Ecological Modelling 493 (2024) 110750

Contents lists available at ScienceDirect

Ecological Modelling

journal homepage: www.elsevier.com/locate/ecolmodel

Short communication

# neonPlantEcology: An R package for preparing NEON plant data for use in ecological research

Adam L. Mahood [a,b,c,*], Ranjan Muthukrishnan [d], Jacob A. Macdonald [a], David T. Barnett [e], Eric R. Sokol [e], Samuel M. Simkin [e]

[a] Water Management & Systems Research Unit, USDA-Agricultural Research Service, Fort Collins, Colorado, USA
[b] Earth Lab, University of Colorado Boulder, Boulder, Colorado, USA
[c] Geography, University of Colorado Boulder, Boulder, Colorado, USA
[d] Boston University Department of Biology, Boston, Massachusetts, USA
[e] National Ecological Observatory Network, Battelle, Boulder, Colorado, USA

ARTICLE INFO

*Keywords:*
National ecological observatory network
Neon
Plant Data
Plant Ecology
R package

ABSTRACT

The National Ecological Observatory Network (NEON) is a continental-scale endeavor of ecological data collection for 30 years. We created a software package, *neonPlantEcology* that automatically arranges the raw data from the plant presence and percent cover (DP1.10058.001) data product from NEON into tables familiar to plant ecologists. Because of the broad scale of the observatory, it is necessary to tailor the data collection to the idiosyncrasies of each of 47 different ecosystems. Furthermore, data collection practices are occasionally modified for various reasons. These complexities, along with the volume and multiscalar nature of the data, need to be understood and accounted for in order to correctly process the data. This is particularly true for the plant diversity data product. We present three case studies using the package, centered around the three primary functions of *neonPlantEcology*. By automating the process of preparing NEON's plant diversity data, *neonPlantEcology* makes it more accessible to a wide range of users.

## 1. Introduction

In most terrestrial ecosystems, plants provide both the energetic foundation and the physical structure for ecological communities. Plants also lie at the interface between biogeochemical fluxes in the soil and in the atmosphere. Plant communities can be thought of as an expression of these fluxes, and thus tracking changes in those communities is critically important in the understanding of ecosystem dynamics. But collecting plant community data is time-consuming, requires deep local expertise, and often must be done at particular times of the year. These challenges make sampling at broad scales difficult. There are collections of plot data from disparate sources (e.g. vegBank (Peet et al., 2012)), but these are often collected by different protocols, which are vulnerable to different types of observer error, making data harmonization an exercise in caution. The need for broad-scale, consistently collected data was one of the reasons for the formation of The National Ecological Observatory Network (NEON) (Keller et al., 2008). NEON began collecting data on a myriad of ecosystem components using consistent protocols and observers at a handful of sites in 2014, eventually coming into full operation at 47 terrestrial sites across the United States in 2019. NEON data have great potential for use in plant ecology studies (Gill et al., 2021; Muthukrishnan et al., 2022), and are just now reaching a point in their lifespan where they have the potential to reveal groundbreaking insights, particularly when joined to an unprecedented array of in situ and remotely-sensed ancillary data collected at each NEON site (Meier et al., 2023). NEON technicians collect plant presence, cover and height annually or sub-annually around peak productivity, in a multiscalar framework (Barnett et al., 2019; NEON, 2023). The nuance in the timing and frequency of data collection, combined with the standardization across sites is the main strength of NEON data products, but if these details are not understood and accounted for it can lead to errors in data preparation and interpretation.

The full set of NEON sites represent the breadth of natural systems that exist across the United States, but because these sites can have vastly different ecological circumstances, there is no one size fits all solution for collecting data. NEON divides the US into 20 domains, and each domain has one to three terrestrial sites where sampling is conducted, for a total of 47 terrestrial sites (Keller et al., 2008). Sampling

* Corresponding author.
*E-mail address:* admahood@gmail.com (A.L. Mahood).

https://doi.org/10.1016/j.ecolmodel.2024.110750
Received 13 January 2024; Received in revised form 16 April 2024; Accepted 3 May 2024
Available online 30 May 2024
0304-3800/Published by Elsevier B.V.

