

## **BIOL203L Semester Project**

### Overview

Phylogenetics is the study of evolutionary relationships. There are many tools and different types of data that can be used to reconstruct evolutionary relationships. Historically, phylogenies (trees) were created using morphological characters. Today many phylogenies are generated using genetic sequences from multiple loci. This project is meant to teach you about the Tree of Life, phylogenetic trees, and some of the tools used to study biodiversity. You will have two labs that introduce you to the techniques for building a phylogenetic tree and then how you use a phylogeny to ask and answer questions in biology. In pairs or groups of 3, you will work together to reconstruct a phylogeny for a portion of the Tree of Life. You will then use what you have learned about phylogenies, evolution, and comparative phylogenetics to address a biological question about that portion of the tree. You will present your results in the form of a poster later in the semester, so that you will gain an appreciation for the entire experience of scientific discovery (from asking a question all the way to finding and presenting the answer).

### Objectives

Learn about scientific process

Gain appreciation for evolutionary connections across the Tree of Life

Interpret a phylogeny

Learn how phylogenetic trees are constructed

Introduce the different ways to study evolutionary relationships

Learn how comparative phylogenetics is used to understand the biology of organisms

### Skills

Hypothesis testing

Database mining

Phylogeny construction

### Materials

Internet access

Poster making materials

### Semester Timeline

Lab 1: Introduce the semester project and assign background readings for phylogeny-building

Assigned readings and tutorials:

**Phylogenetics Tutorial #1** Phylogenetics systematics, a.k.a. evolutionary trees

[http://evolution.berkeley.edu/evolibrary/article/phylogenetics\\_01](http://evolution.berkeley.edu/evolibrary/article/phylogenetics_01)

**Phylogenetics Tutorial #2** Travels in the Great Tree of Life

<http://archive.peabody.yale.edu/exhibits/treeoflife/learn.html>

**Assigned Reading #1** [http://evolution.berkeley.edu/evolibrary/article/0\\_0\\_0/specht\\_01](http://evolution.berkeley.edu/evolibrary/article/0_0_0/specht_01)

**Assigned Reading #2** [http://evolution.berkeley.edu/evolibrary/news/080301\\_elephantshrew](http://evolution.berkeley.edu/evolibrary/news/080301_elephantshrew)

**Database Activity (next page)**

Lab 2: Discussion of phylogeny readings and tutorials. Phylogeny-building lab (Module I)

Lab 6: Comparative phylogenetics lab (Module II), receive taxonomic assignments for project.

Lab 7: Turn in the topics and questions to be addressed with the phylogeny

Lab 8: Turn in draft outline of poster

Lab 10: Turn in final draft of poster, print.

