**Geos 223** **Introductory Paleontology** **Spring 2006**

# Lab 9: Paleobiology and Paleoecology

Name: _____

Section: _____

**AIMS:**

This lab will allow you to put the knowledge you have amassed over the previous few weeks to use! In Parts A and B, you will examine a range of Cretaceous fossils and be faced with the tasks of inferring aspects of the paleobiology of each organism (mode of life, behavior, feeding style, etc.) and reconstructing the paleoecology of this ancient community. In Part C of this lab you will undertake a quantitative analysis of a molluskan community to investigate the effects of time-averaging on important ecological parameters such as species richness, species abundance, and evenness. By the end of this lab you should have an understanding of how paleoecological analyses are conducted, and an appreciation of the nature of (and biases in) paleoecological data.

**INTRODUCTION:**

One of the goals of this course is to impress upon you the fundamental concept that life on Earth has evolved through time, and that the diversity of organisms around us today is the result of approximately 3.5 billion years of change. Ecosystems in the geologic past were very different to those of the modern world in terms of the types of organisms present, the relative abundance of the major groups of organisms, and the mode of life (feeding style, behavior, reproductive strategy, life cycle) of those organisms. Paleontology offers the only direct insight into such ancient communities.

One of the important tasks of paleontology, then, is to decipher not only which organisms were present in a particular environment at a particular moment in geologic time, but also how those organisms lived, fed, behaved, and interacted with each other. The investigation into how particular fossil organisms lived, fed, behaved, grew, etc., falls within the realm of paleobiology. The investigation into how ancient organisms

interacted, competed with each other, partitioned resources, etc., falls within the realm of paleoecology.

Over the past few weeks, you have been introduced to the major groups of organisms which inhabit the Earth today, and to many groups of extinct organisms which played important roles in the history of life. You have been presented with information pertaining to the anatomy, mode of life, feeding style, and behavior of those organisms. In parts A and B of this lab, you will have the opportunity to put all that knowledge to use as you conduct an investigation into the paleoecology of an ancient marine community representative of the Cretaceous Period.

## PART A: CRETACEOUS MARINE BODY FOSSILS.

The Cretaceous Period spanned an interval from 145.5 to 65.5 million years ago. It was a time of generally warm climate and sea level was relatively high, with warm, shallow, epicontinental seas covering much of North America and Europe. Although they do not receive the same headlines as the contemporaneous terrestrial biota of dinosaurs and the earliest flowering plants, the marine communities of the Cretaceous Period were stunning in their diversity and evolutionary importance. Many of the ecological communities we see around us today have their foundations rooted in the late Mesozoic, as several major clades underwent dramatic evolutionary radiations. The end of the Cretaceous was marked by a mass extinction (one of the "big five" mass extinction events in the Phanerozoic). However, although some groups were entirely wiped out by the extinction, Cenozoic ecological communities appear to be generally little changed from their Mesozoic equivalents following the post-extinction recovery interval.

Specimens A1 to A17 and the marine reptiles of A18 are typical body fossils found in marine sediments deposited during the Cretaceous Period. Carefully examine each specimen, and answer the questions pertaining to the paleobiology of the organisms.

### A1: Cretaceous fossil.

Identify the specimen as closely as you can:

_____

What features tell you this?

What was the likely mode of life of this organism?

**A2: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A3: Cretaceous fossils.**

Identify the specimens as closely as you can:

What features tell you this?

What was the mode of life of the organism which bore this structure? How did it feed?

**A4: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A5: Cretaceous fossil.**

Identify the specimen as closely as you can:

What was the mode of life of this organism? How did it feed?

**A6: Cretaceous fossils.**

Identify the specimens as closely as you can:

What features tell you this?

What was the mode of life of these organisms? How did they feed?

**A7: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A8: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism? How did it feed?

To which group does this organism show strong convergent evolution?

**A9: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A10: Cretaceous fossils.**

Identify the specimens as closely as you can:

What features tell you this?

What was the mode of life of these organisms?

**A11: Cretaceous fossil.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A12: Recent specimens, but very similar to ones found in Cretaceous sediments.**

Identify the white organism encrusting the pebble as closely as you can:

How can you tell?

What was the mode of life of this organism?

