Lab 11 – Calculating Diversity Curves

Assignment 1: Learning to Build a Diversity Curve

Step 1: Obtain stratigraphic range data

2. From the “Analyze” menu choose “Analyze Taxonomic Ranges”
3. Enter a taxon name, which should be the name of a group of vertebrates whose diversity you wish to analyze. Choose “species” or “genus” to indicate what level of diversity you want to analyze. For this first exercise enter “Tyrannosauridae” and choose “genus” as the level of analysis.
4. On the next page, choose which genera you want. For this exercise leave all of them ticked.
5. On the next page choose which timescale you want to use as the basis for analysis. This step determines the fineness of scale. For example, you could choose to analyze diversity at a coarse level like Period, which would result in the total diversity for each major geological division being tabulated. For this example we will use the default scale, “Gradstein 7: Stages”, which groups the data according to the time scale recommended by the International Commission on Stratigraphy (http://www.indiana.edu/~g404/GeoTime/ISChart2009.pdf). The other options are less important, but the next steps will be less confusing if you choose “No confidence intervals” as the “Estimate” option and “first appearance” as the “Order taxa by” option.
6. The next page provides the data we need to generate a diversity curve. The figure at the top of the page shows the stages in which each genus occurs as grey squares and the inferred range of the genus in white boxes. The table at the bottom of the page reports the first and last occurrence of each genus in millions of years (or “meganna”, Ma), as well as the number of individual data points in the database for that genus. Note that some genera are well represented, but some are known from only one occurrence.

Step 2: Calculate information needed for a diversity curve.

The first step in calculating a diversity curve is to count the number of originations (“N orig”) and extinctions (“N ext”) in each time period. Some taxa are so poorly represented that they may bias diversity curves, notably “singletons”, which are taxa that occur in only one time bin (in other words, ones that appear to originate and become extinct in the same unit). Tabulate your data with and without singletons using the following table.
<table>
<thead>
<tr>
<th></th>
<th>N. orig</th>
<th>N. ext.</th>
<th>N. singletons</th>
<th>N origin (no singletons)</th>
<th>N ext (no singletons)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barremian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aptian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Albian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cenomanian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Turonian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coniacian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Santonian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Campanian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Maastrichtian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Danian</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Step 3: Calculate the diversity for each bin**

Calculate the diversity in each time unit using the following formula:

\[
 d_t = d_{t-1} - N_{ext_{t-1}} + N_{orig_t}
\]

where \( d_t \) is the standing diversity in time unit \( t \), \( d_{t-1} \) is the standing diversity during the previous time unit, \( N_{ext_{t-1}} \) is the number of extinctions in the previous time unit, and \( N_{orig_t} \) is the number of originations in time unit \( t \). It is useful to record the absolute age of the time unit for graphing (Ma = Megannum, or age of the time period).

<table>
<thead>
<tr>
<th></th>
<th>Ma</th>
<th>d (all taxa)</th>
<th>d (no singletons)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Barremian</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aptian</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Albian</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cenomanian</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Step 4: Draw the diversity curve

Plot the diversity of Tyrannosauridae with and without singletons on the following graph:

What strengths and weaknesses does this graph have for interpreting the changing diversity of tyrannosaurids?

Assignment 2: Generate a curve for a group of your choice

Repeat the steps above for a taxon of your choice. Report the following information and replicate the same tables and graphs above for your group.

Taxon: ___________________  Analyzed by species or genus? (circle one)

Total number of species or genera: __________  Time scale used: ______________
Review information for Lab Exam

The lab exam will consist of 10 stations, each with a specimen, graph, etc. and question(s) to be answered. I’ll break the class in half, each with an hour to take the exam, which means that you’ll have about 5 minutes per station if you need it. Questions will relate directly to assignments that you performed (in other words, you won’t be asked about bones or other information that was not directly relevant to an assignment).

The following is a summary of material that was covered in assignments:

**Bones and Anatomical Terms**

**Diet and dentitions**
Dental formulas, tribosphenic molar morphology, hypocones and herbivore morphology, characteristics of teeth and jaws of insectivores, carnivores, and herbivores

**Locomotion**
Limb segment ratios, Characteristics of ambulatory, scansorial/arboreal, cursorial, saltatorial, and aquatic locomotor specializations. Gear ratio, Efficiency

**Phylogenetic analysis**
Character, character state, plesiomorphy, synapomorphy, homoplasy, tree length, consistency index (CI)

**Geometric morphometrics**
Coordinates, landmarks, Procrustes, Principal Components, Morphospace, Shape model

**CT Scans**
Recognizing basic anatomical structures in scans

**Ecometrics**
Epicondylar index, ecometrics

**Diversity curves**
Diversity curve calculations