INTRODUCTION TO PHYLOGENOMICS

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INSTITUT de BIOLOGIA EVOLUTIVA

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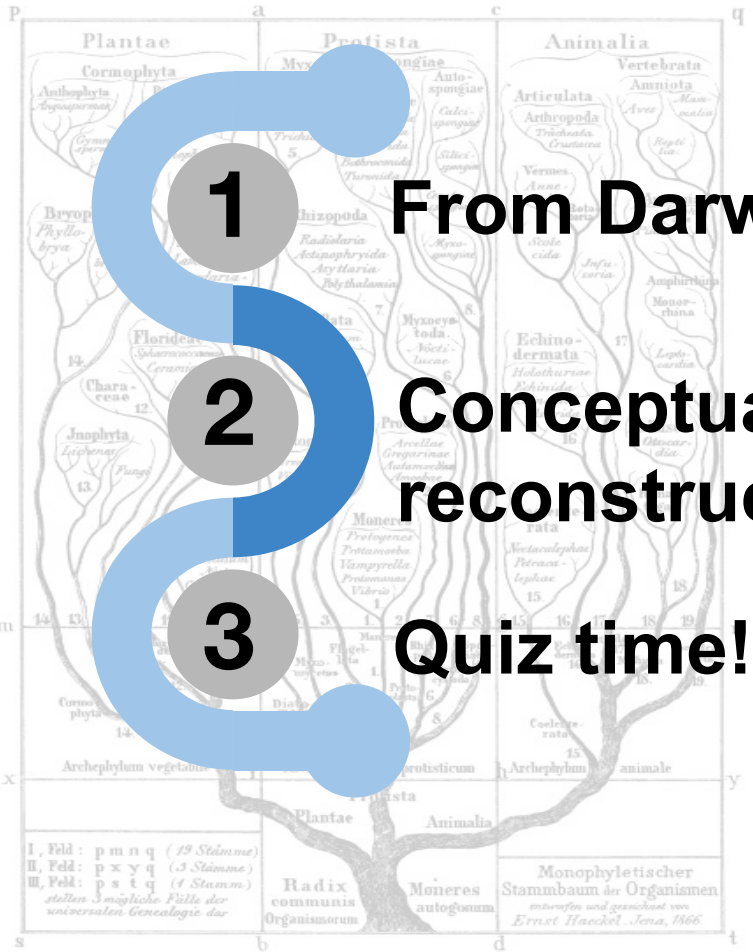
Metazoa Phylogenomics Lab

Content of the lecture



1. From Darwin to phylogenomics
2. Conceptual framework for phylogenomic reconstruction
3. Quiz time!

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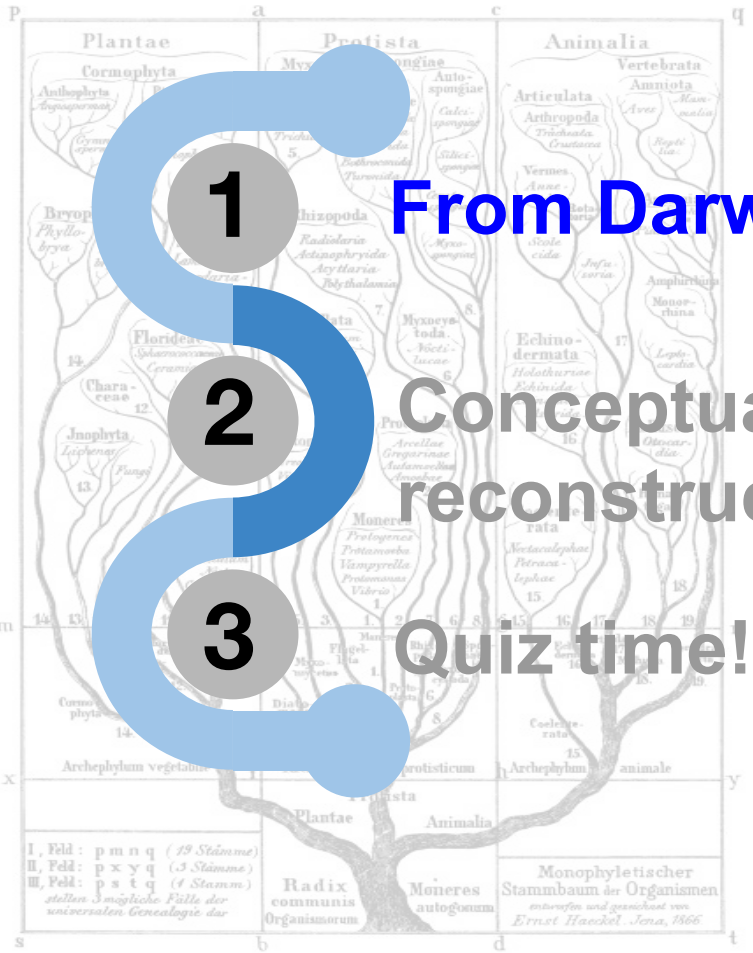

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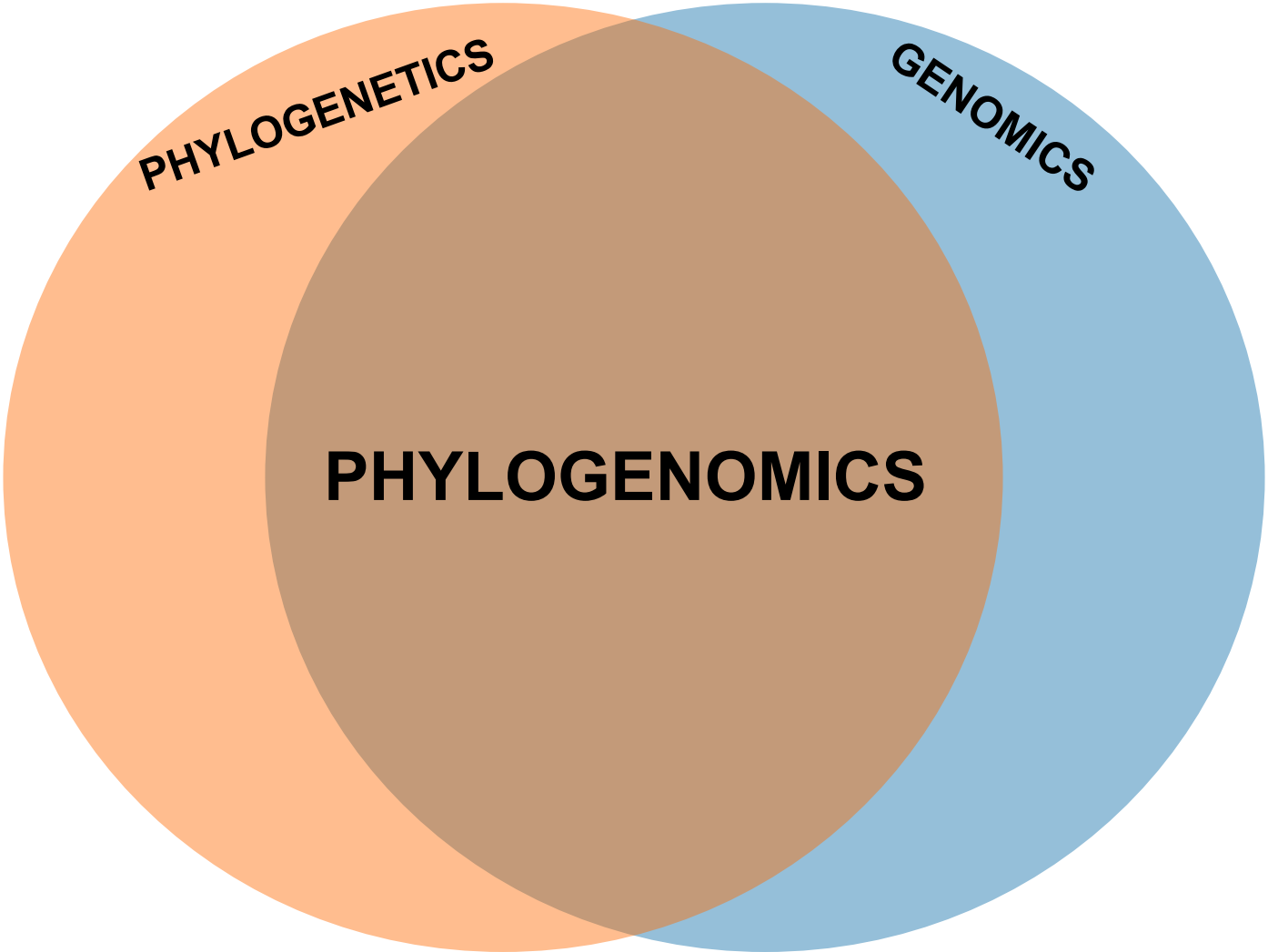
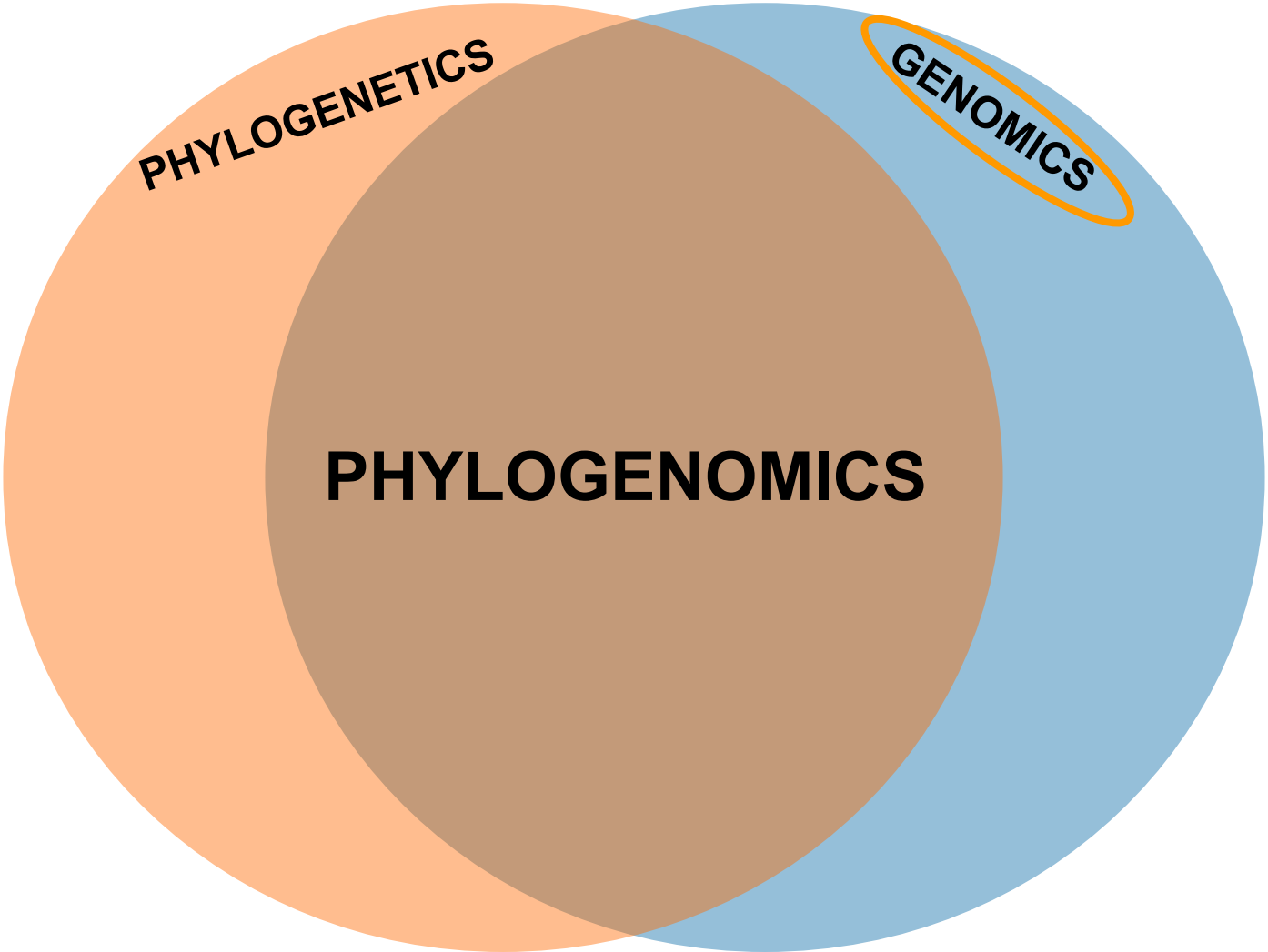

PHYLOGENETICS
GENOMICS
PHYLOGENOMICS


PHYLOGENETICS
GENOMICS
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Genomics

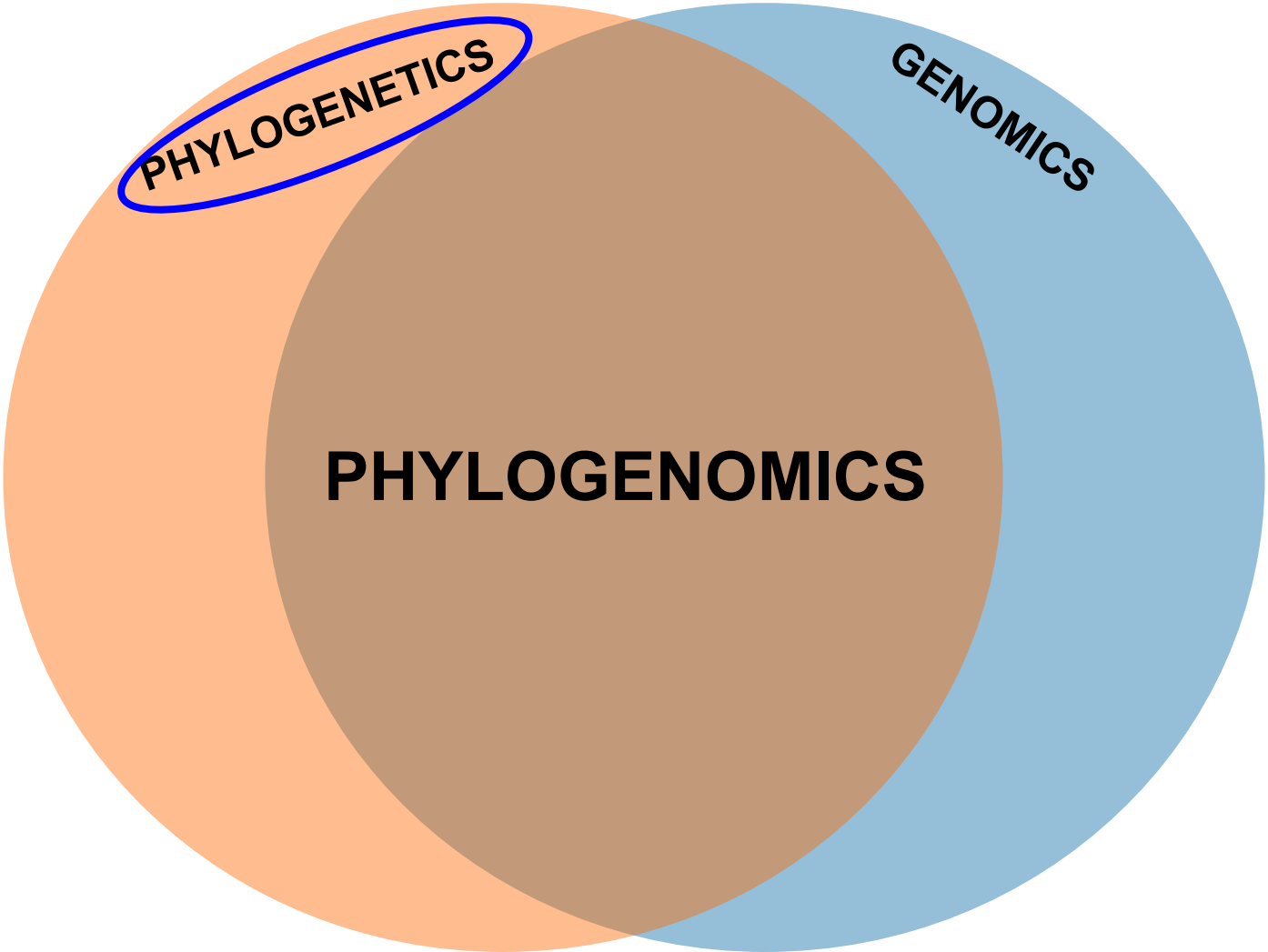
- The study of an organism's complete set of genetic information.
- The genome includes both genes (coding) and non-coding DNA.
- 'Genome': the complete genetic information of an organism.

vs

Genetics

- The study of heredity
- The study of the function and composition of single genes.
- 'Gene': specific sequence of DNA that codes for a functional molecule.

https://www.genomicseducation.hee.nhs.uk/education/core-concepts/what-is-genomics/


PHYLOGENETICS
GENOMICS
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What is a phylogeny…?

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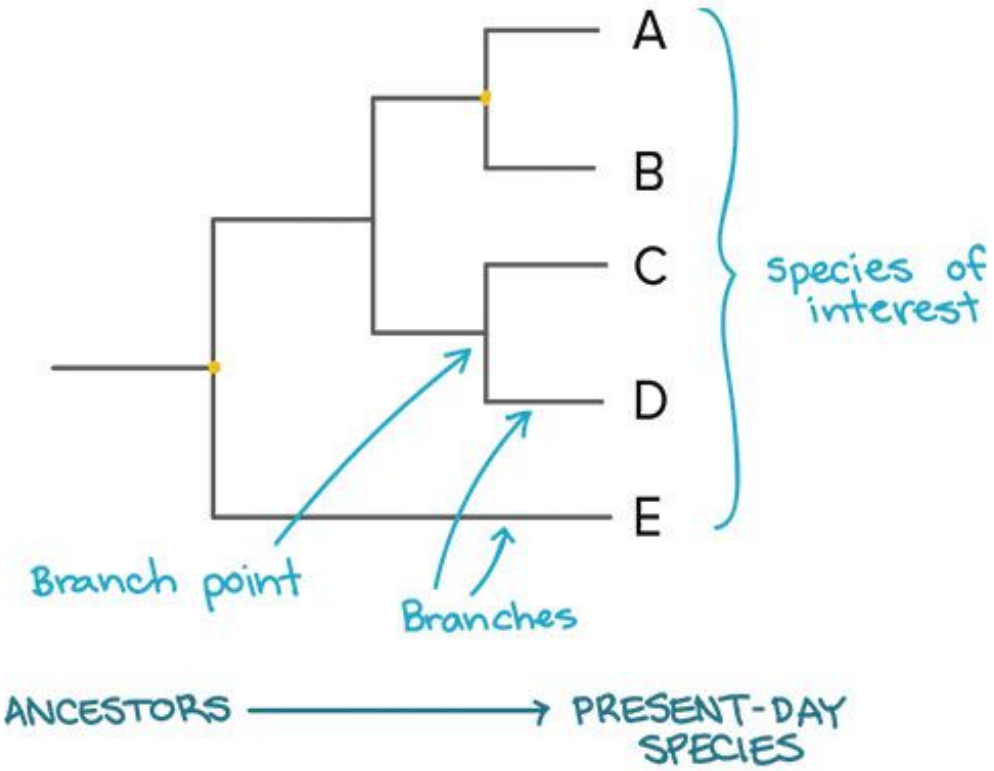
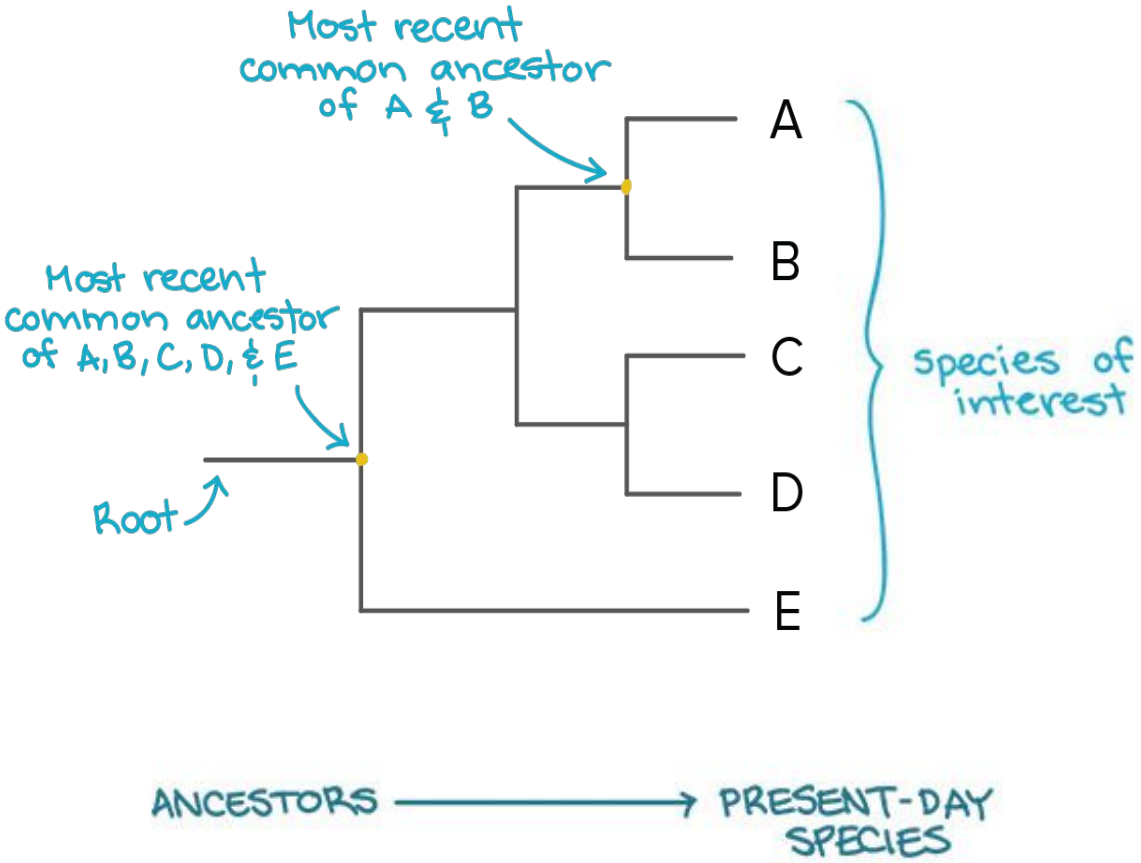


A **phylogenetic tree** is a hypothesis of how species or genes are related through evolution

What is a phylogeny…?



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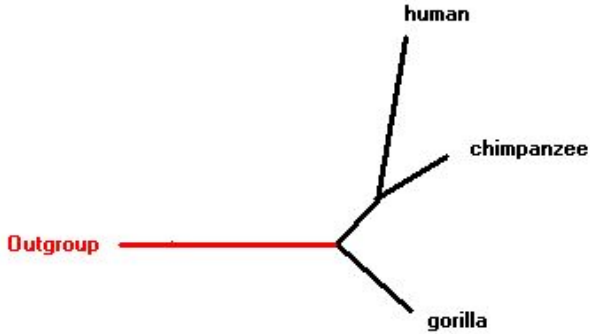
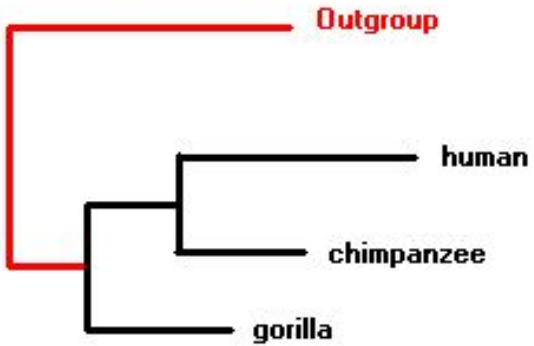
Unrooted tree



Rooted tree



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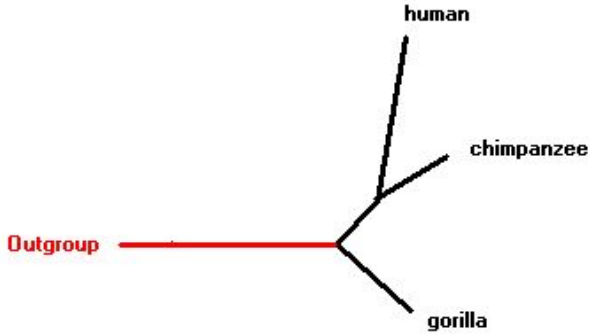

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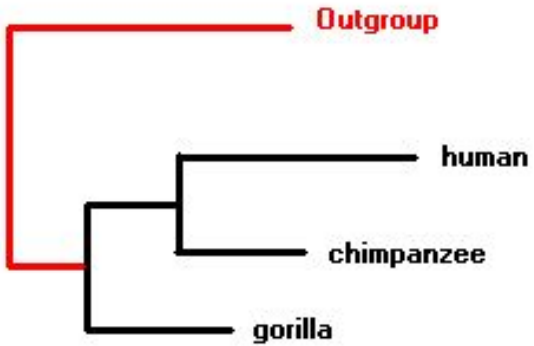

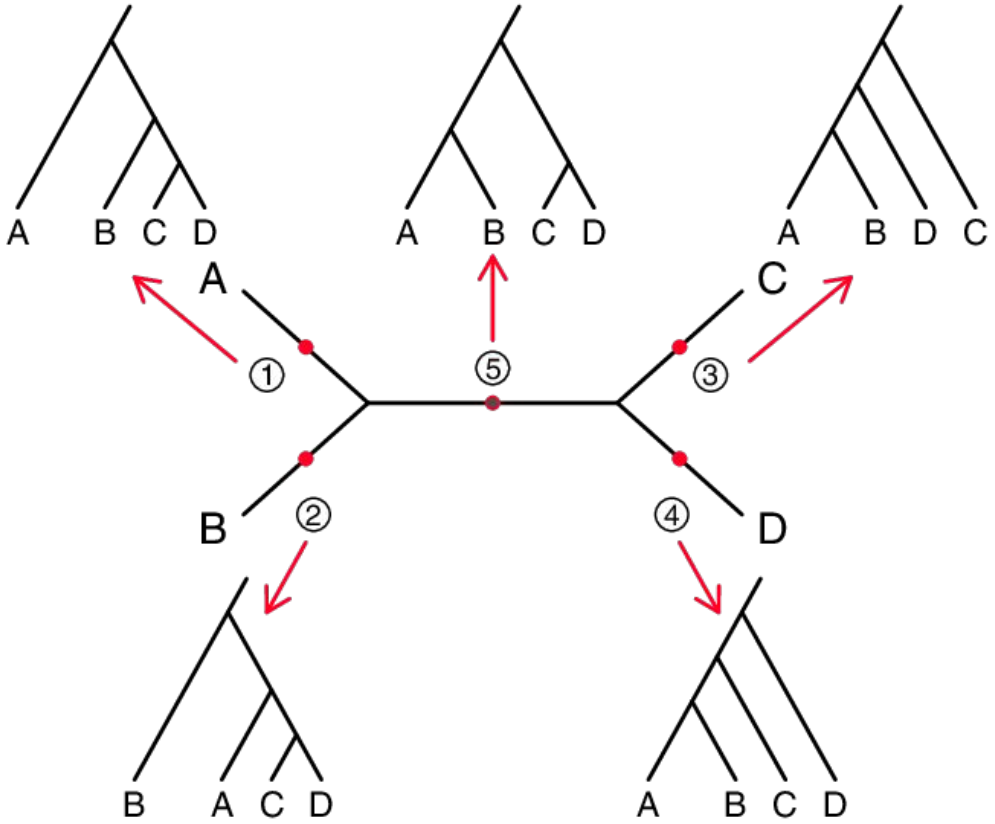

What is a phylogeny, why is it important…?

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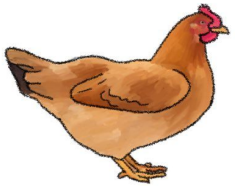
Which came first, the chicken or the egg?



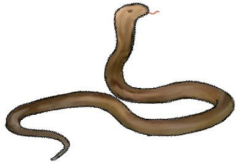
Birds
(Chickens)

What is a phylogeny, why is it important…?

Which came first, the chicken or the egg?

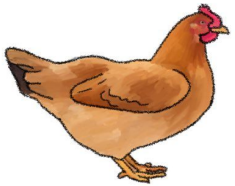
Turtles

Lizards



Snakes

Crocodiles



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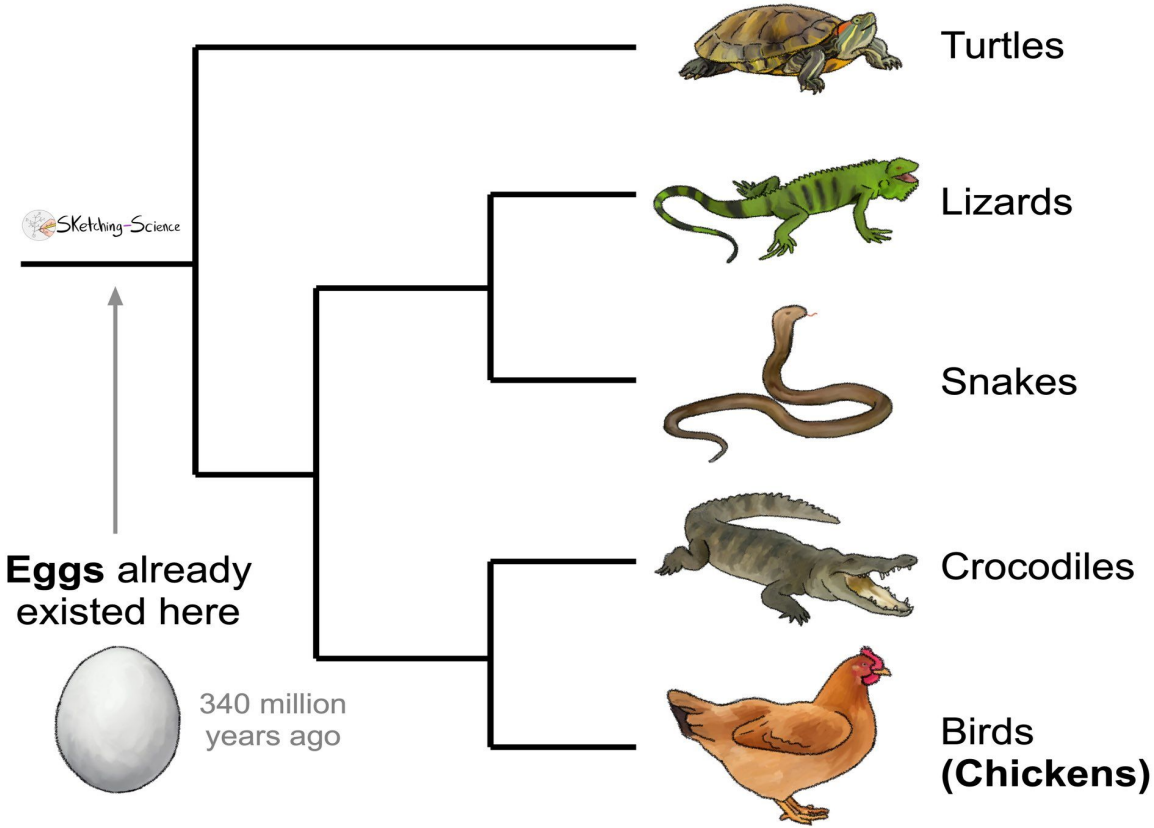
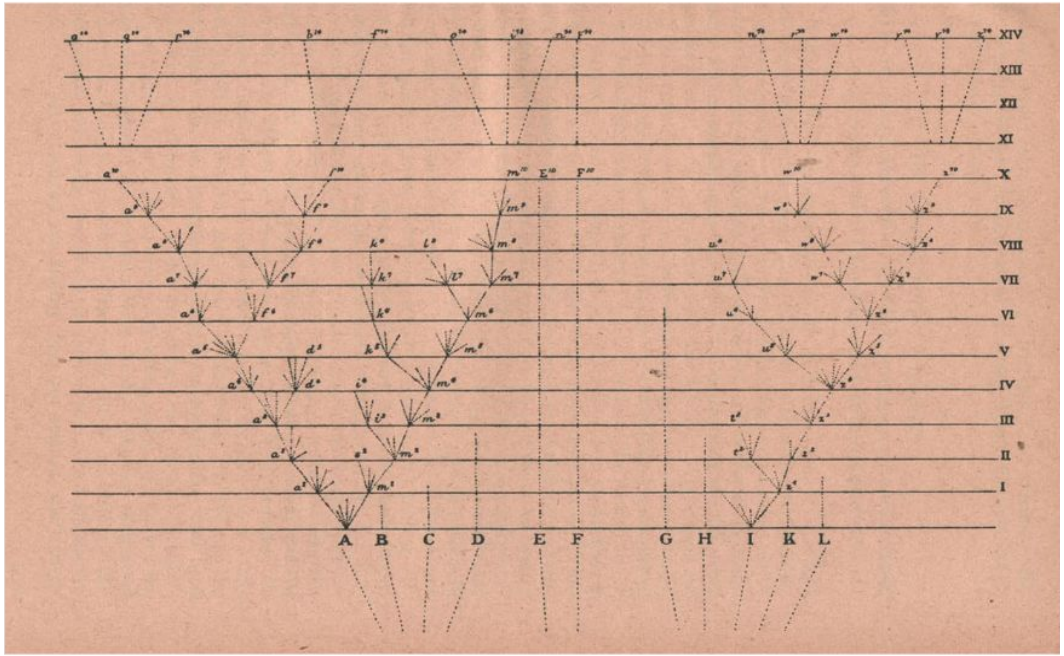


The first phylogenies



(Darwin 1859)

"As buds give rise by growth to fresh buds, and these, if vigorous, branch out and overtop on all sides many a feebler branch, so by generation I believe it has been with the great Tree of Life, which fills with its dead and broken branches the crust of the earth, and covers the surface with its ever branching and beautiful ramifications"

The first phylogenies

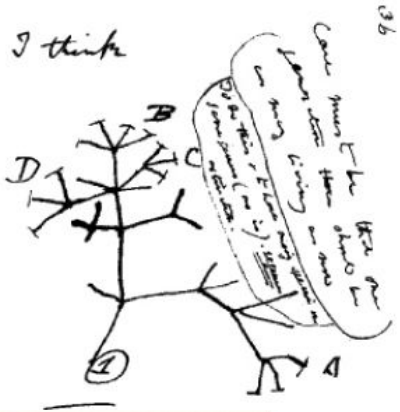
and instinct as the summing up of many contrivances, each useful to the possessor, nearly in the same way as when we look at any great mechanical invention as the summing up of the labour, the experience, the reason, and even the blunders of numerous workmen; when we thus view each organic being, how far more interesting, I speak from experience, will the study of natural history become!

