

# Phylogenetics

Course introduction

RL-V3 MPP

Rachel Warnock

16.04.24



# About this course

Thursdays 14:00–16:00 CET at Henke Str.

8 weeks of lectures + 6 weeks for project work

Classes will consist of lectures and practical exercises

All lecture material available via the [course website](#)

Blue underlined text → [external links](#)

# Course objectives

To learn the **application** of phylogenetics in paleobiology

- Tree building
- Substitution models
- Dating trees
- Clock models
- Tree models
- Diversification rates
- Morphological models
- Continuous trait evolution

# Course evaluation

“**Phylogenetics**” is graded together with “**Introduction to Statistical Modelling**”  
(course code: **RL-V3 MPP**)

Evaluation is based on a **written report** (info available on the [project page](#))

Class exercises will be in [R](#) or the Bayesian phylogenetic software [RevBayes](#)

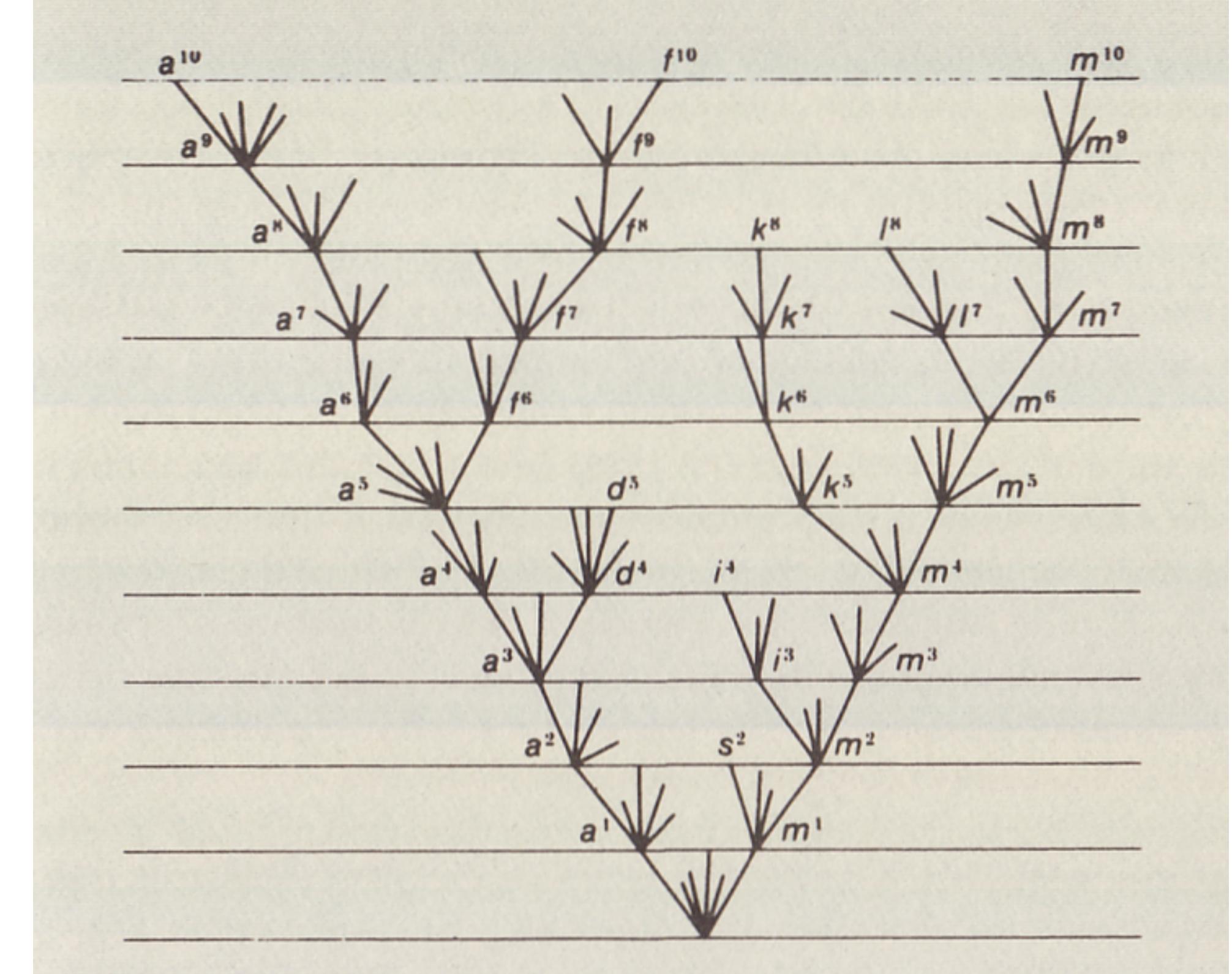
In addition, we have homework exercises that include videos and reading



Please ask questions!

# Today's objectives

- Recap 'tree-thinking'
- Gain an understanding of the **parsimony** approach to tree-building and **statistical inconsistency**



Time tree from Darwin's *Origin of Species*

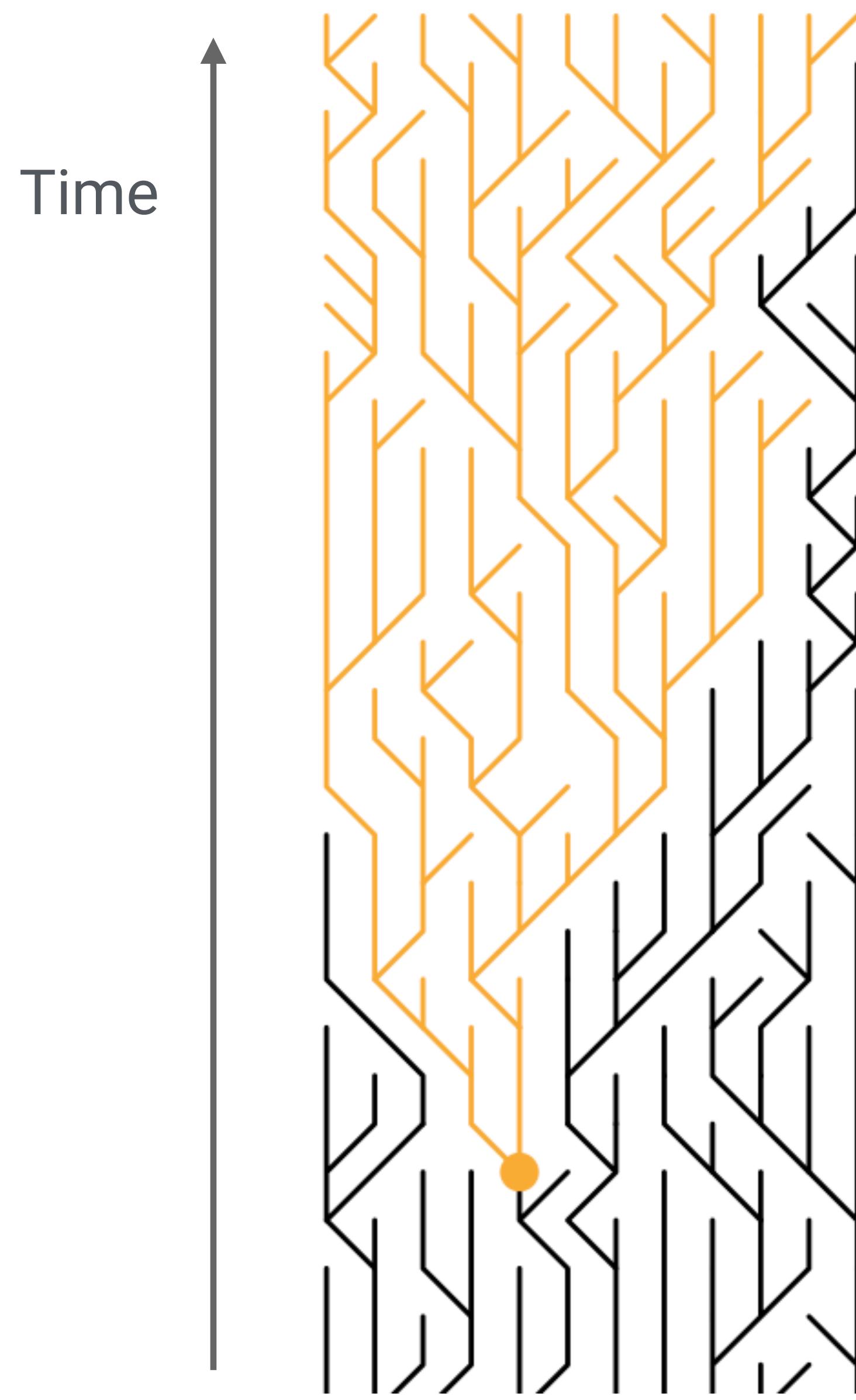
# What is phylogenetics?

# Phylogenetics

**Phylogenetics** aims to reconstruct the phylogeny of individual samples based on molecular or morphological character data

A phylogeny captures part of evolutionary history that is otherwise not directly observable

**Phylogenetics** aims to quantify the processes that gave rise to the tree,  
e.g., speciation, extinction



- populations
- species
- viruses
- cells
- languages

In this course we mainly focus on trees that include **one representative per species**

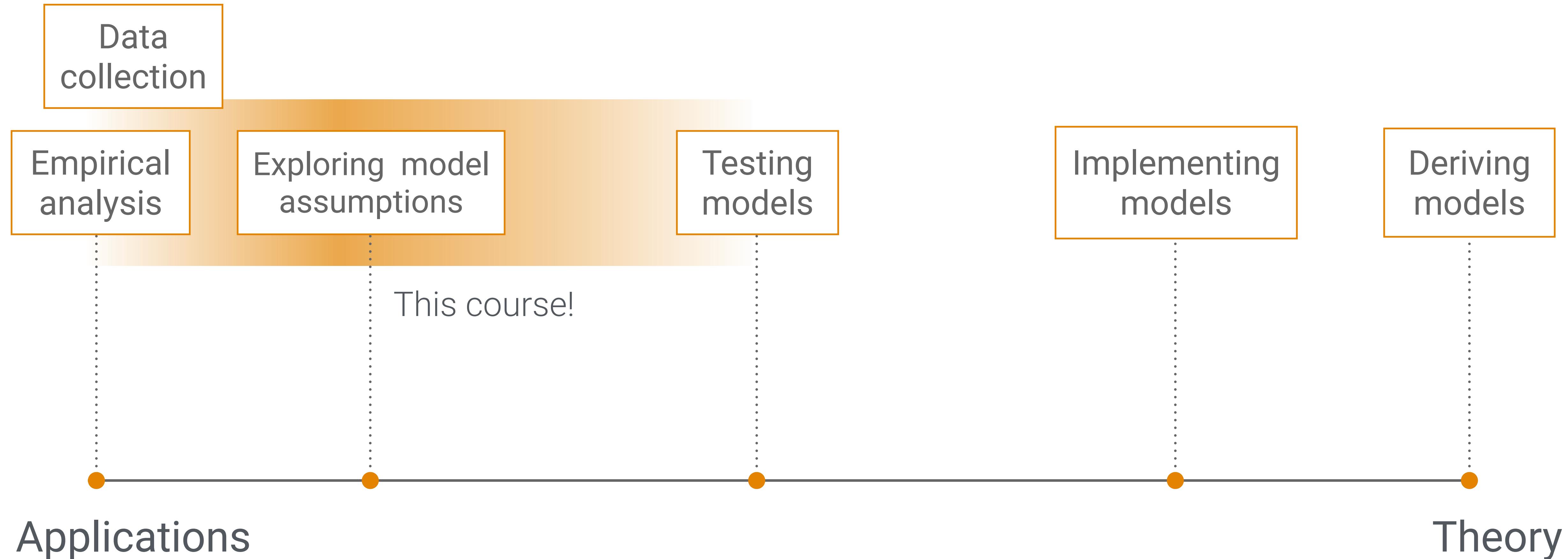
## Data

- DNA
- morphology
- words



[Scots poem](#) - also the [BEAST2](#) logo!

# Research topics in phylogenetics

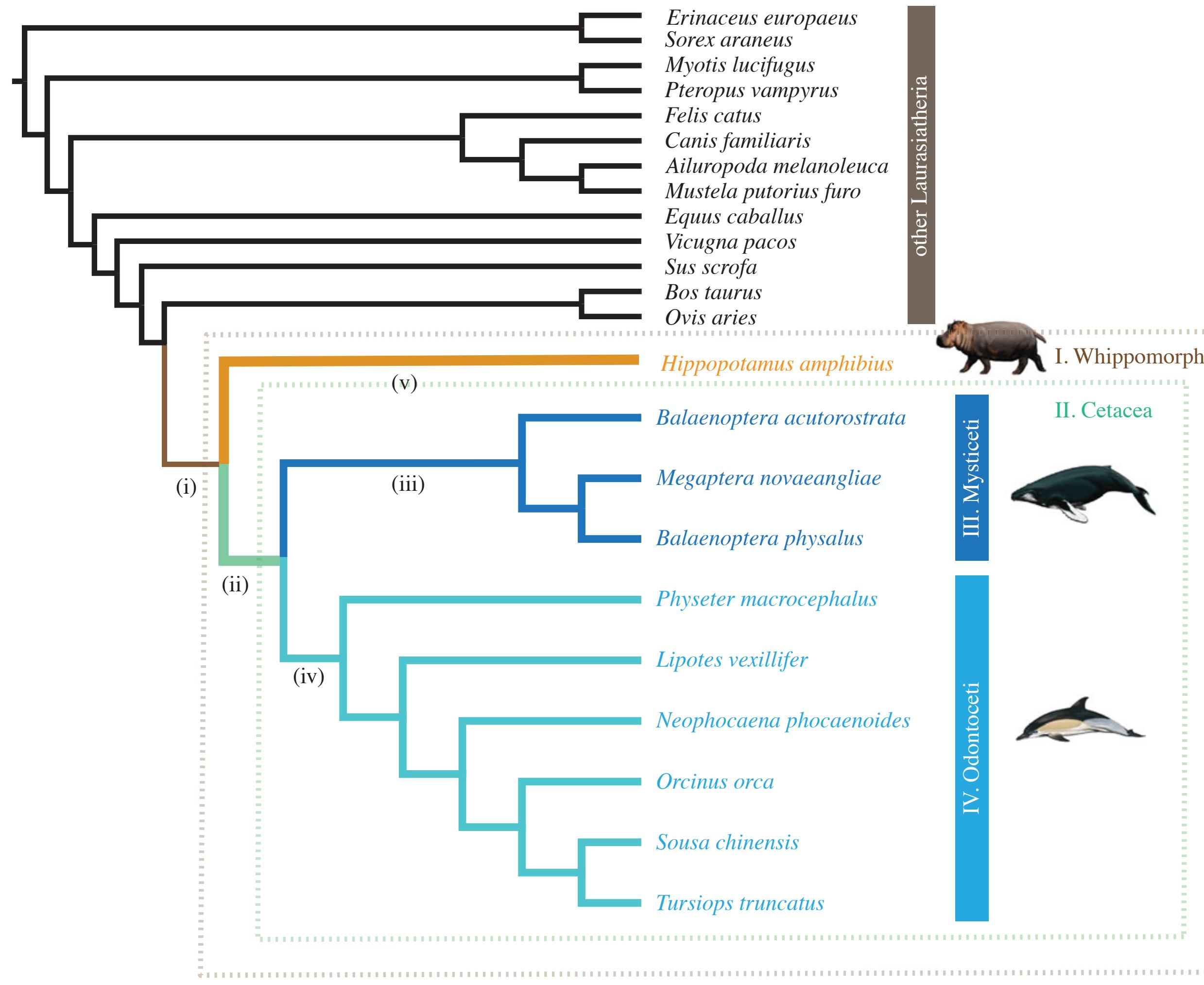


*Nothing in biology makes sense except in the light of evolution* – Theodosius Dobzhansky ([1973](#))

