



Modern Trends in Plant Taxonomy

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Modern Trends in Plant Taxonomy (in NEP syllabus) includes

- Brief idea of Phenetics
- Biometrics
- Cladistics (Monophyletic, polyphyletic and paraphyletic groups)
- Plesiomorphy and apomorphy

What is Phenetics?

Phenetics (Greek: phainein= to appear) also known as taximetrics, is an attempt to classify organisms based on overall similarity, usually in **morphology** or other **observable traits**, regardless of their phylogeny or evolutionary relation.

Phenetics is also called as numerical taxonomy.

As against phenetic system, in phylogenetic system, the emphasis is on evolutionary relationships among organism.

Biometrics is the statistical research on biological phenomena.

- **Numerical taxonomy** is the technique of classifying plants (or organisms) using numerical methods.
- Presently it is also called **phenetics** or **taximetrics** .
- Phenetics is the numerical evaluation of the similarities or affinities of taxonomic units, which are typically classified into taxa based on their affinities.
- Concept was proposed by **Michael Adanson**, a French Botanist in 18th century and therefore called ADANSONIAN TAXONOMY.
- **SNEATH AND SOKAL** published a paper - “ **Principles of numerical taxonomy**” in 1963.



Peter Sneath



Robert R.
Sokal

- **Phenetic relationships**: Relationships among organisms based on **morphological** and other **observable traits**.
- **Phylogenetic relationships**: Relationships among organisms based on degree of **relatedness** due to a **common ancestor**.
- **Cladograms**: The **evolutionary** classification generates trees called cladograms.
- **Clad**: A clad is a **group** of organisms that includes an **ancestor** and **all its descendants**.

Basic definitions in biometrics used in taxonomy

Biometrics is the statistical research on biological phenomena. It is the use of mathematics and statistics in understanding living beings.

Some basic definitions of biometrics are as follows:

Scientific study- *An important feature of a scientific study is the commonly accepted criteria of validity of scientific evidence. objectivity in presentation and evaluation of data (singular datum) and general ethical code of scientific methodology must be constant.*

Data- *It deals with populations or groups of individuals. Thus data always deals with quantities of information, not with the single datum.*

Numerical- unless the data of study can be quantified in one way or the other, they would not be amenable to statistical analysis.

Natural phenomena- It includes all those events that happen in animate and inanimate surroundings not under the control of man.

Description- It is the assignment of features or attributes to a taxon. The features are called characters. Two or more forms of a character are called **character states**. E.g., one example of a character is petal colour for which two character states are pink and white.

Descent- It is the transfer of genetic material from parents to off springs over a time period. Descent may occur by simple clonal reproduction or by complex sexual reproduction. Descent through time results in the formation of a lineage or clade by the transfer of genetic material from parent to off springs.

Evolution- Evolution is viewed as decent with modification. The modification component of evolution refers to a change in the genetic material that is transferred from parents to off springs.

Phenetics (Numerical taxonomy)

It is a type of classification based on the analysis of taxonomic data (numerical comparison) of equally weighted characters by mathematical or computerised methods and numerical evaluation of the similarities or affinities between taxonomic units; these are then arranged into taxa on the basis of their affinities.

The concept was proposed by **Adanson** and later **Sneath and Sokal** (1963) published a book “ **Principles of Numerical Taxonomy**”.

Principles

- The **more characters**, the better a given classification will be.
- Every character should be given **equal weightage**.
- Classification is based on **phenetic similarity**.

Operational Taxonomic Units (OTUs)

- Any sample/item/ individual which is selected /used for analysis is called an **OTU**.
- It is the **basic unit** of numerical taxonomy.
- It may be an individual, species, genus, family, order or class.
- In case OTU is above level of individual, then adequate relationship of various forms become essential. E.g., when genera is OTU then it should be represented by different species.

Methods and procedures of Numerical Taxonomy

- **Selection of Taxa (OTUs).**
- **Selection of characters or traits.**
- **Cluster analysis via computer software.**
- **Determination of taxonomic relationship between OTUs.**
- **Classification based on the basis of overall similarities.**

Selection of characters

- Characters which are used are called unit characters.
- Unit characters can be classified as follows:
 - a) Binary character:** A character having only two states and recorded as present or absent e.g., cell wall present/absent
coding: **Present:** + or 1 **Absent:** - or 0 **Missing:** NC (no comparison)
 - b) Qualitative multistate characters:** These characters possess three or more contrasting forms e.g., flower colour- red, white, yellow.
 - c) Quantitative multistate characters:** They represent measures of size of continuous scale such as weight or length e.g., length of a spore or amount of a chemical produced by a bacterial strain.