**Table 1**
Functions in neonPlantEcology.

| Name: npe_<**name**> | purpose | input | output |
|---|---|---|---|
| 1. download | Download data | Site abbreviation(s) | List object of raw data |
| 2. site_info | Get site metadata | No input | Shapefile of site coordinates with metadata |
| 3. longform | Turn raw data into longform cover data frame | Raw diversity data (1) | Longform data frame with each row as a cover value for each species at each subplot or plot |
| 4. community_matrix | Create community matrix from raw data | Raw diversity data (1) | Data frame with each row as a site, each column as a species, and each cell value is either cover or occurrence |
| 5. summary | Summary diversity info at a chosen scale | Raw diversity data (1) | Summary diversity data |
| 6. plot_centroids | Get plot centroids | Output from 3–5 | Data frame of plot centroids |
| 7. cm_metadata | Get metadata from community matrix | Community matrix from (4) | Data frame with rownames from 2, translated to metadata for each plot |
| 8. change_native_status | Post-hoc change native status | Longform output (3) | Altered longform output |
| 10. groundcover | Get ground cover estimates | Raw Diversity Data (1) | Ground cover for each species at each spatial unit in a longform data frame |
| 11. heights | Get height estimates | RawDiversity Data (1) | Height for each species at each spatial unit in a longform data frame |
| 12. site_ids | Get 4-letter site codes | none | Vector of 4-letter site codes |
| 13. eventID_fixer | Internal function to fix errors in the eventID column | | |
| 14. update_subplots | Internal function to update subplot names to the version in the 2024 release | | |

**Table 2**
NEON's broader R package ecosystem.

| Package Name | Description | Source |
|---|---|---|
| neonUtilities | Access NEON data | CRAN |
| ecocomDP* | Access and work with NEON and LTER biodiversity data in an analysis-ready, standardized format | CRAN (O'Brien et al., 2021) |
| neonstore | Access, store and organize NEON data files | CRAN |
| neonOS | Tools for wrangling NEON observational data products, including checking for duplicate records and joining tables | CRAN |
| geoNEON | Access geolocation data from the NEON API | https://github.com/NEONScience/NEON-geolocation/geoNEON |
| neonPlants | Formats plant data into an presence/absence table | https://github.com/NEONScience/neonPlants |

* At the time of this writing ecocomDP does not have full functionality for the Plant Presence and Percent Cover product.

designs are aligned across all sites but at each site sampling approaches are adapted to reflect local considerations (Barnett et al., 2019; Thorpe et al., 2016). For example, higher latitude areas typically have their growing season peak in the mid to late summer, and so plant sampling is conducted in one bout during the peak of the growing season in order to capture peak productivity. But for hot deserts in the southwest productivity peaks in the spring and fall, and different plant species are abundant in these respective seasons. In these systems, plant sampling is conducted in two bouts corresponding to the bimodal peaks in productivity. The NEON protocols also occasionally see small changes that are implemented due to logistical challenges, and these must be accounted for as well.

Here, we present an R package called *neonPlantEcology* that facilitates the retrieval and initial processing of NEON plant diversity data. The *neonPlantEcology* package processes the raw Plant Presence and Percent Cover data product from NEON (DP1.10058.001) (NEON, 2023), retrieved using NEON's API, into structures familiar to plant ecologists that are compatible with commonly-used packages like *vegan* (Oksanen et al., 2022). *neonPlantEcology* converts the raw data into either a long data frame where each row is an observation of the cover of one plant species at one location, or a wide community matrix, where each row is a sampling location, and each column is a species, at any spatial or temporal level of aggregation. The package contains functions for obtaining height and groundcover data, as well as calculating biodiversity metrics from those same data objects (Table 1). It also has site- and plot-level geographic coordinates and polygons as included datasets. To support broad usage and easy modification, *neonPlantEcology* is coded in *tidyverse* syntax, which is easy to interpret and modify by end users in the community, and it is fast through use of a *data.table* backend via *dtplyr* (Dowle and Srinivasan, 2023; Wickham et al., 2023). The package is currently focused on plant diversity data. Planned future updates will incorporate more functionality to seamlessly integrate ancillary data including vegetation structure, herbaceous biomass, remotely-sensed products and flux tower measurements to link to the plant community data outputs.

