ranacapa: An R package to explore environmental DNA data with exploratory statistics and interactive visualizations

Gaurav S. Kandlikar (1,+), Zachary J. Gold (1), Madeline C. Cowen (1), Rachel S. Meyer (1), Amanda C. Freise (2), Nathan J.B. Kraft (1), Jordan Moberg-Parker (2), Joshua Sprague (3), David Kushner (3), and Emily E. Curd (1)

### Affiliations and Contact Information

1. Department of Ecology and Evolutionary Biology, University of California – Los Angeles
2. Department of Microbiology and Molecular Genetics, University of California – Los Angeles
3. National Park Service

(+) Corresponding Author

* Email: [gkandlikar@ucla.edu](mailto:gkandlikar@ucla.edu)
* Phone: (+1) 952-288-7351
* Mailing Address: Dept. of Ecology & Evolutionary Biology, 621 Charles E. Young Drive S., Los Angeles, CA 90095

**Keywords**: environmental DNA; data visualization; citizen science; community science; shiny; metabarcoding; education; community ecology

## Abstract

Environmental DNA (eDNA) metabarcoding is becoming a core tool in biodiversity monitoring and conservation, and is a promising way to go beyond species inventory to systems-level analyses of community ecological dynamics. Results from eDNA analyses can inform and inspire research scientists, natural resource managers, students, community scientists, and naturalists; however, there is a dearth of easily accessible data exploration tools for this diverse audience. Here we present the R package ranacapa, at the core of which is a Shiny web-app that helps perform exploratory biodiversity analyses and visualizations of eDNA results. The web-app accepts multiple formats of taxonomy tables, and requires a simple metadata file with descriptive information about each sample. The app allows users to explore the data with interactive figures for instant community ecology analysis. We demonstrate the usability of ranacapa by multiple user groups, including the National Park Service, a public community science program, and an undergraduate microbiology course.

## Introduction

The targeted amplification and sequencing of DNA that living organisms shed into the physical environment they occupy (termed “environmental DNA metabarcoding”, or “eDNA sequencing”) is revolutionizing microbiology, ecology, and conservation research. (Taberlet *et al.* 2012; Deiner *et al.* 2017). Sequencing of environmental DNA extracted from field-collected soil, water, or sediment samples holds great promise to shed light on a range of questions, ranging from tracking the dynamics of bacterial communities or profiling the composition of ancient plant and animal communities (Pedersen *et al.* 2014; Props *et al.* 2016), to motoring populations of rare or endangered species (Balasingham *et al.* 2017). As the cost of eDNA sequencing declines and sample collection techniques become more streamlined (e.g. Thomas *et al.* (2018)), professional research scientists are increasingly using eDNA sequencing as a platform to partner with members of the community, such as natural resource managers, undergraduate students, and citizen scientists (collectively referred to in this manuscript as “community scientists”), in primary research. However, developing robust and impactful community science programs that engage community partners in all steps of the research process remains a challenge.

eDNA sequencing-based projects work well for community science partnerships because non-experts can be quickly trained to collect samples in the field, and because eDNA sequencing is an exciting framework for research pertinent to disciplines such as medicine, agriculture, ecology, and geography (Deiner *et al.* 2017). Community partners in such programs can have heterogeneous backgrounds, ranging from curious members of the public for whom collecting samples in the field is the first scientific research experience (e.g. University of California’s CALeDNA program, <http://www.ucedna.com/>), to professional natural resource managers who regularly collaborate with research scientists (e.g. Center for Ocean Solutions’ eDNA project, <https://oceansolutions.stanford.edu/project-environmental-dna>). In these partnerships (as in any other), community participants should be able to participate across multiple stages of the project, not only in sample collection (Pandya 2012; European Citizen Science Association 2015). This can be a challenge for eDNA sequencing-based community science programs because although it is relatively easy to train community partners to collect eDNA samples, it is far more challenging to train them to interact with and visualize the results from these studies: learning the bioinformatic tools necessary for visualizing and analyzing the large, multidimensional datasets generated in eDNA sequencing studies can be difficult for professional researchers (Carey & Papin 2018), let alone for the diverse community partners of community science programs.

