# BHARATHIDASAN UNIVERSITY

Tiruchirappalli- 620024,
Tamil Nadu, India.

## Programme : M.Sc., Biomedical Science

**Course Title : Bioinformatics**
**Course Code : BM35S1BI**

## Unit- III

## TOPIC: PHYLOGENETIC ANALYSIS

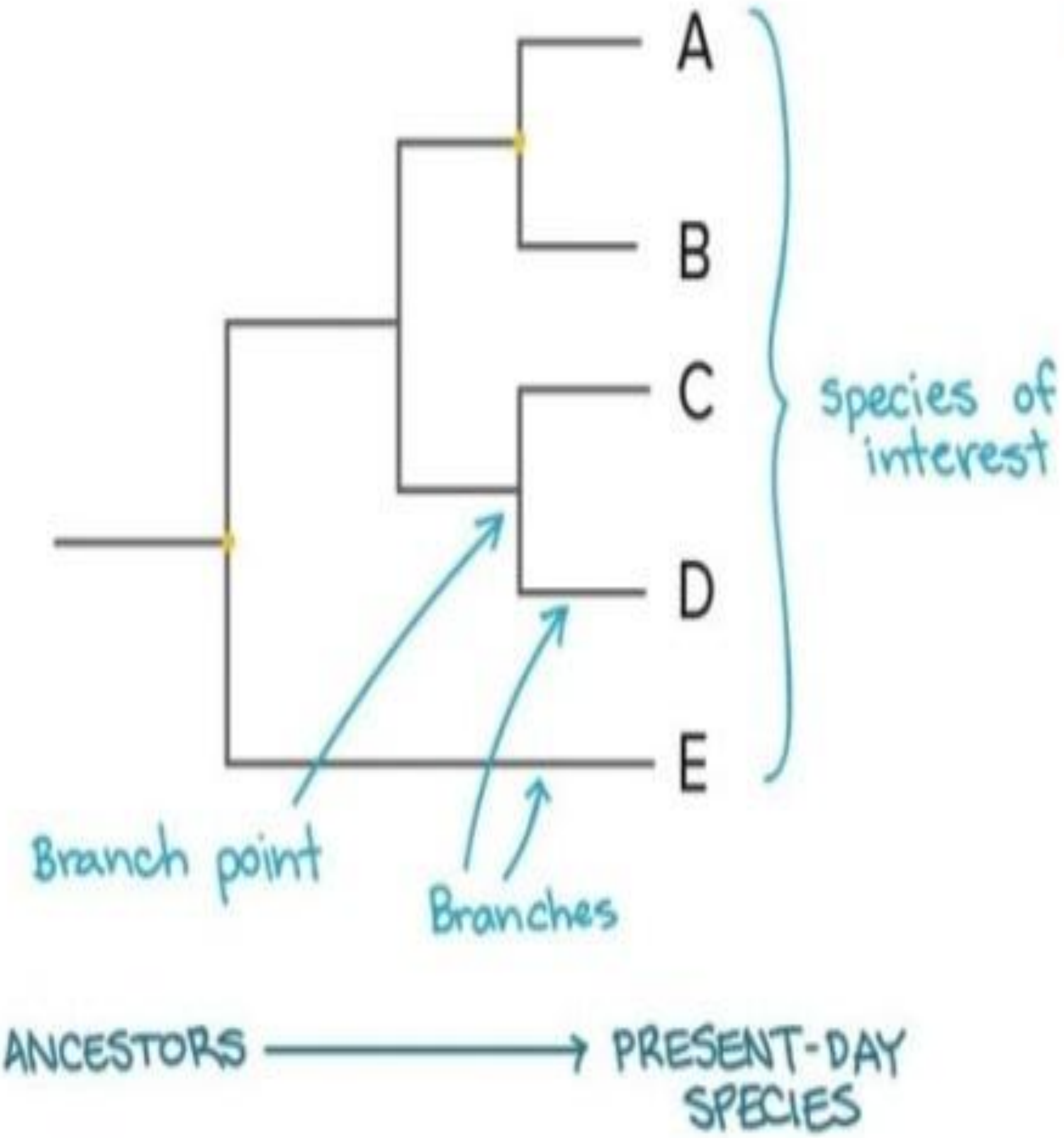
**Dr. P. JEGANATHAN**
Guest Lecturer
Department of Biomedical Science