## 2. Package description

### 2.1. Plant diversity sampling structure

The aim of *neonPlantEcology* is to function within the broader ecosystem of NEON software (Table 2) to help ecologists acquire and process NEON Plant Presence and Percent Cover data (NEON, 2023) into familiar formats for ecological analyses. There are several facets to the NEON plant diversity data to which attention needs to be paid to

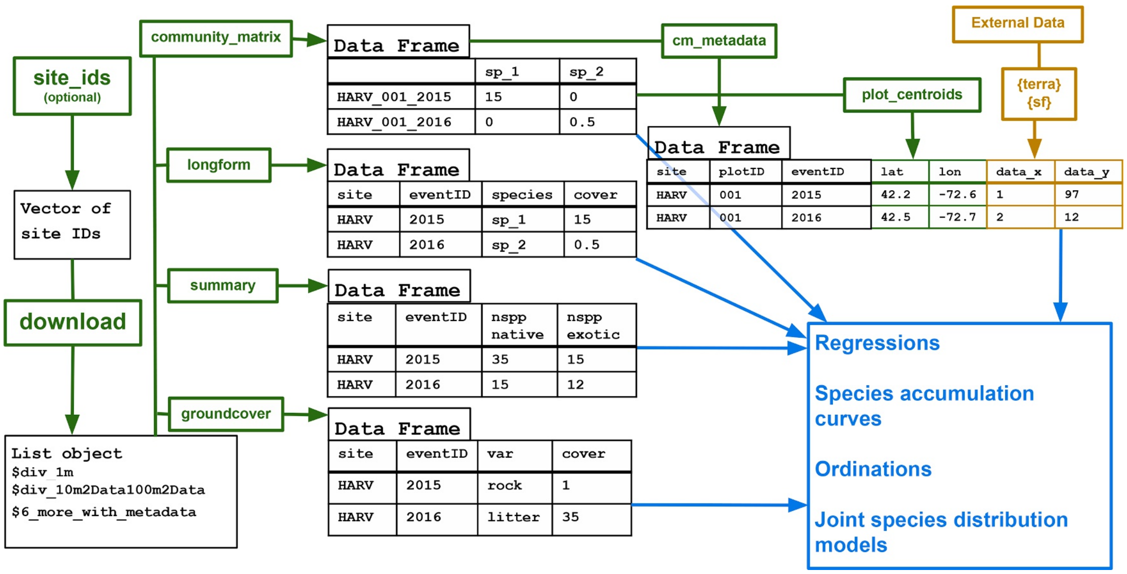


**Fig. 1.** The main functions. `**npe_site_ids**` can be used to assist in site selection. Raw data is acquired through `**npe_download**`. It is then formatted to the desired structure and spatial and temporal scales of interest via `**npe_longform**` for long format, or `**npe_community_matrix**` for wide format. Metadata can be obtained from `**npe_cm_metadata**`, which can be used in concert with `**npe_plot_centroids**` to join community data with external ancillary data. `**npe_groundcover**` extracts ancillary data collected on site, and `**npe_summary**` calculates higher-level information from the community matrix.

properly format it at different scales. First two different types of data are collected within each plot at 4 spatial scales (Barnett et al., 2019). In each 400m$^2$ (20 m x 20 m) plot, technicians estimate percent cover and height for all species within 6–8, 1m$^2$ subplots. Then, they record the occurrence of all species that did not occur in the 1m$^2$ subplots in 10m$^2$ (3.16 m x 3.16 m) subplots that surround each 1m$^2$ subplot. Occurrence is recorded again in two 100m$^2$ (10 m x 10 m) subplots, each of which surrounds one of the 10m2 subplots.