Lab 11: Present posters

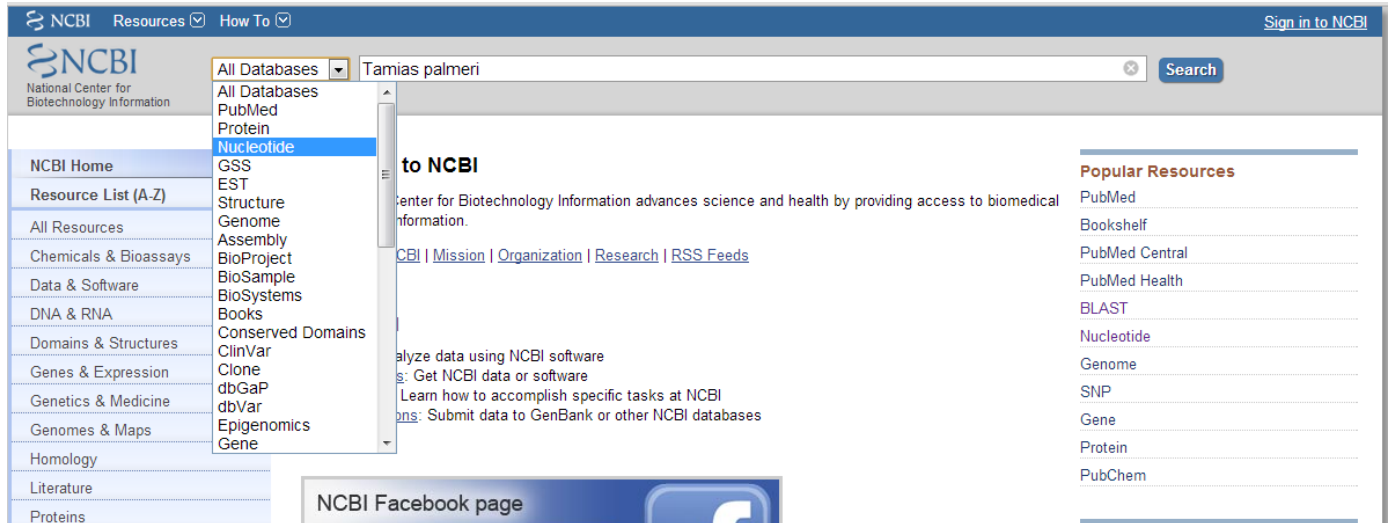
### Tips

Do NOT wait until the last minute to pick a topic and a question. You need to put some careful thought into this and do a little preliminary research BEFORE you turn in a topic. This project requires some critical thinking on your part and spending time developing an interesting question. Your grade will be based on the quality of the question you propose and how well you address it.

## Database Activity

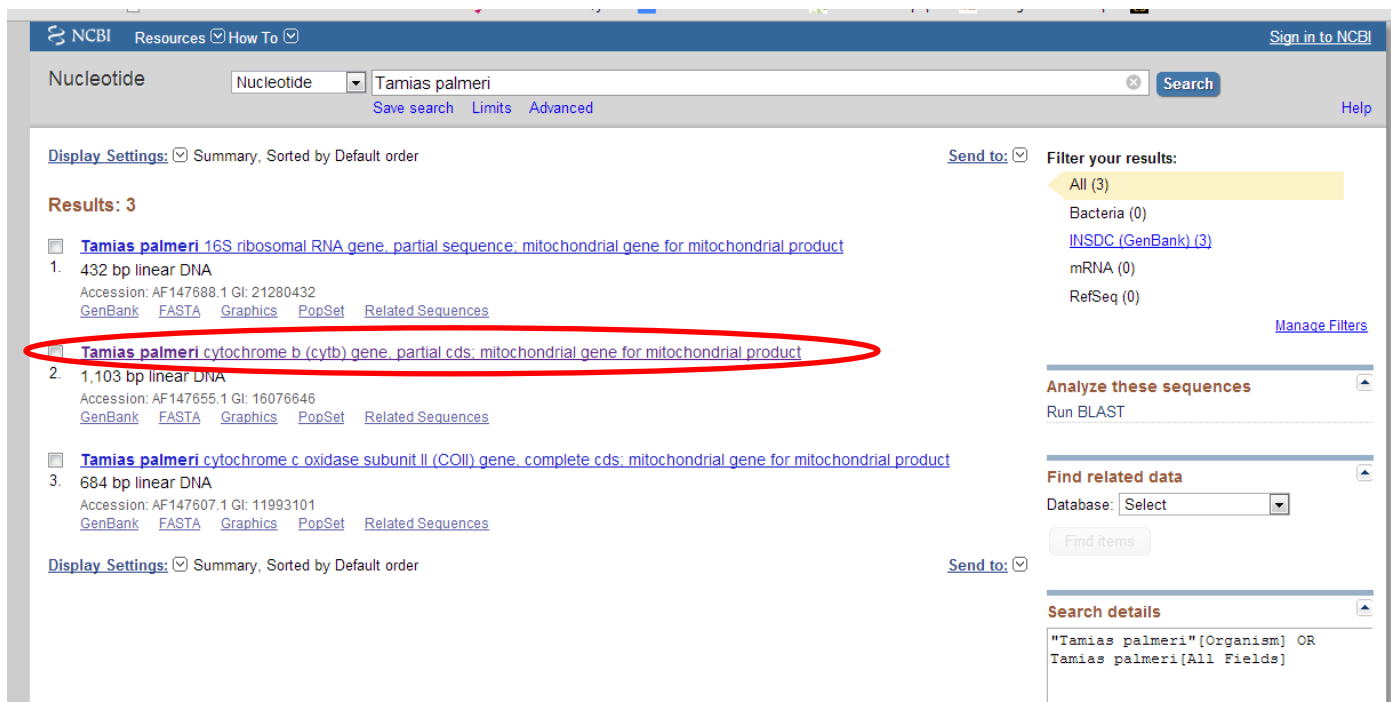
Follow the steps below to begin exploring some of the databases that might be useful for your semester project. Some of these databases will also be valuable when you are exploring the diversity of life throughout the semester. Bring your answers to the questions at the end to the next lab.

