

Digitization reveals and remediates challenges to research on dispersed museum collections from Florissant fossil beds, Colorado

Gwen S. Antell

This document is GSA Data Repository Item 2018190, an elaboration of data sources and methods. It is available at www.geosociety.org/datarepository/2018/.

MATERIALS AND METHODS

Data Acquisition

Florissant Fossil Beds National Monument (FLFO)

FLFO is located in Florissant, CO, and the fossil collection is housed in the Visitor Center and Paleontology Lab on-site (Figure 1B). The author identified all specimens between 2016 and 2017; a total of 1940 invertebrate specimens were examined. Database records were downloaded on 14 February 2017.

Museum of Comparative Zoology (MCZ)

The MCZ is located in Cambridge, MA, and the Florissant collection is housed in the Invertebrate Paleontology collections, in the Harvard Northwest Science Building. Locality coordinates were not recorded for specimens in the MCZ collection, but the main site is indicated in archived notes and photographs. Data are the results of a query for “Florissant” in the “any general locality” search field of MCZbase (mczbase.mcz.harvard.edu) on 6 February 2017; entries were checked by hand to remove neontological specimens. Higher taxonomic classifications of MCZ type specimens were not available in MCZbase exports, and nomenclatural revisions are not updated in the MCZ museum database. Instead, the Linnaean taxonomy of MCZ specimens was inferred from the taxonomic hierarchy of the FLFO database of Florissant type specimens (planning.nps.gov/flfo). Ricardo Perez de la Fuente (MCZ) identified the non-type collections (2017, personal commun.). The databased MCZ collection included 152 insect type specimens with higher taxonomic information and 4511 fossil insects identified to taxa traditionally ranked as families, for a total of 4663 fossil insects included in analysis. An additional 2189 non-type and 10 type specimens at the MCZ had identifications with insufficient taxonomic information and were excluded.

University of Colorado Museum of Natural History (UCM)

The UCM is located in Boulder, CO, and the Florissant collection is housed in the Paleontology Division, in the Bruce Curtis Building (Museum Collections). Database records were downloaded on 21 February 2017. The database contained 1785 identified fossil invertebrates, including 127 insect type specimens and 725 non-type specimens identified to insect taxa traditionally ranked as families.

Smithsonian National Museum of Natural History (USNM)

The USNM collections belong to the Smithsonian Institution, located in Washington, D.C., and the Florissant collection is housed in the Department of Paleobiology. Florissant fossils in the USNM primarily come from the Peale Survey, 1906 Cockerell expedition, and Princeton expedition. These collections include type specimens published by Carpenter, Cockerell, Scudder, and others. The total number of plant and invertebrate fossils in these collections has been estimated at 10,000 specimens (Meyer et al., 2008). The author examined 510 specimens, the top two drawers (~30%) of the uncataloged Cockerell insect collection, in 2017.

Diversity Analysis

Diversity indices calculate diversity as the sum of weighted taxa abundances. The Shannon-Wiener index and Simpson index are given by equations 1 and 2, respectively, where S is the total number of taxa in the community and p_i is the proportional abundance of species i (Hill, 1973). The Shannon-Wiener index is more sensitive to rare species (Oksanen et al., 2017). Variations of this metric use a logarithm with a different base in place of a natural logarithm.

$$H' = -\sum_{i=1}^S p_i \ln(p_i). \quad (1)$$

$$D = 1 - \sum_{i=1}^S p_i^2. \quad (2)$$

It is a well established trend in ecology that the number of taxa observed in a sample increases with the number of individuals sampled. Rarefaction allows diversity comparisons among samples of unequal size by accounting for differences in sample size. The method subsets a sample (i.e. a ‘collection’ as used in the main text) to a given number of individuals; the mean richness over many subsamples is the estimated richness. For a more detailed discussion, including calculation of standard error, see Heck et al. (1975) and Hurlbert (1971).

Rényi diversity and evenness of order α are given by equations 3 and 4, respectively (Hill, 1973; Oksanen et al., 2017). Special cases of Rényi diversities simplify to other indices. For instance, $H_0 = \log(S)$ and $H_1 = H'$.

$$H_\alpha = \frac{1}{1-\alpha} \ln \sum_{i=1}^S p_i^\alpha. \quad (3)$$

$$E_\alpha = H_\alpha - H_0. \quad (4)$$

In assessing two samples, one with a greater α index (H_α or E_α) for all values of α is interpreted as more diverse (Tóthmérész, 1995), but no such statements can be made about profiles that intersect.

All analyses were conducted in the computing environment R, version 3.3.3 (R Core Team, 2017). Diversity metrics were calculated with the {vegan} package (Oksanen et al., 2017) and plotted with the {BiodiversityR} package (Kindt and Coe, 2005).

INTERPRETATION OF RAREFACTION CURVES

Rarefaction curves provide a visual aid to determining adequate sample size (Heck, 1975). Ideally, ecologists would collect observations to increase sample size until the slope decreases, at which point the asymptotic form of the curve is apparent. The curves representing FLFO and MCZ collections are complete enough to show approach to an asymptote, while those representing UCM and USNM collections are near an inflection point in the derivative of richness as a function of sample size. Additional identifications of UCM and USNM specimens would improve the precision of their diversity metrics; however, the results of examining the plotted curves (Figure DR1) justified the inclusion of all four collections in the diversity analysis presented in the main text (Table 2).