The raw data are packaged as a list containing one data frame for cover and heights recorded in the 1m$^2$ subplots, and one data frame with occurrences recorded in the 10m$^2$ and 100m$^2$ subplots. After 2019, the two central 1m$^2$ and 10m$^2$ subplots were excluded from sampling to minimize trampling at the plot centroid. Within a given year, the data are collected in bouts. Most sites have only one bout, but some have multiple bouts to account for multiple peaks in greenness, which may correspond to different species being active and abundant. The site, bout and year are recorded in the data in the "eventID" column in the raw data. *neonPlantEcology* allows the user to select a temporal resolution of subannual, annual or the whole time series, and this will be reflected in the eventID column. Subannual preserves bout-level information, and the eventID column will be formatted "site.bout.year". Annual uses the maximum cover if a species is observed in the same subplot in both bouts, and the eventID column will be the year. If the entire time series is used, the eventID will be the range of years.

### 2.2. Functions

The neonPlantEcology package is based on a set of functions that pull data from the NEON API and process it into more easily usable formats or that provide other useful data about specific NEON sites or plots, providing the components of a workflow starting at the raw data and ending with analysis-ready data (Fig. 1).

`**npe_download**` uses `**loadByProduct**` from *neonUtilities* to download any data product from the NEON API. It downloads the Plant Presence and Percent Cover product (NEON, 2023) by default. `**npe_site_ids**` creates a vector of four letter site codes based on the domain, Koppen-Geiger climate classification, or aridity index that one can feed into `**npe_download**.` There are four data sets included in the package that can be loaded with the data function. **"site_polygons"** is polygons of each terrestrial NEON site location, along with some basic metadata in the row names (site, plot number, subplot ID and event ID). **"sites"** is a data frame of all terrestrial sites with additional metadata of aridity index and Koppen-Geiger climate classifications. **"Plot_centroids"** is point locations of each individual plot for the entire network. **"D14"** is the raw Plant Presence and Percent Cover data for domain 14 (NEON, 2023), which includes the Jornada and Santa Rita Experimental Ranges.

`**npe_longform**` creates a *long* data frame where each row has one cover value for one species, and there are columns defining the plot, subplot, site, eventID and so on. This function processes two list objects from the raw data, one which contains the 1 m$^2$ cover data and one which contains 10 and 100 m$^2$ occurrence data. It aggregates to the spatial scale (1m$^2$, 10m$^2$, 100m$^2$, the whole 400m$^2$ plot, or the site) and at a temporal scale (annual, sub-annual, or the full time series) chosen by the user. If the scale is 1m$^2$, the 10 and 100 m$^2$ subplots are discarded. If the scale is greater, the 10 and 100 m$^2$ subplots are given a trace value (default is 0.05 %), then cover is calculated at the scales specified by the user.

`**npe_community_matrix**` creates a *wide* data frame, where each row is a site, plot or subplot, and each column is a species. The user can specify whether to return an abundance matrix (values 0–100) or an occurrence matrix (values 0 or 1).

`**npe_summary**` creates a longform data frame from the raw data, which it uses to calculate biodiversity and cover indices at the scales specified by the user. It returns a data frame with Shannon-Wiener diversity index (Shannon, 1948) number of species, percent cover, and relative percent cover at each site. Each index is calculated for native, exotic, unknown, native and unknowns summed (notexotic), and all species together (**Table S1**). It optionally calculates all of these metrics for families specified by the user (**see Example 3**). The user also has the option of getting the beta diversity indices of turnover and nestedness (Baselga, 2012) among the 1m$^2$ subplots for each plot, or among plots at each site.