To address this challenge, we created an R package “ranacapa”, at the core of which is a Shiny webapp with which users can visualize and perform simple community ecology analyses on results from eDNA sequencing studies. ranacapa complements existing visualization platforms (e.g. Phinch, Phyloseq-Shiny, QIIME2 Viewer), because in addition to interactive visualizations, ranacapa includes brief explanations and links to additional educational resources to provide users with an overview of basic data analyses used in eDNA studies. ranacapa works with community matrices generated via QIIME () and stored as BIOM tables or with community matrices generated with the Anacapa sequence analysis pipeline (<https://github.com/limey-bean/Anacapa>), which is used extensively by the CALeDNA program. In the remainder of this manuscript, we describe ranacapa and demonstrate its use by two community science partnerships based at the University of California, Los Angeles (UCLA): first, a collaboration between eDNA researchers and resource managers at the National Park Service, and second, a partnership between community ecology researchers and an undergraduate microbiology course at UCLA. As we show in the Use Cases, empowering community partners to interact with the data and perform simple but insightful community ecology analyses can help make these collaborations more enriching and valuable to both parties.

## Implementation

ranacapa consists of a Shiny webapp (Chang *et al.* (2018)) and two categories of helper functions (Table 1). The first set of functions works to connect the taxonomy tables, generated either by the Anacapa eDNA sequence analysis pipeline (<https://github.com/limey-bean/Anacapa>; Curd et al. in prep) or QIIME (Caporaso 2010), into phyloseq objects that can be used for downstream visualizations and analyses. The second set of functions, which includes two externally written functions openly available on GitHub, extends the visualization and statistical functionality of the phyloseq (McMurdie & Holmes 2013) and vegan (Oksanen *et al.* (2018)) packages.

The Shiny app (<http://gauravsk.shinyapps.io/ranacapa> or rancapa::runRanacapaApp()) allows users to interact with eDNA results through statistical summaries and interactive plots, displayed in the following tabs:

* **Sample rarefying**: This tab explains the basic logic behind rarefying samples in metagenomics studies, and allows users to choose the sampling depth (Figure 1). Users can control the number of times the samples are rarified. The documentation on this tab also acknowledges recent disagreement regarding the value of rarefying in metabarcoding and eDNA sequencing studies (McMurdie & Holmes (2014)), and allows users to proceed through the rest of the app without rarefying samples.

#### Figure 1

## PhantomJS not found. You can install it with webshot::install\_phantomjs(). If it is installed, please make sure the phantomjs executable can be found via the PATH variable.

Figure 1: Taxon accumulation curve as shown in the first tab of ranacapa.

* **Taxonomy heatmap**: This tab shows the taxonomy-by-sample matrix as an interactive heatmap made using heatmaply::heatmaply(), where the color represent the number of times a given taxon was sequenced in a sample (Figure 2).

#### Figure 2

Figure 2: Taxonomy heatmap as shown in the ranacapa Shiny app. Taxonomy is shown at the Order level in this figure; in the app, users can choose the taxonomic level to show in the heatmap.

* **Taxonomy barplot**: This tab shows the taxonomy-by-sample matrix as an interactive barplot (Figure 3).

#### Figure 3

Figure 3: Taxonomy barplot as shown in the ranacapa Shiny app. Taxonomy is shown at the Order level in this figure; in the app, users can choose the taxonomic level to show in the barplot

* **Alpha diversity plots**: This tab introduces the concept of Alpha diversity and that diversity can be calculated using a variety of metrics. Users can plot Alpha diversity as observed taxon richness or as Shannon Diversity per sample (or in samples grouped according to a variable in the metadata file, Figure 4).

#### Figure 4

Figure 4: Alpha diveristy boxplots as shown in the ranacapa Shiny app. Users can select the X-axis variable using a dropdown menu in the app.

