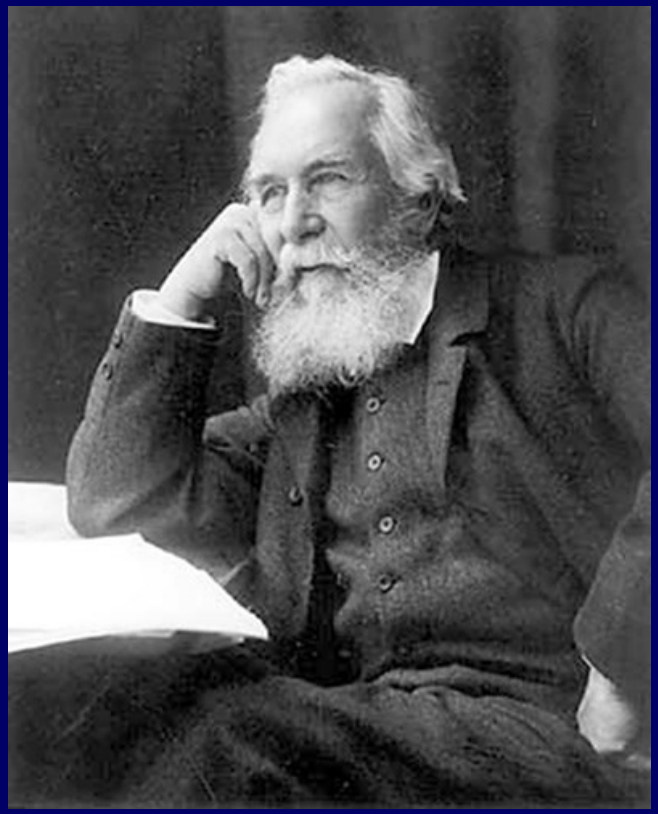
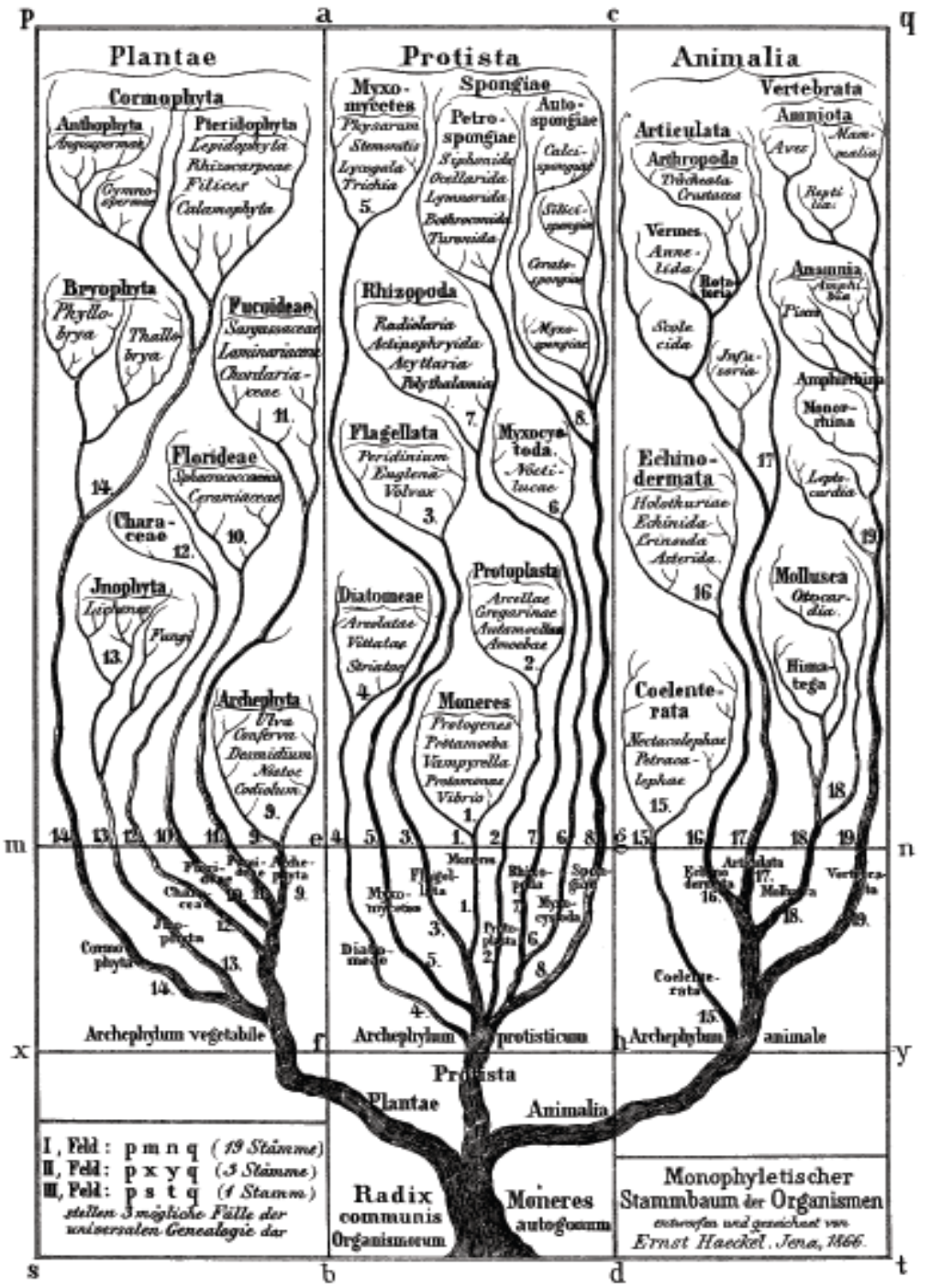
Molecular Phylogeny



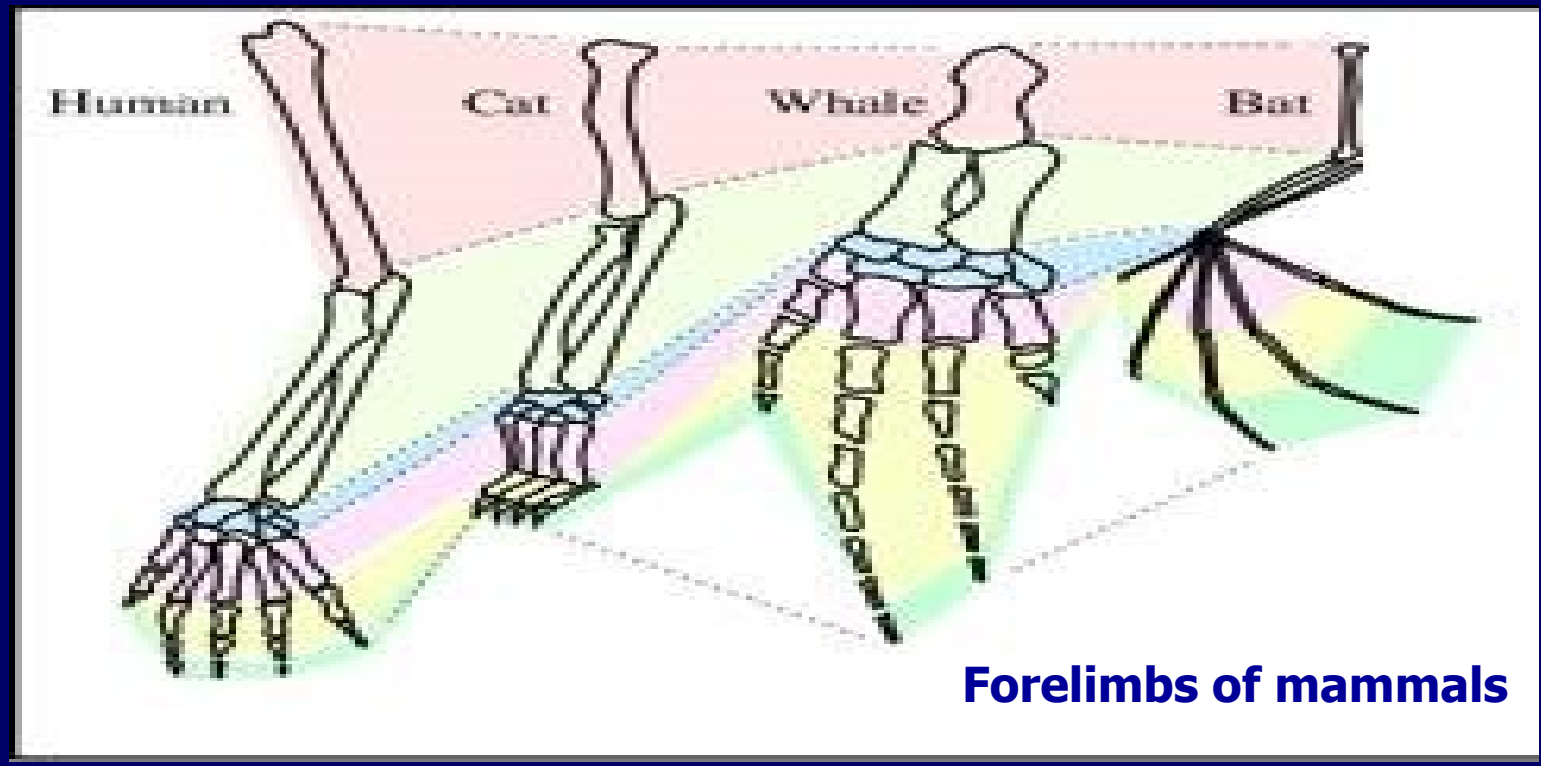
Ernst Haeckel, who coined the word ‘phylogeny’ illustrated evolutionary relationships using trees

