## Round #2

## Decision

*by Samraat Pawar, 2020-01-16 12:59* Manuscript: <u>https://doi.org/10.1101/276592</u> version 3

## Second decision on manuscript

Dear Authors,

I think you have done a thorough job of addressing reviewers' comments and revising the paper.

I have two further suggestions/comments before I feel comfortable with recommending this preprint:

- What is the scaling of search rate (a<sub>i</sub>)? Authors say "Following classical allometric food web models (Brose, 2008; Heckmann et al., 2012), that are based on carbon flows, species biological parameters and trophic interactions scale with species body mass.", but I see no scaling relationship defined. None of the reviewers noticed this, but a model with scaling of birth and death rates but not of interaction rates would behave very differently than one with. As such, the scaling of handling time and search rates can have a significant impact on system dynamics, and the direct sensitivity analysis of a<sub>i</sub> will likely not capture the variation introduced by variation in the scaling model structure and parameter values of a<sub>i</sub> (or the scaling model/parameters of h<sub>i</sub>). Can the authors please clarify? For an example of a paper with scaling of all parameters, see Tang, et al. 2014. "Correlation between Interaction Strengths Drives Stability in Large Ecological Networks." Ecology Letters 17 (9): 1094– 1100. https://doi.org/10.1111/ele.12312.
- 2. The SI has four different files, and not all of the sections/files are cited, as far as I can tell. And even if they are, it's hard to follow the structure of the SI, so I suggest that you combine them into one document with a TOC.

Thanks,

Samraat

## Dear Samraat Pawar,

Thank you for your positive evaluation of our revisions. Please find our response to your two final requests:

- 1. This is actually an omission in the text,  $a_i$  is allometric in our code (this can be seen at line 117 in the species.cpp file in the release of the code associated to the first submission of this study).  $h_i$  is allometric as well as we used an allometric maximum ingestion rate to calculate the handling time (see the corresponding section in Appendix S1 in the supporting information). We added the expression of  $a_i$  in equation (4) and mentioned its allometric nature in the corresponding text (l.183). We also added the handling time  $h_{ij}$  to the list of allometric parameters (l.184) to avoid any doubt about the handling time. We also updated the description and units in Table 1. We hope this clarifies the parametrisation of the model.
- 2. Unfortunately, I cannot remove the former versions of the supporting information on

bioRxiv and they do not benefit from different version as the main text does. Then, I indicate what is the corresponding file in the "Supporting information, data and code accessibility" section:

*"The supporting information (see Supporting\_information\_final.pdf) contains the following section:* 

- S1 Appendix - Parameter calculation

- S2 Appendix - Complementary results

- S3 Appendix - Sensitivity analysis

The  $C^{++}$  code of the simulations and the R code of the figures are available on Zenodo (doi:10.5281/zenodo.3602316)."

Best regards,

Pierre Quévreux, on behalf of the authors