Rules for selection of unit characters

- Must include **all parts** of the organism.
- Not less than **50** characters.
- Belong to **all stages** of life cycle.
- Due attention be given to morphology, physiology, ecology and distribution etc.

Character weighting

- **Equal weighting:** All characters selected are given equal weightage while creating taxonomic groups and is one of the principles of numerical taxonomy.
- **Successive weighting:** The characters which show the least homoplasy (unique) are identified and given more weightage in the subsequent analysis.

Data Processing

Characters (n)	OTU's (t)			
	A	B	C	D
1	1	1	0	NC
2	1	1	1	1
3	1	1	1	1
4	0	1	NC	NC
5	1	1	1	1
6	1	1	0	1
7	1	1	0	NC
8	NC	0	1	1
9	1	1	1	1
10	1	1	1	0

NC= no comparison; 1= present; 0= absent

Estimation of similarity

Characters	1	2	3	4	5
OTU _j	-	+	+	-	+
OTU _k	+	+	+	-	-

Two OTUs are scored for the 5 characters. They agree in 2nd, 3rd and 4th and disagree in 1st and 5th. The similarity is $3/5 = 60\%$ and dissimilarity is $2/5 = 40\%$

		OTU _j	
		1	0
OTU _k	1	a=12	b=3
	0	c=1	d=4

A, b, c and d are the numbers of the four combinations and the total of four combinations $\mathbf{a+b+c+d=n}$. Number of matches $\mathbf{m=a+d}$; number of mismatches $\mathbf{u=b+c}$, $\mathbf{m+u=n}$. Table also takes an example with 20 characters.

The simple matching coefficient (S_{sm})

$$S_{sm} = m/m+u = m/n = a+d/a+b+c+d$$

$$S_{sm} = 12+4/12+3+1+4 = 0.80$$

The example gives S_{sm}

The Jacard Coefficient (S_j)

$$S_j = a/a+u = a/a+b+c$$

Negative matches (d) are excluded in this similarity coefficient.

$$S_j = 12/12+3+1 = 0.75$$

Taxonomic Structure

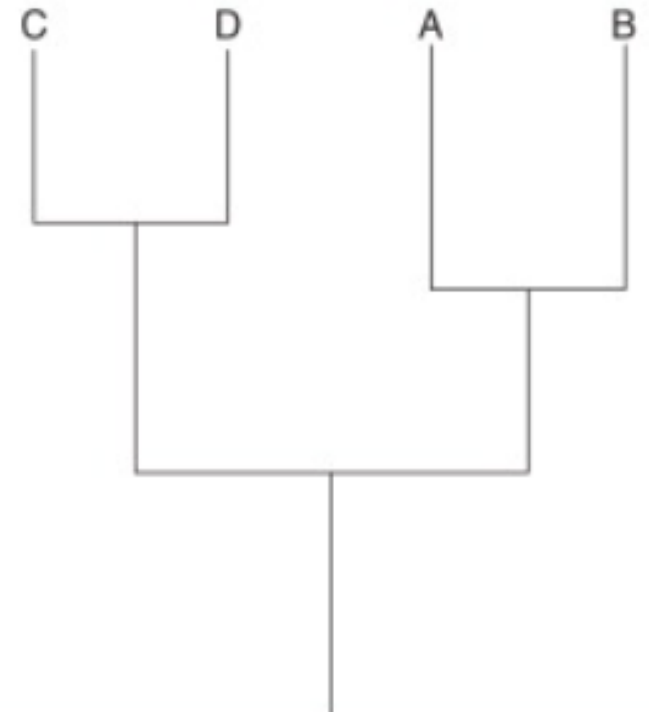
The similarity matrix (resemblance matrix) is the basic evidence available for finding taxonomic structure. In this $t \times t$ matrix of computed similarities are arranged to fall a scale between 0 and 1. Since the similarity of j and k is the same as that of k and j , only one half of this square matrix is filled in. A typical 10×10 similarity matrix of 10 OTUs is given in table 1.