Tree of Life, Ernst Haeckel, 1866



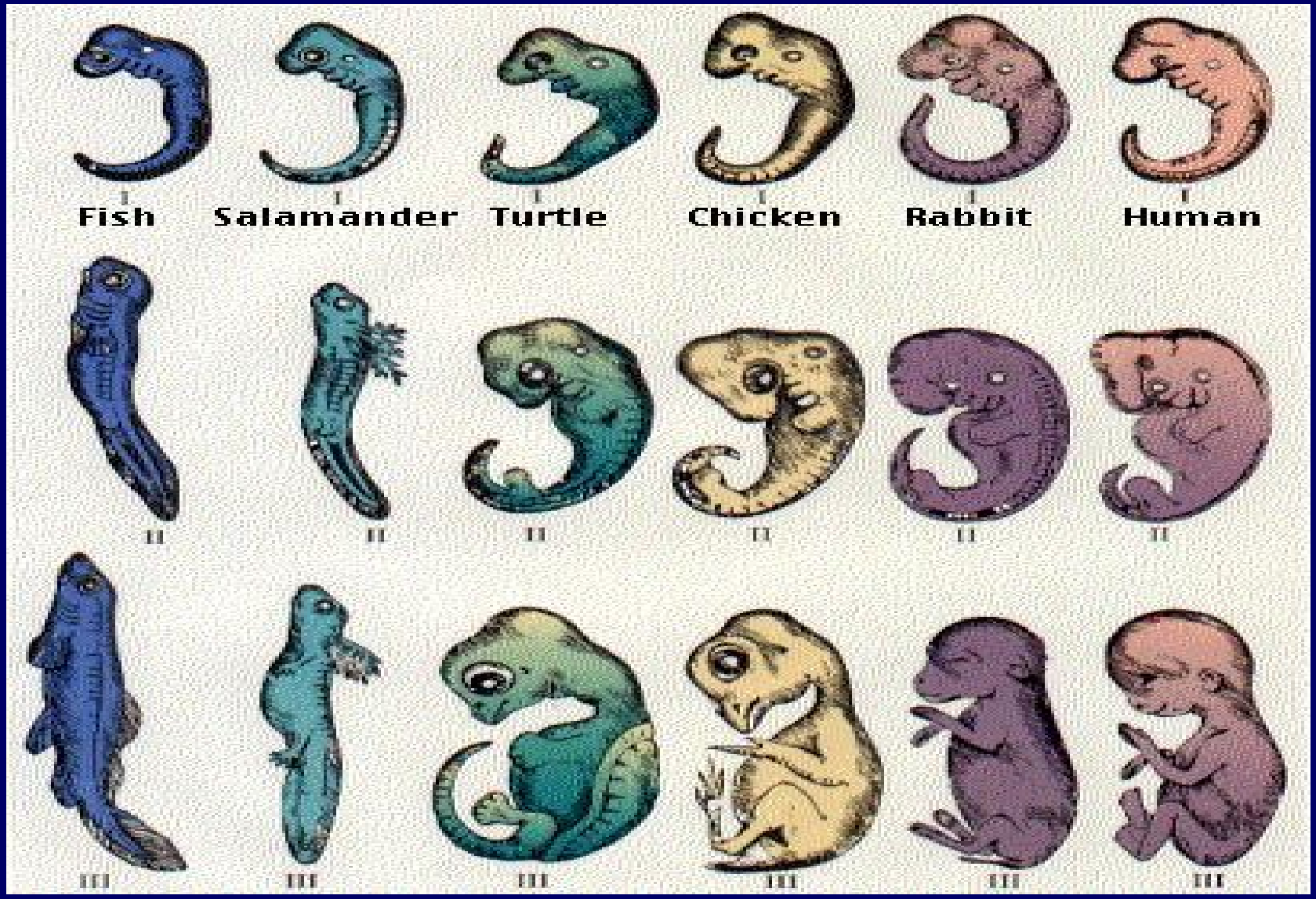
Phylogeny by Anatomy

- Before the birth of molecular biology, phylogeny was derived by looking for homologous anatomical structures or pattern of embryonic development