*Nothing in evolution makes sense except when seen in the light of phylogeny* – Jay Savage (1997)

# Trees in paleobiology

# What can we learn from trees?

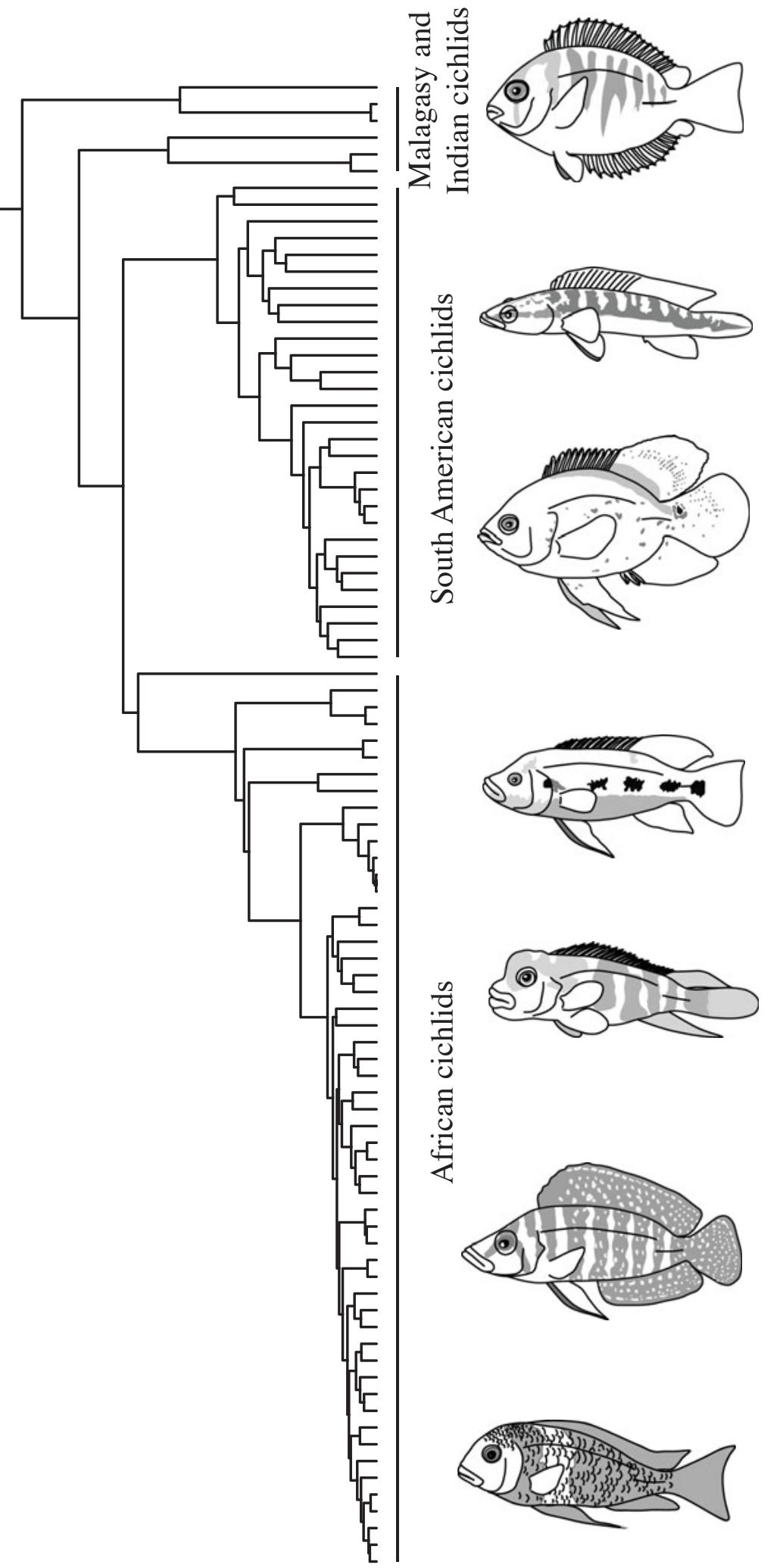


How are our favourite species related?

Does the phylogeny support the taxonomy?

# What can we learn from trees?

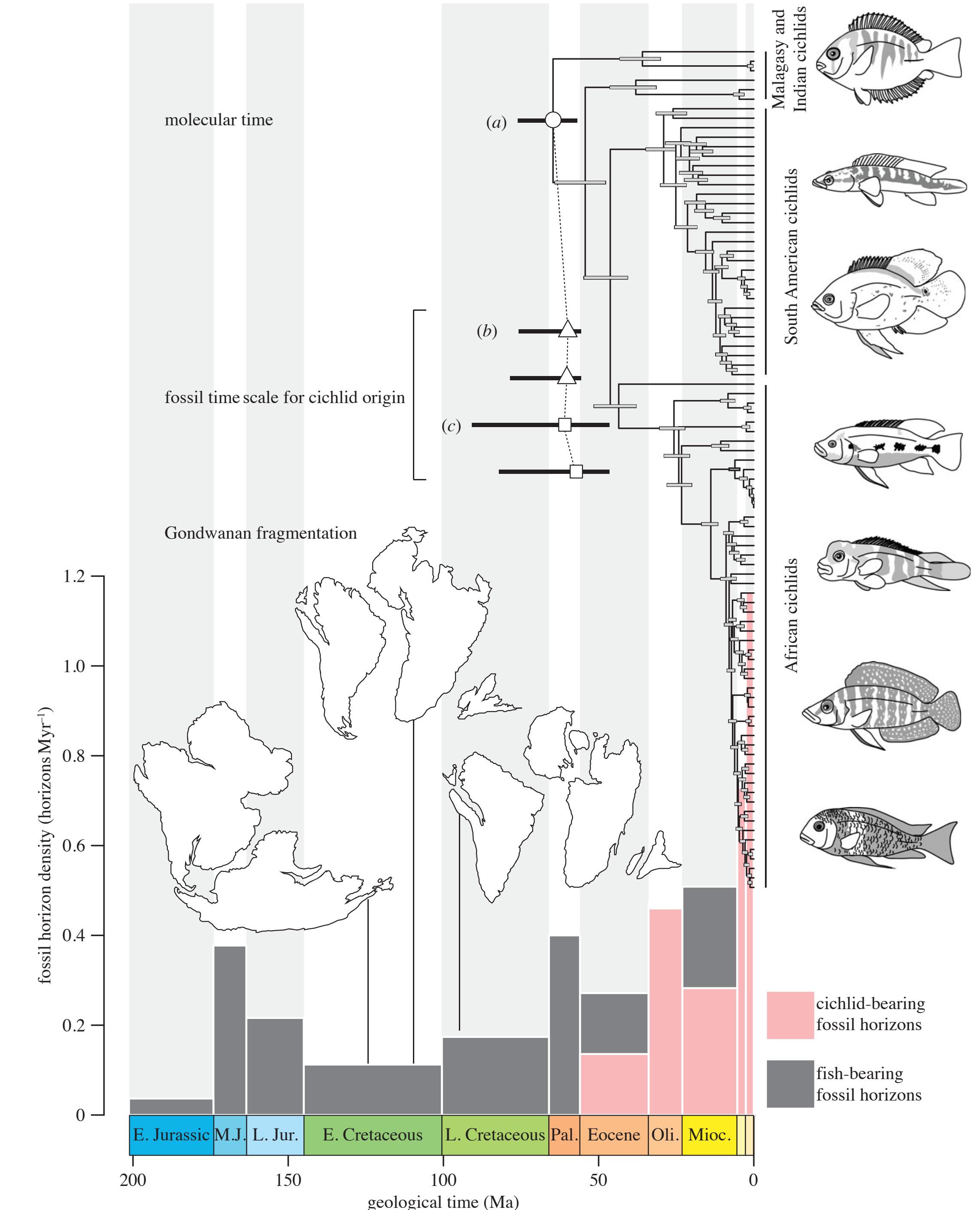
- Evolutionary relationships



# What can we learn from trees?

- Evolutionary relationships
- Timing of diversification events
- Geological context
- Rates of phenotypic evolution
- Diversification rates

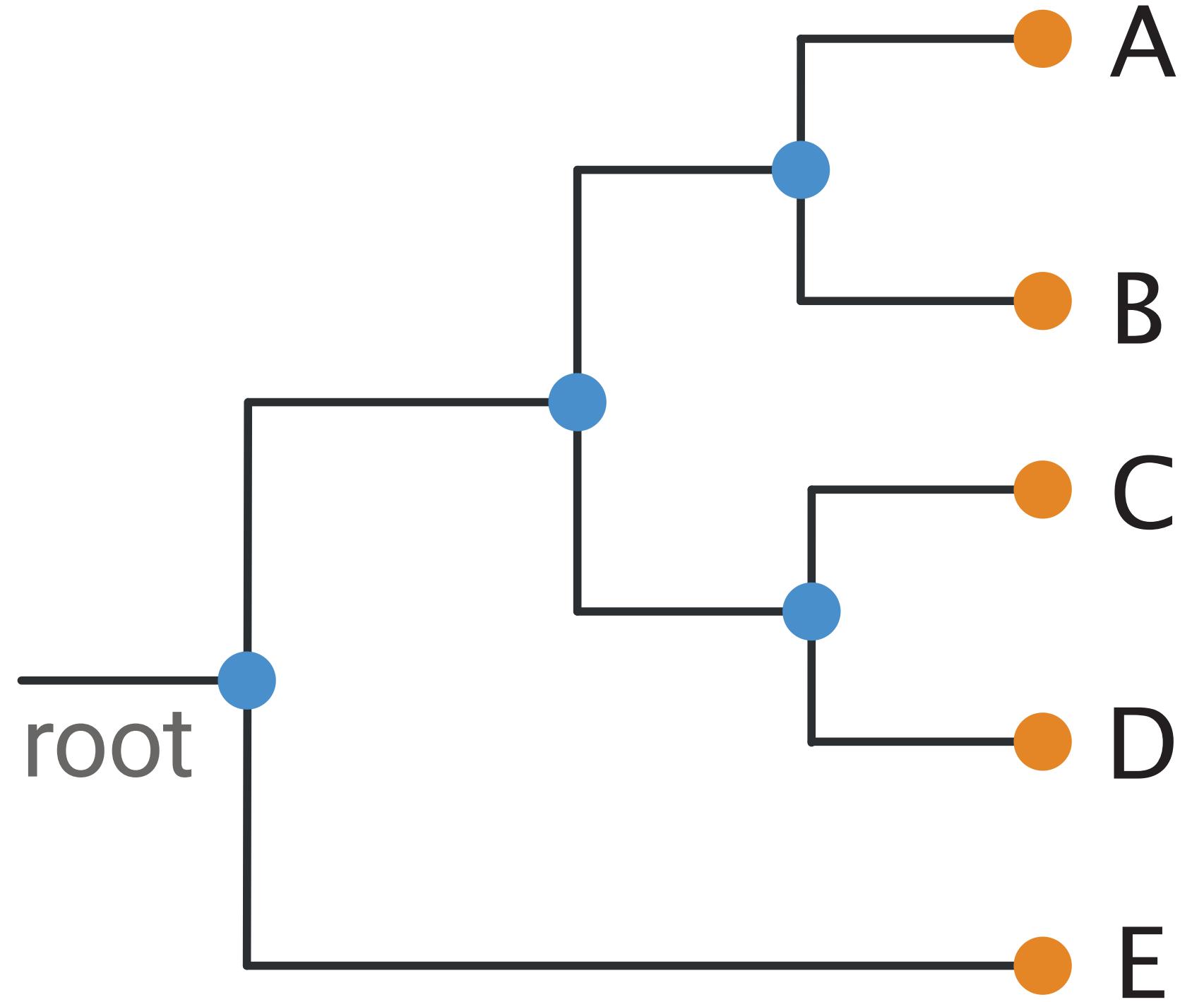
Image adapted from Friedmann et al. (2013)



# Where do we begin?

# Some basic terms

MRCA = most recent common ancestor



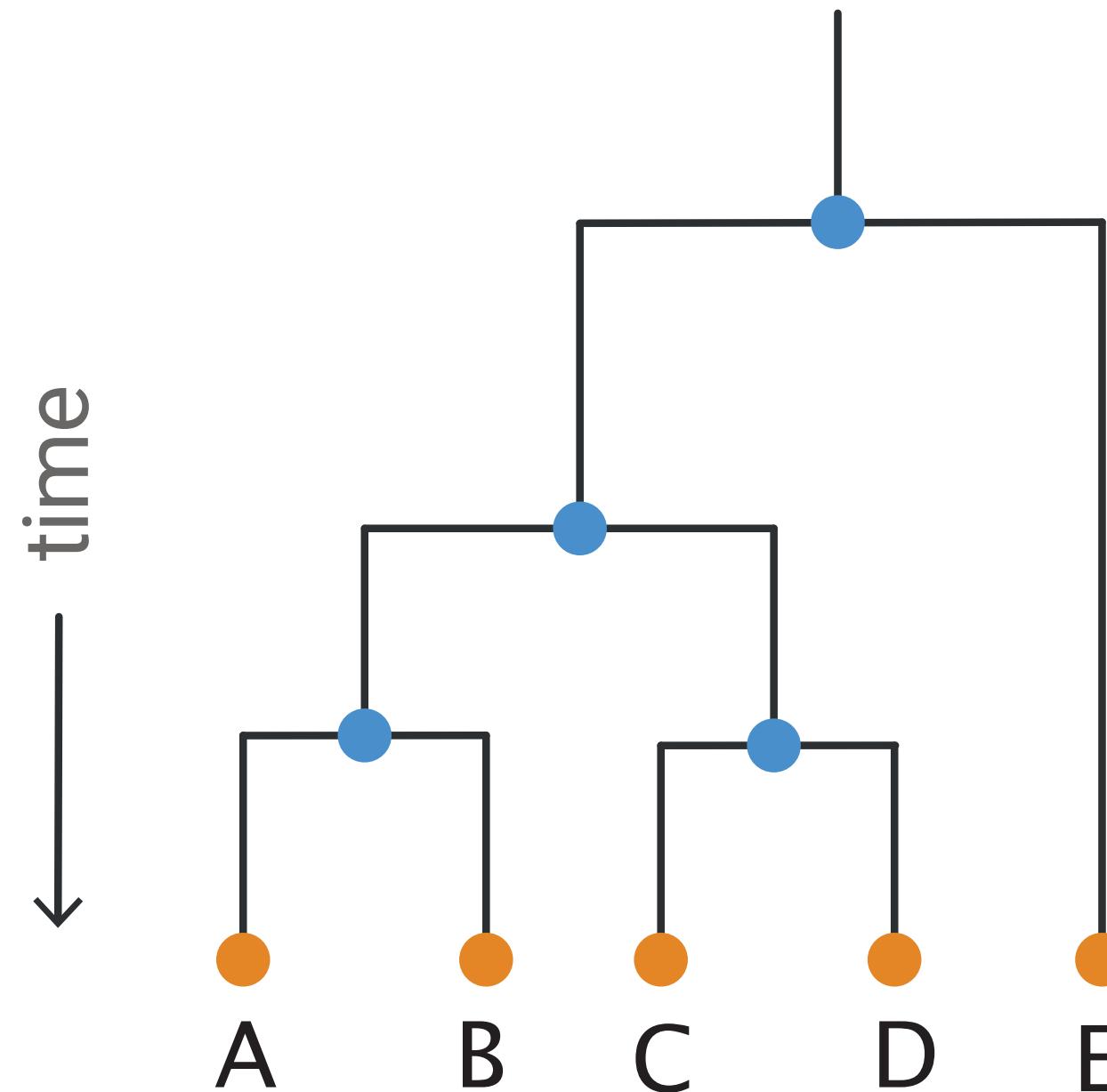
- internal nodes or MRCA
- tips or leaves
- branches or edges

