PHYLOGENETICS

An introductory lecture

Alejandra Vergara-Lope

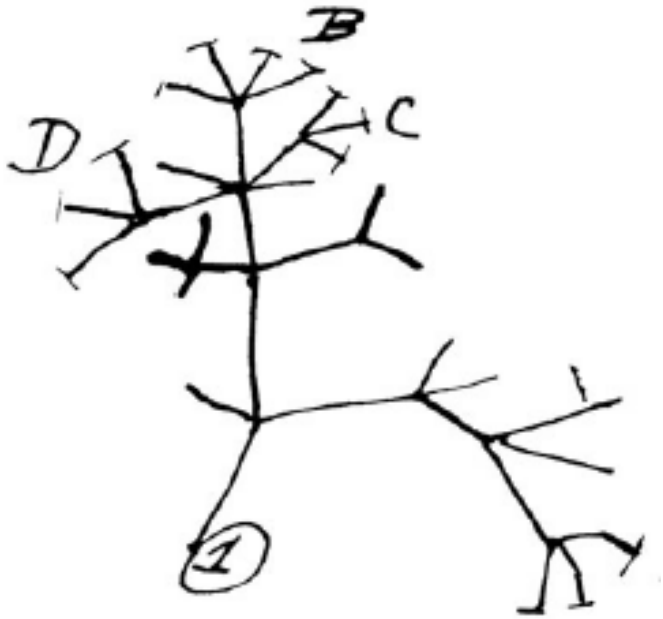
November 13th, 2025

Outline

Introduction to phylogenetics

Origins of phylogenetics

- Since ancient times : Living things are similar and can be grouped
- Several suggestions that organisms could be descended from others
- Darwin proposes natural selection and shows how this could work
- Naturalists, zoologists, ecologists, embryologists initially use morphological and anatomical traits to group organisms
- Mathematical and statistical studies provide sophisticated methods
- Molecular data adds a powerful tool for evolutionary comparisons
- Genomic technologies vastly increase the amount of data available



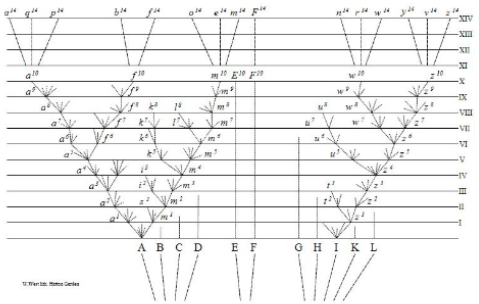
Two Major Tenets of Evolution

1. Heritable Variation

- Within a species, individuals differ from one another (in traits like colour, size, or resistance)
- These differences are genetic and can be passed from parents to offspring
- Sources of variation include mutations, recombination, and genetic drift

2. Descent with Modification

- Over time, species change as traits are passed on and modified across generations
- Populations accumulate small changes that can lead to the formation of new species
- This explains both the unity (shared ancestry) and diversity (differences) of life



Homology, Homoplasy, and Analogy

1. Homology

- Features that share a common ancestry (they may look different or serve different functions, but they come from the same ancestral structure)
- Example : the human arm, bat wing, and whale flipper are homologous structures

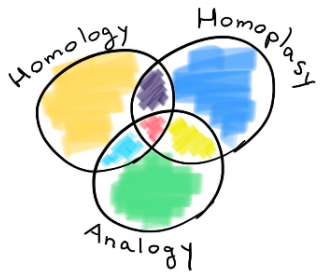
2. Homoplasy

- Similarity based on appearance, not on shared ancestry
- Often results from convergent evolution (independent evolution of similar traits) or evolutionary reversal
- Example : the wings of bats and birds look similar but evolved independently

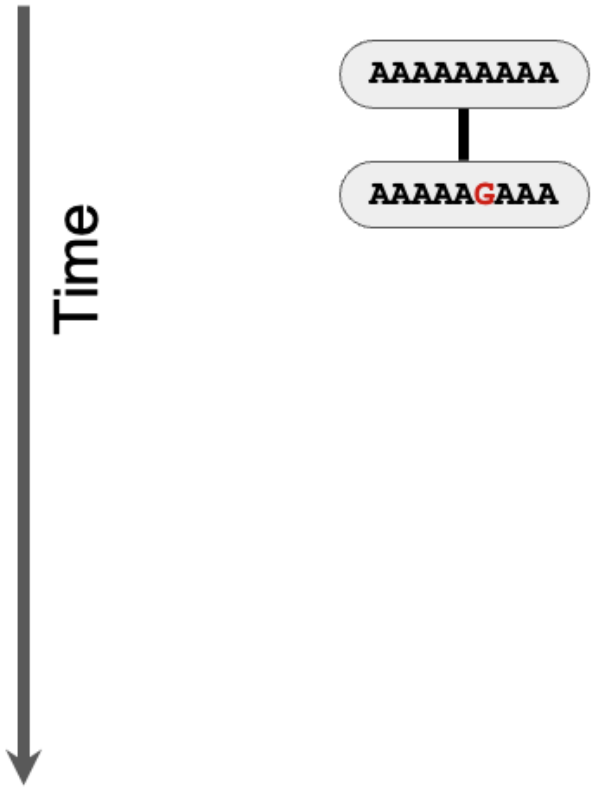
3. Analogy

- Features that have similar functions but do not share a common evolutionary origin
- Example : the wings of insects and birds are analogous because both are used for flying but evolved separately

Key point : Homoplasy and analogy both indicate independent origins, while homology indicates shared ancestry.

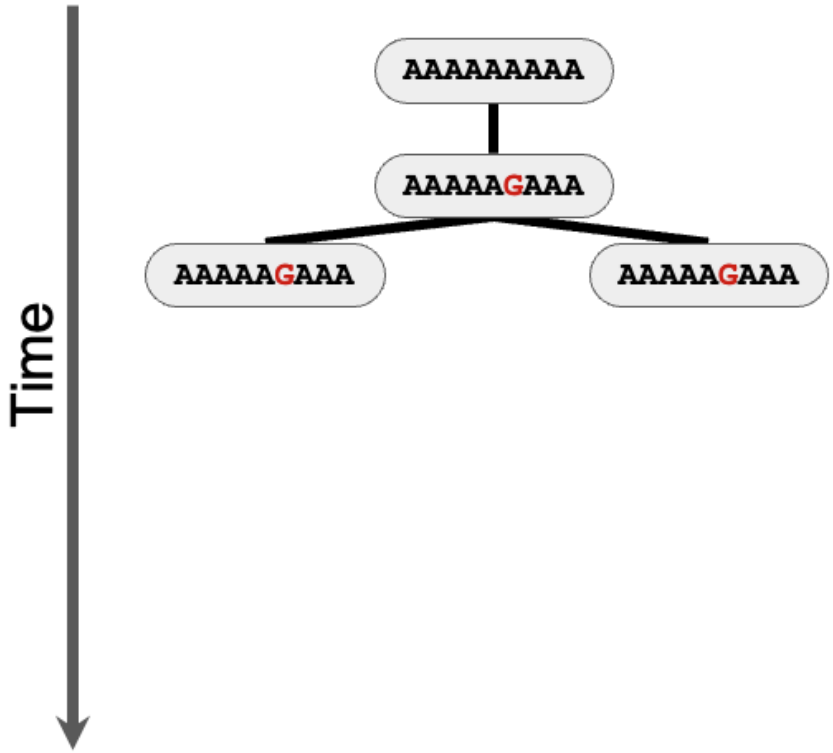


What is a phylogeny ?



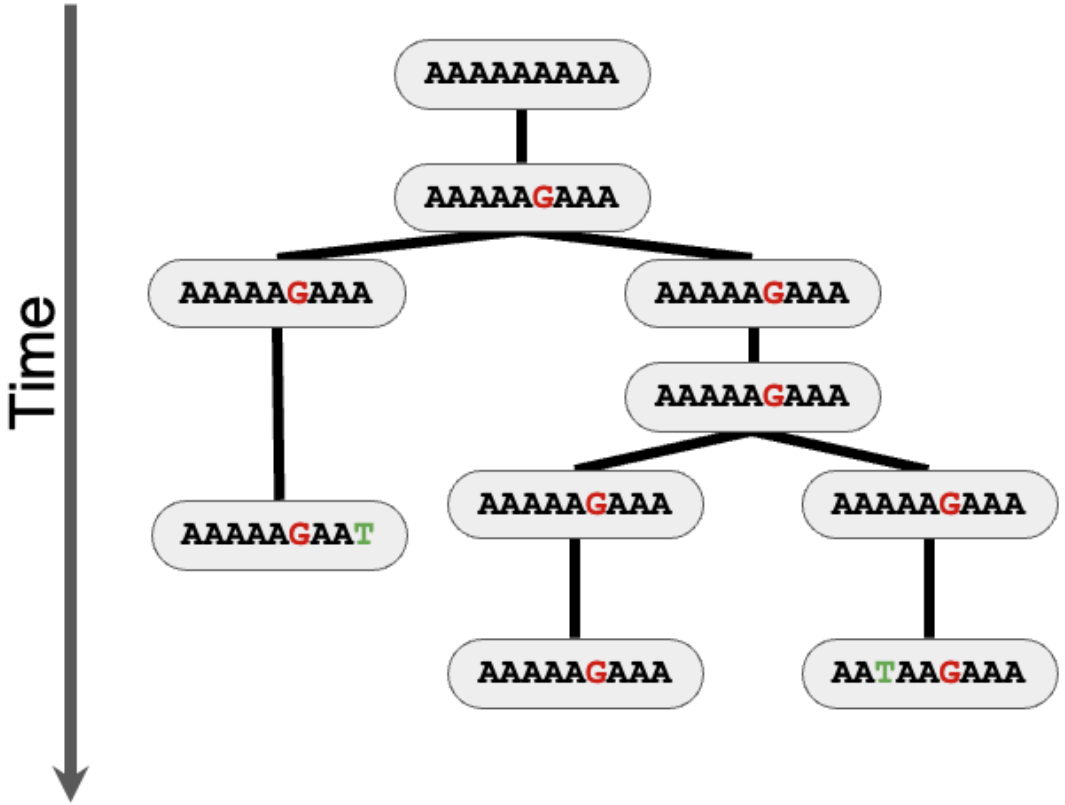
Sequence evolution: mutations alter the genomes being passed on from generation to generation.

What is a phylogeny ?



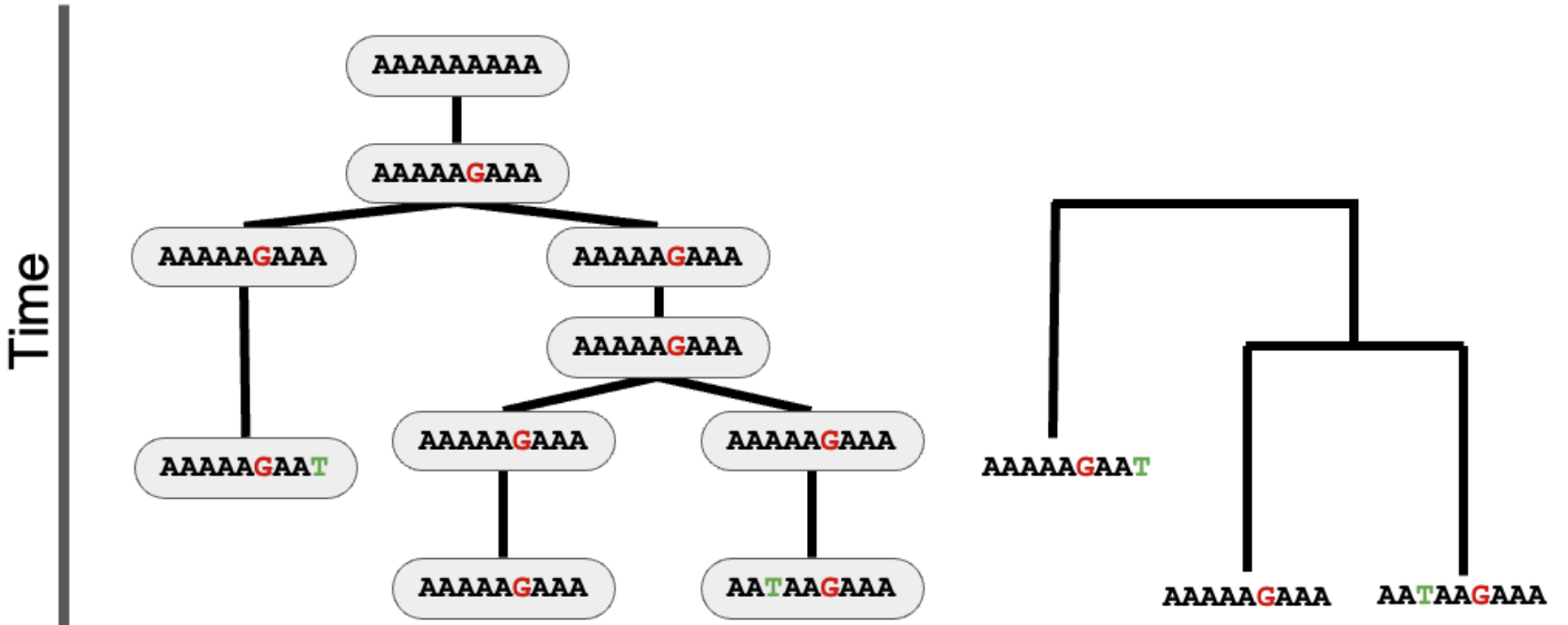
Branching: speciation events, infection of multiple hosts, cell division…

What is a phylogeny ?



Full evolutionary history.

What is a phylogeny ?



Molecular phylogenetics: inferring the evolutionary history from given sequences.

Basic Concepts and Terms

Phylogeny and phylogenetic tree

- A phylogenetic tree is a diagrammatic representation of the evolutionary relationships or phylogeny of a set of entities (organisms, molecules etc)
- Phylogeny reconstruction or inference is deducted from similarities and differences based on evolutionary traits or characters

Traits and characters

- Phenotypic : Morphology (e.g. Size and shape of body parts) Anatomy (Presence/ Absence of anatomical features)
- Molecular : Nucleotide (Genes and other conserved elements) and Proteins

