

Topic : BIOSYSTEMATICS AND NUMERICAL TAXONOMY /PHENETICS

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BIOSYSTEMATICS AND NUMERICAL TAXONOMY /PHENETICS

Systematics and taxonomy are two different concepts related to the study of diverse life forms and the relationships between them through a period of time. While taxonomy is involved in identification, nomenclature and classification, Systematics aims to determine the evolutionary relationship of organisms. Hence in Systematics emphasis is on common ancestry where organisms are grouped based on their evolutionary relationships. Taxonomy can be considered a branch of systematics. Taxonomy is often used as a synonym of systematics (as defined above, while classification is sometimes used rather loosely (and incorrectly) as a synonym of identification. Both in taxonomy and systematic data is obtained from morphological, behavioral, genetics and biochemistry.

According to valentine and Lave, there has been three stages of floristic study

1. Evolutionary phase : involving collection and classification from the Herbarium specimen
2. The Systematic phase: Extensive herbarium and wide study of the taxon undertaken
3. Biosystematics phase : Study of genetical and cytological aspects
4. Encyclopedic phase (introduced by Davis and Heywood):Data to be gathered from wide range of disciplines and assembled to form a good predictive classification of the organism under study.

What is Systematics?

Systematics is the study and classification of living things; in other words, grouping organisms based on a set of rules (or system).Systematics may be defined as the study of the kinds and diversity of organisms and the relationships among them.

Two Kinds of Systematics

Systematics can be divided into two closely related and overlapping levels of classification: taxonomic (known as the Linnaean System) and phylogenetic systems .

Taxonomic classifications group living things together based on shared traits - usually what they look like or what their bodies do. For example, plants that have seeds and flowers we call Angiosperms, and plants that have undifferentiated thallus we call them thallophytes. More specifically, all Angiosperms share the same characteristics and so belong to a group, or **taxon**, of the genus and species.

Phylogenetic classifications:

According to Darwin life evolved and followed the hierarchy of life - all organisms are united in a pattern of increasing similarity. The pattern of relatedness is called **phylogeny** and **systematics** is the field of biology that studies and seeks to determine phylogenies.

It tries to explain how group organisms by how evolutionarily related they are to one another. It's sort of like if you were to introduce someone to a group of people, you might start with their names (taxonomic classification), and then describe who's a sister, uncle, friend, or total stranger.

As for example by looking at each organism's genes, we know that gymnosperms (taxonomic term), say, are more closely related to Angiosperms than they are to fungi or bacteria.

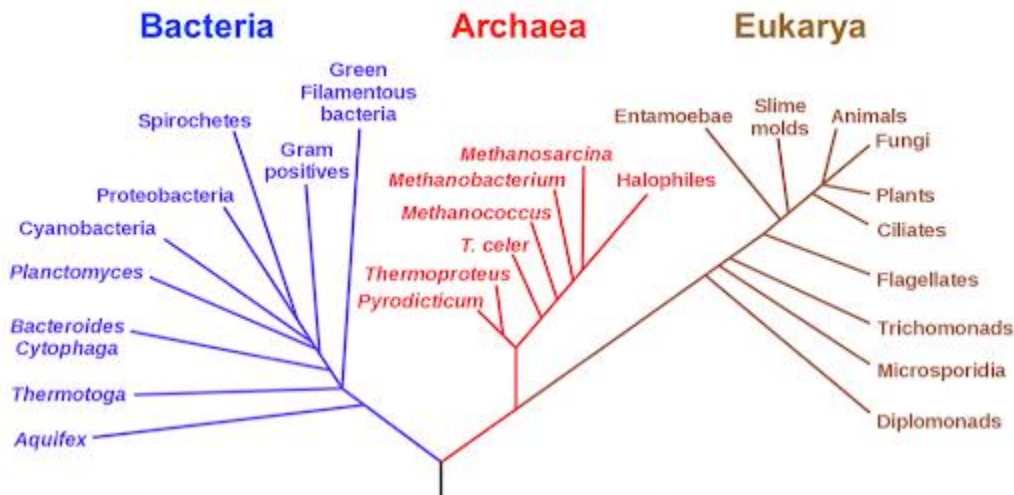


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The data systematists use to reconstruct phylogenies are the attributes or **characters** that organisms have.

These characters source could be :

1. Morphology
2. Developmental Biology
3. Molecular Biology (Genetics, Biochemistry)

1. Morphology

Systematist study external characteristics, examine leaf and flower dissect the ovary systems study the cells and tissues with the electron microscope all to gather comparative evidence for evolution. Along the way, much is added to our knowledge about the basic biology of different organisms.

2. Developmental Pathways (Ontogeny)

The basic embryonic development is constrained and rarely changes because any mutation that affects early development is almost always lethal and selected against. Therefore, developmental evidence can be particularly useful in uncovering evolutionary relationships between diverse adult forms.

3. Molecular and Biochemical Data

The organisms are determined by its genetic content, changes in organisms over the course of evolution should be reflected in their genetic information. However, similarities may not always be a result of common ancestry. Molecules and genes could have similar construction as a result of convergent evolution.

B. Analyzing the Data to Reconstruct Evolution: There are three major ways in which classifications are constructed:

1. **Phenetic** or numerical taxonomy;
2. **Synthetic** or traditional taxonomy;
3. **Cladistic** or phylogenetic taxonomy.

