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## Editors of F1000 Research Software Tool Articles Submission

Dear editors of F1000 Research:

We are pleased to submit our paper "ranacapa: An R package to explore environmental DNA data with exploratory statistics and interactive visualizations" for consideration as a Software Tool Article in your journal. Our paper should be of interest to your readers because it describes an R package and Shiny web app designed to to help make community-wide taxonomy data generate in environmental DNA metabarcoding studies accessible to non-technical audiences. It is a timely contribution in light of recent developments in eDNA sample collection (e.g. Thomas *et al.* (2018)) and taxonomy assignment (Arulandhu *et al.* 2017) techniques, as well as advances in public outreach programs that rely on eDNA metabarcoding to describe and monitor biodiversity.

A growing number of education, biodiversity monitoring, and public outreach programs are using environmental DNA (eDNA) metabarcoding as a platform to engage community partners in primary research. Although it is relatively easy to train non-experts to collect samples in the field, it is difficult to train these partners to interact with other elements of eDNA research, which require considerably bioinformatics skills. This difficulty for community partners to fully engage with the raw results from these studies threatens the long-term value of eDNA metabarcoding-based community science programs, whose success depends on community partners engaging in multiple parts of the research process, including data visualization and analyses (Pandya 2012).

Our R package ranacapa addresses this challenge by enabling users to easily visualize and perform simle community ecology analyses with results from eDNA metabarcoding projects. At the core of our package is a Shiny web app, available online at <a href="https://gauravsk.shinypps.io/ranacapa">https://gauravsk.shinypps.io/ranacapa</a>. ranacapa is designed to work with output files in the BIOM format or the files generated from the Anacapa sequence analysis toolkit, which is being used by the CALeDNA community science project (<a href="https://www.ucedna.com/">http://www.ucedna.com/</a>).

For reviewers, we suggest Dr. Lucie Zinger (CNRS, France), Dr. Holly Bik (Univ. of California-Riverside), and Dr. Jimmy O'Donnell (NOAA).

We confirm that all authors agree to the submission of this article, that this is a novel article, and that it is not currently submitted elsewhere for publication (or already published elsewhere).

Many thanks for your time.

Sincerely,

Gaurav Kandlikar

On behalf of my coauthors: Zachary Gold, Madeline Cowen, Rachel Meyer, Amanda Freise, Nathan Kraft, Jordan Moberg-Parker, Joshua Sprague, David Kushner, and Emily Curd

## References

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