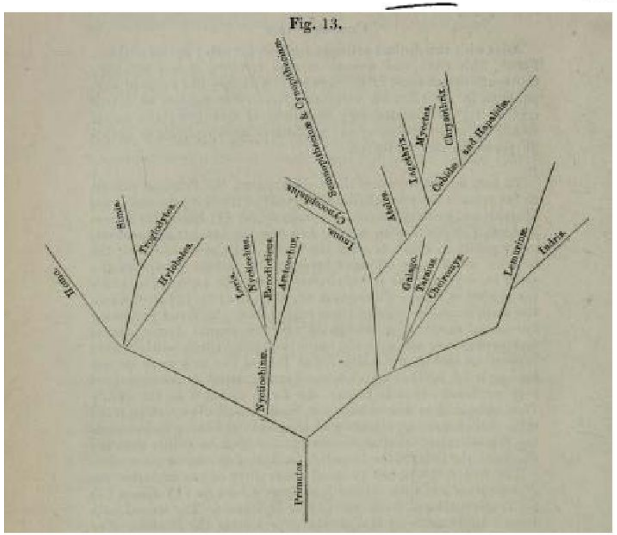
A grand and almost untrodden field of inquiry will be opened, on the causes and laws of variation, on correlation of growth, on the effects of use and disuse, on the direct action of external conditions, and so forth. The study of domestic productions will rise immensely in value. A new variety raised by man will be a far more important and interesting subject for study than one more species added to the infinitude of already recorded species. Our classifications will come to be, as far as they can be so made, genealogies; and will then truly give what may be called the plan of creation. The rules for classifying will no doubt become simpler when we have a definite object in view. We possess no pedigrees or armorial bearings; and we have to discover and trace the many diverging lines of descent in our natural genealogies, by characters of any kind which have long been inherited. Rudimentary organs will speak infallibly with respect to the nature of long-lost structures. Species and groups of species, which are called aberrant, and which may fancifully be called living fossils, will aid us in forming a picture of the ancient forms of life. Embryology will reveal to us the structure, in some degree obscured, of the prototypes of each great class.

When we can feel assured that all the individuals of the same species, and all the closely allied species of most genera, have within a not very remote period de-

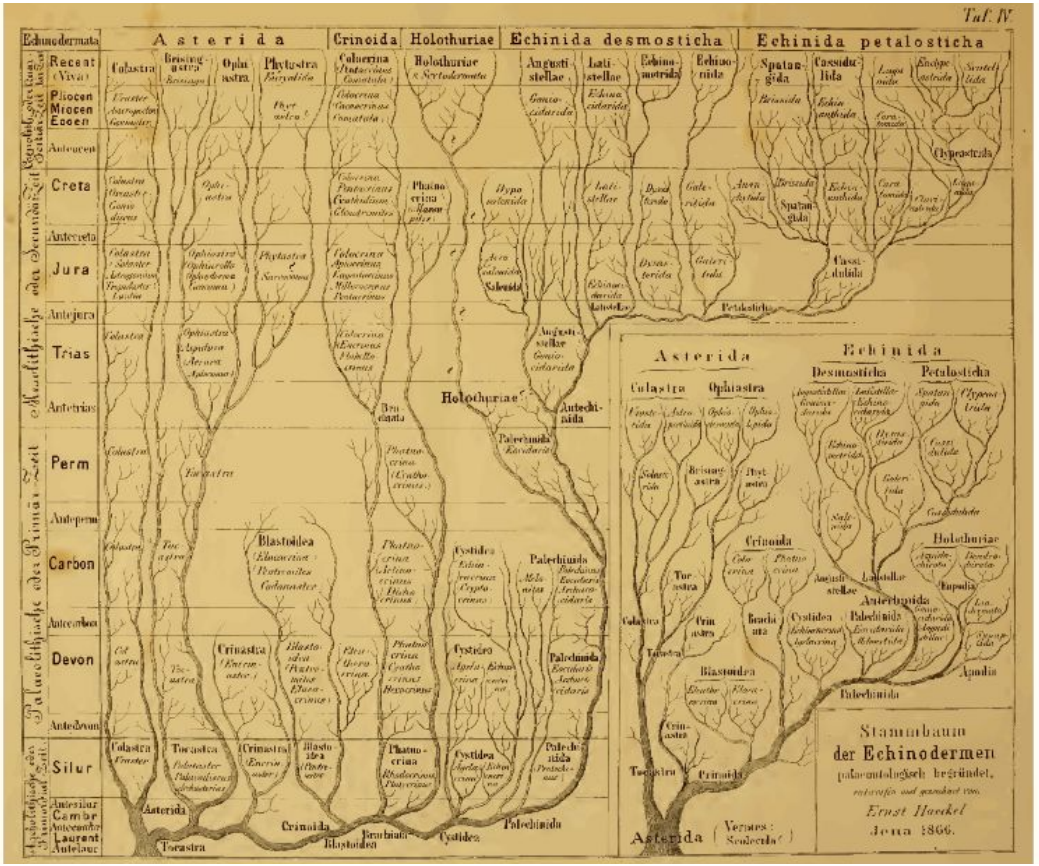
The first phylogenies

The concept:
Darwin's 'I think'
(1837)





Mivart (1865) Proc. Zool. Soc. London



Haeckel (1866)

What is a phylogeny, why is it important… and how do you build one?

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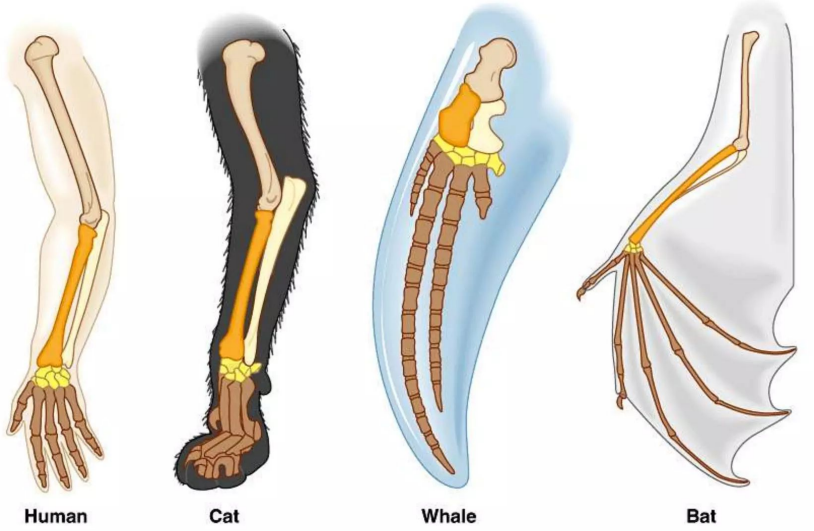
Homologous Structures



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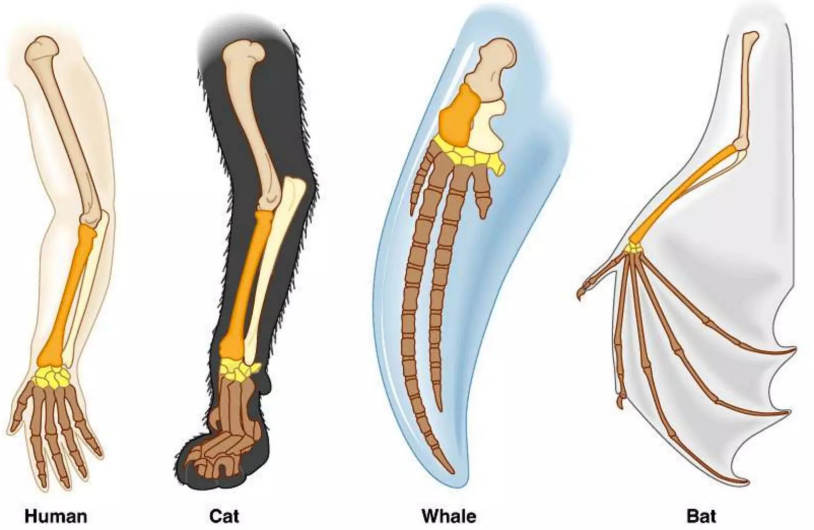

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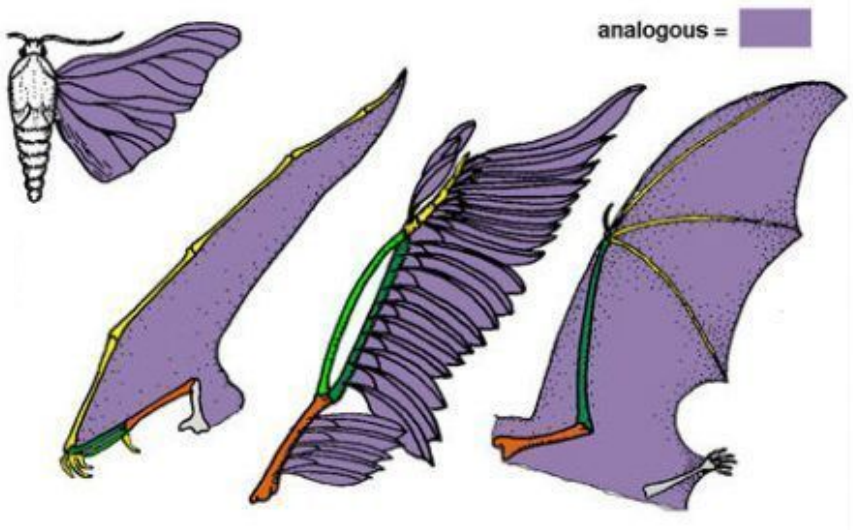
Analogous Structures



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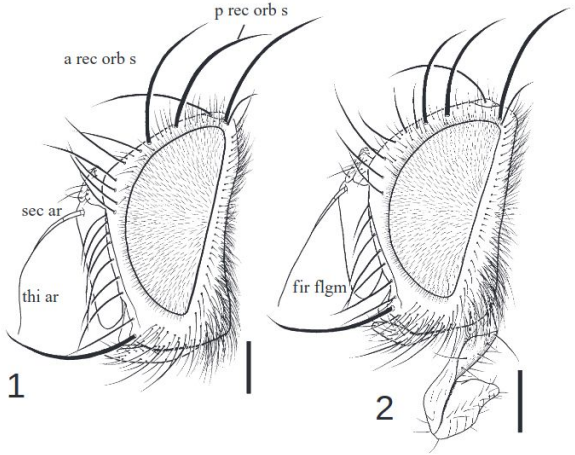
Systematic study of the genus *Phorinia* Robineau-Desvoidy of the Palearctic, Oriental and Oceanian regions (Diptera : Tachinidae)

Takuji Tachi[A,C] *and Hiroshi Shima*[B]

Invertebrate Systematics, 2006, **20**, 255–287



Figs 1–2. Male heads in profile: *1, Phorinia spinulosa*, sp. nov.; *2*, *P. breviata*, sp. nov. (Abbreviations: fir flgm, first flagellomere; sec ar, second aristomere; thi ar, third aristomere; a rec orb s, anterior reclinate orbital seta; p rec orb s, posterior reclinate orbital seta). Scale bars = 0.5 mm.

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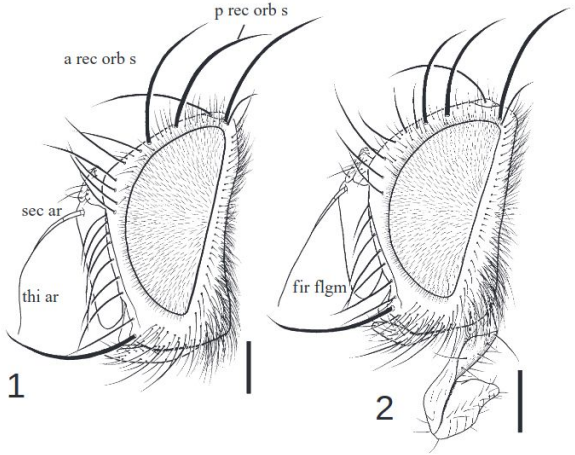

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(*4*) *Occiput:* 0, without black setulae behind postocular row; 1, with black setulae behind postocular row. L = 2; *CI* = 0.50; *RI* = 0.86.
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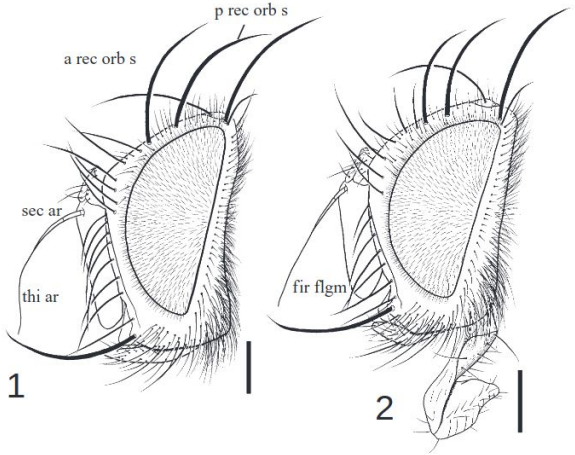

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Table 3. Morphological data matrix used for phylogenetic analysis

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Winthemia venusta	0000000000	0000000000	-000001000	0
Drinomyia hokkaidensis	1000100001	0100000000	-000002000	0
Phorocerosoma vicarium	0000100000	0010000000	-000001000	0
Austrophorocera grandis	0120100000	0101010001	0000003000	1
A. hirsuta	0020100000	0001010001	0000003000	1
Bessa parallela	1021101000	0001010001	1000003000	1

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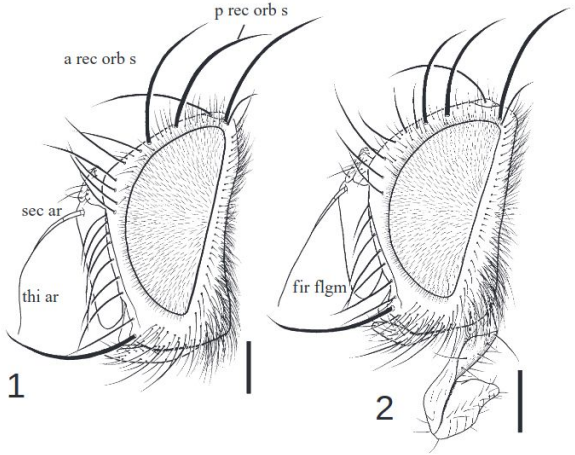

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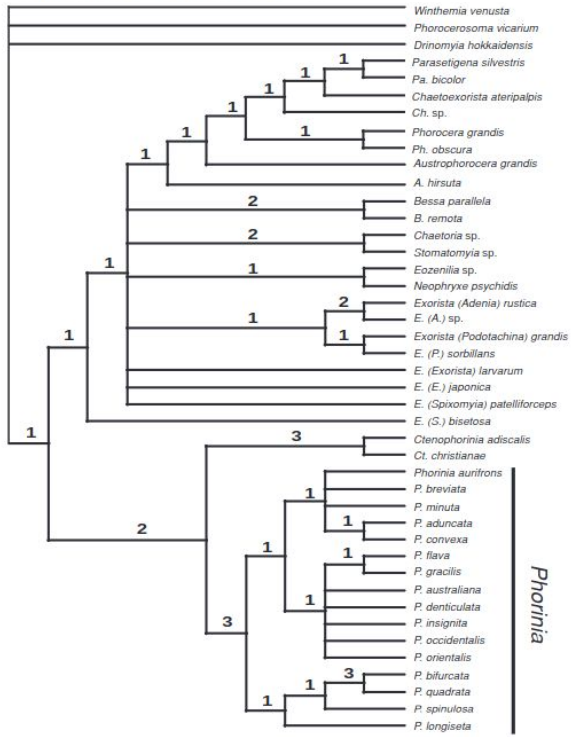
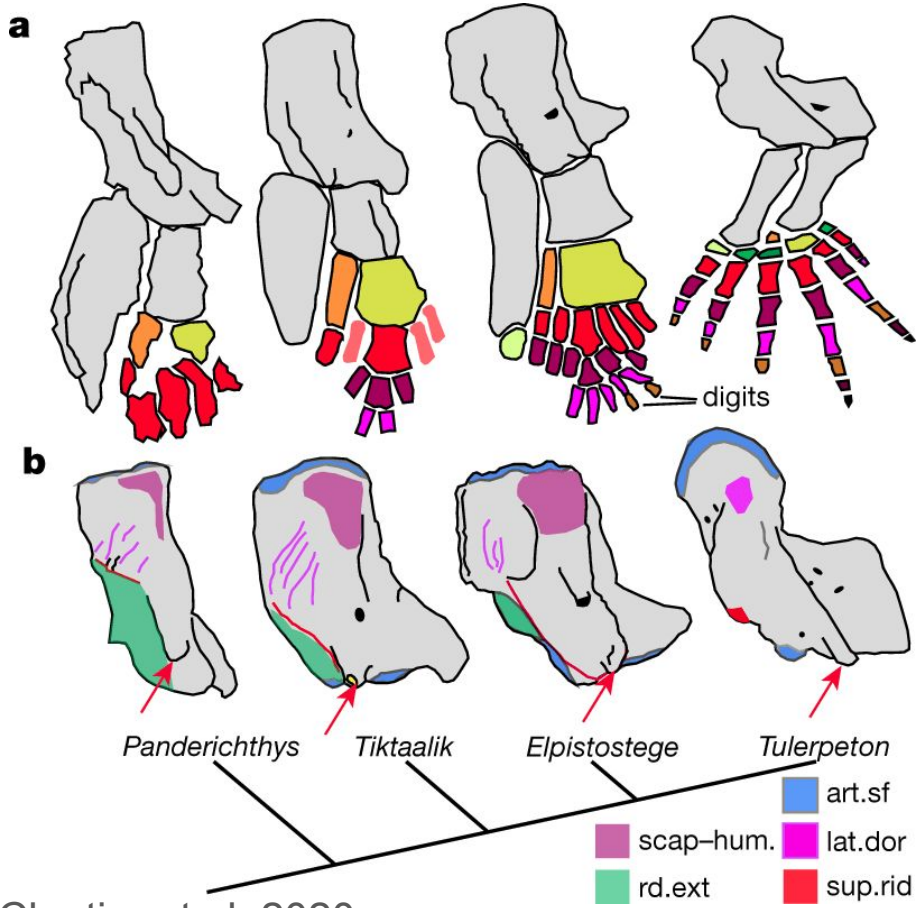


Fig. 79. Strict consensus of 186 equally most parsimonious cladograms (length = 66, consistency index (*CI*) = 0.530, rescaled consistency index (*RC*) = 0.462) generated from an analysis of thirty-one morphological characters. Bremer support values are given on the branches.

What is a phylogeny, why is it important… and how do you build one?



Cloutier et al. 2020

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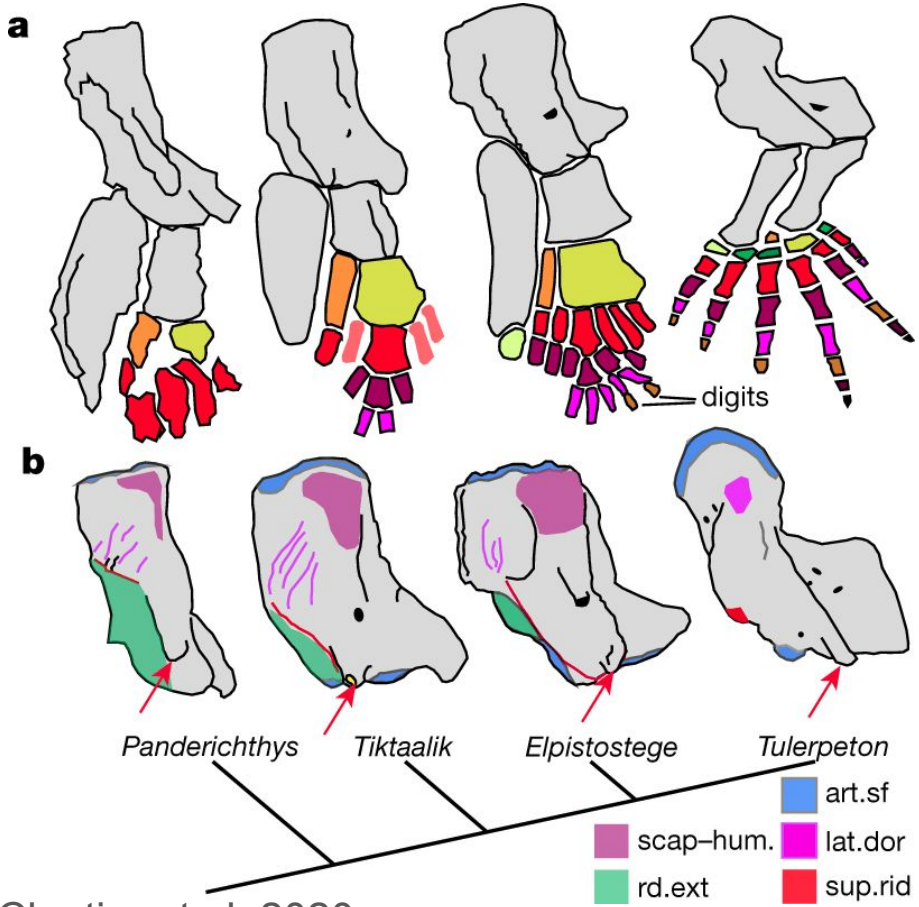

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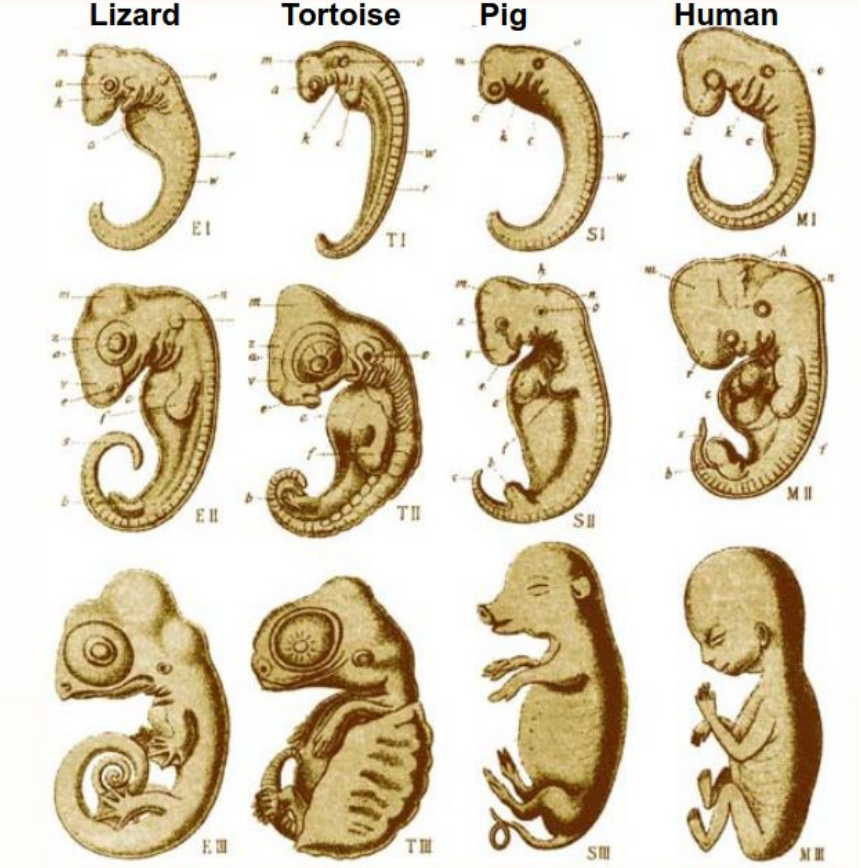


http://www.nature.com/nrg/journal/v7/n11/images/nrg1918-f2.jpg

The origin of molecular phylogenetics

The origin of molecular phylogenetics

BLOOD IMMUNITY
AND
BLOOD RELATIONSHIP

A DEMONSTRATION OF CERTAIN BLOOD-RELATIONSHIPS
AMONGST ANIMALS BY MEANS OF

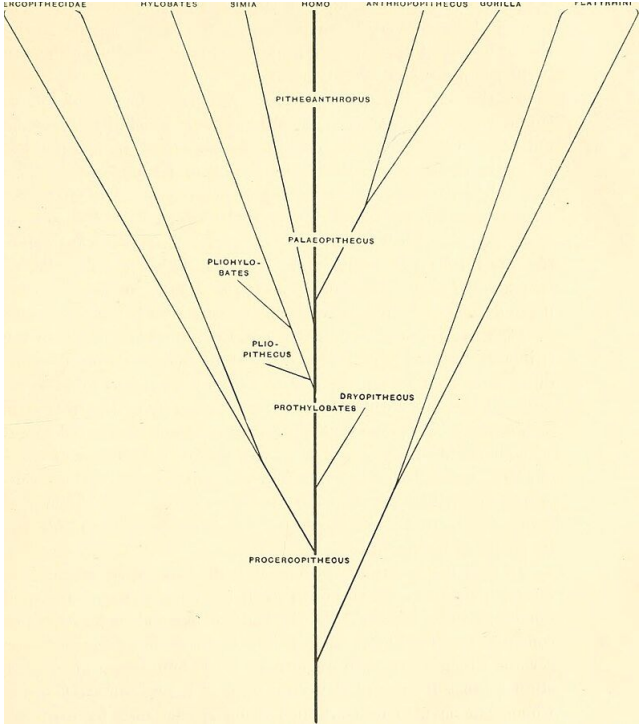
THE PRECIPITIN TEST FOR BLOOD

by
GEORGE H. F. NUTTALL, M.A., M.D., PH.D.
University Lecturer in Bacteriology and Preventive Medicine, Cambridge.

Including
Original Researches by
G. S. GRAHAM-SMITH, M.A., M.B., D.P.H. (Camb.)
and
T. S. P. STRANGEWAYS, M.A., M.R.C.S.

CAMBRIDGE:
at the University Press
1904

Nuttal (1904) - serological cross-reactions were stronger for more closely related organisms -> phylogeny of apes



The origin of molecular phylogenetics

BLOOD IMMUNITY
AND
BLOOD RELATIONSHIP

Nuttal (1904) - serological cross-reactions were stronger for more closely related organisms -> phylogeny of apes

Dobzhansky & Sturtevant (1938) - genomic rearrangements in *Drosophila* as phylogenetic markers

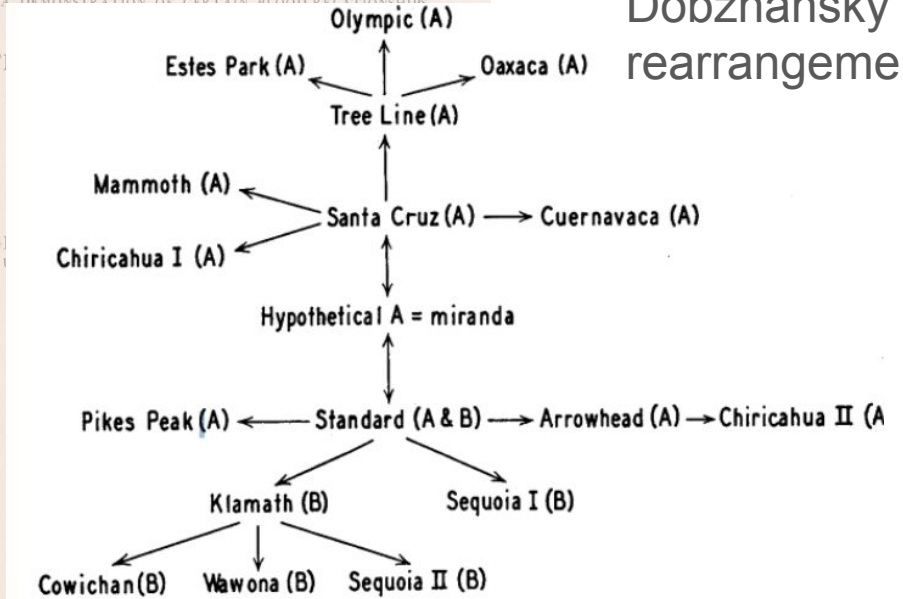
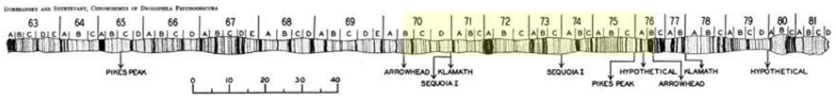
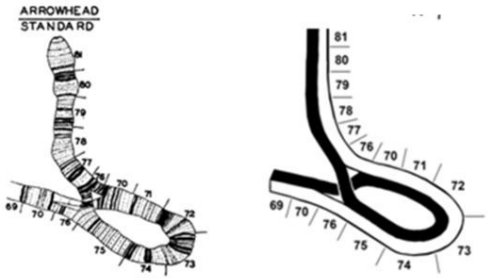


FIGURE 3.—Phylogeny of the gene arrangements in the third chromosome of *Drosophila pse doobscura*. Any two arrangements connected by an arrow in the diagram differ by a single i version. Further explanation in text.