What type of organism could have made the agglutinated tubes also attached to the pebble?

**A13: Jurassic fossil, but very similar to ones found in Cretaceous sediments.**

Identify the specimen as closely as you can:

How can you tell?

What was the mode of life of this organism?

**A14: Jurassic fossil, but very similar to ones found in Cretaceous sediments.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

**A15: Jurassic fossil, but very similar to ones found in Cretaceous sediments.**

Identify the specimen as closely as you can:

What features tell you this?

What was the mode of life of this organism?

What features tell you this?

**A16: Jurassic fossil, but very similar to ones found in Cretaceous sediments.**

Identify the specimen as closely as you can:

What was the mode of life of this organism?

What features tell you this?

**A17: Tertiary fossils, but very similar to ones found in Cretaceous sediments.**

Identify the specimens as closely as you can:

What was the mode of life of this organism?

What features tell you this?

**A18: Cretaceous marine reptiles.**

Go to the following web site to see reconstructions of some Cretaceous marine reptiles:
http://www7.nationalgeographic.com/ngm/0512/feature3/multimedia.html

For each of the following marine vertebrates, record its preferred diet and how it fed:

A18a: *Dakosaurus*.

A18b: *Kronosaurus.*

A18c: *Thalassomedon*.

A18d: *Tylosaurus*.

A18e: *Archelon*.

## PART B: CRETACEOUS MARINE ECOSYSTEM.

B1: Identify which Bombachian megaguild each of the organisms represented in Part A belonged to, and place it in the appropriate cell in the tables below. Some organisms may appear more than once.

**Epifaunal Organisms:**

| | Suspension | Deposit | Herbivore | Carnivore |
|---|---|---|---|---|
| **Mobile** | | | | |
| **Attached Low** | | | | |
| **Attached Erect** | | | | |
| **Reclining** | | | | |

**Pelagic/Nektonic Organisms:**

| Suspension | Herbivore | Carnivore |
|---|---|---|
| | | |

**Infaunal Organisms:**

| | Suspension | Deposit | Carnivore |
|---|---|---|---|
| **Shallow Passive** | | | |
| **Shallow Active** | | | |
| **Deep Passive** | | | |
| **Deep Active** | | | |

B2: Draw a reconstruction of the Cretaceous community in a shallow marine environment during the Cretaceous Period, using the taxonomic, paleobiological, and paleoecological information you have ascertained above.

B3: How well do you think your reconstruction would match that of a true Cretaceous marine community?

B4: Which taxa would you expect to have been present in the original community? Why are they absent from the fossil assemblage?

## PART C: QUANTITATIVE (PALEO)ECOLOGY.

### INTRODUCTION:

When describing any community (modern or ancient) there are several key parameters to determine, including "species richness" (the number of species in the community, also called alpha diversity), "species abundance" (the number or proportion of individuals within the community belonging to a given species), and "evenness" (a measure of how uniformly individuals are distributed among species). These metrics are often assumed to be relatively reliable for censuses of modern communities. However, the reliability of such ecological metrics computed for fossil assemblages is complicated by the fact that fossil assemblages rarely represent "snapshots" of ecological communities. Rather, the number of species sampled and their relative abundances (and therefore "community" evenness) are often distorted through the process of time-averaging.

What is time-averaging?

_____

_____

_____

_____

_____

In this portion of the lab, you will quantitatively investigate: (1) the robustness of these ecological parameters when the same living community is repeatedly sampled over time; (2) how these ecological parameters of a living community are affected by simulated time-averaging; and (3) how these ecological parameters of a living community (with or without simulated time-averaging) compare to a genuinely time-averaged census of the community (i.e., a census of dead members of the community, which accumulated over a long time interval).

