# SEV metadata template

Comprehensive metadata are necessary to support data quality control, efficient dataset archiving and retrieval, and functional re-use of the data both by owners and secondary users. The Sevilleta LTER requires complete documentation for long-term maintenance and distribution of study datasets. Metadata elements requested in this form are consistent with elements required by the Ecological Metadata Standard (EML), which was adopted by the LTER Coordinating Committee in 2004.

Sevilleta metadata consists of information about:

1. Why the study was done
2. Who is involved with study design, data collection, analysis and data management
3. Detailed study methods, so that a secondary user will be able to understand what was done without contacting the study principal investigator.
4. Where the study was done, with GPS points so the site or plots can be relocated.
5. Detailed variable information

Tips for completing a data package (data + metadata):

* Data file and variable names should be brief, yet descriptive.
* Data file names should not contain spaces or symbols (except '\_', '-', and '.'). File names should be descriptive of the data contained in the file.
* Data files should generally be in a flat table format, similar to a SQL database table. Rows are observations, and columns are variables.
* Data files should be in a csv or other delimited text file format. Excel (e.g., .xlsx, .xls, etc.) files are not acceptable.
* Variable names should be descriptive, short, and machine readable. They should not begin with a number or symbol. They should only contain letters, numbers, and underscores ('\_'). They should not contain spaces. (e.g., 'air\_temp' or 'airTemp')
* Variable names used in the data file(s) should match the names used in this metadata document.
* Use ISO 8601 date formats. (e.g., YYYY-MM-DD)

Data should be in csv text file. If starting with an Excel spreadsheet, make sure it does not contain any formulas and comments on cells. If you need comments, put them in their own columns, such as 'field\_notes' and 'qaqc\_notes'. If data were used in a database and major table linking is necessary to analyze the data, de-normalize data into a flat files - do not just export database tables.

Please fill in this metadata form to the best of your ability and submit it to the Sevilleta Information Manager, Kristofer Hall, [khall001@unm.edu](mailto:khall001@unm.edu). If you have questions at any stage, contact the SEV IM.Allow several weeks for review and revision of your data package.

## Dataset Title

Demographic data from long-term symbiont removal experiments with grasses and *Epichloë* fungal endophytes

## Short name or nickname you use to refer to this dataset:

Indiana endo-demog

## Abstract

This project was designed to understand the demographic effects of vertically transmitted fungal endophytes (*Epichloë* spp.) on their grass hosts. The experiment includes seven host-symbiont taxonomic pairs: *Agrostis perennans - E. amarillans, Elymus villosus - E. elymi, Elymus virginicus - E. elymi or EviTG-1,* *Festuca subverticillata - E. starrii, Poa alsodes - E. alsodes, Poa sylvestris - E. PsyTG-1,* *Schedonorus arundinaceus - E. coenophiala*. Experimental plots were established at the Indiana University Lilly-Dickey Woods Research and Teaching Preserve in south-central Indiana, USA in 2007. For each species, 5-10 plots were planted with naturally symbiotic (S+) hosts, and 5-10 plots were plated with hosts that were disinfected of fungal endophytes by heat treatment (S-). Over 15 years (2007-2022) we collected demographic data on the survival, growth, reproduction, and recruitment of all plants in all plots. Beginning in 2018 we also collected data on the locations of all plants in every plot.

## Investigators

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| First Name | Middle Initial | Last Name | Organization | Role | e-mail address | ORCID ID (optional) |
| Joshua | C | Fowler | University of Miami | creator, contact | joshuacfowler1@gmail.com | 0000-0001-8956-0896 |
| Shaun | M | Ziegler | University of New Mexico | creator | shaun.ziegler@gmail.com |  |
| Tom | EX | Miller | Rice Universiy | creator, PI | tom.miller@rice.edu | 0000-0003-3208-6067 |
| Jennifer | A | Rudgers | University of New Mexico | creator, PI, contact | jrudgers@unm.edu | 0000-0001-7094-4857 |
| Kenneth | D | Whitney | University of New Mexico | creator, PI | whitneyk@unm.edu | 0000-0002-2523-5469 |

## Other personnel names and roles

Field crew, data entry, etc. Include an e-mail address, organization and preferably an ORCID ID.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| First Name | Middle Initial | Last Name | Organization | Role | e-mail address | ORCID ID (optional) |
| Mark |  | Sheehan | Rice University | creator | markcsheehan@msn.com |  |
|  |  |  |  |  |  |  |

## License

Select a license for release of your data. We have 2 recommendations: [CC0 – most accommodating of data reuse](https://creativecommons.org/publicdomain/zero/1.0/), and [CCBY – requires attribution](https://creativecommons.org/licenses/by/4.0/)

**CCO**

## Keywords

Demography; symbiosis; fungal endophyte; Lilly-Dickey Woods; population dynamics

## Funding of this work:

Add rows to table if several grants were involved, list only the main PI, start with main grant first:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| PI First Name | PI Middle Initial | PI Last Name | PI ORCID ID (optional) | Title of Grant | Funding Agency | Funding Identification Number |
| Tom | EX | Miller | 0000-0003-3208-6067 | LTREB: Host-symbiont interactions through the lens of stochastic demography | National Science Foundation | 1754468 |