Examples of phylogenies

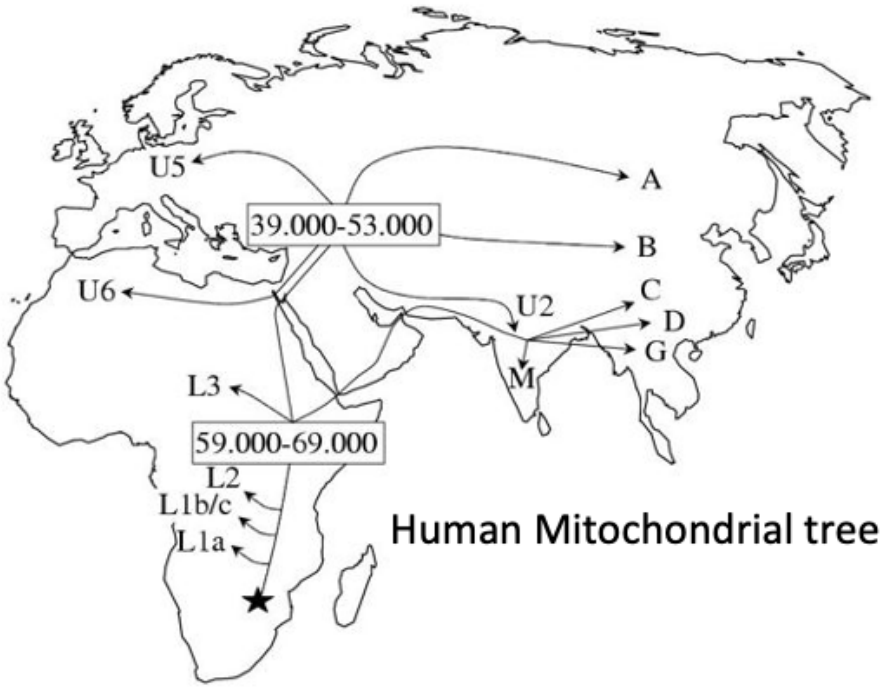


Figure – Taken from http ://tolweb.org and Maca-Meyer et al 2001

Examples of phylogenies

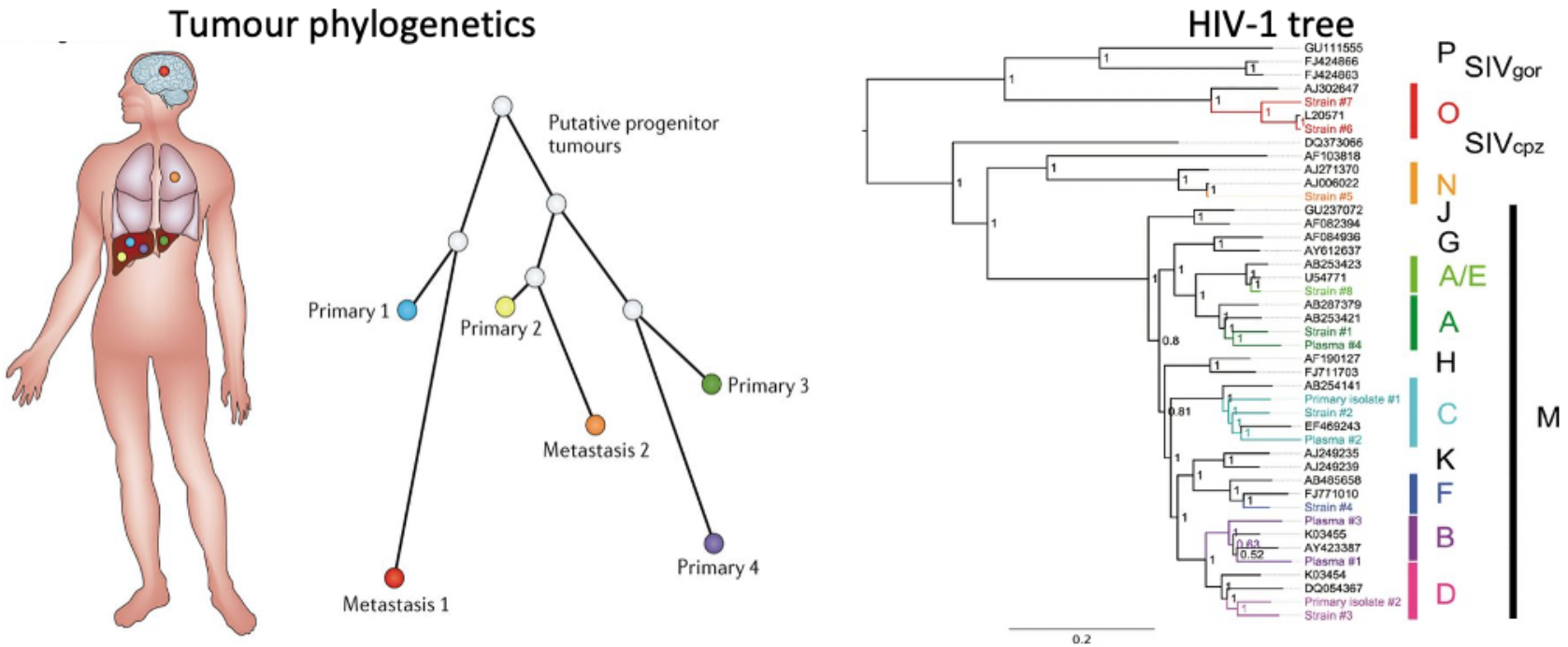


Figure – Taken from Schwartz, Schaffer 2017 and Gall et al 2012

Examples of phylogenies

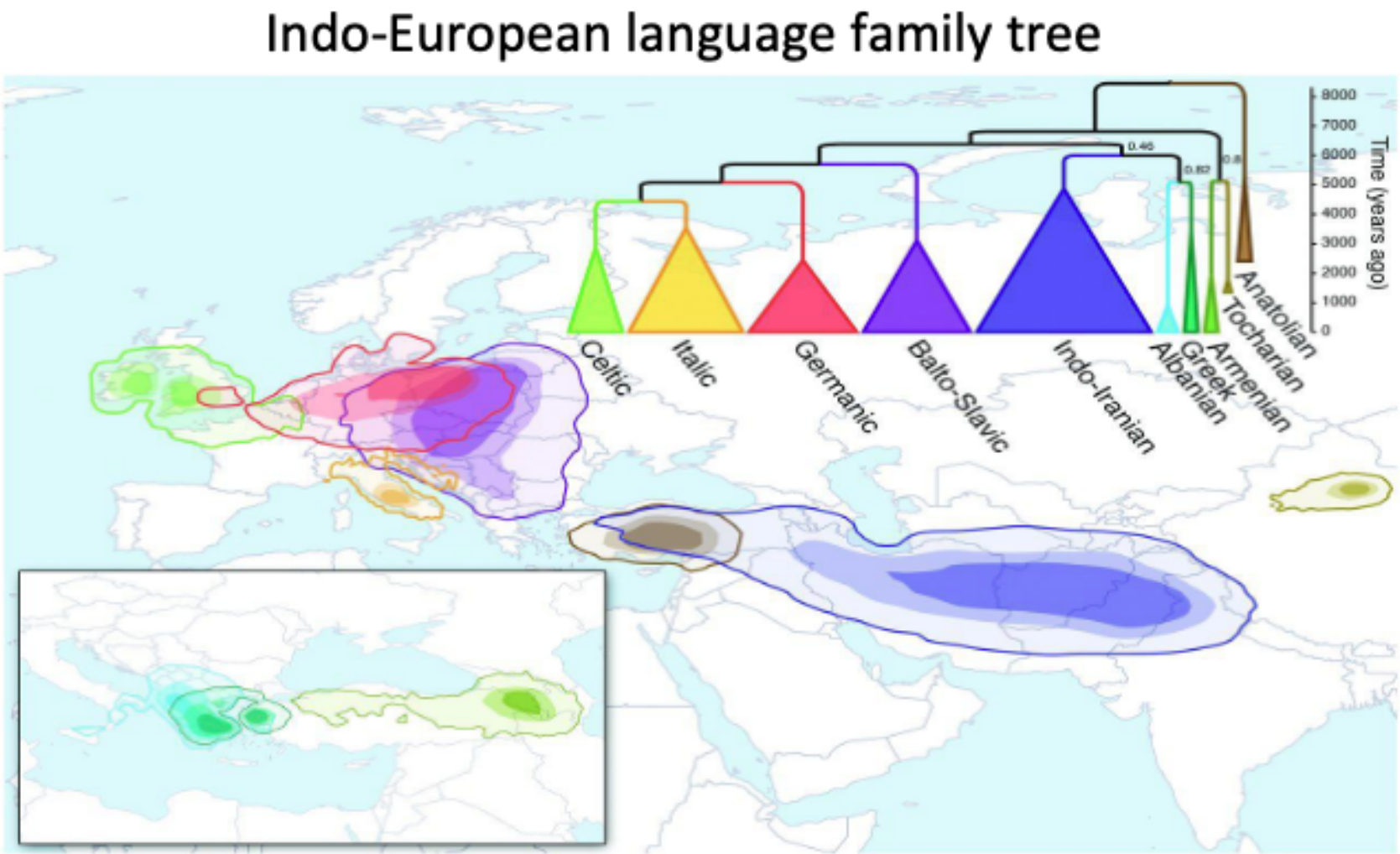
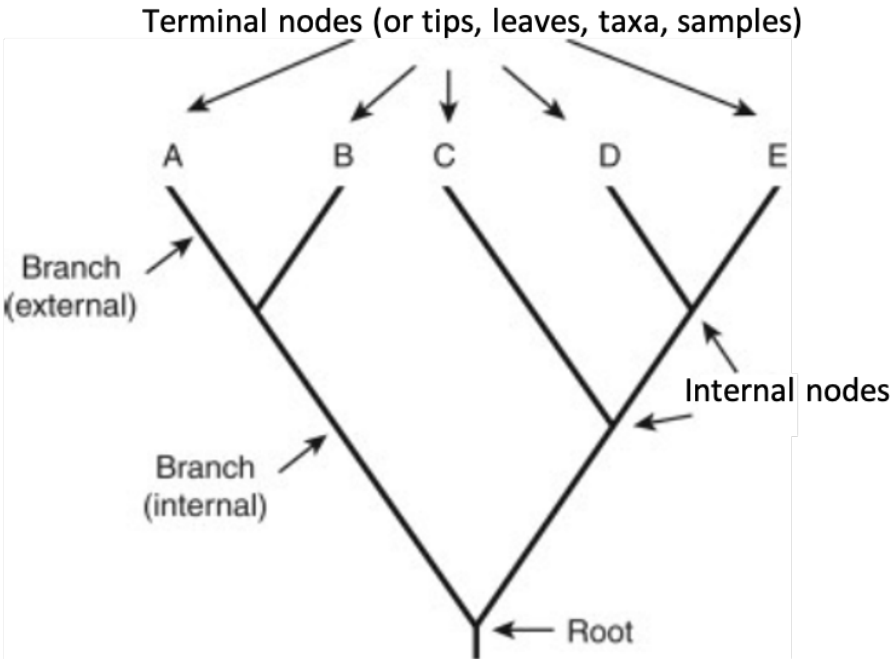


Figure – Taken from Bouckaert et al 2012

Phylogenetic Tree Characteristics, Topology and Types

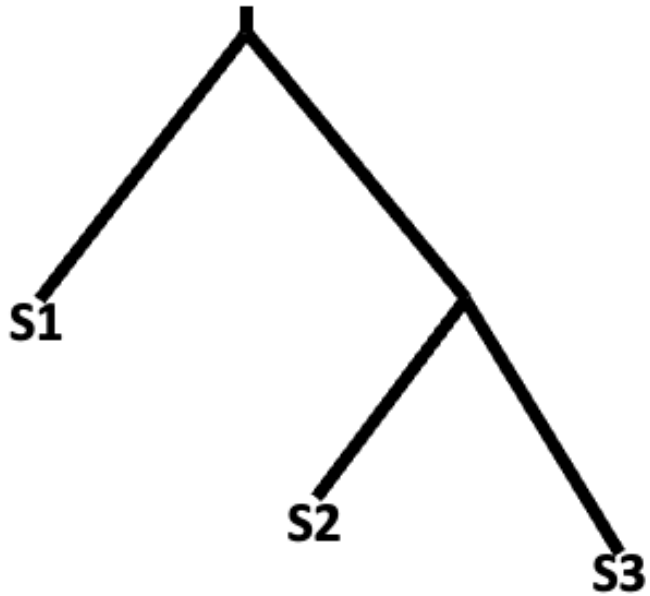
A tree graph - no cycles

- Parts of a tree (nodes and branches)
- Terminal nodes represent the species or entities studied
- Internal nodes represent the last shared ancestor of any two or more species
- A tree may or may not have a root, representing the last common ancestor of everything included in the phylogeny
- Branches connect all nodes showing their relationships and their length may represent change or time
- Basic Types of trees : Dendrogram, Cladogram, Phylogram, Chronogram



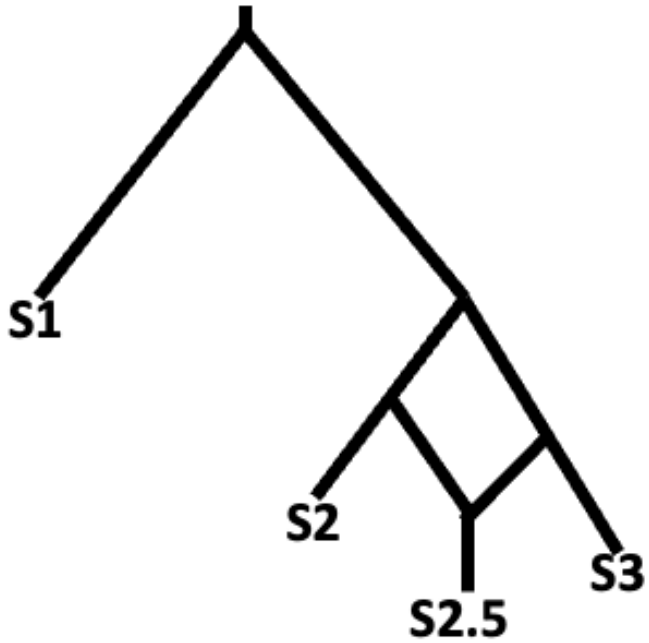
Phylogeny

A tree graph - no cycles



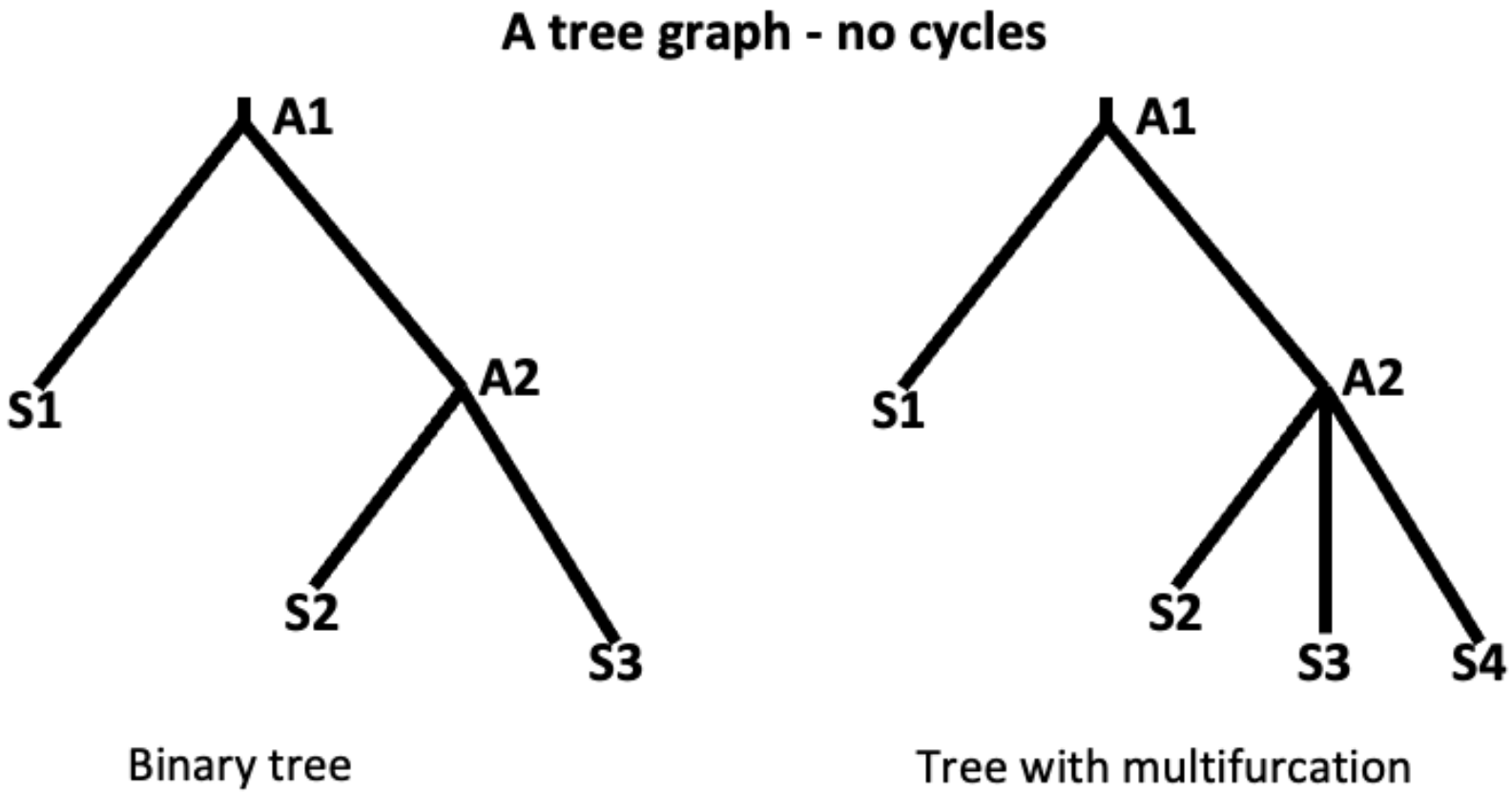
No cycles

Network



Cycle (e.g. hybridization): not a tree!

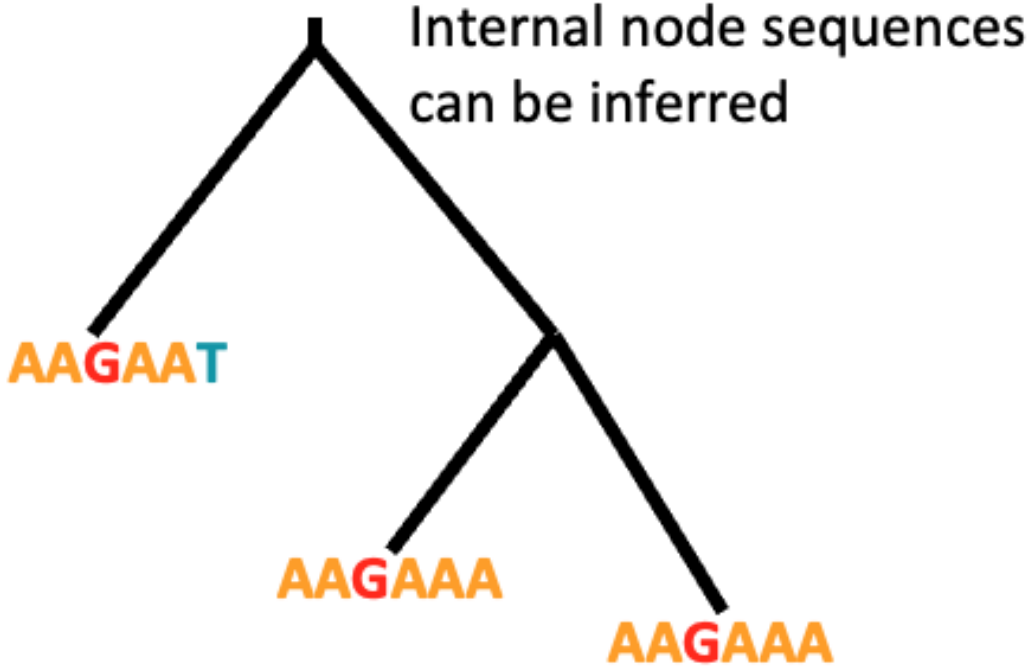
Phylogeny


A tree graph - no cycles
A1
A2
S1
S2
S3
Binary tree
A1
A2
S1
S2
S3
S4
Tree with multifurcation

Phylogeny

A tree graph - no cycles.

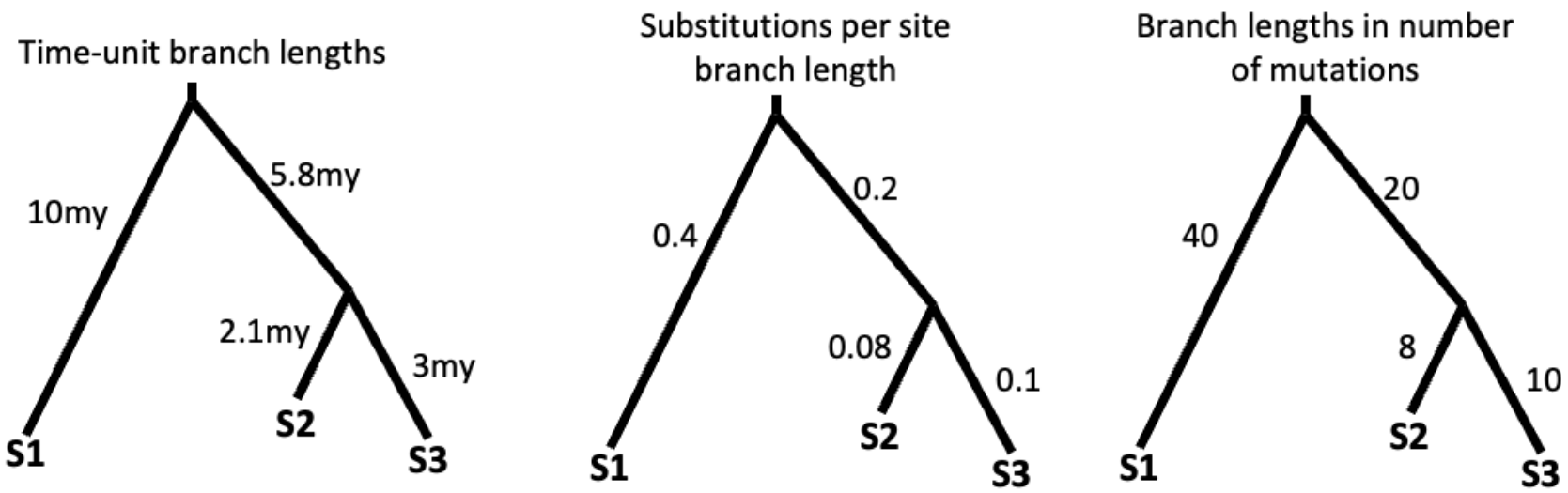
Terminal nodes associated with data



Terminal node sequences are observed

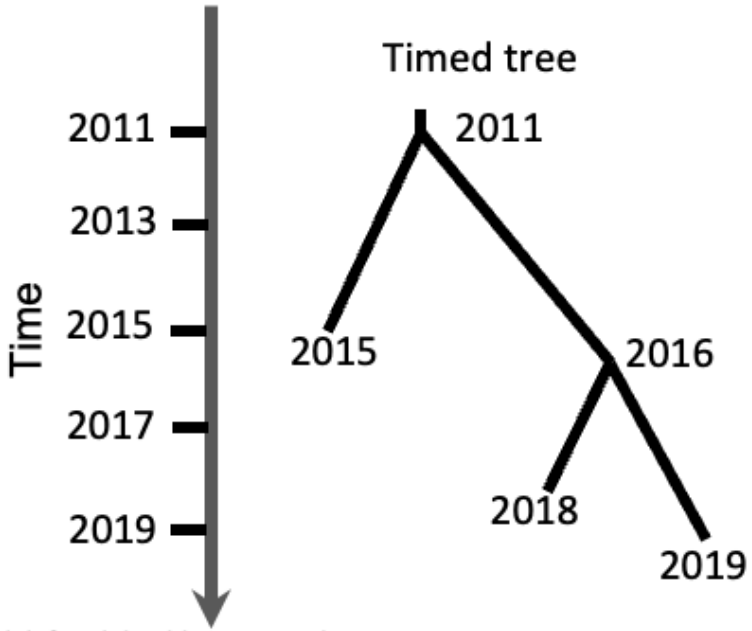
Phylogeny

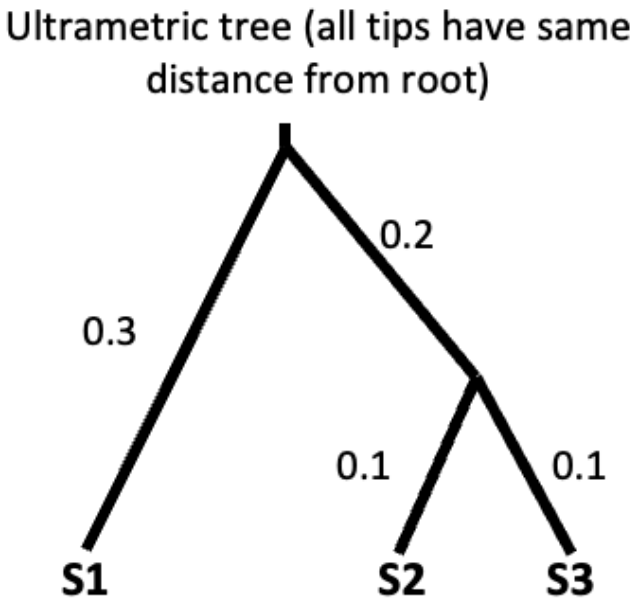
A tree graph - no cycles.
Terminal nodes associated with data.
Branch lengths represent time or divergence.



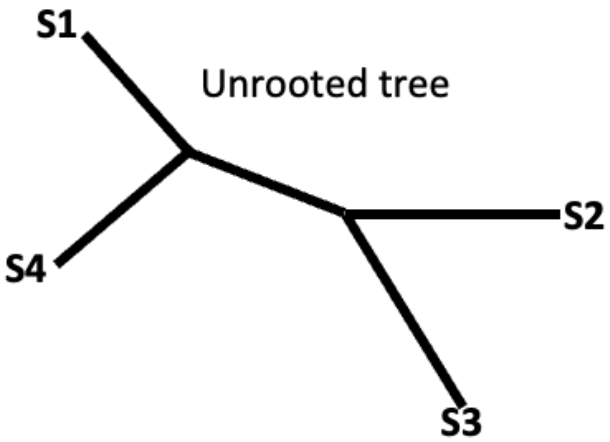
Phylogeny

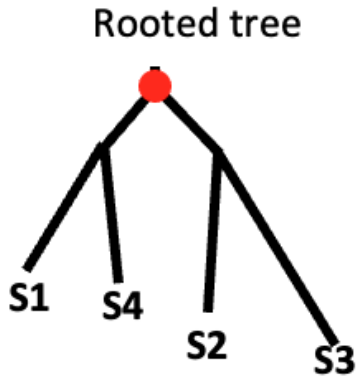
A tree graph - no cycles.
Terminal nodes associated with data.
Branch lengths represent time or divergence.





Tree rooting

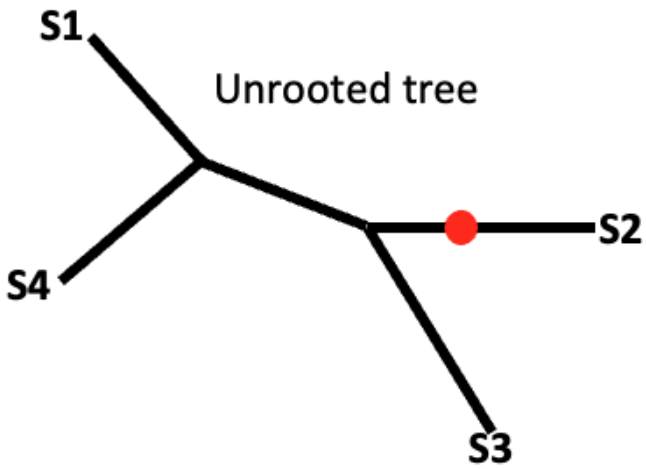


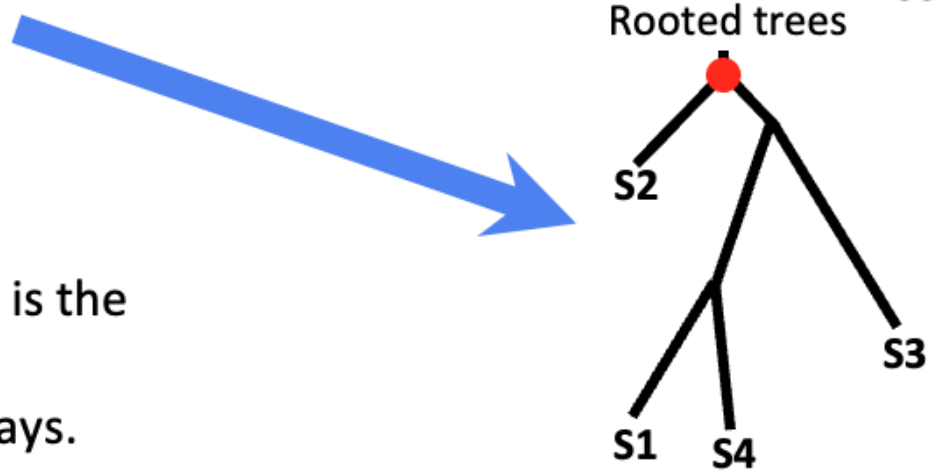


Unrooted trees do not state what is the ancestor of what.
They can be rooted in different ways.