### RAW DATA:

"Live-dead" tests compare the composition of a living community with locally accumulating dead remains. In this study, live and dead individuals of mollusks were

sieved from sediment samples of sand from the shallow subtidal portion of tidal channels in Mugu Lagoon (on the Pacific coast between Los Angeles and Ventura, California). These samples were part of the larger effort of Charles "Pete" Peterson for his dissertation in the early 1970s. Peterson's resulting paper (published in 1976; see reference below) is a classic in taphonomy, and still provides one of the best live-dead datasets available. Peterson's data set utilized here includes:

- "Live data". Seven censuses of a living mollusk community taken over a period of 37 months. Each census represents the pooling of samples from ~20 stations within the habitat (station-level data not provided). Each live census represents a sampled "snapshot" of the molluskan community, and the degree to which the community is observed to be "stable" can be investigated by comparing the seven live censuses. Furthermore, the live censuses can be pooled to varying degrees (by combining the data from two or more censuses) to simulate a "time-averaged" sample of the molluskan community.
- "Dead data". A single census of dead mollusks from the habitat. This dead census includes remains of individuals which accumulated over a relatively long interval, and so is naturally time-averaged relative to any single live census.

Live and dead individuals were sieved from the sediment using a standard mesh size (2 mm opening), and sediment samples were of a standard volume. Numbers of individuals vary among censuses because of differences in absolute abundances (densities) of mollusks over time.

We will investigate live-dead agreement for several common measures of community composition, namely:

(1) Species richness (S); i.e., how many species are present. This is often termed "alpha diversity".

(2) Community evenness; i.e., how uniformly individuals are distributed among species. There are several established ways to quantify evenness. In this exercise we will use the Parker-Berger Index of "dominance" (PDI), which is the proportion of individuals belonging to the most abundant taxon in the species list (using this metric, evenness is basically [1 – dominance]).

(3) Proportional abundance of taxa; i.e., whether each taxon has the same relative abundance in the death assemblage as it does in the local living community. Agreement in proportional abundance between live and dead censuses is generally not expected, owing to differences in the preservation potential of species (even when working among mollusks, all of which have calcareous shells), differences in population turnover rates (individual longevities), and differences in the likelihood of post-mortem transport of shells (either into or out of the local habitat).

The data are listed in the accompanying Excel file (Geos224Lab9Data.xls). The "Raw data" worksheet contains the raw data, which consist of numbers of individuals of each species sampled in each of the seven live censuses, plus a list of numbers of individuals sampled in the single dead census. Note that these are real, non-edited data from Peterson's dissertation.

**DATA FORMATTING:**

Using the equations provided in the top cells of the "Raw data" worksheet in the Excel file:

1. Progressively pool the live census data to generate simulated time-averaged censuses of the mollusk community. Note that the extent of simulated time-averaging increases as more live censuses are pooled.
2. Calculate the proportional abundance of each species in each live census and in each stage of progressive pooling of the live censuses.
3. Calculate the total number of individuals sampled (sample size, N), the number of species sampled (species richness, S), and the Berger-Parker Dominance Index (proportional abundance of the top taxon, PDI) for each live census, for each simulated time-averaged census, and for the dead census.
4. Transfer the results (N, S, PDI) to the "Summary results" worksheet. The information regarding the number of censuses pooled is already provided.

## DATA ANALYSIS AND INTERPRETATION:

### C1: Species Richness in Live and Simulated Time-Averaged Samples.

C1a: Using the data listed in the 'Summary results" worksheet, plot species richness in each live census (non-pooled and progressively pooled; y-axis) as a function of number of censuses pooled (x-axis). There will be seven data points based on non-pooled live censuses, and a series of data points for live-dead agreement representing the successive pooling (increasing simulated time-averaging) of the live censuses.

C1b: How variable is species richness (S) from live census to live census?

C1c: What proportion of the total species richness is represented within live censuses?

C1d: Describe and interpret the effect on species richness of pooling live censuses.

C1e: How does the species richness of a single live census compare with the richness captured by a single census of the dead?

C1f: Describe and interpret how successive pooling of live censuses (simulating progressively greater degrees of time-averaging) affects the live-dead discrepancy in species richness.

**C2: Species Richness and Sample Size.**

Dead shells are almost always more common than live mollusk individuals in a sedimentary sample, resulting in a strong discrepancy in the sample size of live and dead data. Here, the single sampling of the dead yielded ~4600 dead individuals, whereas individual censuses of the living community yielded only 1000-2000 individuals. We might therefore expect the richness (i.e., number of species sampled) of the death assemblage to be larger than that of any live census simply because of differences in sample size. To test whether death assemblages are truly enriched in species owing to time-averaging, we therefore have to remove the effect of larger sample size. There are many ways to do this, including rarefaction (see Lab 6). For convenience, the sample-size standardized richness of the death assemblage (for N values of 1000, 1500, and 2000 individuals) is provided for you on the "Summary results" worksheet.