*neonPlantEcology* has several additional functions to extract and format useful information from the Plant Presence and Percent Cover product. `**npe_cm_metadata**` extracts the metadata from the data frame created by `**npe_community_matrix**` and puts it into a data frame. `**npe_plot_centroids**` downloads the spatial coordinates for each plot. NEON technicians also estimate other ground cover variables (rock, bare ground, etc), which are obtained with `**npe_groundcover**`, and the height of each species in each 1m2 subplot, obtained with

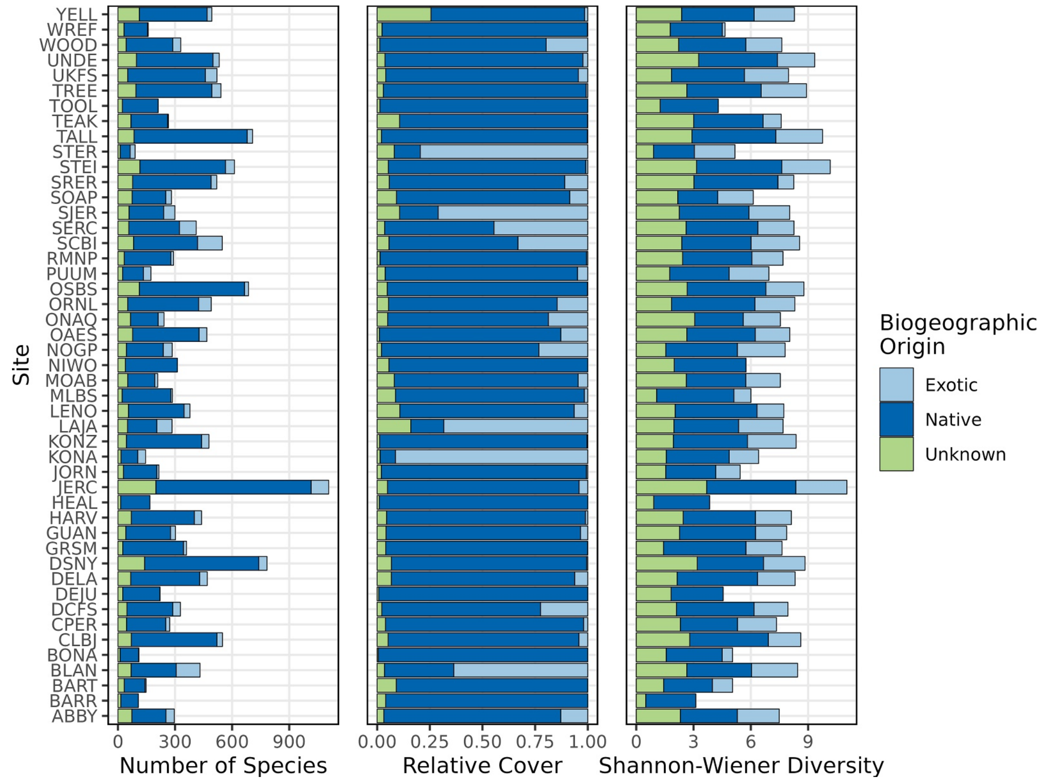


**Fig. 2.** Number of species, relative cover, and Shannon-Wiener diversity grouped by biogeographic origin for all 47 sites. Plotting code for Figs. 2-4 is in the package vignette. In order to recreate Fig. 2, downloading the data for all sites is necessary.