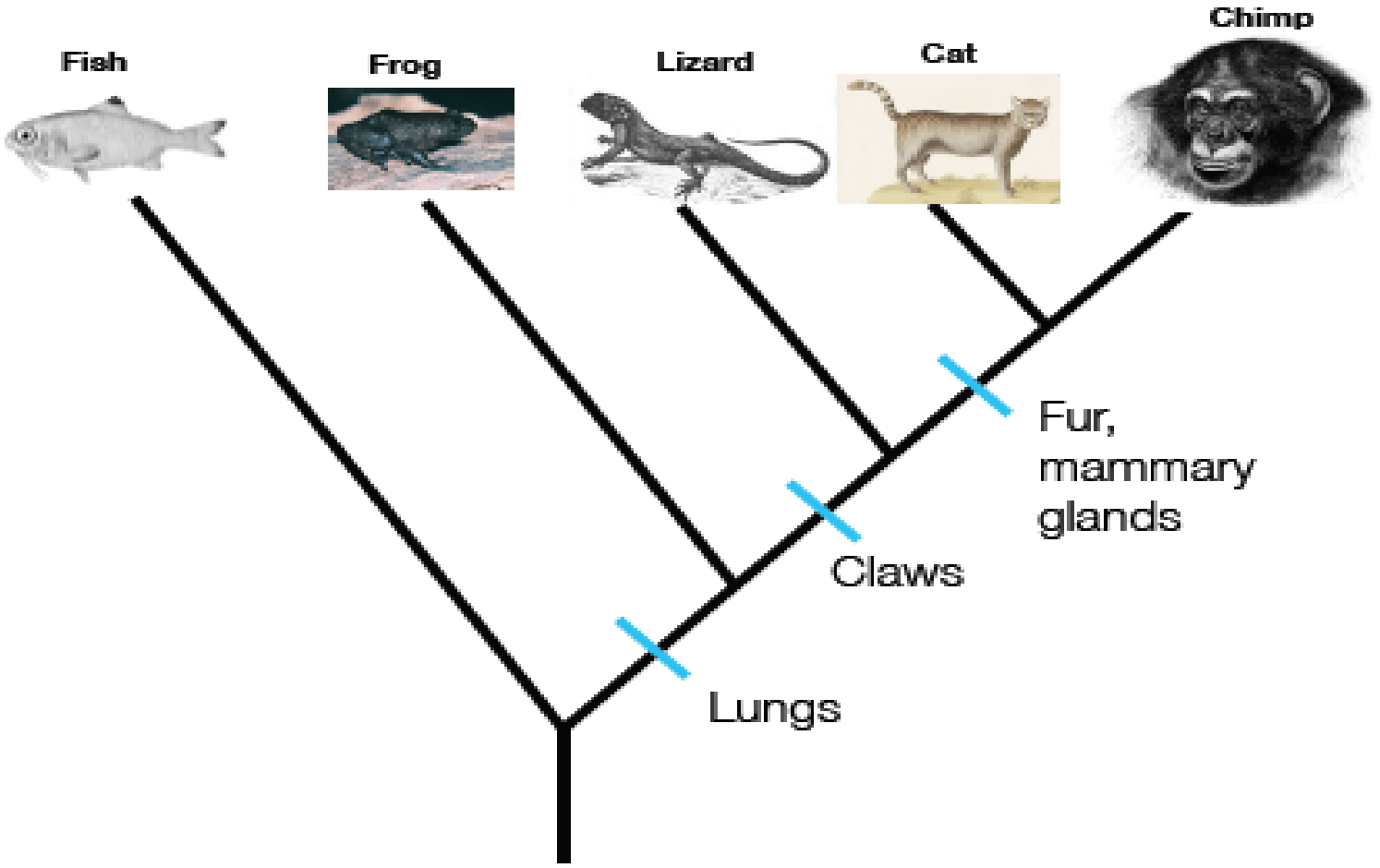


Anatomical Homology

Embryonic Development of Vertebrates



Reconstructing a tree



Molecular homology

Number of mutations between the human haemoglobin alpha chain (142 amino acids long) and

Human beta chain	0
Gorilla	1
Gibbon	2
Rhesus monkey	8
Dog	15
Horse, cow	25
Mouse	27
Gray kangaroo	38
Chicken	45
Frog	67
Lamprey	125
Sea slug (a mollusk)	127
Soybean (leghemoglobin)	124

Now phylogeny is based on proteins & DNA sequences

Molecular Phylogeny

- Mol. Phylogeny is the study of evolution of biological sequences (nucleic acid / protein)
- An MSA is the first step for phylogenetic analysis
- Aligned sequences are represented as outer branches on an evolutionary tree
- In a gene family phylogenetic relationships
  - one can determine, family membership and how the family might have evolved over time
  - helps in identifying genes with equivalent function, (can then be tested by genetic experiments)

Molecular Phylogeny

- Phylogenetic analysis may also be used to follow changes occurring in a rapidly changing species *e.g.* influenza
  - Study rapidly changing genes
  - Next year's strain can be predicted
  - Flu vaccination can be developed
- Analysis of the types of changes (synonymous / nonsynonymous) within a population can reveal, for example, whether a particular gene is under selection

Concept of Evolutionary Tree

- 2-dimensional graph showing evolutionary relationship between organisms, or genes from organisms
- Each sequence referred to as taxon, defined as phylogenetically distinct unit
- Taxa lie as outer branches (leaves) of tree, while internal nodes and branches represent relationship between taxa;

  - closely related taxa are found on neighbouring branches

Concept of Evolutionary Tree

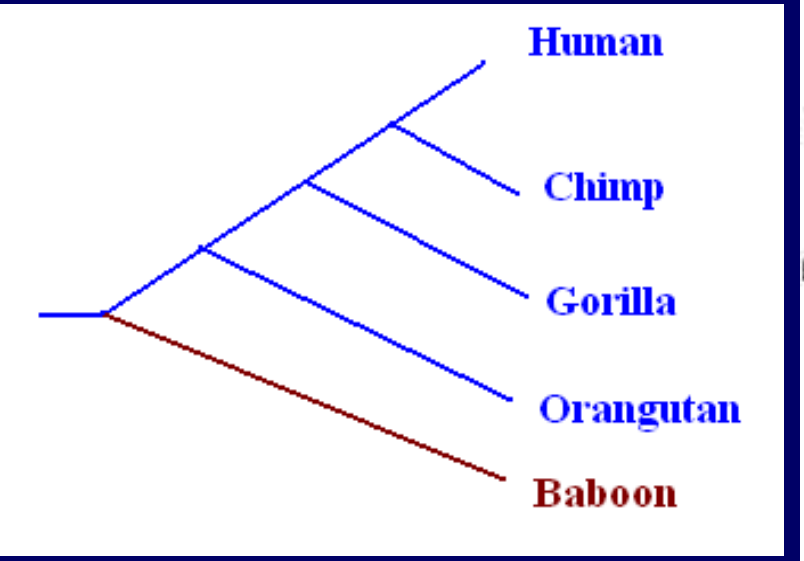
- Branch length indicates the No. of mutations (a measure of evolutionary time) before the next level of separation
- Internal nodes represent the splitting of evolutionary path of the gene into two different species that are reproductively isolated
- Molecular clock hypothesis assumes uniform rate of mutation, suitable for closely related species

  – represented by equal branch lengths from the common ancestor

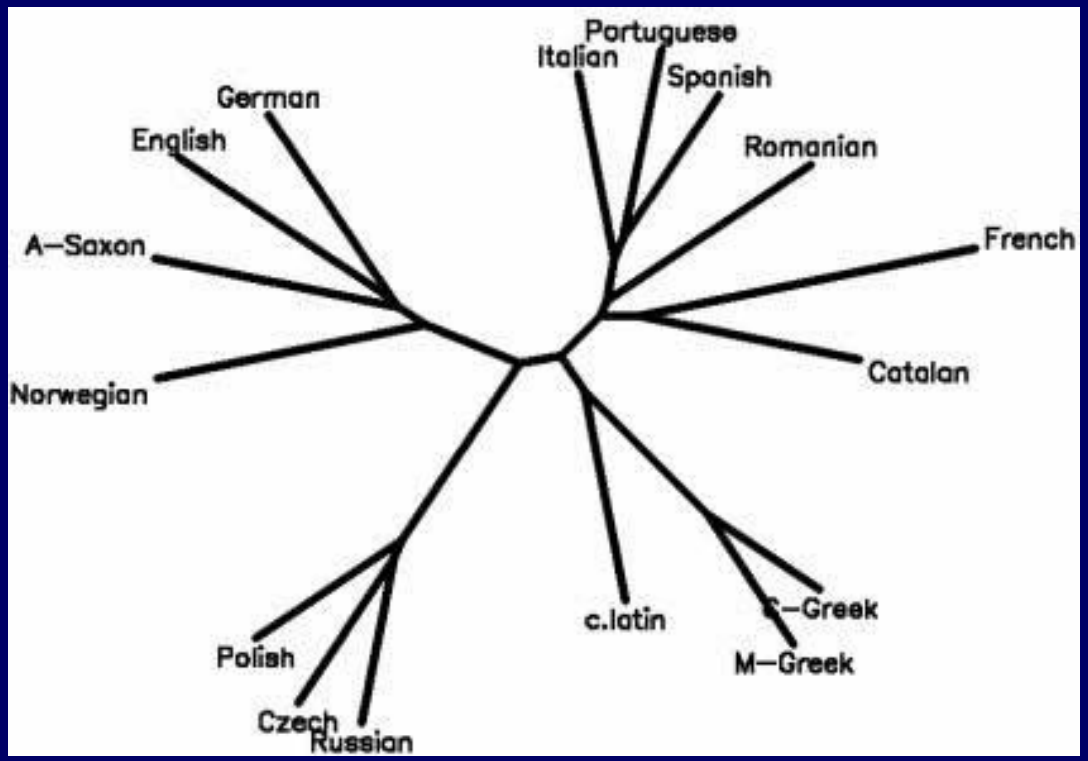
Concept of Evolutionary Tree

- Trees can be rooted or unrooted
- To construct a rooted tree include a taxon that we are reasonably sure branched off earlier than others, also termed as outgroup
- The sum of all branch lengths is termed as the length of the tree
- Trees are usually binary with two branches bifurcating at each node; may have more branches if taxa are too close to be resolved