branch lengths = genetic distance or time

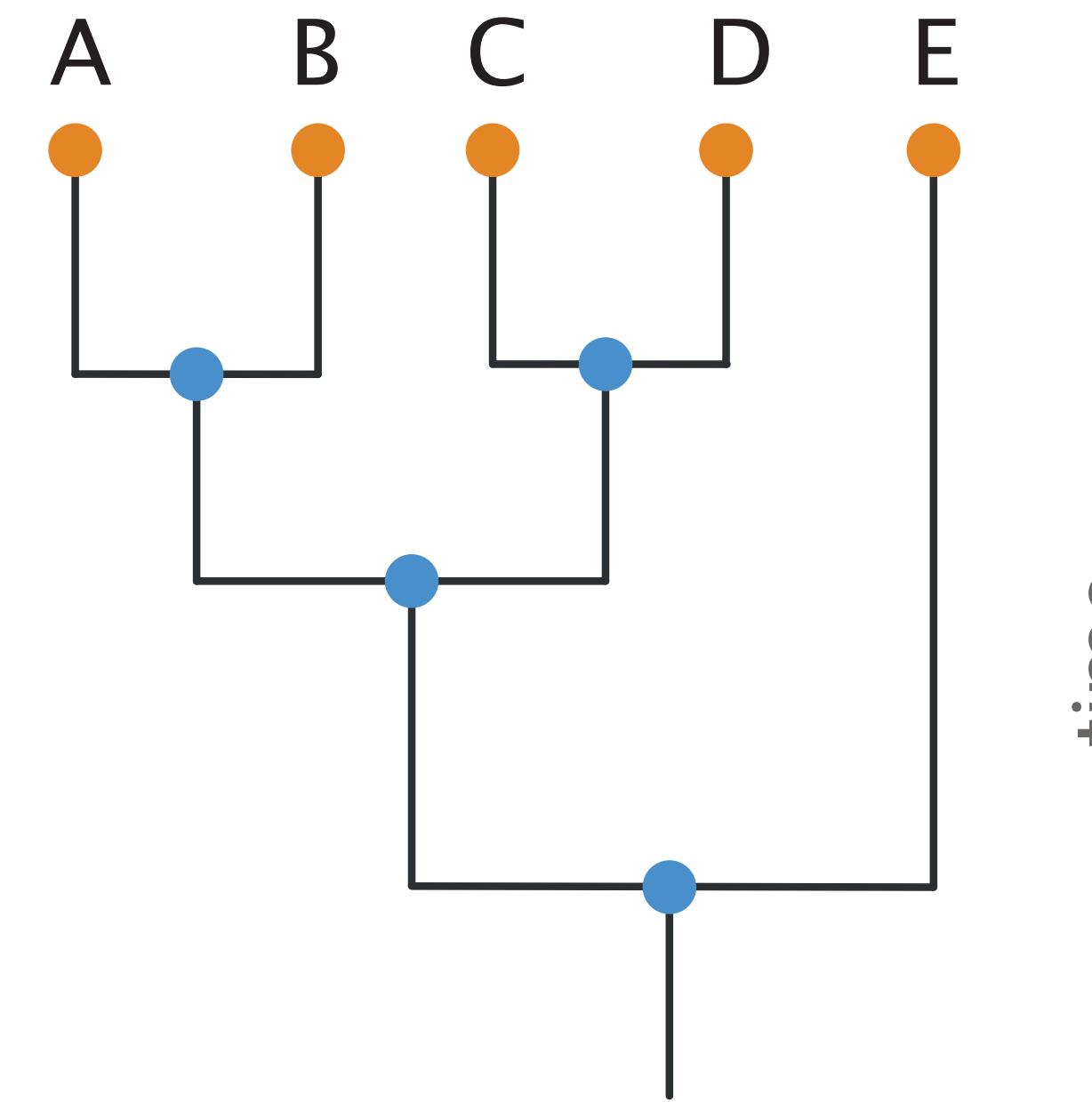
[How to read a phylogenetic tree](#)

# The direction of time

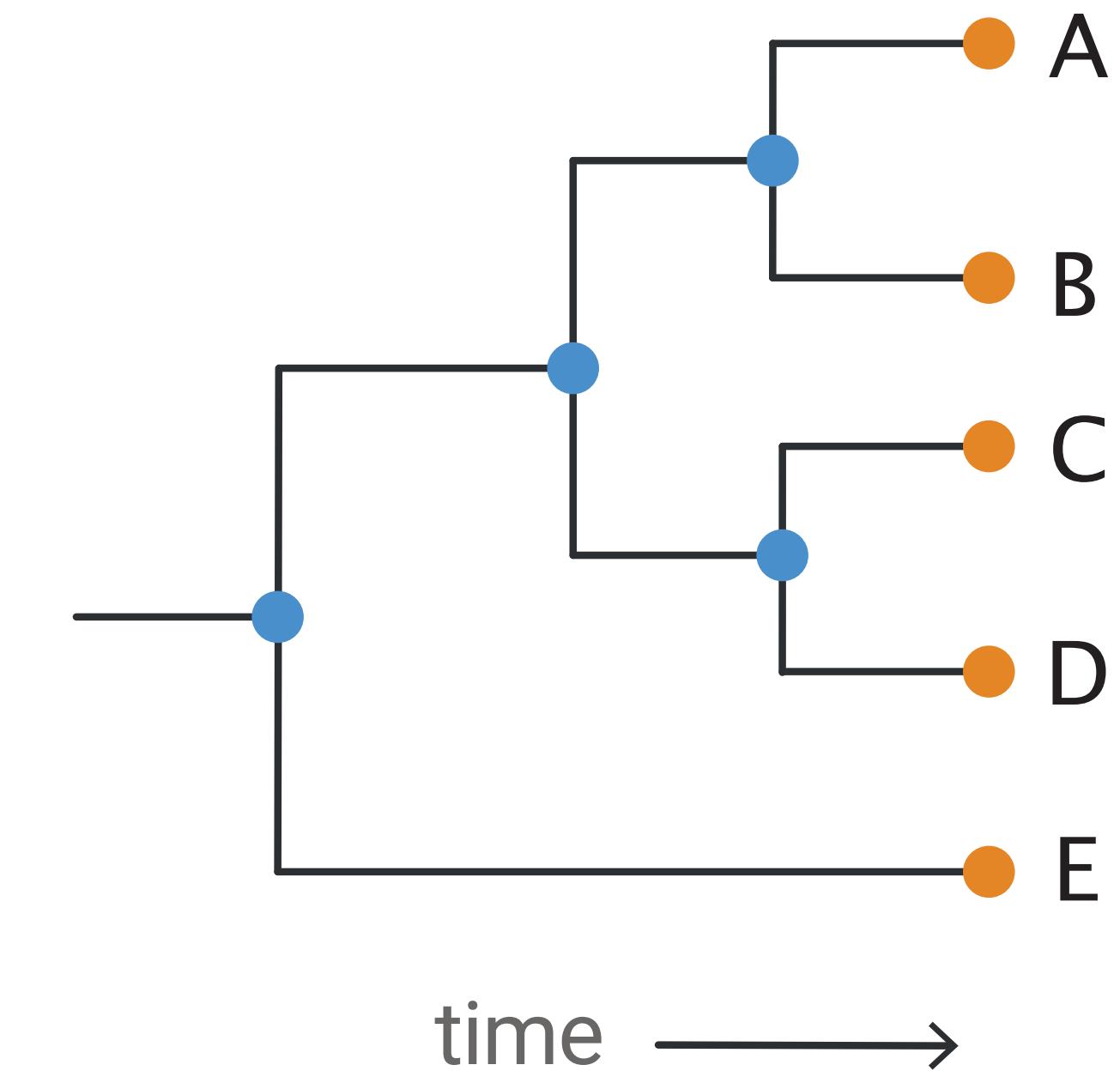
Tip look for the root!



Computer science, maths



Geology

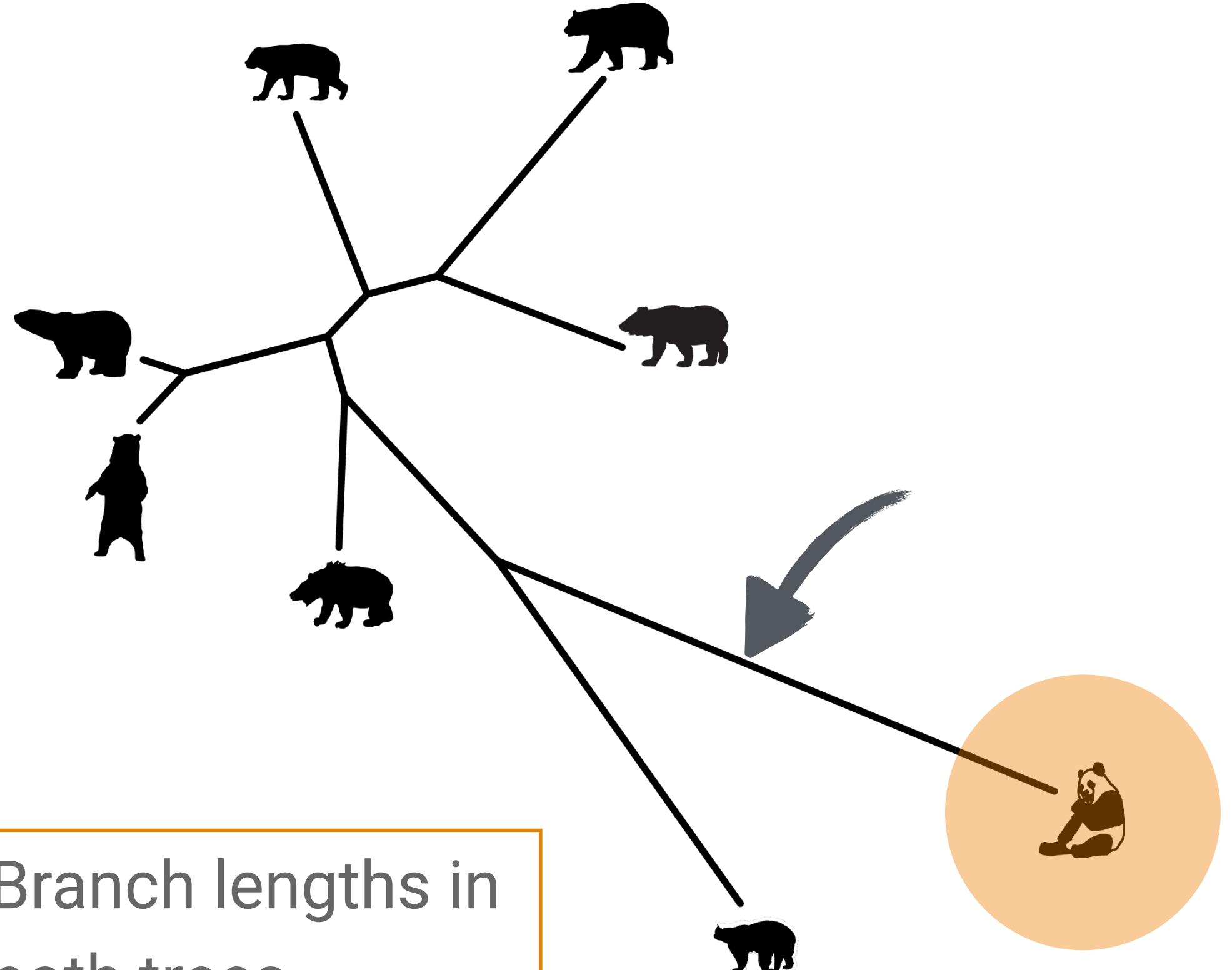


Evolutionary biology

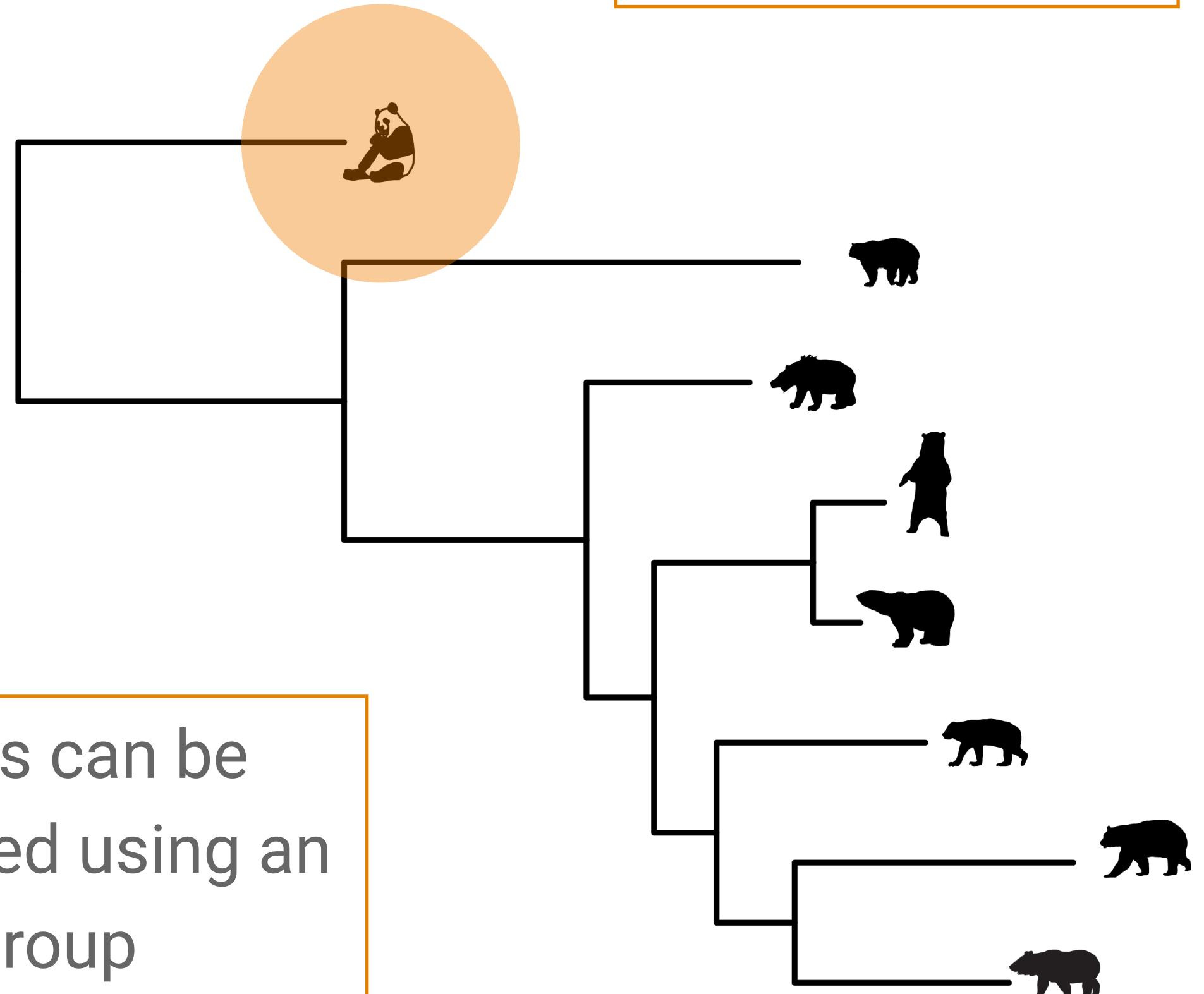
# Two types of trees

Unrooted vs. rooted trees

A rooted tree shows the direction of time



Branch lengths in both trees represents genetic distance



Trees can be rooted using an outgroup

Character	<u>Lamprey</u>	<u>Antelope</u>	<u>Bald eagle</u>	<u>Alligator</u>	<u>Sea bass</u>
Lungs	0	1	1	1	0
Jaws	0	1	1	1	1
Feathers	0	0	1	0	0
Gizzard	0	0	1	1	0
Fur	0	1	0	0	0

- What do you think the correct **rooted** tree should be?  
*Write down your logic*
- How many possible unrooted or rooted trees are there?