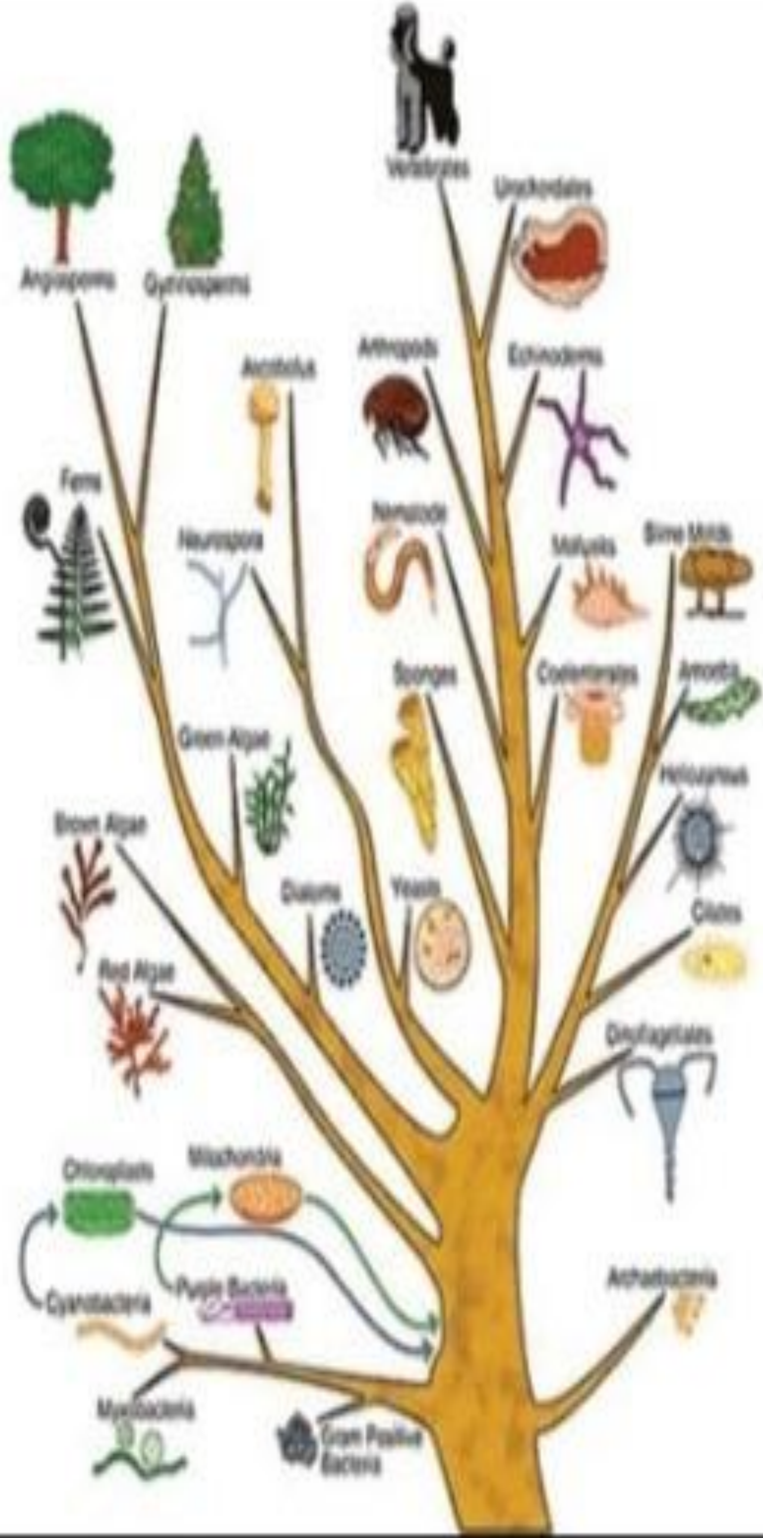
# PHYLOGENETIC ANALYSIS

SEQUENCE –BASED TAXONOMY

# PHYLOGENETIC ANALYSIS

In phylogenetic analysis ,branching diagrams are made to represent the evolutionary history or relationship between different species ,organisms ,or characteristics of an organism ( genes,protiens ,organs,etc..)that are developed from a common ancestor . The diagram is known as a phylogenetic tree. Phylogenetic analysis is important for gathering information on biological diversity ,genetic classification , as well as learning developmental events that occur during evolution.


A
B
C
D
E
species of interest
Branch point
Branches
ANCESTORS → PRESENT-DAY SPECIES


Vertebrates
Urochordates
Angiosperms
Gymnosperms
Acetabularia
Arthropods
Echinoderms
Ferns
Neurospora
Nematode
Molluscs
Slime Molds
Sponges
Coelenterates
Amoeba
Green Algae
Heliozoans
Brown Algae
Diatoms
Yeasts
Ciliates
Red Algae
Dinoflagellates
Chloroplasts
Mitochondria
Purple Bacteria
Cyanobacteria
Archaebacteria
Myxobacteria
Gram Positive Bacteria

# SEQUENCE

Sequence analysis is the process of subjecting a DNA,RNA or Peptide sequence to any wide range of analytical methods to understand its features,function ,structure ,or evolution. Phylogenetic analysis uses nucleotide or amino acid sequence Or other parameters ,such as domain sequence and three – dimensional structure , to construct a tree to show the Evolutionary relationship among different taxa(classification Units ) at the molecular level.

# DNA SEQUENCING

- DNA sequencing is the process of determining the precise orde of nucleotides or order of the four bases – adenine,guanine , cytosine , and thymine ,in a strand of DNA.

- Expressed sequence Tag (EST) is a short sub- sequence of a cDNA sequence . ESTs may be used to identify gene tanscripts , and are instrumental in gene discovery and in gene – Sequence determination .