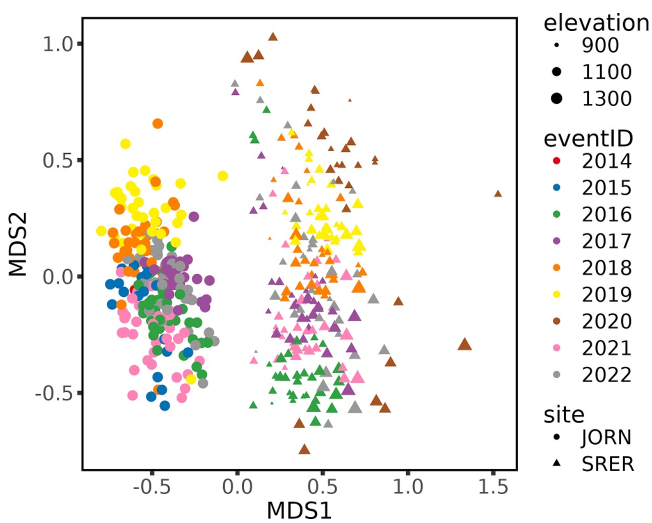


**Fig. 3.** A non-metric, multidimensional scaling analysis for the plant communities at the two sites in Domain 14, the Santa Rita Experimental Range (SRER, triangles) and the Jornada Experimental Range (JORN, circles).

**`npe_heights`**.

## 3. Package installation and examples

The package can be installed from CRAN via `install.packages("neonPlantEcology")`.

**Example 1: summary data for all sites.** For the first example, we downloaded the plant diversity data for all terrestrial sites and used **`npe_summary`** to get site-level information on species richness, relative cover, and Shannon-Wiener alpha diversity for sites, grouped by biogeographic origin (Fig. 2).

```
library(neonPlantEcology)
all_sites <- npe_site_ids(by = "all")
d <- npe_download(sites = all_sites)
di <- npe_summary(d, scale = "site", timescale = "all")
```

**Example 2: community analysis for Domain 14.** Next, we used the included Domain 14 diversity data object via **`data("D14")`**, which was fed to the **`npe_community_matrix`** function to produce a community matrix at an annual time scale and plot-level spatial scale. We then used **`npe_cm_metadata`** to get the plot ID numbers, site, and eventID for each row in the community matrix and joined that with additional plot-level metadata using the location information contained in **`data("plot_centroids")`**. Using these data we conducted a non-metric multidimensional scaling analysis (Minchin, 1987), from which we see separation in plant community composition between the two sites, within-year clustering, and a possible relationship with elevation (Fig. 3).

```
# load packages and data
data("D14"); data("plot_centroids")
library(tidyverse); library(sf); library(vegan); library
  (neonPlantEcology)

# create a community matrix from the raw data
comm <- npe_community_matrix(D14)

# get metadata from community matrix, and use that to get the plot
  info
cm_metadata <- npe_cm_metadata(comm)
metadata <- left_join(cm_metadata, st_set_geometry
  (plot_centroids, NULL))

# do an NMDS on the community matrix, format it in a tidy way, join to
  plot info
```

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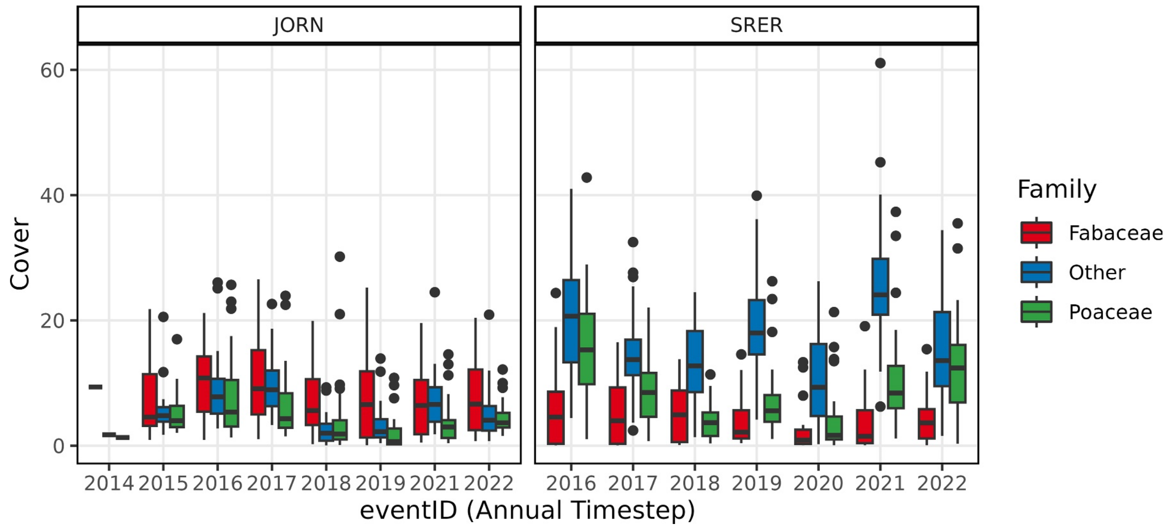