## Timeframe

* Begin date: May 2007
* End date: September 2022
* Data collection ongoing

## Geographic location

* Verbal description (elevation, landform, geology, soils, hydrology, vegetation, climate, site history, etc.): Lilly-Dickey Woods is part of the Eastern broadleaf forests of southern Indiana. Plots are situated among rolling hills in the forest understory. Elevation spans 289 to 343 m.
* North bounding coordinates (decimals): 39.245723, -86.214618
* South bounding coordinates (decimals): 39.241273, -86.214610
* East bounding coordinates (decimals): 39.243131, -86.210058
* West bounding coordinates (decimals): 39.245655, -86.220144

## Taxonomic species or groups

*Agrostis perennans –* AGPE

*Elymus villosus –* ELVI

*Elymus virginicus -* ELVI3

*Festuca subverticillata -* FESU3

*Poa alsodes* – POAL3

*Poa sylvestris -* POSY

*Schedonorus arundinaceus -* SCAR7

## Methods

**Symbiont removal.** Seeds from naturally symbiotic populations of the seven focal host species were collected during summer-fall 2006 from Lilly-Dickey Woods and the nearby Bayles Road Teaching and Research Preserve (39.220167, -86.542683). To generate symbiotic (S+) and symbiont-free (S-) plants from the same genetic lineages, seeds from each species were disinfected with a heat treatment described in Table S1 or left untreated. The heat treatment created symbiont-free plants by warming seeds to temperatures at which the fungus becomes inviable but the host seeds can still germinate. Both heat-treated and untreated seeds were surface sterilized with bleach to remove epiphyllous microbes, cold stratified for up to 4 weeks, then germinated in a growth chamber before transfer to the greenhouse at Indiana University where they grew for ~8 weeks. We confirmed endophyte status by staining thin sections of inner leaf sheath with aniline blue and examining tissue for fungal hyphae at 200X magnification. We established experimental populations with vegetative propagation of clones of similar sizes. By starting the experiment with plants of similar sizes and the same number of unique genotypes, we aimed to limit any potential effects of heat treatments on initial plant growth.

**Field population establishment.** During the fall of 2007 and spring of 2008, we established ten 3x3 m plots for *A. perennans*, *E. villosus*, *E. virginicus*, *F. subverticillata*, and *S*. *arundinaceus* and 18 plots for *P. alsodes* and *P. sylvestris*. Half of the plots were randomly assigned to be planted with either symbiotic or with symbiont-free plants, and initiated with 20 evenly spaced individuals, planted at equal spacing, and labeled with aluminum tags. In spring 2008, we placed plastic deer net fencing around each plot to limit deer herbivory and disturbance; damaged fences were regularly replaced.

**Demographic data collection.** Each summer starting in 2008 through 2022, we censused all individuals in each plot for survival, growth and reproduction, adding new recruits to the census. We censused each species during its peak fruiting stage (May: *P. alsodes*, *P. sylvestris*; June: *F. subverticillata*; July: *E. villosus*, *E. virginicus*, *S*. *arundinaceus*; September: *A. perennans*), such that the censuses were pre-breeding and new recruits came from the previous years' seed production. Leaf litter was cleared out of each plot prior to the census, to aid in locating seedlings. For each plant remaining from the previous year, we determined survival, measured its size as a count of tillers, and collected reproductive data as counts of reproductive tillers and seed-bearing spikelets on all reproductive tillers to a maximum of three. We also tagged all unmarked individuals that were recruits from the previous years' seed production and collected the same demographic data. New recruits typically had one tiller and were non-reproductive. In 2008 and 2009, we took additional counts of seeds per inflorescence for all reproducing individuals in the plots to ground-truth our sub-sample estimates. In 2018, we stopped collecting data for the *S*. *arundinaceus* plots, which had very high survival and low recruitment, and consequently very low variation across years. Beginning in 2018, we used a laser measuring device to measure the distances of every plant to two plot corner posts, labeled “A” and “B”. With these pairs of distances and distances between posts A and B provided in a supplemental data fie, x/y coordinates can be derived using Pythagorean algebra.

**Population re-establishment.** In 2021 and 2022, because plot numbers had strongly declined, we planted new greenhouse-reared from the same source population and endophyte status as the 2007 founders. We planted 6-10 plants in all plots of *P. alsodes*, *P. sylvestris*, *F. subverticillata*, *E. villosus,* and *A. perennans*.

## Data Table

**Table file name:** LDW\_LTREB\_20072022.csv

**Table description:** Long-term demographic data from symbiont-removal experiment. Each row represents one transition year of one individual (from the census in year t to the census in year t+1). Individuals that survive one or more years occur in multiple rows.