1	1.0									
2	0.9	1.0								
3	0.6	0.5	1.0							
4	0.5	0.6	0.5	1.0						
5	0.9	0.8	0.6	0.5	1.0					
6	0.6	0.6	0.8	0.5	0.6	1.0				
7	0.6	0.6	0.8	0.5	0.5	0.8	1.0			
8	0.5	0.5	0.5	0.9	0.5	0.5	1.5	1.0		
9	0.8	0.9	0.6	0.5	0.9	0.6	0.6	0.6	1.0	
10	0.6	0.6	0.7	0.6	0.6	0.8	0.8	0.5	0.6	1.0
	1	2	3	4	5	6	7	8	9	10

Table 1. 10X10 similarity matrix for 10 OTU's

Cluster Analysis

- Cluster analysis is a multivariate data mining technique whose goal is to provide any meaningful picture and need to further condensed to enable a comparison of units.
- In this, the computer sorts out the OTUs according to their overall similarity i.e., according to the characters in common.
- The software produces a **phenogram** that is a **dendrogram** (branching tree diagram) which shows the taxonomic relationship between the taxa.



A Phenogram

Advantages of Numerical Taxonomy

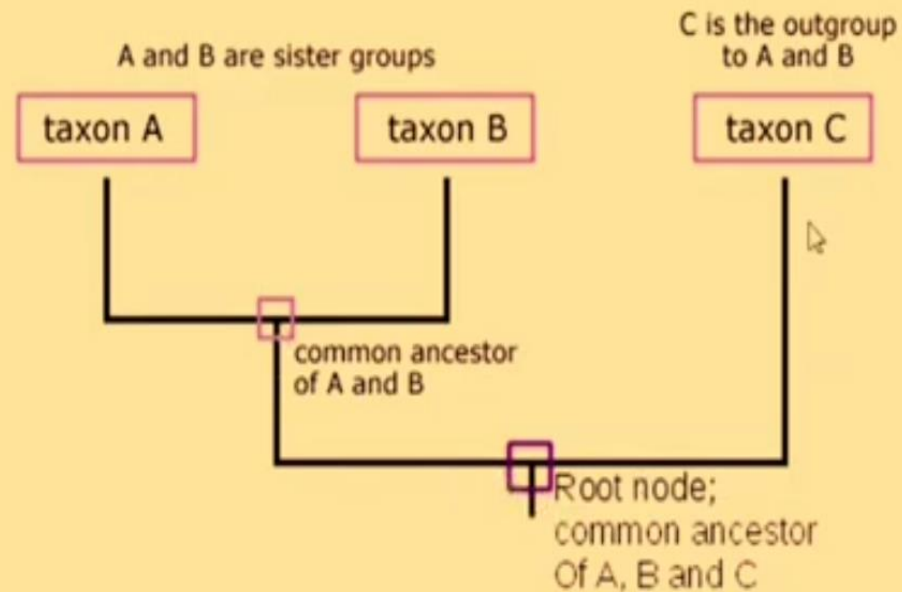
- Provide results that **agree** with established classification.
- Highly **relevant to real problem** of biological classification.
- Provide a **more exact basis** for classification.
- **Integrate data** from various sources viz., morphology, physiology, biochemistry, DNA studies, etc.
- Being quantitative, the methods **provide greater discrimination** along the spectrum of taxonomic differences.
- **Re-examination** of principles of taxonomy.

Demerits of Numerical Taxonomy

- Useful in phenetic classification but **not for phylogenetic** classification.
- **Character selection is crucial** because if character chosen for comparison are inadequate, the statistical methods may give less satisfactory solution.
- Different taxometric procedures may give different results.

Phylogenetic Tree

- A visual representation of the relationships between different organisms, showing the path through evolutionary time from a common ancestor to different descendants.
- Phylogenetic trees are hypothesized reconstructions of evolutionary history.