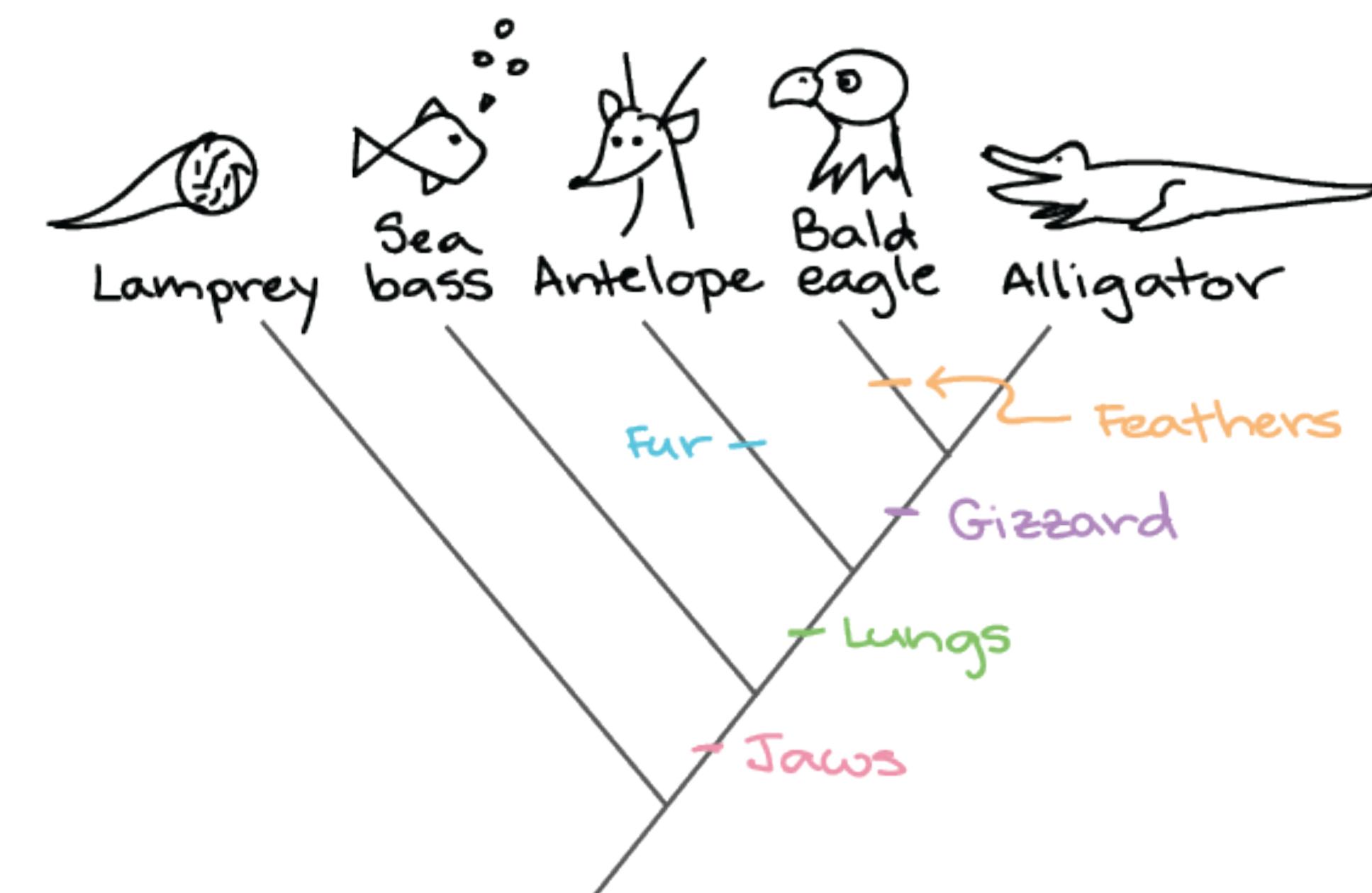
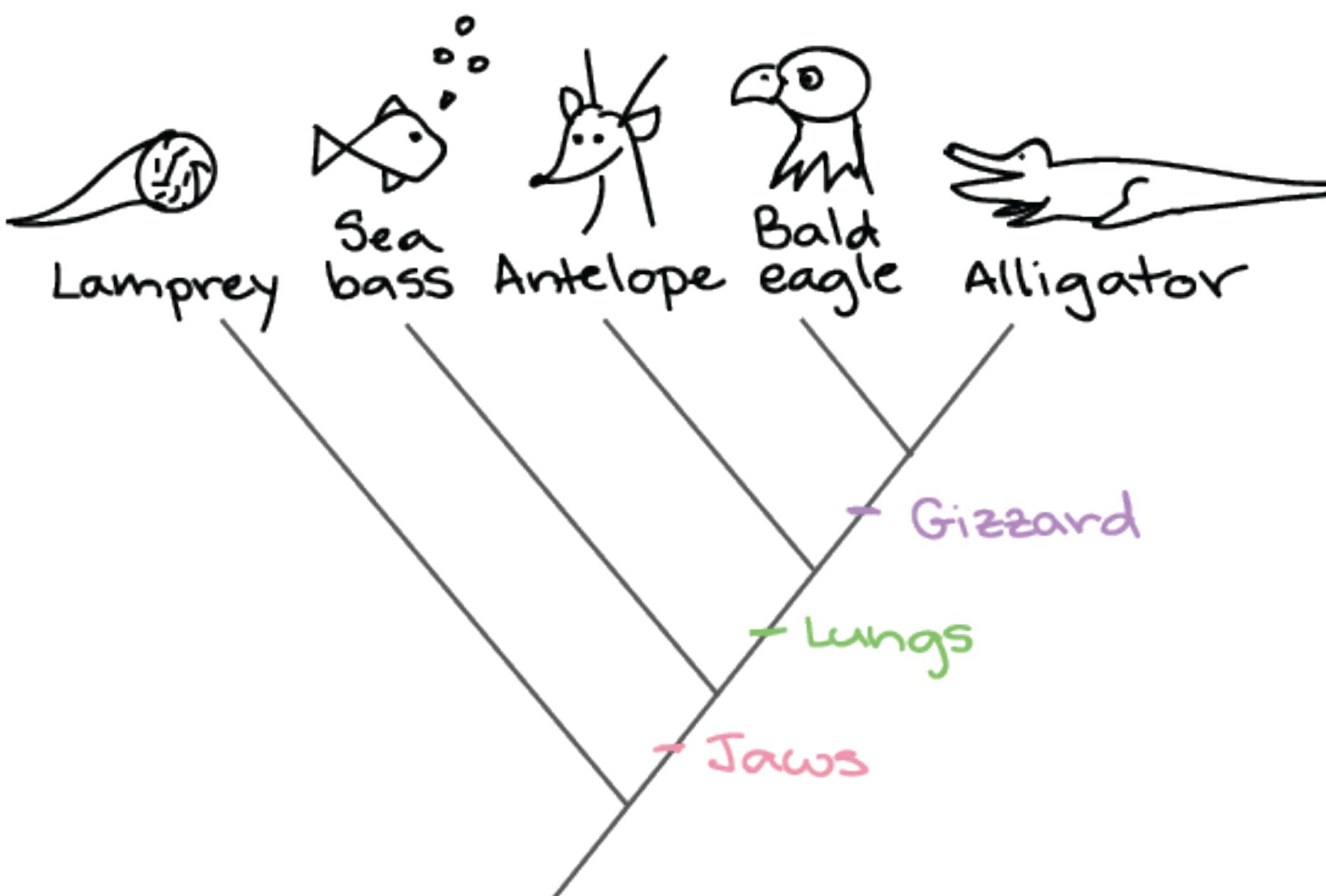
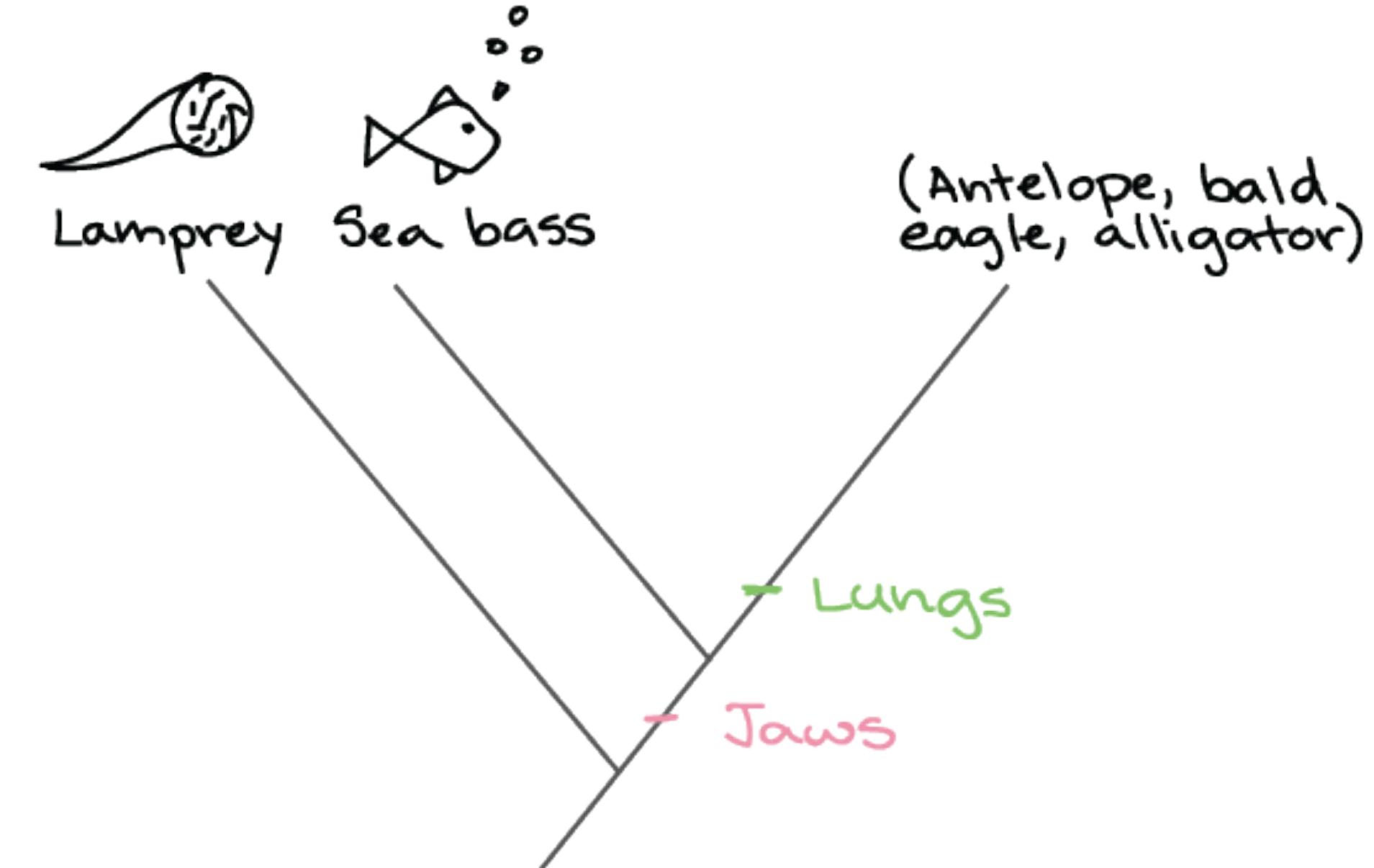
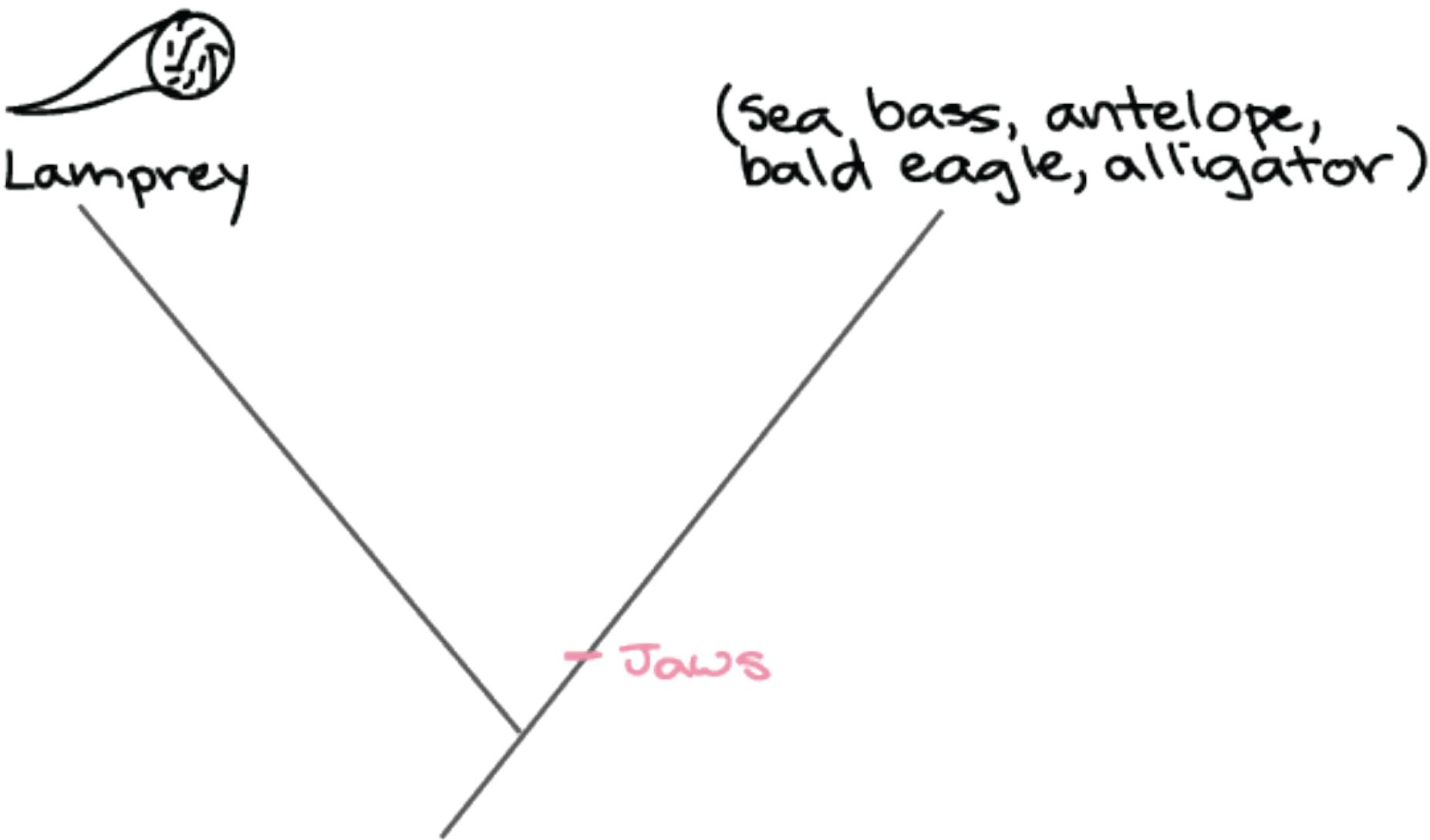
# There are a **huge** number of possible trees!

