

Phylogenetic Analysis: Cladistics and Phenetics

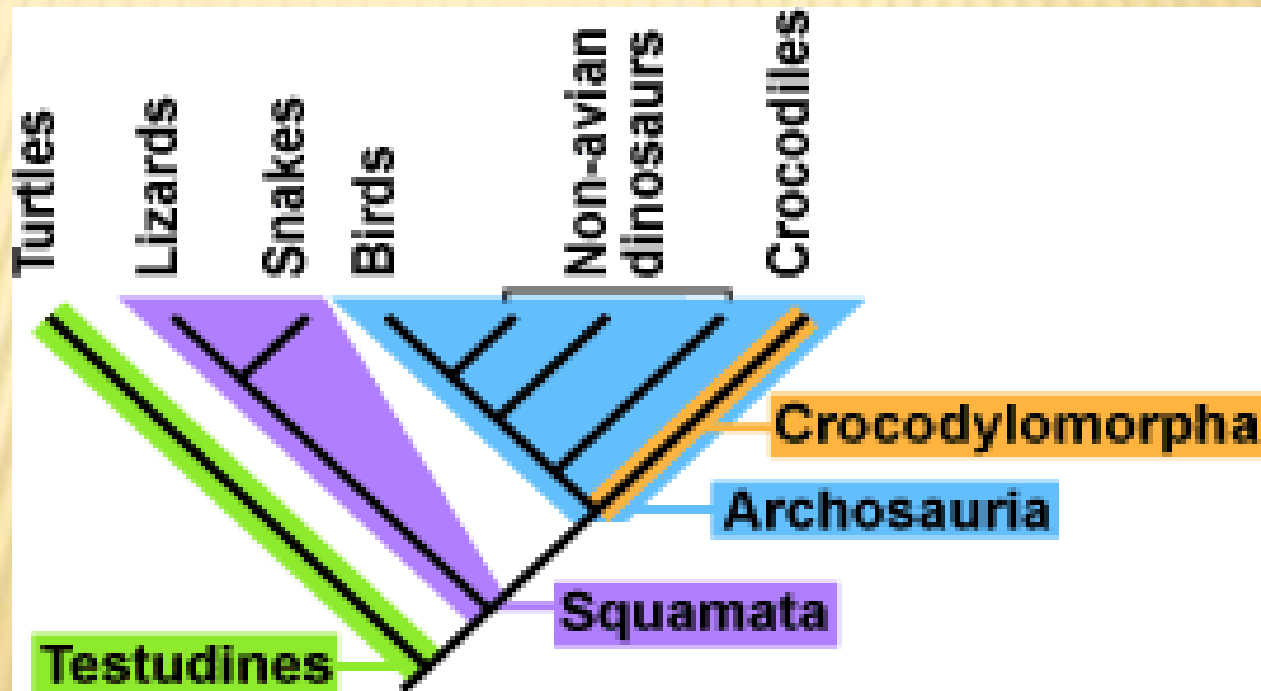
Adopted from Geonyzl L. Alviola

Davao Doctors College

Dr. MZM

Clade: A group of organisms, such as a species, whose members share homologous features derived from a common ancestor.

Cladistics: A system of classification based on the phylogenetic relationships and evolutionary history of groups of organisms.



Three Schools of Phylogenetic Analysis

A crucial consideration in macroevolutionary studies is that of the evolutionary relationships (phylogeny) of the organisms in question. The course begins with an introduction to the scope of macroevolutionary studies and illustrates methods of reconstructing phylogeny, from both morphological and molecular data.

It is important to appreciate the differences between the three methods of phylogenetic analysis that are described, namely

- evolutionary systematics
- phenetics
- cladistics

phylogenetic relationships. In the light of evolution, the hierarchy of taxa could now be seen as reflecting the phylogenetic tree of life.

If the phylogeny of life were itself known, there would be little problem in recognising higher taxa: the only arbitrary part of the exercise, of deciding where to 'sever' the branches to delimit the higher taxa, could simply be a matter of consensus. The problems arise because, as noted earlier, the true phylogeny is unknown, and can only be inferred from the available evidence. In practice, then, organisms are grouped according to criteria deemed to reflect relationship, and phylogeny is construed from these groupings. Conclusions may vary not only according to the characteristics of the organisms which are investigated, but also according to how they are analysed.

1.2 Taxa and relationships

Until the mid-20th century, inferences about evolutionary relationships between species were generally based upon as wide a range of evidence as could be mustered. **Evolutionary systematics** is the name given to this eclectic approach, because of its explicit focus on evolutionary conclusions. The disparate nature of the evidence used (ranging from the taxonomic attributes and geographical distribution of living organisms to the stratigraphical distribution of fossils) meant that there was no single underlying method of analysis, and so the conclusions were reached by a variety of lines of reasoning. Consequently, the discipline became notoriously the domain of widely experienced experts, who tended to acquire an unfortunate reputation in the popular imagination as a sort of unassailable priesthood. Frustration with the lack of a consistent method of analysis, and hence with the ultimately subjective nature of evolutionary systematics, led, in the 1950s, to the development of two new approaches to systematics both of which claimed to be more objective: in **phenetics**, species are clustered according to their overall morphometric similarities; in **cladistics**, relationships are inferred from the extent to which different species share evolutionarily modified features apparently derived from common ancestors. Yet neither new approach proved to be without its problems, and so all three continue to be practised today. The methods and the advantages and disadvantages of each approach will be discussed in the following sections. Nevertheless, **cladistics** has emerged in recent years as the most powerful and widely used method of phylogenetic analysis in most instances, and so most emphasis will be given here to this approach.

