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May 2, 2014

Professor Rob Freckleton
Executive Editor
Methods in Ecology and Evolution
British Ecological Society

Professor Freckleton,

With this letter, my coauthor Matt Lau and I are submitting a revised version of our article entitled *enaR: An R Package for Ecosystem Network Analysis* (MEE-13-11-654) for reconsideration and publication in *Methods in Ecology and Evolution* as an Application paper. With our manuscript revisions, we have attempted to address the main critiques by the associate editor and two initial reviewers, while staying within the constraints of the article type. Texcount indicates that the article currently contains 3110 words. We appreciate the initial evaluation of the work, which has led to an improved final product. In the remainder of this letter, we identify how we addressed the initial comments.

To start, 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 text about the historical development of Ecosystem Network Analysis and extant software tools. Generally, we refocused the text and reduced the overall length by removing unnecessary details.

The reviewers also recommended that we clarify both how the package is to be used and how it can be extended by the community. We accomplished this in several ways. First, throughout the manuscript we replaced the term “Ecological Network Analysis” with “Ecosystem Network Analysis” to make the scope of the work 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. For example, we do not include algorithms to find structural motifs in networks (as suggested) because while this is an important structural network analysis, it is currently outside of the core ecosystem network analysis. Second, we have expanded the description of the package as a whole, and identify specific functions and their use in Tables 1, 2 and 3. As the package includes 34 different functions including nine main analysis functions that each perform multiple subanalyses, it is unfortunately impossible to extensively describe and illustrate all of them 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. Third, we have added more ecological interpretation to the example analysis shown in Table 4. We have also revised this to ensure that the example is reproducible without the need for supplementary (This does require the most recent enaR release that fixes a bug in the “pack()” function. The ecological interpretation of the example Flow Analysis is now presented in a paragraph added to the Example Application sub-section. Fourth, we added text clarifying the model 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 have included an annotated version of the R script that generates Figure 1, which we expect will help potential users learn to use the package.

Another concern was that our claim that the software was more available and extensible was not sufficiently supported. We have addressed this in two specific ways. First, we have clarified that because this is an R package, all R functions are available for review and local editing by executing the `edit(function_name)` command. Second, as suggested 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.

To address some more specific concerns, we revised and clarified language as requested. First, the text stating that the package is “built on” existing packages has been modified to better explain that the package uses a data type that is defined by and used in previously developed R network analysis packages that don’t include the specific ecosystem network analysis algorithms. Second, we added text describing the input data types and methods, partly through the introduction of Tables 1 through 3. Third, confusing text referring to the package as professional grade has been eliminated. Finally, software version numbering issues were removed by deleting specific reference to the version of the package. We should emphasize, however, that if accepted this will be the first paper to introduce this R package to the ecological community.

Finally, throughout the manuscript we have attempted to clarify the novelty of this application. While we have encoded some newer analyses and algorithm revisions, most of the analyses and algorithms in the package are not new to ecology; some are more than 20 years old. However, there are four key novel aspects to this software. 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. We posit that this synthesis is an essential next step for this science. 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 development (GitHub), the algorithms are available for inspection and are adaptable and extensible as the user needs, in a way that few of the extant software allow. 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 by their original creators (with selected analyses), they have not been collected and made available in this way. This curated set of models is likely to become an important resource for the ENA and systems ecology community. 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. The strength of this application is the novel combination of these key features. Thus, 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,

A handwritten signature in black ink, appearing to read 'Stuart R. Borrett', with a stylized, cursive script.

Stuart R. Borrett