# PROTEIN SEQUENCING

Protein sequencing is a technique to the determine amino acid sequence of a protein ,as well as which conformation the protein adopts and the extent to which it is complexed with any Non- peptide molecules.

# SEQUENCE ALIGNMENT

Sequence alignment is a way of arranging the sequences of DNA ,RNA or protein to identify regions of similarity that May be a consequence of functional, structural , or Evoluntionary relationships between the sequences.  it involves the identification of the correct location of deletions and insertions that have occurred in either of the two lineages since the divergence from a common ancestor.

# TYPES

On the basis of number of comparing sequencing strand ,
It is of two types:

- Pair –wise alignment
- Multiple sequence alignment

# Pair –wise sequence alignment

Pair –wise sequence alignment only compares two sequence at a time A pairwise alignment consists of a series of paired bases,on bas from each sequence.there are three types of pairs:

matches= the same nucleotide appears in both sequence
mismatches= different nucleotides are found in the two sequence
gaps = a base in one sequence and null base in the other.

# Multiple sequence alignment

Multiple sequence alignment (MSA) is a sequence alignment Of three or more biological sequence ,generally protein,DNA, Or RNA.

# TAXONOMY

Taxonomy is the branch of biology that deals with identification (placement of a new organism into a previously described group), Nomenclature ,and classification.

# Phylogenetic taxonomy

1859Darwin insisted classification should reflect genetic Relatedness. 1900 emil willi henning grouped organisms by inferred Evolutionary relatedness  homologous structures inherited from common ancestors So were related.

Carolus linnaeus designed our hierarchical classification Sc he me .