Phenetics or Numerical Taxonomy:

Sneath and Sokal (1957) introduced the concept of Phenetics. And published it published a textbook “Principle of Numerical Taxonomy” in 1963 and revised it in 1973 as Numerical Taxonomy.

There are many examples of numerical taxonomy solving taxonomic problems. Clifford (1977) studied Alismidae, Lilidae, Commelinidae, and Arecidae. On the basis of results of cluster analysis Alismidae was kept away from others.

Phenetics, or numerical taxonomy uses biological character to assess overall similarity to assess the relationship between two organisms . It makes no attempt to reflect evolution .Taxa are treated on the basis of presence or absence of character and states reflected. The character of choice is Unit or single character. Each character is given equal weight.

In numerical taxonomy the terms Phenon replaces taxon, i.e., rank of any level and the particular phenons are designated by numerical prefixes showing the level of resemblances by which they are defined.

Similarity in the attributes over which they were scored, and they are physically delinked by drawing horizontal straight lines or Phenon lines at the appropriate level across a phenogram. Thus , 50 phenon or 70 phenon means phenons defined by a 50 percent or 70 percent.

Numerical Taxonomy is based on Phenetic evidences, i.e., on similarities by observed and recorded characters of taxa, and not on phylogenetic probabilities. Since, numerical taxonomy is operational in the sense that it is divided into a series of repeated steps, allowing its results to be checked back step by step.

Seven principles of phenetics are as:

- (1) The greater the content of information in the taxa of a classification and the more characters on which it is based, the better a given classification will be.
- (2) A Priori every character is of equal weight in creating natural taxa.

- (3) Overall similarity between any two entities is a function of their individual similarities in each of the many characters in which they are being compared.
- (4) Distinct taxa can be recognized because correlation of characters differs in the group of organisms under study.
- (5) Phylogenetic inferences can be drawn from the taxonomic structure of a group and from character correlations, given certain assumptions about evolutionary pathways and mechanism.
- (6) Taxonomy is practiced as an empirical sciences as opposed to interpretative or intrusive science.
- (7) Classification are based on phenetic similarity.

Most of these principles bear resemblance to the aims and methods of Adanson and are therefore, known as Neo-Adansonian principles.

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The logical steps are:

(1) Choice and Number of units to be Studied:

The basic unit of numerical taxonomy is operational taxonomic Unit (OTU). The term is given to the lowest term being studied in a particular investigation.

The number of characters needed to achieve are at least 60 characters or more like 80 or 100 as desirable. In listing characters only homologous (common evolutionary origin) characters are to be compared.

(2) Character Selection and Taxon Matrix:

Character is a feature of an individual or taxonomic group, which can be measured, counted or assessed. In angiosperms mostly morphological, physiological or distributional ones are used as OTU, resulting in Data-matrix of attributes. (OTUs X characters or taxon).

If one is classifying 30 OTUs and using 100 characters the data matrix will consist of 3000 attributes. A computer is essential to calculate the data because of number and variety of operational units. The use of a computer necessitates the codification of the attributes in some simple form which can be feed into the computer, and this presents great problem. The simplest codification is a Binary or two state system, e.g., \pm and $-$ or 0 and 1 where each character exists in only two states.

		Characters (n)									
OTUs (t)		a	b	c	d	e	f	g	h	i	j
Species 1	1	+	-	-	+	+	+	+	+	+	+
	2	+	\pm	\pm	+	-	+	+	-	-	-
	3	-	\pm	-	+	\pm	+	+	+	+	+
	4	-	+	-	-	-	\pm	+	-	+	+
	5	+	+	+	-	+	\pm	+	+	\pm	+
	6	+	+	+	-	\pm	-	+	+	+	+

+ = attribute present , - = Attribute absent

\pm = May be present in some species

Cluster Analysis:

Data presented in OTUs x OTUs (t x t) matrix are much exhaustive and difficult to give correct picture. In cluster analysis the OTUs are arranged in order of decreasing similarity.

An acceptable data matrix is prepared for computer programme, using the matrix, the computer sorts out clusters OTUs according to their overall similarity. They can be

(i) Polythetic- are defined by the possessions of the greatest number of shared features

(ii) Monothetic- defined by the possession of unique set or feature which is necessary and sufficient to define the groups.

Advantage of Numerical Taxonomy over Conventional Taxonomy:

- (i) It has the power to integrate data from a variety of sources-, e.g., morphology, physiology, phytochemistry, embryology, anatomy, palynology, cytology, etc.
- (ii) (ii) Automation of data processing promotes efficiency.
- (iii) The data can be used for creation of description key, catalogue, maps etc.
- (iv) It can provide better classification.
- (v) Description can improve conventional taxonomy.
- (vi) A number of evolutionary concepts are interpreted by this method.

Aims of Numerical Taxonomy:

Main aim is to determine phenetic relationship between organisms or Taxa. According to Sneath and Sokal (1973) phenetic relationship means similarity or resemblance based on a set of phenotypic characters. Cladistic relationship means expression of the recency of common ancestry and it is represented by branching network of ancestor-descendent relationship.

Calculation of Affinity:

The calculation of affinity between pairs of OTUs is based on some clearly stated statistics.

Sneath and Sokal (1973) recognized four basic types:

- (a) Association coefficient.
- (b) Distance coefficient.
- (c) Correlation coefficient.
- (d) Probabilistic coefficient.

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