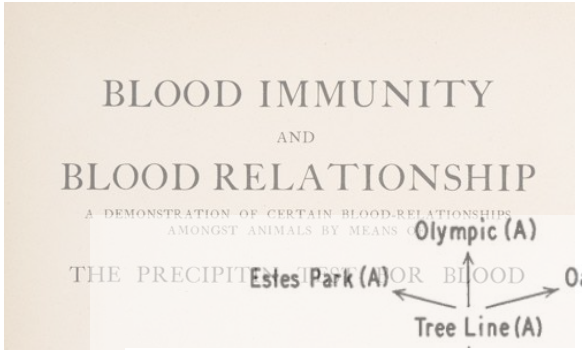


Chromosome 3 of *Drosophila pseudoobscura*



Standard and Arrowhead arrangements differ by an inversion from segments 70 to 76

The origin of molecular phylogenetics


BLOOD IMMUNITY
AND
BLOOD RELATIONSHIP
A DEMONSTRATION OF CERTAIN BLOOD-RELATIONSHIPS
AMONGST ANIMALS BY MEANS
THE PRECIPIT
OR BLOOD
Olympic (A)
Estes Park (A)
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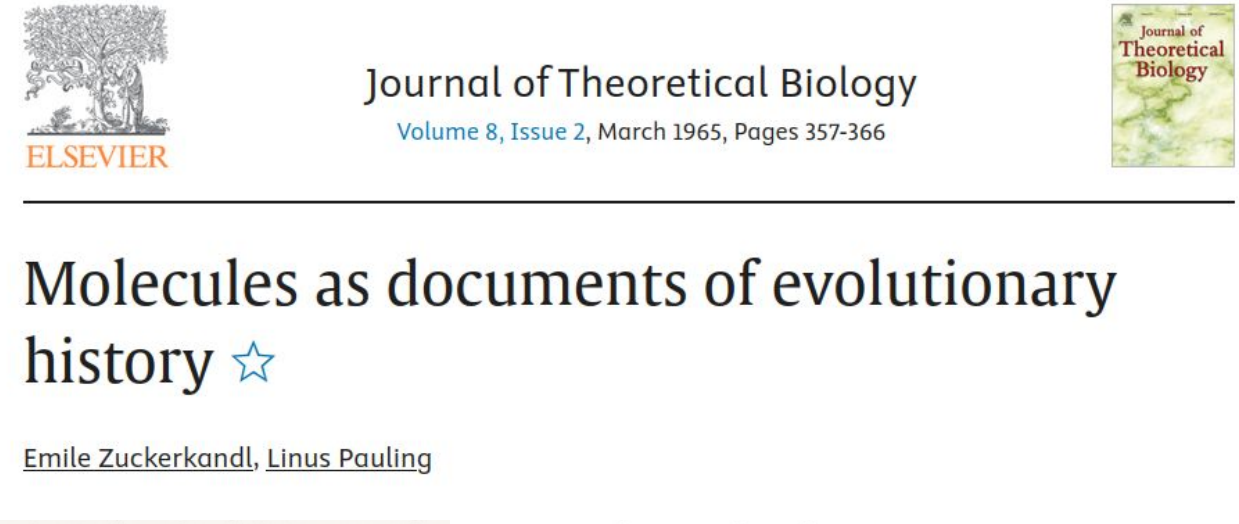

ELSEVIER

Journal of Theoretical Biology

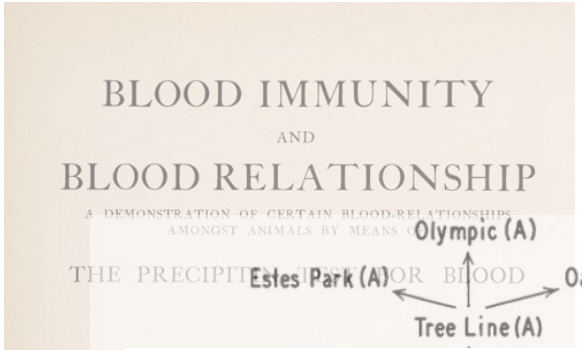
Volume 8, Issue 2, March 1965, Pages 357-366

Molecules as documents of evolutionary history ☆

Emile Zuckerkandl, Linus Pauling

Zuckerkandl & Pauling (1965) -

The origin of molecular phylogenetics


BLOOD IMMUNITY
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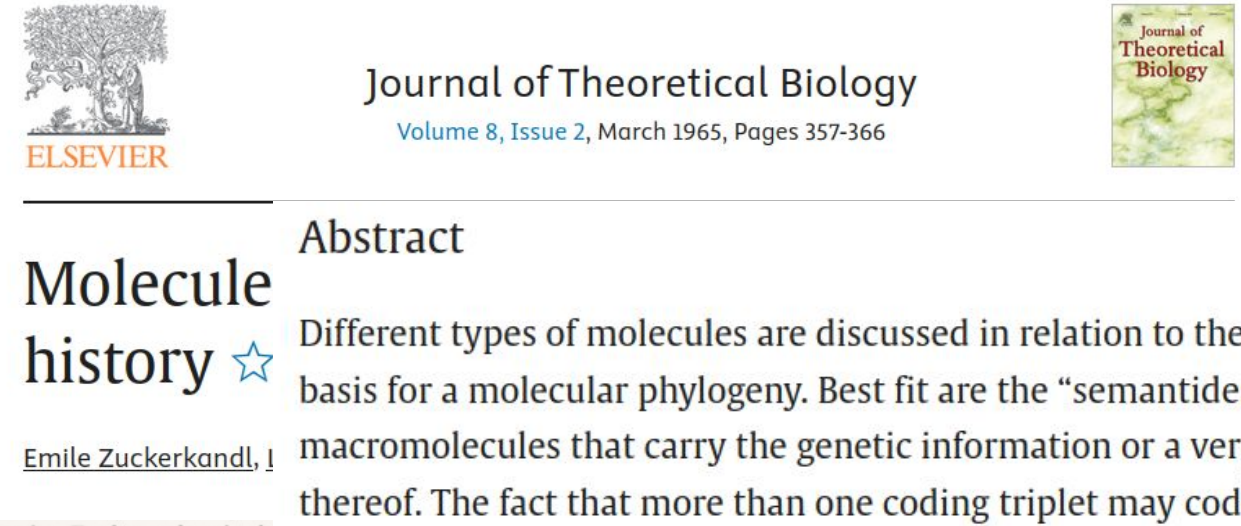
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Journal of Theoretical Biology

Volume 8, Issue 2, March 1965, Pages 357-366

Zuckerkandl & Pauling (1965) -

Molecule history ☆

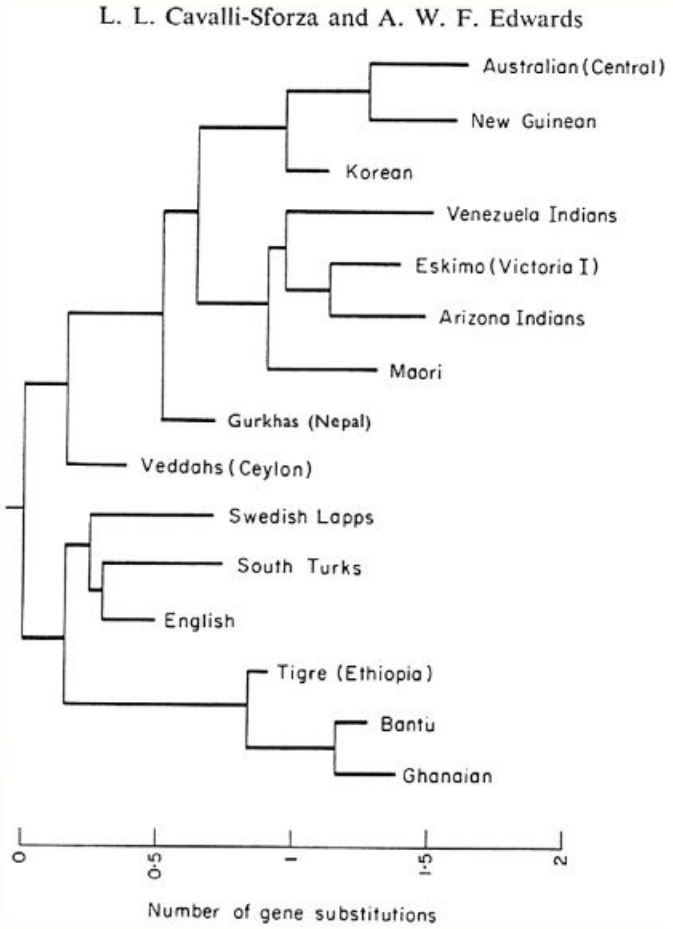
Emile Zuckerkandl, I

version. Further explanation in

Abstract

Different types of molecules are discussed in relation to their fitness for providing the basis for a molecular phylogeny. Best fit are the “semantides”, i.e. the different types of macromolecules that carry the genetic information or a very extensive translation thereof. The fact that more than one coding triplet may code for a given amino acid

Molecular phylogenetics: the new wave

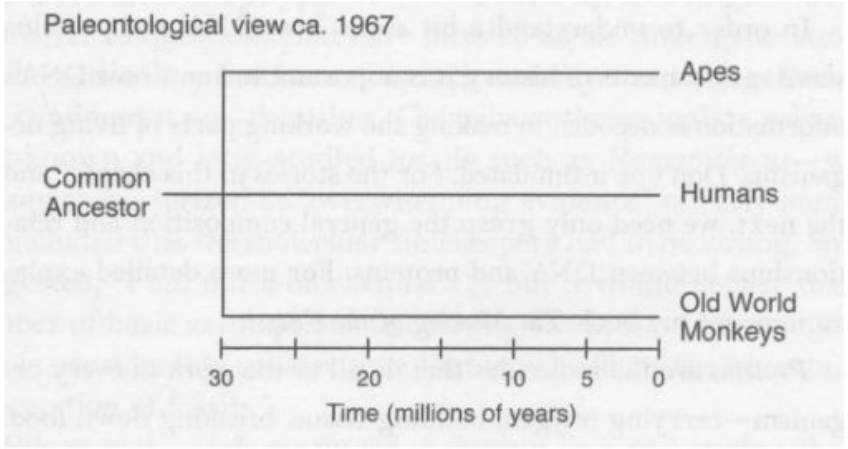


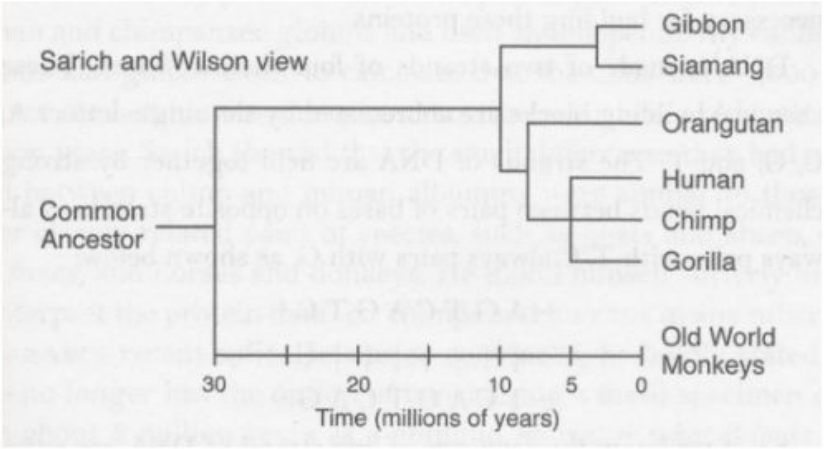
Phylogeny inferred from blood group allele frequencies from 15 populations

Cavalli-Sforza & Edwards (1965) in Genetics Today

Molecular phylogenetics: the new wave

Divergence times were estimated by measuring the immunological cross-reaction of blood serum albumin between pairs of primates





"no fuss, no muss, no dishpan hands. Just throw some proteins into a laboratory apparatus, shake them up, and bingo! – we have an answer to questions that have puzzled us for three generations."

Sarich & Wilson (1967) Science

Molecular phylogenetics: the new wave

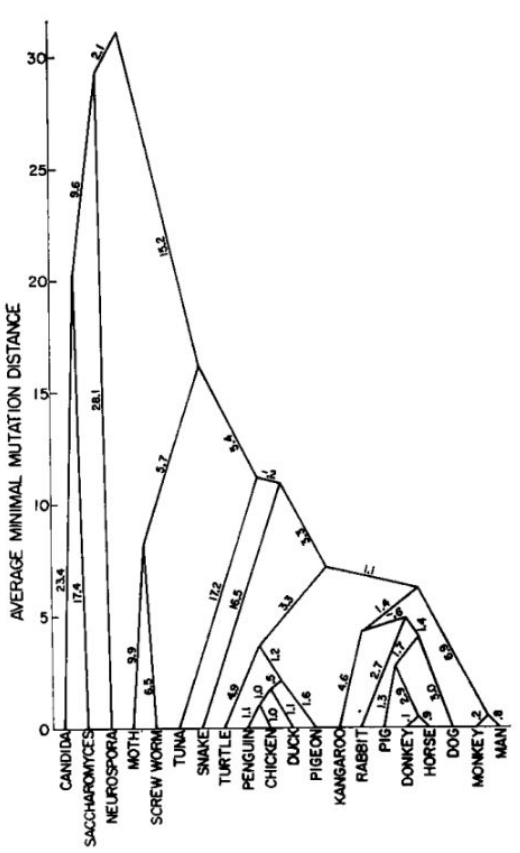
Construction of Phylogenetic Trees

A method based on mutation distances as estimated from cytochrome *c* sequences is of general applicability.

Walter M. Fitch and Emanuel Margoliash

Biochemists have attempted to use quantitative estimates of variance between substances obtained from different species to construct phylogenetic trees. Examples of this approach include studies of the degree of interspecific hybridization of DNA (*1*), the degree of cross reactivity of antisera to purified proteins (*2*), the number of differences in the peptides from enzymic digests of purified homologous proteins, both as estimated by paper electrophoresis-chromatography or column chromatography and as estimated from the amino acid compositions of the proteins (*3*), and the number of amino acid replacements between homologous proteins whose complete primary structures had been determined (*4*). These methods have not been completely satisfactory because (i) the portion of the genome examined

20 JANUARY 1967



Molecular phylogenetics: the new wave

Proc. Natl. Acad. Sci. USA
Vol. 74, No. 11, pp. 5088–5090, November 1977
Evolution

Phylogenetic structure of the prokaryotic domain: The primary kingdoms

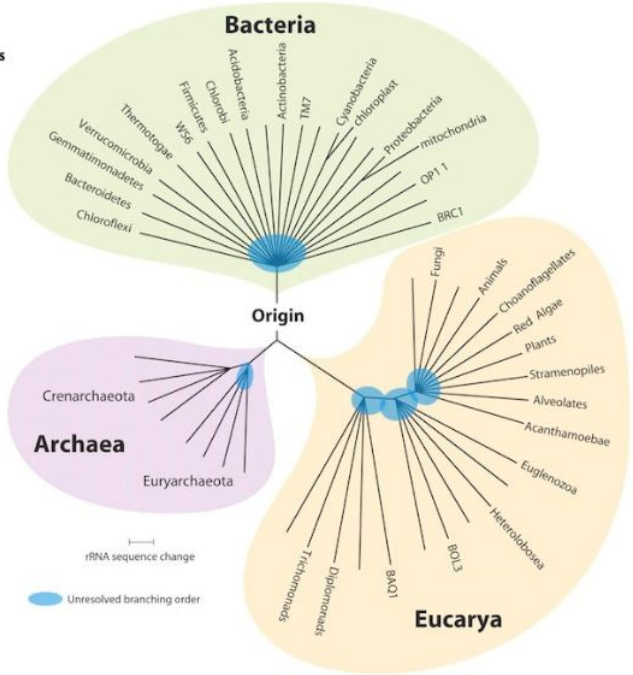
(archaebacteria/eubacteria/urkaryote/16S ribosomal RNA/molecular phylogeny)

CARL R. WOESE AND GEORGE E. FOX*

Department of Genetics and Development, University of Illinois, Urbana, Illinois

Communicated by T. M. Sonneborn, August 18, 1977

ABSTRACT **A phylogenetic analysis based upon ribosomal RNA sequence characterization reveals that living systems represent one of three aboriginal lines of descent: (*i*) the eubacteria, comprising all typical bacteria; (*ii*) the archaebacteria, containing methanogenic bacteria; and (*iii*) the urkaryotes, now represented in the cytoplasmic component of eukaryotic cells.**



The dawn of phylogenomics

The dawn of phylogenomics

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Insight/Outlook

Phylogenomics: Improving Functional Predictions for Uncharacterized Genes by Evolutionary Analysis

Jonathan A. Eisen[1]

Department of Biological Sciences, Stanford University, Stanford, California 94305-5020 USA

The ability to accurately predict gene function based on gene sequence is an important tool in many areas of biological research. Such predictions have become particularly important in the genomics age in which numerous gene sequences are generated with little or no accompanying experimentally determined functional information. Almost all functional prediction methods rely on the identification, characterization, (e.g., Altschul et al. 1989; Goldman et al. 1996). In this commentary, I discuss the use of evolutionary information in the prediction of gene function. To appreciate the potential of a *phylogenomic* approach to the prediction of gene function, it is necessary to first discuss how gene sequence is commonly used to predict gene function and some general features about gene evolution.

convergence (the exact threshold for such an inference is not well established).

Improvements in database search programs have made the identification of likely homologs much faster, easier, and more reliable (Altschul et al. 1997; Henikoff et al. 1998). However, as discussed above, in many cases the identification of homologs is not sufficient to make specific functional predictions be-

Phylogenomics: prediction of gene function and gene family evolution

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Phylogenomics: prediction of gene function and gene family evolution

Sequence Similarity, Homology, and Functional Predictions

To make use of the identification of sequence similarity between genes, it is helpful to understand how such similarity arises. Genes can become similar in sequence either as a result of *convergence* (similarities that have arisen without a common evolutionary history) or descent with modification from a common ancestor (also known as *homology*). It is imperative to recognize that sequence similarity and homology are not interchangeable terms. Not all homologs are similar in sequence (i.e., homologous genes can diverge so much that similarities are difficult or impossible to detect) and not all similarities are due to homology (Reeck et al. 1987; Hillis 1994). Similarity due to convergence, which is likely limited to small regions of genes, can be useful for some functional predictions (Henikoff et al. 1997). However, most sequence-based functional predictions are based on the identification (and subsequent analysis) of similarities that are thought to be due to homology. Because homology is a statement about common ancestry, it cannot be proven directly from sequence similarity. In these cases, the inference of homology is made based on finding levels of sequence similarity that are thought to be too high to be due to

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Phylogenomics: prediction of gene function and gene family evolution

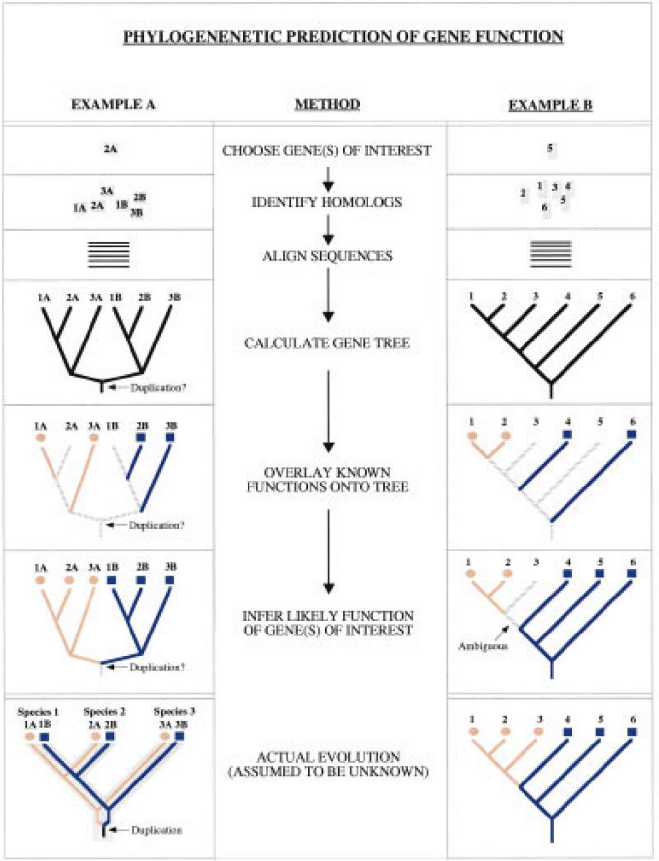

Figure 1 Outline of a phylogenomic methodology. In this method, information about the evolutionary relationships among genes is used to predict the functions of uncharacterized genes (see text for details). Two hypothetical scenarios are presented and the path of trying to

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1414–1419 | PNAS | February 5, 2002 | vol. 99 | no. 3 www.pnas.org/cgi/doi/10.1073/pnas.032662799

The analysis of 100 genes supports the grouping of three highly divergent amoebae: *Dictyostelium*, *Entamoeba*, and *Mastigamoeba*

Eric Bapteste*, Henner Brinkmann†, Jennifer A. Lee‡, Dorothy V. Moore‡, Christoph W. Sensen§, Paul Gordon¶, Laure Duruflé*, Terry Gaasterland‡, Philippe Lopez*, Miklós Müller‡, and Hervé Philippe*‖

The phylogenetic relationships of amoebae are poorly resolved. To address this difficult question, we have sequenced 1,280 expressed sequence tags from *Mastigamoeba balamuthi* and assembled a large data set containing 123 genes for representatives of three phenotypically highly divergent major amoeboid lineages: Pelobionta, Entamoebidae, and Mycetozoa. Phylogenetic reconstruction was performed on ≈25,000 aa positions for 30 species by using maximum-likelihood approaches. All well-established eukaryotic groups were recovered with high statistical support, validating our approach. Interestingly, the three amoeboid lineages strongly clustered together in agreement with the Conosa hypothesis [as defined by T. Cavalier-Smith (1998) *Biol. Rev. Cambridge Philos. Soc.* 73, 203–266]. Two amitochondriate amoebae, the free-living *Mastigamoeba* and the human parasite *Entamoeba*, formed a significant sister group to the exclusion of the mycetozoan *Dictyostelium*. This result suggested that a part of the reductive process in the evolution of *Entamoeba* (e.g., loss of typical mitochondria) occurred in its free-living ancestors. Applying this inexpensive expressed sequence tag approach to many other lineages will surely improve our understanding of eukaryotic evolution.

Phylogenomics: species tree inference

The dawn of phylogenomics

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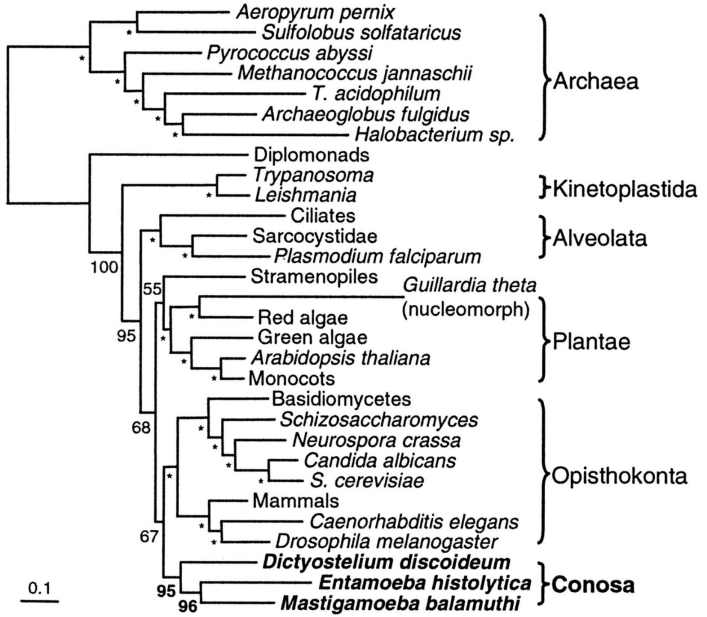
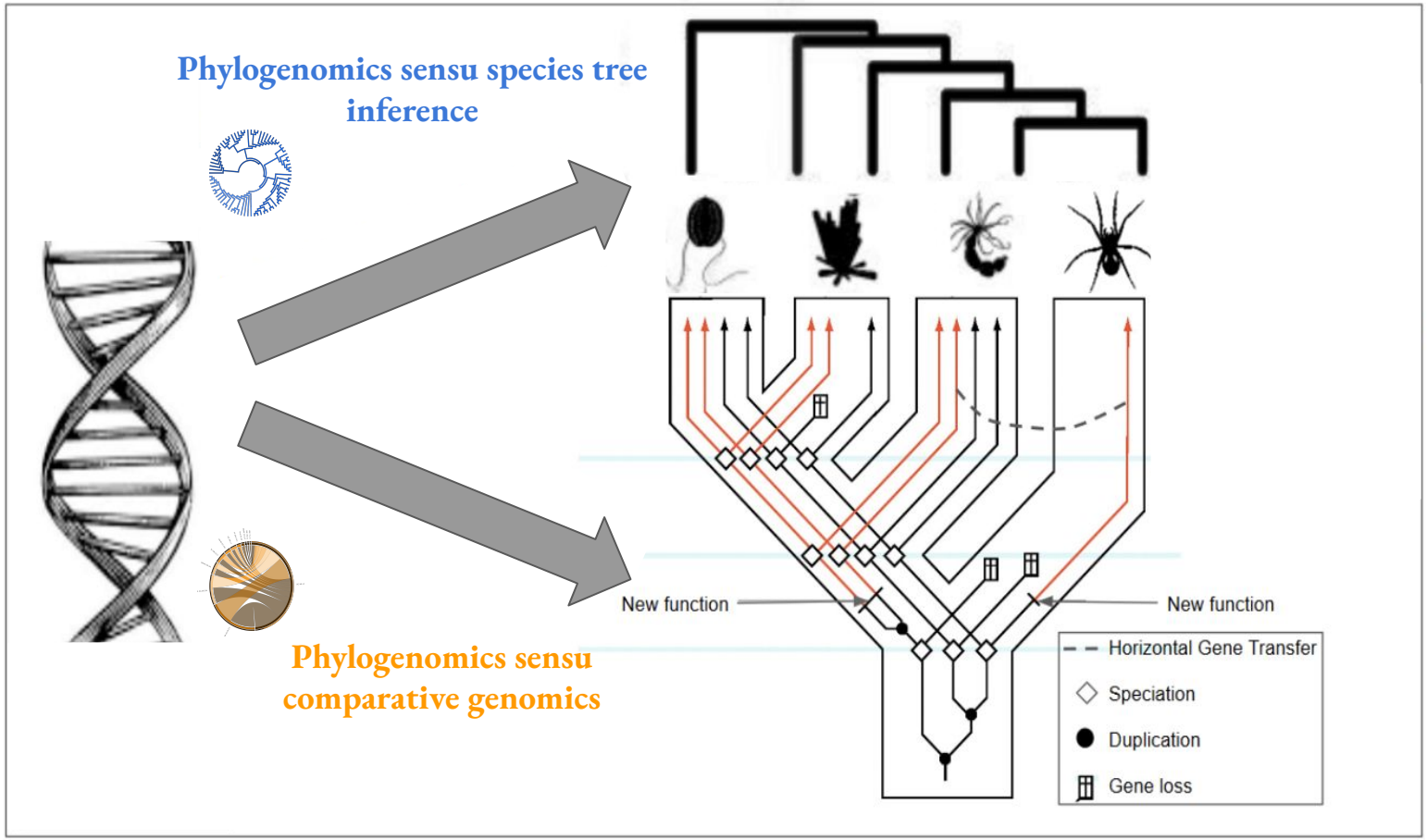


*ML tree based on 25,032 aa positions. * indicates a constrained node. We used the JTT model, without taking into account among-sites rate variation. The branch lengths have been computed on the concatenated sequences. BVs were obtained by bootstrapping the 123 genes.*

The dawn of phylogenomics



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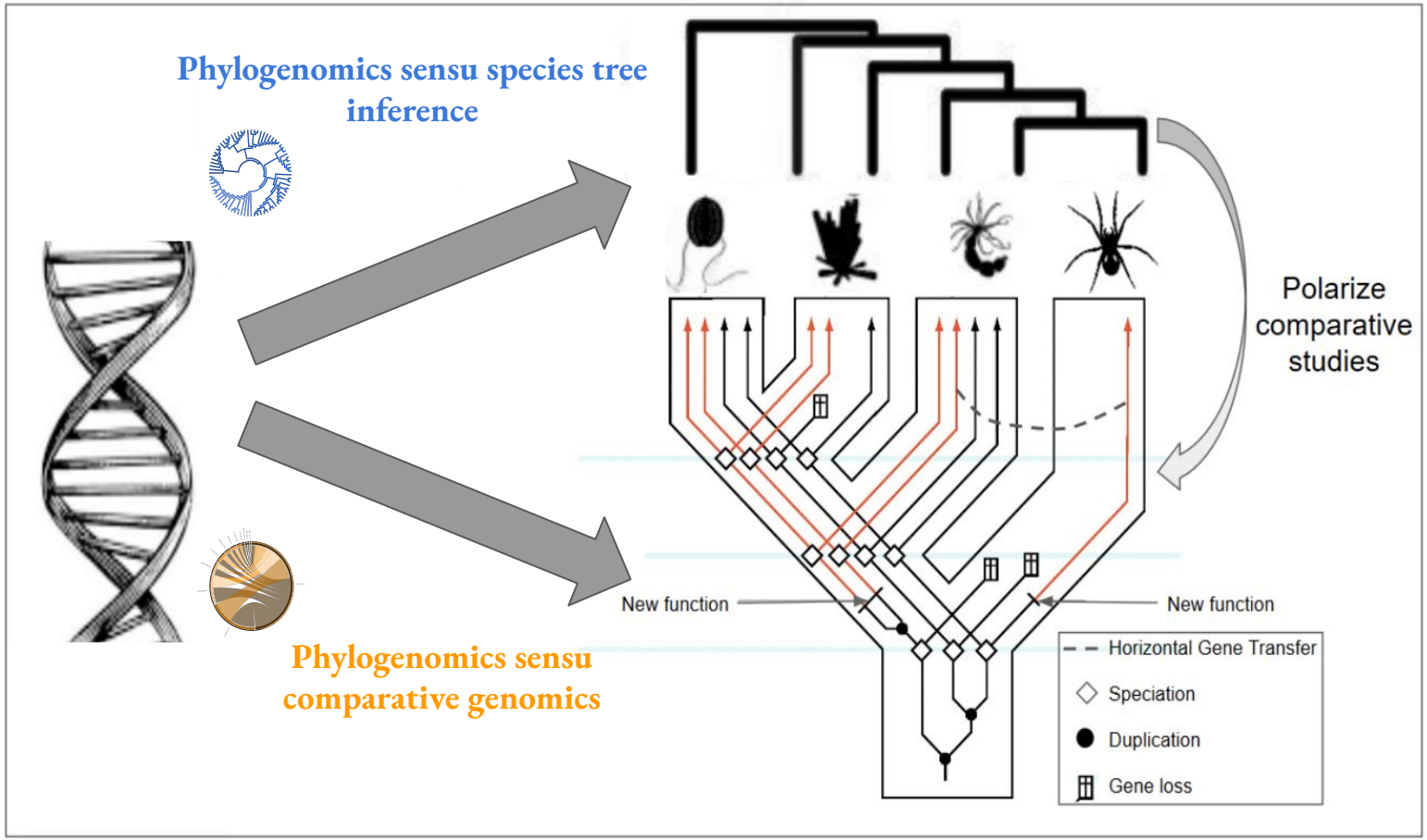

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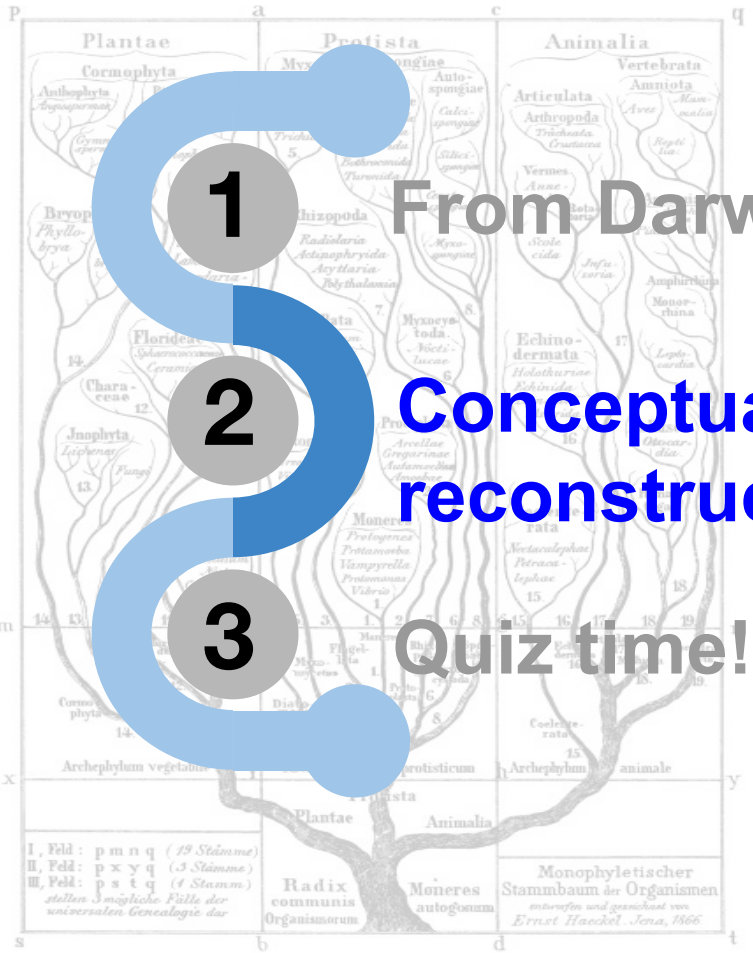
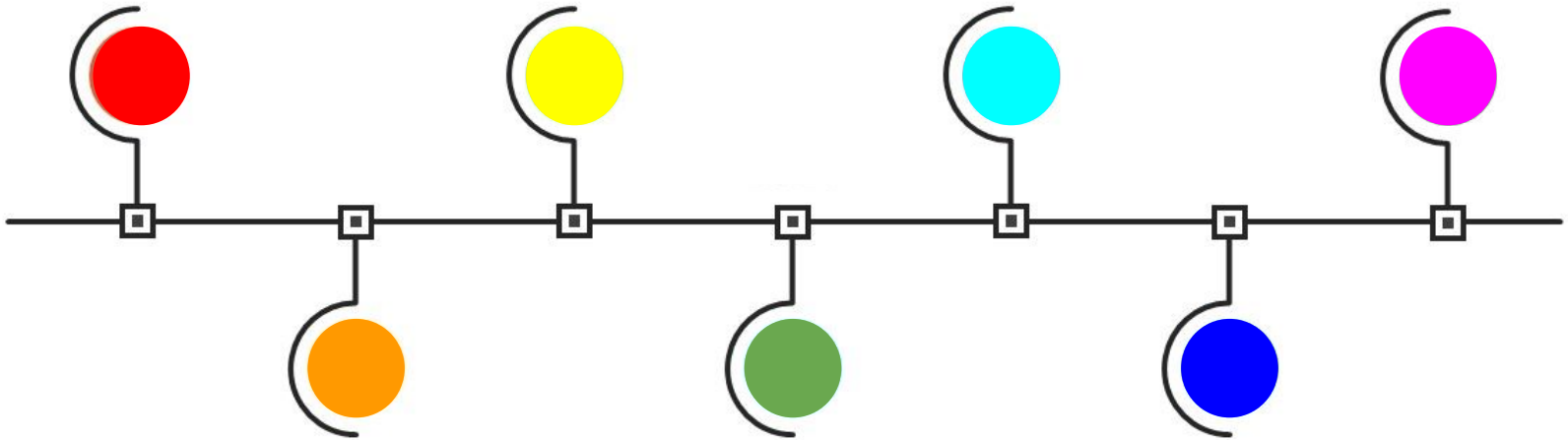


1. From Darwin to phylogenomics
2. **Conceptual framework for phylogenomic reconstruction**
3. Quiz time!



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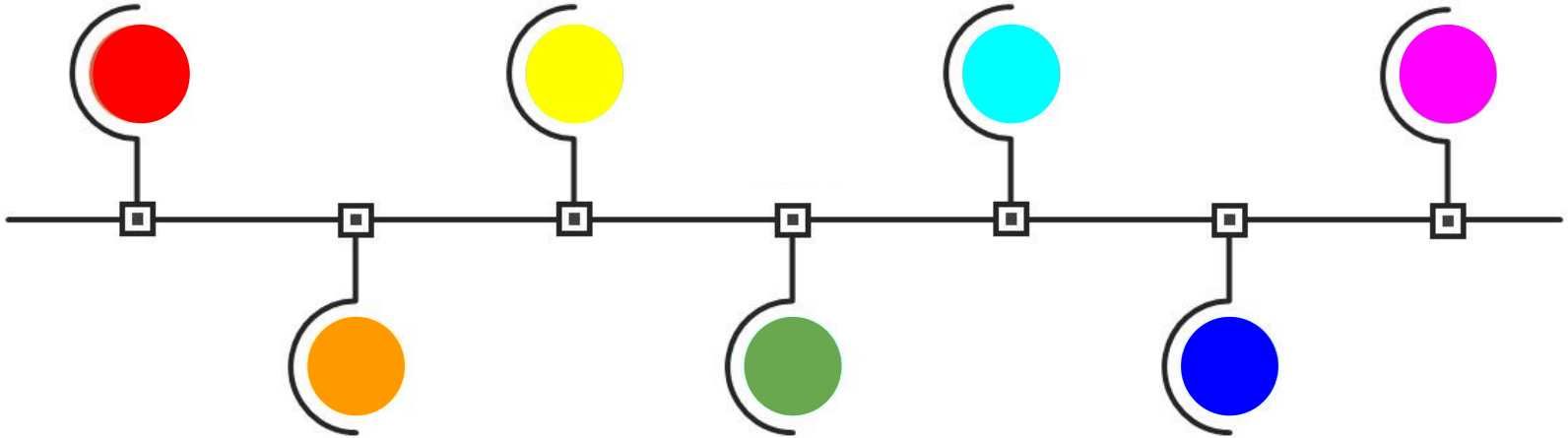