Go to GenBank, <http://www.ncbi.nlm.nih.gov/>, in the “All Databases” drop down menu select “Nucleotide”, then type “Tamias palmeri” into the search box and hit the “Search” button.



The screenshot shows the NCBI homepage with the search bar at the top. The 'All Databases' dropdown menu is open, and 'Nucleotide' is selected. The search box contains 'Tamias palmeri' and the 'Search' button is visible. The page also shows a navigation menu on the left and a 'Popular Resources' section on the right.

The results page should look like this, click on the entry for Tamias palmeri cytochrome b (Accession AF147655.1)



The screenshot shows the search results page for 'Tamias palmeri'. The search results are displayed, and the entry for 'Tamias palmeri cytochrome b (cytb) gene, partial cds: mitochondrial gene for mitochondrial product' is highlighted with a red circle. The results are sorted by Default order and show 3 results. The highlighted entry has an accession number of AF147655.1 and a length of 1,103 bp linear DNA. The page also shows a 'Filter your results' section on the right and a 'Search details' section at the bottom.

This page leads you to all of the information for that accession, including the type of sequence data, the source of the data, the publication, the authors on the publication, additional information about the data, and the actual sequence itself. If the sequence is associated with a museum specimen (which is what you will be looking for), there is a link on the right side of the page to the database entry for that specimen, in this instance “MSB Mammals 59000”, click on that link.

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Search Limits Advanced Help

Display Settings: GenBank Send:

**Tamias palmeri cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product**

GenBank: AF147655.1

FASTA Graphics PopSet

Go to:

LOCUS AF147655 1103 bp DNA linear ROD 12-OCT-2001

DEFINITION Tamias palmeri cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product.

ACCESSION AF147655

VERSION AF147655.1 GI:16076646

KEYWORDS .

SOURCE mitochondrion Tamias palmeri (Palmer's chipmunk)

ORGANISM [Tamias palmeri](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Scuriidae; Xerinae; Marmotini; Tamias.

REFERENCE 1 (bases 1 to 1103)  
AUTHORS Piaggio,A.J. and Spicer,G.S.  
TITLE Molecular phylogeny of the chipmunks inferred from Mitochondrial cytochrome b and cytochrome oxidase II gene sequences  
JOURNAL Mol. Phylogenet. Evol. 20 (3), 335-350 (2001)  
PUBMED [11527462](#)

REFERENCE 2 (bases 1 to 1103)  
AUTHORS Spicer,G.S.

Change region shown

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

LinkOut to external resources

**MSB Mammals 59000**

Related information

Related Sequences

Full text in PMC

PopSet

Now you are on the museum specimen page for that individual in the Arctos database. This page has a lot of useful information about this specimen, including types of material archived from that individual and the publication that it was used in. If you scroll down you will see the geographic information about where this individual was collected.