Example: Rooted & Unrooted

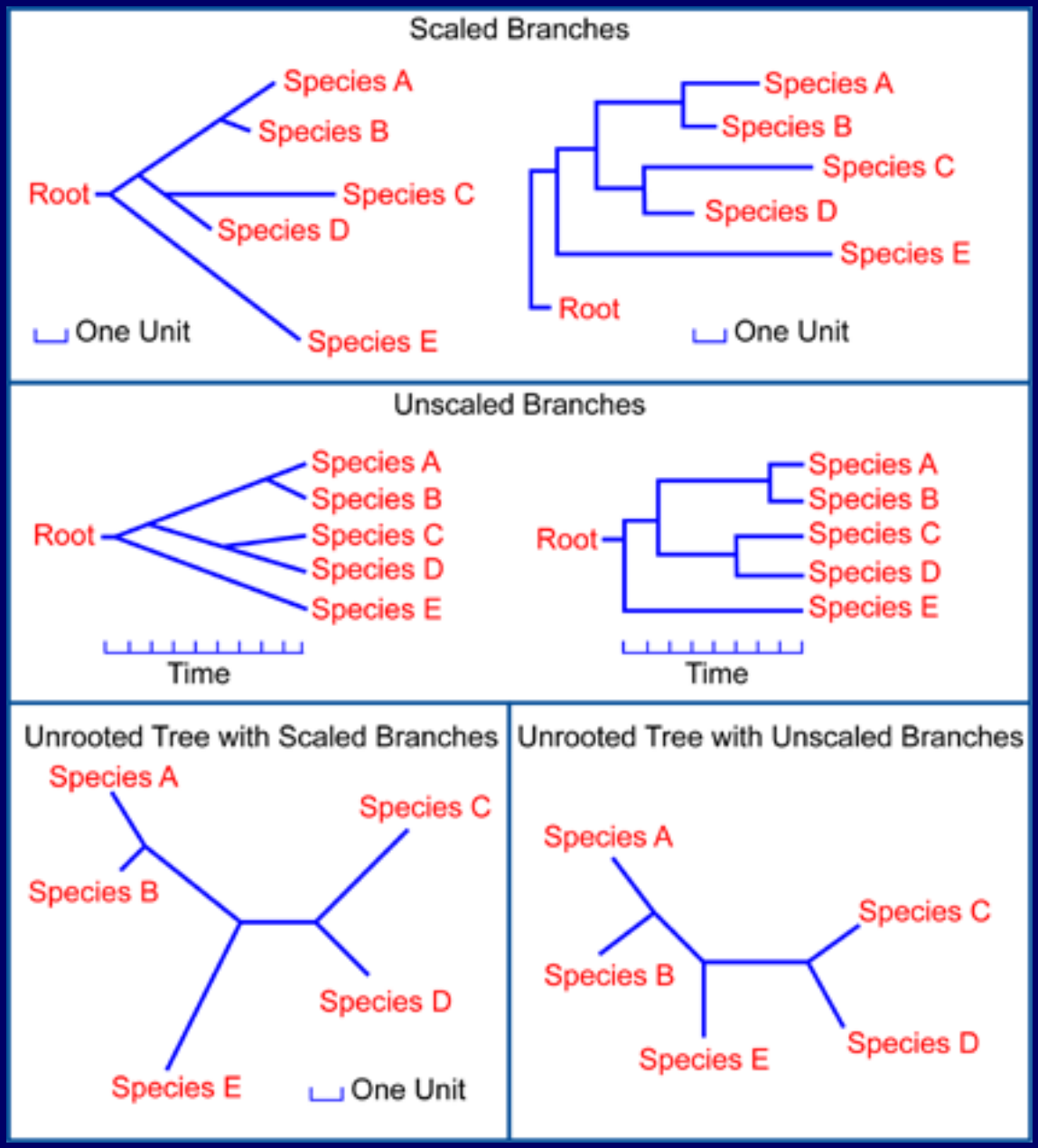


Rooted



Unrooted

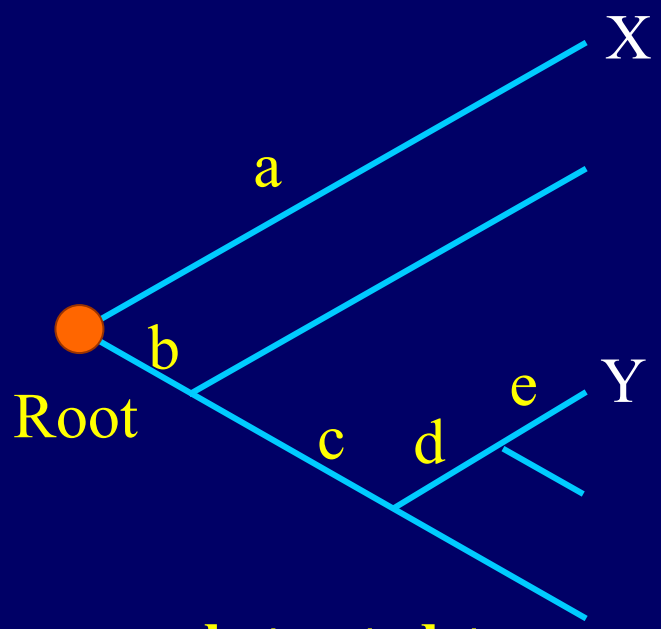
Example: Scaled & UnScaled



Concept of Evolutionary Tree

Ultrametricity

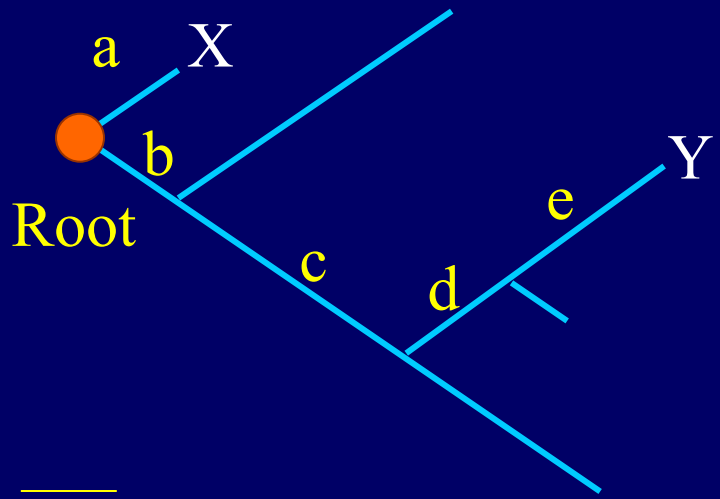
All tips are at equal distance from the root.



$$a = b + c + d + e$$

Additivity

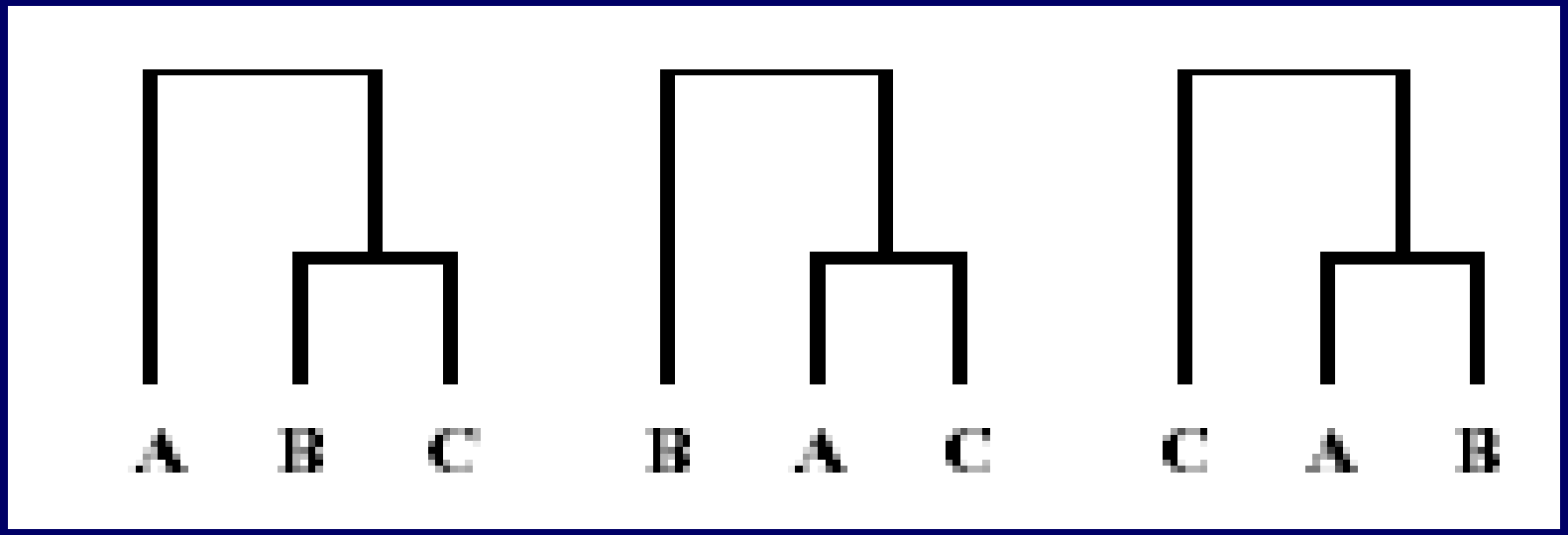
Distance between any two tips equals the total branch length between them.