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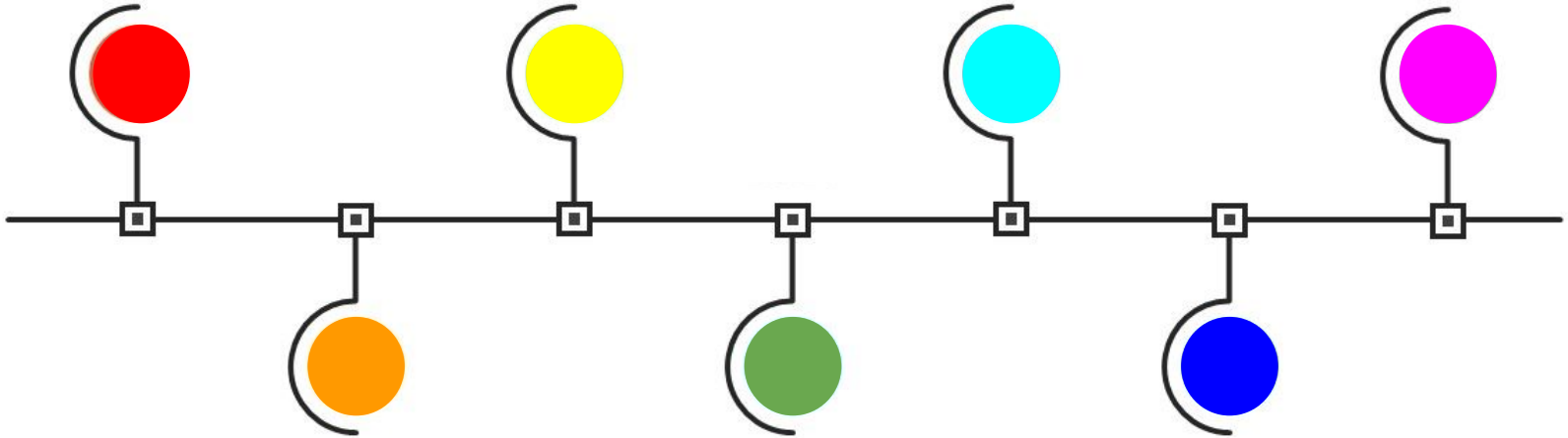
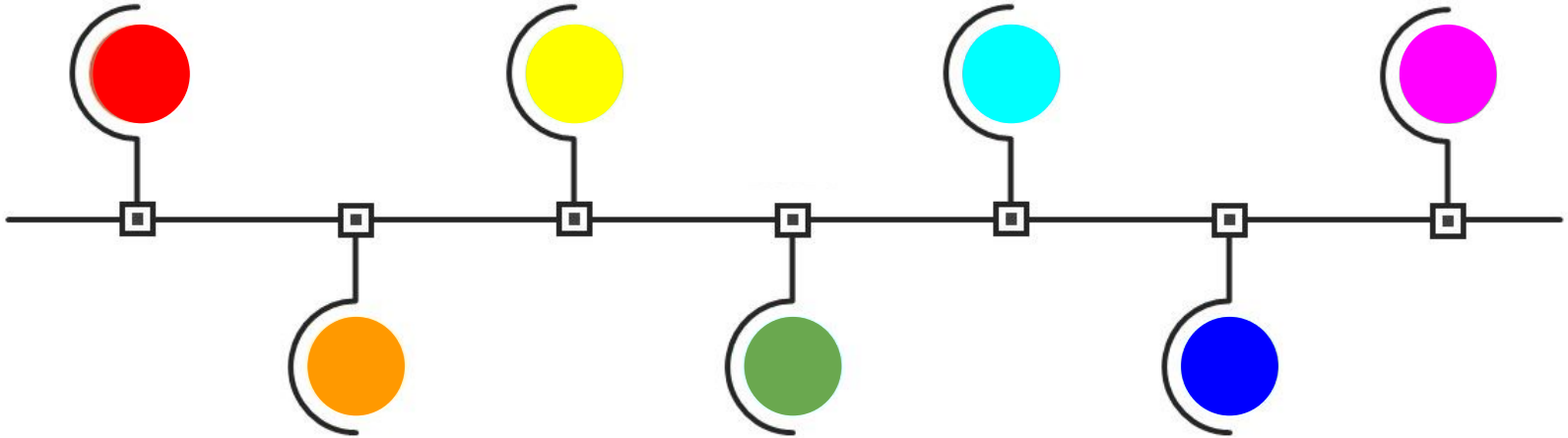


02 ORTHOLOGY INFERENCE

01 DATA

03 ALIGNMENT & TRIMMING



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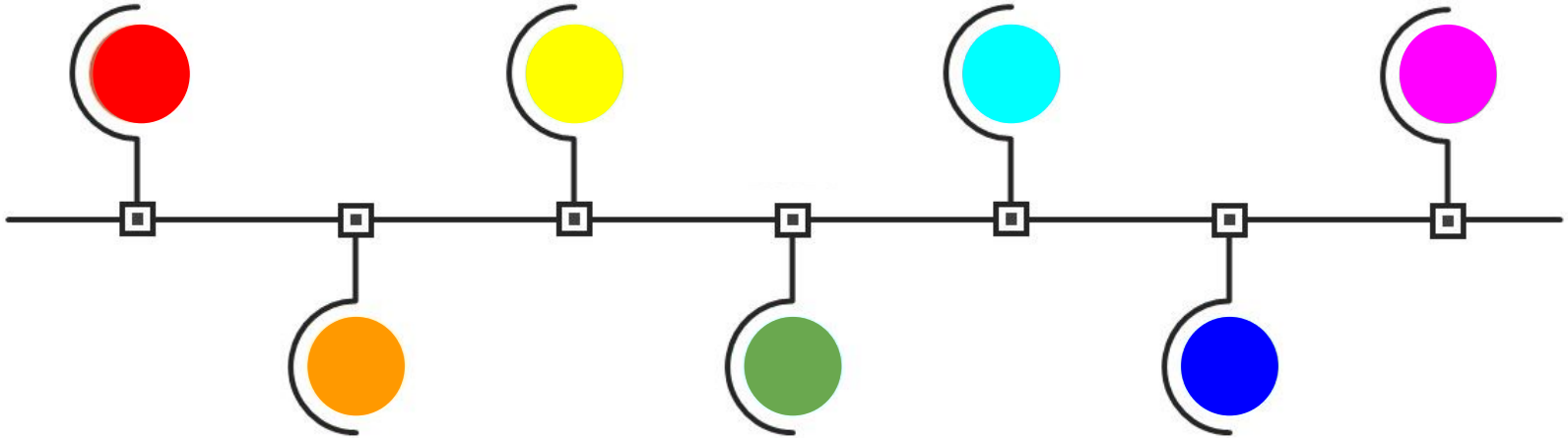

02 ORTHOLOGY INFERENCE

04 PHYLOGENOMIC SUBSAMPLING

01 DATA

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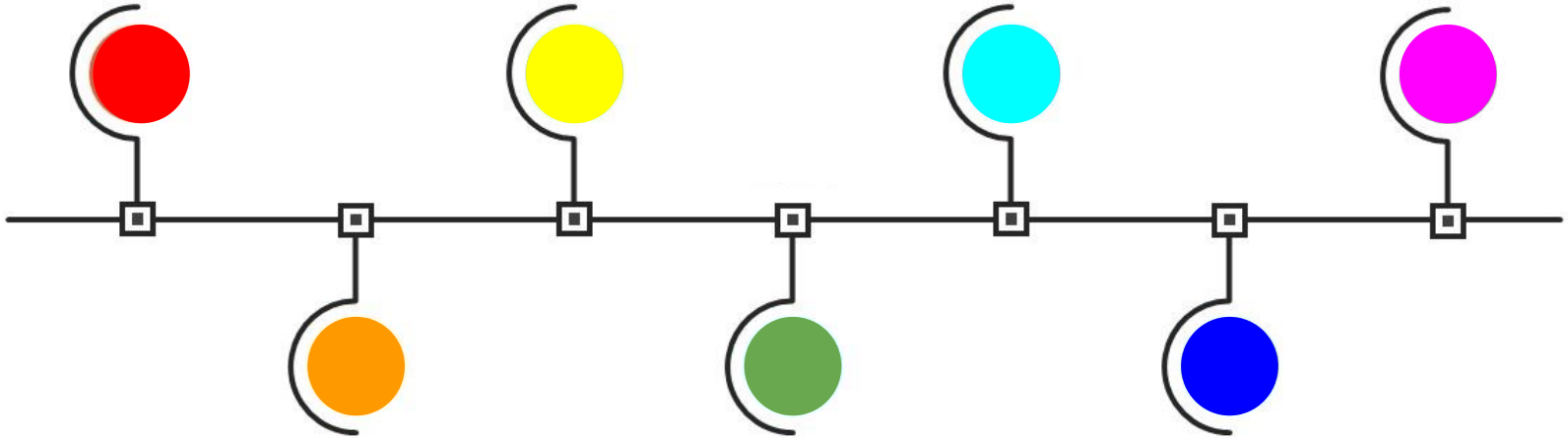
05 SUPERMATRIX VS INDIVIDUAL GENES



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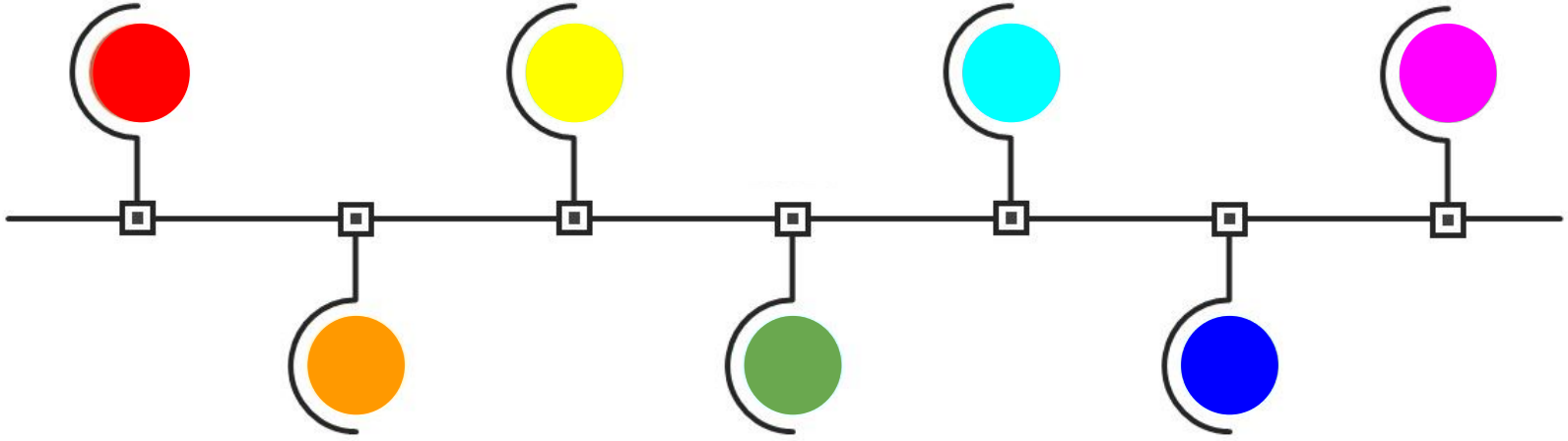
06 MODEL SELECTION & PHYLOGENETIC INFERENCE



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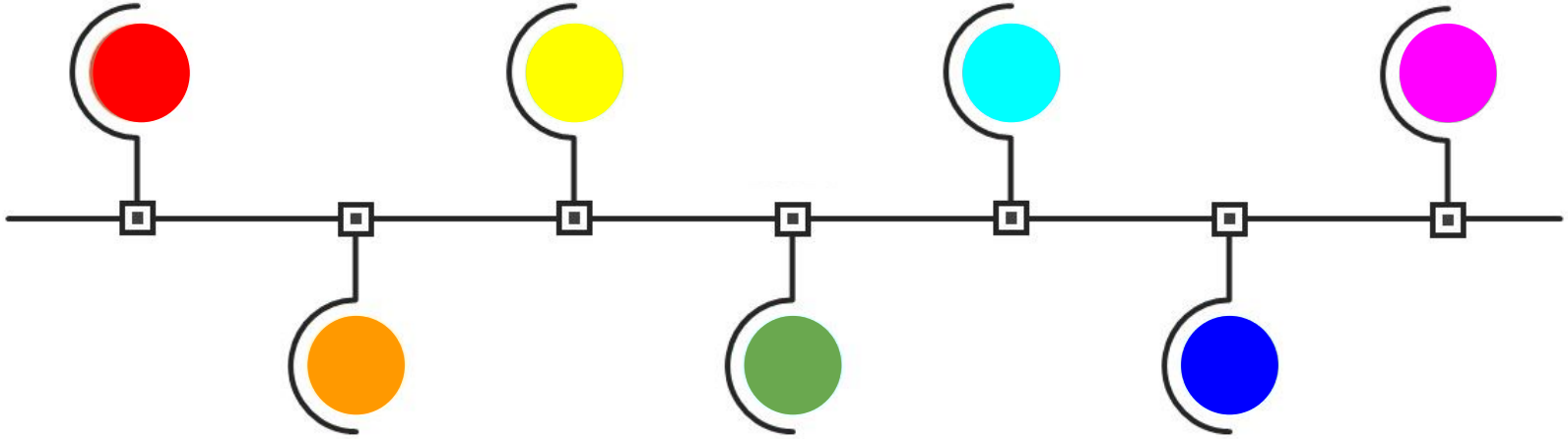
06 MODEL SELECTION & PHYLOGENETIC INFERENCE

07 TESTING THE ROBUSTNESS OF YOUR TREE



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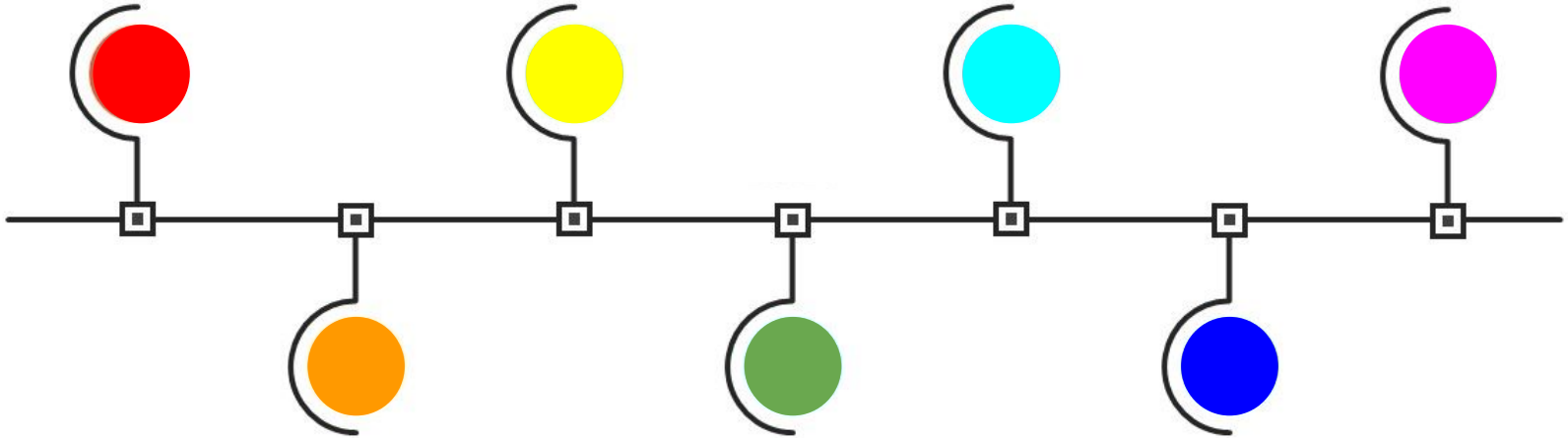

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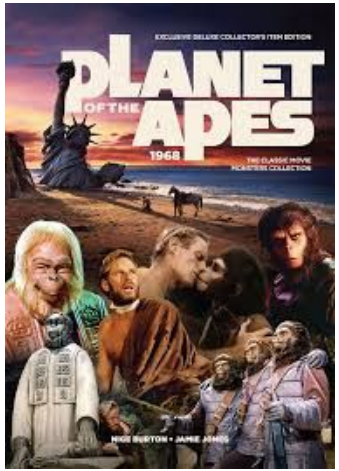

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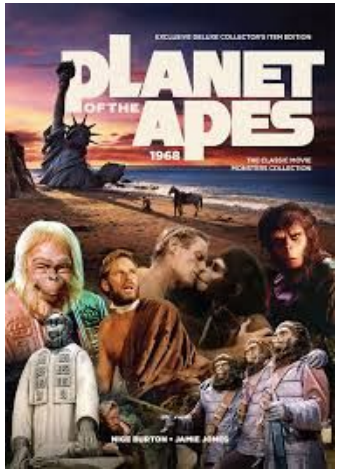

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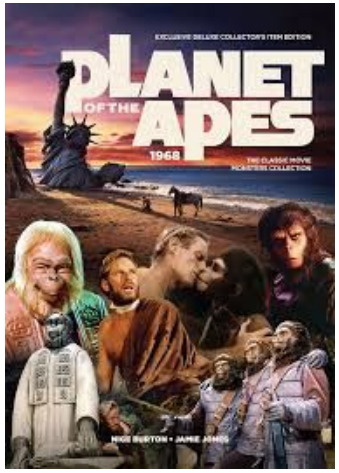

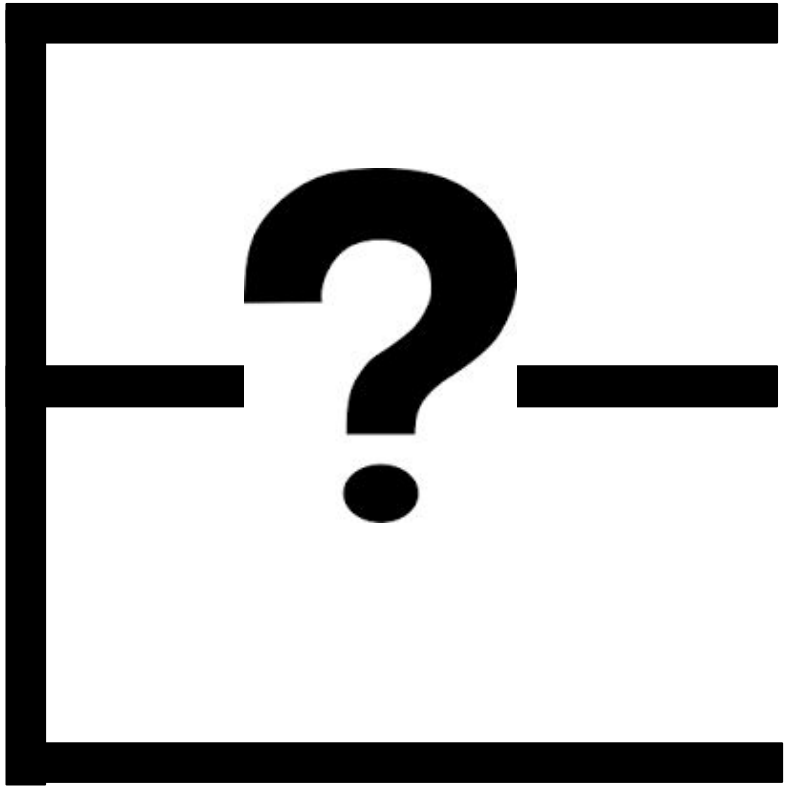

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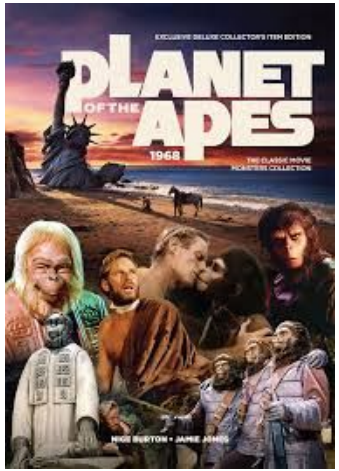

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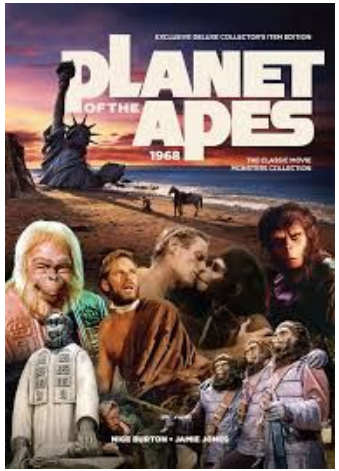

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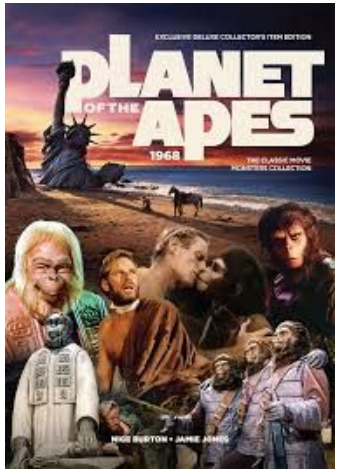

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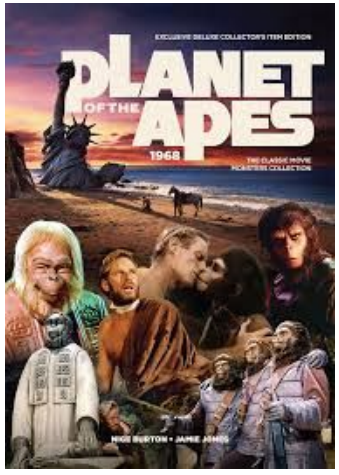

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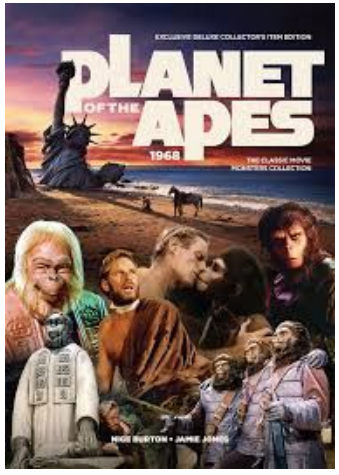

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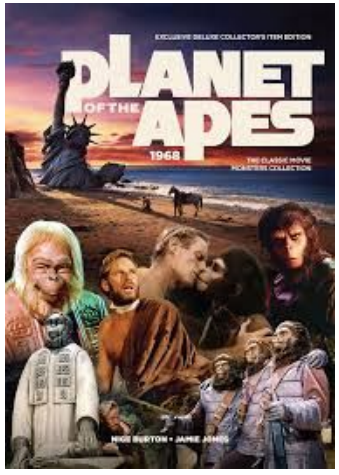

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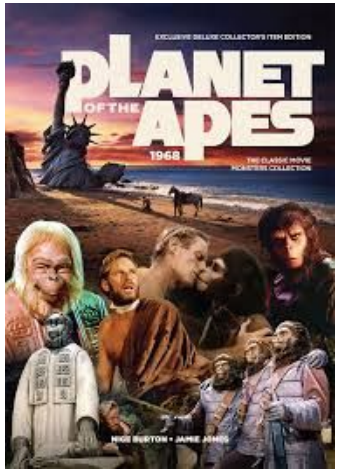

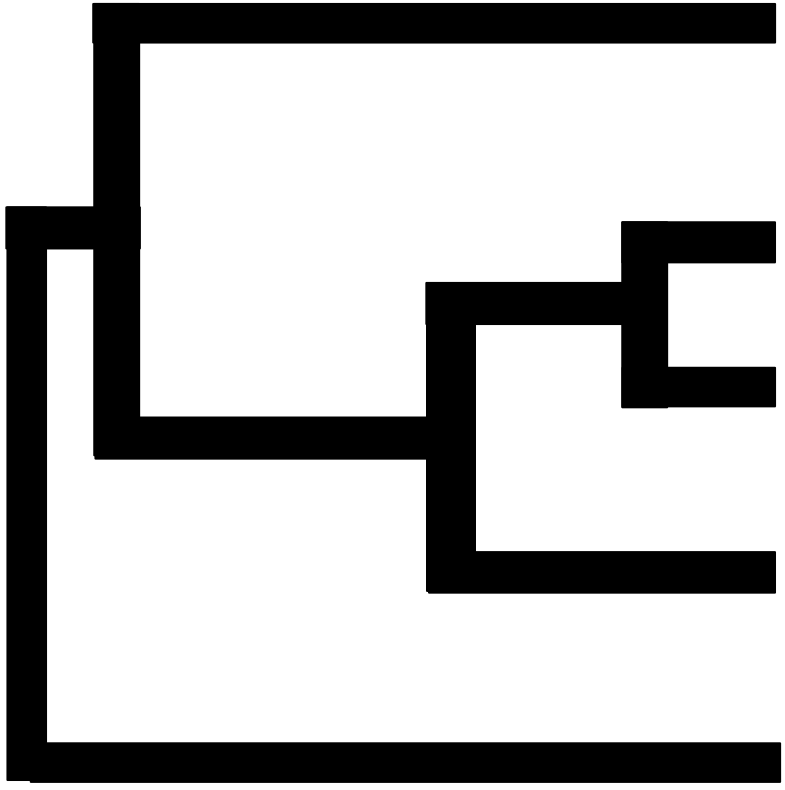

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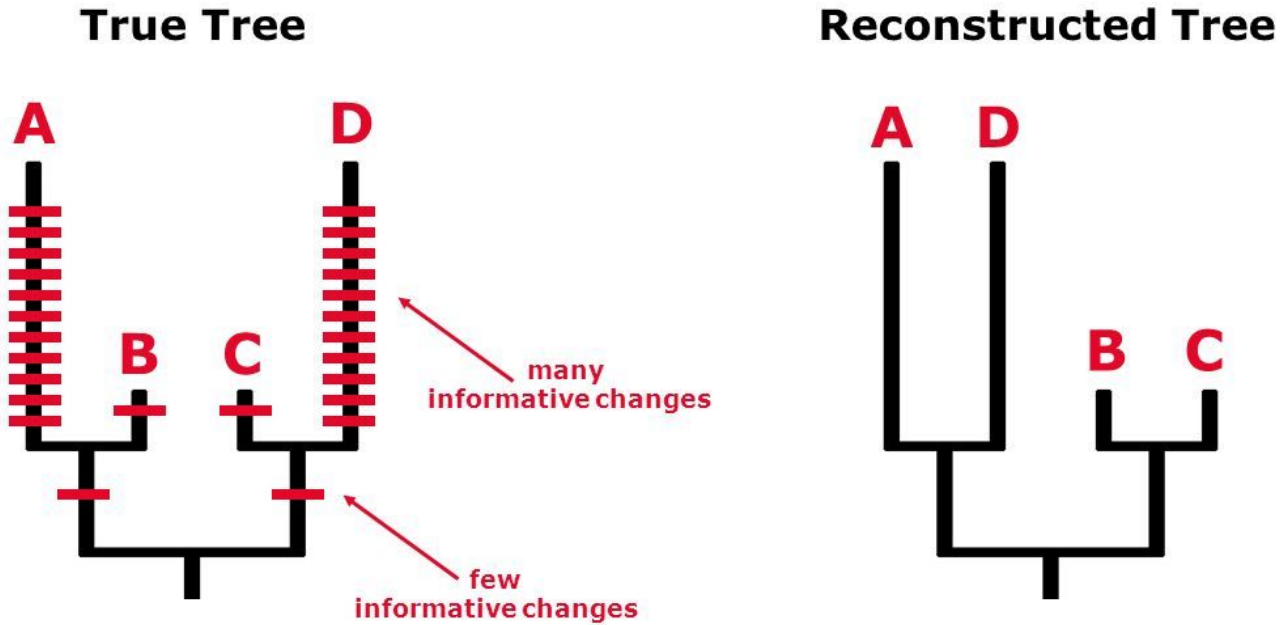
Incomplete, biased, or improper **taxon sampling** can lead to misleading results in reconstructing evolutionary relationships.

Long Branch Attraction

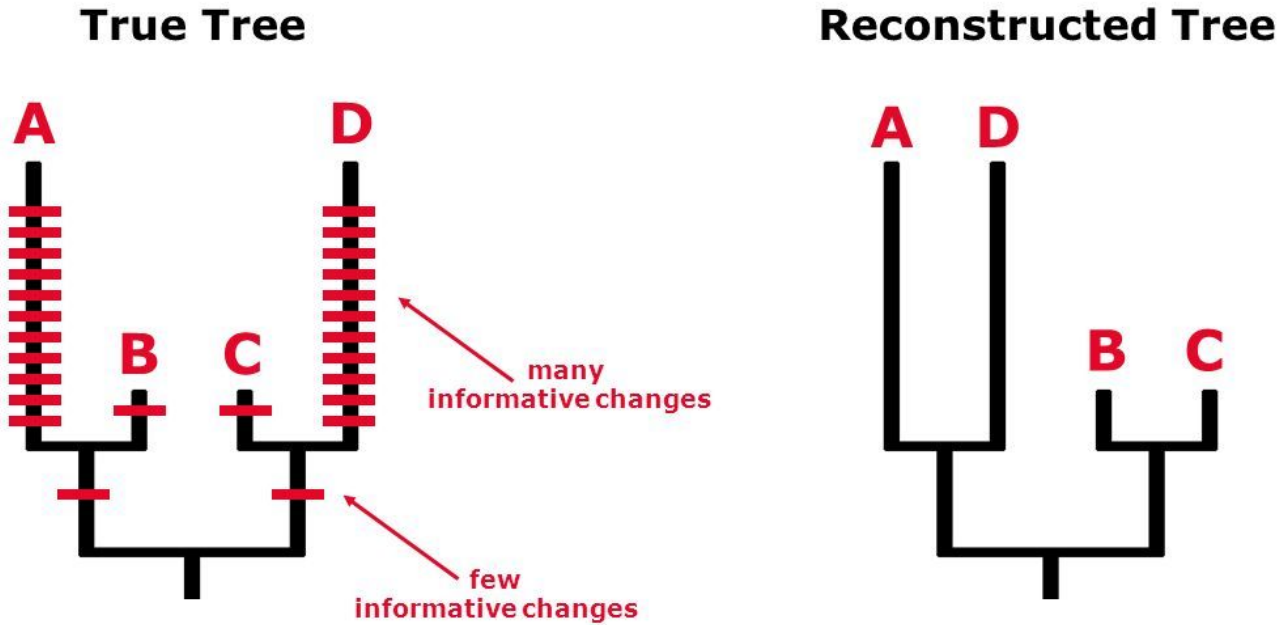


01 DATA

Incomplete, biased, or improper **taxon sampling** can lead to misleading results in reconstructing evolutionary relationships.

Long Branch Attraction

Outgroups / Fast-evolving lineages / Missing data



01 DATA

Source of your data

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GENOMES

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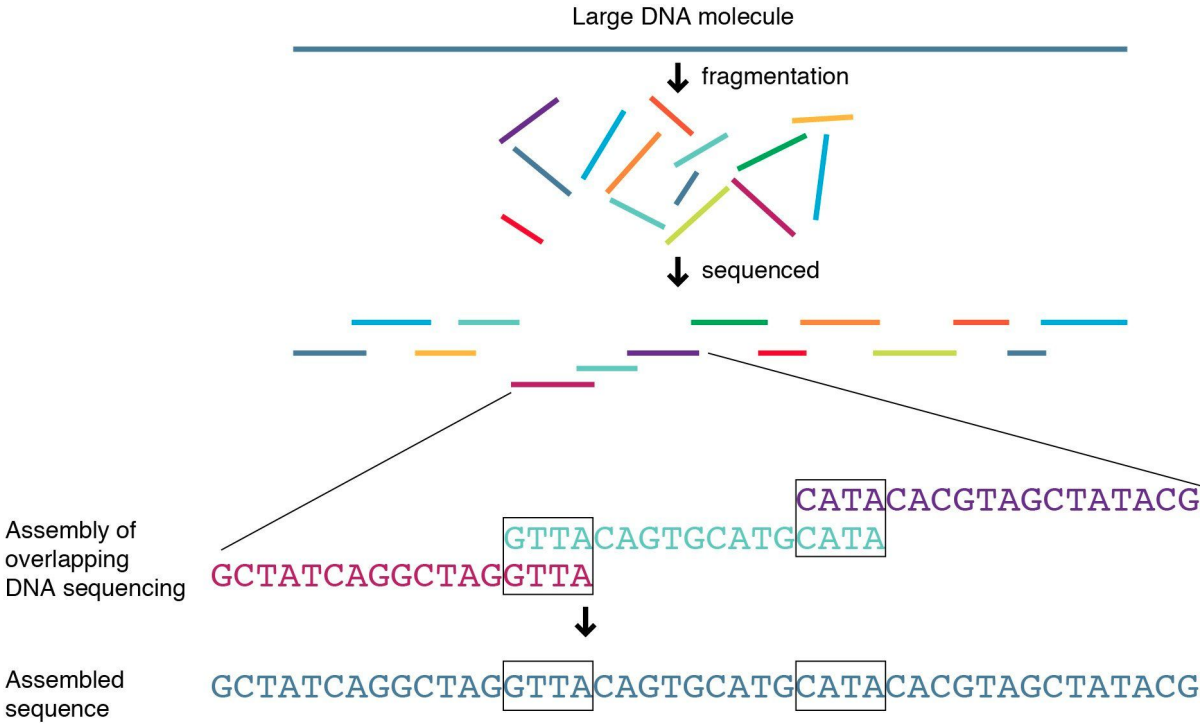

https://knowgenetics.org/whole-genome-sequencing/

- Assembled and annotated.
- Coding genes are retrieved (longest isoform) -> this is your dataset!