REFERENCES CITED

- Heck, K.L., van Belle, G., and Simberloff, D., 1975, Explicit calculation of the rarefaction diversity measurement and the determination of sufficient sample size: *Ecology*, v. 56, no. 6, p. 1459–1461.
- Hill, M.O., 1973, Diversity and evenness: A unifying notation and its consequences: *Ecology*, v. 54, no. 2, p. 427–432.
- Hurlbert, S.H., 1971, The nonconcept of species diversity: A critique and alternative parameters: *Ecology*, v. 52, no. 4, p. 577–586.
- Kindt, R., and Coe, R., 2005, *Tree diversity analysis: A manual and software for common statistical methods for ecological and biodiversity studies*: Nairobi, Kenya, World Agroforestry Centre, 196 p.
- Meyer, H.W., Wasson, M.S., and Frakes, B.J., 2008, Development of an integrated paleontological database and web site of Florissant collections, taxonomy, and publications, *in* Meyer, H.M., and Smith, D.M., eds., *Paleontology of the Upper Eocene Florissant Formation*, Colorado: Boulder, Colorado, Geological Society of America Special Paper 435, p. 159–177.
- Oksanen, J., et al., 2017, *vegan: Community ecology package*, R package version 2.4-2, <https://CRAN.R-project.org/package=vegan>.
- R Core Team, 2017, *A language and environment for statistical computing*: R Foundation for Statistical Computing, Vienna, Austria, <https://www.R-project.org/>.
- Tóthmérész, B., 1995, Comparison of different methods for diversity ordering: *Journal of Vegetation Science*, v. 6, no. 2, p. 283–290.

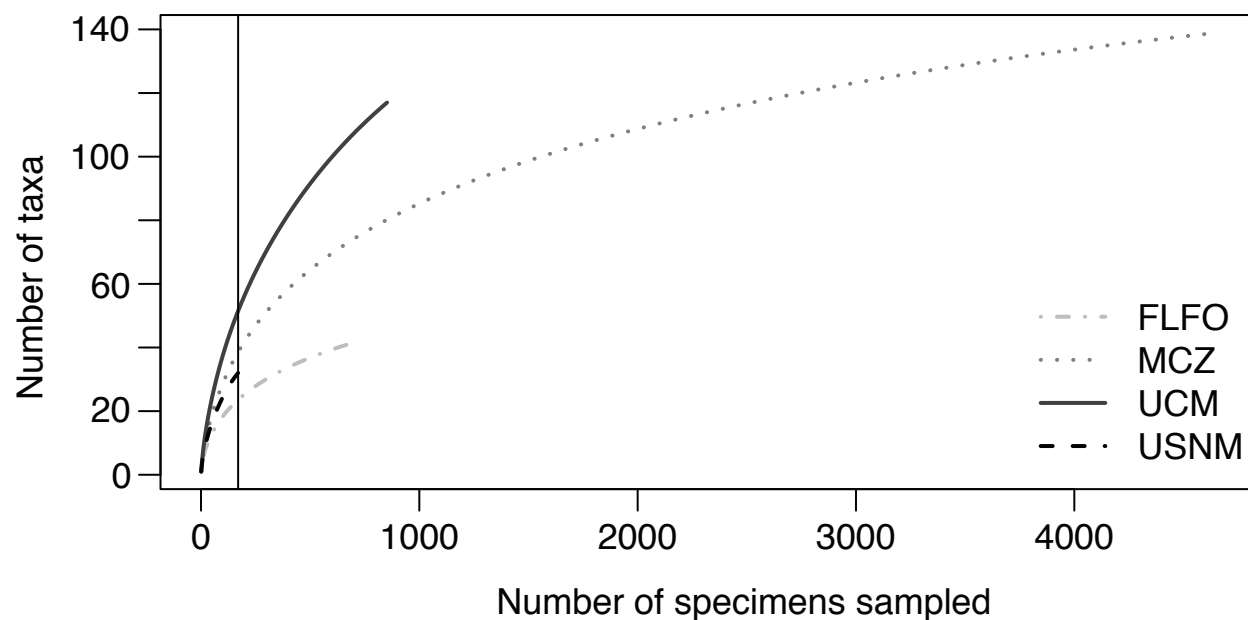


Figure DR1. Rarefaction curves show the estimated number of taxa occurring in subsamples of a given size. The vertical line at $x = 170$ represents the minimum sample size of any collection, at which rarefied taxonomic richness was calculated (Table 2, main text). Curves plot the rarefied diversity of fossil insect specimens from Florissant Fossil Beds National Monument (FLFO), Harvard Museum of Comparative Zoology (MCZ), University of Colorado Museum (UCM), and Smithsonian National Museum of Natural History collections (USNM). Specimens were identified to taxa traditionally ranked as families.