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 shared evolutionary history or characters

Phenetics: physical attributes, numerical taxonomy

(resemblance: Based on phenotypic similarities)

Cladistics (Phylogenetics): evolutionary relationships

(descent: Based exclusively on shared /derived evolutionary features or traits or characters)

ASSUMPTIONS OF CLADISTICS

- ✘ All species in a group must have share a common ancestor.
- ✘ All species derived from a common ancestor must be included in the taxon.

PHENETICS

Does not necessarily reflect genetic similarity or evolutionary relatedness. Instead, groups are based on convenient, observable characteristics.

Is based on the organism characters, compared to give the expression of similarities and differences.

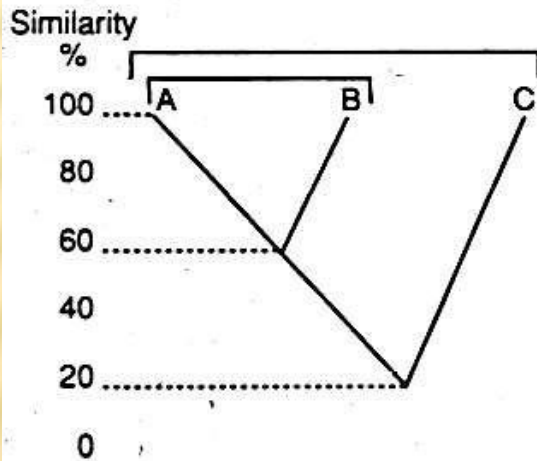
A priori, every character is of equal weight in creating natural taxa or every character has an equal taxonomic value.

PHENETICS VS CLADISTIC

PHENETIC

Overall similarities

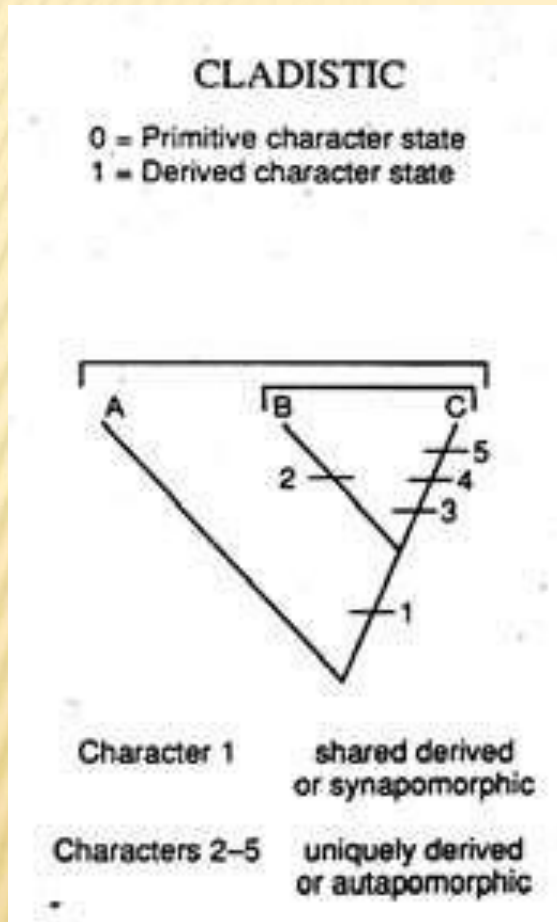
| | A | B | C |
|---|---|-----|-----|
| A | - | .60 | .20 |
| B | | - | .20 |
| C | | | - |



| Species | Characters | | | | |
|---------|------------|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| A | 0 | 0 | 0 | 0 | 0 |
| B | 1 | 1 | 0 | 0 | 0 |
| C | 1 | 0 | 1 | 1 | 1 |

- Phenetics uses “overall similarity” - all characters Used
- Graphical representation is called a phenogram, dendrogram, network

PHENETICS VS CLADISTIC



| | | Characters | | | | |
|---------|---|------------|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 |
| Species | A | 0 | 0 | 0 | 0 | 0 |
| | B | 1 | 1 | 0 | 0 | 0 |
| | C | 1 | 0 | 1 | 1 | 1 |

- Cladistics uses only phylogenetically informative characters
- Derived state is shared by 2 but not all taxa - “shared derived character states

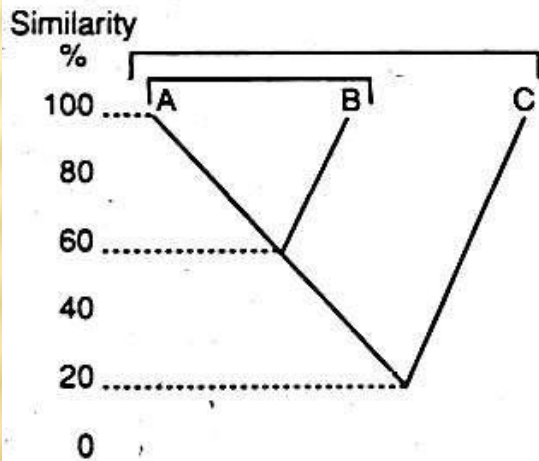
PHENETICS VS CLADISTIC

PHENETIC

Overall similarities

| | A | B | C |
|---|---|-----|-----|
| A | - | .60 | .20 |
| B | | - | .20 |
| C | | | - |

Phenogram is not equal
Cladogram



CLADISTIC

0 = Primitive character state

1 = Derived character state