Mammal Collection Museum of Southwestern Biology

Search Portals My Stuff About/Help

Log In or Create Account

**MSB Mammals 59000** TOIYABE NAT. FOREST, KYLE CANYON, MT. CHARLESTON C. T19S R56E SEC36

*Tamias palmeri*

skin; skull; postcranial skeleton; heart, kidney (frozen); karyotype (frozen); liver (frozen); liver (frozen) sample; liver (frozen) sample

North America, United States, Nevada, Clark County  
24-Sep-1987

Map of collection site in Nevada, USA.

Log in or Create Account MSB Mammals

Identifiers

GenBank: [AF147655](#)

GenBank: [AF147607](#)

NK: 2473

preparator number: 363

Part Name	Condition	Disposition	#	Label	Remarks
heart, kidney (frozen)	unchecked	in collection	1		
karyotype (frozen)	unchecked	in collection	1		
liver (frozen)	unchecked	in collection	1		
liver (frozen)	unchecked	on loan	1		
liver (frozen)	unchecked	on loan	1		
postcranial skeleton	unchecked	unchecked	1		
skin	unchecked	unchecked	1		
skull	unchecked	unchecked	1		

sex: female

Details

**Tamias palmeri**  
Animalia Chordata Mammalia Rodentia Sciurognathi Scuriidae Scurinae Tamias palmeri  
Palmer's chipmunk  
Identified by unknown on 2005-02-15  
Nature of ID: legacy

**Tamias palmeri**  
Animalia Chordata Mammalia Rodentia Sciurognathi Scuriidae Scurinae Tamias palmeri  
Palmer's chipmunk  
sensu Piaggio and Spicer 2001  
Identified by Toni Piaggio, Greg S. Spicer  
Nature of ID: type specimen  
Remarks: ID from citation in Piaggio and Spicer 2001.

**Tamias palmeri**  
Animalia Chordata Mammalia Rodentia Sciurognathi Scuriidae Scurinae Tamias palmeri  
Palmer's chipmunk  
sensu Piaggio and Spicer 2000  
Identified by Toni Piaggio, Greg S. Spicer  
Nature of ID: type specimen  
Remarks: ID from citation in Piaggio and Spicer 2000.

Now, use Animal Diversity Web (<http://animaldiversity.ummz.umich.edu/>), Tree of Life (<http://tolweb.org/tree/>), and Global Biodiversity Information Facility (<http://www.gbif.org/>) to answer the questions below.

1. Search for *Tamias palmeri* on the Animal Diversity Web.

- A. What is the common name for this species? \_\_\_\_\_
- B. What state is this species found in? \_\_\_\_\_
- C. What family is this species in? Classification information is on the right side of the page.  
\_\_\_\_\_

2. On the Tree of Life website, search for the family name from question 1C.

- A. What is the common name for this family? \_\_\_\_\_
- B. How many species are in this family? \_\_\_\_\_
- C. Name a continent this family is **not** found on. \_\_\_\_\_

3. Now search the Global Biodiversity Information Facility for *Tamias palmeri*. On the homepage, click on the "Access Data Portal" button on the right. On the next page, enter *Tamias palmeri* in the search box on the left. There should be one result under the "Scientific Names" section of the results page. Click on that entry and answer the questions below.

- A. How many occurrence records are there for this species? \_\_\_\_\_
- B. Name **one** of dataset resources for the map (table at the bottom of the page).  
\_\_\_\_\_

## Vocabulary

Definitions taken from Merriam-Webster (m-w.com) and UCMP Glossary (<http://www.ucmp.berkeley.edu/glossary/gloss1phylo.html>), some slightly modified.

**Adaptation:** change in a population resulting from natural selection; a structure which is the result of such selection.

**Analogous:** a trait or an organ that appears similar in two unrelated organisms, but was not present in the common ancestor of those two organisms (also called **homoplasy** or **convergence**).