* **Alpha diversity statistics**: This tab allows users to choose a variable from the metadata, and generates an Alpha diversity ANOVA table according to the user-selected variable. The tab also shows the output from a post-hoc Tukey test.
* **Beta diversity plots**: This tab introduces the concept of Beta diversity and shows a PCoA plot differentiating each sample. Points on the PCoA plot are colored according to a user-selected metadata variable (Figure 5). The tab also shows dissimilarity among sites according in a dendrogram generated with Ward’s cluster analysis (stats::hclust(distance\_object, method = "ward.d2"), where distance\_object is made using phyloseq::distance(). For both figures, users can toggle between using Jaccard and Bray-Curtis dissimilarity.

#### Figure 5

Figure 5: PCoA ordination of the samples as shown in the ranacapa Shiny app. Users can select the grouping variable with a dropdown menu in the app.

* **Beta diversity statistics**: This tab shows results from two statistical tests of species turnover across site: first, a multivariate ANOVA (implemented with vegan::adonis()) and an associated pairwise comparison (implemented with ranacapa::pairwise\_adonis()); second, heterogeneity of variances can be assessed using vegan::betadisper().
* **More references**

## Operation

ranacapa depends on Bioconductor v 3.7, which in turn relies on R v 3.5.0. The Shiny app has been tested on Chrome and Firefox on Windows, Mac-OSX, and Ubuntu. The package can be installed using the command devtools::install\_github("gauravsk/ranacapa"), and the Shiny app is available at <http://gauravsk.shinyapps.io/ranacapa>.

### Workflow

ranacapa genereteas interactive visualizations based on two input files. The first required input is a site-by-species matrix, uploaded either as a .biom or as a .txt file. If the site-by-species matrix is uploaded as a .biom file, the file should contain taxonomy and abundance information; thus, .qza files generated by QIIME2 are not immediately suitable for ranacapa. If the site-by-species matrix is uploaded as a .txt file, the file should match the specifications of the output files from the Anacapa eDNA sequence analysis pipeline (). Specifically, each row in the .txt file must represent the taxonomic identification for one Amplicon Sequence Variant (ASV), and each column, save one, must represent the number of times that ASV appears in each sequenced sample. One column, named sum.taxonomy must contain the taxonomic identification, with taxonomic rank separated by a ;. as follows:

site\_1 site\_2 site\_3 site\_4 site\_5 site\_6 site\_7 site\_8 site\_9 sum.taxonomy   
 1 0 0 0 0 0 0 0 0 Annelida;Clitellata;Haplotaxida;Megascolecidae;Amynthas;Amynthas sze…  
 0 0 0 0 0 0 0 0 0 Nemertea;Palaeonemertea;NA;Cephalothricidae;Cephalothrix;Cephalothri…  
 0 0 0 0 0 0 0 0 0 ""   
 0 0 0 0 0 0 0 0 0 Nematoda;Chromadorea;Monhysterida;Monhysteridae;NA;Monhysteridae sp.…  
 0 1 0 0 0 0 0 0 0 NA;Oomycetes;Pythiales;Pythiaceae;Pythium;Pythium rostratifingens

The second required input is a sample metadata file uploaded as a .txt file.

s with the following specification: ranacapa also expects sample metadata to be uploaded as a tab-delimited .txt file. The ranacapa function validate\_input\_files() verifies that both the taxonomy table and the metadata files match certain structural requirements, which are documented in the function help files. The current version of ranacapa accepts both categorical and continuous metadata columns, but in the latter case, continuous values are categorized into bins.

## Use Cases

We designed ranacapa to be used by eDNA researchers to share the results from their research with community partners. Specifically, we expect that researchers with bioinformatic expertise will use best-practices to assign taxonomy to eDNA datasets using the pipeline of their choice and generate clean taxonomy and metadata files. Researchers will then use ranacapa to share results with their community partners, emphasizing the analyses or visualizations most appropriate to their use case. We document two such partnerships below that showcase how ranacapa can facilitate authentic communication between researchers and community scientists.

