ELE4120 Bioinformatics
Tutorial 8
Content

• Classifying Organisms
  – Systematics and Speciation
  – Taxonomy and phylogenetics
  – Phenetics versus cladistics

• Phylogenetic trees
Biological classification

• Goal:
  - To develop a system of categories that provides (‘useful’) information about living things
Classifying Organisms

- **Systematics** is the science of the relationships of organisms
  - how organisms are related and the evidence for those relationships

- **Speciation** -- the origin of new species from previously existing ones
  - anagenesis - one species changes into another over time
  - cladogenesis - one species splits to make two

Reconstruct evolutionary history

Phylogeny
In the western scientific tradition:

1. Biological Taxonomy - Aristotle - mid 300’s BCE
2. Hierarchical Taxonomy & Binomial nomenclature - Linnaeus - early to mid 1700’s
3. Phenetic taxonomy - Adanson - 1750s
4. Phylogeny - Darwin, Haeckel - mid 1800’s
5. Evolutionary taxonomy - Mayr and Simpson - mid 1900’s
6. Phenetic taxonomy - Sneath and Sokal - 1960’s
7. Cladistic taxonomy - Hennig - 1960’s
Species Classification

- **Phenetic**: physical attributes, numerical taxonomy
  - (resemblance: Based on phenotypic similarity)

- **Cladistic (Phylogenetic)**: evolutionary relationships
  - (descent: Based exclusively on the branching patterns of phylogeny)

- **Evolutionary**: synthesis of the two
Phenetic Classification

• “Like with like”
• Use many characters to define overall similarity
• Linnaean
  – “God created, Linnaeus arranged”
  – Before Darwin so not based on Evolution (but may reflect history)
• Problem: uses all types of characters (analogies, ancestral & derived homologies)
Taxonomy and phylogenetics

- **Taxonomy** is the science of the classification of organisms.

- Taxonomy deals with the naming and ordering of taxa.

- The *Linnaean* hierarchy:
  1. Kingdom
  2. Division
  3. Class
  4. Order
  5. Family
  6. Genus
  7. Species

**Taxonomic Classification of Man**

*Homo sapiens*

- Superkingdom: Eukaryota
- Kingdom: Metazoa
- Phylum: Chordata
- Class: Mammalia
- Order: Primata
- Family: Hominidae
- Genus: *Homo*
- Species: *sapiens*
- Subspecies: *sapiens*
Classification Systems

• Taxonomy:
  – Classification of living organisms into groups

• Phylogenetic Classification System:
  – Groups reflect genetic similarity and evolutionary relatedness

• Phenetic Classification System:
  – Groups do not necessarily reflect genetic similarity or evolutionary relatedness. Instead, groups are based on convenient, observable characteristics.
Phylogenetics

- **Phylogenetics** is the science of the pattern of evolution.
- Evolutionary theory states that groups of similar organisms are descended from a **common ancestor**.
  - **Phylogenetic systematics** is a method of taxonomic classification based on their evolutionary history.
- Evolutionary biology versus phylogenetics
  - Evolutionary biology is the study of the **processes** that generate diversity.
  - Phylogenetics is the study of the **pattern** of diversity produced by those processes.
Phenetics *versus* cladistics

- Within the field of taxonomy there are two different methods and philosophies of building phylogenetic trees: **cladistic** and **phenetic**

  - **Phenetic** methods construct trees (*phenograms*) by considering the current states of characters without regard to the evolutionary history that brought the species to their current phenotypes; *dendrograms* are based on **overall similarity**

  - **Cladistic** methods construct trees (*cladograms*) rely on assumptions about ancestral relationships as well as on current data; *cladograms* are based on **character evolution** (e.g. shared derived characters)

- Cladistics is becoming the method of choice; it is considered to be more powerful and to provide more realistic estimates, however, it is slower than phenetic algorithms
Phenetic Classification of Vertebrates

Amphibians  Reptiles  Birds  Mammals

Are the phenetic reptiles a valid phylogenetic group?

To create a phylogenetically valid class of reptiles, what groups would need to be included?
Possible Phylogenetic Classification of Vertebrates

Are the *phenetic* reptiles a valid phylogenetic group?

To create a phylogenetically valid class of *reptiles*, what groups would need to be included?
Character and Distance Data

The molecular data used to generate phylogenetic trees fall into one of two categories:

1. Characters: a well-defined feature that can exist in a limited number of different states.
2. Distances: a measure of the overall, pairwise difference between two data sets.
Phylogenetic trees

• The central problem of phylogenetics:
  --how do we determine the relationships between taxa?

In phylogenetic studies, the most convenient way of presenting evolutionary relationships among a group of organisms is the **phylogenetic tree**.
Phylogenetic trees

- **Node**: a branchpoint in a tree (a presumed ancestral OTU)
- **Branch**: defines the relationship between the taxa in terms of descent and ancestry
- **Topology**: the branching patterns of the tree
- **Branch length** (scaled trees only): represents the number of changes that have occurred in the branch
- **Root**: the common ancestor of all taxa
- **Clade**: a group of two or more taxa or DNA sequences that includes both their common ancestor and all their descendents
Phylogenetic trees

• There are many ways of drawing a tree
Phylogenetic trees

• There are many ways of drawing a tree
Phylogenetic trees

• There are many ways of drawing a tree

\[
\begin{align*}
A & \quad B & \quad C & \quad D & \quad E \\
\text{no meaning}
\end{align*}
\]
Phylogenetic trees

• There are many ways of drawing a tree

Diagram:
- Bifurcation
- Trifurcation

≠
Phylogenetic trees

- Trees can be scaled or unscaled (with or without branch lengths)
Phylogenetic trees

- Trees can be unrooted or rooted
Phylogenetic trees

- Trees can be unrooted or rooted

These trees show five different evolutionary relationships among the taxa!
Example: Cladograms
---Restate steps in other words

1) select group of organisms
2) determine characters & states
3) for each character, classify ancestral & derived
   - comparison to outgroup
   - traits shared with outgroup = ancestral
4) group by shared derived characters (synapomorphies)
5) choose most parsimonious tree (fewest evolutionary transitions)
## Example: Seed Plants

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<tr>
<th>TAXA</th>
<th>Cotyledon #</th>
<th>Carpels</th>
<th>Perianth</th>
<th>Seeds</th>
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</tr>
<tr>
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<td>Present</td>
<td>Present</td>
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<tr>
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</table>
Example: Parsimonious Tree