$n$ tips	unrooted trees	rooted trees
3	1	3
4	3	15
5	15	105
6	105	945
7	945	10395
8	10395	135135
9	135135	2027025
10	2027025	34459425

**Number of branches**

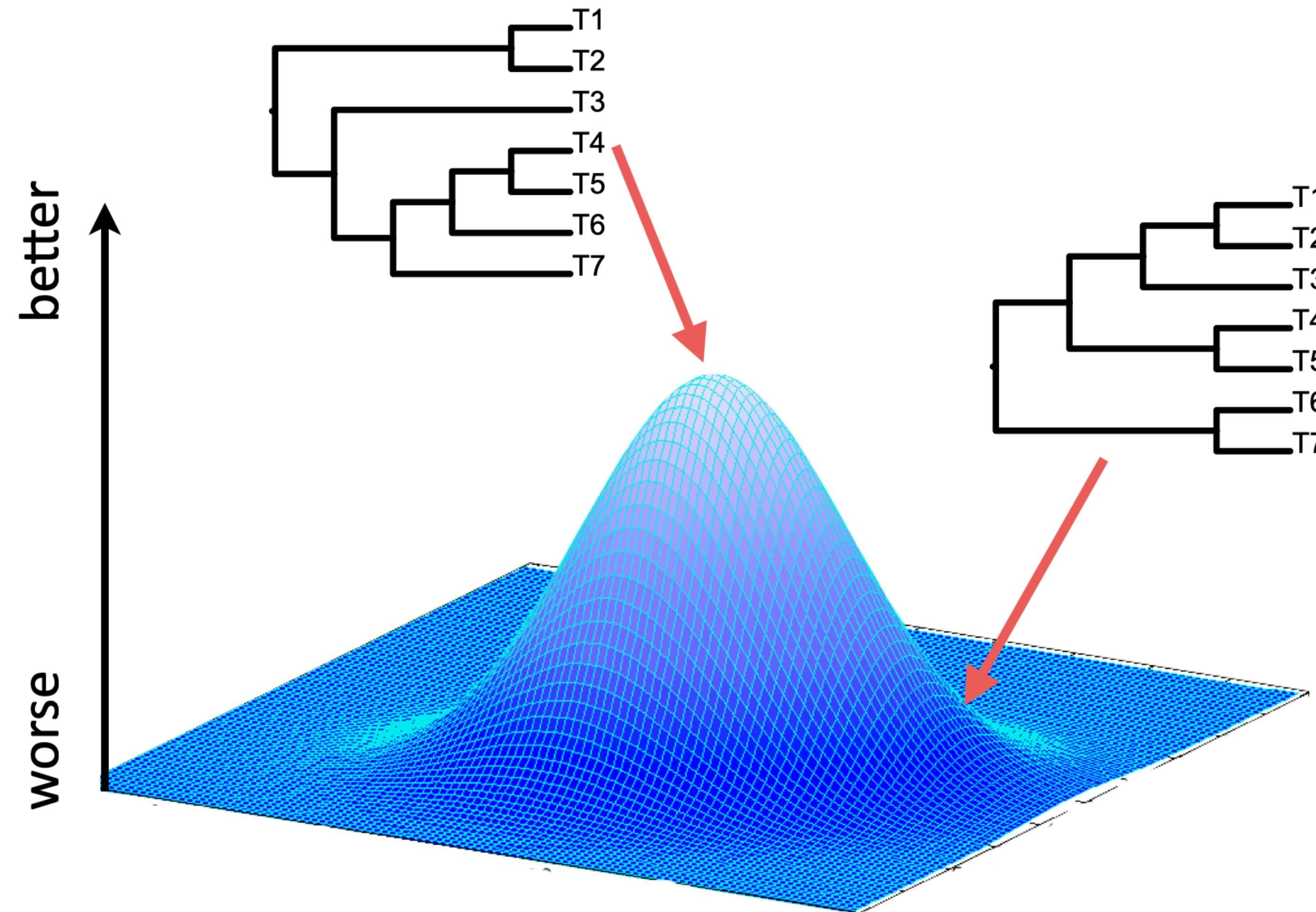
unrooted tree	$2n-3$
rooted tree	$2n-2$

See wiki for more on [where these numbers come from](#)



- *Write down your logic*
  - Most people intuitively assume the tree with the **fewest** changes is correct
  - This approach to tree building is called **maximum parsimony**

# How do we find the ‘best’ tree?



# It depends how you measure ‘best’

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Method	Criterion (tree score)
Maximum parsimony	Minimum number of changes
Maximum likelihood	Likelihood score (probability), optimised over branch lengths and model parameters
Bayesian inference	Posterior probability, integrating over branch lengths and model parameters

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Both maximum likelihood and Bayesian inference are model-based approaches

Note these are not the only approaches to tree-building but they are the most widely used

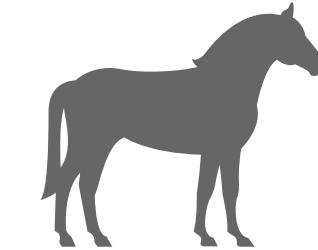
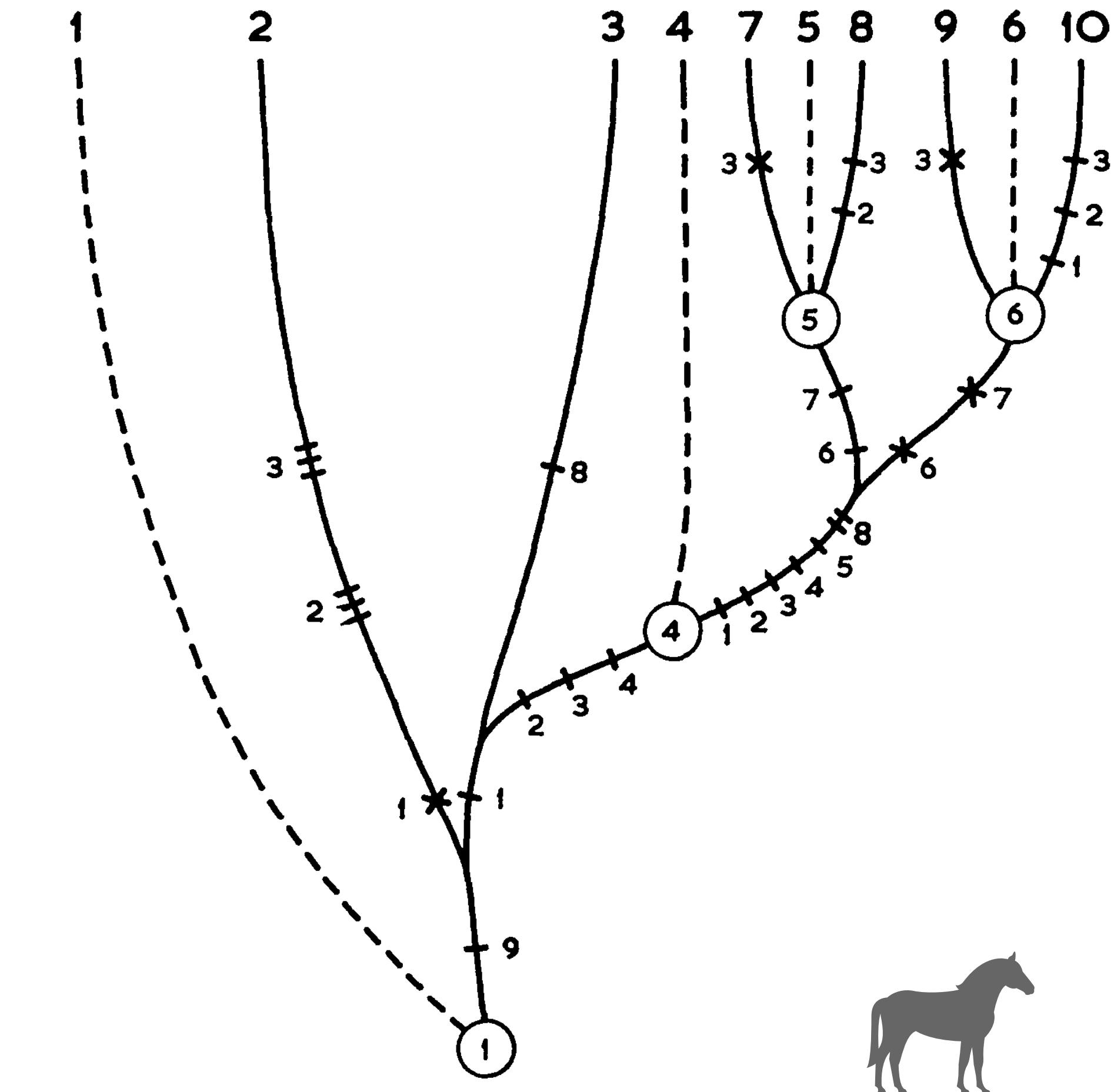
# Maximum parsimony

# Maximum parsimony

The **maximum parsimony** tree is the unrooted tree with the *lowest parsimony score*

The **parsimony score** of a tree is defined as the *minimum number of changes* required to explain the data summed across characters

Maximum parsimony first described in Edwards and Cavalli-Sforza ([1964](#))



Phylogeny of fossil horses. It was (I think) the first tree constructed using parsimony and discrete morphological characters by Camin and Sokal ([1965](#)) – this study popularised the use of parsimony among systematists



This tree is *less* parsimonious than the one on the left



# Maximum parsimony

Parsimony can not identify the location of the root, so we can use an outgroup to root the tree

There can be more than one tree with the same parsimony score

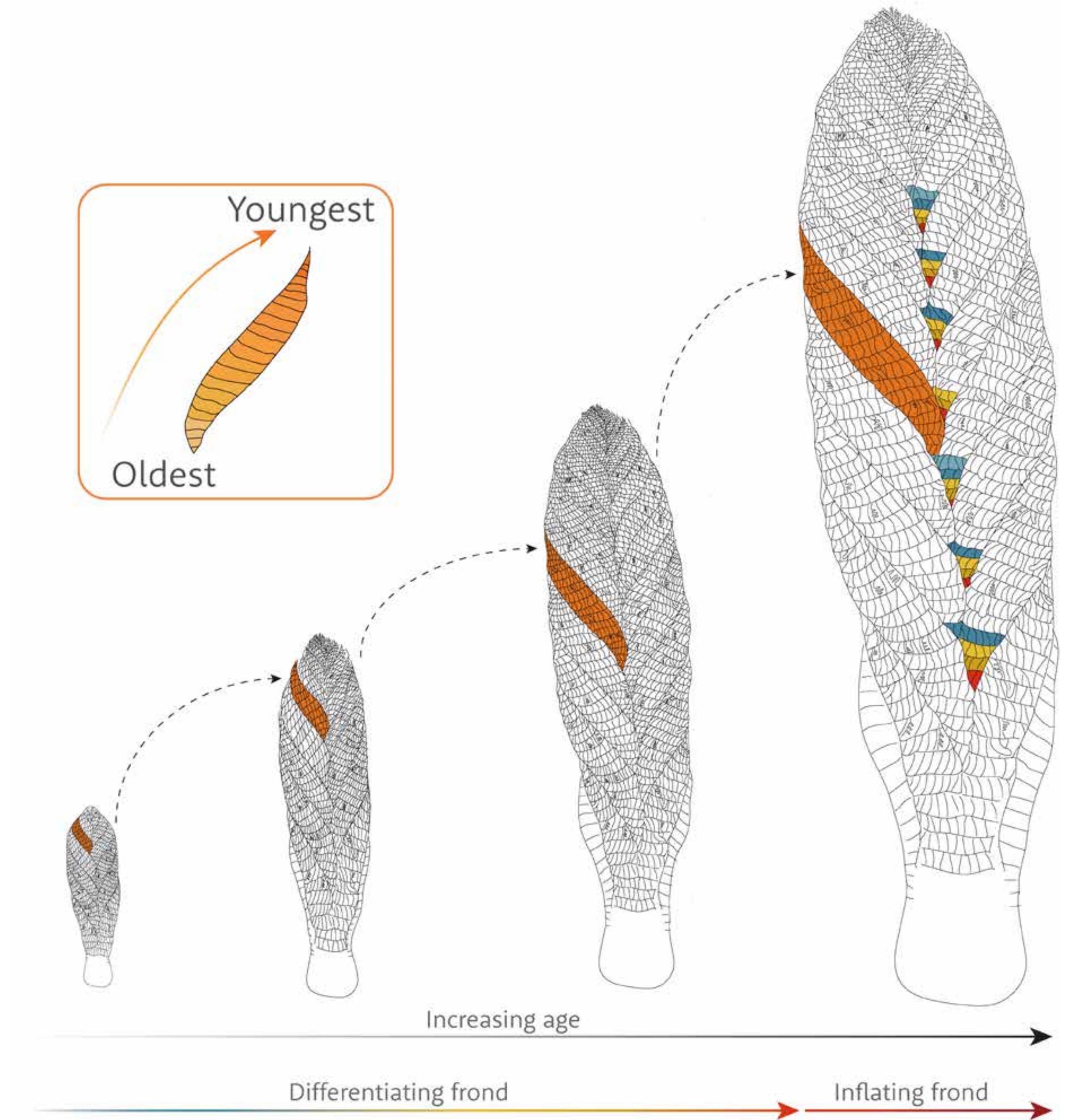
Parsimony does not make **explicit** assumptions about the evolutionary process

Maximum parsimony can only be used to estimate tree topology

# Exercise

Tree building using parsimony

Data from Dunn (2016). See also Dunn et al. (2021)  
Phylogenetic affinity of the enigmatic Charnia



#NEXUS

Initiates the nexus block

[Matrix modified from Dunn (2016) ]

BEGIN DATA;

DIMENSIONS NTAX=10 NCHAR=117;  
FORMAT DATATYPE = STANDARD SYMBOLS= " 0 1 2 3" MISSING=? GAP=- ;

MATRIX

Charnia	00?1??1????????0???1?211201??????0-?-???????
Laccaria	110?0010000000000-000--00--00---0-----000-
Capsaspora	001011-00----000-00---00-----0-----0-0-
Monosiga	001000-11----000-00---00-----0-----0-0-
Sycon	00110011111111110100110--0000000000----0---000-
Amphimedon	00110011111111121100110--0000000000----0---000-
Trichoplax	00110011111100000-0000210--0111110000--00---000-
Mnemiopsis	00110011111100000-0011211200110010111121110011110
Nematostella	001100111111000000011211100110010111111101111111
Hydra	00110011111100000-001121110011001011111110111111

;

END;

```
#NEXUS
```

```
[Matrix modified from Dunn (2016)]
```

**Comments go in square brackets**

**Great for keeping track of data sources**

```
BEGIN DATA;
```

```
DIMENSIONS NTAX=10 NCHAR=117;  
FORMAT DATATYPE = STANDARD SYMBOLS= " 0 1 2 3" MISSING=? GAP=- ;
```

```
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```

Charnia	00?1??1????????0???1?211201??????0-?-???????
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Sycon	00110011111111110100110--0000000000----0---000-
Amphimedon	00110011111111121100110--0000000000----0---000-
Trichoplax	00110011111100000-000210--0111110000--00---000-
Mnemiopsis	00110011111100000-0011211200110010111121110011110
Nematostella	001100111111000000011211100110010111111101111111
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```
;
```

```
END;
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Hydra	00110011111100000-001121110011001011111110111111

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END;

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[Matrix modified from Dunn (2016) ]
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Hydra	00110011111100000-001121110011001011111110111111

