# USGS metrics calculation method

A database of binary trait information was provided by \_\_\_\_\_\_. This database was merged to the WY diatom taxa list (provided by \_\_\_\_\_\_). Ambiguous taxa were excluded at this step (“undetermined pennate”, “unknown centric”, and “unknown genus”). Seven other taxa (*Halamphora*, *Kolbesia ploenensis, Kolbesia suchlandtii*, *Parlibellus , Rhoicosphenia, Rossithidium, Staurophora brantii*) were present in the dataset but did not have traits in the USGS database. These taxa were added in rows of all zeros (no trait information) to the trait database.

From the merged taxa/trait dataset, three types of metrics were calculated: trait richness (the number of taxa in each sample possessing a certain trait), proportion trait richness (the proportion of taxa in each sample possessing a certain trait), and proportion trait abundance ( the proportional abundance of of taxa in each sample possessing a trait).

The R code used to calculate the above metrics was modified for this dataset from code originally written by S. Spaulding (2020).