The tree root is the inferred most recent common ancestor (MRCA) of the considered sequences.

Tree rooting in practice



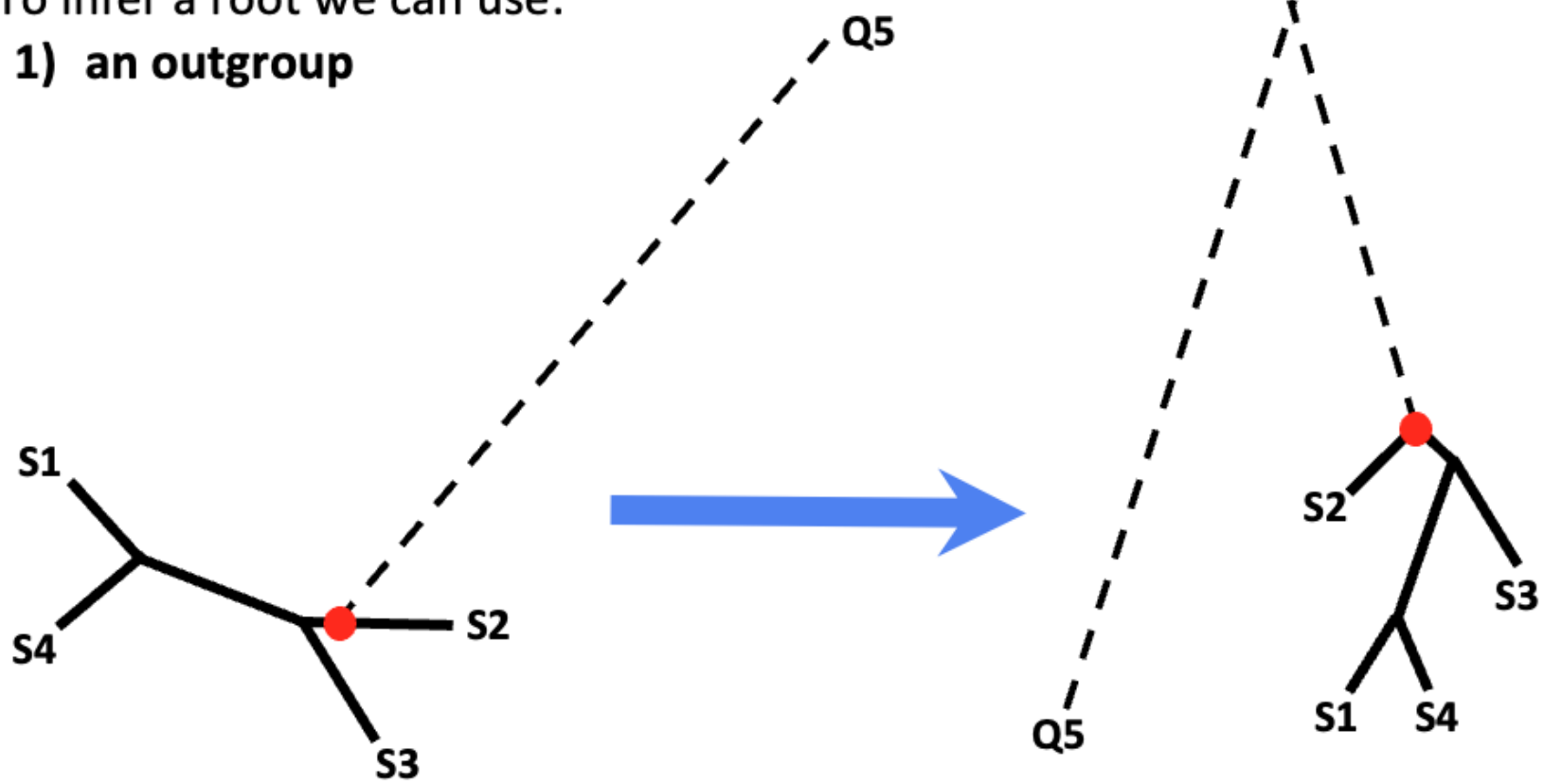


Unrooted trees do not state what is the ancestor of what.
They can be rooted in different ways.

Tree rooting in practice

To infer a root we can use:

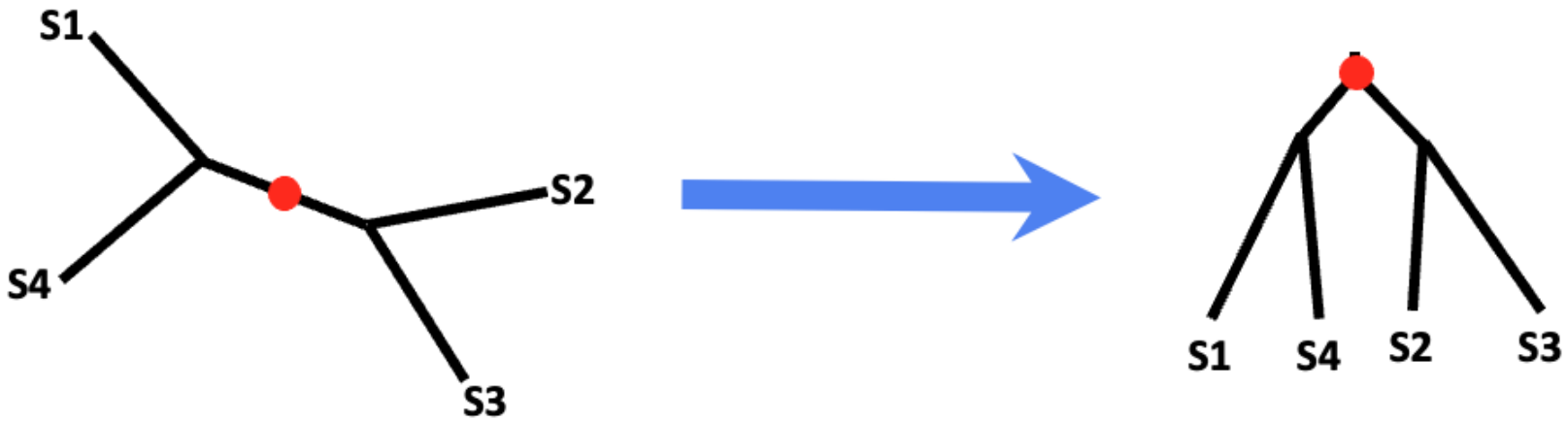
1) **an outgroup**



Tree rooting in practice

To infer a root we can use:

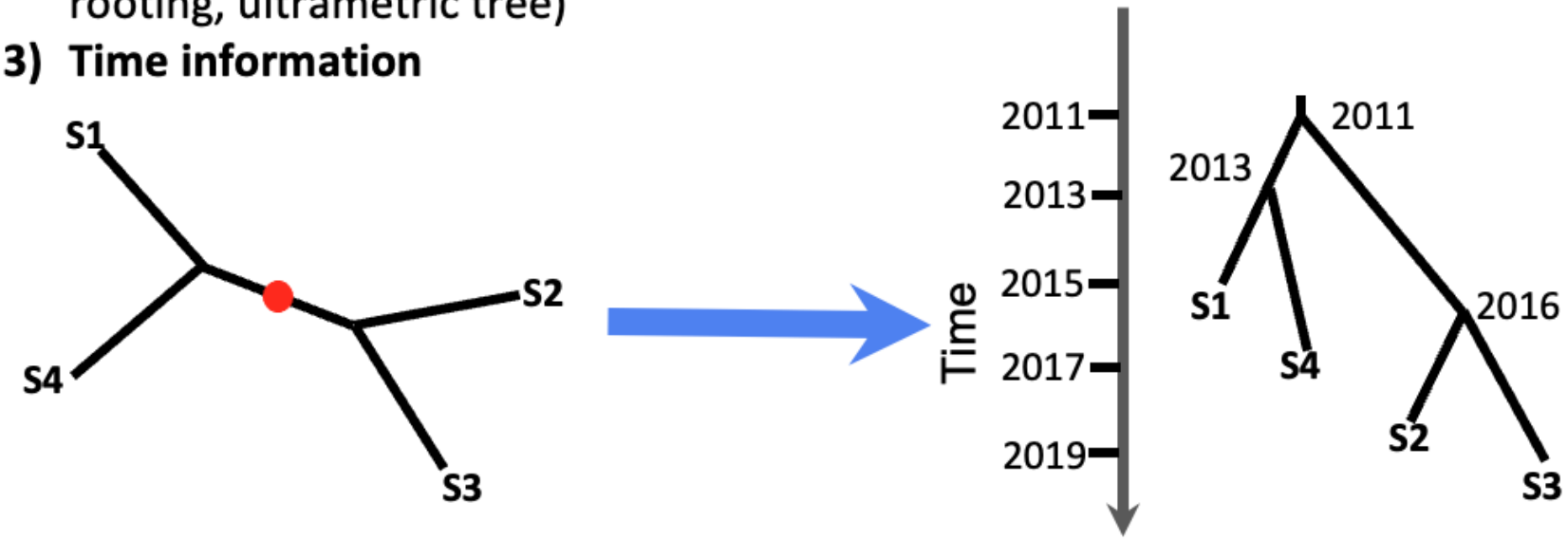
1) an outgroup
2) **constant evolution rate (midpoint rooting, ultrametric tree)**



Tree rooting in practice

To infer a root we can use:

1) an outgroup
2) constant evolution rate (midpoint rooting, ultrametric tree)
3) **Time information**



Tree rooting in practice

To infer a root we can use:

1) an outgroup
2) constant evolution rate (midpoint rooting, ultrametric tree)
3) Time information
4) **A non-reversible model**

Often genome composition (e.g. GC content) changes with time.
We can use this to root a tree.

Software | Open Access | Published: 01 May 2021

Root Digger: a root placement program for phylogenetic trees

Ben Bettisworth & Alexandros Stamatakis

BMC Bioinformatics **22**, Article number: 225 (2021) | Cite this article

Tree rooting in practice

To root a tree we can use:

1) an outgroup
2) constant evolution rate (midpoint rooting, ultrametric tree)
3) Time information
4) A non-reversible model
5) **All of the above!**

Science

The Huanan Seafood Wholesale Market in Wuhan was the early epicenter of the COVID-19 pandemic

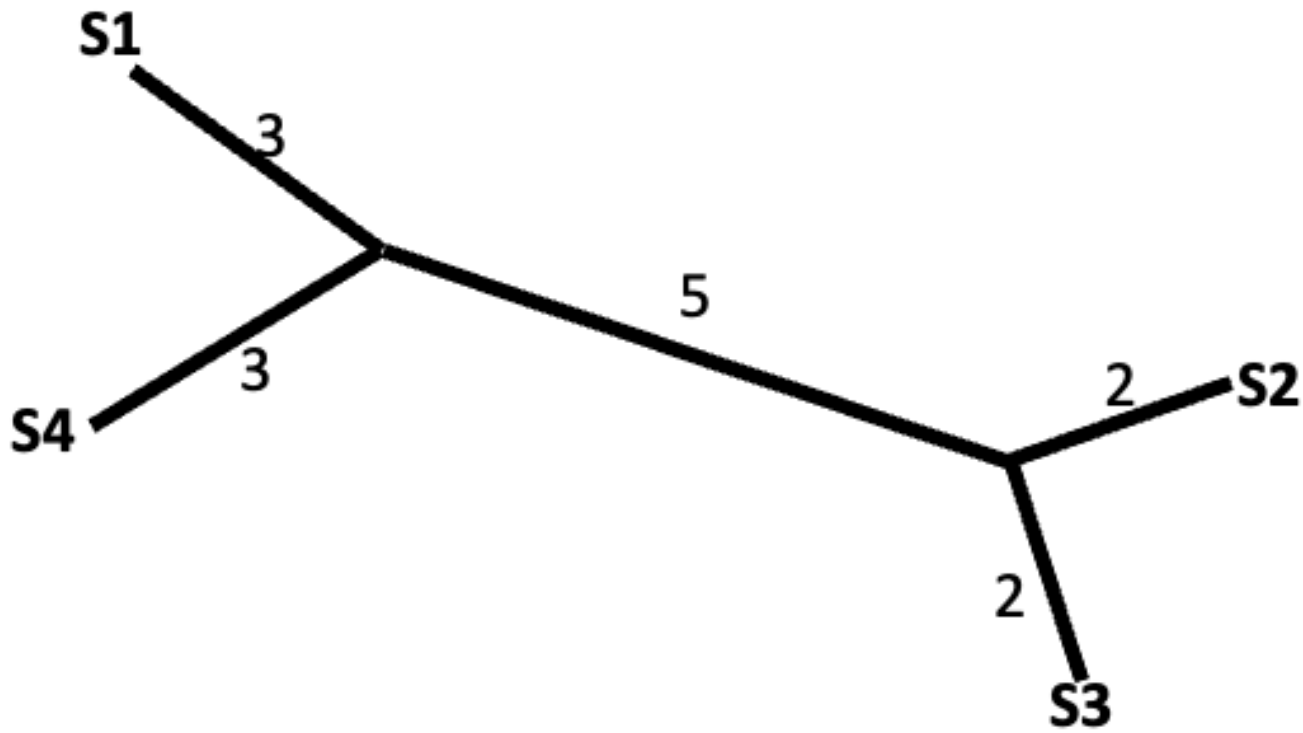
MICHAEL WOROBEY, JOSHUA I. LEVY, LORENA MALPICA SERRANO, ALEXANDER CRITS-CHRISTOPH, JONATHAN E. PEKAR, STEPHEN A. GOLDSTEIN, ANGELA L. RASMUSSEN, MORITZ U. G. KRAEMER, CHRIS NEWMAN, [...] KRISTIAN G. ANDERSEN +9 authors Authors Info & Affiliations

The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2

JONATHAN E. PEKAR, ANDREW MAGEE, EDYTH PARKER, NIEMA MOSHIRI, KATHERINE IZHIKEVICH, JENNIFER L. HAVENS, KARTHIK GANGAVARAPU, LORENA MARIANA MALPICA SERRANO, ALEXANDER CRITS-CHRISTOPH, [...] JOEL O. WERTHEIM +20 authors Authors Info & Affiliations

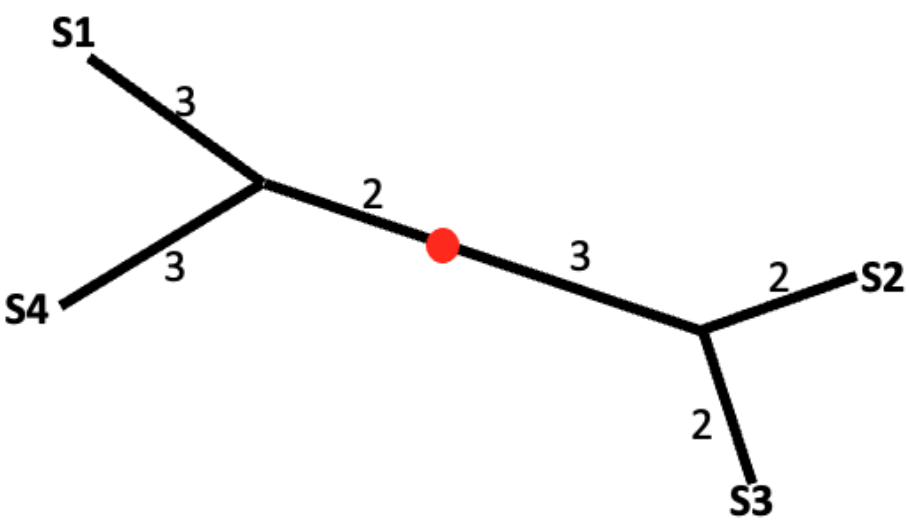
Practical

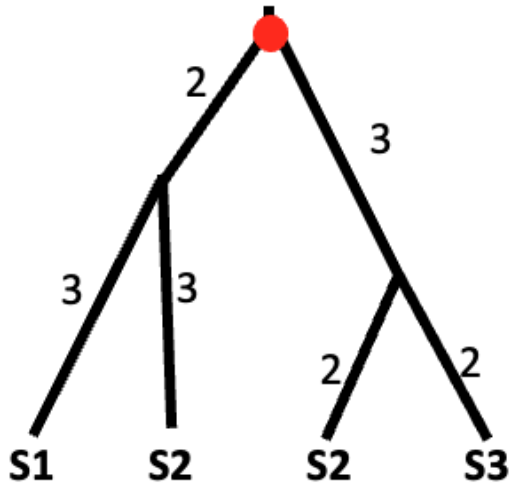
Root this tree by making it ultrametric (all terminal nodes with same distance from the root)



Answer

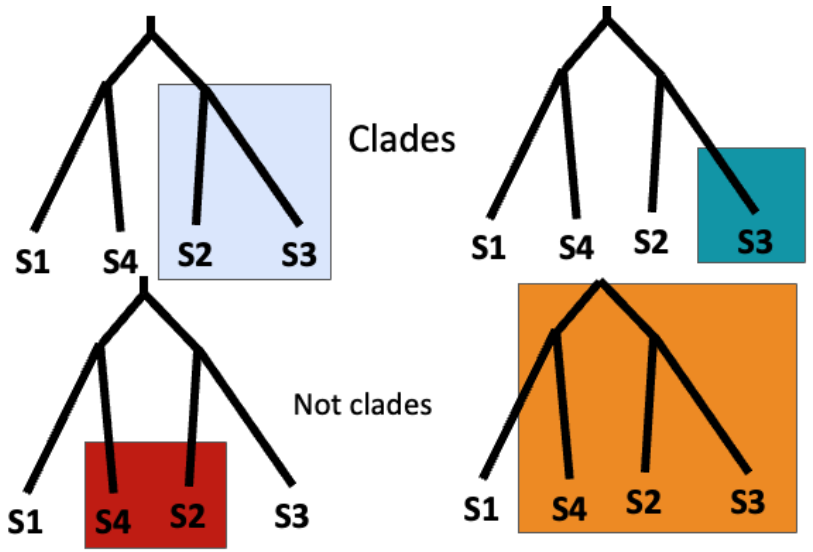
Assuming : Root this tree by making it ultrametric (all terminal nodes with same distance from the root)



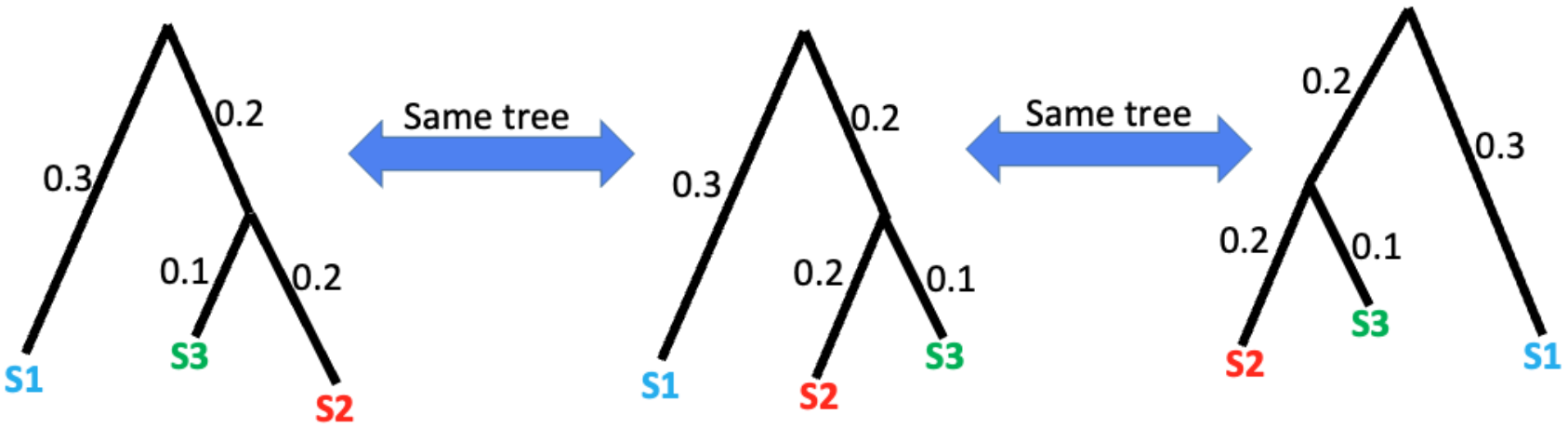


Tree topology

- A clade is a set of all sequences descending from node/ancestor
- Each node and each branch in a rooted tree correspond to one clade
- If two trees have the same clades, we say they have the same topology
- If two trees have the same topology and branch lengths, they are the same