$$\overline{XY} = a + b + c + d + e$$

Tree reconstruction

- Tree reconstruction becomes difficult if all possible trees have to be scored before deciding on the optimal tree
- For three species there are only three possible trees



Tree reconstruction

- With 4 species the No. of rooted trees becomes 15, 105 for 5 species and over 13 billion for 12 species
- For *n* species, the No. of rooted trees is given by

$$(2n - 3)!/(2^{(n-2)}[n - 2]!)$$

- For unrooted trees, the No. is significantly smaller (1 for n=3, 3 for n=4, 15 for n=5, and over half a billion for n=12):

$$(2n - 5)!/(2^{(n-3)}[n - 3]!)$$

- This problem has been shown to be NP-hard

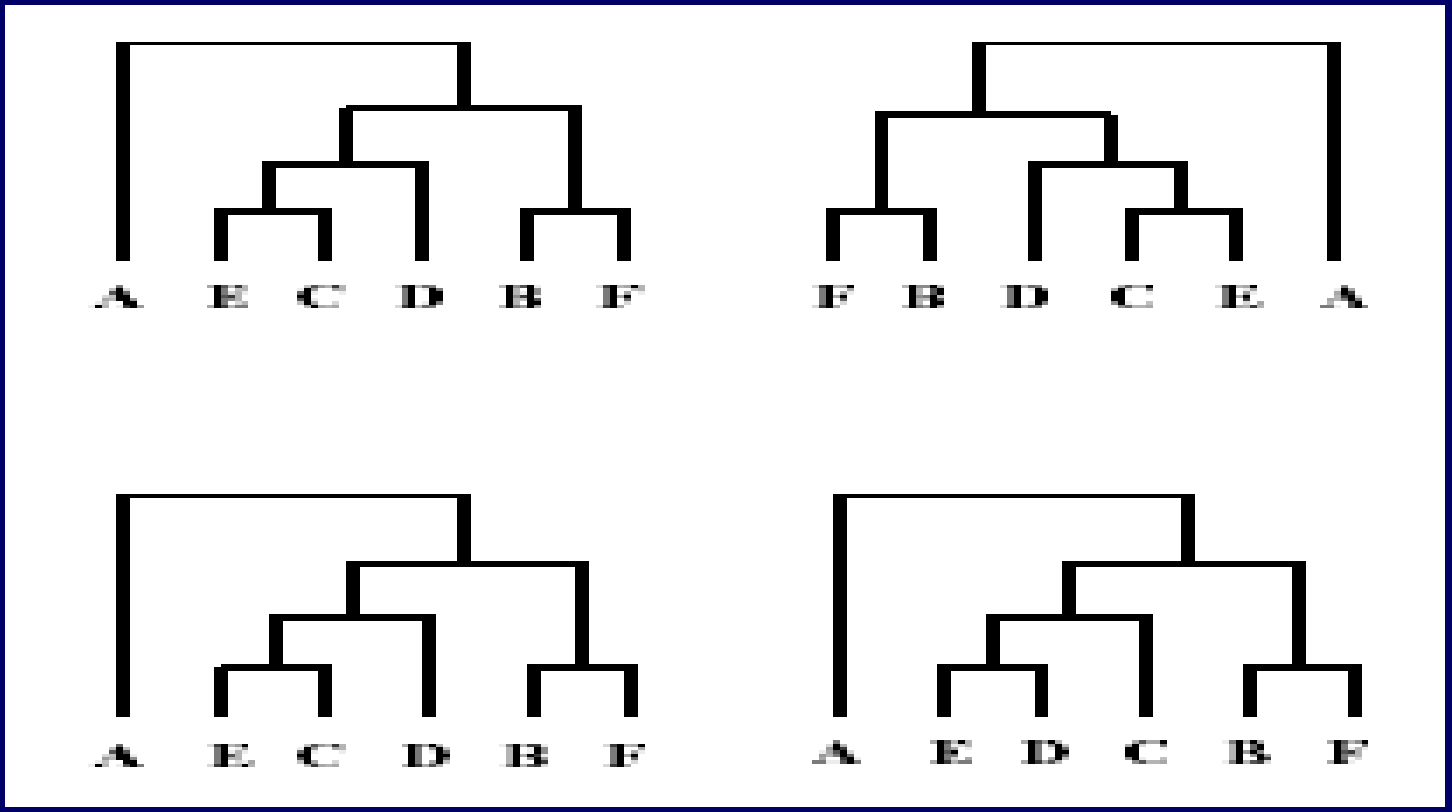
Number of possible evolutionary trees to consider as a function of number of sequences

Taxa or sequence no.	No. of rooted trees	No. of unrooted trees
3	3	1
4	15	3
5	105	15
—	—	—
7	10,395	954

Terminology

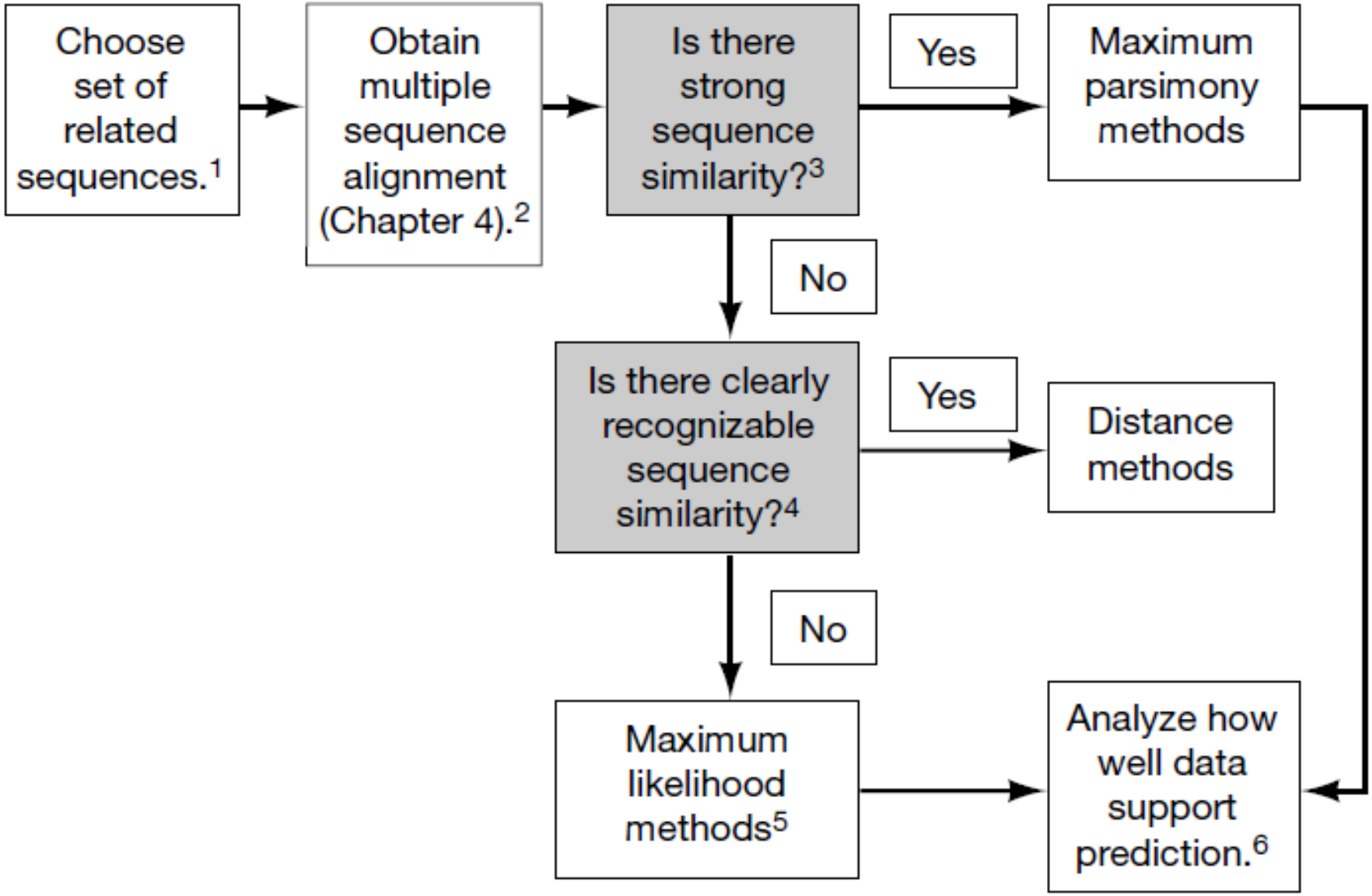
- **Tree topology: ordering of species independent of branch lengths**