C2a: Plot species richness in live censuses (for non-pooled and pooled data; y-axis) as a function of number of individuals sampled (x-axis). The relationship between these variables might be better displayed if sample size is plotted on a logarithmic scale (in Excel, click on the x-axis then choose "log" from the scale menu).

C2b: Describe and interpret the relationship between species richness (S) and total sample size (N) for the live censuses.

C2c: How does species richness in the dead census change as its sample size is rarefied down to values comparable to those of live censuses? Plotting this as a graph will make the nature of this relationship clearer.

C2d: Describe and interpret the agreement (or disagreement) in species richness between the live and dead censuses, and how this is affected by rarefaction of the dead census.

**C3: Species Abundance and Evenness I.**

C3a: Plot the Parker-Berger Dominance Index (PDI; y-axis) against the number of censuses pooled (x-axis, ranging from 1 to 7), including data for all live censuses and for the successively pooled live censuses.

C3b: How variable is PDI from live census to live census?

C3c: Describe and interpret the effect of pooling the live censuses on observed PDI.

C3d: How does the PDI of a single live sample compare with the PDI captured by a single census of the dead?

C3e: Describe and interpret how successive pooling of live censuses (simulating progressively greater degrees of time-averaging) affects the live-dead discrepancy in PDI.

## C4: Species Abundance and Evenness II.

The analysis above investigated how the proportional dominance of the most abundant taxon differed among censuses (and with varying degrees of time-averaging, simulated or natural), but did not determine whether the identity of the most abundant taxon differed among samples. This issue of differences in abundance of particular species among samples will be investigated here.

C4a: Create a list of all mollusk species sampled in any of the live census or in the dead census. Tabulate the proportional abundance of each of these species in the dead census and in the maximally-pooled live census.

C4b: Plot a graph of proportional abundance of all taxa in the dead census (y-axis) against proportional abundance of all taxa in the maximally pooled live census (x-axis). There should be several species that have values of zero on one axis or the other, but no species that have zero values on both axes. Change each axis to a log scale. Ignore any warning messages that result from there being values of zero in the source data which should not be logged. Click on any data point, then under the "Graph" menu specify the fitting of a linear trendline and the printing of an r-squared value. Although species with values of zero on either axis are not shown on the graph, they do enter into the calculation

of the regression. [Note that this simplistic regression method is not strictly valid for several technical reasons and would not be appropriate for publication, but is used here because it provides an intuitive understanding of the issue with minimal mathematical complication.]

C4c: According to this plot, how well do (maximally pooled) live and dead censuses match in terms of the proportional abundance of the sampled species?

C4d: What do these results signify in terms of quality of death assemblages as sources of proportional abundance information for taxa in living communities, and for any correction factor that needs to be applied before estimating original live relative abundances?

C4e: On the same graph, plot live-dead proportional abundances again but using only a single live census (your choice) as the source of the proportional abundance of the live data. Once again calculate the linear regression and associated r-squared value.

C4f: How does such a (non-pooled) live-dead comparison compare to that resulting from use of the maximally pooled live data (above)?

C4g: What do these differences (or similarities) signify in terms of the value of death assemblages for ecological inference?

C4h: Compare the agreement between any two non-pooled live censuses using this procedure. How does the degree of agreement in proportional abundance of species between live and dead censuses compare to that between live censuses of the same community?

**Reference:**

Peterson, C. H. 1976. Relative abundances of living and dead molluscs in two Californian lagoons. *Lethaia* **9**: 137-148. [Raw data are from his 1972 PhD dissertation at UC Santa Barbara, used by SM Kidwell with his permission]

## PART D: DEVONIAN MARINE ECOSYSTEM.

Take a swim through the Devonian oceans on the web site:

www.geocities.com/christiandarki/fish.htm

See many armored fish (agnathans, placoderms, acanthodians), ammonoids, and trilobites in this fun interactive program.

List two odd things about the shells of the Devonian ammonoids in this program:

_____

_____

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_____