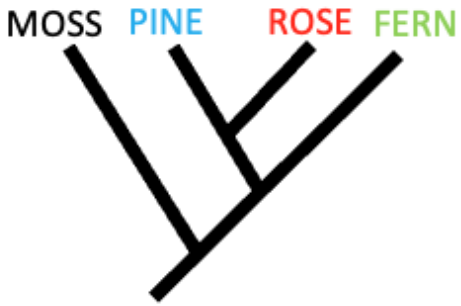


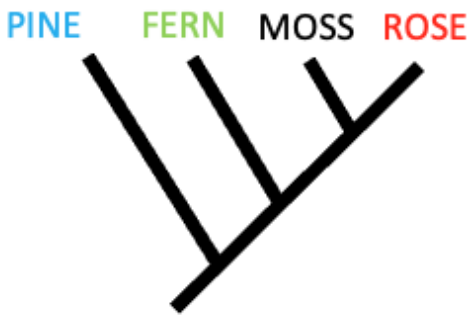
Tree topology

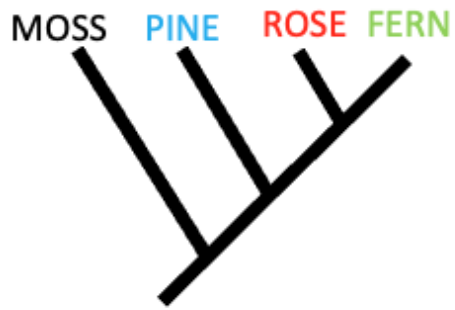


Practical

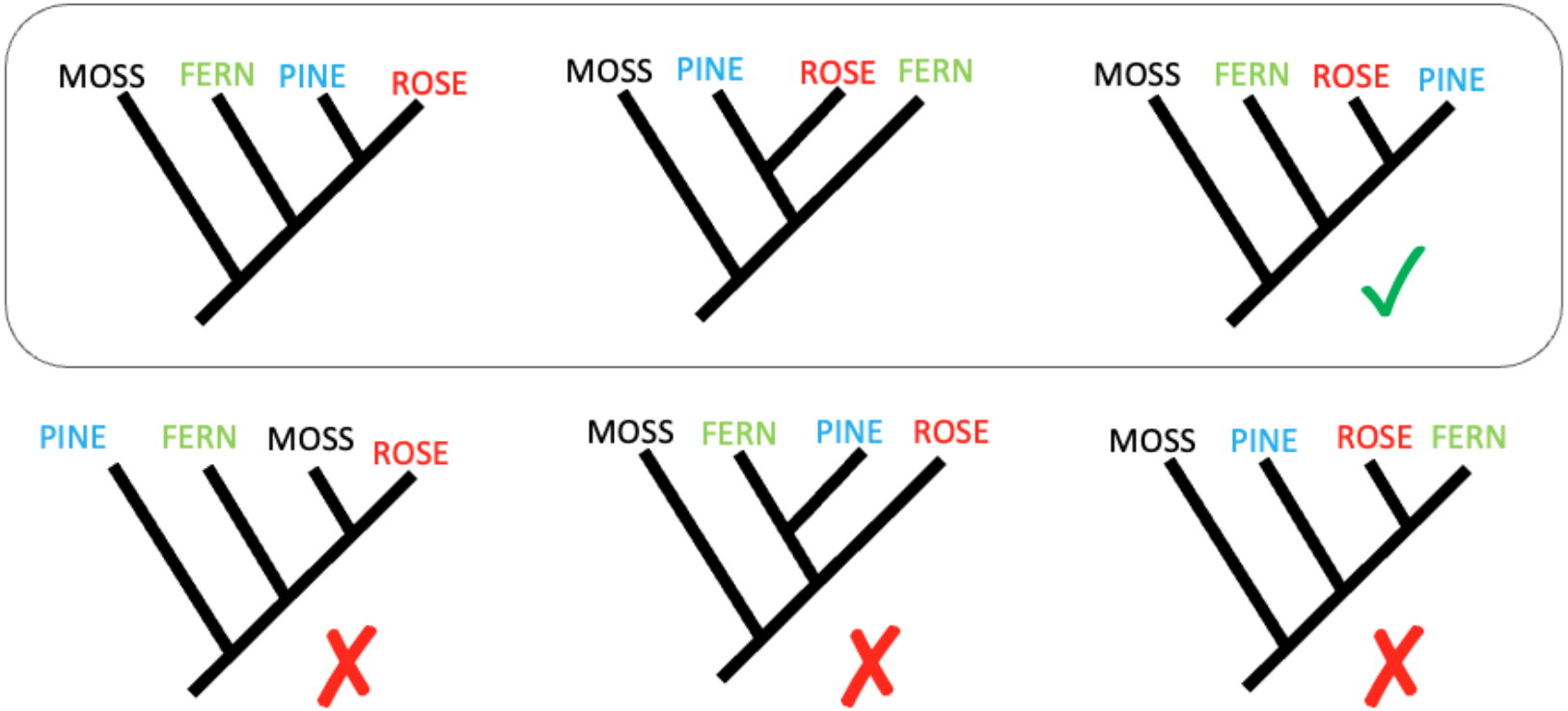
Which trees have the same topology ?





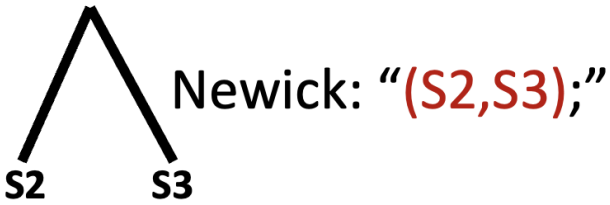


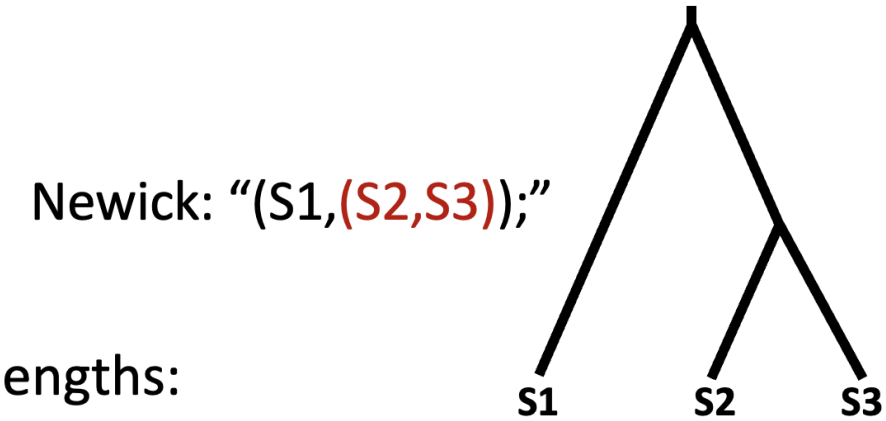
Answer

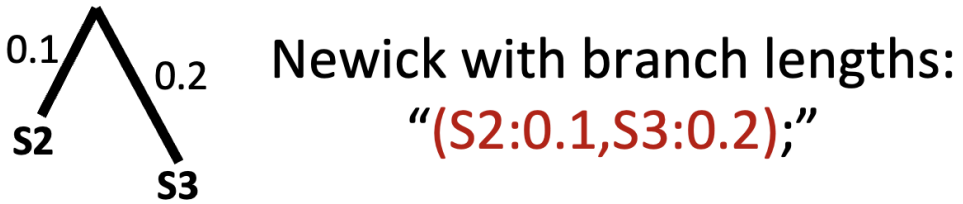

MOSS FERN PINE ROSE
MOSS PINE ROSE FERN
MOSS FERN ROSE PINE
PINE FERN MOSS ROSE
MOSS FERN PINE ROSE
MOSS PINE ROSE FERN

Newick format

Newick format The Newick format represents phylogenetic trees as text Usual for input/output in phylogenetic software

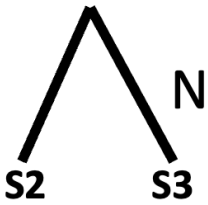






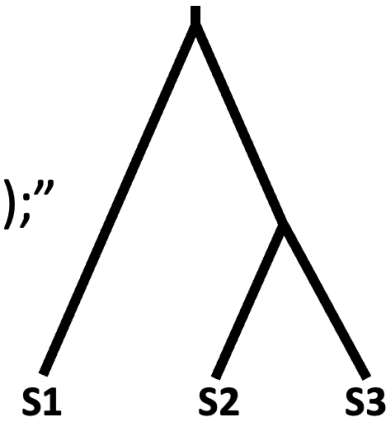
Newick format

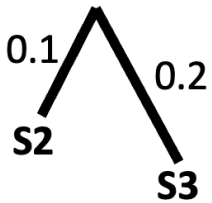
Newick format The Newick format represents phylogenetic trees as text. In Newick format, a nested structure of brackets is used to define the tree topology. Usual for input/output in phylogenetic software



Newick: “(S2,S3);”

Newick: “(S1,(S2,S3));”



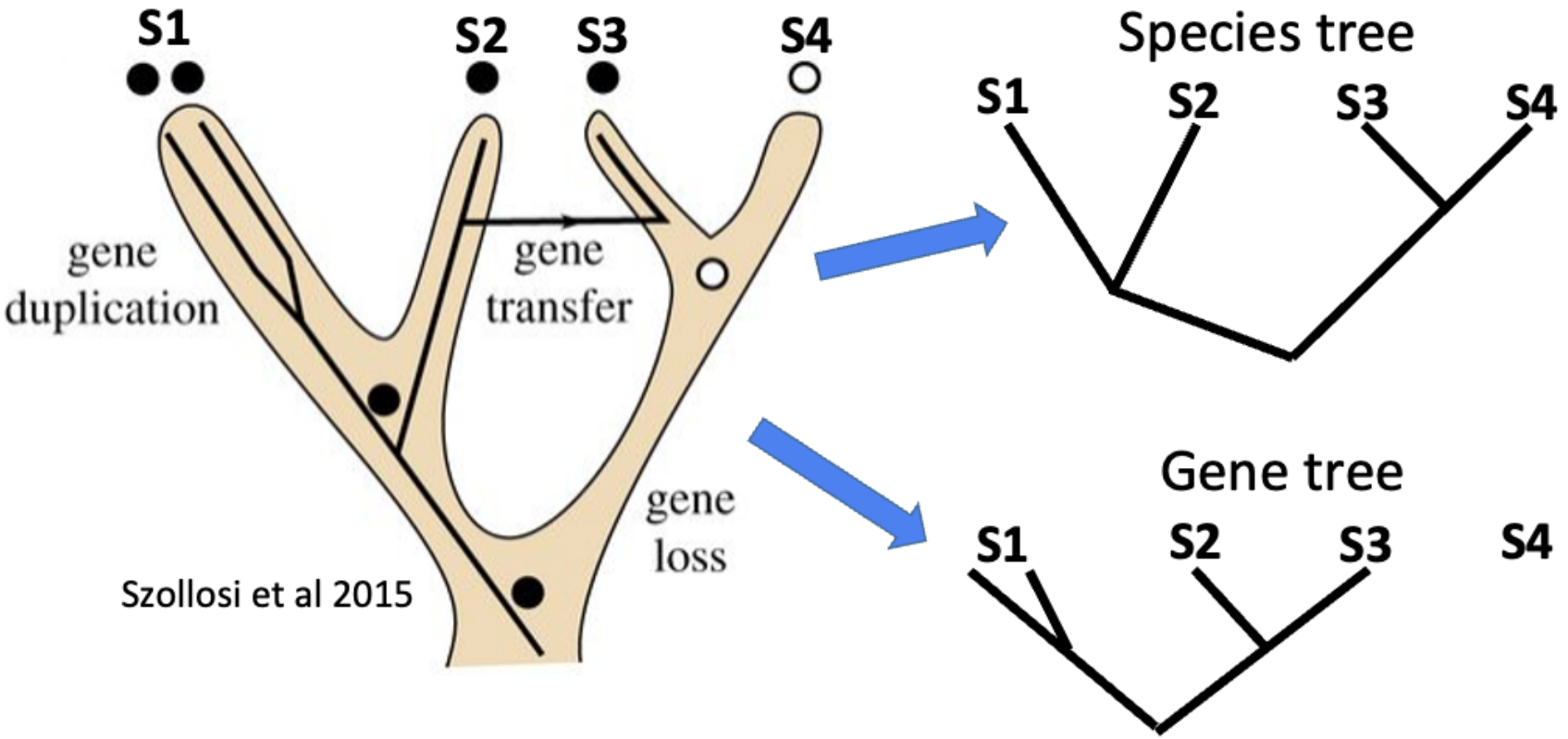


Newick with branch lengths:
“(S2:0.1,S3:0.2);”

Practical 1

Tree terminology

Gene duplication, loss, and horizontal transfer



Tree terminology

Hybridization

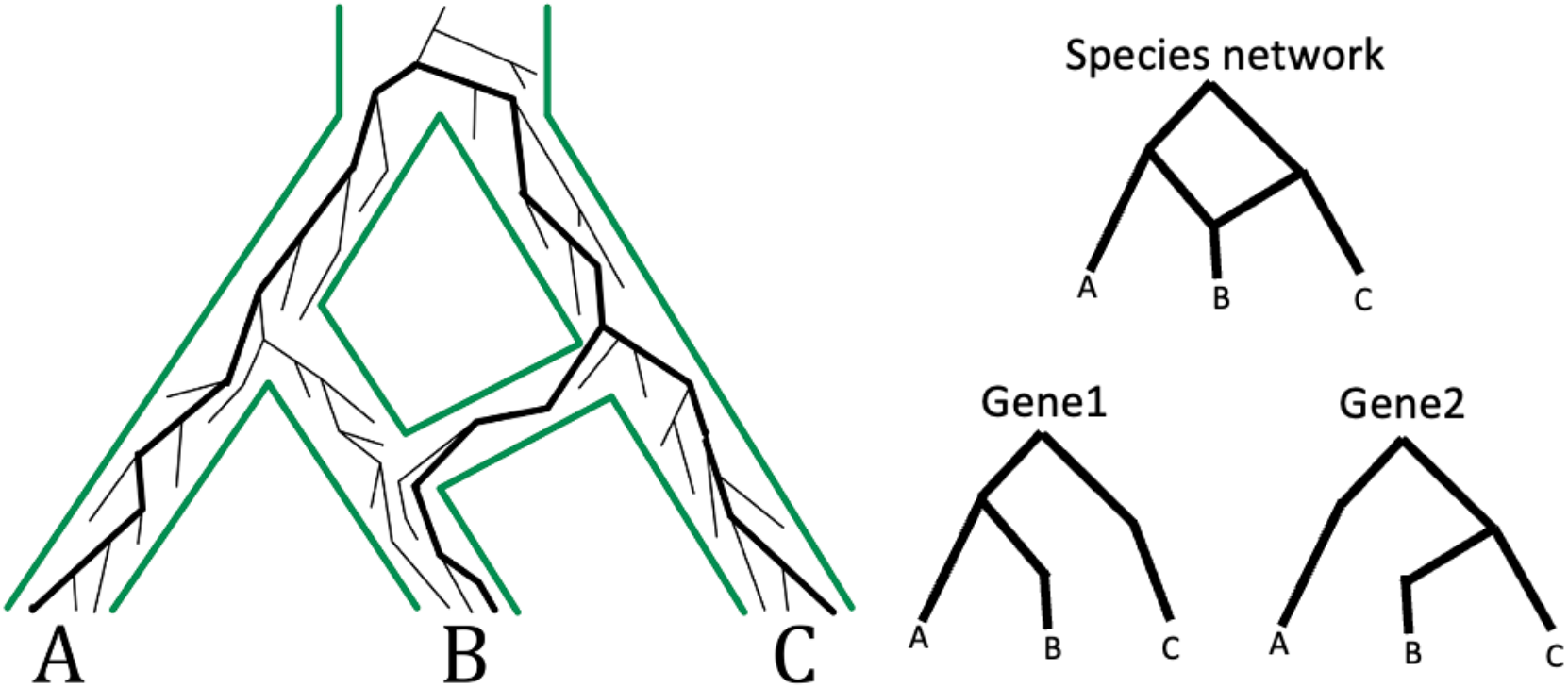


Figure – Taken from Wen and Nakhleh 2016, Software : phyloNet

Tree terminology

Due to recombination, different loci are within-species trees :

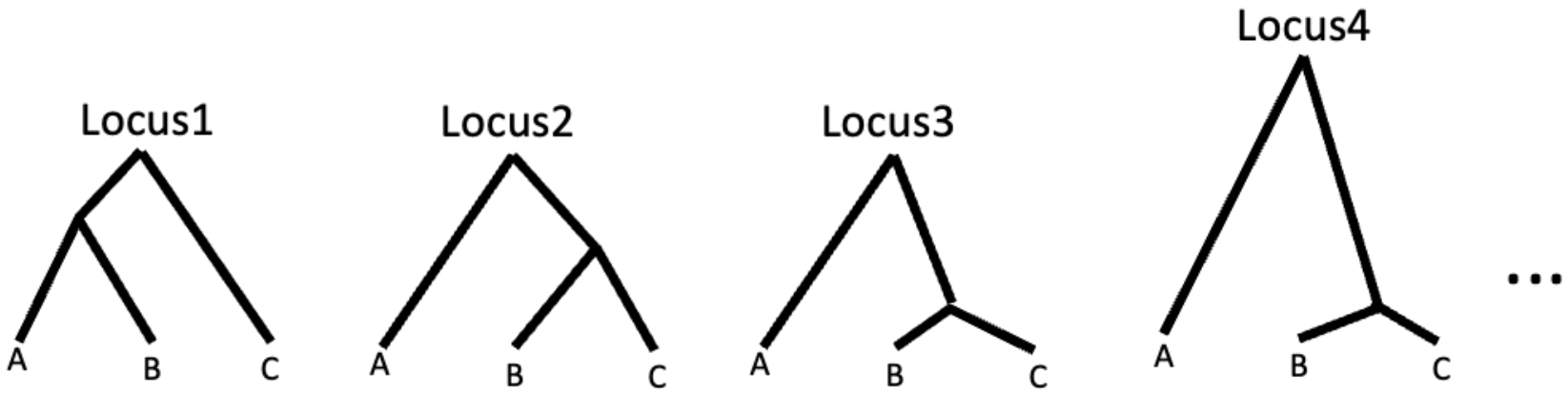


Figure – Software :ClonalFrameML, Gubbins

Tree terminology

Incomplete lineage sorting

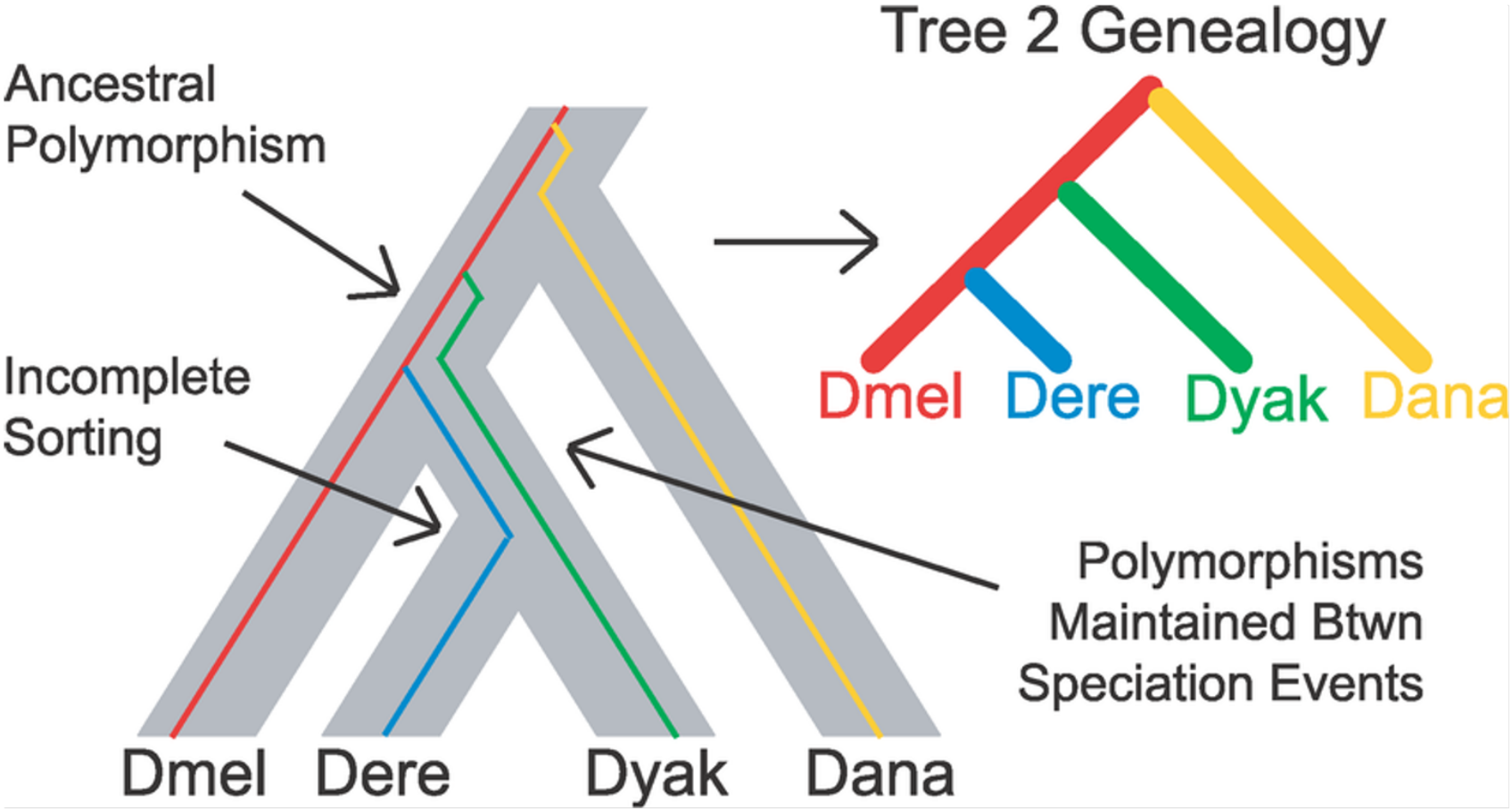


Figure – Taken from Pollard et al 2006, Some software : star-BEAST, SNAPP, BP&P

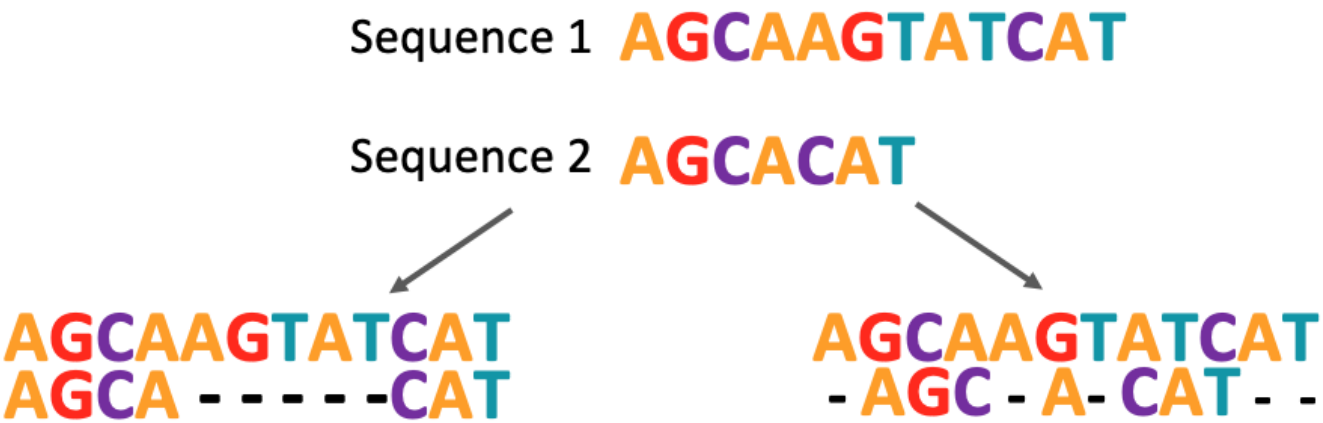
Summary

- A phylogeny is made of topology and branch lengths. It can be rooted or unrooted, binary or with multifurcations, ultrameric and/or timed. A phylogeny represents an evolutionary history.
- The Newick format is used for input and output by phylogenetic software.
- Sometimes there is not a single tree. Beware of hybridization, recombination, lateral gene transfer, gene duplications or losses, and incomplete lineage sorting.