Same topology



Different topology

METHODS

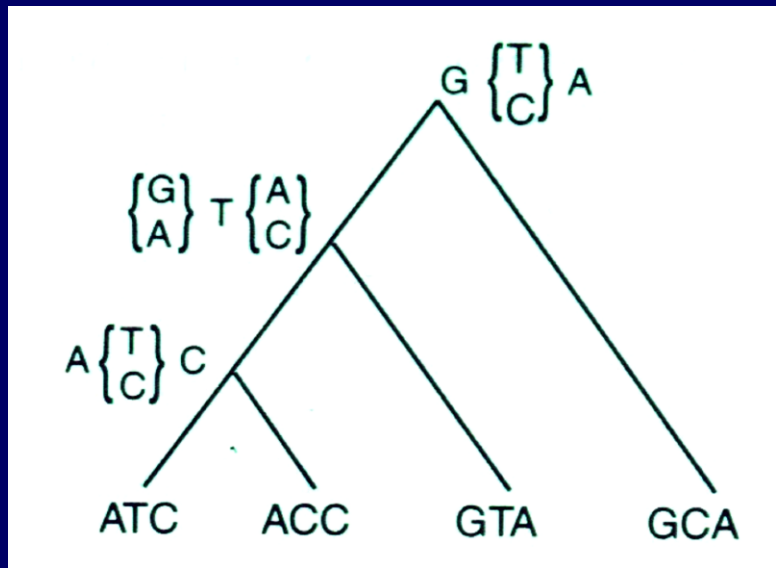

Choose set of related sequences.[1]
Obtain multiple sequence alignment (Chapter 4).[2]
Is there strong sequence similarity?[3]
Yes
Maximum parsimony methods
No
Is there clearly recognizable sequence similarity?[4]
Yes
Distance methods
No
Maximum likelihood methods[5]
Analyze how well data support prediction.[6]

Methods for Phylogeny

- Maximum parsimony approach is used for closely related sequences, and the variation is similar among all pairs of sequences
- Distance methods are used when more variation and intermediate level of similarity is present
- Maximum likelihood methods work for any set of sequences, but they are useful when sequences are very variable

Maximum Parsimony Method

- Predicts trees that minimize the No. of steps to generate observed variation
- For each aligned position, trees that require smallest no. of evolutionary steps to explain the observed changes are identified
- Finally the trees that produce the smallest no. of changes overall for all aligned positions are identified
- Works best for a small no. of closely related sequences



parsimony score = 4

Maximum Parsimony Method

- Maximum Parsimony method does not use any model of molecular evolution.
- It is based on an implicit assumption that mutation is rare, and the best explanation of evolutionary history is the one that requires the least mutation.

Phylip Programs: Parsimony

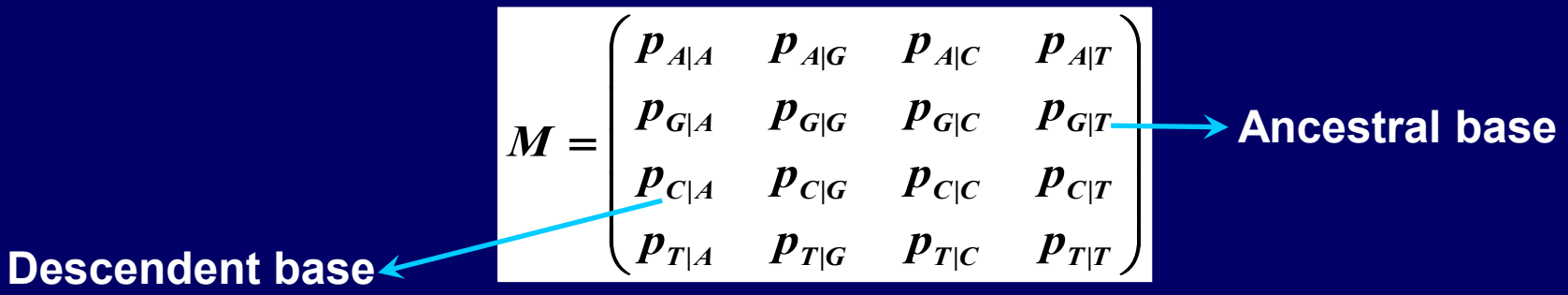
- **dnapars**: treats gaps as 5th state
- **dnapenny**: uses branch and bound method
- **dnacomp**: based on compatibility criteria; finds tree that supports largest number of sites
- **dnamove**: performs parsimony and compatibility interactively
- **protpars**: based on no. of mutations to change a codon for aa1 to codon for aa2 for non-synonymous changes only

Distance Methods

- Uses No. of changes between pairs of sequences in a group to construct a tree
- Sequences with fewest changes are neighbours, *i.e.* they share a node to which they are joined by a branch
- Aim is to position neighbours correctly and to compute branch lengths that best fit the data
- Methods for tree construction: UPGMA, Fitch-Margoliash, Neighbour-Joining, etc., based on distance matrix that gives substitution rates.

Distance Methods

- Distance is computed based on conditional probability of observing a change.
- A simplest model, called Jukes-Cantor assumes all substitutions have same rate of mutation, while more complex one define different rates for each type of substitution.



Jukes-Cantor model

Transition matrix for Jukes-Cantor model:

$$M = \begin{pmatrix} 1-\alpha & \alpha/3 & \alpha/3 & \alpha/3 \\ \alpha/3 & 1-\alpha & \alpha/3 & \alpha/3 \\ \alpha/3 & \alpha/3 & 1-\alpha & \alpha/3 \\ \alpha/3 & \alpha/3 & \alpha/3 & 1-\alpha \end{pmatrix}$$

$$d_{JC}(S_0, S_1) = t\alpha \approx -\frac{3}{4}\ln\left(1 - \frac{4}{3}p\right)$$

Value of α depends on the **time step** we use and **features** of the particular DNA sequence being modeled.