01 DATA

Source of your data

GENOMES

Pros:

- Very large set of genetic markers
- Good identification of full-length genes, less chimeras (if the assembly and annotation are of good quality)
- Good for shallow and deep evolutionary distances
- Ethanol-fixed tissue OK (for draft genomes)

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Pros:

- Very large set of genetic markers
- Good identification of full-length genes, less chimeras (if the assembly and annotation are of good quality)
- Good for shallow and deep evolutionary distances
- Ethanol-fixed tissue OK (for draft genomes)

Cons:

- Annotation may vary quite a lot between species (source, software, etc), may not be comparable.
- Expensive (money and computing time)
- More difficult to have a high number of species
- Fresh tissue needed (for chromosome-level genomes)

01 DATA

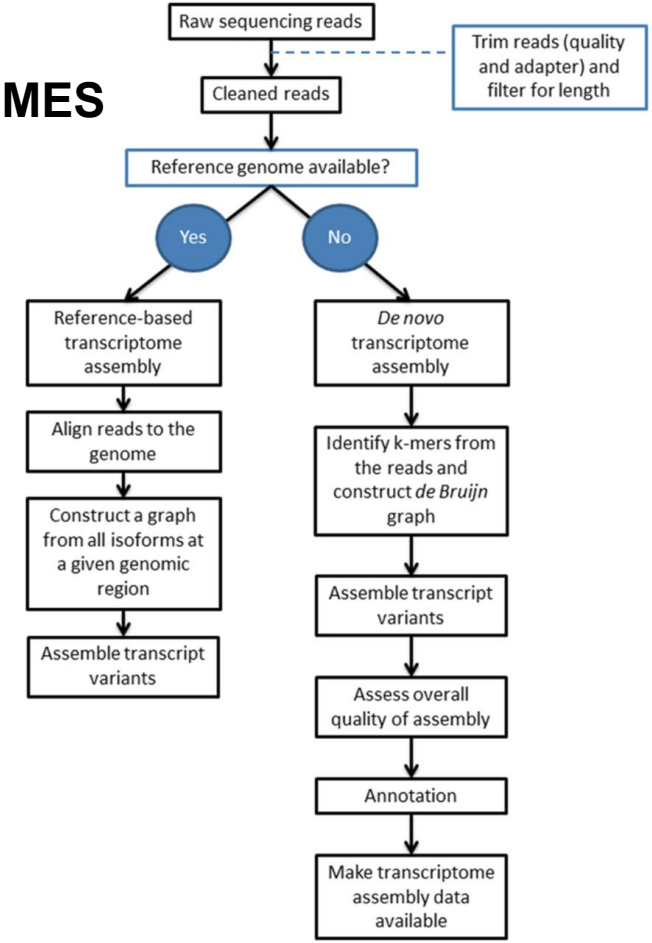
Source of your data

TRANSCRIPTOMES

01 DATA

Source of your data

TRANSCRIPTOMES



Moreton et al. 2016

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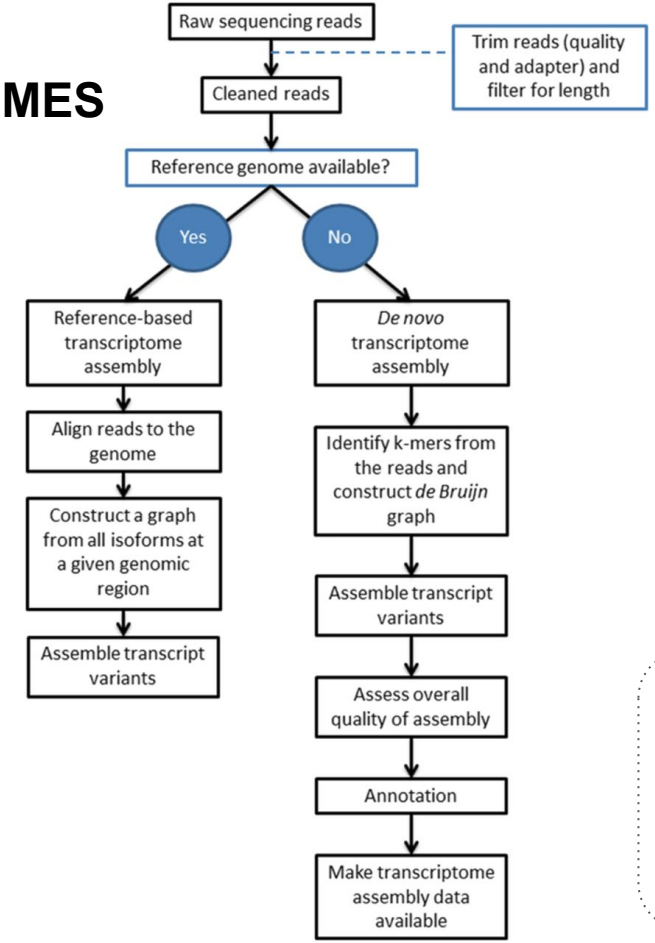
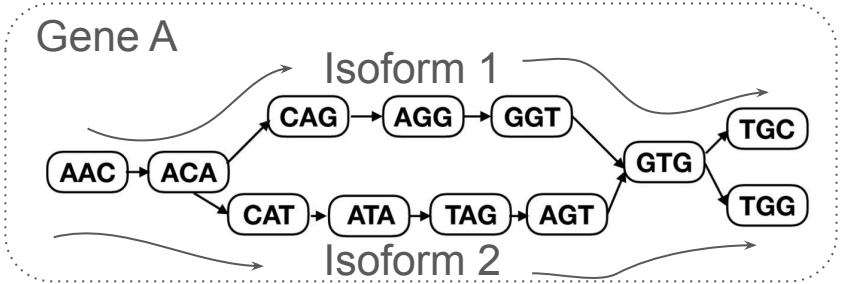


- Assembled de novo

De Bruijn Graph



Moreton et al. 2016

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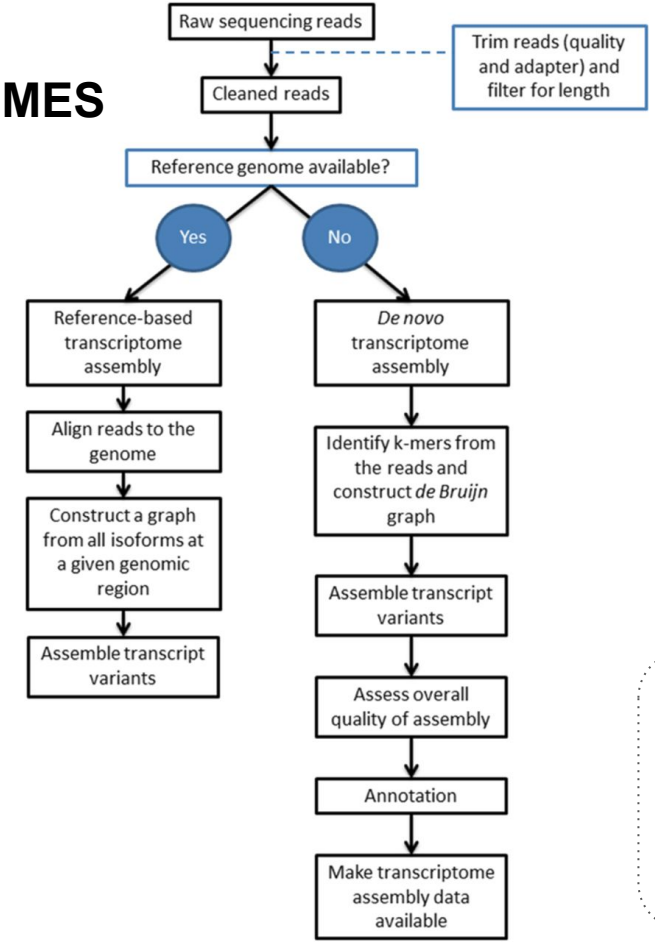

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- Coding genes are retrieved (after inferring ORFs; longest isoform) -> this is your dataset!

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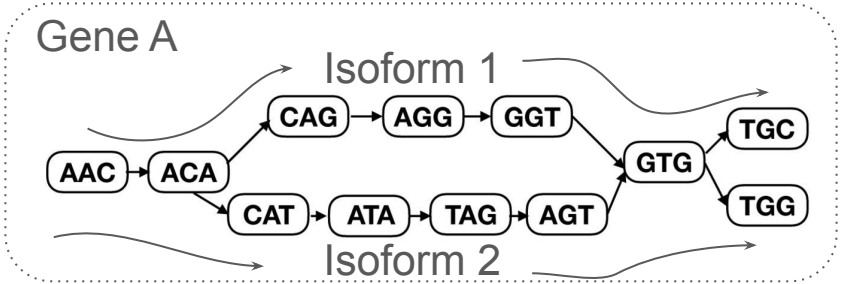

Moreton et al. 2016

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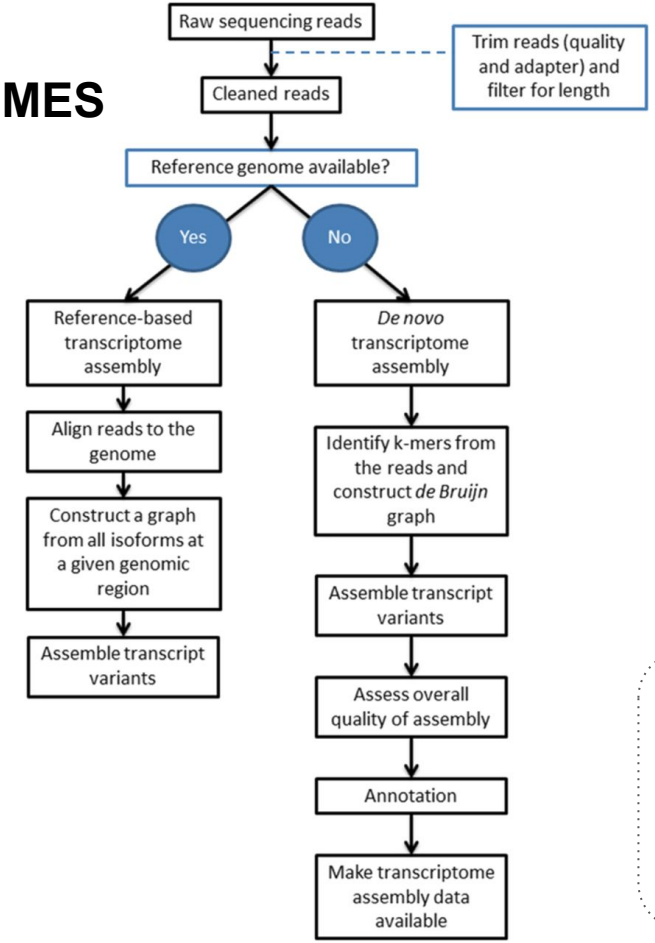

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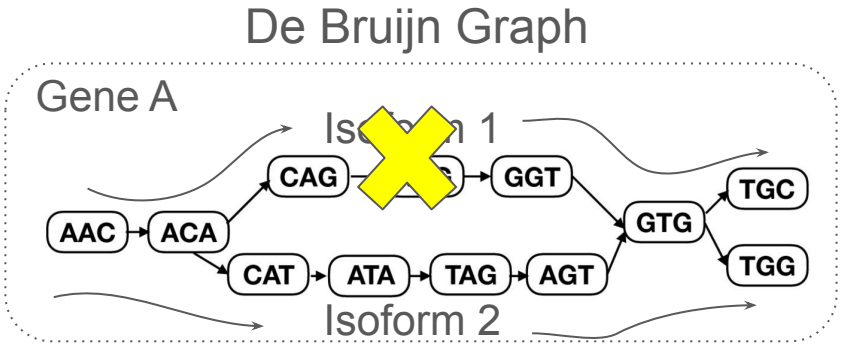

Moreton et al. 2016

01 DATA

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TRANSCRIPTOMES

Pros:

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- Much cheaper than sequencing genomes -> easier to have a high number of species
- Not dependent upon a reference genome
- Good for shallow and deep evolutionary distances

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Source of your data

TRANSCRIPTOMES

Pros:

- Very large set of genetic markers
- Much cheaper than sequencing genomes -> easier to have a high number of species
- Not dependent upon a reference genome
- Good for shallow and deep evolutionary distances

Cons:

- Incomplete identification of full-length genes and single-copy transcripts.
- Potential misassembly of transcripts (especially when duplicates are present)
- Missing data as a product of the transcriptome representing a snapshot of expression (but this could also affect genome annotation)
- Fresh tissue needed

01 DATA

Source of your data

ULTRACONSERVED ELEMENTS (UCEs)

01 DATA

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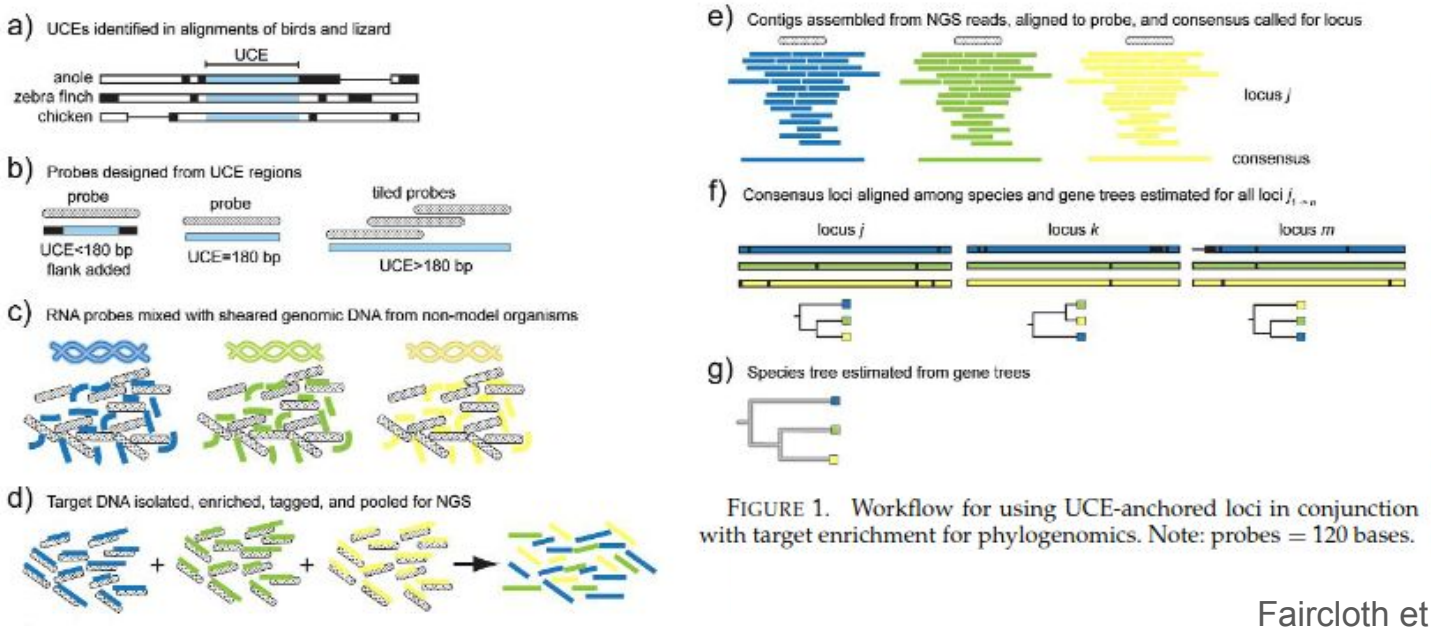

FIGURE 1. Workflow for using UCE-anchored loci in conjunction with target enrichment for phylogenomics. Note: probes = 120 bases.

Faircloth et al. 2012

The UCEs are designed a priori -> after hybridization, sequencing, assembly and mapping, this is your data!

01 DATA

Source of your data

ULTRACONSERVED ELEMENTS (UCEs)

Pros:

- Medium-large set of genetic markers
- Much cheaper than sequencing genomes -> easier to have a high number of species
- Not dependent upon a reference genome
- Tissues fixed in EtOH or museum specimens are OK

01 DATA

Source of your data

(Lisa Pokorny's talk on 31st Jan)

ULTRACONSERVED ELEMENTS (UCEs)

Pros:

- Medium-large set of genetic markers
- Much cheaper than sequencing genomes -> easier to have a high number of species
- Not dependent upon a reference genome
- Tissues fixed in EtOH or museum specimens are OK

Cons:

- Limited availability of markes outside the designed ones.
- Potential misassembly (if probes are designed with a limited amount of species)
- Retrieval success dependent on DNA quality
- Usefulness of markers known a posteriori
- No proper orthology inference

01 DATA

Source of your data

REDUCED REPRESENTATION (RADseq, GBS)

01 DATA

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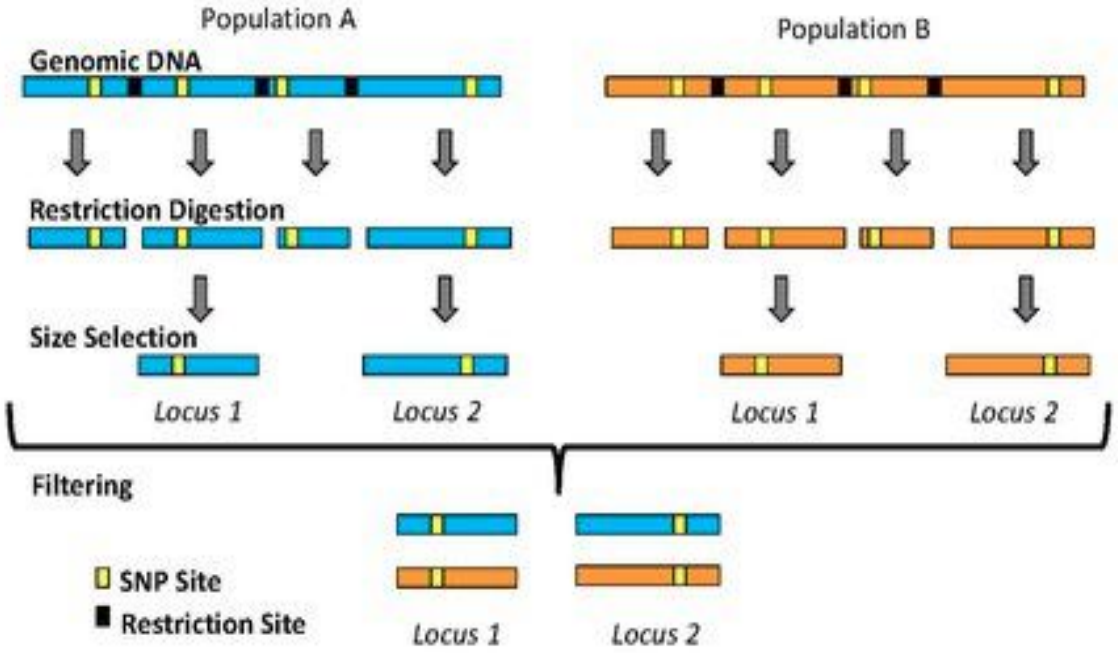


After digestion, sequencing and mapping, this is your data!

01 DATA

Source of your data

REDUCED REPRESENTATION (RADseq, GBS)

Pros:

- The cheapest of the methods
- Not dependent upon a reference genome
- Samples fixed in ethanol OK
- Markers distributed evenly across the genome

01 DATA

Source of your data

REDUCED REPRESENTATION (RADseq, GBS)

Pros:

- The cheapest of the methods
- Not dependent upon a reference genome
- Samples fixed in ethanol OK
- Markers distributed evenly across the genome

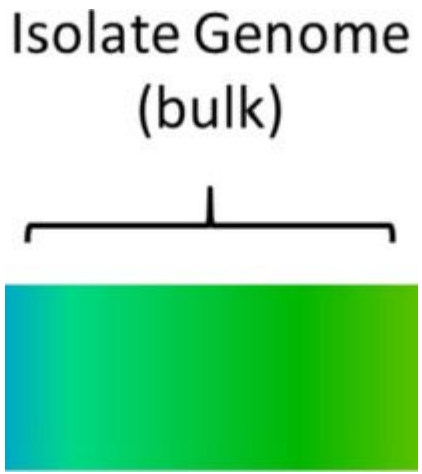
Cons:

- No full genes, only SNPs
- Only for population genomics or phylogeny including closely-related species
- Missing data as a product of the transcriptome representing a snapshot of expression (but this could also affect genome annotation)
- No proper orthology inference

01 DATA

Source of your data

METAGENOMICS/METATRANSCRIPTOMICS



One individual, multiple cells

01 DATA

Source of your data

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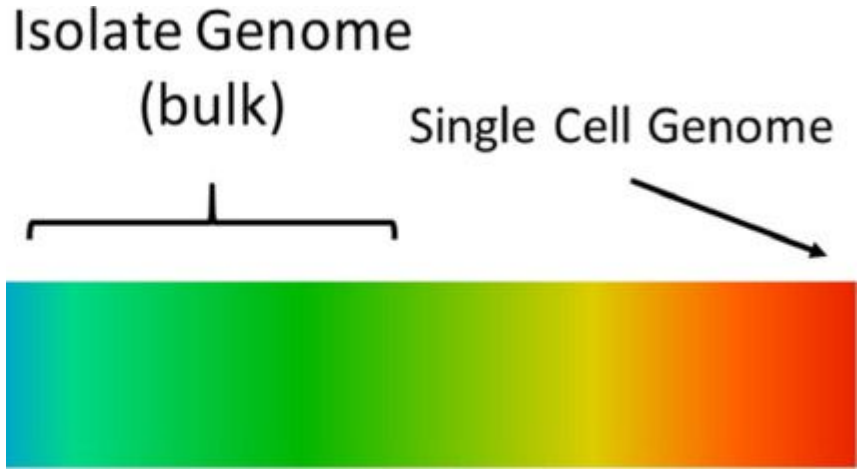

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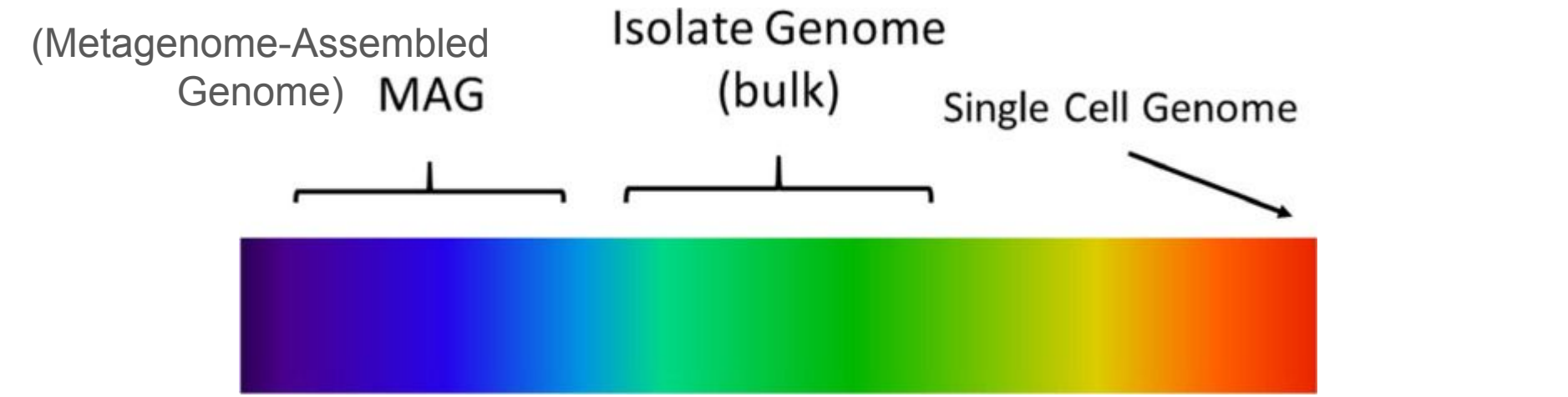

01 DATA

Source of your data

METAGENOMICS - single cell

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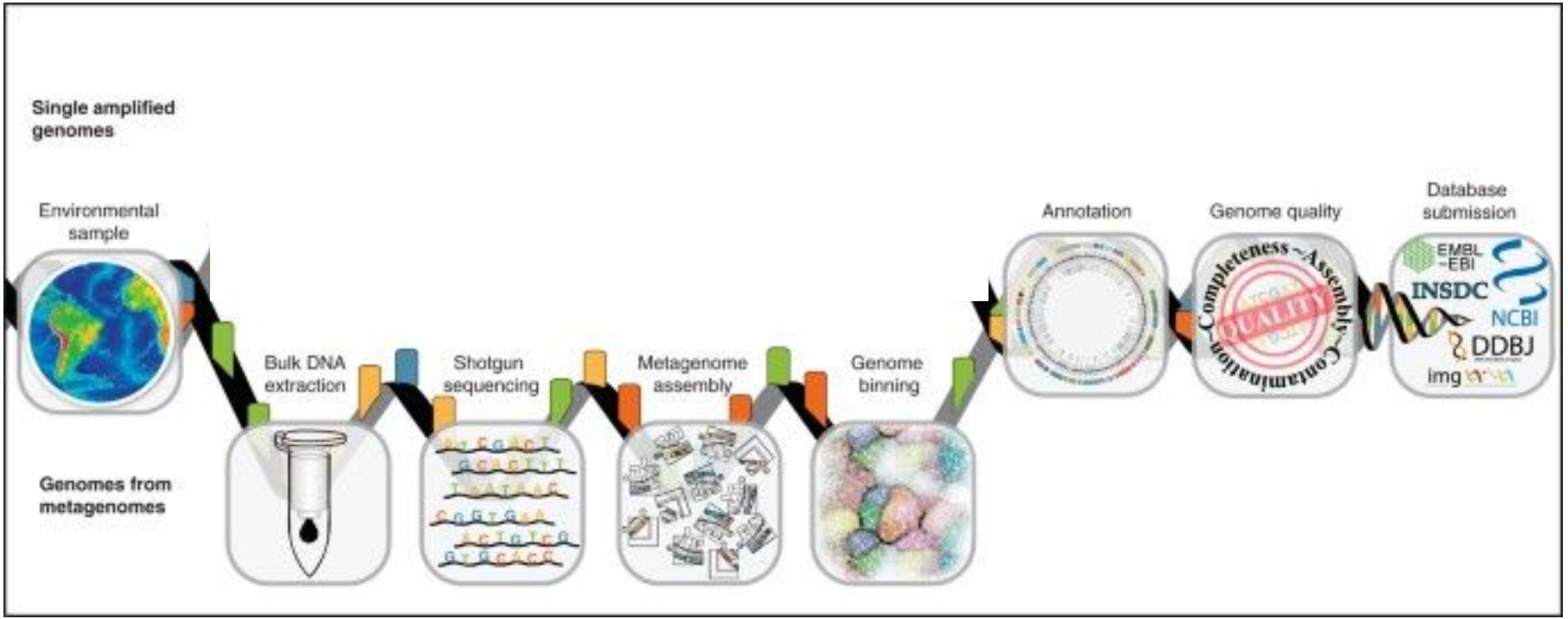

Bowers et al. 2017

01 DATA

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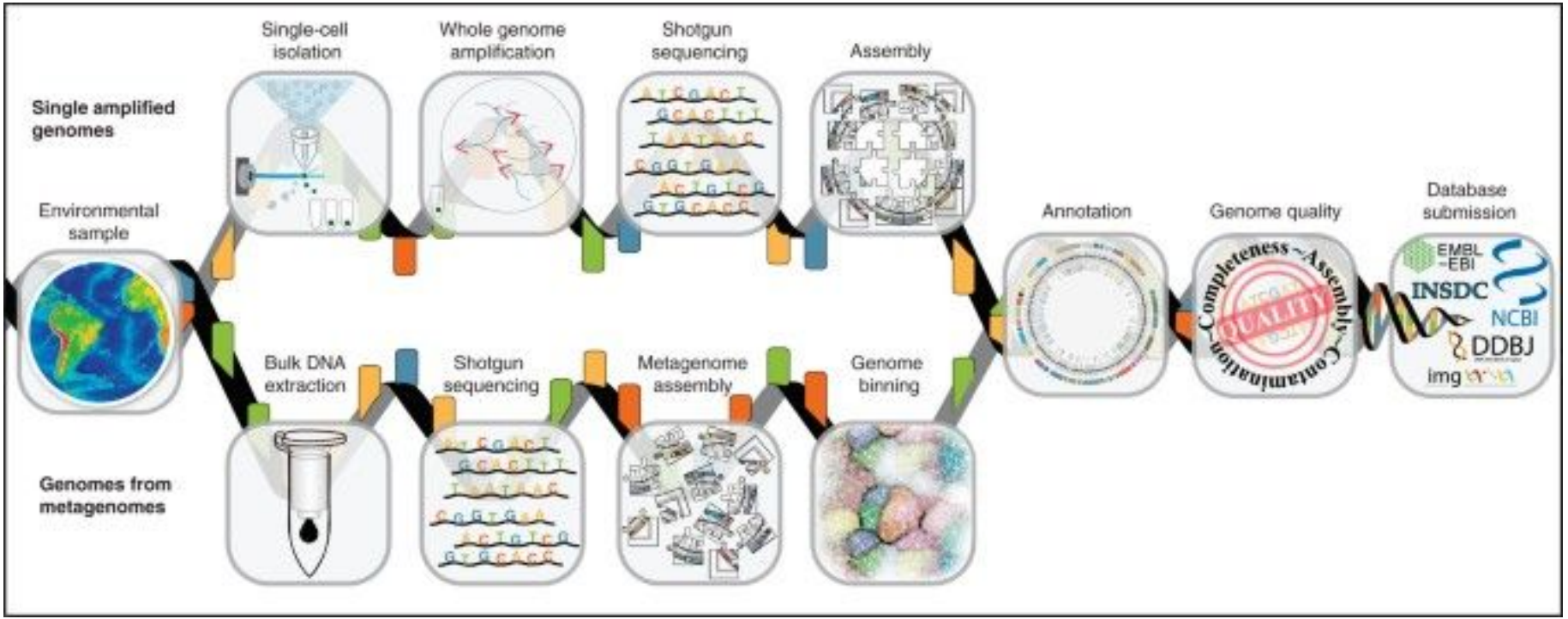
METAGENOMICS - single cell vs MAGs



Bowers et al. 2017

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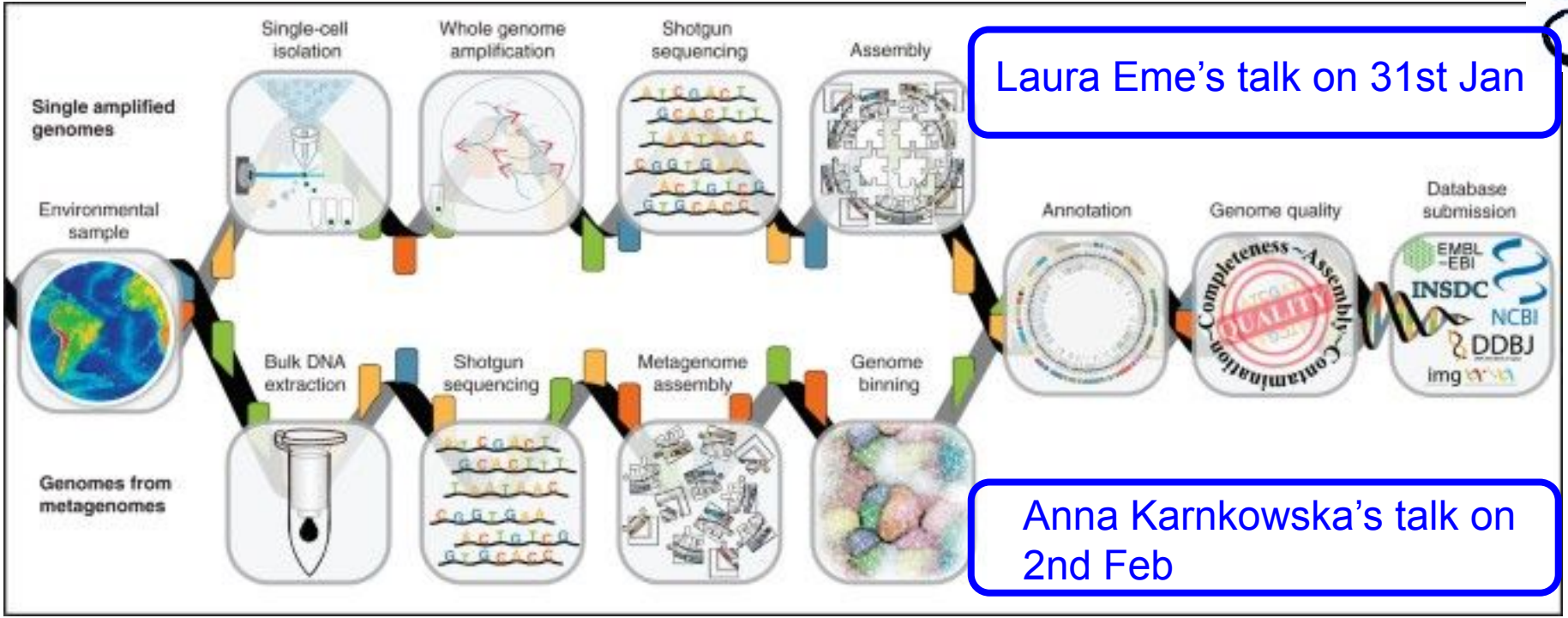

Laura Eme's talk on 31st Jan

Anna Karnkowska's talk on 2nd Feb

Bowers et al. 2017

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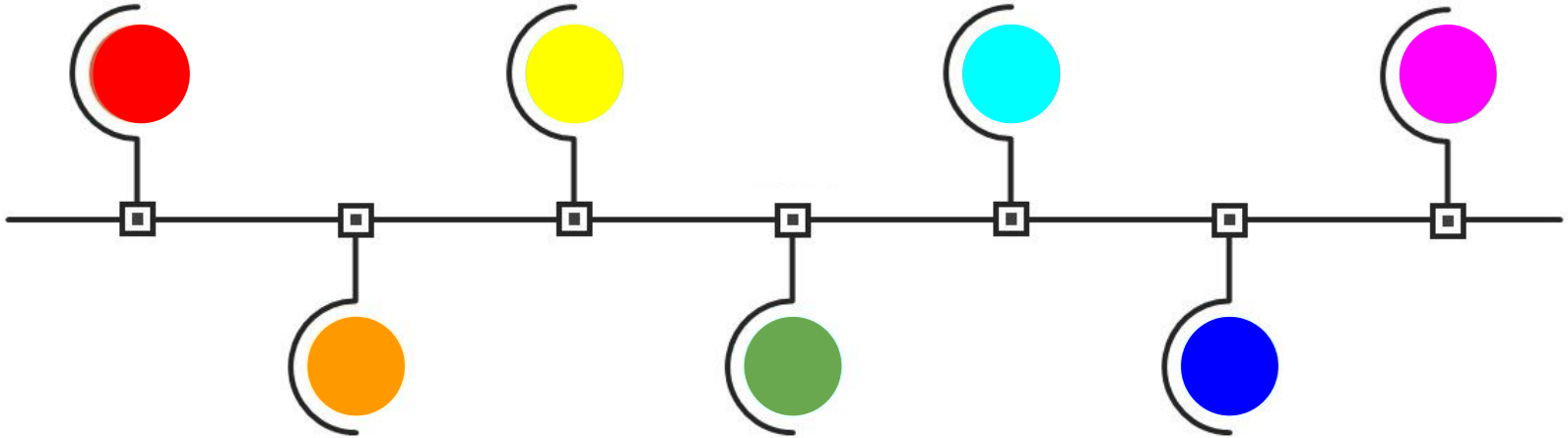