Sequence alignment

Molecular data : alignment

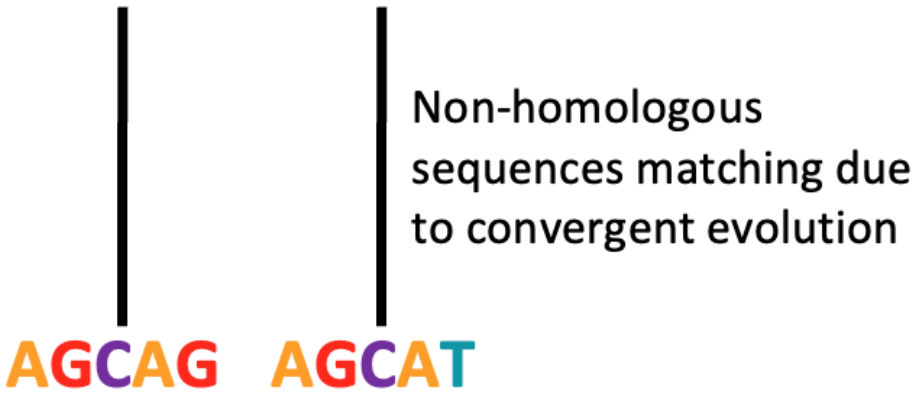
- Some phylogenetic methods are alignment-free (e.g. based on k-mers)
- However, most phylogenetic methods need sequence alignments
- Aligning means putting sequence data in a matrix
- We do not consider genome alignment (which might also be needed). Here, we focus on small scale gene alignment



Molecular data : alignment

There are 2 types of alignment :

- Evolutionary alignment, defined by homology
- Structural alignment, exploring functional and structural similarity
- In phylogenetics we need evolutionary alignments



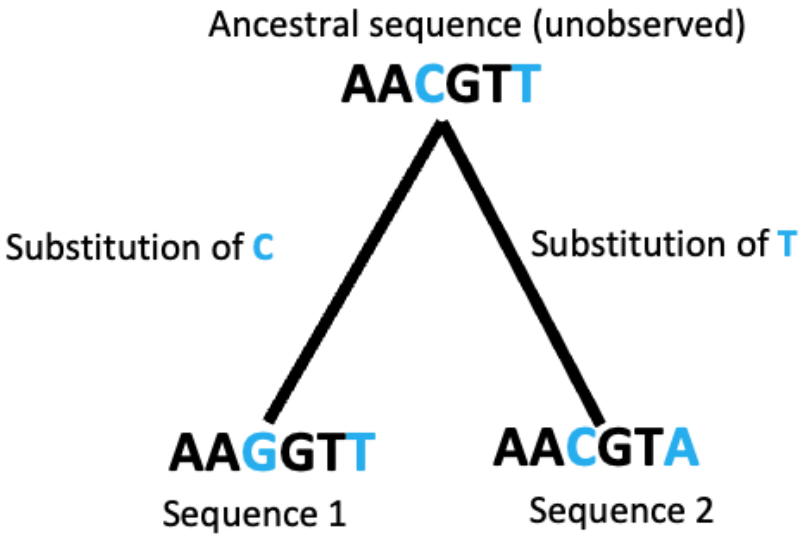
Which alignment is correct?

1) AGCAG - - - - -
- - - - - AGCAT

2) AGCAG
AGCAT

Molecular data : alignment

Pairwise alignment for two sequences

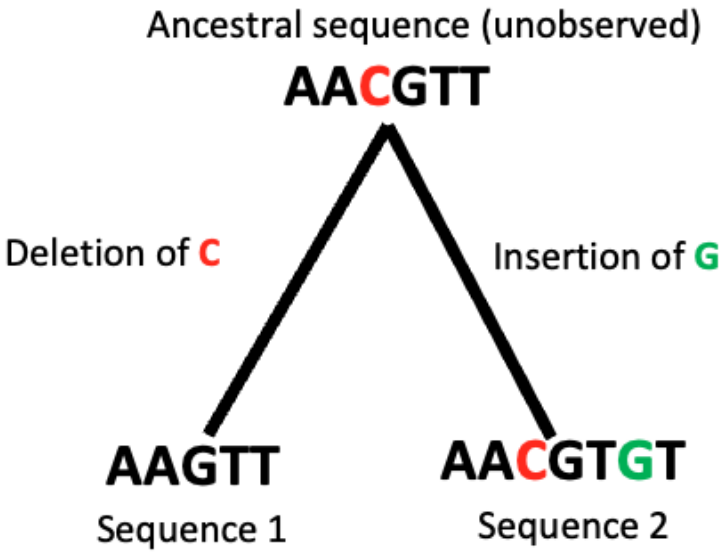


Correct pairwise alignment:

Sequence 1	A	A	G	G	T	T
Sequence 2	A	A	C	G	T	A

Molecular data : alignment

Pairwise alignment for two sequences

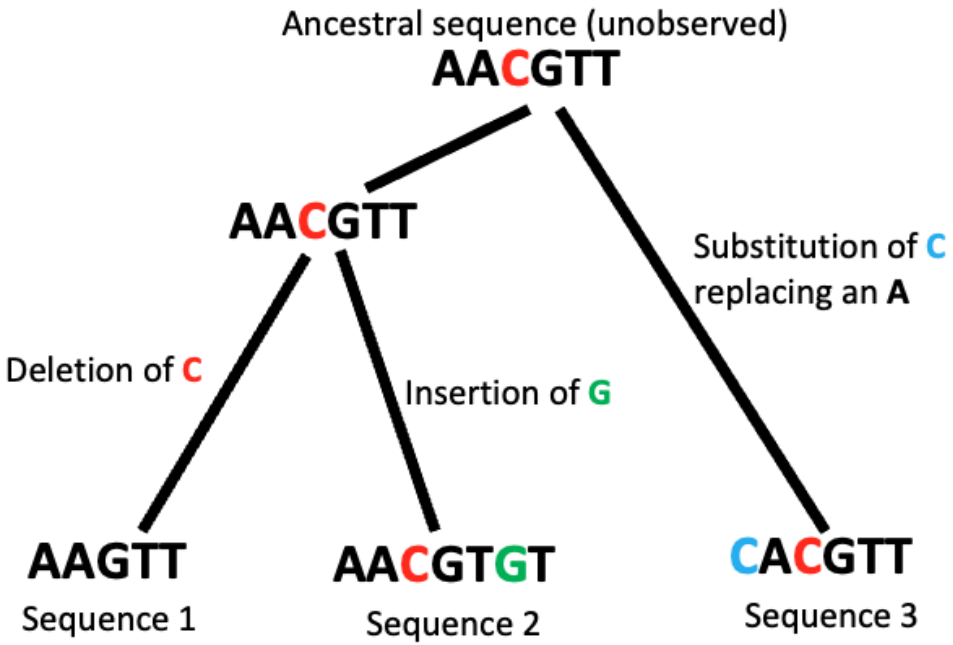


Correct pairwise alignment:

Sequence 1	A A - G T - T
Sequence 2	A A C G T G T

Molecular data : alignment

Multiple sequence alignment (MSA) is the alignment of multiple (more than 2) sequences



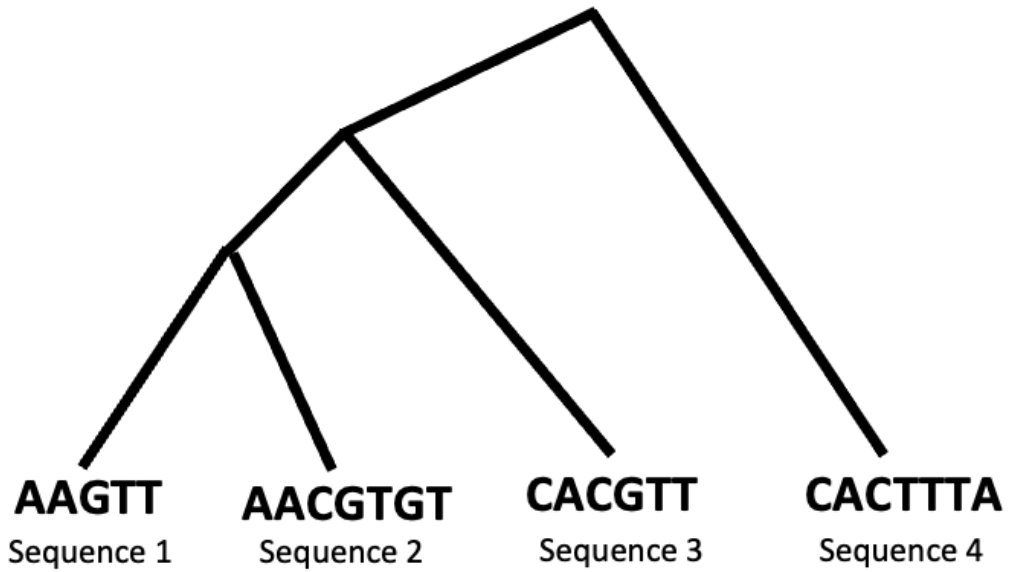
Correct MSA:

Sequence 1	A A - G T - T
Sequence 2	A A C G T G T
Sequence 3	C A C G T - T

Multiple sequence alignment (MSA)

Progressive alignment

- Align the two most closely related sequences
- Grow the MSA while keeping the previous sub-alignments constant
- Repeat until all sequences are aligned
- **Note** : Early errors in alignment can snowball

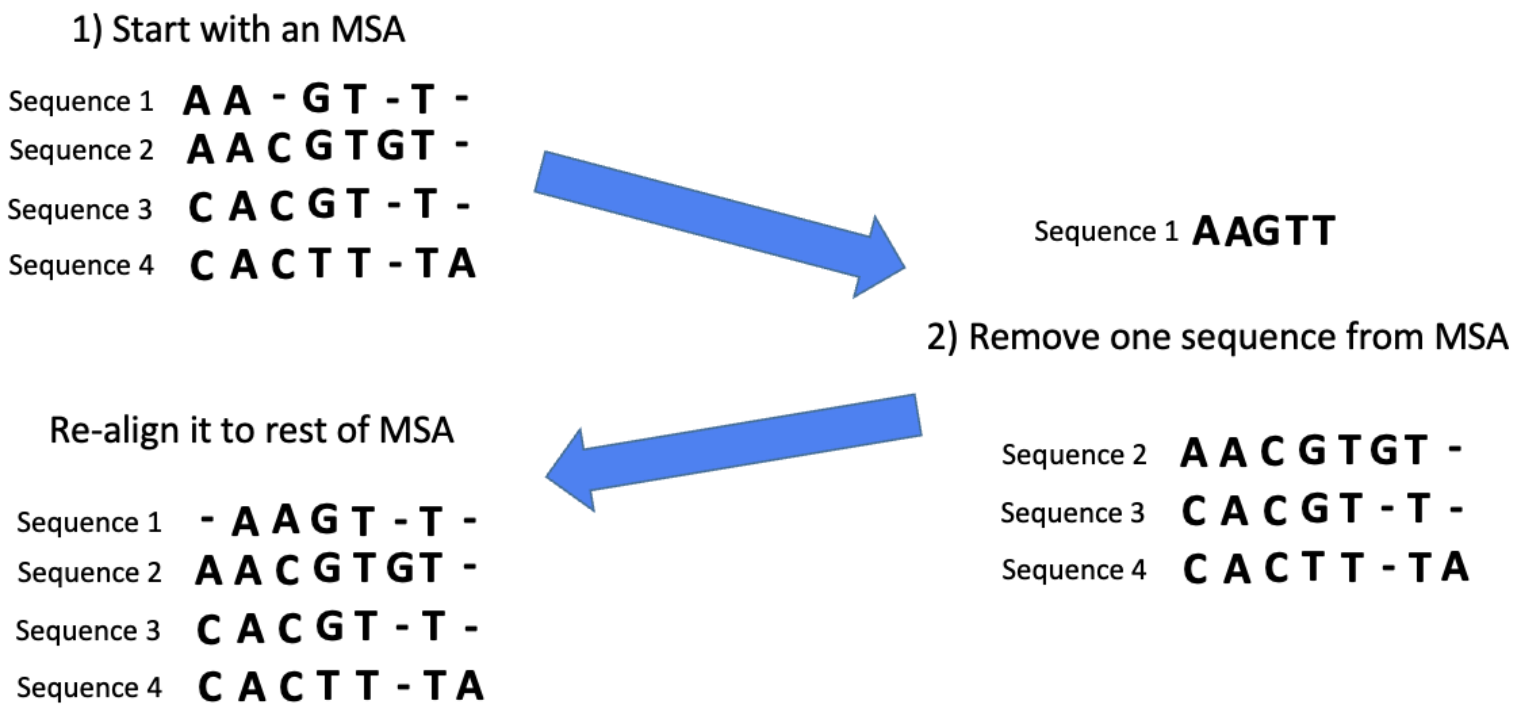


Sequence 1	A A - G T - T -
Sequence 2	A A C G T G T -
Sequence 3	C A C G T - T -
Sequence 4	C A C T T - T A

Multiple sequence alignment (MSA)

Iterative alignment

- There are many MSA methods : Clustal, MAFFT, MUSCLE, PRANK, T-Coffee, ProbAlign, . . .
- When sequences are similar, alignment is easy, and aligners will infer similar alignments
- At high divergence, different aligners or parameter values can give very different alignments



Multiple sequence alignment (MSA)

Recommendations

- MAFFT provides good accuracy and very good efficiency in most practical applications
- With high-divergence small datasets, PRANK can be more robust
- With very small datasets, BaliPhy can bypass alignments altogether

Nucleotide, amino acid, or codon ?

Nucleotide, amino acid, or codon ?

- Nucleotide alignments are highly informative at short divergence, but can be misleading at higher divergence due to saturation
- Amino acid alignments are preferred at high divergence ; they can also be used as a first step to create a codon alignment
- Codon alignments can be useful for coding sequences in particular for positive selection scans

Summary

- Usually, molecular phylogenetic methods require a multiple sequence alignment (MSA)
- Alignments can impact analyses of high-divergence data
- Alignment is easy at short divergence, but is hard and uncertain at high divergence
- Choice of nucleotide vs amino acid alignment mostly depends on divergence

Practical 2

Phylogenetic inference

Molecular Tree construction methods

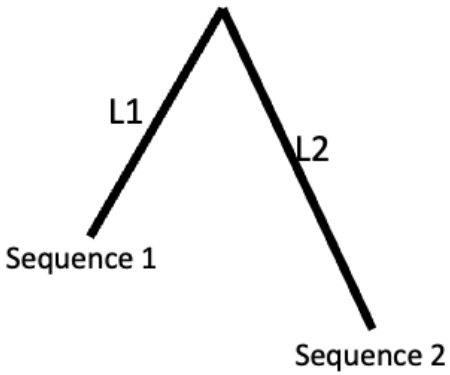
Molecular Tree construction methods

- Distance based methods
- Maximum Parsimony
- Maximum Likelihood
- Bayesian Inference

Important concepts

- Substitution Model selection
- Obtaining statistical support (bootstrapping)

Distance-based phylogenetics



Evolutionary distance = L1 + L2

Sequence 1 A A - G T - T A A T G T G T A A G T
Sequence 2 A A C G T G T T A C G T G T A A G T

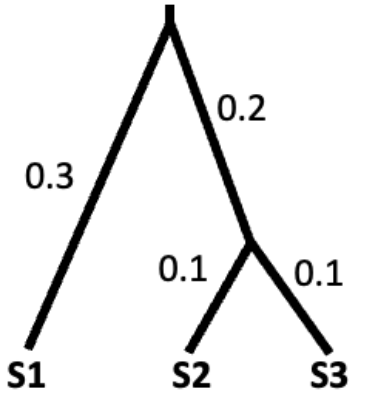
2 substitutions out of 16 match columns: **S**=2/16

More distance, more substitutions. If **S** is the proportions of substitutions, the evolutionary distance D between sequences is estimated as:

$$D = -\frac{3}{4}\ln(1 - \frac{4}{3}S)$$

Distance-based phylogenetics

Distance-based phylogenetics Starting from the distances between all pairs of sequences (the distance matrix) we infer a phylogeny using Neighbor-Joining (NJ) or UPGMA. NJ is popular for fast tree inference, and as initial tree for more complex phylogenetic and alignment inference.



D(S1,S2)=0.6
D(S1,S3)=0.6
D(S2,S3)=0.2

?

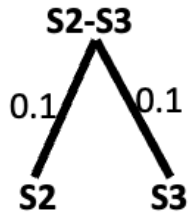
	S1	S2	S3
S1	0	0.6	0.6
S2	0.6	0	0.2
S3	0.6	0.2	0

Distance-based phylogenetics

Neighbor-Joining

	S1	S2	S3
S1	0	0.6	0.6
S2	0.6	0	0.2
S3	0.6	0.2	0

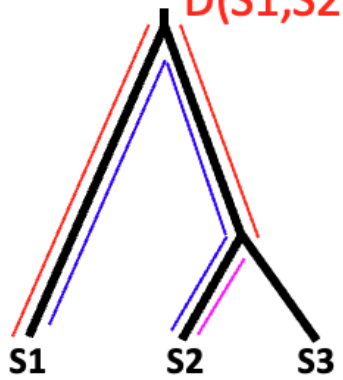
S2 and **S3** are closest to each other, so create clade (**S2**,**S3**) and internal node **S2-S3**

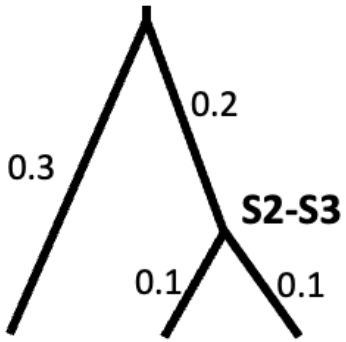


Replace **S2** and **S3** with **S2-S3**

D(S1,S2-S3)=D(S2,S1)-D(S2,S2-S3)

	S1	S2-S3
S1	0	0.5
S2-S3	0.5	0





75

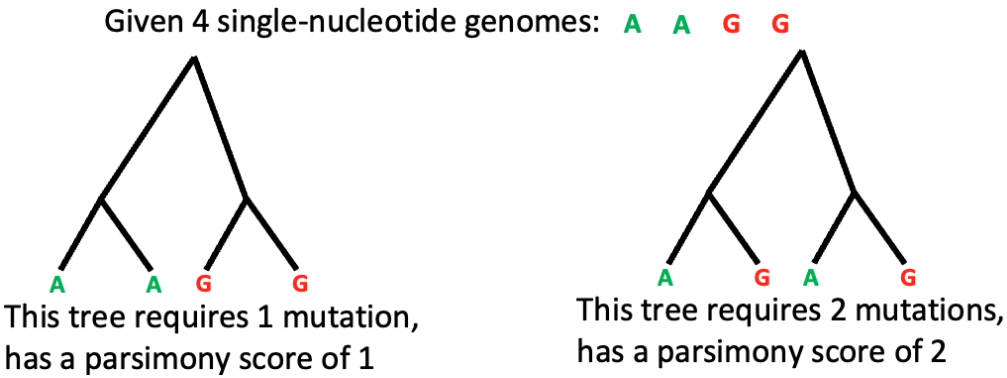
Distance-based phylogenetics

Summary

- Distance-based phylogenetic reconstruction uses pairwise evolutionary distances (the distance matrix)
- There are different methods to build a phylogeny from the distance matrix, like NJ
- Distance-based methods are fast but are considered less reliable. They are used for guide trees in MSA inference

