

A protocol for reproducible functional diversity analyses

The widespread use of species traits to infer community assembly mechanisms or to link species to ecosystem functions has led to an exponential increase in functional diversity analyses, with >10,000 papers published in 2010–2019, and >1,500 papers only in 2020. This interest is reflected in the development of a multitude of theoretical and methodological frameworks for calculating functional diversity, making it challenging to navigate the myriads of options and to report details to reproduce a trait-based analysis. Therefore, the study of functional diversity would benefit from the existence of a general guideline for standard reporting and good practices in this discipline. We devise an eight-step protocol to guide ecologists in conducting and reporting

functional diversity analyses. We do so by streamlining available terminology, concepts, and methods, with the overarching goal of increasing reproducibility, transparency and comparability across studies. The protocol is based on the following key elements: identification of a research question, a sampling scheme and a study design, assemblage of community and trait data matrices, data exploration and preprocessing, functional diversity computation, model fitting, evaluation and interpretation, and data, metadata and code provision. Throughout the protocol, we provide information on how to best select research questions and study designs, and discuss ways to ensure reproducibility in reporting results. To facilitate the implementation of this protocol, we further developed an interactive web-based application (stepFD) in the form of a checklist workflow, detailing all the steps of the protocol and providing tabular and graphical outputs that can be merged to produce a final report. The protocol streamlined here is expected to promote the description of functional diversity analyses in sufficient detail to ensure full transparency and reproducibility. A thorough reporting of functional diversity analyses ensures that ecologists can incorporate others' findings into meta-analyses, the shared data can be integrated into larger databases for consensus analyses, and available code can be reused by other researchers. All these elements are key to push forward this vibrant and fast-growing field of research.