α is a probability, but can be interpreted as a rate at which observable base substitutions occur over one time step and is measured in units of

α = (substitutions per site) / time step

Kimura Models

Kimura 2-parameter model allows for different rates for transitions (β) and transversions (γ), while substitution rates to be different:

$$M = \begin{pmatrix} * & \beta & \gamma & \gamma \\ \beta & * & \gamma & \gamma \\ \gamma & \gamma & * & \beta \\ \gamma & \gamma & \beta & * \end{pmatrix}$$

$$M = \begin{pmatrix} * & \beta & \gamma & \delta \\ \beta & * & \delta & \gamma \\ \gamma & \delta & * & \beta \\ \delta & \gamma & \beta & * \end{pmatrix}$$

with diagonal entries being 1-β-2γ, and 1-β-γ-δ, respectively.

$$d_{K2} = -\frac{1}{2}\ln(1-2p_1-p_2) - \frac{1}{4}\ln(1-2p_2)$$

$$d_{K3} = -\frac{1}{4}(\ln(1-2\beta-2\gamma)+\ln(1-2\beta-2\delta)+\ln(1-2\gamma-2\delta))$$

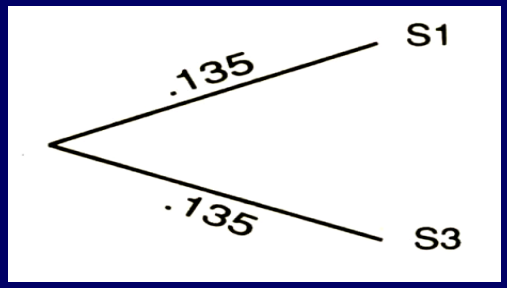
Tree Construction: UPGMA

Unweighted Pair-Group Method with Arithmetic Means (UPGMA), also called the average distance method.

- assumes that rate of change along the branches of a tree is a **constant**, i.e., it assumes a molecular clock.

	S_1	S_2	S_3	S_4
S_1		.45	.27	.53
S_2			.40	.50
S_3				.62

Distances Between Taxa



Step -1: pick the two closest taxa, S1 and S3, .27 distance apart.

Draw the edges, each of length 0.27/2 = 0.135, equidistant from the common ancestor.

UPGMA

Combine S1 & S3 into a group

	S_1	S_2	S_3	S_4
S_1		.45	.27	.53
S_2			.40	.50
S_3				.62

e.g., distance between S1-S3 and S2 is

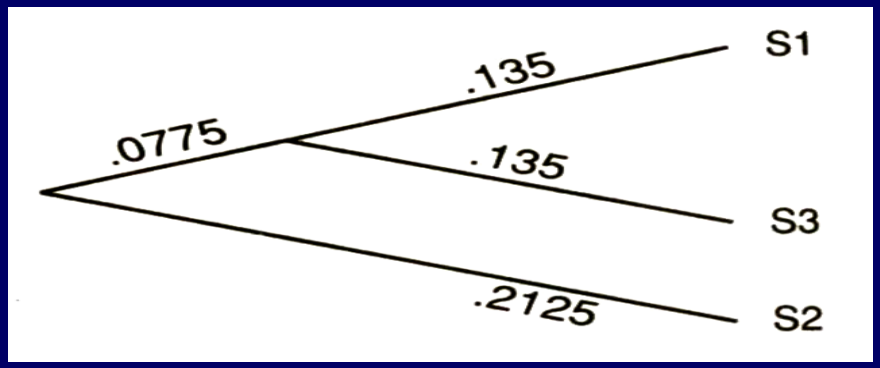
(.45 + .40)/2 = .425

The table then collapses to:

	S1-S3	S2	S4
S1-S3		.425	.575
S2			.50

UPGMA

Step-2: Repeat the process, using the collapsed distance table. Because the closest taxa and/or groups in the new table are S1-S3 and S2, .425 apart:



Edge to S2 will have length .425/2 = .2125, while the other new edge will be (.425/2) - .135 = .0775

	S1-S3	S2	S4
S1-S3		.425	.575
S2			.50

UPGMA

Step-3: Again combining taxa, we form a group S1-S2-S3, and compute its distance from S4 by averaging the original distances from S4 to each of S1, S2, and S3: (.53 + .5 + .62)/3 = .55

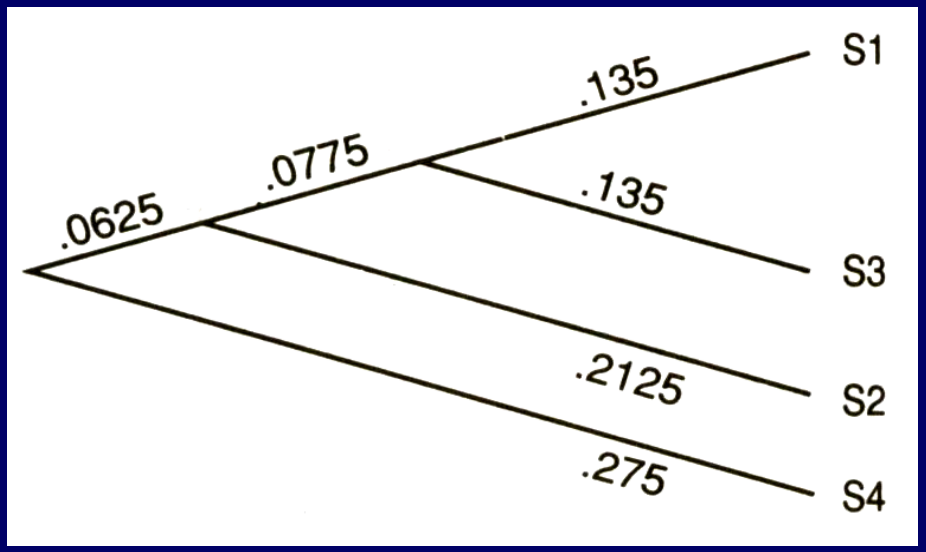
	S1-S2-S3
S4	.55

Final tree is drawn by estimating S4 as .55/2 = .275 from the root.

The other edge has length 0.275 – 0.2125 = .0625, since that places all other taxa .275 from the root as well.

UPGMA

	S_1	S_2	S_3	S_4
S_1		.45	.27	.53
S_2			.40	.50
S_3				.62



Does the constructed tree exactly fit the data?

Distance on the tree from S3 to S4 =.55, while according to the original data, it is.62!

To an approximation, the tree distances are reasonably close to the distances given by the data

UPGMA

Note: molecular clock assumption is implicit in UPGMA.

In this example, when we placed S1 & S3 at the ends of equal length branches, we assumed that the amount of mutation each underwent from their common ancestor was equal.

UPGMA always places all the taxa at the same distance from the root, so that the amount of mutation from the root to any taxon is identical.

UPGMA always produces a rooted tree.

Phylip Programs: Distance Methods

- **dnadist** is the Phylip program for computing distance among DNA sequences
- **protdist** is the program for computing distances for protein sequences
- **fitch** estimates branch length assuming additivity of branch lengths using Fitch-Margoliash method; molecular clock not assumed
- **kitsch** same as fitch but assumes molecular clock
- **neighbor** estimates phylogeny using the neighbour-joining or UPGMA method

Maximum Likelihood

- Maximum likelihood is similar to maximum parsimony, in that analysis is performed for each column of the alignment, all possible trees are considered, and trees with fewest changes are usually more likely
- ML allows corrections for variations in the mutation rates by considering explicit evolutionary models
- Method can be used to explore relationships among more diverse sequences

Maximum Likelihood

The basic approach of maximum likelihood is:

- Specify a particular model of molecular evolution (e.g., Jukes-Cantor (all substitutions are equally likely), Kimura (different rates for transitions and transversions).
- Consider a specific tree for relating our taxa. Assuming the model of evolution and specific tree are correct, compute the probability that the DNA sequence in our data could have been produced.

- This is the likelihood of the tree, given our data.

