

Lab 7: The Paleobiology Database: Diversity and Extinction in the Phanerozoic (as viewed through the eyes of bivalves and brachiopods)

Due: In class on Tuesday (one typed copy per group is fine!)

A key question in paleobiology is how diversity, origination, and extinction have changed over time. Given that species are missing from the fossil record this is hard to determine directly. However, we can measure how *fossil* diversity has changed over time, in the hope that the pattern of diversity change seen in the fossil record accurately reflects the pattern of true diversity change.

We all know that bivalves are doing much better these days than brachiopods. But why? In this lab, we'll use PBDB to explore their diversity over the Phanerozoic and try to get into more of the dynamics that have led to their respective rise and fall. In addition, we'll take a look at the fact that the way that we count our fossil taxa can change our view of the diversity of life through time, so in this lab we will play around with a few different methods of data analyses to try to get at a picture of "true" biodiversity.



The scallop is watching you.

You may be asking yourself WHY DO WE KEEP DOING STUFF ABOUT BRACHIOPODS AND BIVALVES?! The answer for this week is that a) they both are around for the entire Phanerozoic and so we can compare their entire ranges b) they are similar in that they are (mostly) benthic marine invertebrates - much tougher to make comparisons between dinosaurs and brachiopods, for example, and c) you're already familiar with their morphology and paleoecology so you can actually say something about their similarities and differences!

Goals of the lab:

1. To learn how to make diversity curves using raw data.
2. To understand and appreciate that the way that we count our fossil taxa can change our view of the diversity of organisms through time.
3. To examine long term trends in extinction and origination.
4. To compare major groups of Phanerozoic marine invertebrates to get a more nuanced view of diversity and extinction dynamics.

Skills you will learn:

1. How to download diversity data from PBDB.
2. How to create diversity curves in a spreadsheet program.
3. How to analyze different ways of measuring and counting diversity.

Your Mission: Using the PBDB, analyze the differences in diversity dynamics between *Bivalvia* and *Brachiopoda* over the course of the Phanerozoic.

To Do: Describe (in graphs and a descriptive paragraph of text) each groups':

- A. overall Phanerozoic diversity
- B. response to "big 5" mass extinctions/depletions
- C. long term (Phanerozoic) trends in origination and extinction

Some graphs will cover more than one of these areas, or you can put things on the same axes, etc.

To Do: Discuss the following points:

- D. Discuss the different metrics you have for measuring diversity and defend your use of your preferred metrics in your analysis. For example, if you only used one or two diversity metrics to make the graphs you used for A-C, explain why you used the ones you did and not others (1-2 paragraphs).
- E. Explain what might be *causing* the overall changes you have observed, and *why* they are different in the two groups. You don't need to re-summarize what you wrote for A-C above. To help you with this, incorporate information we've covered in previous labs and in lectures. There's no right answer here, so use your existing knowledge and what you've done so far in lab to try to figure it out! (2-3 paragraphs, don't exceed ~500 words)

Occurrences
 Specimens / Measurements
 Geological strata
 Collections
 Diversity over time
 Taxa
 Opinions
 Bibliographic references / Taxa by ref

Comma-separated values (csv)
 Tab-separated values (tsv)
 JSON
 RIS

Simple form
 Show all available parameters

Clear form

[https://paleobiodb.org/data1.2/occs/diversity.csv?
datainfo&rowcount&base_name=Bivalvia&count=genera&time_reso=epoch&recent](https://paleobiodb.org/data1.2/occs/diversity.csv?datainfo&rowcount&base_name=Bivalvia&count=genera&time_reso=epoch&recent)

Test Download

Use one or more of the following sections to select a set of records and choose output options. If you close a section, you remove those parameters from the download URL until the section is opened again.

▼ Select by taxonomy



Taxon or taxa to include:

Bivalvia

Taxonomic resolution:

genera

▼ Select by time



Interval or Ma range:

through

Temporal resolution:

epoch Assume extant taxa range through to present

Use graphs and text to explain your analyses. See below for tips, help, etc, and ask questions! You can also use PBDB Navigator, but you must also use the raw download data as described below in your analysis.

What are boundary crossers?: For range-through data (i.e., FAD-LAD ranges) we assume that all the originations occurred before all the extinctions within an interval. That is, we have assumed that all the genera recorded in an interval co-existed at least at some point in the interval. But perhaps some of the genera had become extinct before some of the new ones had originated. So it is quite likely that, ignoring all other problems, that the standard method for estimating diversity curves *overestimates the diversity in each interval*.

To circumvent the fact that we usually don't know *when* in an interval each genus actually appeared or disappeared, Richard Bambach (then at Virginia Tech, and now at the Smithsonian) proposed that we only count taxa known to cross stratigraphic boundaries (e.g., the boundary between the Ordovician and Silurian). The reasoning is simple; all the taxa that cross a stratigraphic boundary, (i.e., are known to exist both before and after the boundary) *must have co-existed at the boundary*. Thus, using the boundary-crosser method we have point estimates of the diversity of taxa known to co-exist at each point in time (the boundaries between our stratigraphic intervals).