Add rows as needed. Use a separate table for each data file in your data package.

|  |  |  |  |
| --- | --- | --- | --- |
| Column name | Description | Unit or  code explanation or date format | Empty value code |
| species | Host grass species | AGPE = *A. perennans*  ELRI = *E. villosus*  ELVI = *E. virginicus*  FESU = *F.* subverticillata  LOAR = *S*. *arundinaceus* (formerly *Lolium arundinaceum*)  POAL = *P. alsodes*  POSY = *P. sylvestris* | NA |
| plot | Plot identified | Arbitrary integer | NA |
| endo\_01 | Endophyte status assigned to plot | 0 = endophyte-free (S-), 1 = endophyte-symbiotic (S+) | NA |
| id | Unique ID of focal plant. For original founders, a unique four-digit tag number. For recruit plants, a concatenation of plot number and recruit number (e.g., the first recruit observed in plot 111 has id = 111\_1) | Arbitrary integer | NA |
| origin\_01 | Whether or not the individual was greenhouse-reared and planted by the investigators or recruited into the population | 0 = greenhouse-reared “original” plants (2007 founders plus 2021-22 additions), 1 = natural recruit | NA |
| dist\_a | Distance to post A | meters | NA |
| dist\_b | Distance to post B | meters | NA |
| birth | Year in which the plant recruited into the population; NA when birth year is unknown | Year (YYYY) | NA |
| endo\_status\_from\_check | Individual-level endophyte status observed during spot-checks. Values are means of one or more endophyte checks on the same individual in multiple years. | 0 = endophyte-free (S-), 1 = endophyte-symbiotic (S+), values between 0 and 1 indicate conflicting scores in re-checks. | NA |
| year\_t | Calendar year at the start of the census interval | Year (YYYY) | NA |
| size\_t | Number of tillers at the start of the census interval | Count | NA |
| flw\_count\_t | Number of flowering tillers at the start of the census interval (always less than or equal to number of tillers) | Count | NA |
| spike\_a\_t | Count of spikelets on one of three arbitrarily chosen flowering tillers at the start of the census interval | Count | NA |
| spike\_b\_t | Count of spikelets on one of three arbitrarily chosen flowering tillers at the start of the census interval | Count | NA |
| spike\_c\_t | Count of spikelets on one of three arbitrarily chosen flowering tillers at the start of the census interval | Count | NA |
| spike\_d\_t | Count of spikelets on a fourth flowering tiller at the start of the census interval (recorded infrequently) | Count | NA |
| year\_t1 | Calendar year at the end of the census interval | Year (YYYY) | NA |
| surv\_t1 | Survival status at the end of the census interval | 0 = dead, 1 = alive | NA |
| size\_t1 | Number of tillers at the end of the census interval | Count | NA |
| flw\_count\_t1 | Number of flowering tillers at the end of the census interval (always less than or equal to number of tillers) | Count | NA |
| spike\_a\_t1 | Count of spikelets on one of three arbitrarily chosen flowering tillers at the end of the census interval | Count | NA |
| spike\_b\_t1 | Count of spikelets on one of three arbitrarily chosen flowering tillers at the end of the census interval | Count | NA |
| spike\_c\_t1 | Count of spikelets on one of three arbitrarily chosen flowering tillers at the end of the census interval | Count | NA |
| spike\_d\_t1 | Count of spikelets on a fourth flowering tiller at the end of the census interval (recorded infrequently) | Count |  |

**Table file name:** LDW\_LTREB\_AB\_distance.csv

**Table description:** Data table contains the distances between posts A and B of each plot. These distances can be used with the dist\_a and dist\_b variables of LDW\_LTREB\_20072022.csv to generate x/y coordinates for each individual.

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| --- | --- | --- | --- |
| Column name | Description | Unit or  code explanation or date format | Empty value code |
| plot | Plot number, corresponding to plot numbers in the demographic data | Arbitrary integer value | NA |
| AB\_distance | Distance between corner post A and corner post B | meters | NA |
| Notes | qualitative observations regarding any difficulties measuring AB distance | NA | NA |

## Articles

List articles that cite this dataset (optional)

|  |  |  |
| --- | --- | --- |
| Article DOI or URL (DOI is preferred) | Article title | Journal title |
| https://github.com/joshuacfowler/Grass-Endophyte-Stochastic-Demography/blob/master/Manuscript/submission\_to\_PNAS/Endo\_stoch\_demo.pdf | Microbial symbionts buffer host-plants from the demographic costs of environmental stochasticity | In review |
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## Scripts/code (software)

List any software scripts/code you would like to archive along with your data. These may include processing scripts you wrote to create, clean, or analyze the data. Submit copies of the scripts as part of the data package.

|  |  |  |
| --- | --- | --- |
| File name | Description | Scripting language |
| endo\_demog\_data\_processing.R | This script cleans and harmonizes several raw data sources to produce the derived data product archived here. | R |
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## Data provenance

Were these data derived from other data? If so, document this information so data users will know where the data came from.

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| --- | --- | --- | --- |
| Dataset title | Dataset DOI or URL | Creator (name & email) | Contact (name & email) |
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## QA/QC Procedures

Data distributions and variable classes were inspected in R. Any data issues were corrected in our data processing script, providing a record of how derived data relate to raw data inputs.

## Notes and Comments