Second review for "Predicting species distributions in the open oceans with convolutional neural networks"

General remarks

My main remarks in the first round of review were:

1. the need for a baseline model to compare the CNN with

2. a discussion regarding the goal of this model and whether it was a "niche" model

3. the sometimes surprising choice of species

4. the fact that the model was a classifier, not a regression and that it could have unexpected consequences

5. the inclusion of geographical predictors (hemisphere etc.) which led to artefacts in the predicted distributions

6. the caricatural aspect of the 2°C increase simulation

I understand that the authors are not in a position to re-run the analyses presented in the paper. This makes it impossible to fully answer some of my remarks or those of other reviewers. They made a significant effort to review what they could and modify the text. I leave it to the recommender to decide whether this is enough to warrant a recommendation in the end.

Regarding my main remarks:

1.

The addition of the punctual DNN is welcome and clearly shows the advantage of using the spatial information. This is a good addition to the paper. Thank you.

2.

This is now better presented in the introduction and the word "niche" is not used anymore in the context of this paper, which is appropriate.

The discussion of the fit with theoretical distributions (in section 3.2) is now more cautious.

3.

The selection of species could not be changed. The introduction was altered to mention that the species selected were expected to have different distribution characteristics.

Most are mobile species, for which the dynamic SDM approach makes sense. I still think including the Acropora coral, the only sessile species in the list, does not make sense, in particular in light of the following remark.

4.

The nature of the model (i.e. a classifier) is now better presented, in a paragraph starting at line 206. A short paragraph in the discussion (line 345 and following) helps with the interpretation, but I think it is not enough, because the maps are actually very different from usual SDMs.

What is represented by each map is the *proportion* of each species among the 38 selected (assuming no sampling bias etc. as the authors point out).

This means the following, assuming a model with two species, A and B:

- in a pixel in which the conditions are maximally favourable for species A but absolutely not for species B, the value predicted for species A will be 1

- in a pixel in which the conditions are barely correct for A but still not favourable for B, the prediction will still be 1

- in a pixel in which the conditions are equally favourable for both, the predicted value will be 0.5 (as stated line 220)

This makes it very difficult to interpret a single map in isolation from others. It also explains some of the very spotty aspect of the maps: when conditions are still favourable for species A but also become favourable for another species, the predicted value for A drops. This is exemplified by the following image where blue is for *Caretta caretta*, green is *Carcharhinus falciformis* and red is *Carcharinus albimarginatus*; while the whole region may be favourable for the green turtle, the extra favourability of some pixels for the sharks make the habitat suitability for the turtle drop. This is purely a numerical artefact, not an ecological feature: these sharks only rarely eat green turtles. This is not wrong per se, but it will likely be wrongly interpreted by an unprepared reader (I know I was mistaken during my first review and I only realised this now because we have been working with proportions too and scratching our heads trying to interpret the maps).



So, overall, it should be made much more obvious that all maps are maps of proportions among the 38 species (more frequently and strongly than the mention at line 246) and their discussion should be made in light of that fact. For example, the absence of a species within its distribution range (section 3.3) may be caused by differences in season, immediate vs. long term conditions, etc. as discussed, but also by the fact that another species dominates in one part of the range of the target species. Do not hesitate to repeat yourselves; it is quite difficult to wrap one's head around the interpretation of maps of proportions.

Another way to present this is to say that your model is not a model of species distribution but rather a model of *community composition*: you are trying to define the proportion of each target species in each pixel and, in particular, which one dominates. In terms of representation, to make this obvious, with few species, you could plot a single map with a colour in each pixel, resulting from a mix of colours proportional to the probability of each species; with three species, you could take Red, Green and Blue and the resulting RGB colour would inform on which species dominates. With 38 species, I am not sure what to do, but maybe you can restrict yourselves to a few?

In light of this fact, the selection of Acropora makes even less sense: all others share similar habitats, some may compete for the same food source, etc. It makes more or less sense to consider them as a community and study their relative abundance; this is not the case for Acropora. It could have had little effect on the results since it is a very coastal species while the others are all pelagic (therefore their distributions are not "competing"), but that supposes that the coastal conditions are different enough from the pelagic ones, which is not true given its distribution map (and your discussion at line 415). This is briefly discussed in the new version of the paper but is a serious limitation for the predictions in the inter-tropical Pacific.

As you note, a way to circumvent this "relative abundance" problem is to predict many species at once: this was, each species is coexisting with, probably, many others in each pixel (i.e. each set of conditions), the predicted values do not approach 1 but their value is closer to the true habitat of the species. But the example above shows that 38 is not enough here.

5.

This is not presented as a limitation of the study. I am not convinced by the solution ("blurring" the limits rather than having hard ones): there will still be a fake boundary, which makes no sense to animals around the equator for example.

I was looking for papers discussing the inclusion of such specific geographic predictors in SDMs but could not find a definitive paper. This search probably needs to be deepened and the discussion of the consequence a bit more advanced (in the absence of the possibility to re-run the model).

6.

The simulation was removed, which I think was the right decision.

Detailed remarks

56: While simple averaging indeed erases dynamic structures, it is still possible to use another summary in climatologies. For example, to predict the most favourable habitat of tuna, a climatology of the frequency of presence of fronts (from FSLE snapshots) is likely to be a relevant information. So add "If one uses simple averaging, the use of climatological..." and possibly rephrase this sentence a bit.

88: CNNs can be used for regression also, there is nothing specific to classification. I understand you added this sentence to highlight that *yours* is a classifier, but the current sentence is not specific enough.

133: Cleaning up species records was advised by another reviewer; you explained that it was impossible to perform all manually. I agree but some automated solutions could at least allow you to automatically spot outliers in geographical/environmental space (e.g. kernel density estimation).

Seeing some of the initial point distributions, this would be worthwhile, with Acropora records in Southampton for example...

Discussion: while I appreciate the effort to include many remarks from the reviewers in the discussion, they often only amount to an acknowledgement of a problem and a statement that this needs to be further explored. I would have preferred a bit more depth, in discussion in general

PS: draftable.com was super useful. Thank you for using it!