Maximum Parsimony

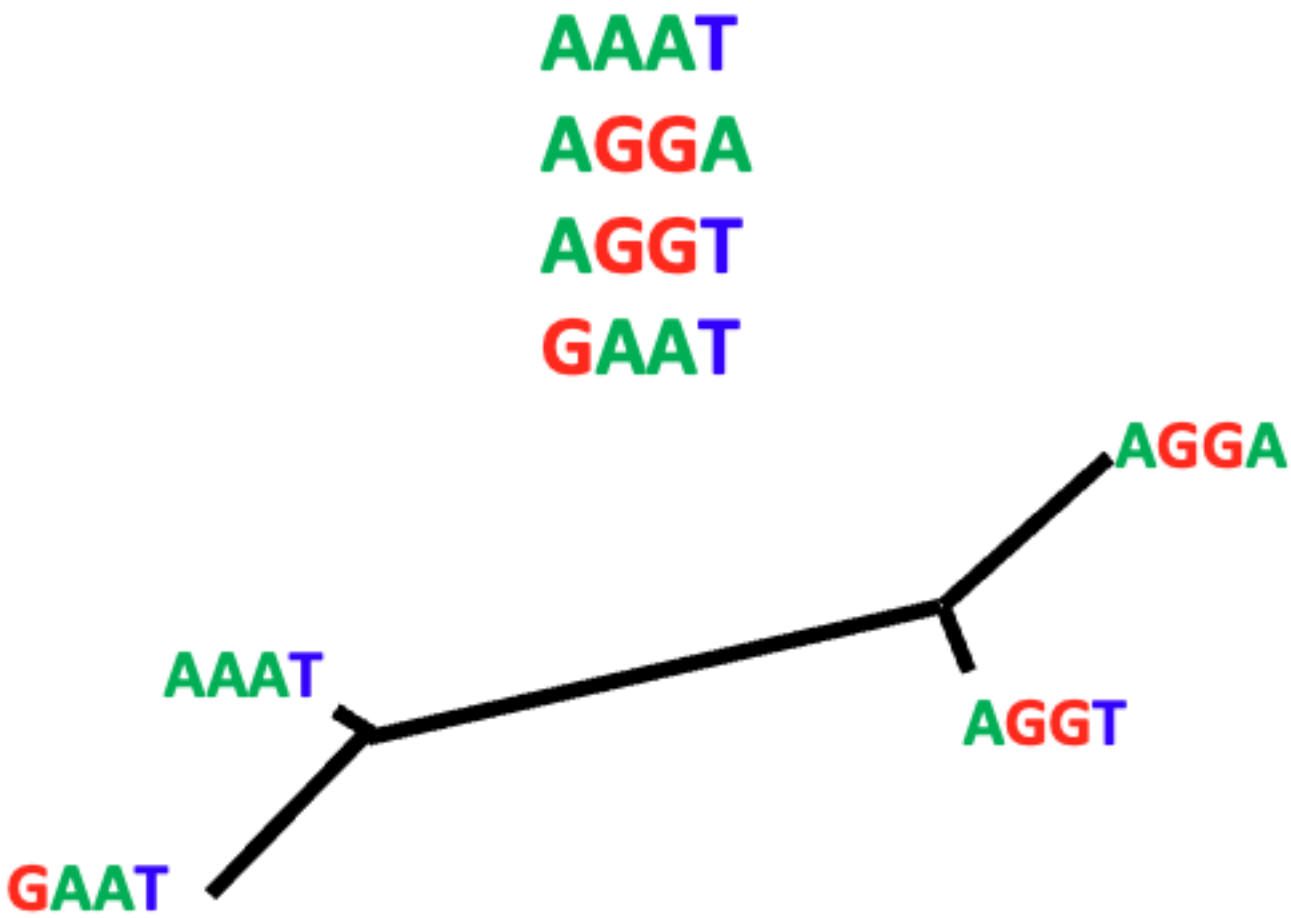
- Maximum parsimony methods assume the best tree requires the fewest mutations to explain the alignment
- What is the smallest number of evolutionary steps that lead to the observed state
- Simple enumeration is the simplest way, but not feasible for large data
- Heuristic algorithms needed for large datasets
- Often underestimates evolutionary change
- Long branch attraction
- More commonly used for morphological data



Maximum Parsimony

Example

- Maximum Parsimony tree relating these genomes



Maximum likelihood phylogenetics

Maximum likelihood phylogenetics

Conditional probability

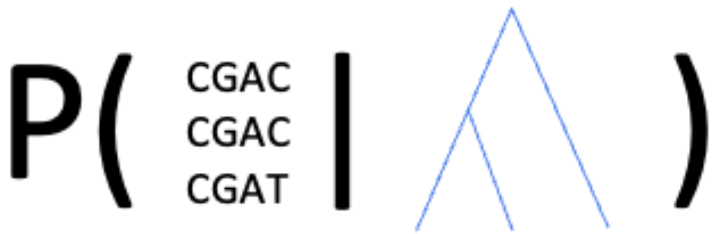
- The probability of A conditional on B, or P(A|B), is the probability of A assuming that B is true. If I work from home 50% of the time when it rains, and 80% when it doesn't :

P( | )=0.5

P( | )=0.8

Maximum likelihood phylogenetics

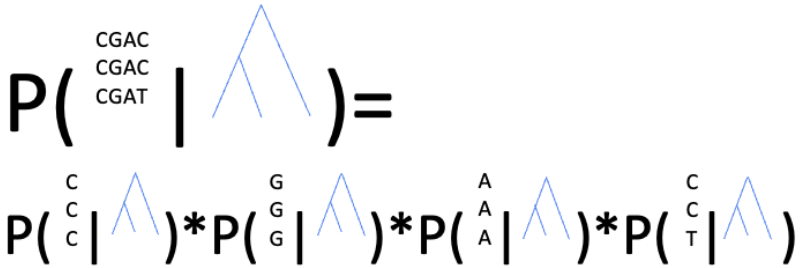
Likelihood - Given data (an alignment) and a hypothesis (a tree) the likelihood is the probability of the data conditional on the hypothesis



- A hypothesis with a higher likelihood explains the data better - Maximum Likelihood aims at finding the tree with the highest likelihood

Maximum likelihood phylogenetics

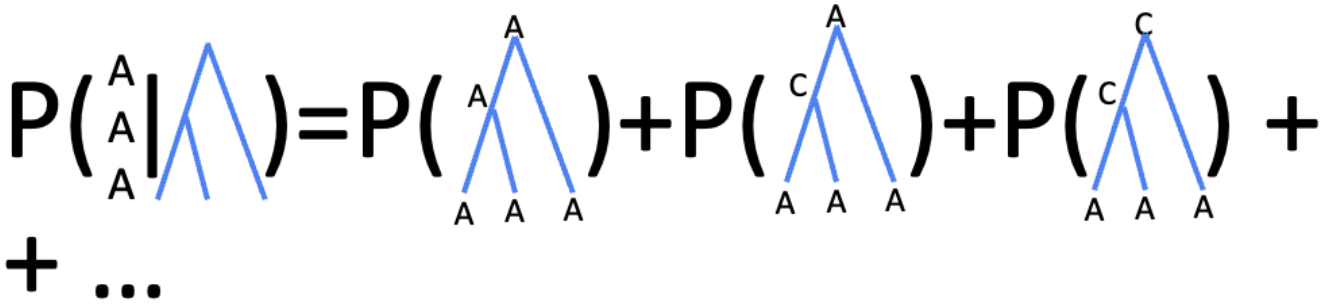
Phylogenetic Likelihood The likelihood of a tree is the product of the likelihood of the alignment columns (columns are assumed to evolve independently)



$$L = L_1 L_2 \cdots L_N = \prod_{j=1}^{N} L_j$$

Maximum likelihood phylogenetics

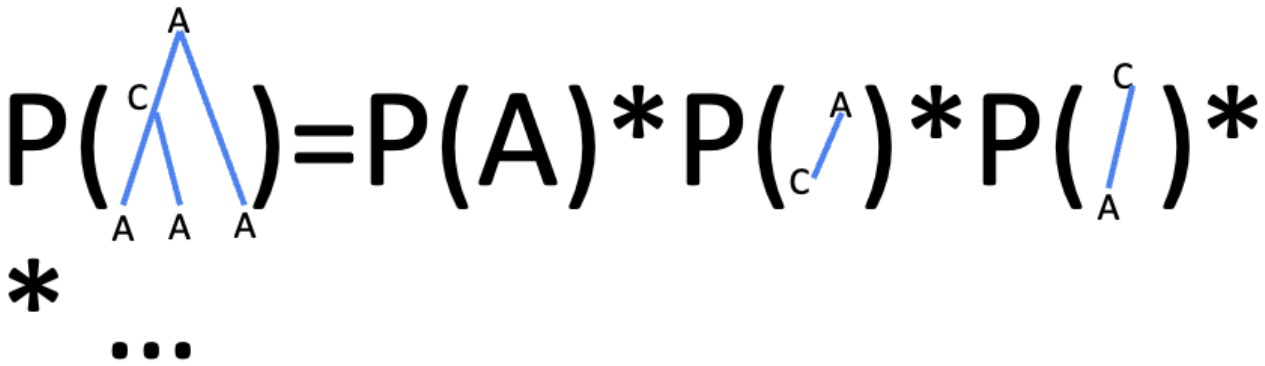
Phylogenetic Likelihood The likelihood of one alignment column is calculated by considering all possible states of the ancestors



This is done efficiently using dynamic programming (Felsenstein 1981 pruning algorithm)

Maximum likelihood phylogenetics

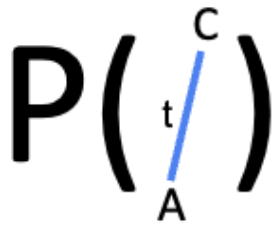
Phylogenetic Likelihood The probability of one nucleotide history can be calculated as the product of the probabilities of each branch



These probabilities are calculated using substitution matrices and matrix exponentiation

Maximum likelihood phylogenetics

Phylogenetic Likelihood



Probabilities depend on the branch length and the two nucleotides A substitution matrix Q describes how often a nucleotide evolves into another

For short branch lengths: $P(C \rightarrow A) \cong tq_{CA}$

In general we use matrix exponentiation: e^{Qt}

Maximum likelihood phylogenetics

Substitution Models Substitution models can be parametric or empirical. Nucleotide models are usually parametric : defined from a few parameters estimated from the current data. For example :

JC69

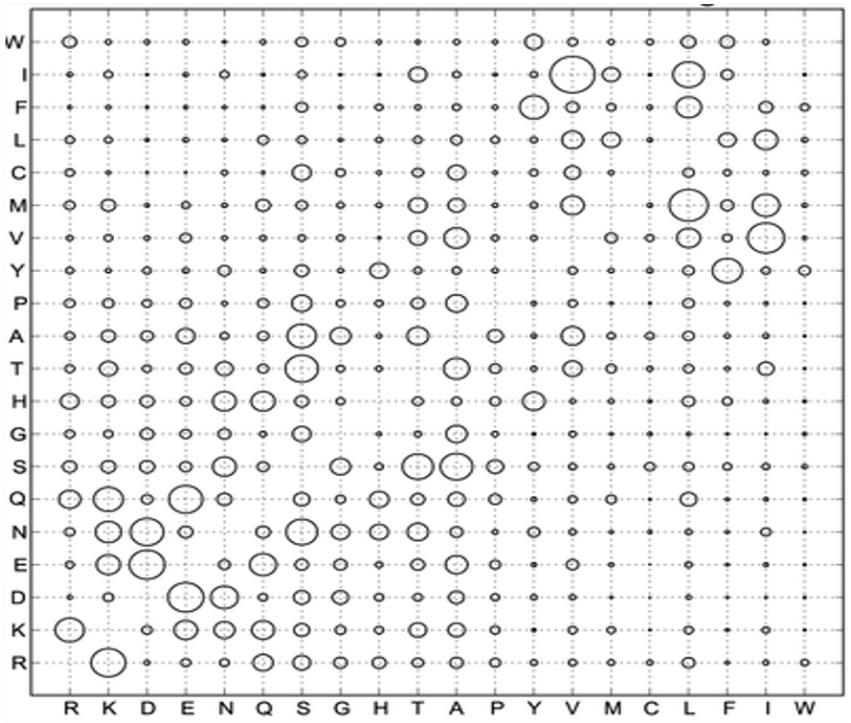
$$\begin{pmatrix} * & \frac{\mu}{4} & \frac{\mu}{4} & \frac{\mu}{4} \\ \frac{\mu}{4} & * & \frac{\mu}{4} & \frac{\mu}{4} \\ \frac{\mu}{4} & \frac{\mu}{4} & * & \frac{\mu}{4} \\ \frac{\mu}{4} & \frac{\mu}{4} & \frac{\mu}{4} & * \end{pmatrix}$$

HKY85

$$\begin{pmatrix} * & \kappa\pi_G & \pi_C & \pi_T \\ \kappa\pi_A & * & \pi_C & \pi_T \\ \pi_A & \pi_G & * & \kappa\pi_T \\ \pi_A & \pi_G & \kappa\pi_C & * \end{pmatrix}$$

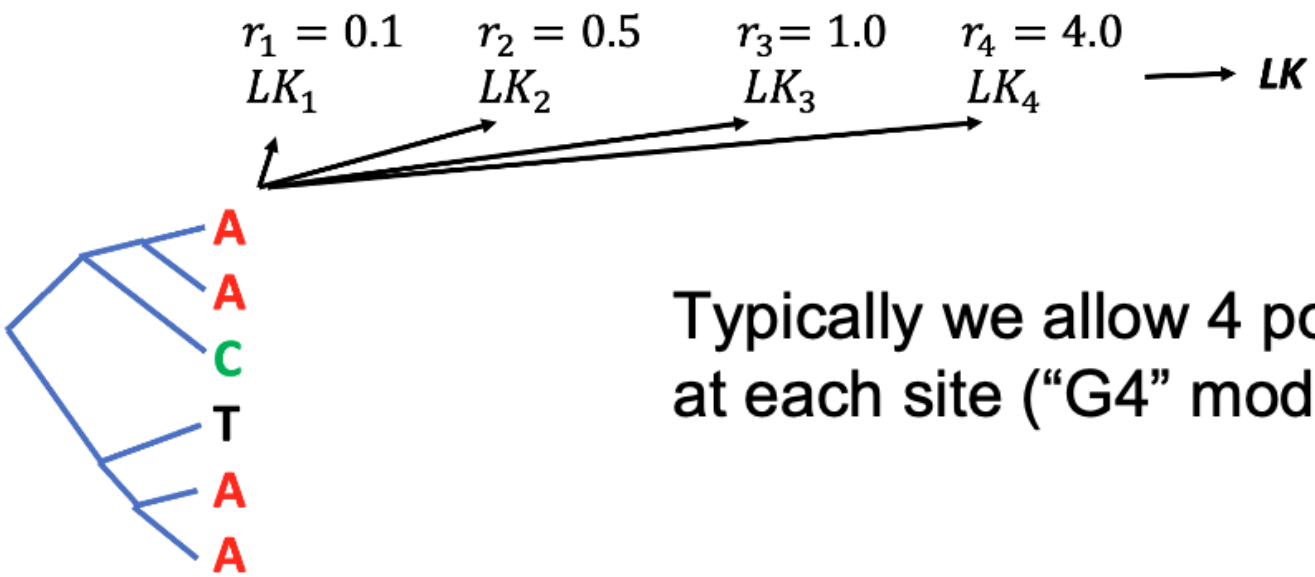
Maximum likelihood phylogenetics

Substitution Models Amino acid models are usually empirical : estimated from large datasets and then applied to smaller ones without changes E.g., WAG (Whelan and Goldman 2001)



Maximum likelihood phylogenetics

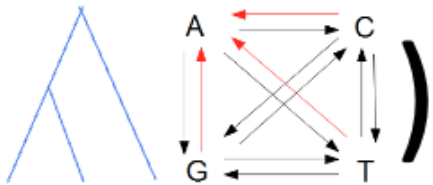
Rate variation By default, we assume all genome positions and species evolve in the same way. This is not realistic, and rate variation along the genome can be modelled to improve inference.



Typically we allow 4 possible rates at each site ("G4" model)

Maximum likelihood phylogenetics

Maximum Likelihood

Likelihood: $P($ CGAC / CGAC / CGAT $|$ 

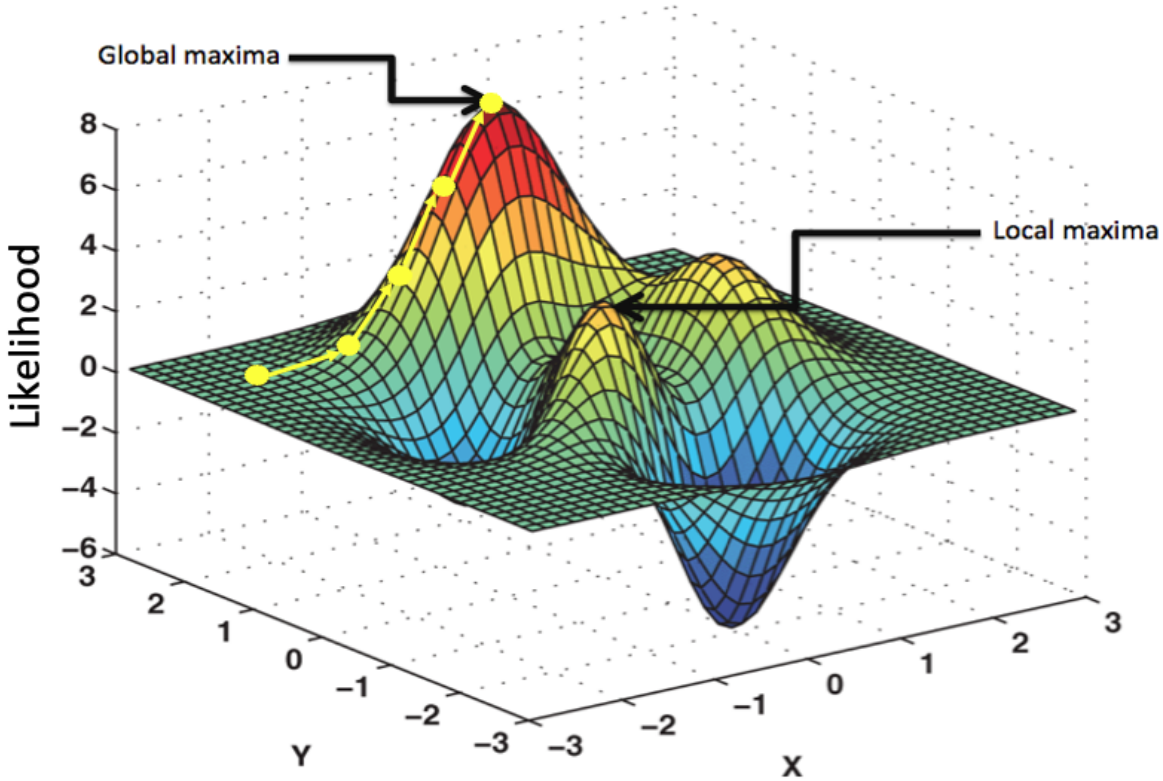
$)$

- Maximum likelihood infers not only the tree, but also model parameters in case of parametric models
- The number of possible trees is huge
- Instead of trying all possible trees, we heuristically modify a starting tree until no improvements can be found

Maximum likelihood phylogenetics

Maximum Likelihood

- The likelihood landscape
- We start from an initial random or NJ tree
- We propose new, similar trees, and accept them if they have higher likelihood
- When we reach an unimprovable tree, we stop



Maximum likelihood phylogenetics

Maximum Likelihood : Summary

- Maximum Likelihood (ML) searches for the tree with the highest likelihood as the best explanation for the data
- It infers one tree ; bootstrap can be used to assess uncertainty
- Slower than distance or parsimony methods, but still adequate for datasets with thousands of sequences
- It allows many models/features/analyses/tests, and is the most popular approach for tree inference due to its robustness