- kingdom
- phylum
- class
- order
- family
- genus
- species

All animals are placed in kingdom animalia Binomial nomenclature is the system Linnaeus used for naming species.

# Ranking system

Today naming is regulated by nomenclature codes allowing names to be divided into ranks

**Animals**
Organisms able to move on th
own.

**Chordates**
Animals with a backbone.

**Mammals**
Chordates with fur or hair an
milk glands.

**Primates**
Mammals with collar bones
grasping fingers.

**Hominids**
Primates with relatively flat
and three-dimensional vision.

**Homo**
Hominids with upright post
and large brains.

**Homo sapiens**
Members of the genus Homo w
hightforehead and thin skull b

## Clade system:

Clade are organisms or species that share derived character states and form a subset within a larger group.

A synapomorphy is a derived character shared by the members of the clade.

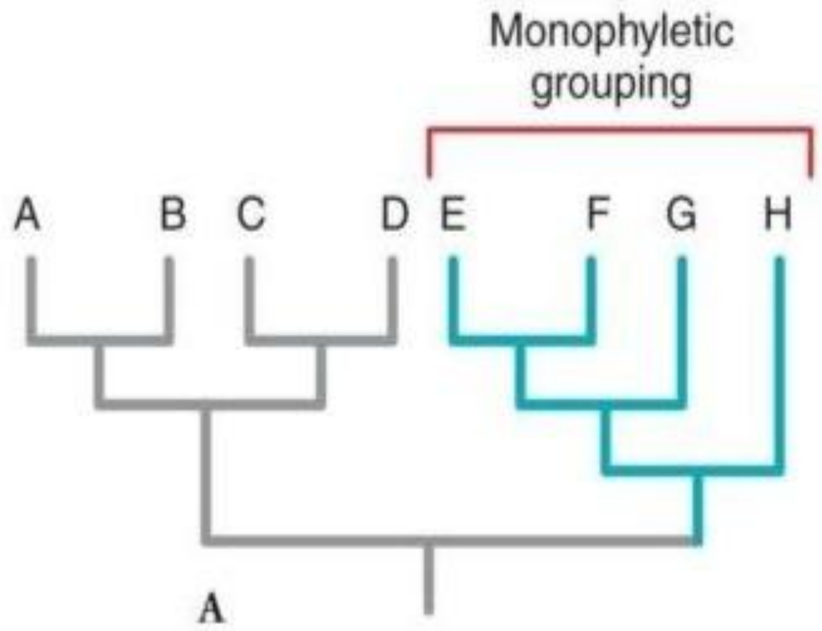
A nested hierarchy is formed by the derived states of all characters in a study group.

The nested hierarchy of clade can be represented as a cladogram that is based on shared synamorphies .

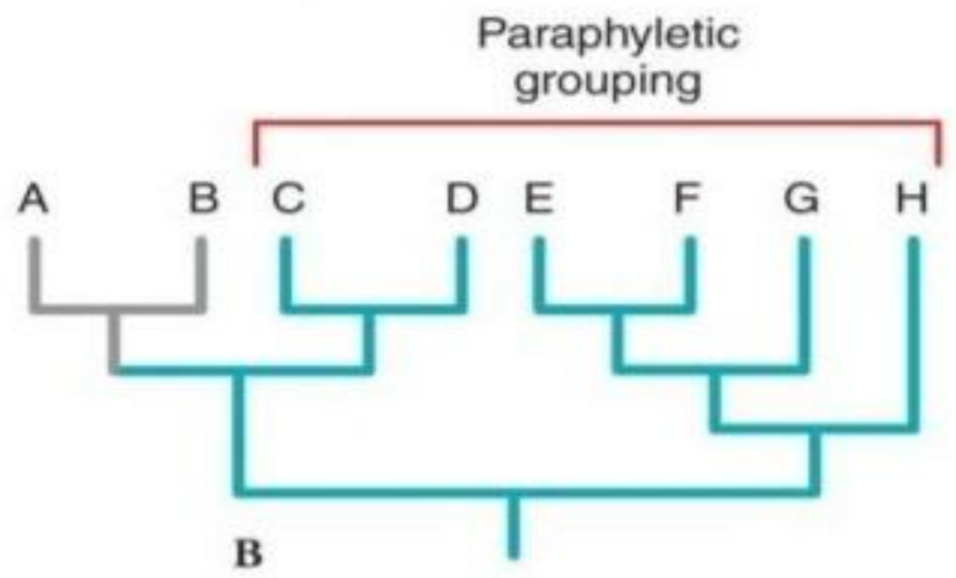
Cladistic system: 1960's scientists started using DNA sequences to determine common ancestry ignoring ranks. International code of phylogenetic nomenclature ( phylocode) is currently under development.