02 ORTHOLOGY INFERENCE

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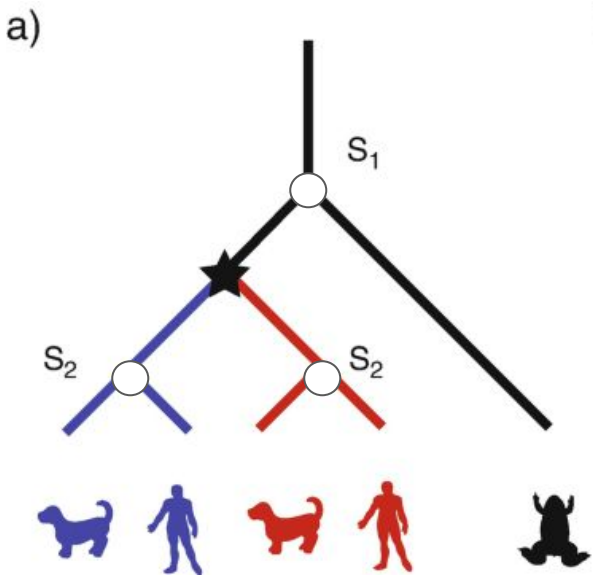
Definitions

- Two genes are **orthologs** if their MRCA is a ***speciation***:○



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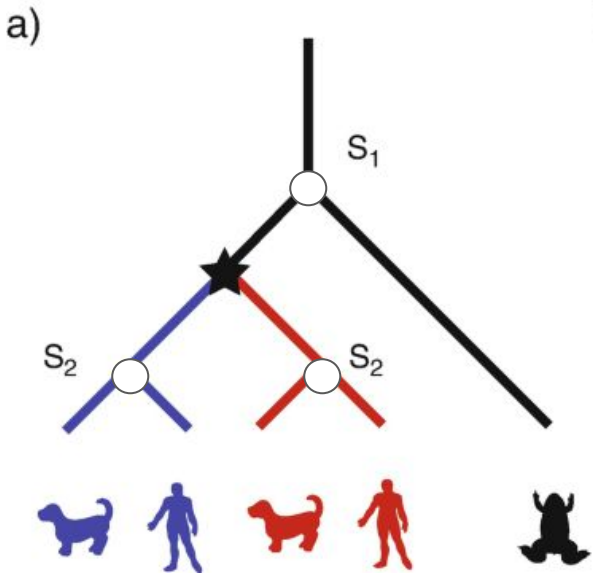

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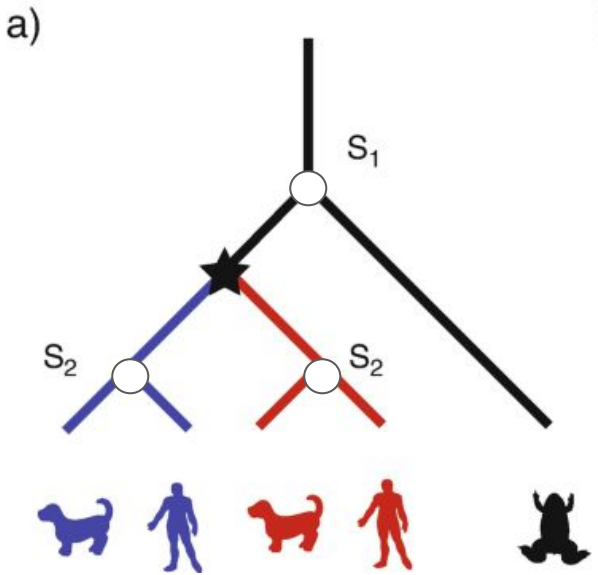
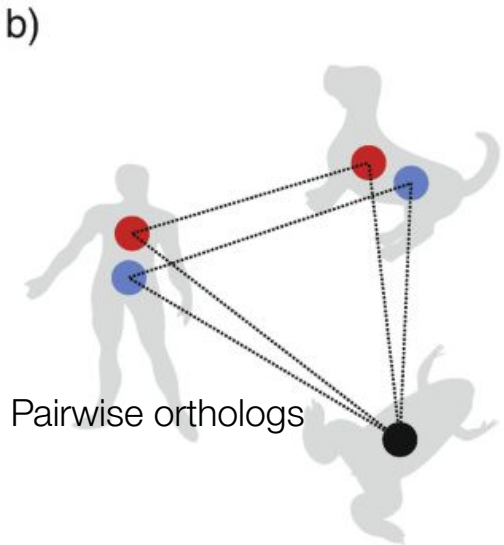
Orthology relationships are inferred *pairwise*





Altenhoff, Glover & Dessimoz 2019

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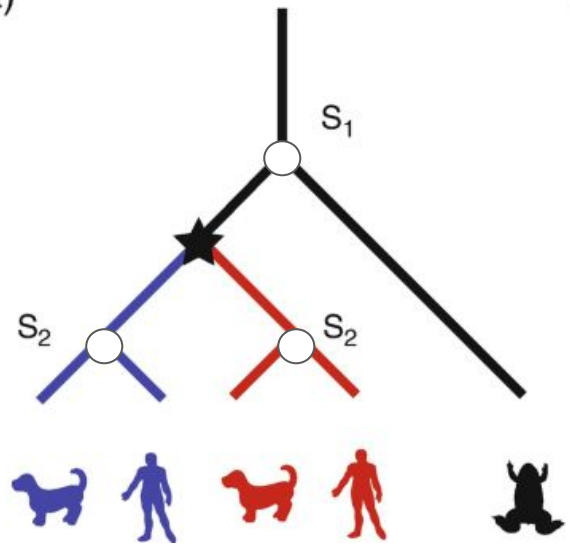
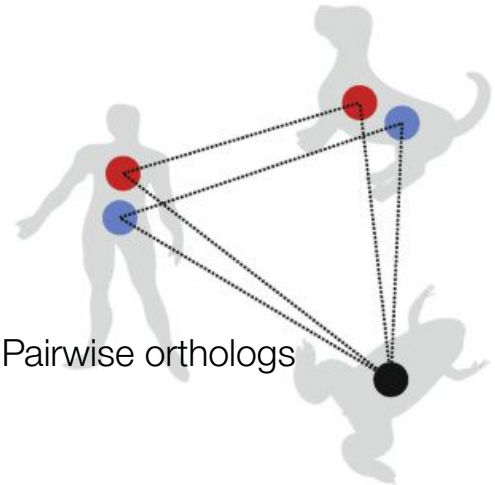


b)



Pairwise orthologs

Orthology relationships are inferred *pairwise*

When we have multiple species, we should consider the concept of *orthogroup*

Altenhoff, Glover & Dessimoz 2019

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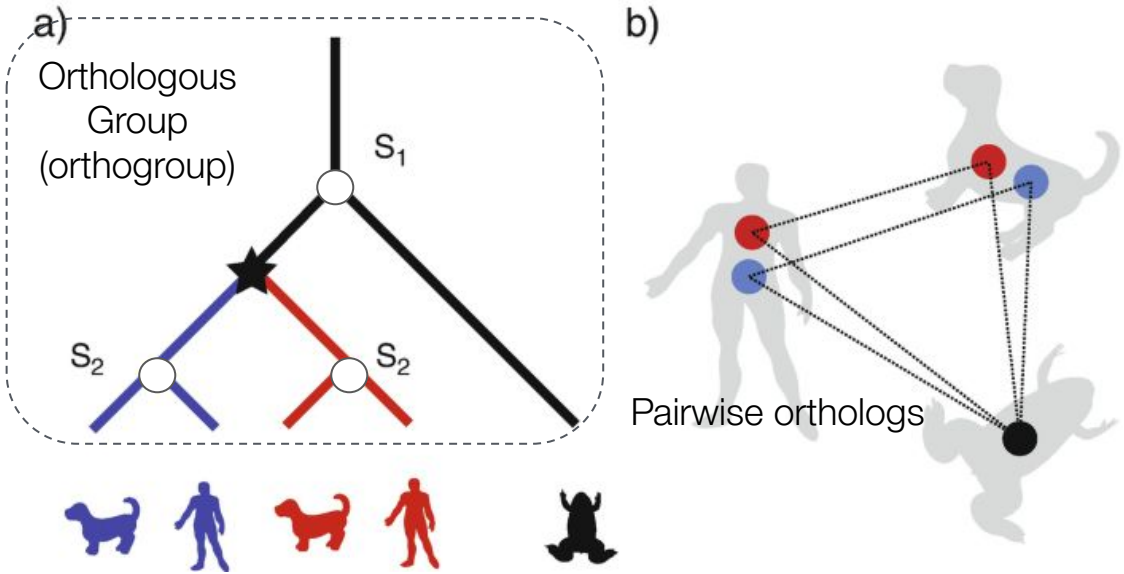

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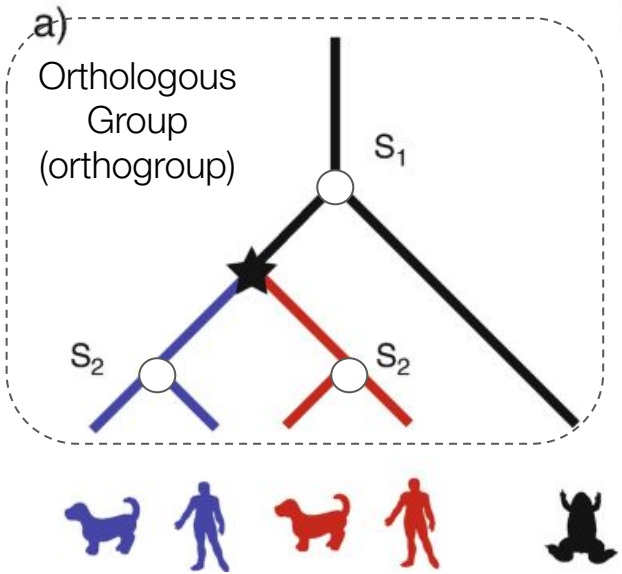

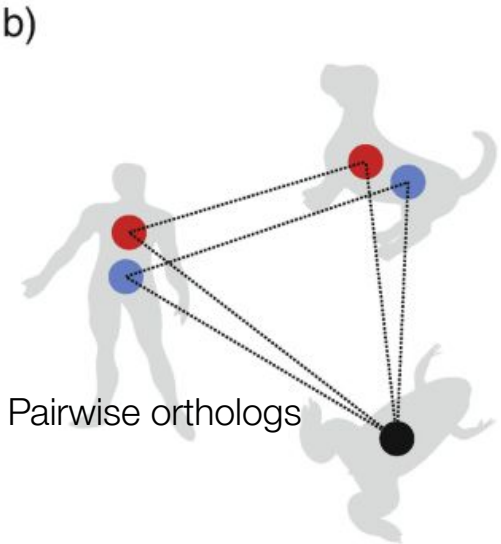

Orthology relationships are inferred *pairwise*

When we have multiple species, we should consider the concept of *orthogroup*

Orthology inference is essential for phylogenomics, as you want to consider only genes that arouse through speciation events

Altenhoff, Glover & Dessimoz 2019

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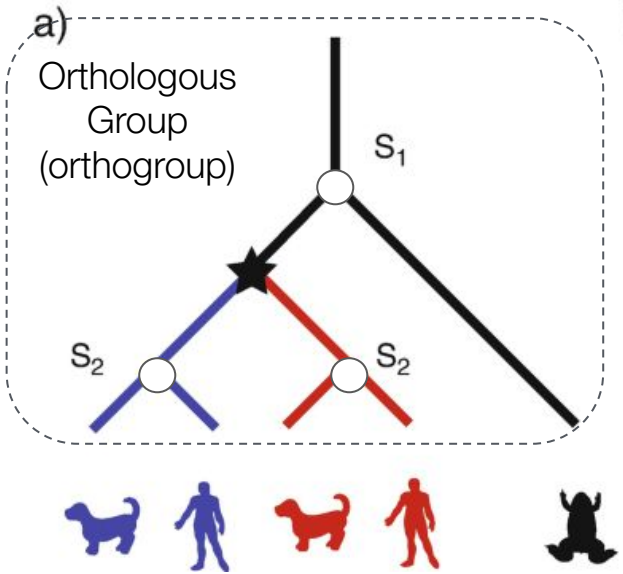

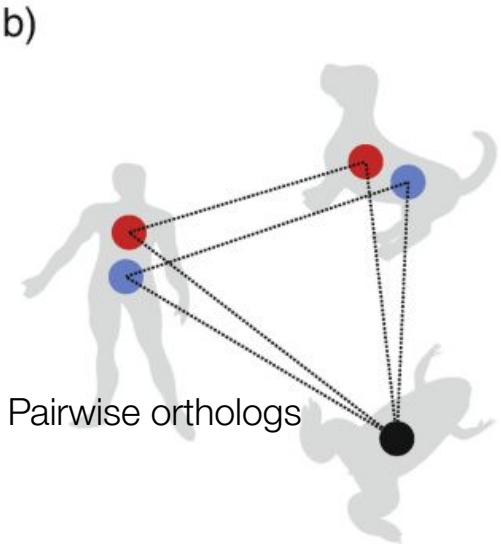

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For phylogenomic inference, we want either:

Altenhoff, Glover & Dessimoz 2019

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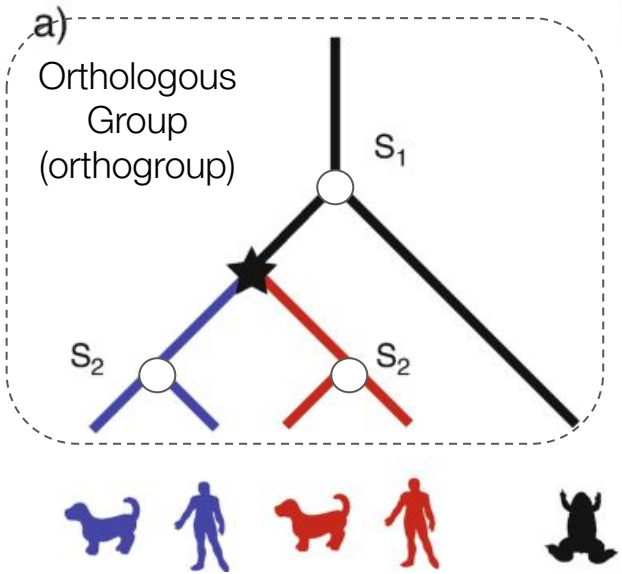

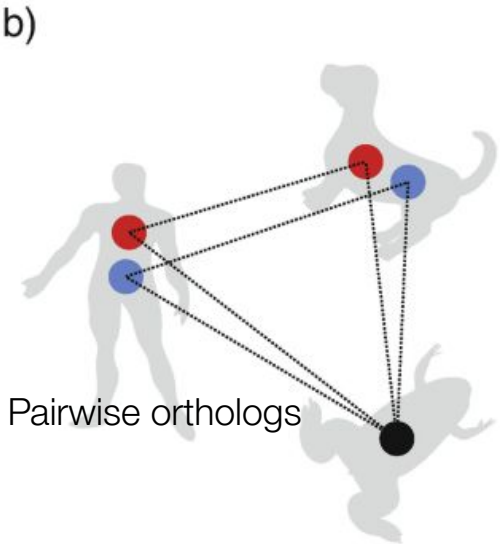

Orthology relationships are inferred *pairwise*

When we have multiple species, we should consider the concept of *orthogroup*

For phylogenomic inference, we want either:

- Single-copy orthogroups (ie, one gene per species)

Altenhoff, Glover & Dessimoz 2019

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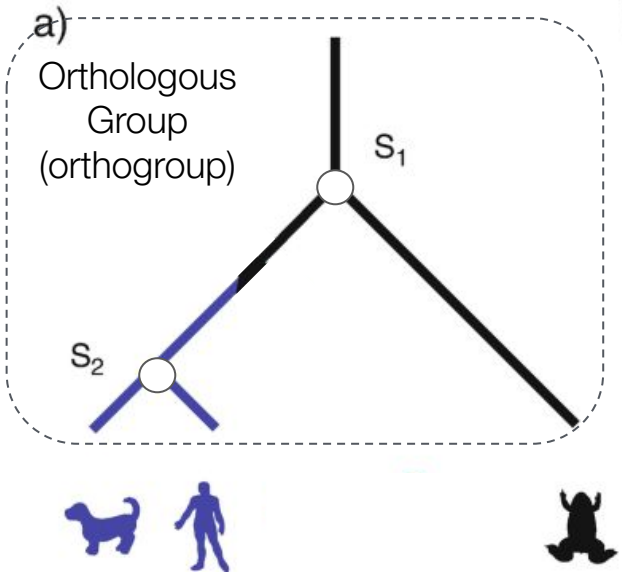

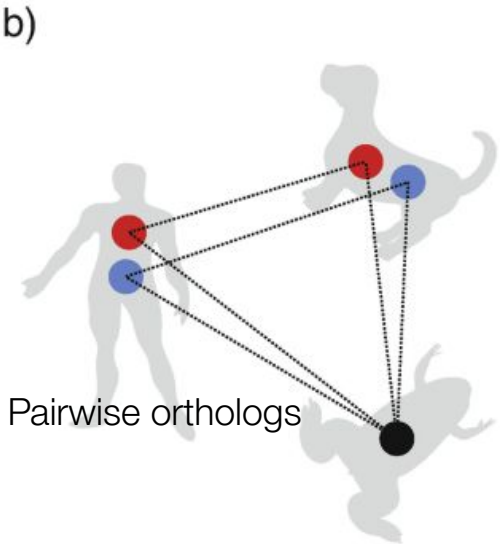

Orthology relationships are inferred *pairwise*

When we have multiple species, we should consider the concept of *orthogroup*

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Altenhoff, Glover & Dessimoz 2019

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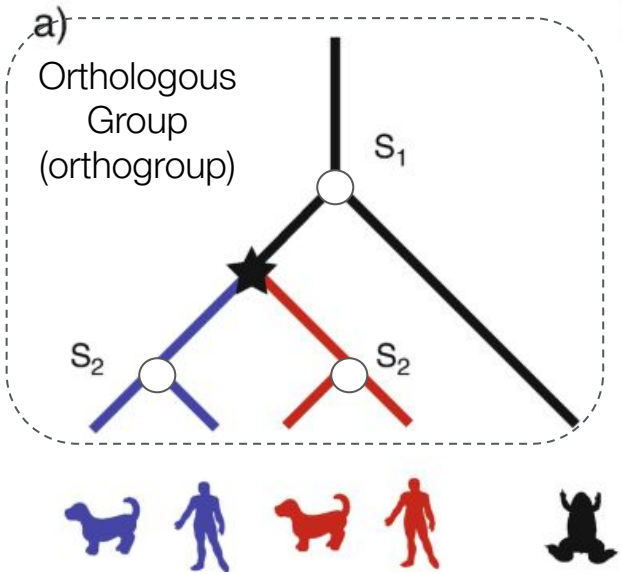

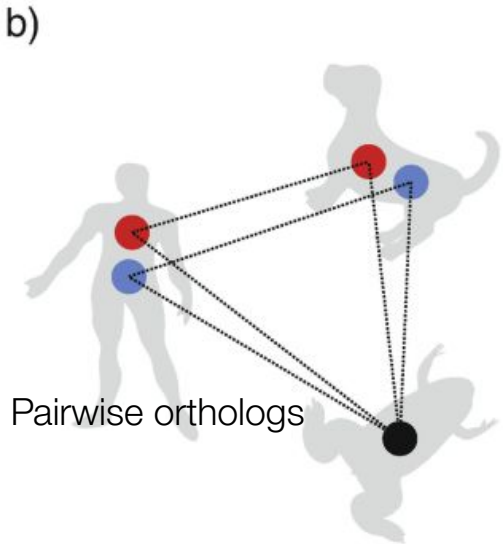

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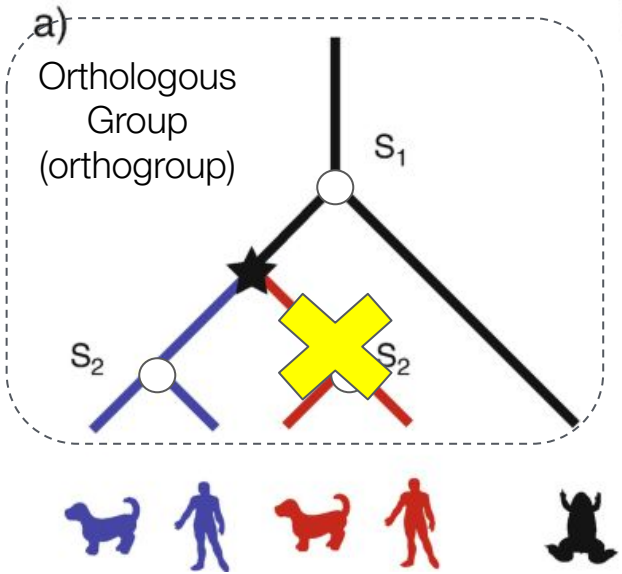

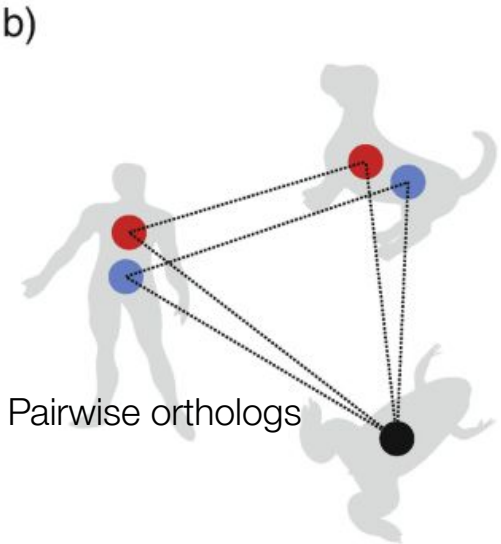

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Altenhoff, Glover & Dessimoz 2019

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Marina Marcet-Houben tomorrow

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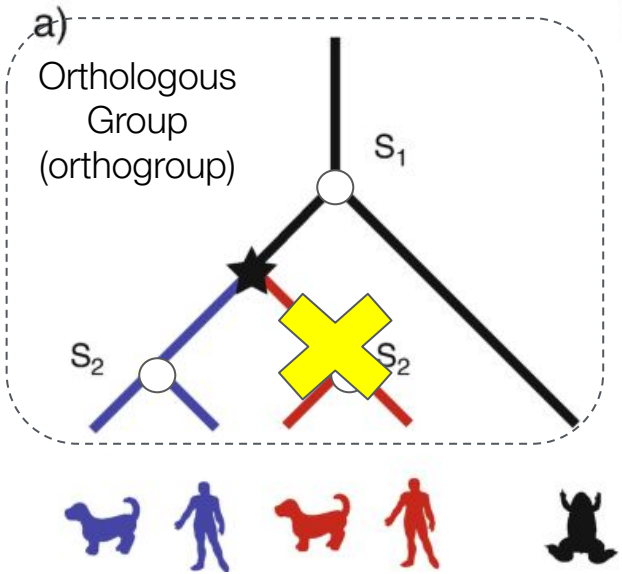

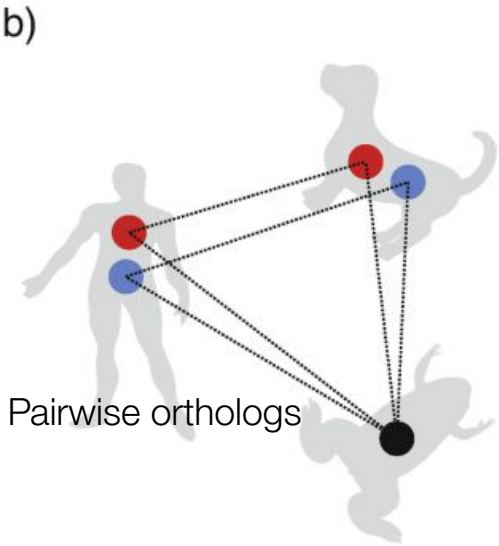

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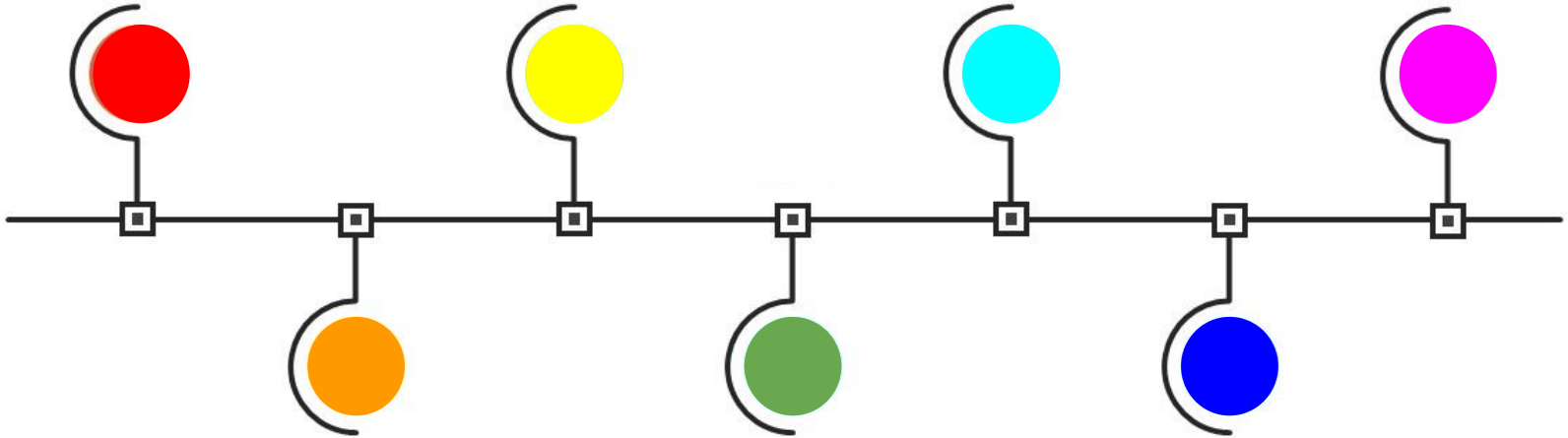
03 ALIGNMENT & TRIMMING



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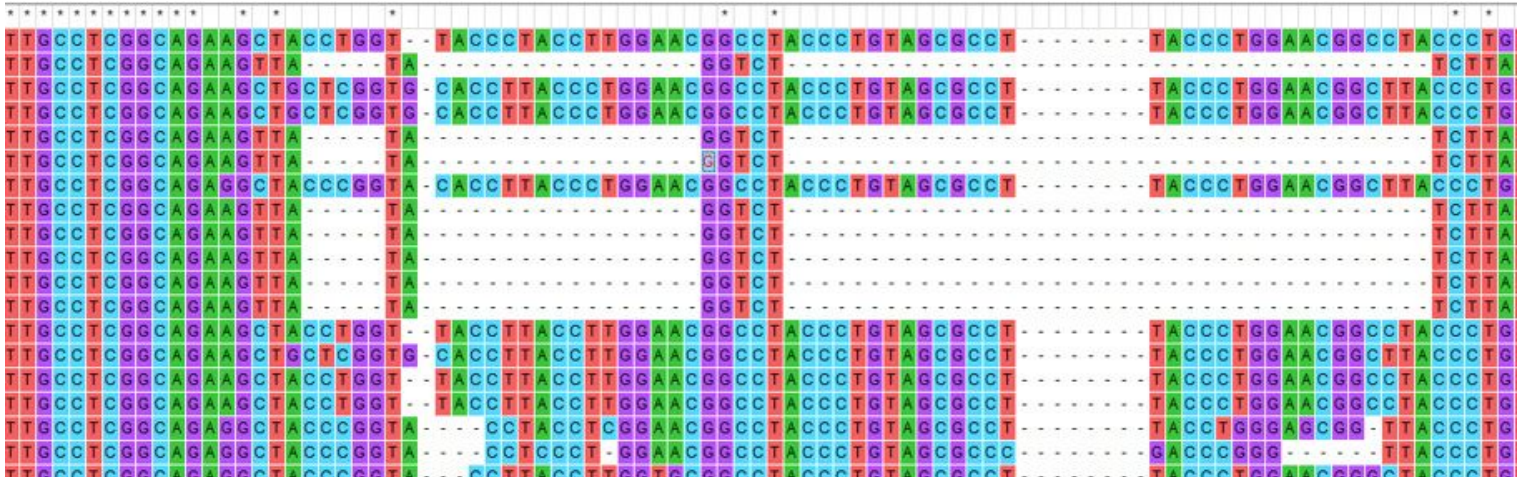

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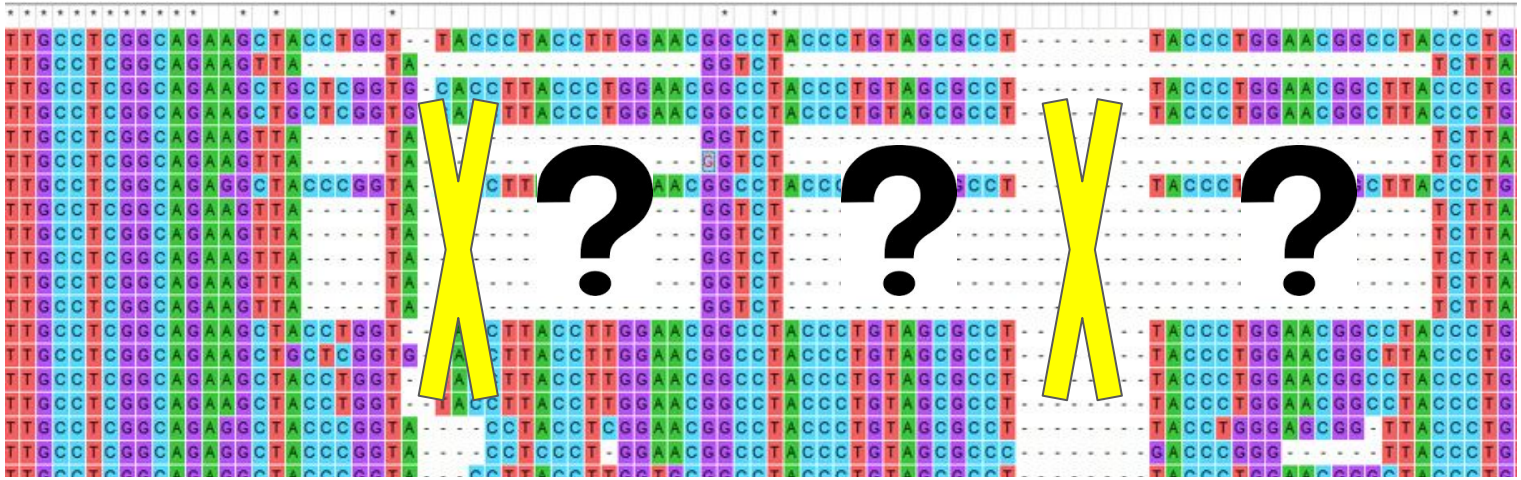

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Jacob and Marina today

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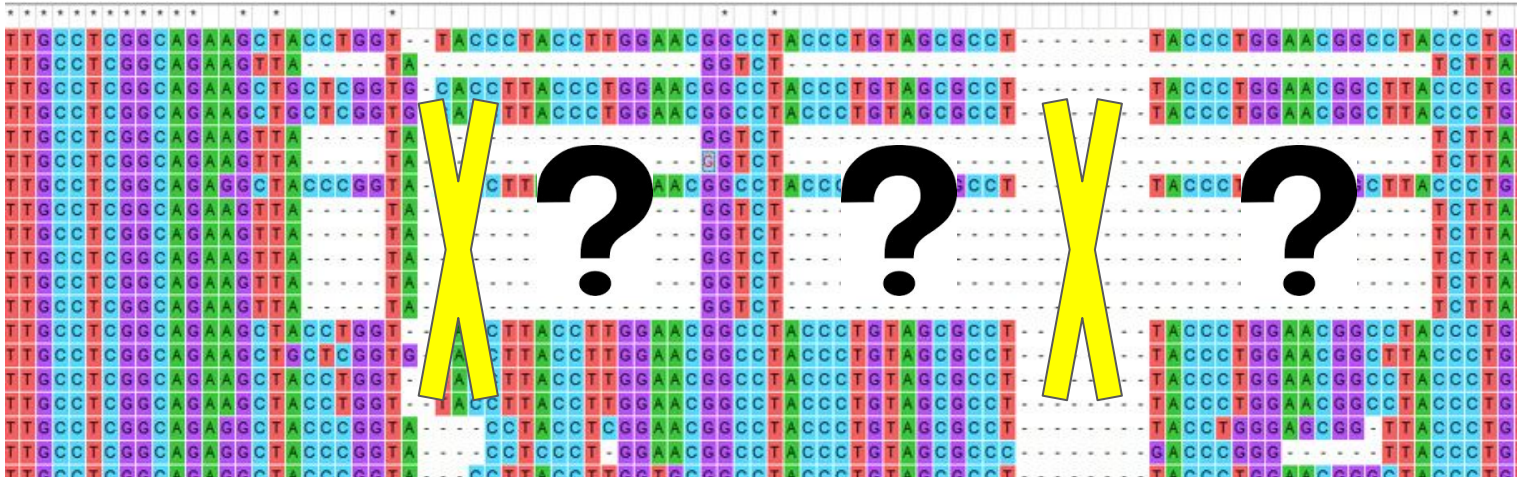

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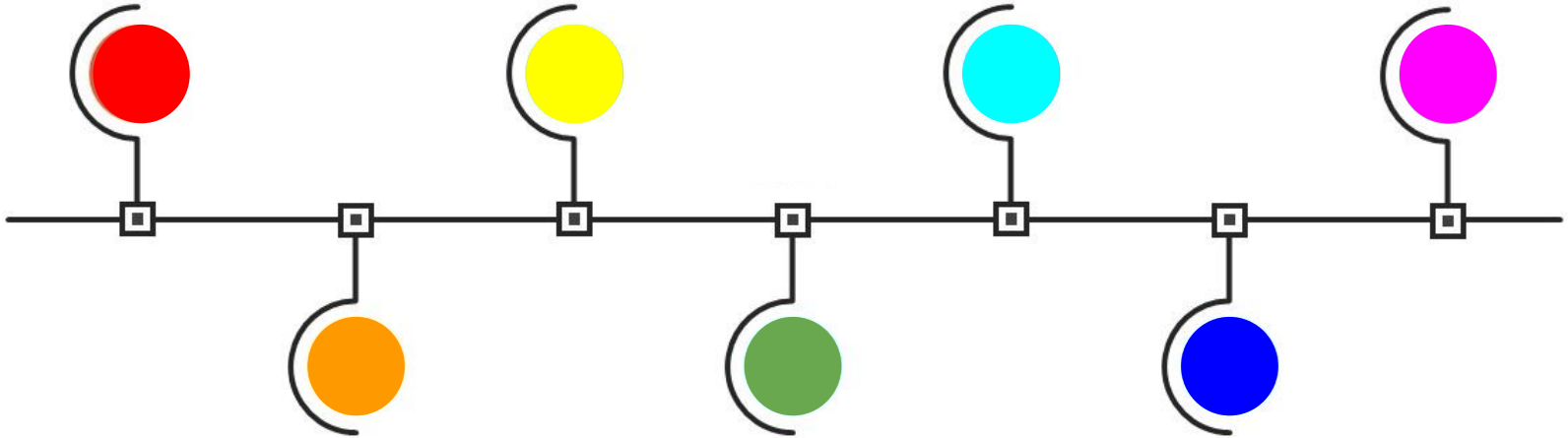

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04 PHYLOGENOMIC SUBSAMPLING

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This step can be used to *explore phylogenetic conflicts*, *test specific hypotheses* of relationships, measure the impact of *different sources of bias*, and allow for a *better modeling* of evolutionary processes.