Step 1: Download Diversity over Time data for Bivalvia and Brachiopoda using the PBDB download interface. Set temporal resolution to **Epoch** and assume range through (see screen shot)

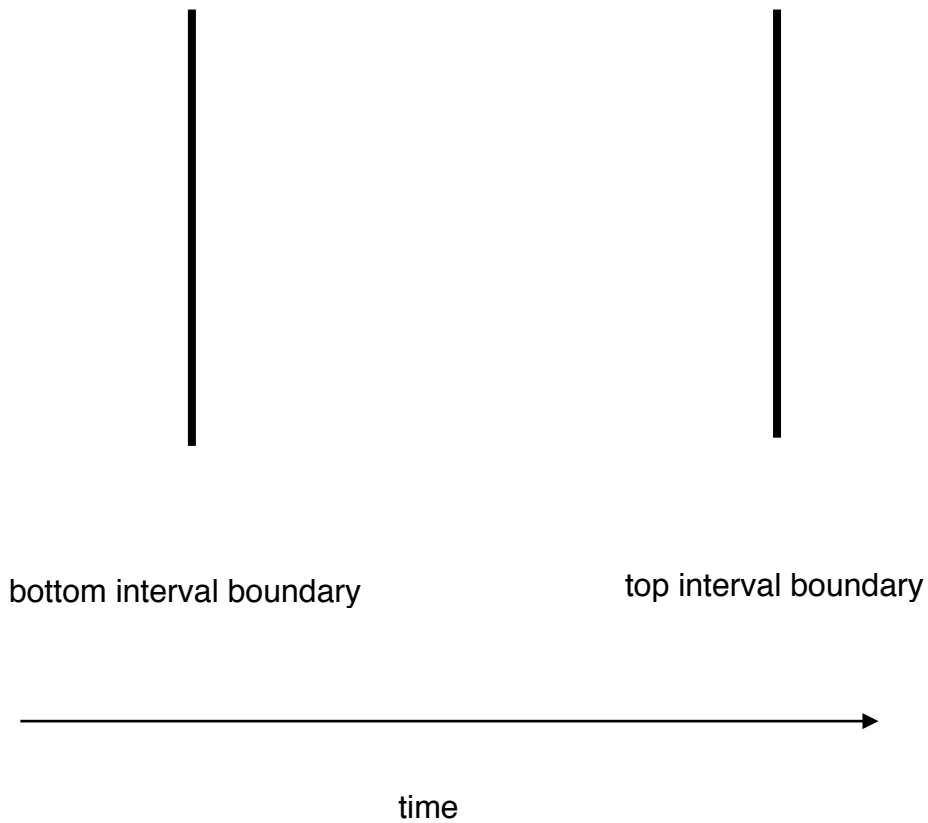
Open the file in Excel and delete the header rows in your spreadsheet. You'll now have a spreadsheet with the following columns with the following definitions:

interval_no	interval_name	max_ma	min_ma	X_Ft	X_bL	X_FL	X_bt	sampled_in_n_occ
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- Interval_no: this is just a PBDB code which you can basically ignore.
- Interval_name: the time interval - you downloaded data at the Epoch level
- max_ma: the maximum age of the time interval in millions of years
- min_ma: the minimum age of the time interval in millions of years
- X_Ft: number of taxa crossing top boundary and first appearing in interval
- X_bL: number of taxa crossing bottom boundary and last appearing in interval
- X_FL: number of taxa with first and last appearance *within* the interval
- X_bt: number of taxa crossing *both* bottom and top interval boundaries

- `sampled_in_bin`: this is the number of unique taxa sampled in each time bin
- `n_occs`: this is the number of fossil occurrences in each time bin — there may be multiple occurrences for a single taxon.

To help you understand what each of these means, draw a line that represents one taxon range for each of the following metrics: `X_Ft`, `X_bL`, `X_FL`, `X_bt`



Make the following new columns:

- Mean bin age: the mean of the max and min bin ages (i.e., the midpoint of the time interval)
- `Total_D`: the **total** taxonomic diversity within each bin. This will be the sum of some number of columns in your spreadsheet. Examine your drawing above to help you determine which ones.

- Total_D with no singletons: Total_D without taxa that are present in one bin only (you'll need to figure out which column this is! - again, consult your drawing)

More tips and suggestions:

A good way to display your data is through marked line scatter plots with the time bin midpoints as the X-axis (to get the time running in the correct direction, right / control click on your x-axis, go to format axis, and then click values in reverse order; ask me if your Excel looks different and I can help you find this).

Adding **linear trend lines** can help you see Phanerozoic-scale trends. Chart design -> add chart element -> linear trend line (ask me if your Excel looks different and I can help you find this).

Mass Extinction	Myrs
End-Ordovician	444
Devonian	360
Permo-Triassic	251
Triassic-Jurassic	199
Cretaceous-Paleogene	66