### Use Case 1: How ranacapa facilitated a collaboration between eDNA researchers and managers at the National Park Service

eDNA research scientists can use ranacapa to share results, especially interactive taxonomy lists, with natural resource managers. For example ranacapa was used by researchers at UCLA who partner with resource managers at the Channel Islands National Park to assess the potential for eDNA as a biodiversity monitoring tool in the Southern California Channel Islands. The goal of this ongoing collaboration is to assess whether eDNA metabarcoding studies can provide insights to supplement ongoing management efforts at the park, which are currently done with expensive and time-intensive visual surveys (Lessios (1996), Murphy & Jenkins (2010), Usseglio (2015)). Implementing streamlined eDNA-based monitoring may allow a dramatic expansion in the scope and scale of marine ecosystem assessment in the California (Edgar *et al.* (2007), Deiner *et al.* (2017)).

To begin exploring whether eDNA-based studies can supplement visual underwater surveys, resource managers at the Channel Islands National Park Service collected and filtered thirty-1L water samples for eDNA analysis at permanent monitoring sites inside and adjacent to MPAs in the park. Research scientists at UCLA performed metabarcode sequencing of the mitochondrial 12S and CO1 gene regions from these samples targeting bony fishes, elasmobranches, and invertebrate taxa. The researchers processed sequences and assigned taxonomy using the Anacapa toolkit. When taxonomy tables were ready, researchers used the ranacapa Shiny app to share results from this pilot study with National Park resource managers.

The taxonomy heatmap (Figure 3) was the most valuable vizualation to this collaboration, because it allowed the resource managers to focus on a particular set of key taxa. The heatmap showed that this pilot study detected 36 of the 70 key metazoan taxa monitored by the managers at the species level, and the remaining 34 at the genus, family, or order level. This indicates that eDNA-based studies can likely supplement ongoing management efforts and provide new insights into the spatial and temporal distributions of these key species, especially rare and difficult to observe taxa such as endangered or invasive species. The resource managers were also interested in the PCoA plot, which was used to explore whether well-known major biogeographic patterns in the Channel Islands (e.g. turnover of fish communities across gradients in sea surface temperature, ) are detected using eDNA analyses. The value of ranacapa in this scenario was to highlight the strengths and areas for concern in using eDNA to monitor diversity in the Channel Islands. Due to the potential for eDNA to help improve detection of rare species (especially endangered species or newly introduced exotics), which are difficult to observe visually, this collaboration is continuing. The data from this study are packaged as the demo dataset for the ranacapa Shiny web-app and are available online at XXX.

### Use Case 2: How ranacapa helps undergraduate environmental microbiology students pursue sophisticated microbiome analyses

Students can use ranacapa to interact with results from metabarcoding studies and to learn the basic structure of eDNA datasets. A research-based environmental microbiology course at UCLA (Shapiro *et al.* 2015) used eDNA metabarcoding approaches to study the impact of a recent local wildfire on the plant and soil microbial community. The goal of this twenty-week course was to provide students an authentic experience in basic microbiology and microbial community ecology research. The instructors helped students develop a research question, design a sampling regime to test their hypotheses, and conduct fieldwork to collect soil samples for eDNA analyses in burned and unburned natural areas. Over the first ten weeks of the course, the instructional team (which included eDNA research scientists) extracted total DNA and sequenced the ITS2 (Gu *et al.* 2013) and 16S SSU RNA (Caporaso *et al.* 2012) metabarcoding region to characterize the plant, bacterial, and archaeal communities in the student-collected soil samples. The researchers then processed the sequences and assigned taxonomy using the Anacapa toolkit.

