Laura Twardochleb

1/10/20

Data-paper read-me for R scripts and .csv files

**Occurrence data cleaning**

* “WQP\_occurrence\_cleaning.R” conducts initial data cleaning on biological monitoring data downloaded from the Water Quality Portal and assigns names and ranks to taxa. It requires the following files:
* macroinvertebrate\_biological.csv
* macroinvertebrate\_site.csv
* invertebrate\_biological.csv
* invertebrate\_site.csv

This script writes also writes two intermediate files: “WQP\_invertebrate\_1979\_2016\_2.csv” and “WQP\_insect\_w\_ranks.csv”. Final output is “insects2001v3.csv”.

* “State\_cleaning\_6\_26\_19.R” conducts cleaning of raw state data files. It reads all .csv files in the folder “state\_data”. The script outputs “state\_data.csv”.
* “WQP\_state\_merge\_10\_3\_19.R” conducts remaining cleaning of occurrence data. The script requires the following files:
* state\_data.csv
* insects2001v3.csv
* raw\_trait\_table.csv

The script writes “occurrence22.1.csv”, which is the final cleaned occurrence dataset with genus only records for Ch. 3 analysis paper. It also writes “ancillary\_taxonomy\_occurrence.csv” to create the ancillary taxonomy table. The script writes “occurrence22.csv”, which contains all of cleaned occurrence data, and “genus\_occurrence\_table\_edi.csv”, which contains the genus occurrence table for the data paper and hosting by EDI. Finally, it writes, “raw\_community\_table.csv”, which is the raw occurrence table for EDI.

**Trait data cleaning**

* “WQP\_insect\_2001.R” conducts initial cleaning of USEPA traits database and outputs two files, “biotraits\_11\_30\_17.csv”, which contains cleaned data from the USEPA traits database, and “biotraits8.csv”, which contains taxa not in USEPA database for which Ethan Hiltner added trait data. The script requires the following files:
  + - * insects2001v3.csv
      * freshwater\_biotraits\_transposed.csv
* “Pyne\_traits\_8\_17\_18.R” combines and harmonizes data between Matthew Pyne’s trait dataset and the USEPA traits database. It reads the Pyne data and the USEPA database that was added to by Ethan Hiltner:
* biotraits8\_6\_15\_18.csv
* Pyne2016\_genus.csv

The script writes the data marge to “biotraits\_8\_23\_18.csv”. It also writes to subsets of the trait dataset to file for Ethan Hiltner, Minali Bhatt and Erika Ralston to work from: “Hiltner\_biotraits.csv”, “Ralston\_biotraits.csv” and “Bhatt\_biotraits.csv”. Further modifications were made in the script to Bhatt and Ralston subsets of the data and output to “Ralstin\_biotraits\_11\_16\_18.csv” and “Bhatt\_biotraits\_11\_16\_18.csv”.

* “Trait\_cleaning\_12\_10\_19.R” conducts remaining data cleaning of traits database by combining all subsets of the database from Ethan Hiltner, Minali Bhatt, and Erika Ralston. It requires Bhatt, Hiltner, and Ralston .csv files, with code to read them in from Google Drive. The script outputs “biotraits\_wide2.csv”, which contains the cleaned, raw trait data.
* “Calc\_trait\_affinity\_mode.R” calculates trait affinities and modal trait values for two tables: Genus\_Trait\_Affinities (“trait\_affinities\_table.csv”) and Genus\_Traits (“trait\_mode\_table.csv”). It also produces an Ancillary\_Taxonomy\_Table (“ancillary\_taxonomy\_table\_master.csv”) and the Raw\_Traits table (“raw\_trait\_table\_EDI.csv”) formatted for EDI. It requires the following files:
* biotraits\_wide2.csv
* ancillary\_taxonomy\_occurrence.csv