```
;
```

```
END;
```

**Number of taxa and  
characters in the matrix**

```
#NEXUS
```

```
[Matrix modified from Dunn (2016) ]
```

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Nematostella	001100111111000000011211100110010111111101111111
Hydra	00110011111100000-001121110011001011111110111111

```
;
```

```
END;
```

## Details about the data

```
#NEXUS
```

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[Matrix modified from Dunn (2016)]
```

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Hydra	00110011111100000-001121110011001011111110111111

```
;
```

```
END;
```

**Initiates the data matrix**

```
#NEXUS
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[Matrix modified from Dunn (2016)]
```

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```

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Hydra	00110011111100000-0011211100110010111111101111111

```
;
```

```
END;
```

## Phylogenetic data matrix

**Taxon names left, characters right after tabs or spaces**

```
#NEXUS
```

```
[Matrix modified from Dunn (2016) ]
```

```
BEGIN DATA;
```

```
DIMENSIONS NTAX=10 NCHAR=117;  
FORMAT DATATYPE = STANDARD SYMBOLS= " 0 1 2 3" MISSING=? GAP=- ;
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```
MATRIX
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Monosiga	001000-11-----00-00---0-----0-----0-0-
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Nematostella	001100111111000000011211100110010111111101111111
Hydra	00110011111100000-001121110011001011111110111111

```
;
```

**Initiates the end of the data matrix**

```
END;
```

```
#NEXUS
```

```
[Matrix modified from Dunn (2016) ]
```

```
BEGIN DATA;
```

```
DIMENSIONS NTAX=10 NCHAR=117;  
FORMAT DATATYPE = STANDARD SYMBOLS= " 0 1 2 3" MISSING=? GAP=- ;
```

```
MATRIX
```

Charnia	00?1??1????????0???1?211201??????0-?-???????
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Hydra	00110011111100000-001121110011001011111110111111