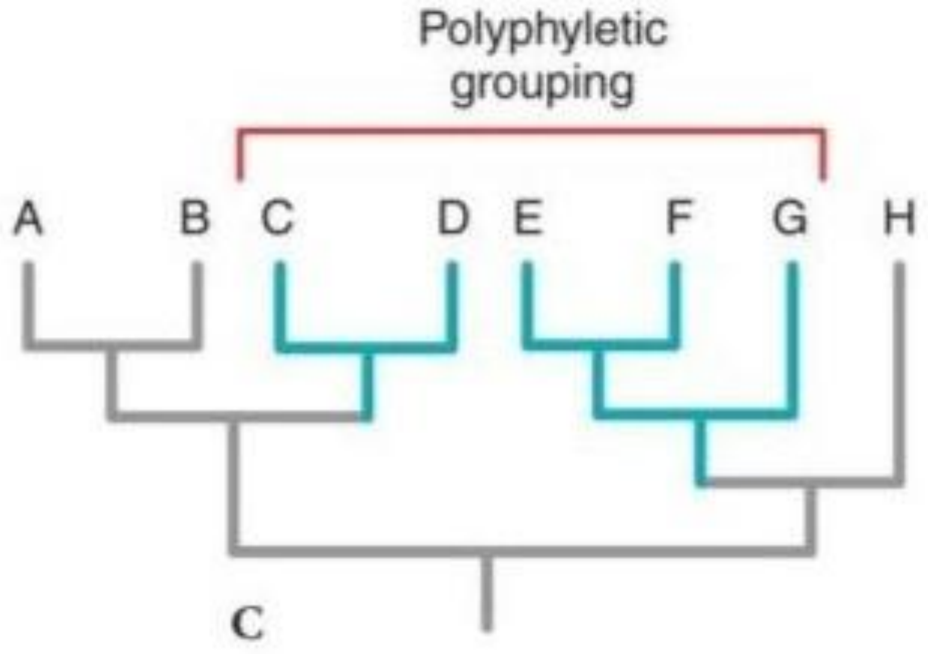
MONOPHYLOLETIC: signifying that it consists

of the ancestors species and all its descendants.



PARAPHYLETIC: Clade is grouping that consists of an ancestral species and some,but not all of the descendants.





POLYPHYLETIC: grouping includes numerous types of organisms that lack a common ancestor.

# THEORIES OF TAXONOMY

A theory of taxonomy allows us to rank taxonomic groups:  Two popular theories

- Evolutionary taxonomy
- Phylogenetic systematics

Both based on evolutionary principles, sometimes results conflict

EVOLUTIONARY TAXONOMY  Evolutionary taxonomy utilizes common descent and the amount of adaptive evolutionary change to rank higher taxa. Sometimes this type of classification includes paraphyletic groupings.

PHYLOGENETIC SYSTEMATICS or cladistic, emphasize common descent and is based on cladogram All taxa must be monophyletic Cladistic taxonomists have moved chimpaces, gorillas,and orangutans into the family hominidae

Humans and chimps form a sister group,as do the human /chimp group and gorillas .