Shortly after taxonomy tables were generated, the course instructors introduced students to eDNA data exploration and simple statistical analyses using ranacapa. A key strength of using ranacapa was that despite having no prior bioinformatics experience, students began exploring on the an online instance of Shiny app (<http://gauravsk.shinyapps.io/ranacapa>) within a single class period. Thus, using ranacapa allowed the instructors to focus their time with the students on biological questions rather than on troubleshooting bioinformatics problems, as had been the case in previous sessions of the course. The course instructors noted that this basic exploration in ranacapa, which was not part of the curriculum in previous iterations of the course, had several positive impacts on students and their research projects. First, ranacapa helped students explore the basic structure of the dataset and begin to understand the relationships between community profile and the various metadata they had collected in the field. Second, ranacapa opened the door to basic diversity analyses– for example, students could easily test their hypotheses regarding the taxonomic diversity of microbes in burned and unburned soils. Third, by significantly reducing the time and difficulty in visualizing soil microbial diversity patterns, ranacapa helped students develop and pursue more sophisticated analyses during the remaineder of the course using tools such as STAMP. The taxonomy tables and metadata files used in this course are available online at XXXX.

## Summary and Future Directions

Metabarcode sequencing of environmental DNA is becoming a key tool in a wide variety of ecological studies, and results from these studies are of interest to a broad audience. Our R package and Shiny web-app ranacapa helps users conduct exploratory analyses and visualizations on eDNA datasets, and is a step toward making data and analyses from eDNA sequencing-based studies more accessible and understandable for a wide range of community research partners.

We propose three avenues for future work in ranacapa. First, we plan to use ranacapa as the primary tool to present eDNA results from hundreds of samples sequenced by the CALeDNA community science program. The positive experience with reserve managers suggests open forums to discuss ranacapa output will be fruitful to strengthen the feedback loop between community partners and researchers. Second, ranacapa will be a key tool in the upcoming undergraduate curriculum module “Pipeline for Undergraduate Microbiome Analysis”, which is being built as a complete suite of analysis and data visualization tools which will be made openly available to undergraduate researchers. Finally, in the long-term, we believe that there is great promise in connecting ranacapa to packages that connect with APIs of online biodiversity databases (e.g. Taxize, rinat). This will help users explore a much wider range of biodiversity questions, for example, by programmatically asking whether their samples include invasive species that are absent from other nearby sites. Such apps that allow non-technical audiences to easily interact with results from eDNA sequencing studies have great potential to engage community partners with a wide range of backgrounds and interests in primary research.

## Software availability

* A Shiny web-app, including a dataset generated for demonstrations, is available at <https://gauravsk.shinyapps.io/ranacapa>
* ranacapa is available for installation at <https://github.com/gauravsk/ranacapa>
* Link to source code as at time of publication (F1000Research TO GENERATE)
* Link to archived source code as at time of publication (F1000Research TO GENERATE)
* Software license (GPL-3)
* Data availability
* Figshare: [DOI]
* License: CC-BY 4.0

## Author contributions

GSK led the development of ranacapa, with help from MCC. ZJG and EEC provided feedback regarding which analyses and visualization options to include. ZJG performed the MPA eDNA study in collaboration with JS and DK. NK, GSK, EC, and RM collaborated with AF and JMP, who used ranacapa in their microbiology undergraduate course. GSK wrote the first draft of this manuscript; all authors contributed to revisions.

## Competing interests

No competing interests were disclosed

## Grant information

GSK and ZJG were supported by the US-NSF Graduate Research Fellowship (DEG No. 1650604) during the development of this package. EEC is supported by the CALeDNA program, with funds from University of California President’s Research Catalyst Award (CA-16-376437).

## Acknowledgments

We thank Sabrina Shirazi, Rachel Turba, Chris Dao, and Keith Mitchell for providing feedback on developmental versions of this package. Ranacapa builds on numerous functions that have been made openly available online with a GPL-3 License, namely the “phyloseq-extended” toolkit written by Mahendra Mariadassau (<https://github.com/mahendra-mariadassou/phyloseq-extended>) and “pairwise.adonis” written by Pedro Martinez Arbizu (<https://github.com/pmartinezarbizu/pairwiseAdonis>).

## References

Balasingham, K.D., Walter, R.P., Mandrak, N.E. & Heath, D.D. (2017). Environmental DNA detection of rare and invasive fish species in two great lakes tributaries. *Molecular Ecology*, 27, 112–127.