```
;
```

```
END;
```

**Initiates the end of the nexus block**

# Statistical inconsistency

The following slides are adapted from Tracy Heath (in turn adapted from Mark Holder)

# Statistical consistency

Ideally, we want an inference method to return the correct answer if we provide enough data

An estimator is **statistically consistent** if it is guaranteed to get the correct answer with an infinite amount of data

It has been demonstrated that in some scenarios parsimony is statistically inconsistent. The issue is known as **long branch attraction**

# Convergent evolution

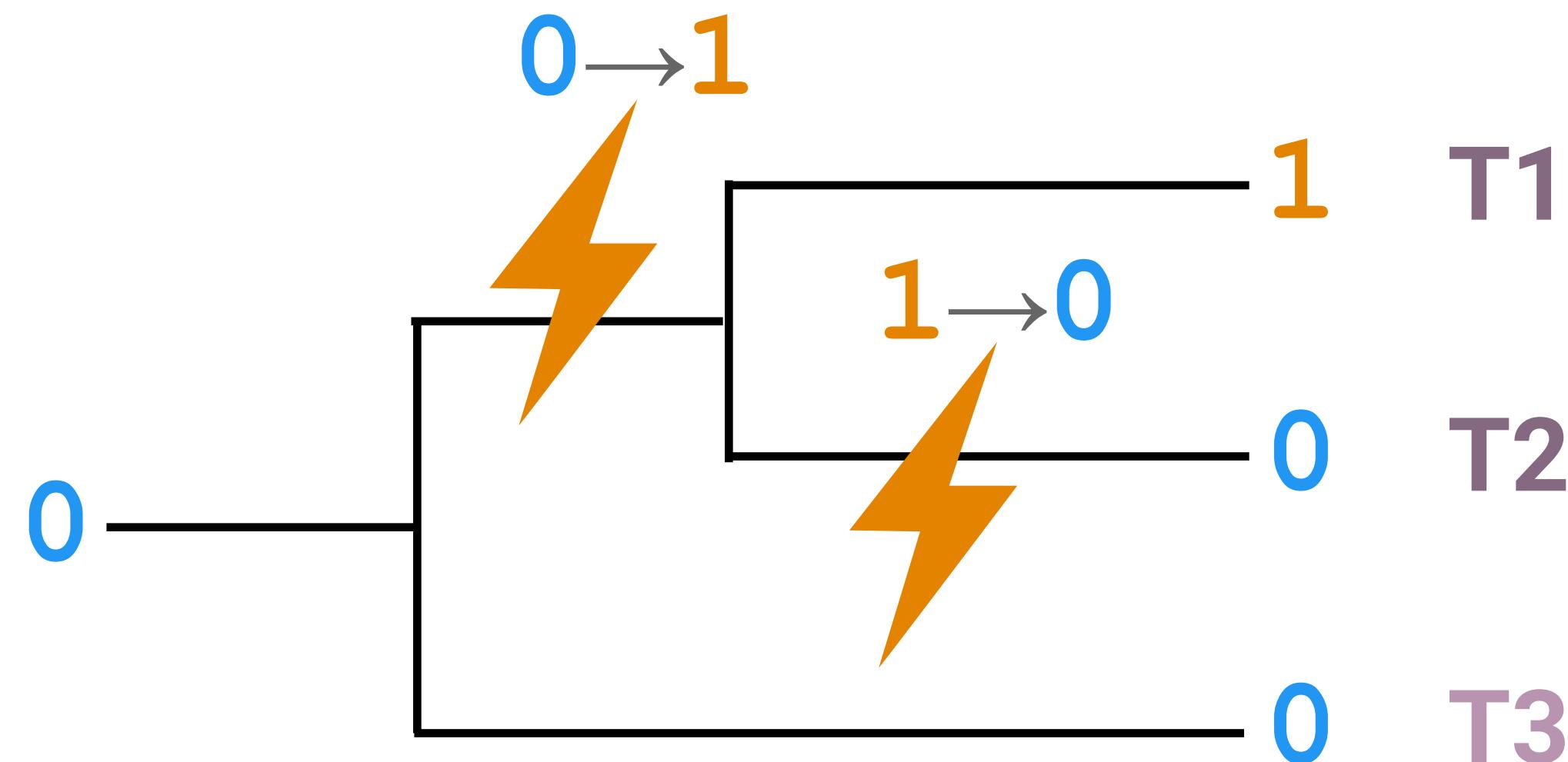
A trait that is found in two species, but not in their common ancestor is an example of **homoplasy**

We find widespread homoplasy in both morphological and molecular datasets



Bird, Pterosaur (extinct), fruit bat: 3 different vertebrates independently lightened bones and transformed hands into wings

# Convergence and parsimony



Hypothetical tree showing multiple transitions at the same character

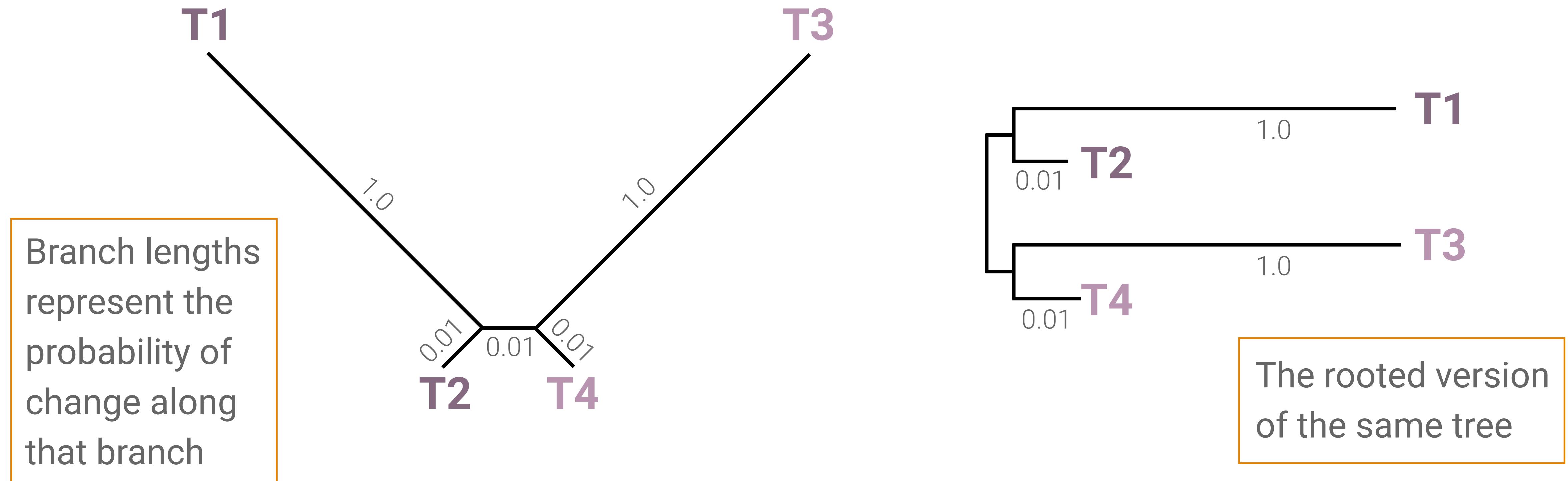
Parsimony will always favour the tree with the smallest number of changes

The method does not account for multiple transitions (or “hits”), e.g.,  
 $0 \rightarrow 1 \rightarrow 0$

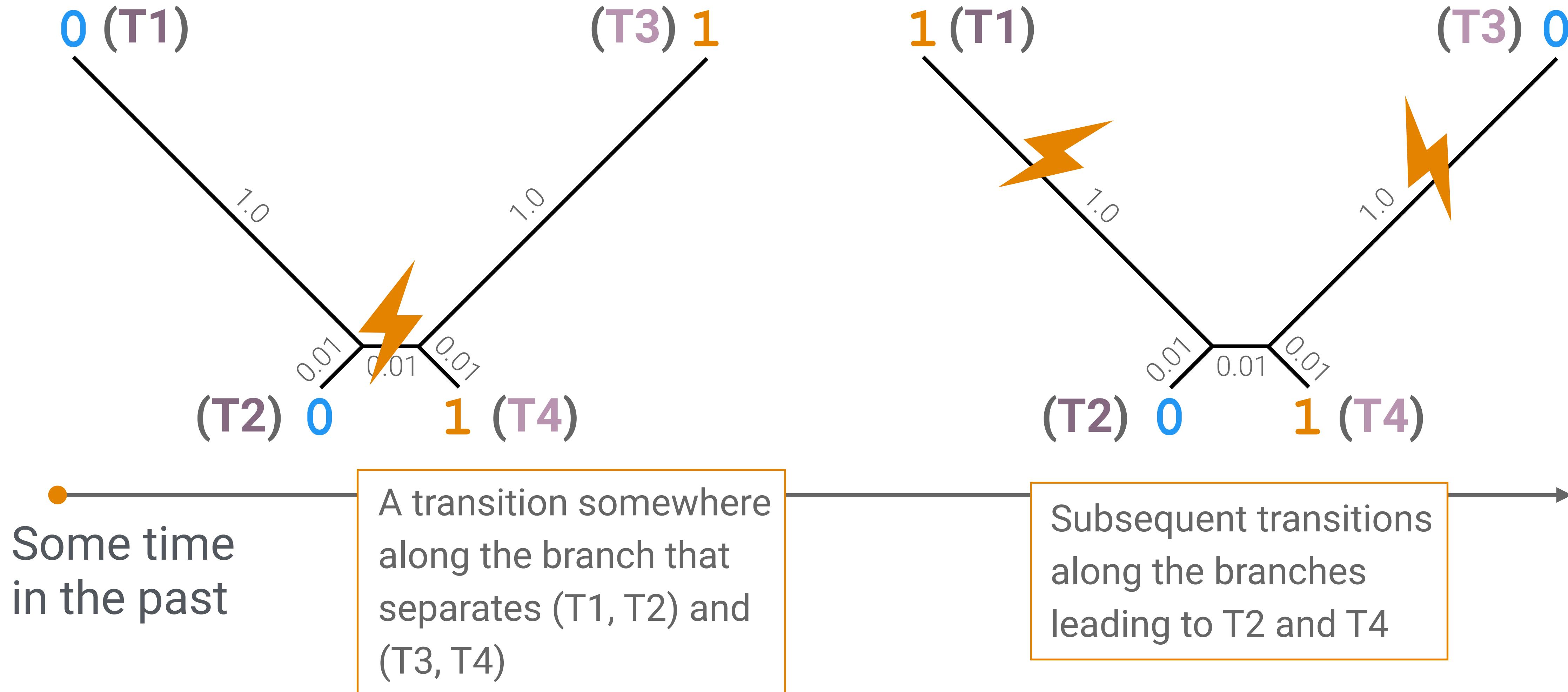
We can only invoke convergent evolution *ad hoc* after inference

# Long branch attraction

Say we have the following tree, with 2 long and 2 short branches



# Long branch attraction

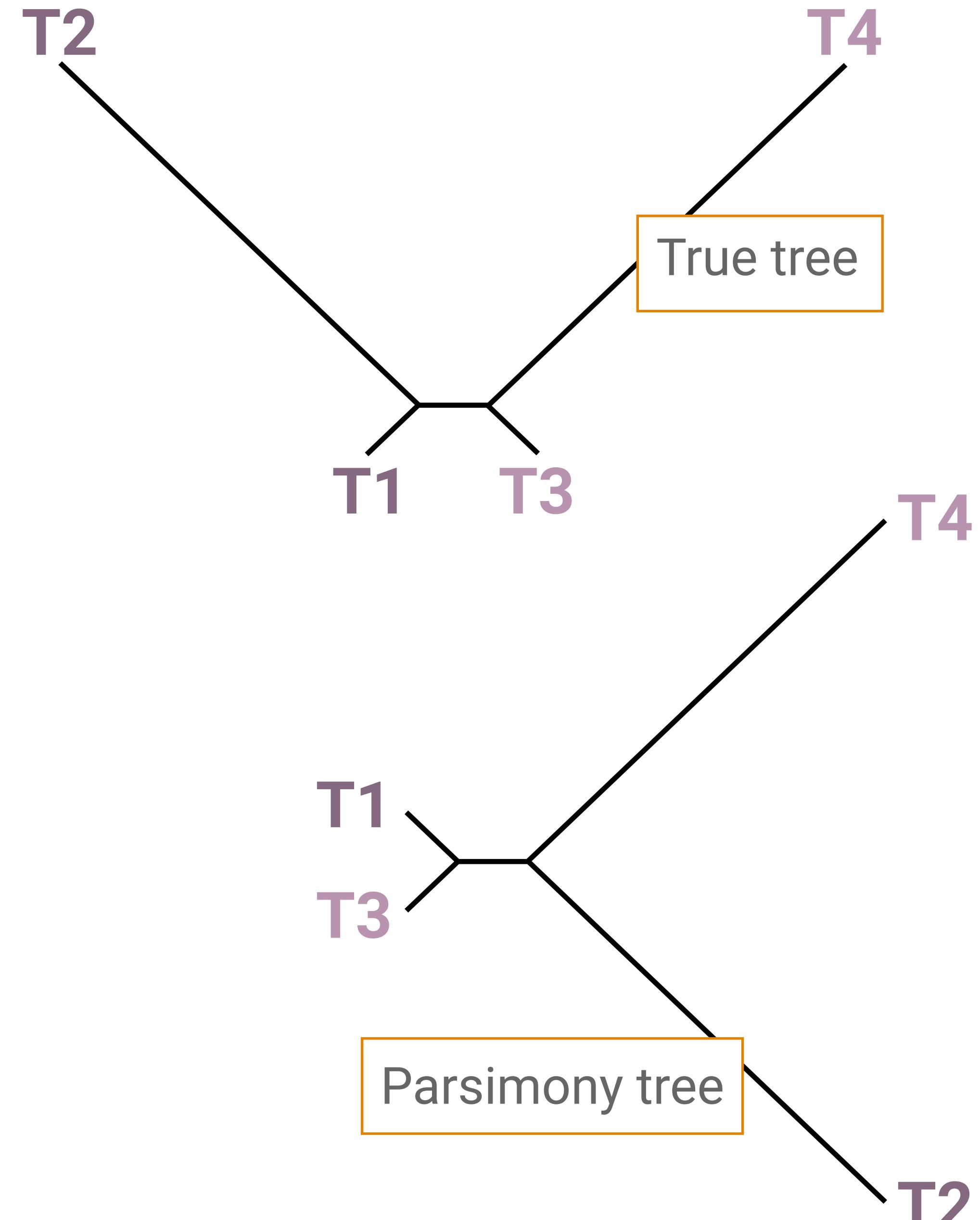


# Long branch attraction

Parsimony is almost guaranteed to get this tree wrong

And more data makes this problem worse, meaning this approach is statistically inconsistent

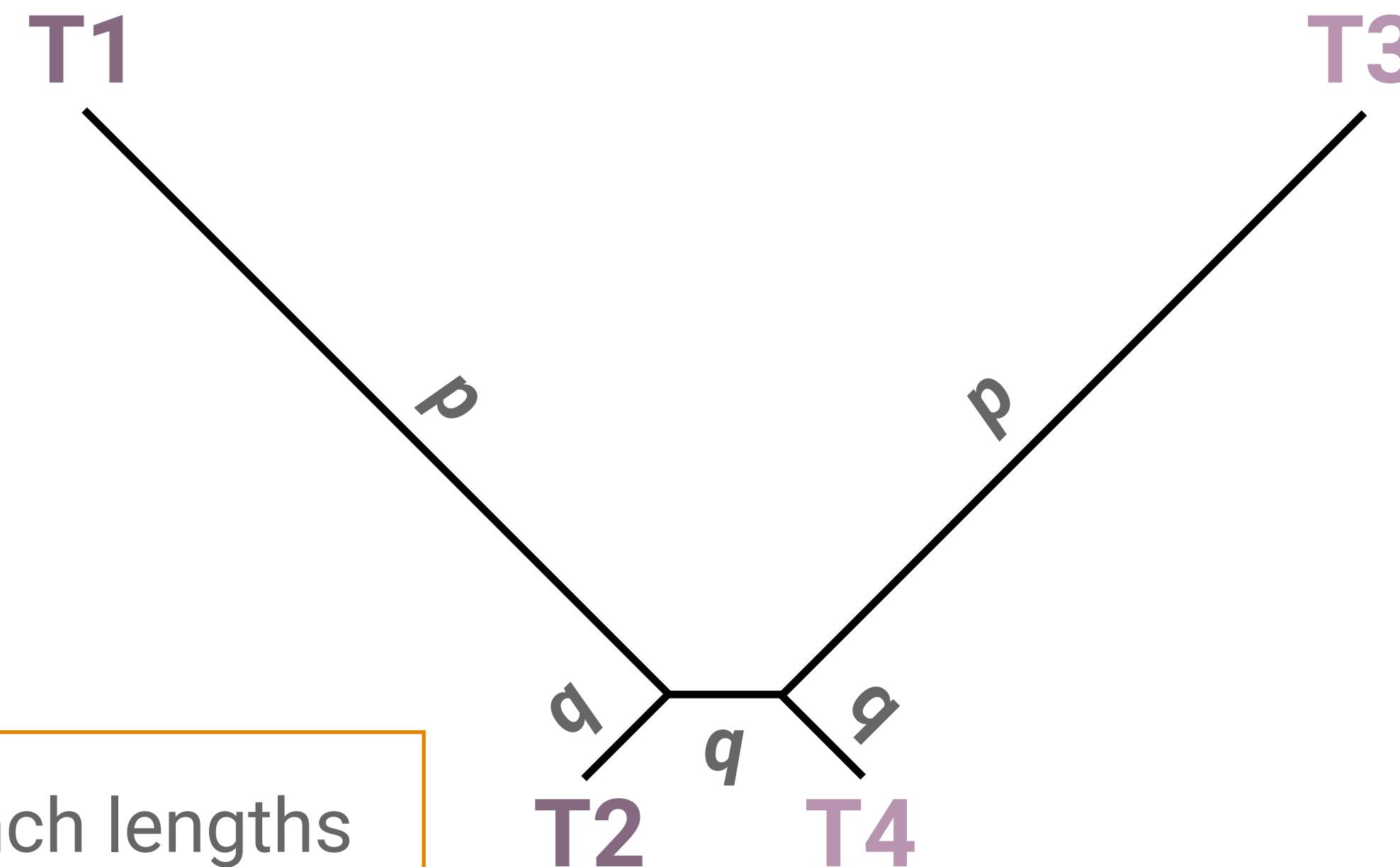
This issue has been thoroughly characterised for molecular data



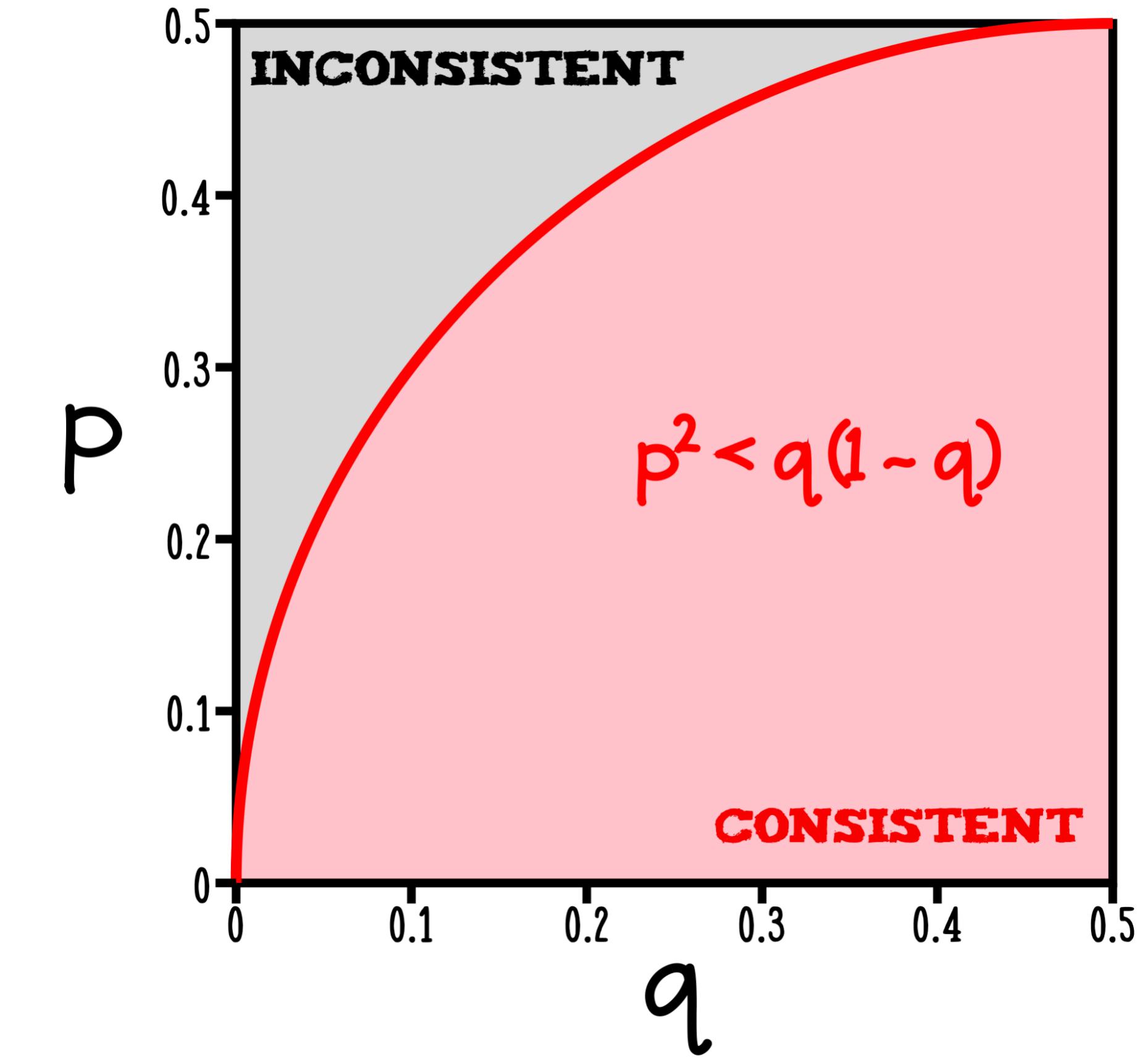
Felsenstein (1978)

Felsenstein (2004), Inferring Phylogenies

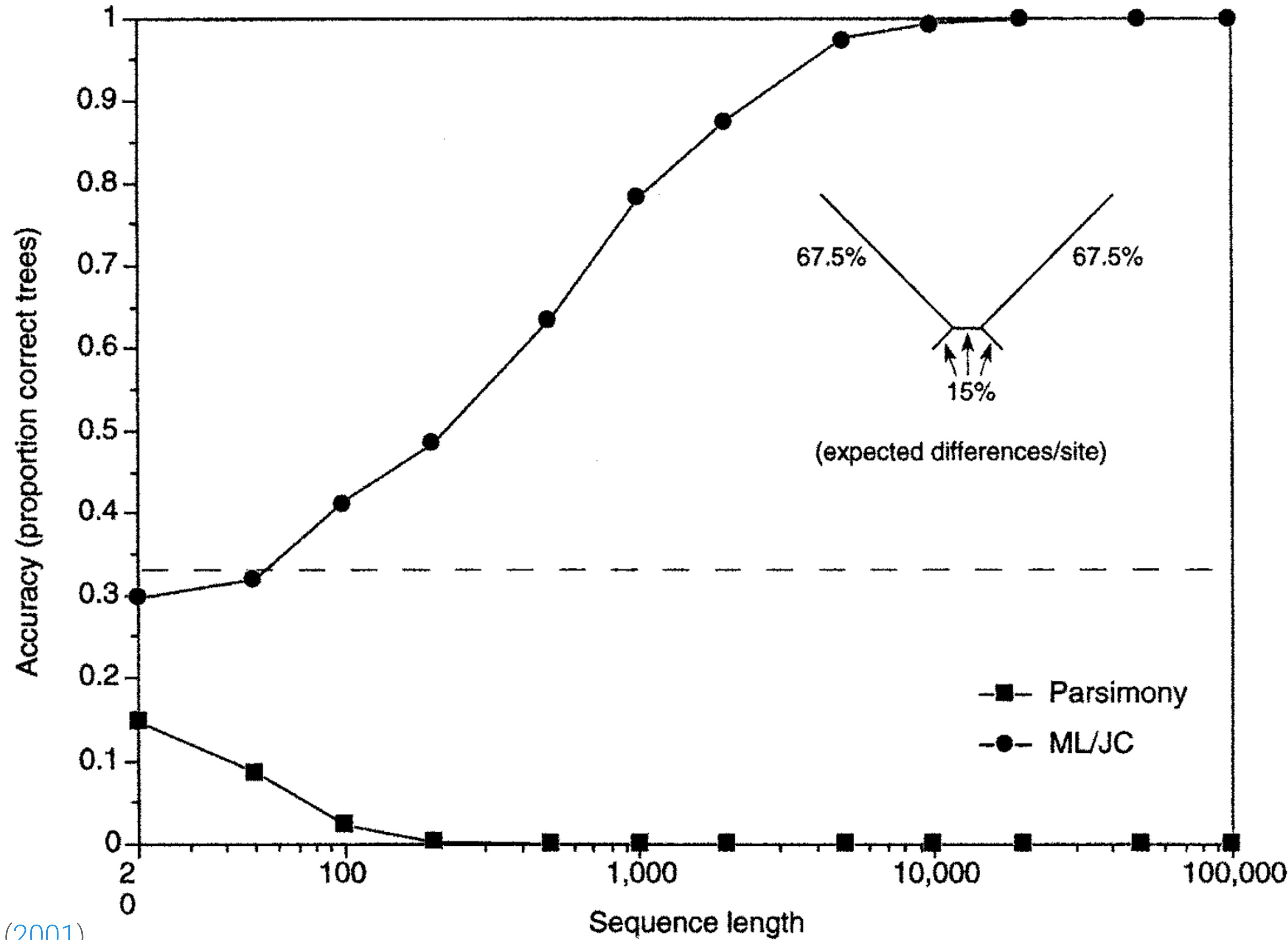
# Long branch attraction



Branch lengths represent the probability ( $p, q$ ) of change along that branch



The area in grey, is the area of parameter space where you are almost guaranteed to recover the wrong tree, with increasing certainty the more data you have

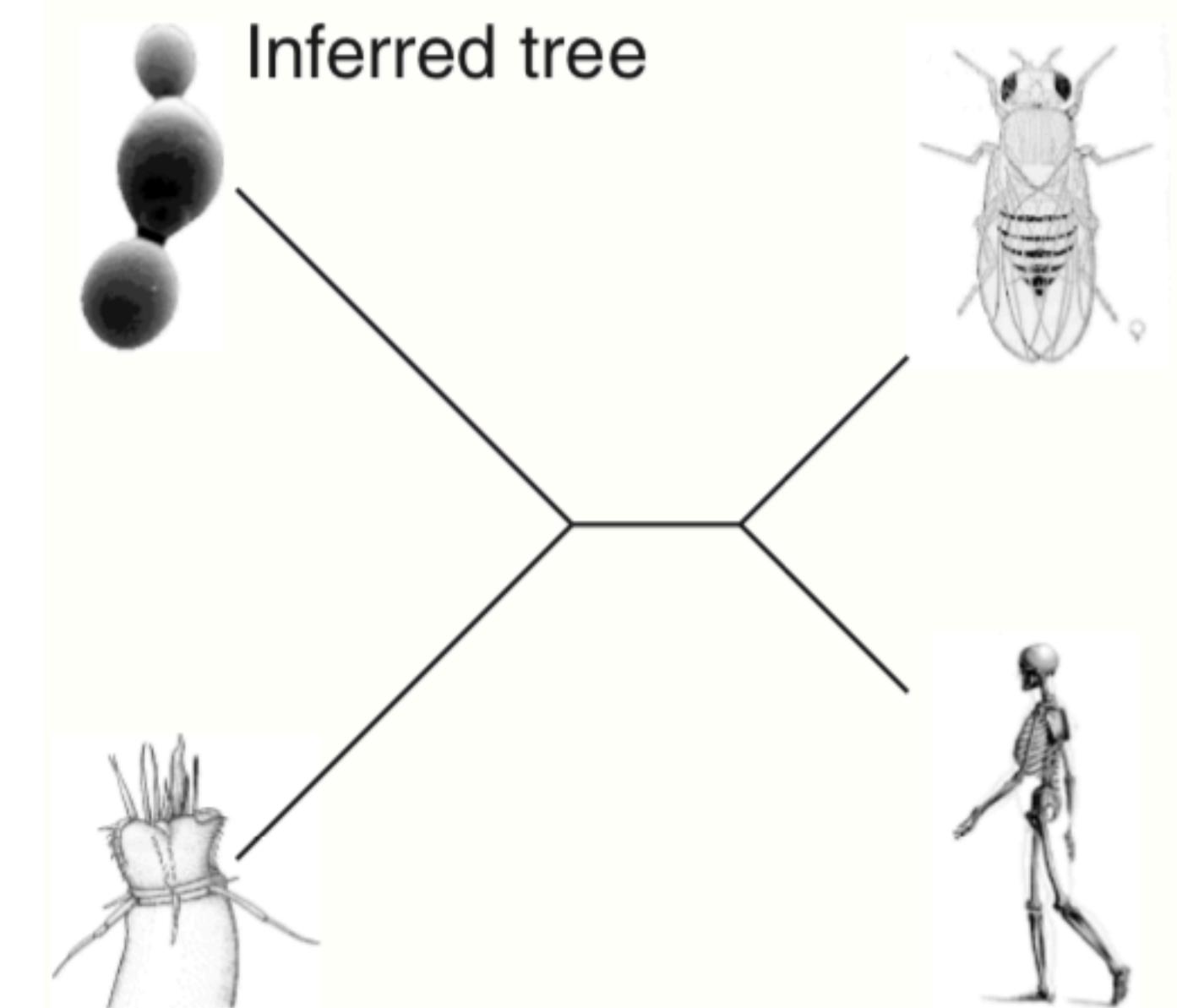
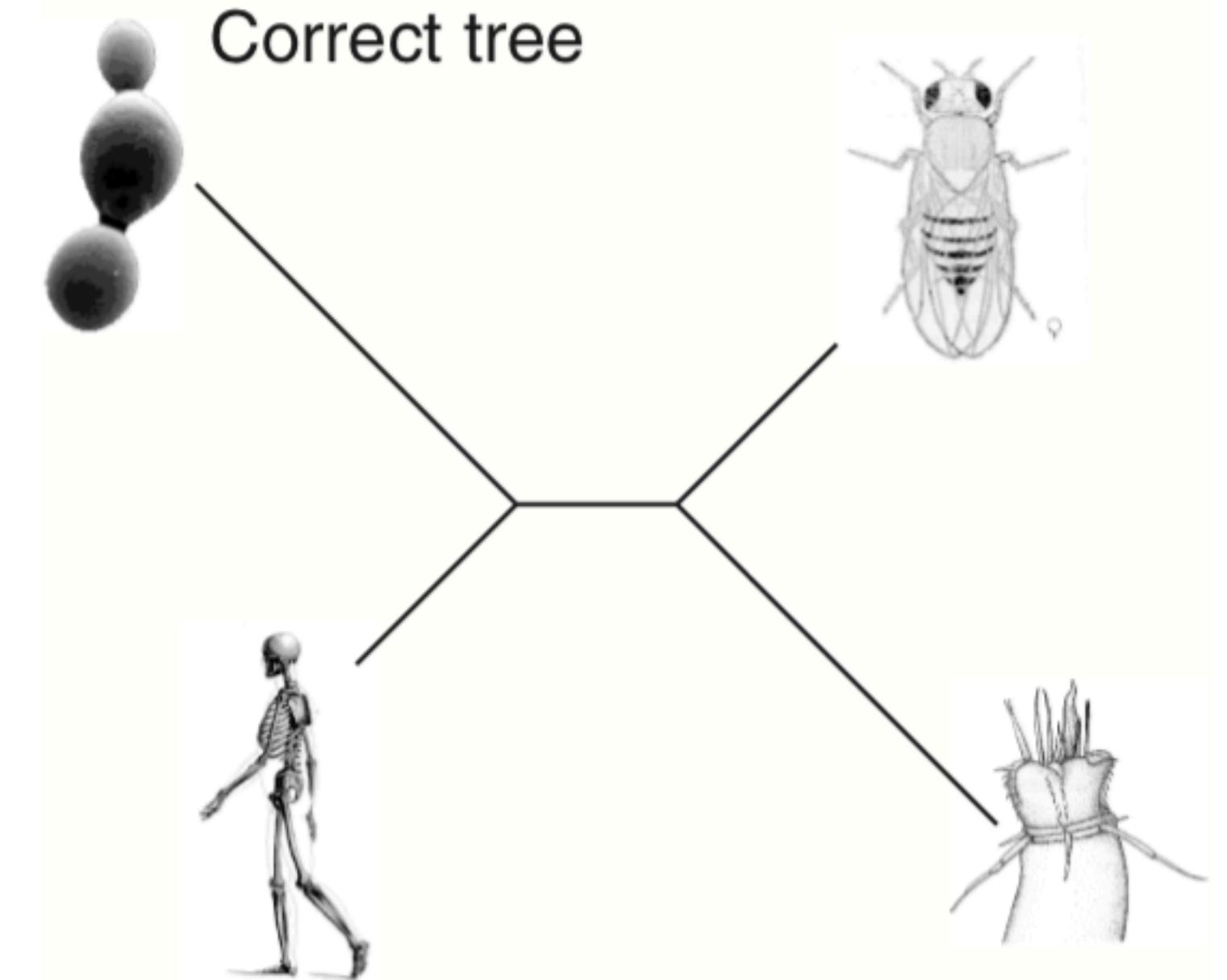


# A classic case of LBA

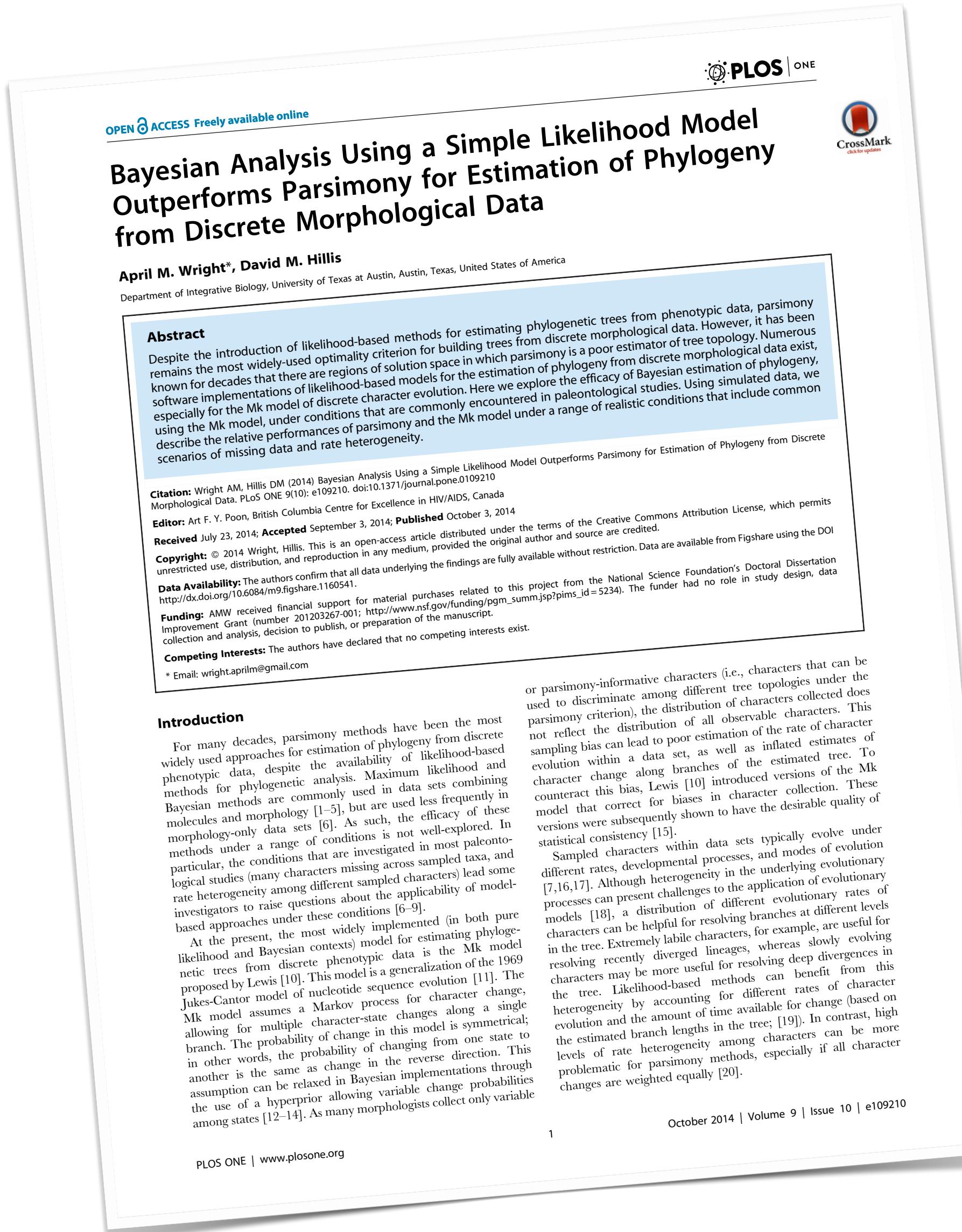
The relationship between nematodes, arthropods, and chordates was misunderstood for a long time

- **Ecdysozoa\***  
(arthropods, nematodes), vertebrates
- **Coelomata**  
(arthropods, vertebrates), nematodes

\*widely accepted today, Image: Telford et al. ([2005](#))



# Parsimony in paleobiology



This was the first paper to show that the same LBA issues that affect molecular data probably also affect morphology

Wright and Hillis (2014)

A slew of papers followed...

OPEN ACCESS Freely available online

# Bayesian Analysis Using a Simple Likelihood Model Outperforms Parsimony for Estimation of Phylogeny from Discrete Morphological Data

April M. Wright\*, David M. Hillis

Department of Integrative Biology, University of Texas at Austin, Austin, Texas, United States of America



ONE



## Abstract

Despite the introduction of likelihood-based methods for estimating phylogenetic trees from phenotypic data, parsimony remains the most widely-used optimality criterion for building trees from discrete morphological data. However, it has been known for decades that there are regions of solution space in which parsimony is a poor estimator of tree topology. Numerous software implementations of likelihood-based models for the estimation of phylogeny from discrete morphological data exist, especially for the Mk model of discrete character evolution. Here we explore the efficacy of Bayesian estimation of phylogeny, using the Mk model, under conditions that are commonly encountered in paleontological studies. Using simulated data, we describe the relative performances of parsimony and the Mk model under a range of realistic conditions that include common scenarios of missing data and rate heterogeneity.

**Citation:** Wright AM, Hillis DM (2014) Bayesian Analysis Using a Simple Likelihood Model Outperforms Parsimony for Estimation of Phylogeny from Discrete Morphological Data. PLoS ONE 9(10): e109210. doi:10.1371/journal.pone.0109210

**Editor:** Art F. Y. Poon, British Columbia Centre for Excellence in HIV/AIDS, Canada

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## Introduction

For many decades, parsimony methods have been the most widely used approaches for estimation of phylogeny from discrete phenotypic data, despite the availability of likelihood-based methods for phylogenetic analysis. Maximum likelihood and Bayesian methods are commonly used in data sets combining molecules and morphology [1–5], but are used less frequently in morphology-only data sets [6]. As such, the efficacy of these methods under a range of conditions is not well-explored. In particular, the conditions that are investigated in most paleontological studies (many characters missing across sampled taxa, and rate heterogeneity among different sampled characters) lead some investigators to raise questions about the applicability of model-based approaches under these conditions [6–9].

At the present, the most widely implemented (in both pure likelihood and Bayesian contexts) model for estimating phylogenetic trees from discrete phenotypic data is the Mk model proposed by Lewis [10]. This model is a generalization of the 1969 Jukes-Cantor model of nucleotide sequence evolution [11]. The Mk model assumes a Markov process for character change, allowing for multiple character-state changes along a single branch. The probability of change in this model is symmetrical; in other words, the probability of changing from one state to another is the same as change in the reverse direction. This assumption can be relaxed in Bayesian implementations through the use of a hyperprior allowing variable change probabilities among states [12–14]. As many morphologists collect only variable