BOTH EVOLUTIONARY AND CLADISTIC TAXONOMY:
Accept monophyletic groups  Reject polyphyletic groupsv  Differ on accepting paraphyletic groups

Evolutionary taxonomy does
Phylogenetic systematics does not .

## MODERN SYSTEM

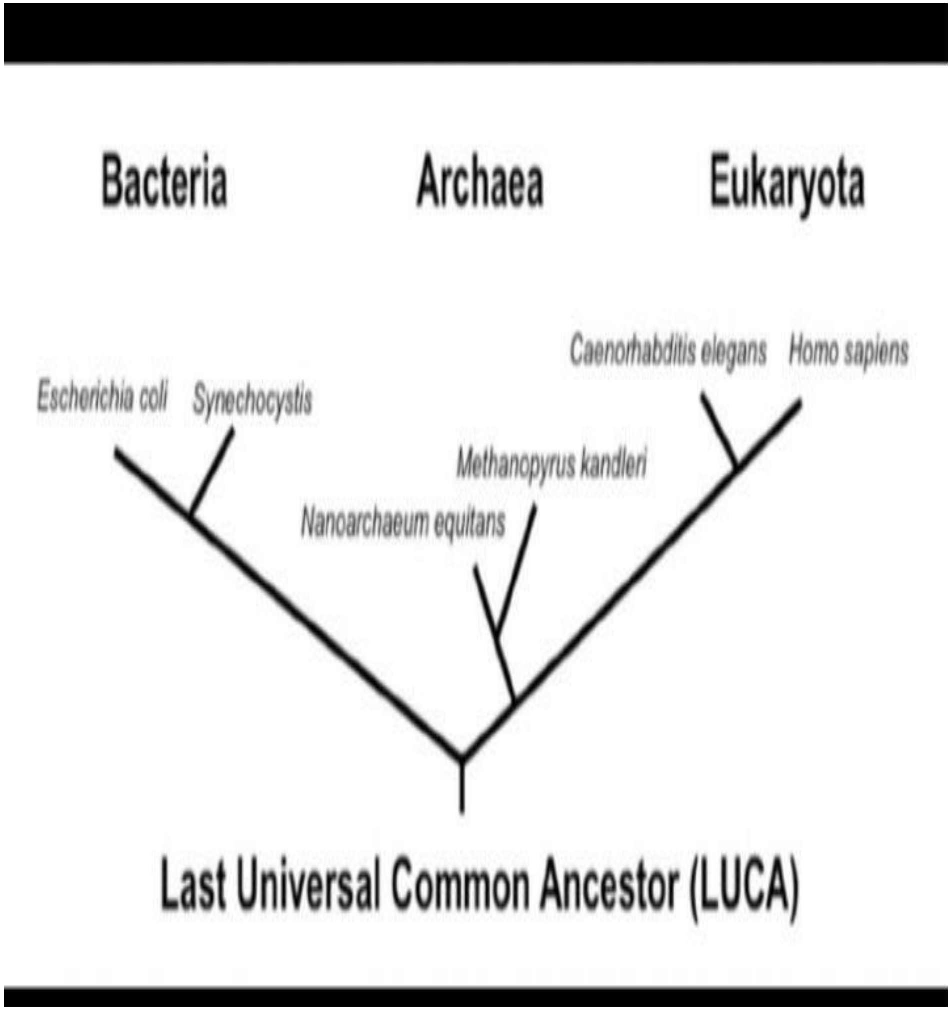
Three - domain system

- Compares ribosomal
- RNA

  all cells have ribosome

Bacteria,archaea ,eukarya

- With six kingdoms as subgroups



# References

Hall BG. 2011. Phylogenetic trees made easy: a how-to manual. 4th ed.Sunderland (MA): Sinauer Associates.

Hall BG, Barlow M. 2006. Phylogenetic analysis as a tool in molecular epidemiology of infectious diseases.Ann Epidemiol. 16:157–169.

THANK

YOU !!