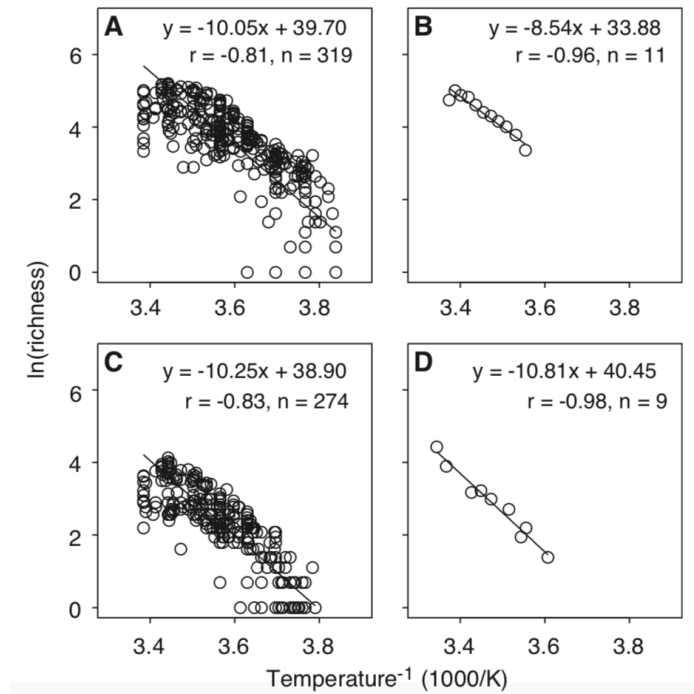


Figure 1. Relationships reported by Allen et al. (2002) on the relationship between the inverse of ambient temperature (1.000/K) and the natural logarithm of species richness in different terrestrial taxonomic groups. (A) North American trees (latitudinal gradient), (B) Costa Rica trees (altitudinal gradient), (C) North American amphibians (elevational gradient) and (D) Ecuadorian amphibians (elevational gradient).

Table 1. Slope, 95% CI, intercept, r score and sample size of the relationships shown in Figure 1 plus those displayed for aquatic taxa (not show in Fig. 1).

Group	Data set	Slope	95% CI	Intercept	<i>r</i>	<i>n</i>
Trees						
	Latitudinal gradient, North America	-10.05	-10.88 to -9.18	39.70	-0.81	319
	Elevational gradient, Costa Rica	-8.54	-10.10 to -6.48	33.88	-0.96	11
Amphibians						
	Latitudinal gradient, North America	-10.25	-11.01 to -9.58	38.90	-0.83	274
	Elevational gradient, Ecuador	-10.81	-12.10 to -8.83	40.45	-0.98	9
Aquatic taxa						
	Riverine fish, global	-9.16	-11.09 to -7.66	35.55	-0.43	165
	Marine gastropods, Americas	-7.17	-7.65 to -6.71	30.51	-0.91	116
	Marine ectoparasites, Pacific	-8.51	-9.88 to -7.17	30.99	0.60	93
Average						
		-9.21			-0.79	

The author provided slopes, p-values for the t-test on the slopes of segmented models and AIC values. However, such descriptors do not provide information on the goodness-of-fit of the models. I am not particularly familiar with quantile regression, yet I suspect the classical R^2 used for models that are based on the conditional mean are not valid for quantile regression. However, a quick search in google suggests that some alternatives exist (e.g. Koenker, R and Machado, J. 1999. Goodness of Fit and Related Inference Processes for Quantile Regression, Journal of the American Statistical Association, 94, 1296-1310). I think the manuscript will much benefit from including any suitable goodness-of-fit metric for the models. After all, the AIC criteria serves to choose the best model, but it does not tell anything about whether the selected model is actually a good descriptor of the data (as the devil's advocate, I may argue that the author is choosing the best model among very bad ones, which might invalidate the conclusion of the study).

Figure 1. Just a suggestion. If the author is going to present this figure in colour, consider using a colour palette instead of just red for a better visual impact.

The results of the residual analysis are very interesting. I wonder if the author has considered splitting the dataset between tropical (including both humid and dry tropics, where frost days may not be a big issue but water availability does) and temperate (where frost days may be an important issue rather than water availability) regions to test the hypothesis separately for each group of plots. This analysis should not imply much of an effort, and it may serve to get further insight on the biological response of tree species to environmental thresholds.

The final sentence of the article reads: "The structure of wet-tropics rich versus dry-tropics and extratropics poor seems more feasible than the famous pattern of the latitudinal gradient of species richness". I do not get the meaning of such statement.

Figure S1. While I have no problem with this figure, I think it is unnecessary.

Abstract. Please, describe the fact that you analyzed upper bonds rather than central tendencies when introducing the hypothesis. This is indeed the main novelty of the manuscript, and yet it is presented when introducing the results instead. I think this section requires some rewriting.