Reply to Reviewers' comments

**ID:** remotesensing-454161

**Title:** Looking for ticks from Space: using remotely sensed spectral diversity to assess *Amblyomma* and *Hyalomma* tick abundance

**Authors:** Da Re et al.

We would like to thank the reviewer for his/her stimulating comments. We also believe that, thanks to his/her suggestions, the manuscript is now greatly improved.

**Reviewer #1**

In this study the authors advance the use of spectral diversity, from Satellite Remote Sensing (SRS -- MODIS, specifically), as an improved predictor over NDVI for the abundance of two disease-vector tick taxa. The study is concise and well-written. There are few if any typographical or grammatical problems, and the paper follows a logical structure. I have several worries about the ground-truth data and other revisions to suggest.

However, even if these problems can all be rectified with revision, the performance of the models with spectral diversity is modest and incremental at best. In other words, my concern is that the approach offered by the authors is unlikely to advance the basic science or its application in improved spatial epidemiology to better predict the risks from tick vectors on a landscape. Although it is better to know than to not know, the study is unlikely to improve our understanding of the phenomenon under study or illuminate similar systems under study elsewhere.

Reply: We thank the reviewer for his/her comment. We highlighted better in the text that we got a moderate contribution to the explained variance and that there is likely a scale and sensor issue (L385-95 of the revised manuscript). Nevertheless, to our knowledge the relationship between arthropod vectors and spectral diversity was never tested. Though our approach showed modest results in term of goodness-of-fit between predicted and observed value, we consider the R² = 13-20% a promising result for a single-variable model, taking in consideration the sampling and scale limitations.

A strength of the study is that it pairs ground sampling of ticks across the country to the SRS (Satellite Remote Sensing). In other words, there are empirical abundance estimates for the two tick taxa that come from sampling of 104 randomly selected how herds throughout the country. The methods report the timeframe of these surveys (Oct-Dec in one year), but without an explicit link to the timeframe of the MODIS imagery for the SRS. What does “as close as possible” [line 118] actually mean? Were the images also from this range of October-December, or? It would make a big difference in NDVI and spectral diversity.

Reply: We now specify metadata on satellite images in section “2.4 Satellite images and predictor variables”.

The study calculates NDVI and spectral diversity for the whole country of Benin, which includes various habitats and land use including pasture and forest. However, the samples for ticks could only come from cow habitat, which likely excludes forests (and some other land use covers). Thus, is this analysis missing a step? Should it not first attempt to predict the abundance of cows, and
then look at the variation in tick loads within the areas where cows are possible? I wonder if a better approach understand tick ecology and disease risk is to measure cow populations and use environmental predictors of their abundance and health?

Reply: We accounted for cow presence in the sampling strategy. We used the GliPha maps on gridded livestock of the world to exclude areas outside of cow habitat. As stated in the manuscript, Benin has a very mixed land cover pattern, with most forest patches being small patches of degraded forest, which is also used for grazing of pastoral cattle. In short, we can state that cows are everywhere, they can be seen grazing along the roads, in fields after harvest, on the beach, and also in the forest, unless it is very protected. This is why we excluded the national parks. Cattle ticks are linked to cattle, but their abundance is not proportional to cattle density. Cattle presence is a constraint, not a risk factor. In the absence of cattle, the adults will feed on other wild or domestic mammals (goat, sheep, antelope ...). Furthermore, the spatial and temporal accuracy of cattle density maps in this region is insufficient for this study.

Given the low amount of variance explained, and for one species the modest incremental improvement of the spectral index over NDVI, is it likely that we can hope for epidemiological prediction for ticks using SRS? The authors mentions the “population dynamic” of ticks [line 306], which probably was not synchronous but also can vary a lot through a year, and abundances themselves will not strongly predict the incidence of disease. Thus, there are gaps that seem to make it unlikely this study can have a large impact.

Reply: we are focusing here on the potential of using remote sensing spectral diversity to predict tick abundance. As the Reviewer said, the results are modest, and we have highlighted in the text how this approach is really taxa- and scale-dependent. However, this approach was never tested for parasitic arthropod, and the theoretical background is robust.

Strictly speaking, the code for the study is not freely available online at the authors gitlab website. The code is available only after registration with gitlab. Although registration is free, a reviewer potentially must disclose their identity before logging into the author’s page. The authors must provide the code on a site with no restrictions to access at all.

Reply: Though codes are increasingly provided through GitHub or GitLab, we provided the code as supplementary material.

Table 3 is unnecessary. These very simple descriptive stats can be given in the results text. Table 4 and 5 are, in my opinion, too much. Can the authors distill out the most important pieces of the model selection and the parameter estimate for the top model(s)? Additionally, where is the Vuong test, and what is the model set for the AIC values? It seems there are 4 model sets for each species (spectral count & ZIP, NDVI count & ZIP), but only 2 AIC sets for model selection. The table legend or its footnotes should also have a key for the abbreviations used, such as GLCM, which have to be hunted down in the body of the manuscript.

Reply: As suggested by the Reviewer, Table 3 was deleted and its information included in the text. In contrast, we find Tables 4, 5 (now 3, 4) are sufficient to represent the double component (Poisson and binomial) of the Zero Inflated Poisson model, which is also the reason why only one AIC is provided. We added in the tables legend the abbreviations requested.