Review of: "Listening to the Bats of Carajás: Applied Bioacoustics for Species Inventory and Environmental Use in a Mosaic of Forests, Savannas, and Industrial Mining in the Brazilian Amazonia"

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Potential competing interests: No potential competing interests to declare.

I carefully read Gomes & Bernard's article on bats in Carajás. Your research is essential for filling gaps in our knowledge about bats in the Amazon. It also has the potential to significantly impact our understanding of the ecological dynamics in areas bordering hotspots of environmental degradation. Congratulations on this significant contribution.

Some suggestions:

- The citations need to be reviewed. Some places are in a different format than the general text.

- Reference 27 is unnecessary in the last sentence of the second paragraph of the introduction since it does not directly assess the effect of habitat loss or degradation.

- In the third paragraph of the introduction and in other parts of the text, include this paper: https://onlinelibrary.wiley.com/doi/10.1111/aec.13550

- Confirm that reference 29 is correct to be cited at the end of the third paragraph of the introduction.

- In item 2.4 of the methods, the first sentence of the first paragraph: What parameters were used for the species richness curves? Was there randomisation? If so, how much? If the curves were extrapolated, as mentioned at the beginning of the sentence, how much was extrapolated? Were sonotypes also used for these analyses?

By default, iNext extrapolates the curve up to twice the maximum observed value of the sample, following the criteria described in the package. However, in Figure 2, there is a cutoff at a maximum number of minutes. What is this number, and why is there a cutoff? My suggestion for a fairer comparison would be to use the cutoff of up to twice the size of the smallest sample, which would be the "cave in an area planned for mining." Alternatively, if you do not want to make such a strong cutoff in the curves with more records, either use the interpolated value that corresponds to the value sampled at the end of the curve or the one that corresponds to the value extrapolated up to twice the last observed value of the curve. In any case, there is no description of which value is used to run the GLMMs or whether the interpolated value corresponds to the largest observed or extrapolated value.

Also, the curves were constructed based on the sampling time, as shown in Figure 2. In other words, did you do a matrix for each sampling site containing presence and absence according to the minute it was recorded? It would be good to have a description of this in the methods so that other people can repeat this type of analysis.

- In item 2.4 of the methods, the third sentence of the second paragraph: Did you check whether or not there is spatial autocorrelation by analysing the residuals of the models? How did you ensure spatial independence since some groups of points seem to have points very close to each other?

- About the estimated richness values in Table 2: Perhaps indicate the percentage (%) of the estimated richness observed in parentheses. This would give a better idea of the sampling coverage. This could also have been done with the sampling coverage curves from iNEXT, using the sampled coverage option in the R function.

- Item 3.3 of the Results, first sentence of the first paragraph: Using the confidence intervals (CIs) of the iNEXT curves, you could also have compared the richness between the sampled habitats since an overlap of the CIs would indicate no difference between the habitats. Again, you would need to choose and justify the value of the curve at which this comparison would be made.

- Item 3.3 of the Results, second sentence of the fourth paragraph: Why was no index used to effectively analyse the composition (similarity or dissimilarity) between the sampled habitats? You could use anything from ANOSIM/SIMPER to β-diversity, remembering that verifying the spatial autocorrelation for any of these is necessary. For example, Figure 3 shows that the richness is similar for some habitats in very close sites.

- In the summary and discussion, you mention *areas of metallophilic savannas (canga)*, but there is no explanation in the methods that cangas are a savanna type. Include this in the methods.

- End of the first paragraph of the discussion: However, the species composition was not effectively analysed.