Caporaso, J.G., Lauber, C.L., Walters, W.A., Berg-Lyons, D., Huntley, J. & Fierer, N. *et al.* (2012). Ultra-high-throughput microbial community analysis on the illumina HiSeq and MiSeq platforms. *The ISME Journal*, 6, 1621–1624.

Chang, W., Cheng, J., Allaire, J., Xie, Y. & McPherson, J. (2018). *Shiny: Web application framework for r*.

Deiner, K., Bik, H.M., Mächler, E., Seymour, M., Lacoursière-Roussel, A. & Altermatt, F. *et al.* (2017). Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. *Molecular Ecology*, 26, 5872–5895.

Edgar, G.J., Russ, G.R. & Babcock, R.C. (2007). Marine protected areas. In: *Marine ecology* (eds. Connell, S. & Gillanders, B.). Oxford University Press, pp. 534–565.

European Citizen Science Association. (2015). Ten principles of citizen science. [*https://ecsa.citizen-science.net/sites/default/files/ecsa\_ten\_principles\_of\_citizen\_science.pdf*](https://ecsa.citizen-science.net/sites/default/files/ecsa_ten_principles_of_citizen_science.pdf).

Gu, W., Song, J., Cao, Y., Sun, Q., Yao, H. & Wu, Q. *et al.* (2013). Application of the ITS2 region for barcoding medicinal plants of selaginellaceae in pteridophyta. *PLoS ONE*, 8, e67818.

Lessios, H.A. (1996). METHODS for quantifying abundance of marine organisms. In: *Methods and techniques of underwater research* (eds. Lang, M. & Baldwin, C.). American Academy of Underwater Sciences (AAUS), pp. 149–157.

McMurdie, P.J. & Holmes, S. (2013). Phyloseq: An r package for reproducible interactive analysis and graphics of microbiome census data. *PLoS ONE*, 8, e61217.

McMurdie, P.J. & Holmes, S. (2014). Waste not, want not: Why rarefying microbiome data is inadmissible. *PLoS Computational Biology*, 10, e1003531.

Murphy, H.M. & Jenkins, G.P. (2010). Observational methods used in marine spatial monitoring of fishes and associated habitats: A review. *Marine and Freshwater Research*, 61, 236.

Oksanen, J., Blanchet, F.G., Friendly, M., Kindt, R., Legendre, P. & McGlinn, D. *et al.* (2018). *Vegan: Community ecology package*.

Pandya, R.E. (2012). A framework for engaging diverse communities in citizen science in the US. *Frontiers in Ecology and the Environment*, 10, 314–317.

Pedersen, M.W., Overballe-Petersen, S., Ermini, L., Sarkissian, C.D., Haile, J. & Hellstrom, M. *et al.* (2014). Ancient and modern environmental DNA. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 370, 20130383.

Props, R., Kerckhof, F.-M., Rubbens, P., Vrieze, J.D., Sanabria, E.H. & Waegeman, W. *et al.* (2016). Absolute quantification of microbial taxon abundances. *The ISME Journal*, 11, 584–587.

Shapiro, C., Toma, S., Roth-Johnson, E.A., Hancock, S.P., Ayon, C. & Zimmerman, H. *et al.* (2015). Comparing the impact of course-based and apprentice-based research experiences in a life science laboratory curriculum. *Journal of Microbiology & Biology Education*, 16, 186–197.

Taberlet, P., Coissac, E., Hajibabaei, M. & Riesberg, L.H. (2012). Environmental DNA. *Molecular Ecology*, 21, 1789–1793.

Thomas, A.C., Howard, J., Nguyen, P.L., Seimon, T.A. & Goldberg, C.S. (2018). ANDe : A fully integrated environmental DNA sampling system. *Methods in Ecology and Evolution*, 9, 1379–1385.

Usseglio, P. (2015). Quantifying reef fishes: Bias in observational approaches. In: *Ecology of fishes on coral reefs* (ed. Mora, C.). Cambridge University Press, pp. 270–273.