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letterProfessor Rob Freckleton  
Professor Freckleton,

With this letter, my coauthor Matt Lau and I are submitting a revised version of our article entitled enaR: An Package for Ecosystem Network Analysis for reconsideration and publication in Methods in Ecology and Evolution as an Application paper.

With our manuscript revisions, we have done our best to address the previous critiques by the associate editor and two reviewers. We appreciate their initial evaluation of the work and help improving the final product. In the remainder of this letter, we systematically identify how we addressed the initial comments.

There were multiple comments to focus and clarify the introduction. In response, we completely rewrote the introduction to focus on the broad MEE audience. Specifically, we added text to make the ecological motivation of the analyses more clear and reduced or eliminated the text about the historical development of Ecosystem Network Analysis and extant software tools. We generally focused the text and reduced the overall length introduction by removing any unnecessary details. In addition, throughout the manuscript we replaced the term “Ecological Network Analysis” with “Ecosystem Network Analysis” to make the goal/intent of the analyses more clear. While “Ecological Network Analysis” is the historical key term for these analyses, it was clear in some of the comments that this generated confusion due to the growth of network ecology.

It was also suggested that we improve the clarity of how the package is to be used and extended by the community. With the goal of improving the pedagogy of the manuscript, we have added more ecological interpretation to the example analysis text and annotation in the example, i.e., Table 4, which we have updated so that it is now completely reproducible. The ecological interpretation of the example Flow Analysis is now presented in a paragraph added to the Example Application sub-section. The previously difficult to access, supplementary data file, oyster.dat, is no longer referred to for the example. We also added text clarifying the data requirements and inputs, model library contents, batch processing, visualizations, and links to other packages to those respective sub-sections or figure legends. Missing references in the description of the example results have also been added. Further, as online supplementary material we plan to publish an annotated version of the script that generates Figure 1, which we expect will help potential users learn to use the package.

In response to several specific comments, we have expanded the description of the package as a whole and the specific functions with Tables 1, 2 and 3. As the package includes 34 different functions including nine primary analysis functions that each perform multiple subanalyses, it is not possible to describe them all in depth in this short Application article. Thus, we have worked to provide enough detail to identify the main types of analyses that are available, supply ecological motivation for why they might be useful, and to give a reference to additional literature that interested readers can use to learn more about each analysis.

One concern was that our claim that the software was more available and extensible was not sufficiently supported. We have addressed this in a couple of ways. First, we have clarified that because this is an package, all functions are available for review and local editing by executing the `edit(function.name)` command. Second, we have established a GitHub repository for enaR to manage the collaborative development of this coding project. This should enable a broad community to contribute to the package and view code directly with all annotation visible in the code for each function.

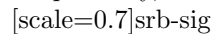
We also revised and clarified some language in the paper as requested. The text stating that the package is “built on” existing packages has been improved to explain that the package uses a data type that is used with previously developed packages used for network analyses. We have also added text describing the input data types and methods, partly through Tables 1 through 3. Confusing text referring to the package as professional grade has now been removed. Version numbering issues have been removed by deleting specific reference to the version of the package. Further, if accepted this will be the first paper to introduce the package to the ecological community.

Finally, throughout the manuscript we have attempted to clarify the novelty of this software. For the most part, the analyses and algorithms in the package are not new to ecology; some of them are more than 20 years old. However, we see four key novel aspects to this tool. First, the package collects the core algorithms

for Ecosystem Network Analysis from both the Patten and Ulanowicz schools of development, which is uncommon amongst existing software. Further, it provides a software foundation that can continue to be expanded to include new developments. Second, due to the open source nature of the chosen environments for execution (`R`) and `developmnet` (GitHub), the algorithms are available for inspection and are adaptable and extensible as the user needs. Third, we have included a library of 100 empirically-based ecosystem models in the package to enable cross-comparisons and new meta-analyses. While these models have been previously published, they have not been collected and made available in this way. Fourth, because of the nature of the programming environment and some of the software design decisions, ecologists using this package have easy access to a range of additional network analysis and statistical tools in `R`. Given these novel features, we expect this software to contribute to the large and rapidly growing area of network ecology and the domain of network science in general.

Thank you in advance for your consideration of this revised article.

Respectfully,

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Stuart R. Borrett