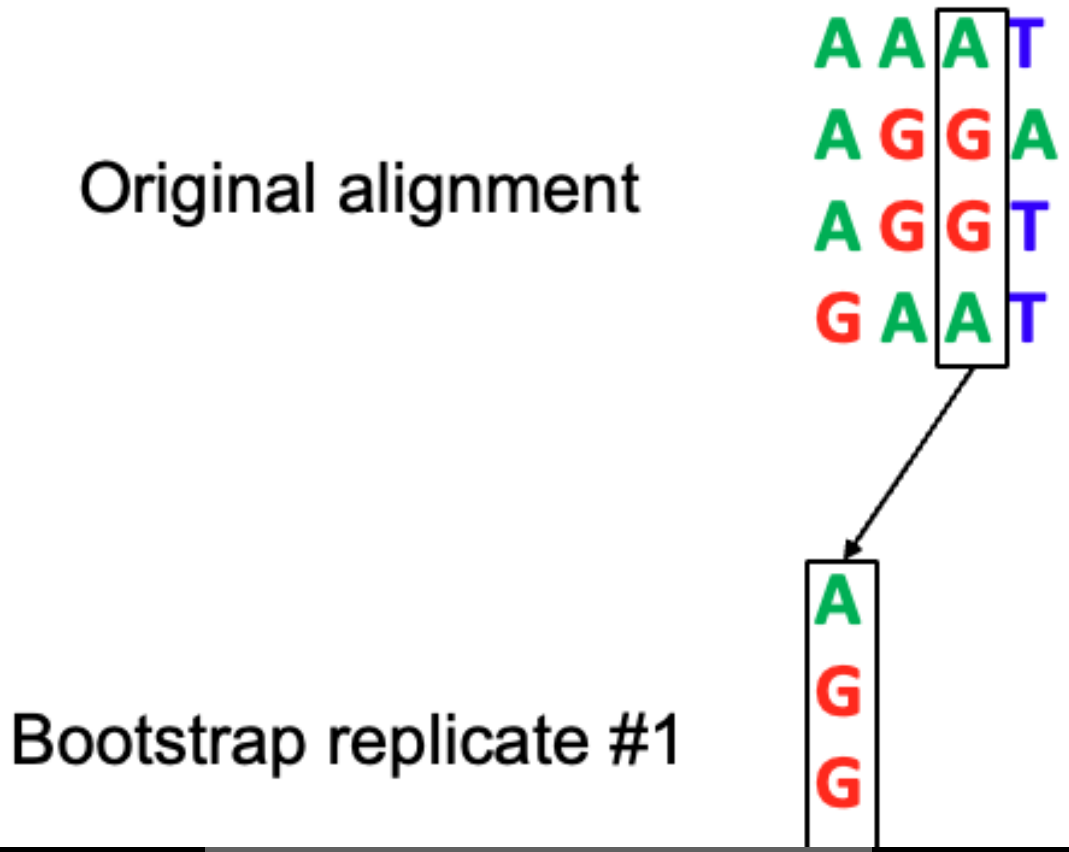
Practical 3

Bootstrap

Bootstrap

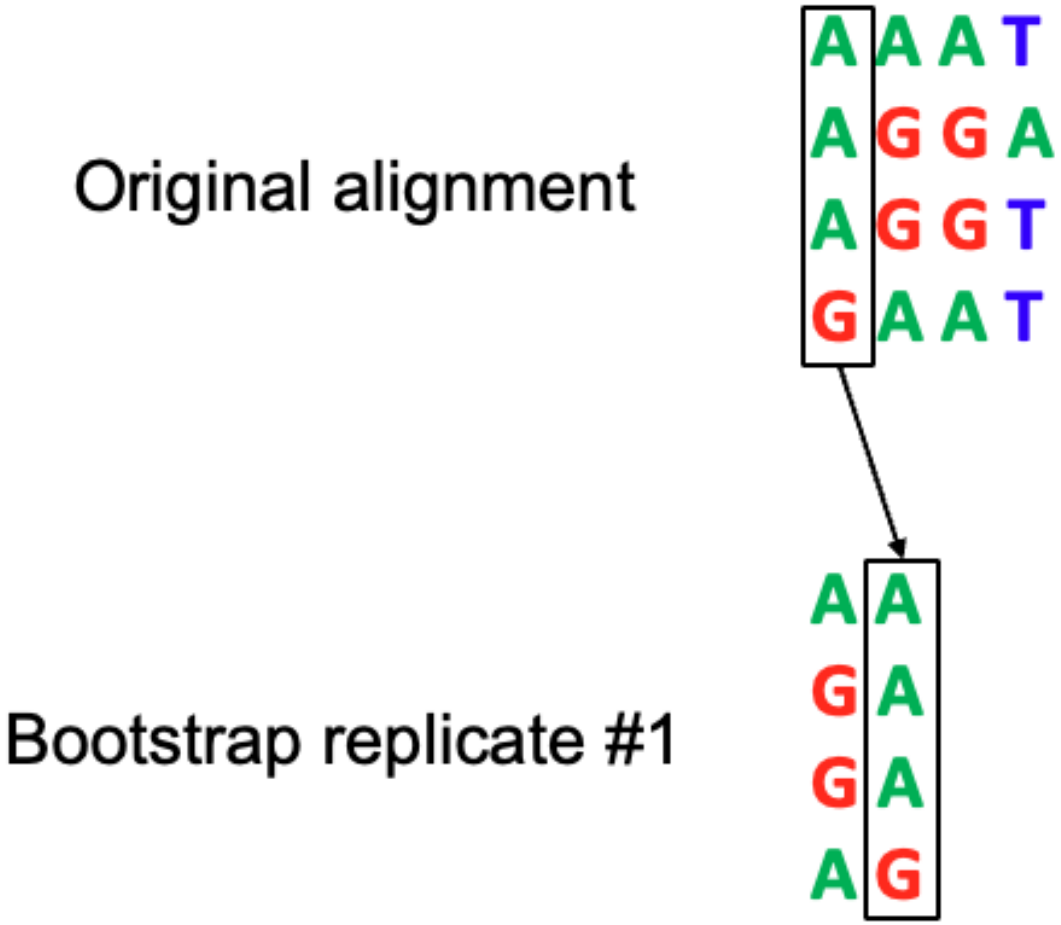
Bootstrap

- Maximum likelihood, parsimony, and distance methods reconstruct one tree
- How to measure confidence in the tree/branches ?
- A popular approach is bootstrap (Felsenstein, 1985)
- Each bootstrap replicate resamples alignment columns (with replacement) to create a new alignment of the same size as the original



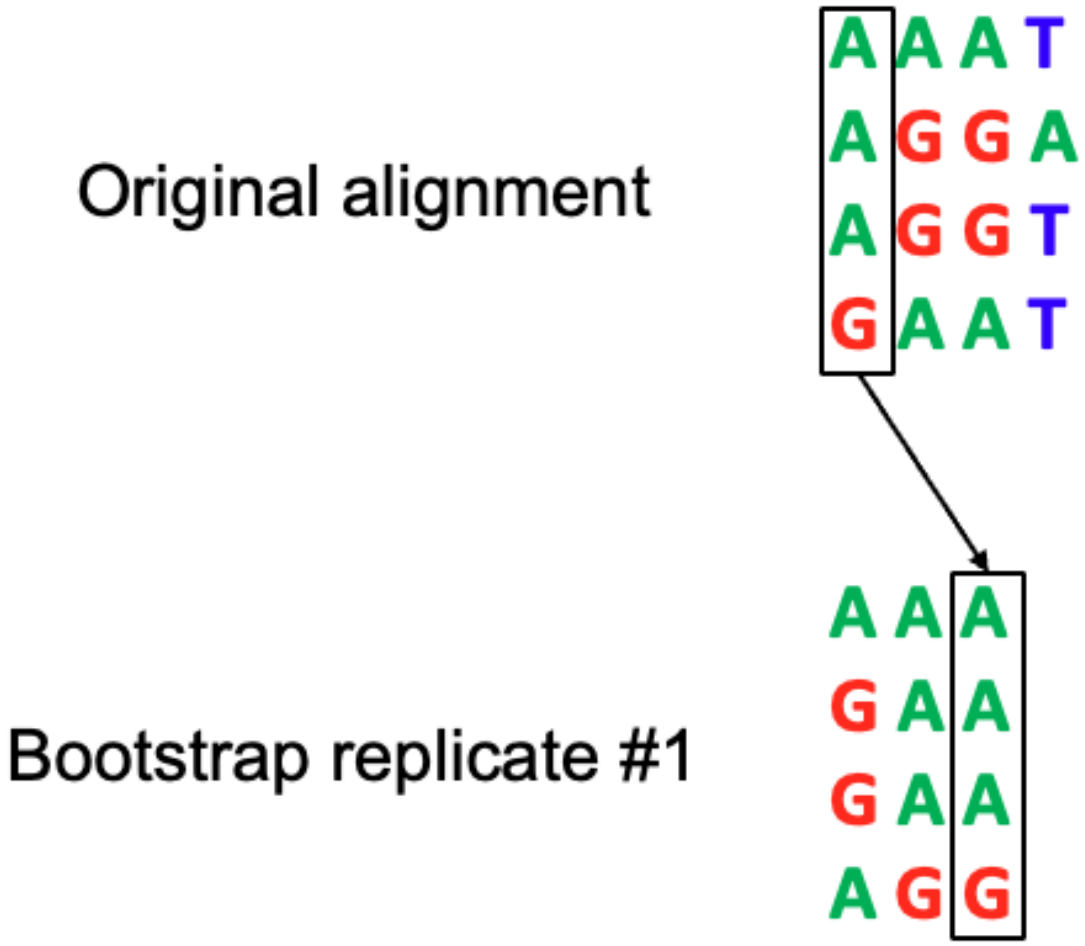
Bootstrap

Bootstrap



Bootstrap

Bootstrap

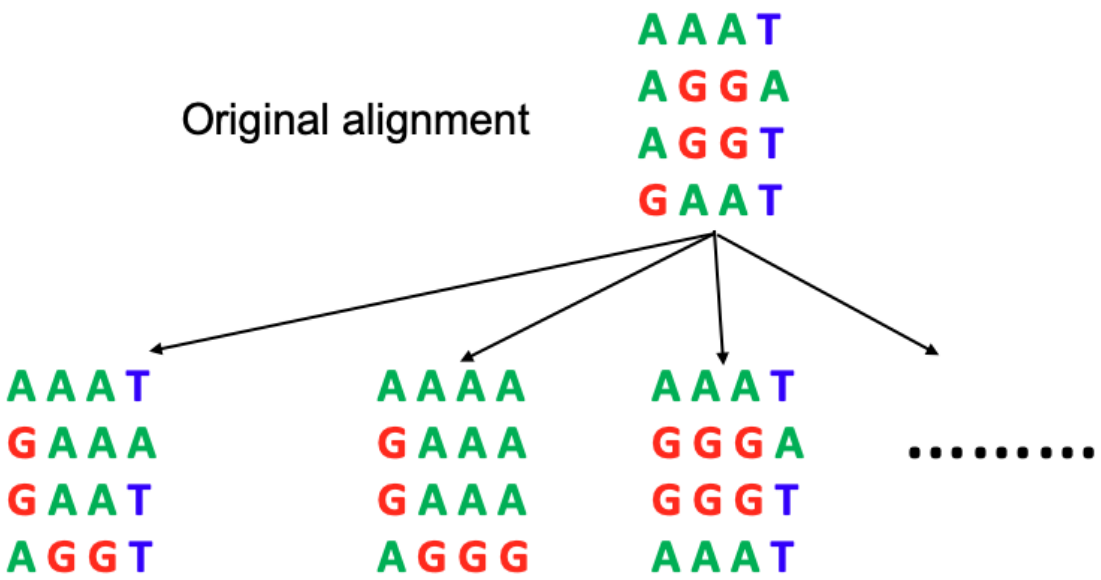


Bootstrap

Bootstrap

Bootstrap

Bootstrap

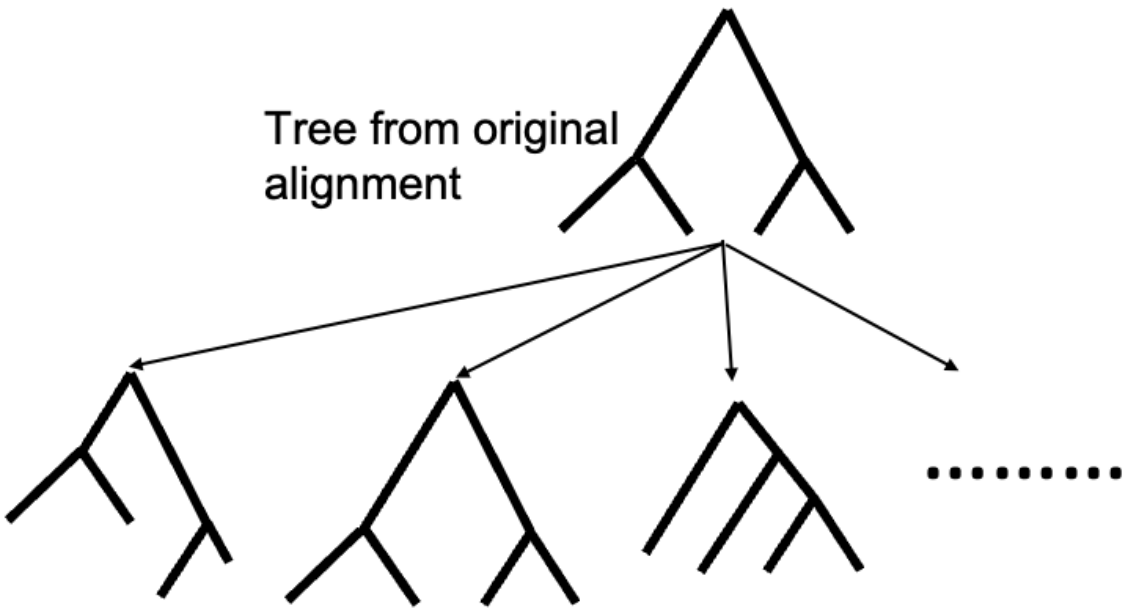


We create hundreds of such bootstrap replicate alignments

Bootstrap

Bootstrap

- From each alignment we then infer a bootstrap tree. The support of a branch in the initial tree is the proportion of times it is present in the bootstrap trees
- Typically 1000 replicates : it can be extremely slow
- There are faster approximations (e.g. UFBoot in IQ-TREE)



Trees inferred from bootstrap replicates

Bootstrap

Bootstrap : Summary

- The bootstrap creates replicate alignments from the true one and counts how often each clade occurs in the replicate trees
- Bootstrap is slow (e.g. 100x or 1000x slower than standard inference). Faster approximations are available such as UFBoot
- Other branch supports have different meaning : TBE represents the proportion of a clade that is stable. aLRT measures the confidence in a specific branching, rather than a clade

Practical 4

Bayesian phylogenetics inference

Bayesian inference

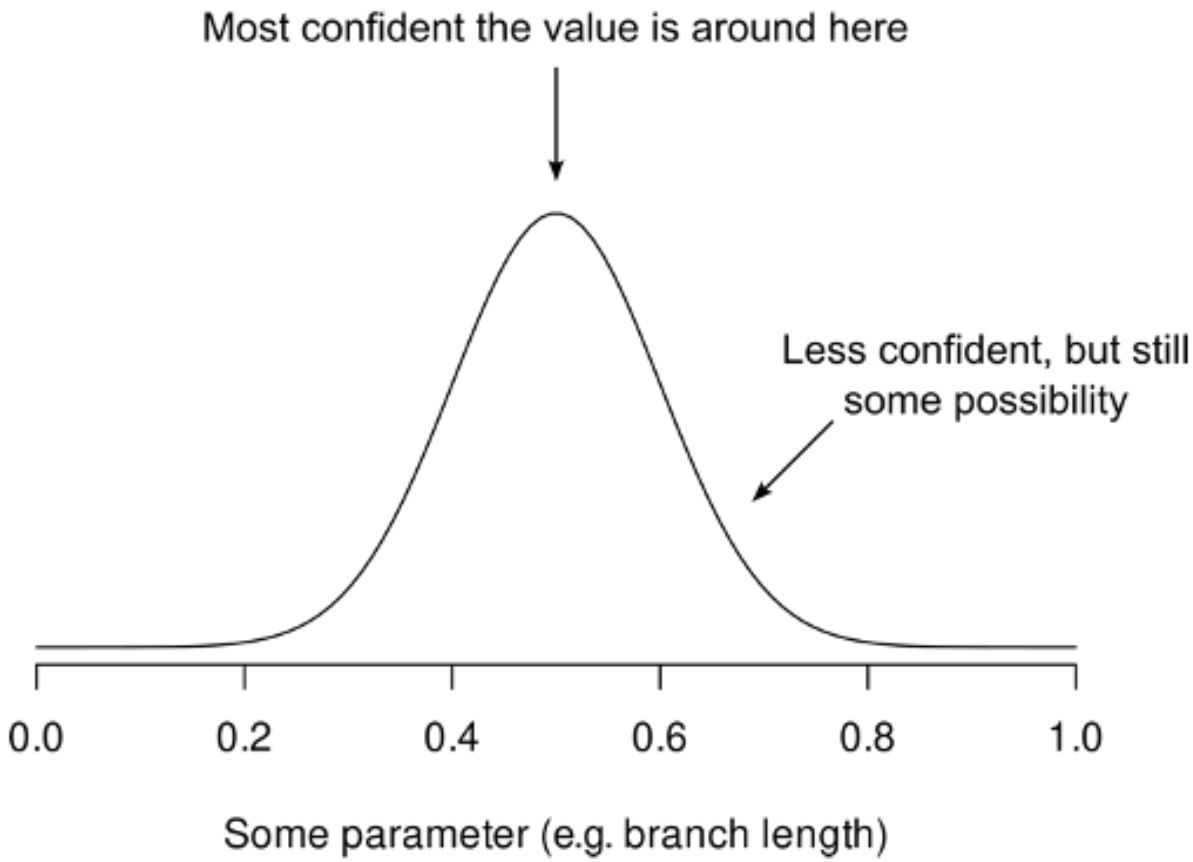
Bayesian inference

- The principle of likelihood asks the question : how probable are our data given our tree
- Many feel that this is the wrong question - generally it seems simpler to ask how probable your hypothesis (tree) is, given some data
- To ask this question, we must use Bayesian inference

Bayesian inference

Bayesian inference

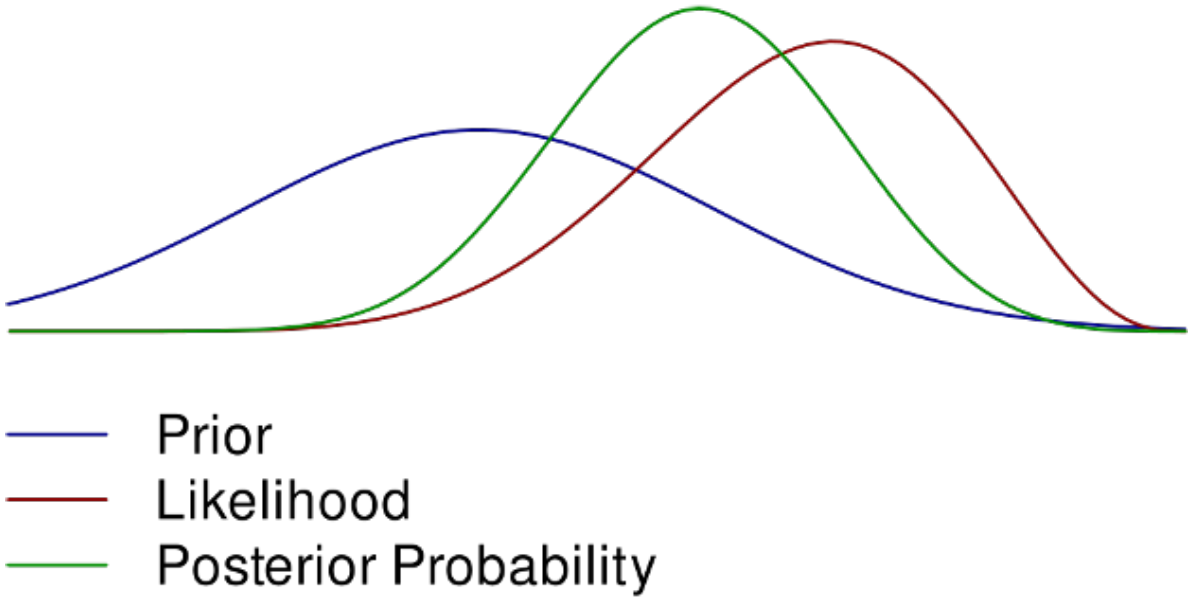
- The Bayesian view is that probability represents a way of encoding beliefs about a hypothesis
- High probabilities mean that I am pretty certain of this hypothesis, but I express my uncertainty about it with a distribution



Bayesian inference

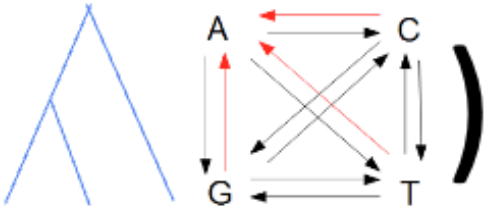
Bayesian inference Conceptually, it combines two sources of information to calculate Posterior Probabilities :

- Information from the data, encoded by the likelihood
- Information from our prior beliefs, the prior distribution



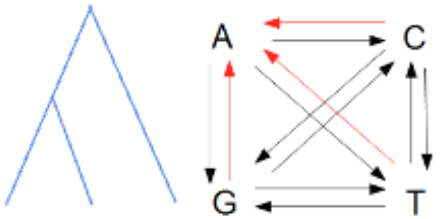
Bayesian inference

Bayesian inference

Likelihood: $P($ CGAC / CGAC / CGAT $|$ 

$)$

Maximum likelihood looks for the tree and parameters that maximize the likelihood

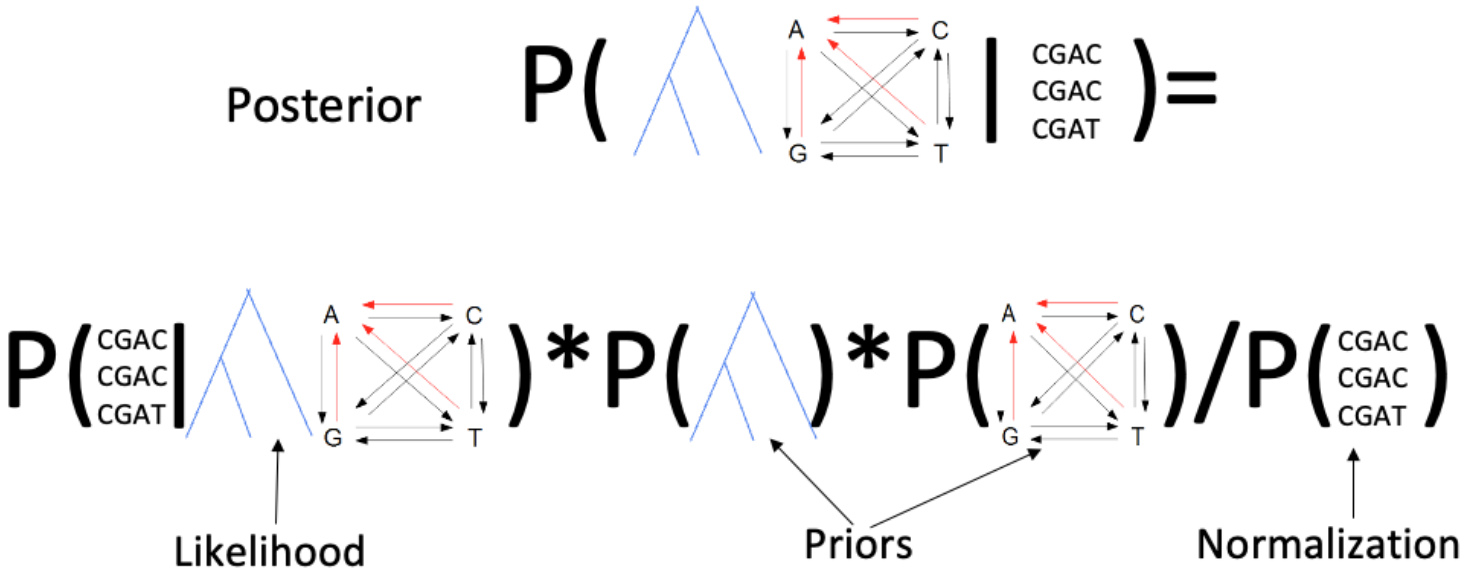
Posterior: $P($ 

$|$ CGAC / CGAC / CGAT $)$

Bayesian methods seek the posterior probability of tree and parameters

Bayesian inference

Bayesian inference



- Priors do need to be specified by the user
- We do not need to calculate the normalization factor if we use Monte Carlo Markov Chain (MCMC) methods