**Ancestor :** any organism, population, or species from which some other organism, population, or species is descended by reproduction.

**Ancestral state reconstruction:** a method to estimate the character state of an ancestor based on phylogenetic relationships and character states of present-day organisms.

**Apomorphy:** a derived state, or a character that has evolved to a different state.

**Basal lineage:** the earliest diverging taxon within a clade.

**Branch:** a line on a phylogeny representing a lineage from a node (branching point) to another node or to terminal taxa.

**Character:** heritable trait possessed by an organism; characters are usually described in terms of their states.

**Character state:** one of the possibilities for a given character. For example, if the character is eye color, states can be blue or brown. Or, if the character is the position in a DNA sequence, the states can be A, C, G, or T.

**Clade:** a monophyletic taxon; a group of organisms which includes the most recent common ancestor of all of its members and all of the descendants of that most recent common ancestor.

**Conserved trait:** a trait that changes its state infrequently across a phylogeny.

**Convergence:** similarities which have arisen independently in two or more lineages that are not sister taxa.

**Derived :** describes a character state that is present in one or more subclades, but not all, of a clade under consideration. A derived character state is inferred to be a modified version of the primitive condition of that character, and to have arisen later in the evolution of the clade.

**Evolutionary tree:** a diagram which depicts the hypothetical phylogeny of the taxa under consideration.

**Homologous :** two structures are considered homologous when they are inherited from a common ancestor which possessed the structure.

**Labile trait:** a trait that changes its state easily or frequently across a phylogeny.

**Lineage:** any continuous line of descent; any series of organisms connected by reproduction.

**Maximum likelihood (in phylogenetics):** a statistical method to estimate the evolutionary relationships among taxa. This method evaluates all the possibly relationships for a given set of taxa.

**Monophyletic :** term applied to a group of organisms which includes the most recent common ancestor of all of its members and all of the descendants of that most recent common ancestor. A monophyletic group is called a clade.

**Node:** the point at which two or more branches (or lineages) come together on a phylogeny.

**Outgroup:** in a phylogenetic analysis, any taxon used to help resolve the polarity of characters, and which is hypothesized to be less closely related to each of the taxa under consideration than any are to each other.

**Paraphyletic:** term applied to a group of organisms which includes the most recent common ancestor of all of its members, but not all of the descendants of that most recent common ancestor.

**Parsimony:** refers to a rule used to choose among possible relationships, which states that the relationships implying the least number of changes in character states is the best.

**Phylogenetics:** field of biology that deals with the relationships between organisms.

**Phylogeny:** the evolutionary relationships among organisms; the patterns of lineage branching produced by the evolutionary history of the organisms being considered.

**Plesiomorphy:** primitive character state for the taxa under consideration.

**Polyphyletic:** term applied to a group of organisms which does not include the most recent common ancestor of those organisms; the ancestor does not possess the character shared by members of the group.

**Primitive:** a character state present in the common ancestor of a clade. A primitive character state is inferred to be the original condition of that character within the clade under consideration.

**Radiation:** event of rapid cladogenesis, believed to occur under conditions where a new feature permits a lineage to move into a new niche or new habitat, and is then called an adaptive radiation.

**Sister group:** the two clades resulting from the splitting of a single lineage.

**Synapomorphy:** a character which is derived, and because it is shared by the taxa under consideration, is used to infer common ancestry.

**Systematics:** field of biology that deals with the diversity of life. Systematics is usually divided into the two areas of phylogenetics and taxonomy.

**Taxon:** any named group of organisms, not necessarily a clade; a taxon may be designated by a Latin name or by a letter, number, or any other symbol; plural: taxa.

**Taxonomy:** the science of naming and classifying organisms.

**Trait:** an inherited characteristic that is a distinguishing quality.

**Vicariance:** speciation which occurs as a result of the separation and subsequent isolation of portions of an original population.