Phenogram	Cladogram
It is a type dendrogram which is based on phenetic data. Lines called phenon lines, drawn at right angles to dichotomously branching dendrogram represent lines of percentage similarity of phenetic features between organisms.	It is a dendrogram that rely on assumption about ancestral relationships as well as on current data.
Phenetic data are based on features in organisms regardless of whether they are analogous or homologous.	Analogy and homology is given importance.
Organisms that are evolutionarily distant may be grouped closely together.	Not so.
Example: Gymnosperm tree evolved in Carboniferous Period (355-290 mya) whereas angiosperm tree did not evolve until 90 mya. But in a phenogram they will be grouped together on the basis of structure.	Not so.
OTUs = Operational Taxonomic Units	OEUs = Operational Evolutionary Units
First proposed by M.Adanson; Sokal and Sneath (1963)	First proposed by W.Hennig (1950,1957)

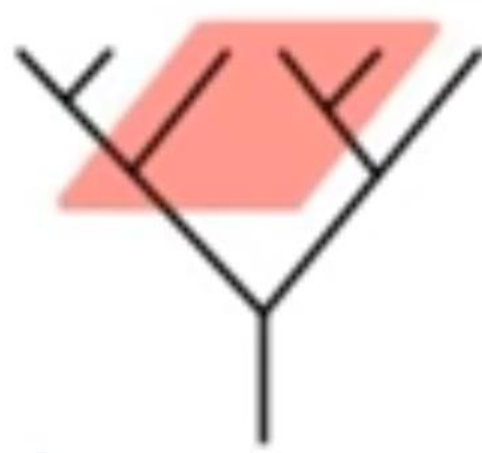
WHAT IS A CLADE?

Group of species that include a single common ancestor and are all descendants of that ancestor

CLADES



NOT CLADES



Apomorphy refers to a **novel** evolutionary character, **unique to a particular clade** and all its descendants. An apomorphy restricted to a single species is called autapomorphy. E.g., presence of feathers in Aves; absence of legs in snakes.

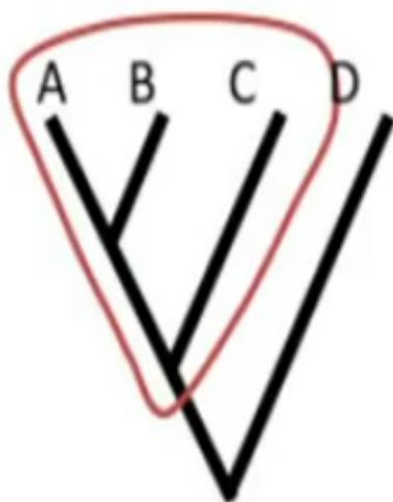
Plesiomorphy refers to an evolutionary **character homologous within a particular clade** but, **not unique** to all members of that particular clade. E.g., presence of legs in reptiles.

Different groups of organisms

Monophyletic ✓	Paraphyletic	Poly phyletic
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Monophyletic group

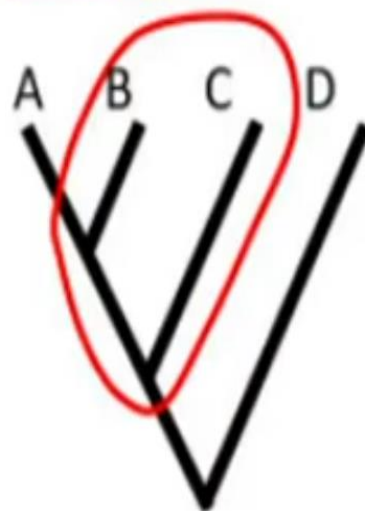
Includes an ancestor
all of its descendants



How could this happen?

Paraphyletic group

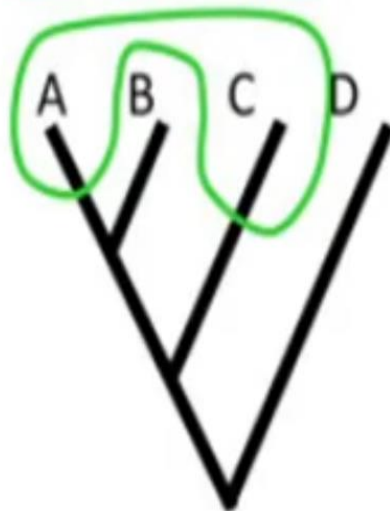
Includes ancestor and
some, but not all of its
descendants



Taxon A is highly derived
and looks very different
from B, C, and ancestor

Polyphyletic group

Includes two convergent
descendants but not their
common ancestor



Taxon A and C share
similar traits through
convergent evolution

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