Bayesian inference

Priors

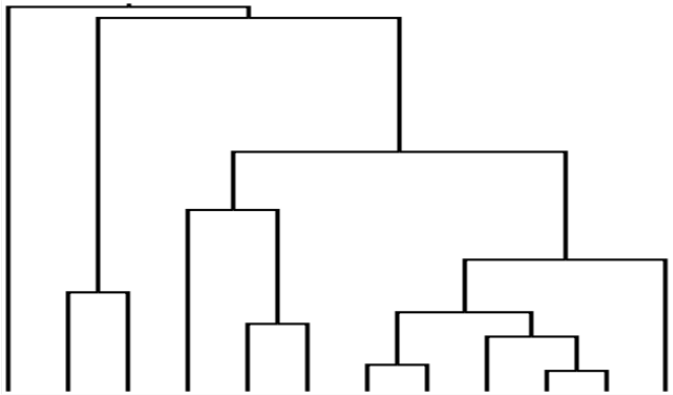


Figure – Yule and Birth-death priors model speciation/extinction and epidemics

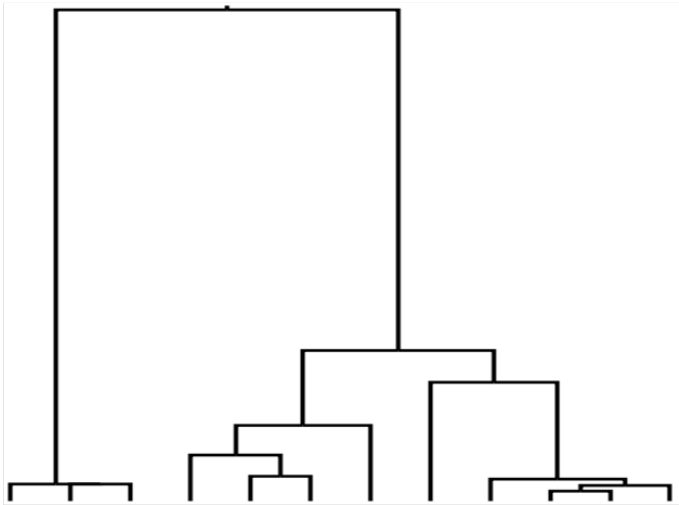


Figure – Coalescent priors are used for within-population data

Bayesian inference

Bayesian inference

- The difference between likelihood and posterior matters the most when data is limited there otherwise uncertainty (e.g., high or low divergence)
- Given this alignment of two species, what is the maximum likelihood divergence ?
- Is this a reasonable estimate ?
- The maximum likelihood divergence is 0
- This would mean the 2 species are the same, which is usually wrong
- A Bayesian method takes into account the uncertainty that comes from small data and low divergence

Monte Carlo Markov Chain

Monte Carlo Markov Chain Similar moves to Maximum Likelihood tree search, but :

- ML (usually) accepts only moves that increase the likelihood
- MCMC can accept moves that decrease the posterior

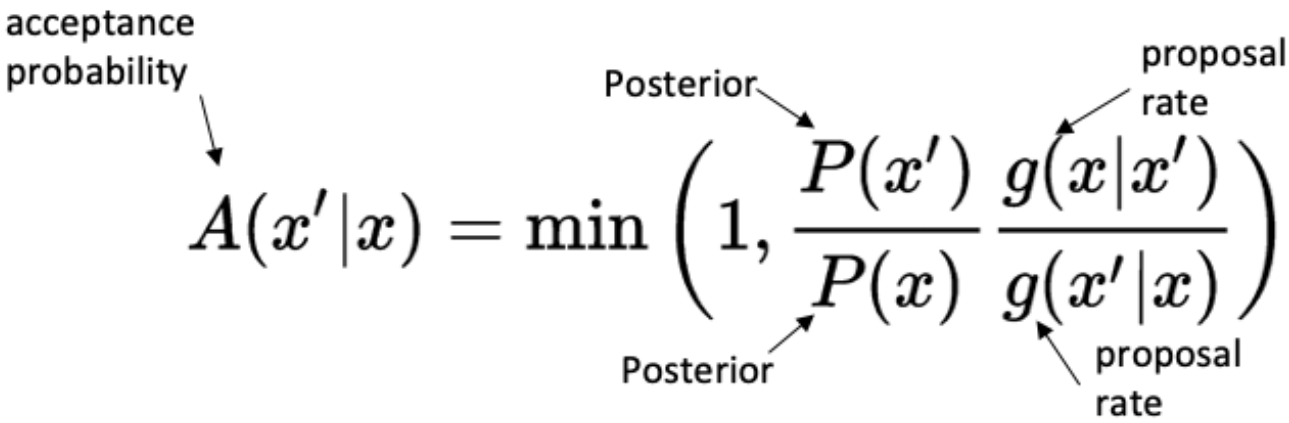
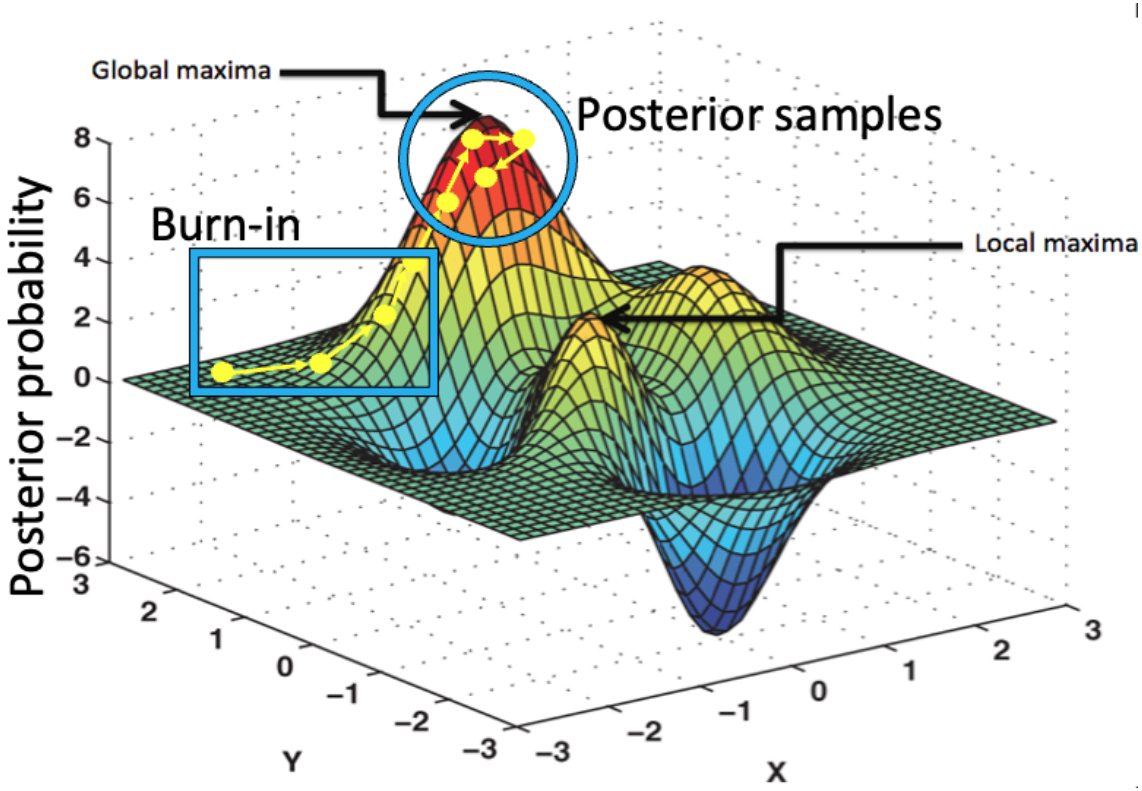


Figure – Metropolis-Hastings acceptance

Monte Carlo Markov Chain

Monte Carlo Markov Chain

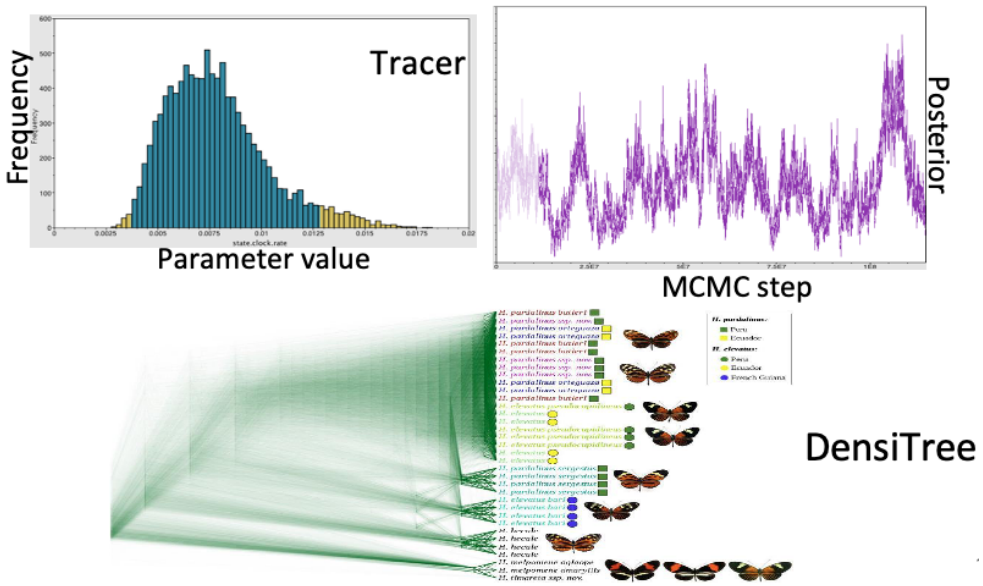
- The start of MCMC looks similar to ML
- MCMC moves can however also decrease the posterior
- Initial samples (“burn-in”) are then discarded
- In the final sample trees are represented proportionally with their probability



Bayesian inference

Bayesian inference

- Methods we have seen so far (distance, parsimony and maximum likelihood) estimate one tree
- Bayesian methods instead assess the probabilities of different trees : the output is a collection of trees
- Bayesian analyses provide multiple trees and parameter values as output



Bayesian inference

Bayesian inference : Summary

- Bayesian methods use prior probabilities of trees and parameters, and infer posterior distributions
- They are generally slower than ML
- They are good at measuring uncertainty
- They can use broad ranges of models and data

Practical 5

Some phylogenetic applications

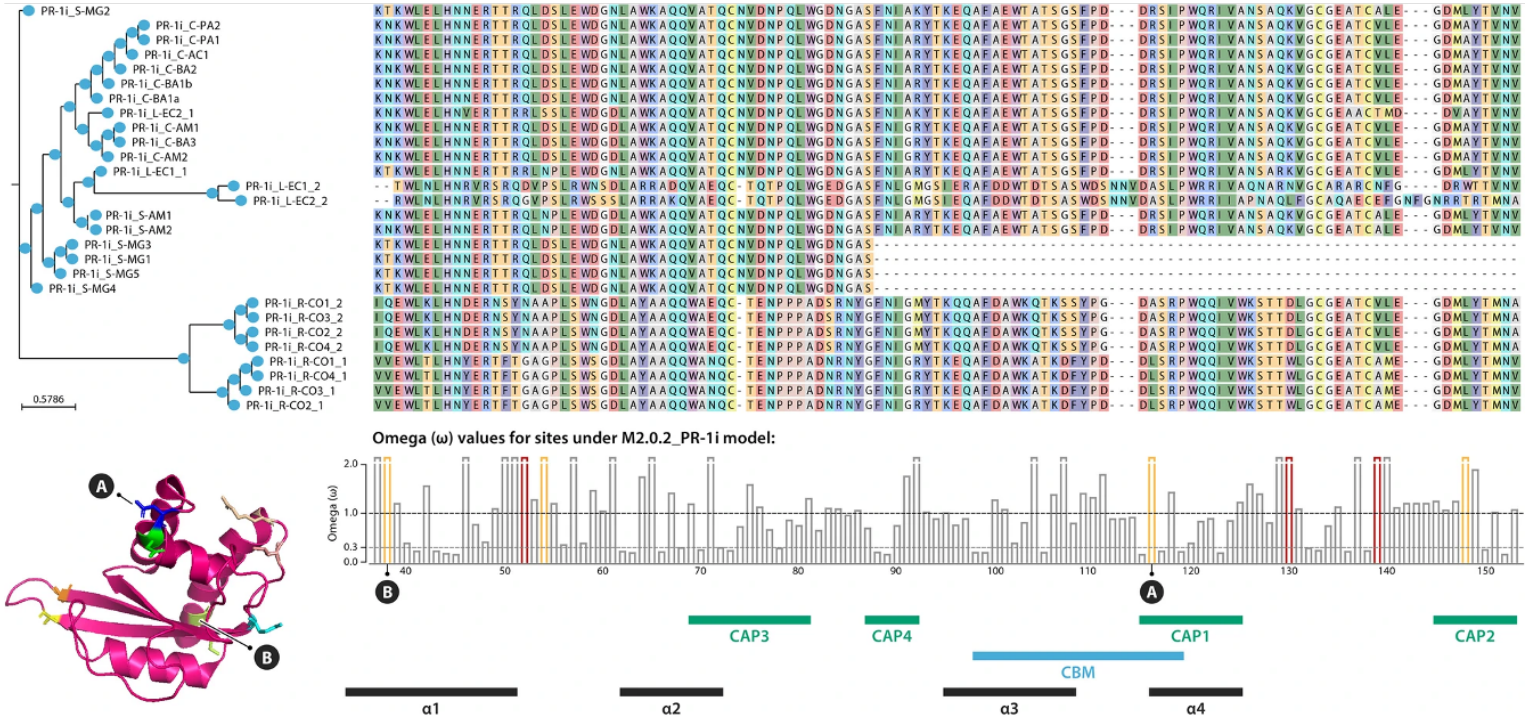
Inference of phylogeny from Molecular data

Inference of phylogeny from Molecular data : Recap

Distance/parsimony	Maximum Likelihood	Bayesian
MEGA ape (R) bioPython UShER	FastTree RaxML IQTree PhyML	MrBayes BEAST
Fast and simple but without complex models	Often more accurate, more computational demand	Slow but accurately measure uncertainty. Broadest range of models and applications.

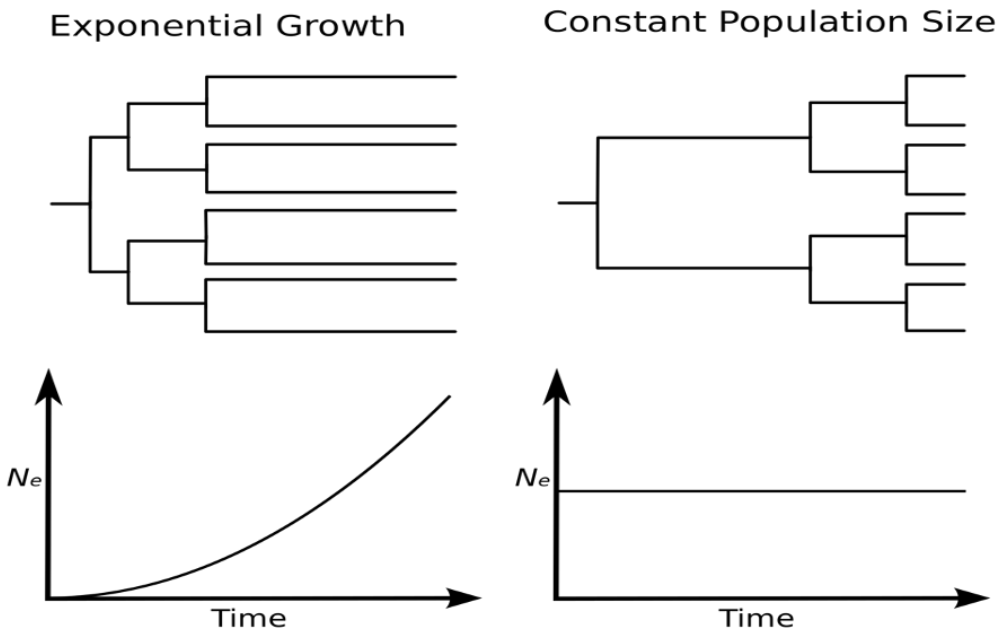
Some phylogenetic applications

Positive selection scans Statistical tests can highlight genes, gene positions, and branches under selection. Software : PAML, HyPhy



Some phylogenetic applications

Phylodynamics The shape of a phylogenetic tree can reveal past population/epidemiological dynamics. This is because the probability of branching/coalescing depends on the population size.



Some phylogenetic applications

Phylodynamics From the tree shape we can reconstruct the history of prevalence or population size changes. Software : BEAST

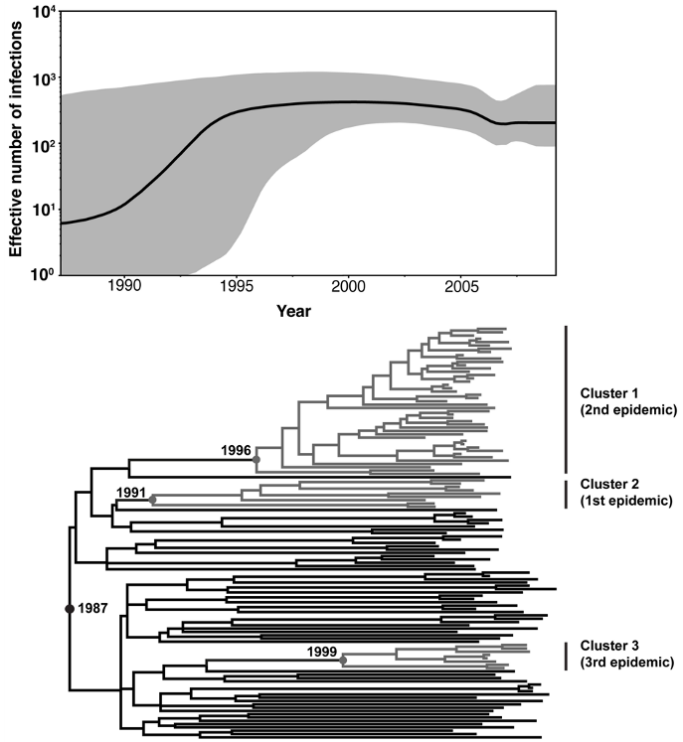
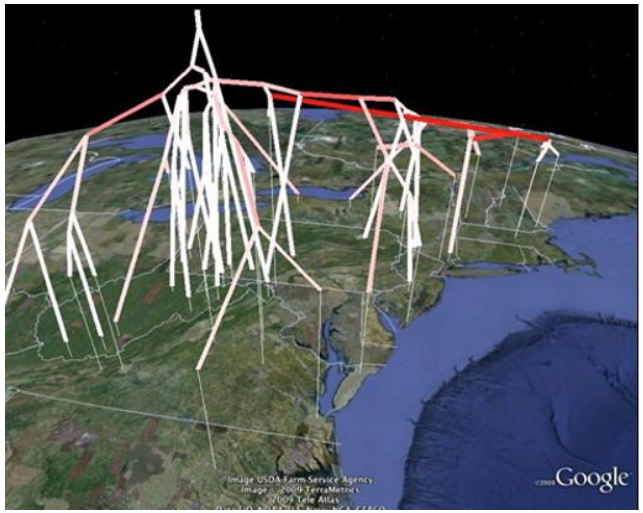


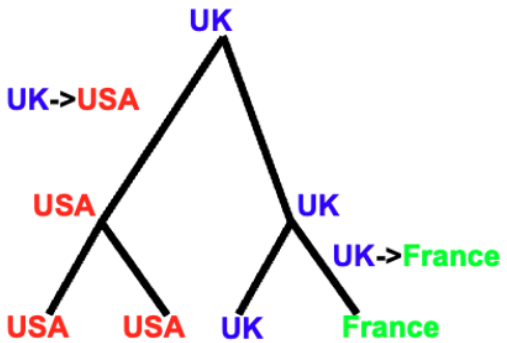
Figure – Hon-Kwan Chen et al 2011

Some phylogenetic applications

Viral Phylogeography

- We can integrate genetic sequences with other data like time, phenotype, or geographic information
- When we use time and geographic information we can do phylogeography : the study of spread in space and time using phylogenies
- Phylogeography can be done in discrete space (e.g. between countries) or continuous space using coordinate data. Software : BEAST
- Statistical tests can highlight genes, gene positions, and branches under selection. Software : PAML, HyPhy





Practical 6