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How? By checking the properties of genes or sites and selecting the ones that minimize bias.

04 PHYLOGENOMIC SUBSAMPLING

Which properties?

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Information content

-> length of alignment
-> missing data
-> level of occupancy

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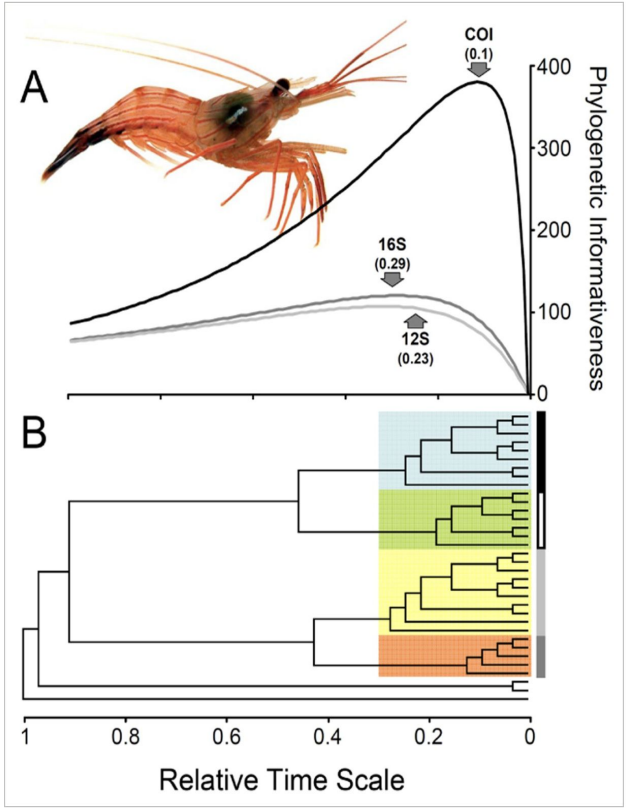

Baeza & Fuentes 2013

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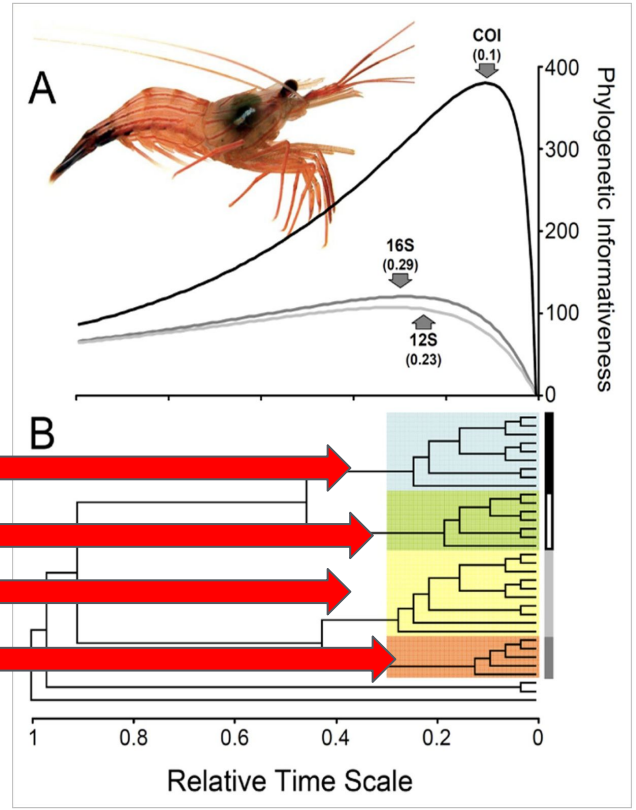
Good information to infer these nodes



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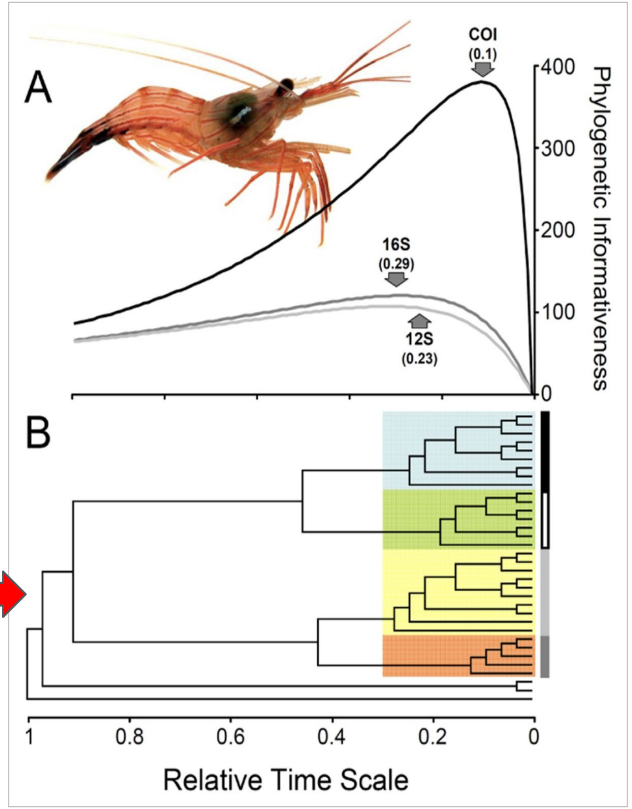
Not enough information to infer these nodes



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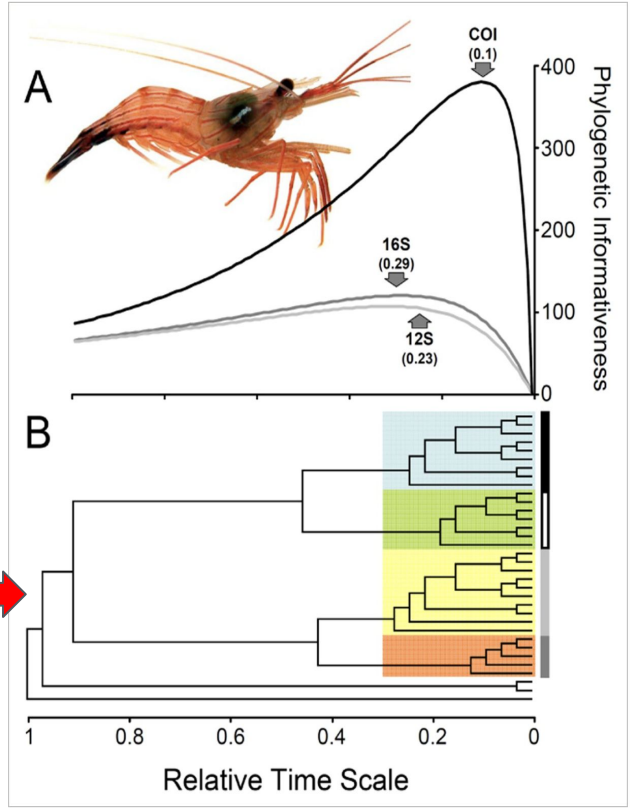

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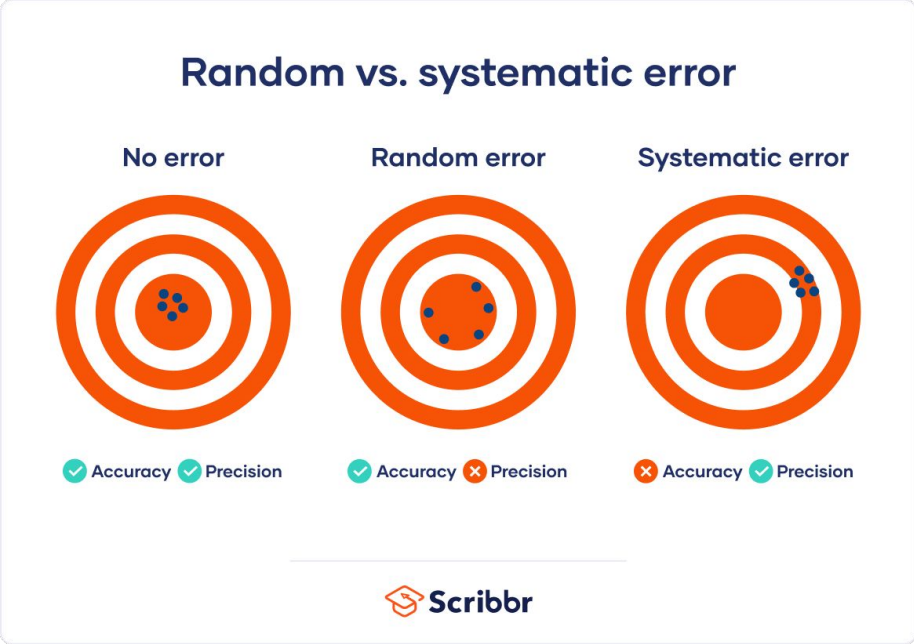
Systematic error: when a calculated value deviates from the true value in a consistent way.



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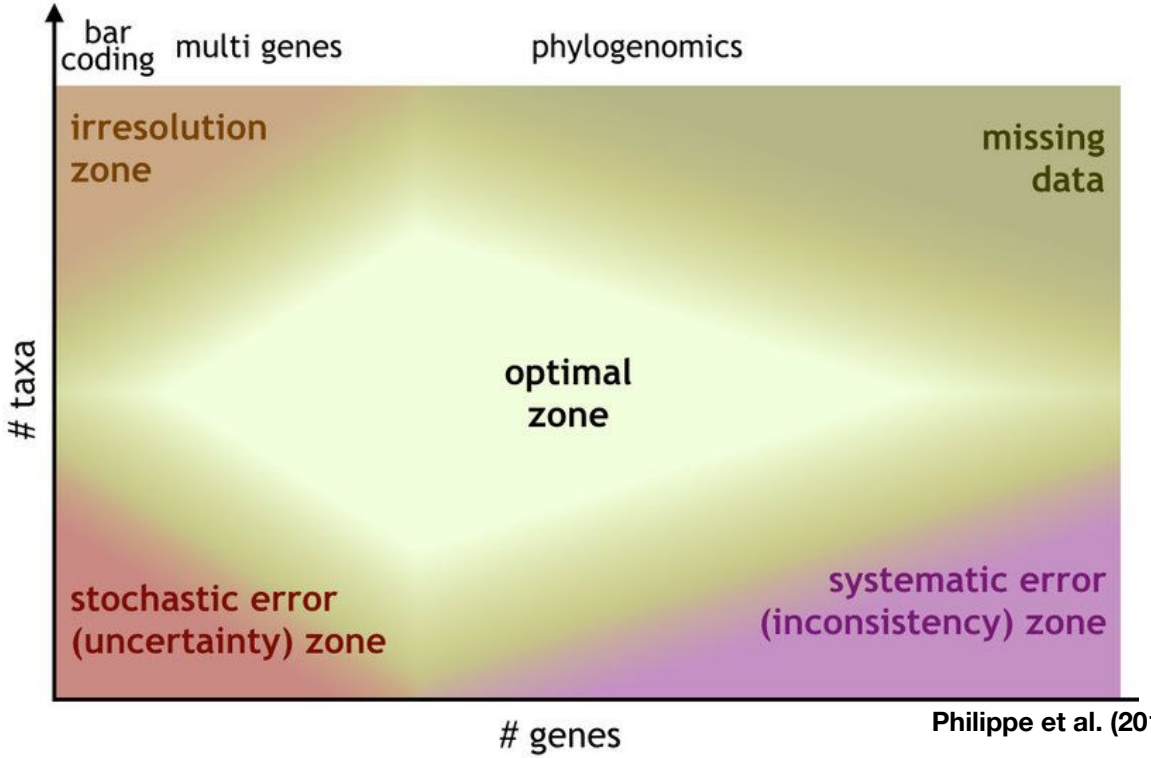

Philippe et al. (2017)

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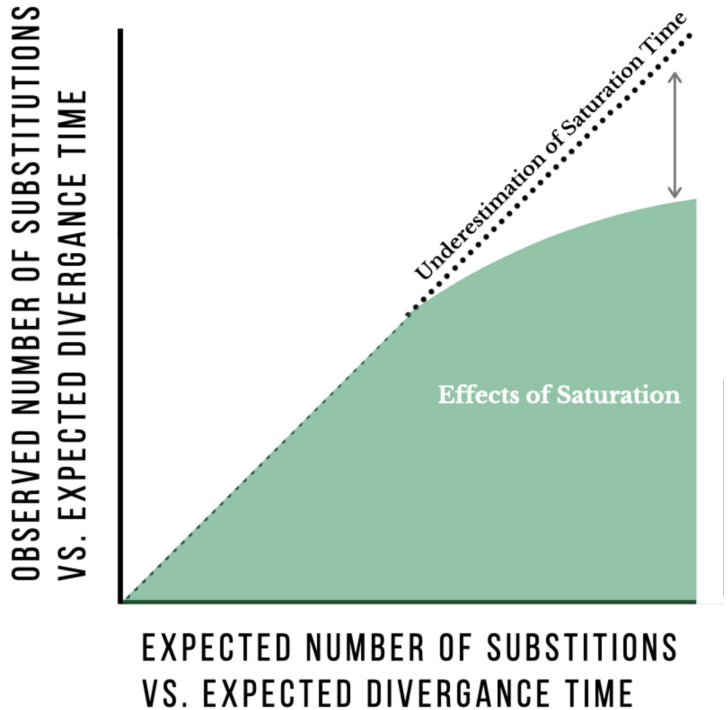

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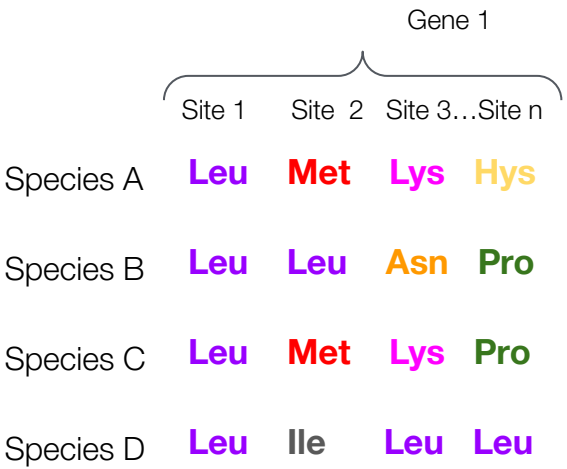

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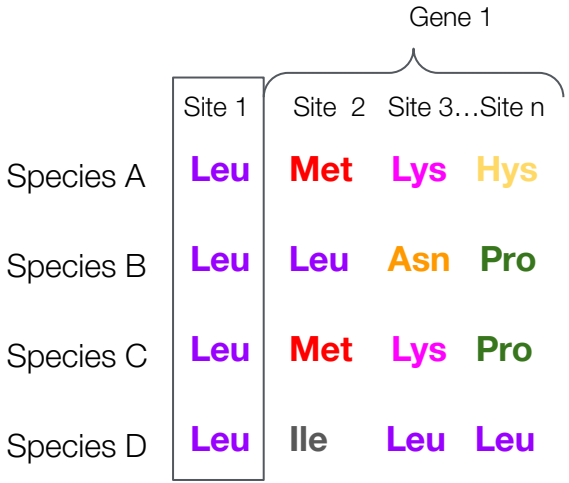

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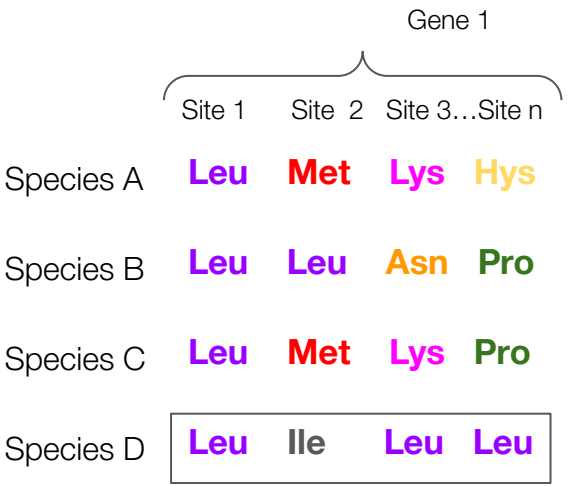

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Jacob and Marina today

Antonis Rokas and Jacob on 29th Jan

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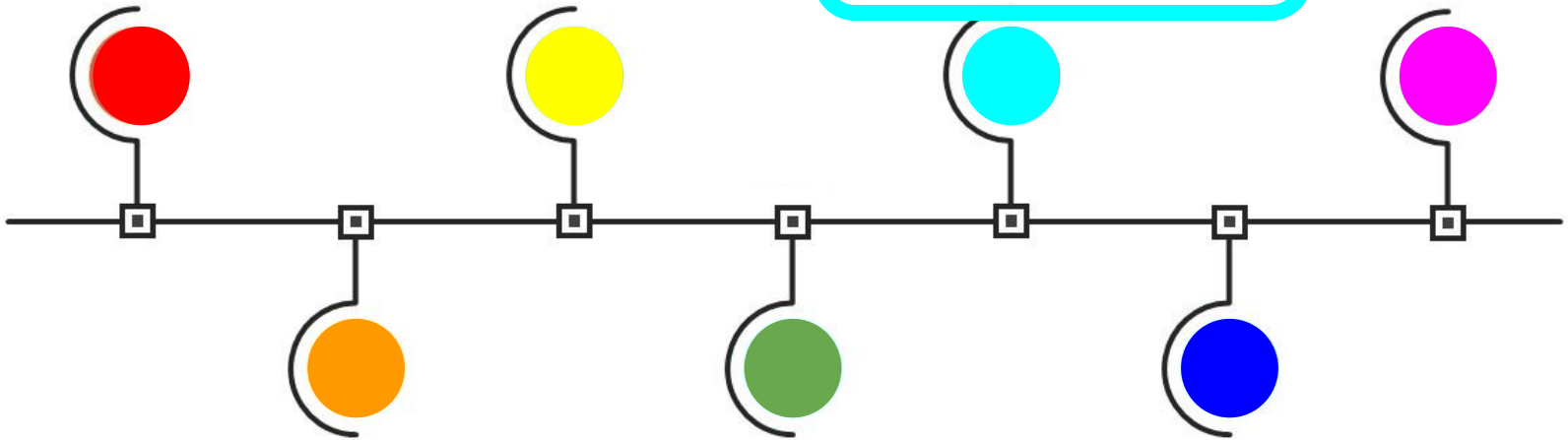
02 ORTHOLOGY INFERENCE

03 ALIGNMENT & TRIMMING

04 PHYLOGENOMIC SUBSAMPLING

05 SUPERMATRIX VS INDIVIDUAL GENES



05 SUPERMATRIX VS INDIV. GENE TREES

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~~Gene tree ≈ Species phylogeny~~

Gene tree ≠ Species phylogeny

05 SUPERMATRIX VS INDIV. GENE TREES

Analytical factors

They lead to failure in accurately inferring a gene tree; these can be either due to **stochastic error** (e.g., insufficient sequence length or taxon samples) or due to **systematic error** (e.g., observed data far depart from model assumptions)

Biological factors

They lead to gene trees that are topologically distinct from each other and from the species tree. Known factors include **stochastic lineage sorting**, **hidden paralogy**, **horizontal gene transfer**, **recombination** and **natural selection**

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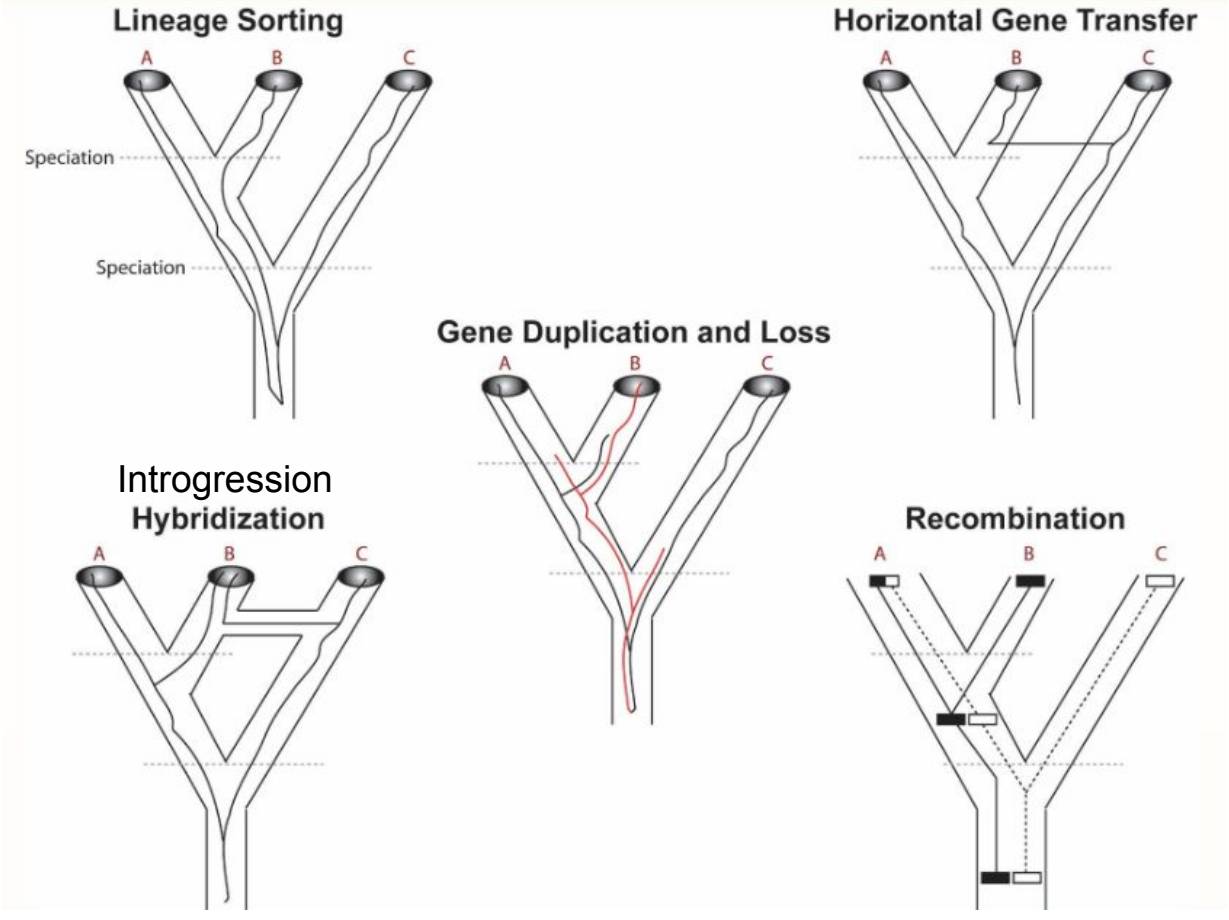

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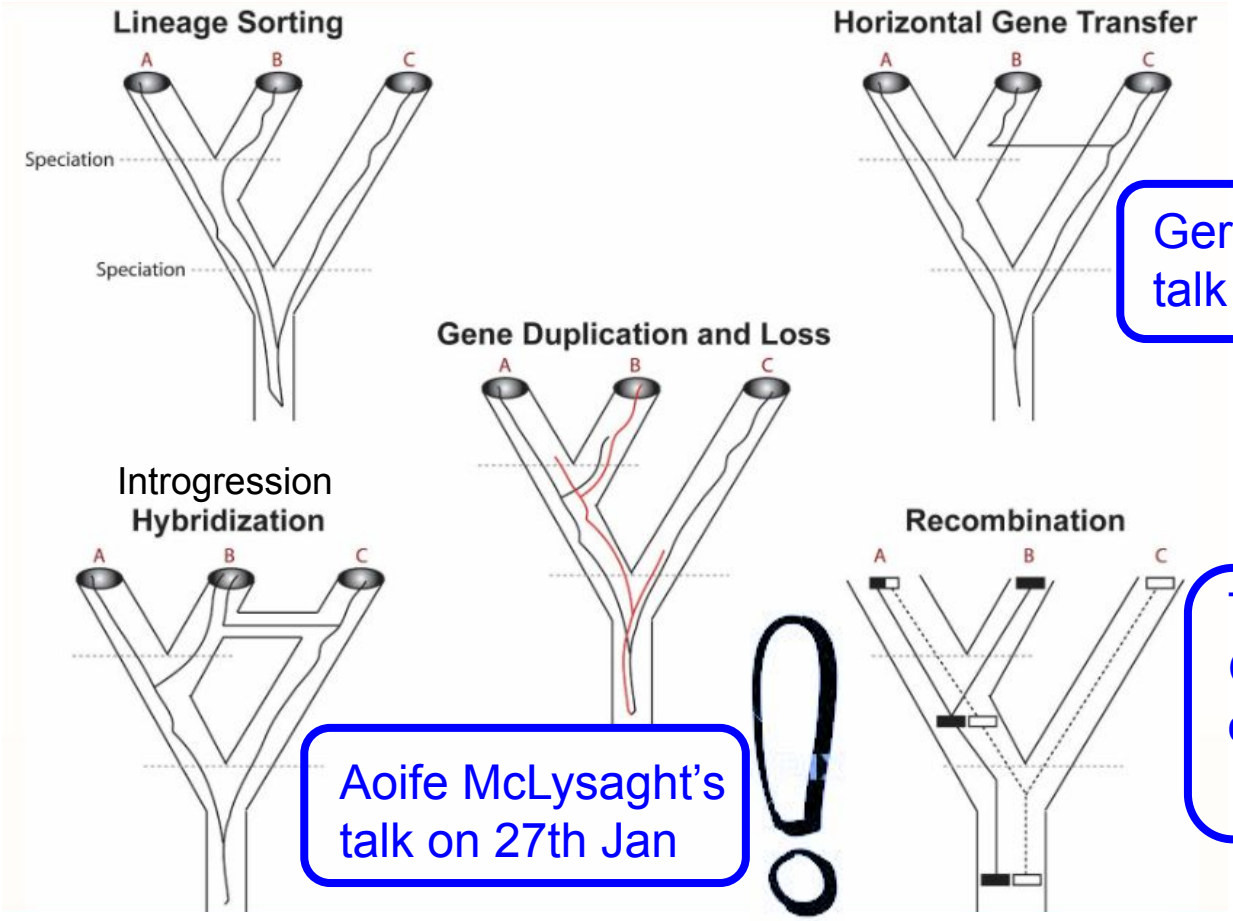

Gergely Szöllősi's talk on 1st Feb

Aoife McLysaght's talk on 27th Jan

Toni Gabaldón's tal on 30th Jan

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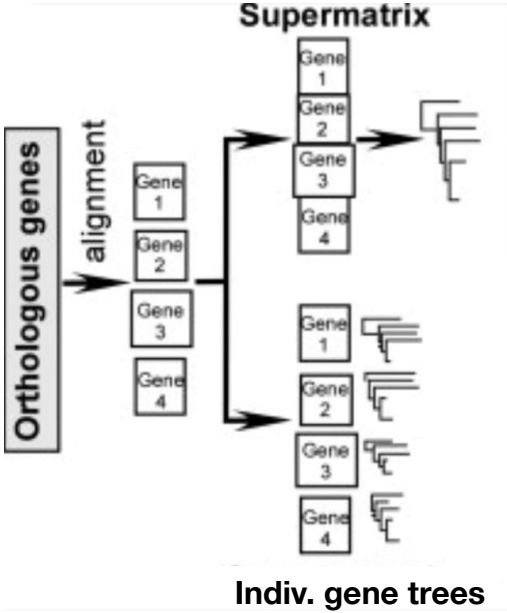

Adapted from Fernández, Hormiga & Giribet (2014)

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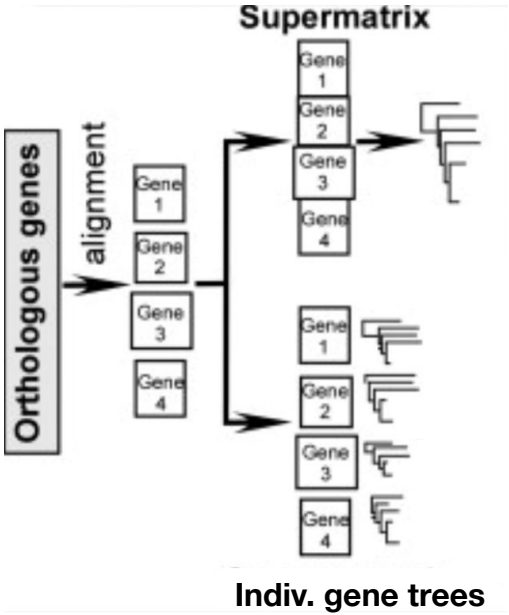

Phylogenetic analysis
(one tree)

Phylogenetic analysis
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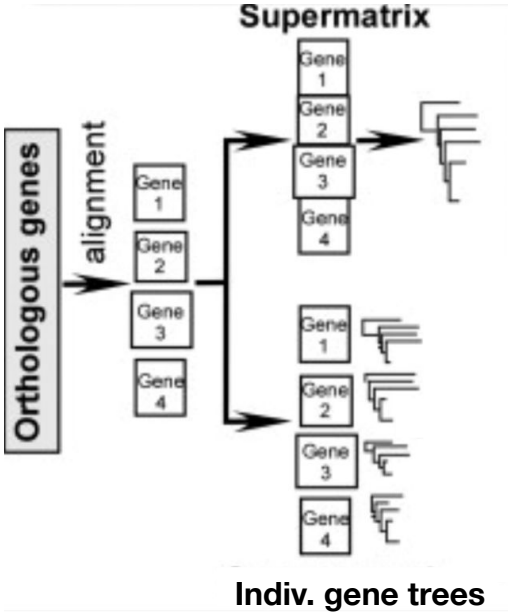

Phylogenetic analysis (one tree)

Phylogenetic analysis (multiple trees)

Estimation of a species tree given a set of gene trees

Multispecies coalescent

Adapted from Fernández, Hormiga & Giribet (2014)

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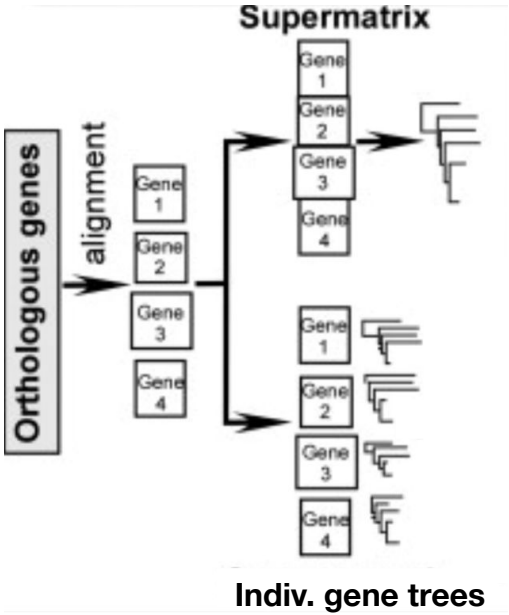