**Fig. 4.** The sum of the annual percent cover of plants in the Fabaceae, Poaceae and all other families for the Jornada Experimental Range (JORN) and the Santa Rita Experimental Range (SRER).

(*continued*)

```
nmds <- metaMDS(comm)
nmds_sites <- left_join(as_tibble(nmds$points,
  rownames = "rowname"), metadata)
```

**Example 3: cover by family through time.** For the third example we use **`npe_longform`** to collect species cover by year at the plot scale, then aggregate by two families of interest: Fabaceae and Poaceae (Fig. 4).

```
# load packages and data
data("D14"); library(tidyverse); library(neonPlantEcology)
# input data and summarize by family
lf <- npe_longform(D14, scale = "plot", timescale = "annual")
lf_f <- lf |>
mutate(family = ifelse(!family %in% c("Poaceae", "Fabaceae"),
  "Other", family)) |>
group_by(site, plotID, eventID, family) |>
summarise(cover = sum(cover, na.rm=T)) |>
ungroup()
```

## 4. Conclusion

*neonPlantEcology* complements the existing software ecosystem for working with NEON data by providing the basic service of conducting all of the steps of processing the plant diversity data from its raw form, accounting for spatial and temporal scale, sampling effort and changes in sampling design, into formats that are readable by programs and packages such as PC-ORD or R vegan which are familiar to ecologists. This is the first and only package that we are aware of that has this functionality for the Plant Presence and Percent Cover product. We aimed to create a package that contains sensible defaults at each decision point, but provides the flexibility for the end user to modify those decisions if it makes sense for their analysis. Wider adoption of this package will simplify the process of acquiring and processing of NEON data and facilitate broader usage by community ecologists, and assist and encourage researchers to conduct more cross site comparisons. Scaling up to multi-site or whole network analyses will be critical for achieving the broadest goals of NEON to understand the robustness or context dependence of ecological theory (Nagy et al., 2021; Record et al., 2021).

## CRediT authorship contribution statement

**Adam L. Mahood:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Ranjan Muthukrishnan:** Writing – review & editing, Writing – original draft, Software, Methodology, Conceptualization. **Jacob A. Macdonald:** Writing – review & editing, Writing – original draft, Visualization, Methodology. **David T. Barnett:** Writing – review & editing, Writing – original draft, Methodology. **Eric R. Sokol:** Writing – review & editing, Writing – original draft, Software, Methodology. **Samuel M. Simkin:** Writing – review & editing, Writing – original draft, Software, Methodology.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Data availability

All code and data is publicly available

## Acknowledgments

This project originated from collaborative partnerships formed at the 2019 NEON Science Summit, which was funded by NSF Award #DBI 1906144. The National Ecological Observatory Network is a program sponsored by the National Science Foundation and operated under cooperative agreement by Battelle. This material is based in part upon work supported by the National Science Foundation through the NEON Program. The authors would like to thank Courtney Meier, Simion A. Detlaff and two anonymous reviewers for constructive feedback that greatly improved the manuscript.

## Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ecolmodel.2024.110750.

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