Maximum Likelihood

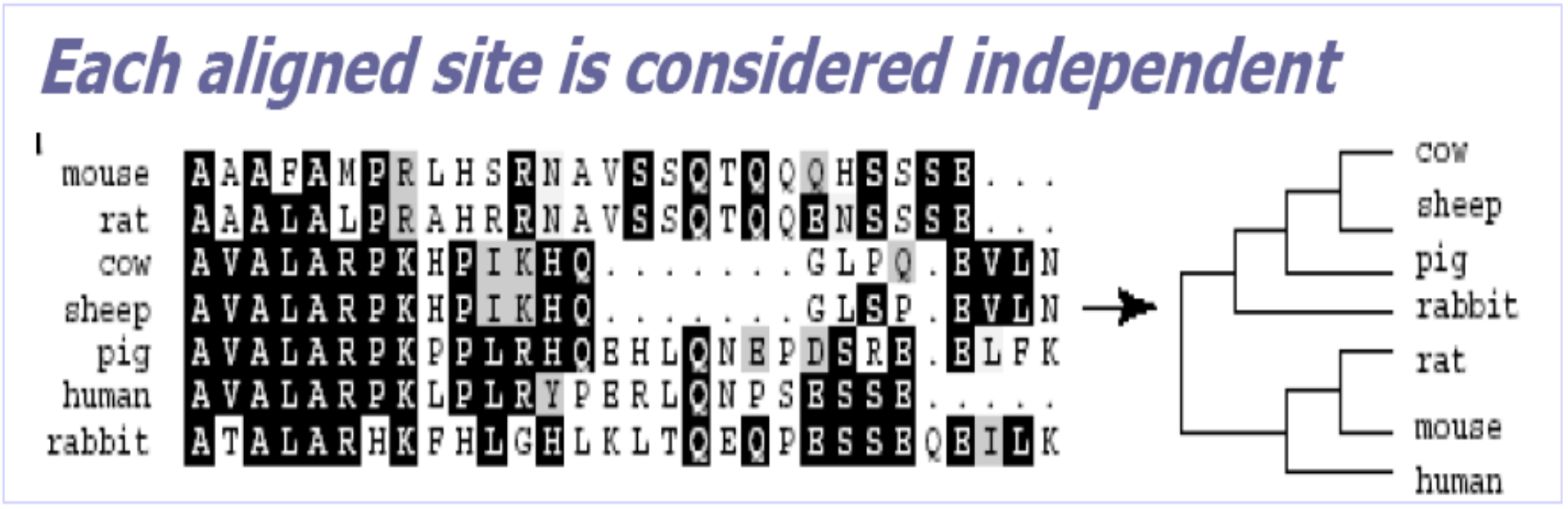
- Compute the likelihood for each tree
- Probability of each tree is the product of mutation rates in each branch
- Likelihoods given by each column are multiplied to give the likelihood of the tree
- Choose the tree with the greatest likelihood as the tree best fitting the data.
- Phylip programs dnaml and dnamlk (same as dnaml except that is assumes a molecular clock) and proml and promlk (for proteins)

Bootstrapping

- Once a tree has been chosen by some method, it would be desirable to quantify how confident one is of it.
- This is given by the statistical technique - bootstrapping.
- In this procedure, the true data sequences are used to create a set of new pseudo-replicate sequences of the same length.
- Bases at a particular site in the new sequences are chosen to be the bases appearing in a randomly chosen site in the original sequences.

Bootstrapping

Initial alignment and tree:

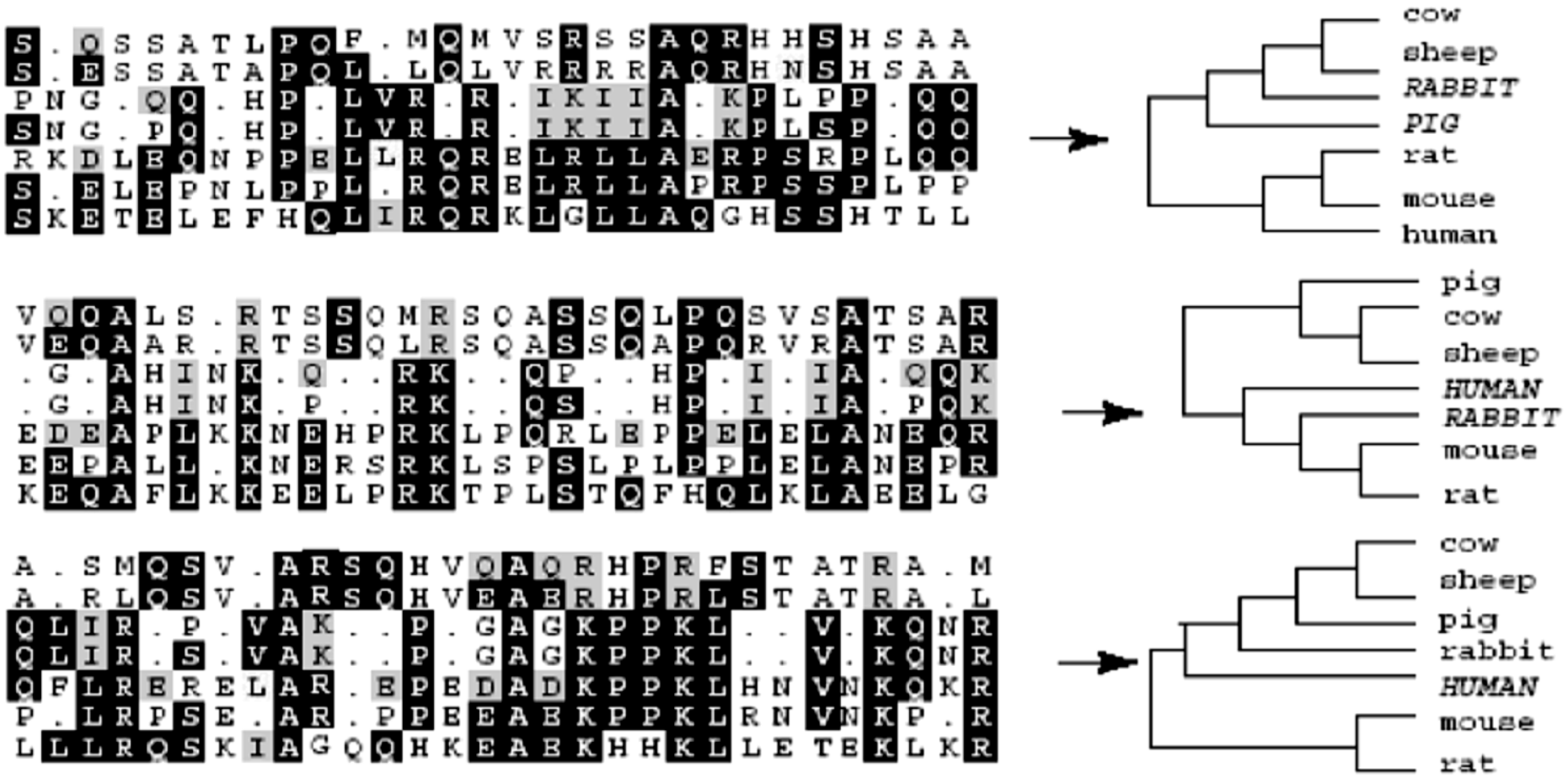


In bootstrap analysis:

- **All sites are considered independent as if freely available in a 'hat' to pick**
- **Available sites are picked up randomly to reconstruct a new alignment of the original size and a new phylogeny**

Bootstrapping

- Process is repeated many times to ascertain the strength of clustering. New “alignment” may contain several sites multiple times while some other sites may be absent - sampling with replacement



Bootstrapping

- Phylogenies are compared to calculate values [Bootstrap value] that signify the number of times a given branch/cluster occurred in the Multiple bootstrap trees
- Higher the value - higher the confidence of phylogenetic inference
- In general values < 50% provide very poor support

Which method is the Best?

One of the difficulties of picking a method is that one can find good arguments for and against them all.

Cautious approach - always use a number of different methods on the data.

Rather than trusting a single method to give an accurate tree, check to see if different methods give roughly the same results.

They often do, and if they do not, it is worth investigating why they don't.

References

- Bioinformatics Sequence & Genome Analysis, David W. Mount
- Biological Sequence Analysis, Probabilistic Models of Proteins and Nucleic Acids, R. Durbin, S.R. Eddy, A. Keoghs and G. Mitchison