or parsimony-informative characters (i.e., characters that can be used to discriminate among different tree topologies under the parsimony criterion), the distribution of characters collected does not reflect the distribution of all observable characters. This sampling bias can lead to poor estimation of the rate of character evolution within a data set, as well as inflated estimates of character change along branches of the estimated tree. To counteract this bias, Lewis [10] introduced versions of the Mk model that correct for biases in character collection. These versions were subsequently shown to have the desirable quality of statistical consistency [15].

Sampled characters within data sets typically evolve under different rates, developmental processes, and modes of evolution [7,16,17]. Although heterogeneity in the underlying evolutionary processes can present challenges to the application of evolutionary models [18], a distribution of different evolutionary rates of characters can be helpful for resolving branches at different levels in the tree. Extremely labile characters, for example, are useful for resolving recently diverged lineages, whereas slowly evolving characters may be more useful for resolving deep divergences in the tree. Likelihood-based methods can benefit from this heterogeneity by accounting for different rates of character evolution and the amount of time available for change (based on the estimated branch lengths in the tree [19]). In contrast, high levels of rate heterogeneity among characters can be more problematic for parsimony methods, especially if all character changes are weighted equally [20].

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# Morphological Phylogenetics Evaluated Using Novel Evolutionary Simulations

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**Abstract.**—Evolutionary inferences require reliable phylogenies. Morphological data have traditionally been analyzed using maximum parsimony, but recent simulation studies have suggested that Bayesian analyses yield more accurate trees. This debate is ongoing, in part, because of ambiguity over modes of morphological evolution and a lack of appropriate models. Here, we investigate phylogenetic methods using two novel simulation models—one in which morphological characters evolve stochastically along lineages and another in which individuals undergo selection. Both models generate character data and lineage splitting simultaneously; the resulting trees are an emergent property, rather than a fixed parameter. Standard consensus methods for Bayesian searches (Mk) yield fewer incorrect nodes and quartets than the standard consensus trees recovered using equal weighting and implied weighting parsimony searches. Distances between the pool of derived trees (most parsimonious or posterior distribution) and the true trees—measured using Robinson-Foulds (RF), subtree prune and regraft (SPR), and tree bisection reconnection (TBR) metrics—demonstrate that this is related to the search strategy and consensus method of each technique. The amount and structure of homoplasy in character data differ between models, and lineage splitting simultaneously—the resulting trees measured using Robinson-Foulds (RF), subtree prune and regraft (SPR), and tree bisection reconnection (TBR) metrics—demonstrate that this is related to the search strategy and consensus method of each technique. 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In 2016 the journal *Cladistics* published an editorial stating

*“If alternative methods give different results and the author prefers an unparsimonious topology, he or she is welcome to present that result, but should be prepared to defend it on philosophical grounds”*

The epistemological paradigm of this journal is parsimony. There are strong philosophical arguments in support of parsimony versus other methods of phylogenetic inference (e.g. Farris, 1983).

The high citation index of *Cladistics* shows that the journal is publishing some of the most groundbreaking empirical and theoretical research on the history of life, and we remain committed to the publication of outstanding systematics research. As a community of scientists, the Willi Hennig Society is always open to new methods and ideas, and to well-reasoned criticisms of old ones. However, we do not hold in special esteem any method solely because it is novel or purportedly sophisticated.

Phylogenetic data sets submitted to this journal should be analysed using parsimony. If alternative methods are also used and there is no difference among the results, the author should defer to the principles of the Society and present the tree obtained by parsimony. Unless there is a pertinent reason to include multiple trees from alternative methods, a tree based on parsimony is sufficient as an intelligible, informative and repeatable hypothesis of relationships, and articles should not be cluttered with multiple, often redundant, trees produced from other methods. If alternative methods give different results and the author prefers an unparsimonious topology, he or she is welcome to present that result, but should be prepared to defend it on philosophical grounds.

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The Editors

The debacle was written up in [Wired Magazine](#)

See also #ParsimonyGate: [The Perspective of a Reformed ‘Hardcore’ Cladist](#) by Prosanta Chakrabarty

# Final notes on parsimony

The greatest advantage of parsimony is its beautiful simplicity (Yang, 2014)

Computationally fast, often produces sensible results and still serves practical purposes

Some argue that parsimony is assumption free. Others argue parsimony does make assumptions, even if we don't know what they are, referred to as **implicit assumptions**

We are often interested in more than just the topology, so we will turn out focus to other methods

# Homework



Re-familiarise yourself with [how to read a phylogenetic tree](#) and [rooting](#)



[A Brief History of Computational Phylogenetics](#)