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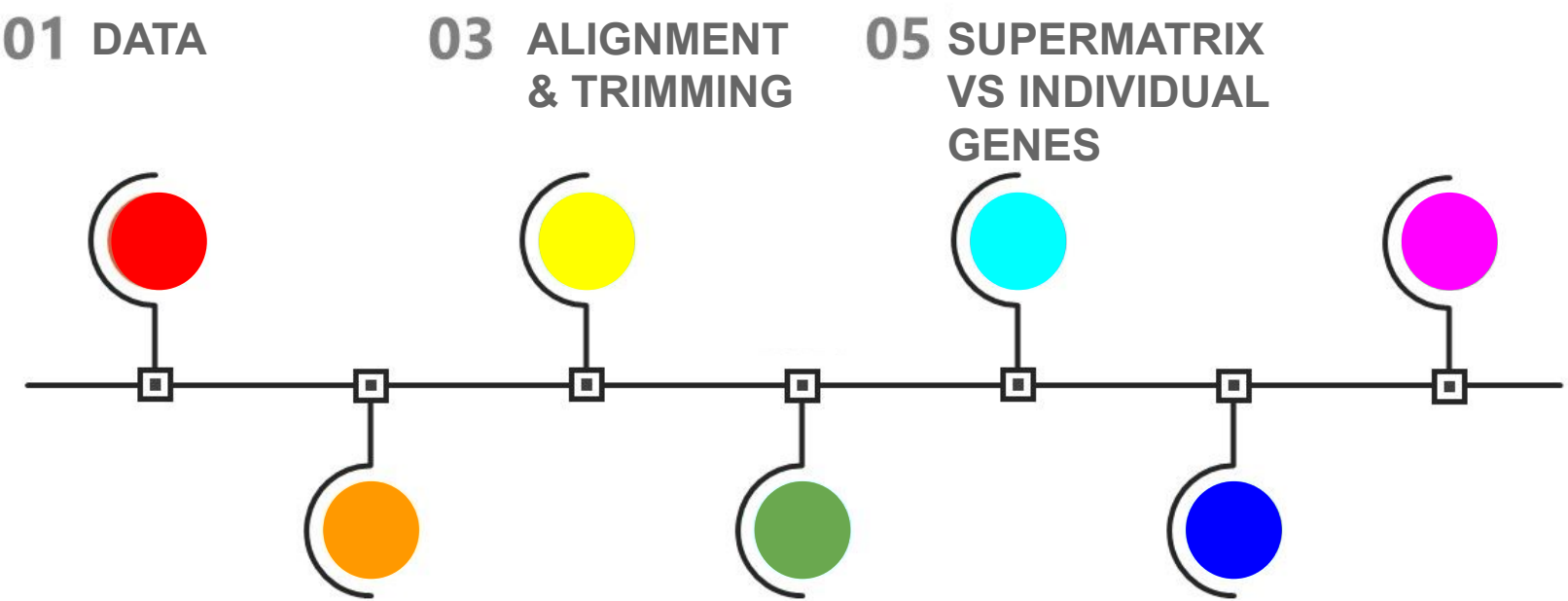
Erin Molloy's talks on 25th and 26th Jan

Adapted from Fernández, Hormiga & Giribet (2014)


01 DATA
02 ORTHOLOGY INFERENCE
03 ALIGNMENT & TRIMMING
04 PHYLOGENOMI SUBSAMPLING
05 SUPERMATRIX VS INDIVIDUAL GENES
06 MODEL SELECTION & PHYLOGENETIC INFERENCE

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DATA

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

DATA + MODEL OF EVOLUTION

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

DATA + MODEL OF EVOLUTION

+ METHOD

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

DATA + MODEL OF EVOLUTION

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+ A WAY TO ASSESS HOW GOOD YOUR HYPOTHESIS IS

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

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DATA + **MODEL OF EVOLUTION** (= substitution model)

A model that describes changes in sequences over evolutionary time and transforms the number of changes in an evolutionary distance

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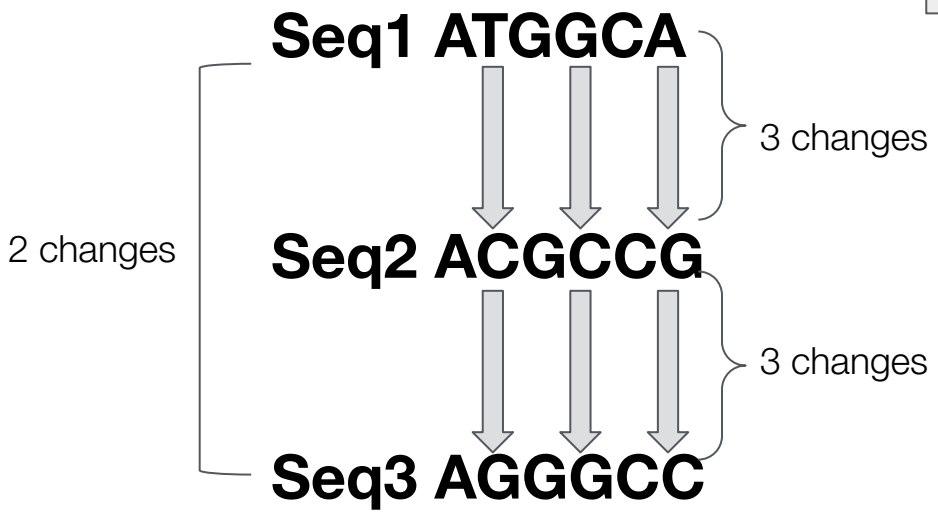

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Seq1 ATGGCA

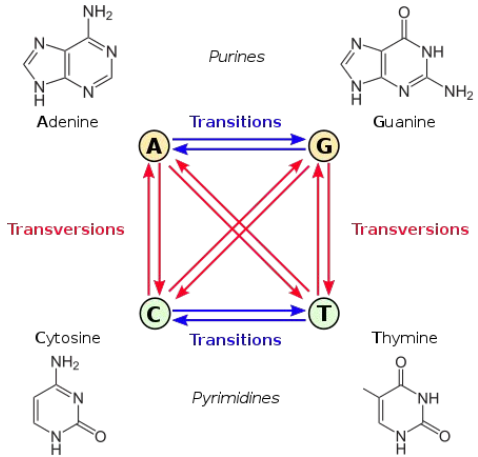
3 changes

2 changes

Seq2 ACGCCG

3 changes

Seq3 AGGGCC



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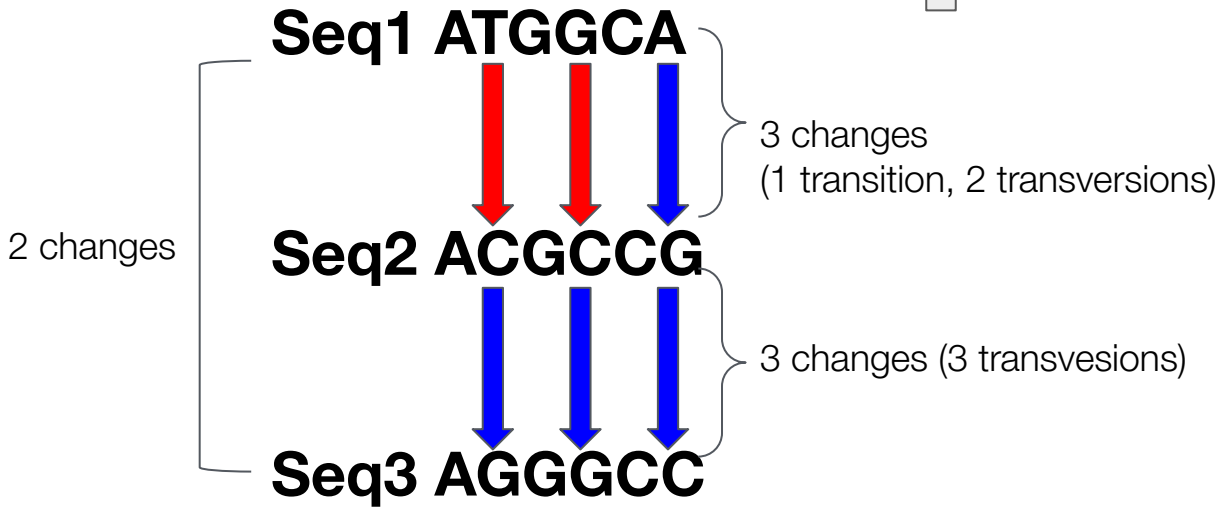

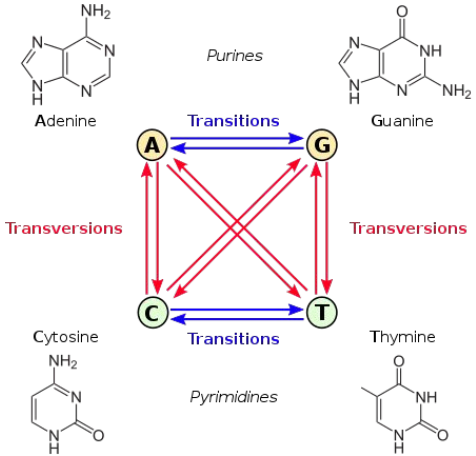

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

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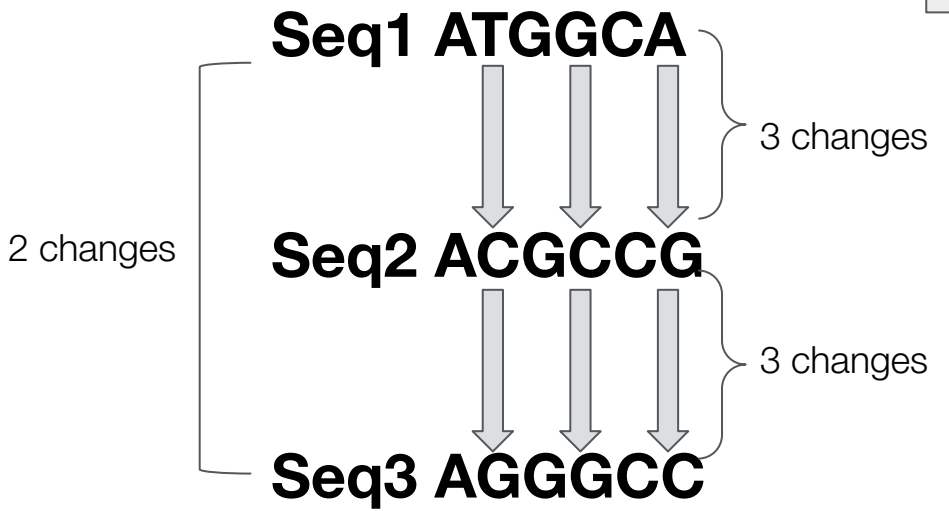

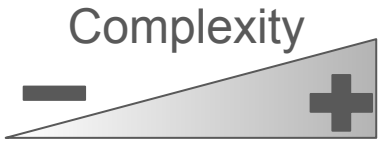

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Complexity

Jukes & Cantor

nucleotides

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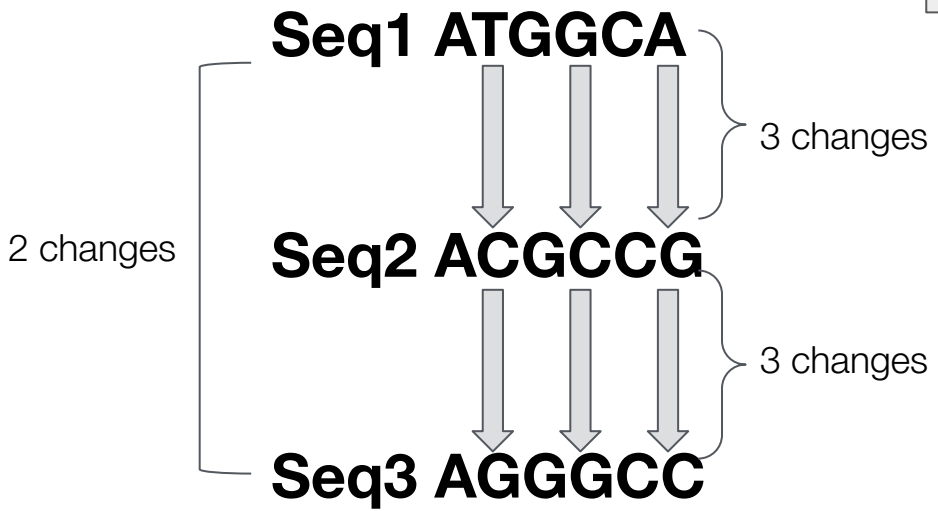

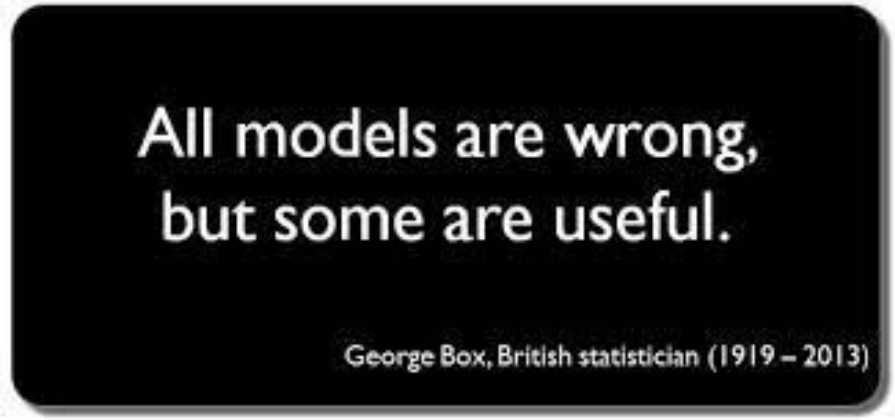

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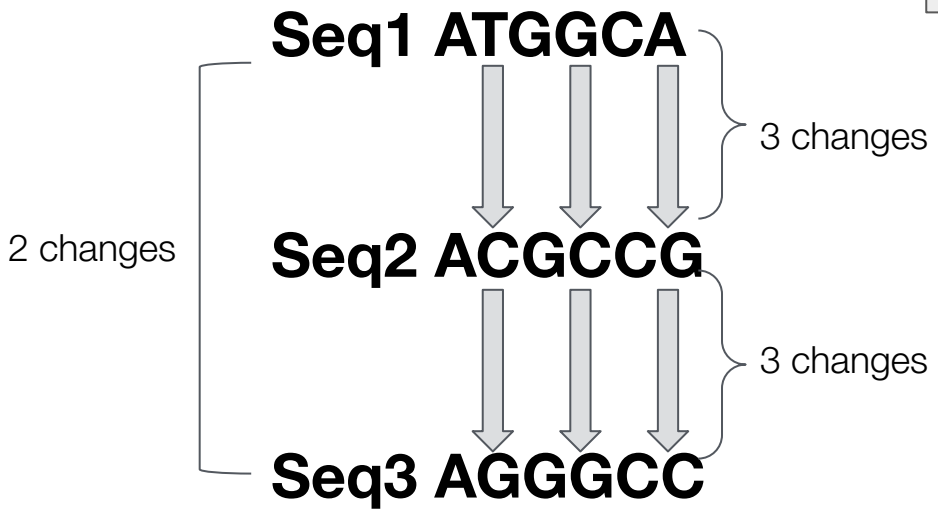

More about models:

Olivier Gascuel's talk on 25th Jan

06 MODEL SELECTION & PHYLOGENETIC INFERENCE

DATA + MODEL OF EVOLUTION + METHOD

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DATA + **MODEL OF EVOLUTION**

+ **METHOD**

Two main methods:

Maximum Likelihood (ML) and **Bayesian Inference (BI)**

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BI seeks P(T|D), while ML maximizes P(D|T)

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DATA + MODEL OF EVOLUTION

+ METHOD

+ A WAY TO ASSESS HOW GOOD YOUR HYPOTHESIS IS

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Traditional metrics:

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- Transfer bootstrap expectation (TBE)

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Olivier Gascuel and Oleksyi Kozlov's talks on 25th Jan

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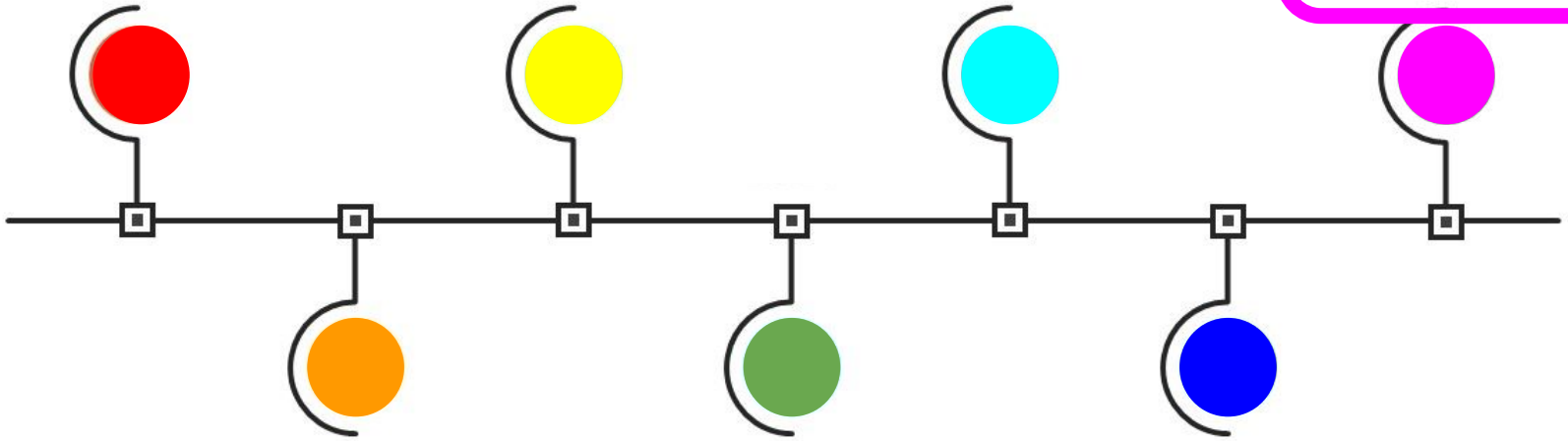
07 TESTING THE ROBUSTNESS OF YOUR TREE



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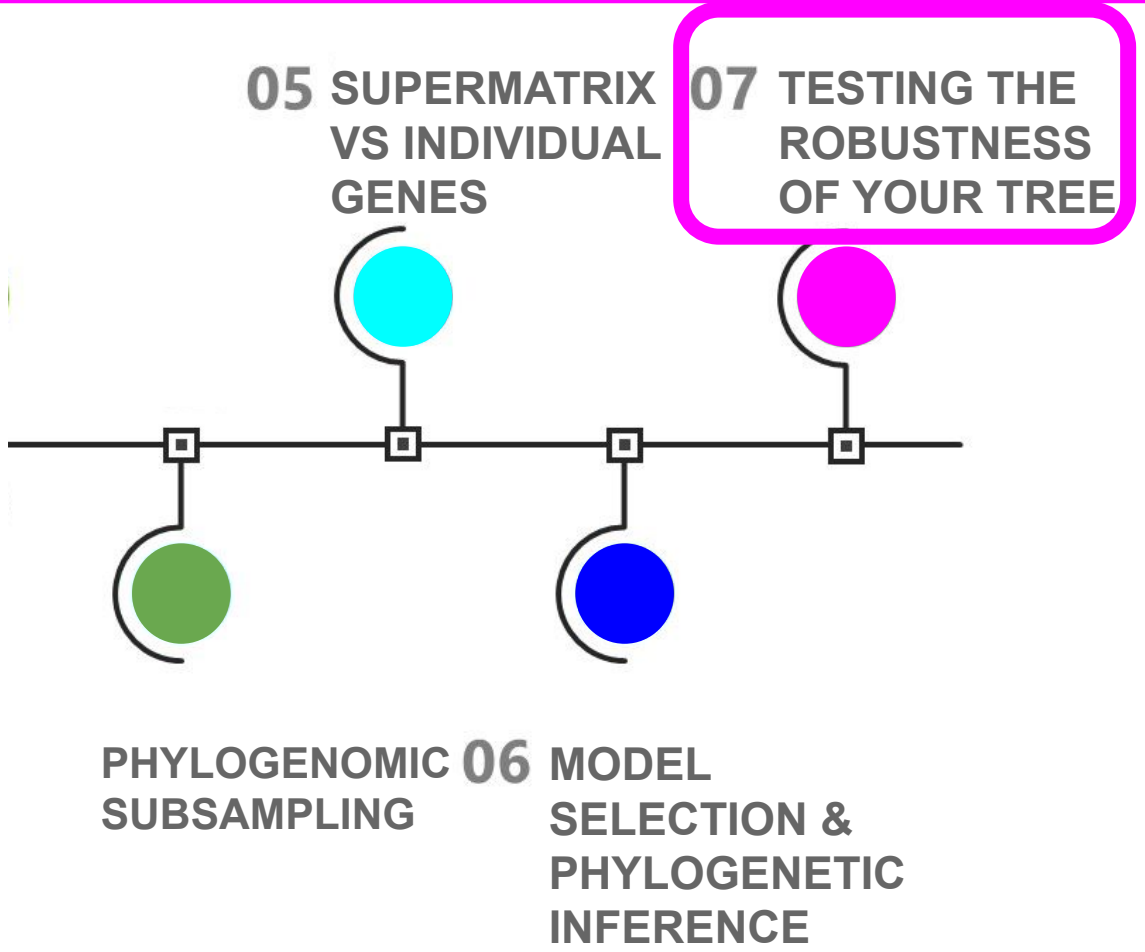

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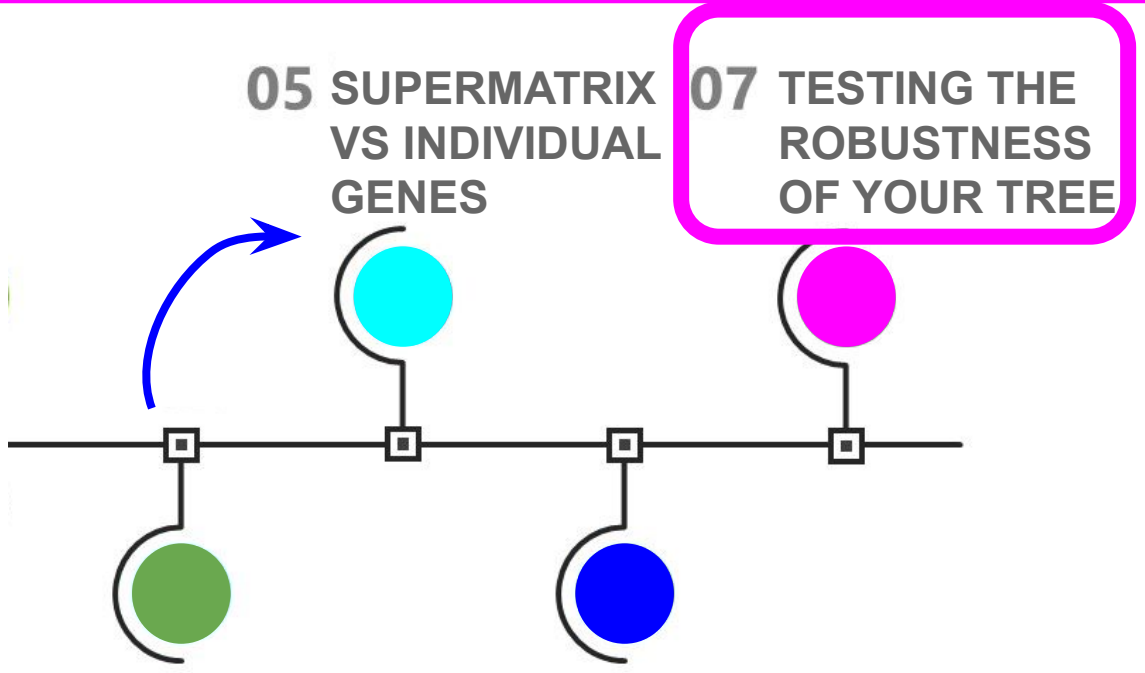

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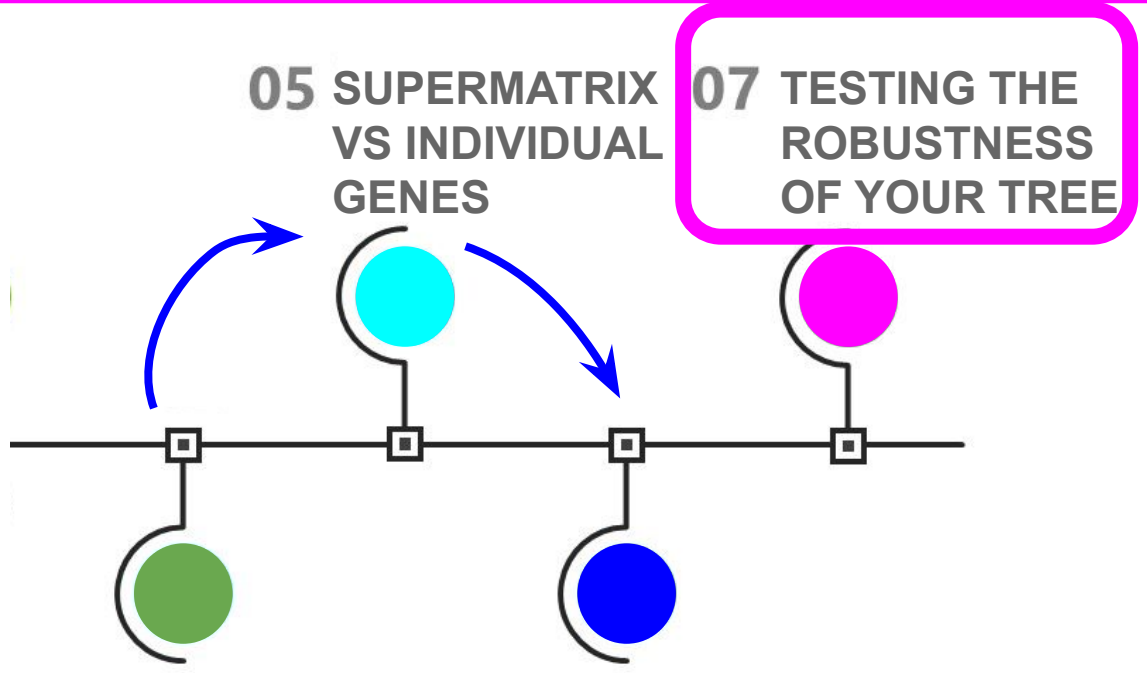

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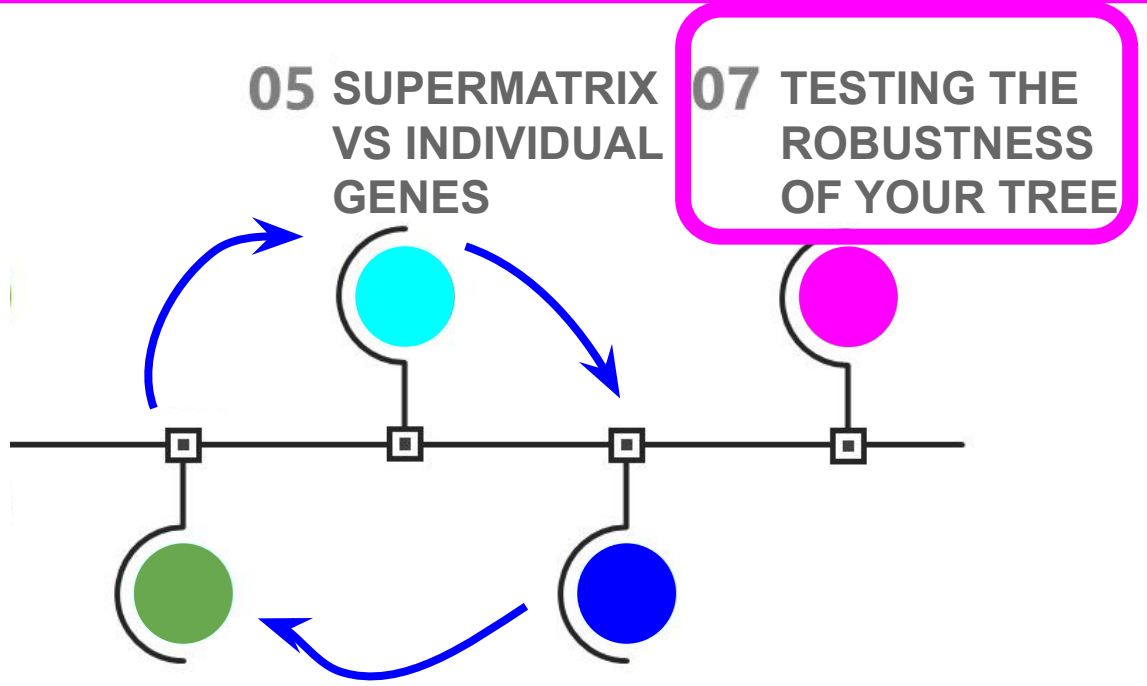

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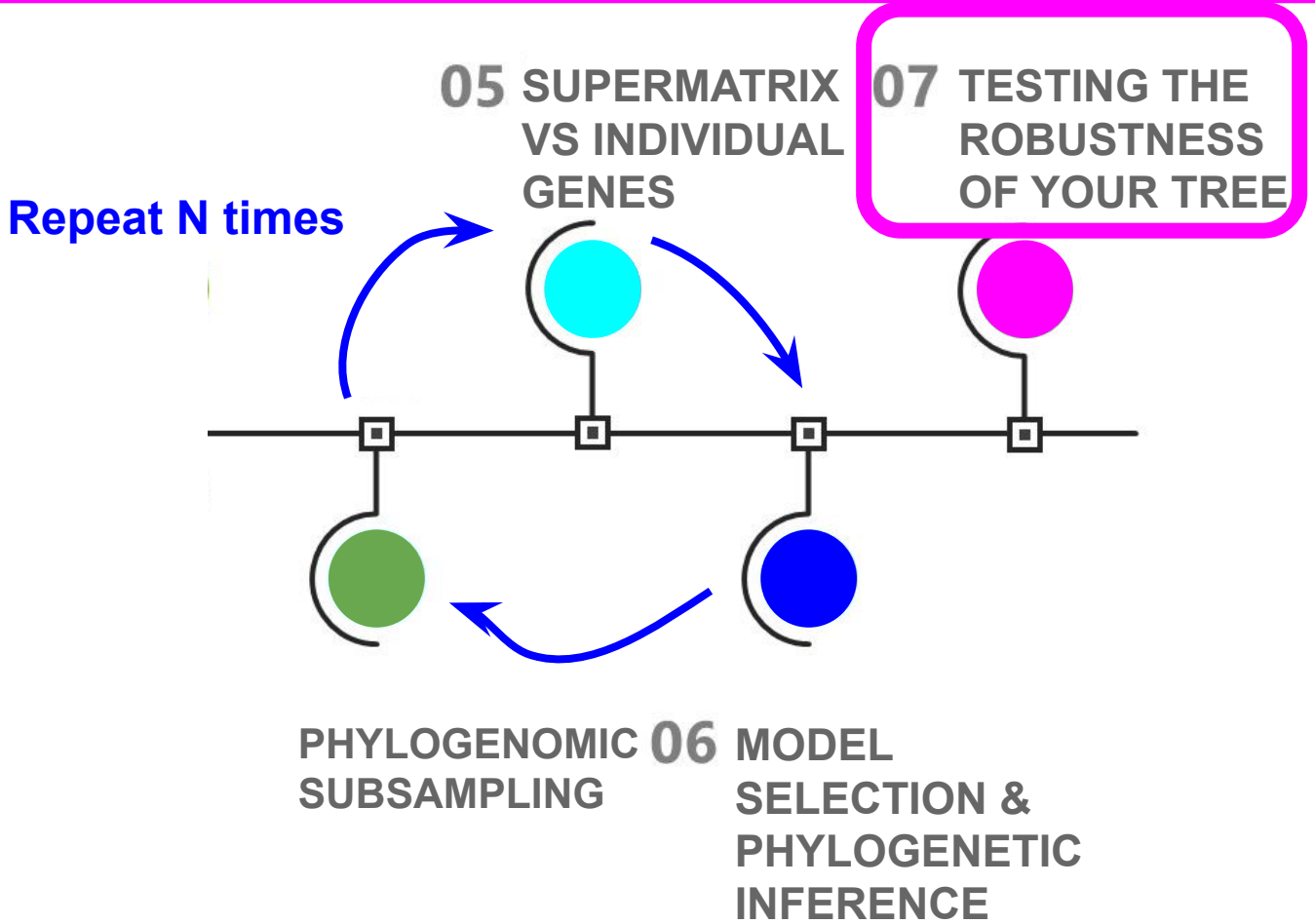

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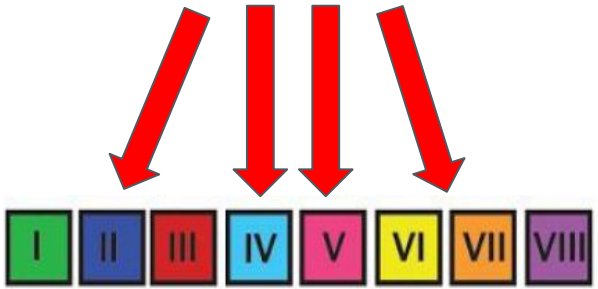
Fernández, Edgecombe & Giribet (2016) Syst Biol

07 TESTING THE ROBUSTNESS OF YOUR TREE

These are **matrices/subsets** of individual gene trees



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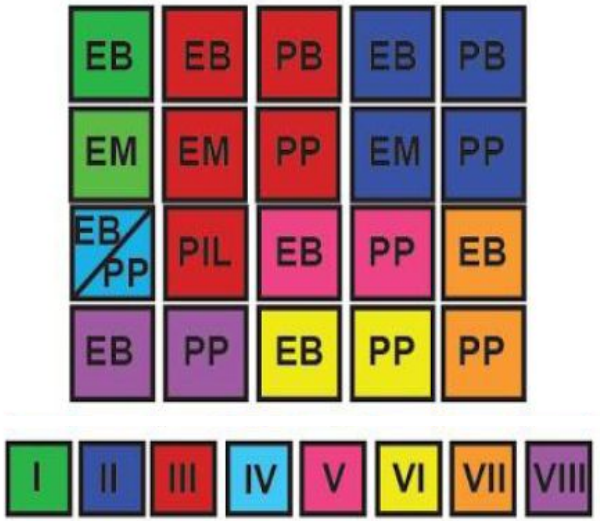
07 TESTING THE ROBUSTNESS OF YOUR TREE

These are **analyses**



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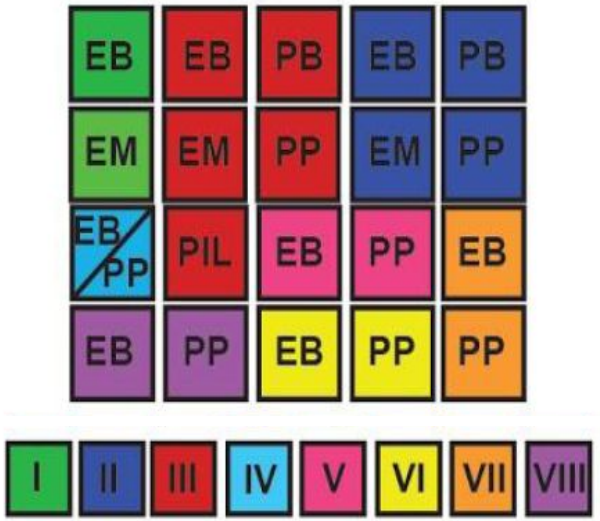

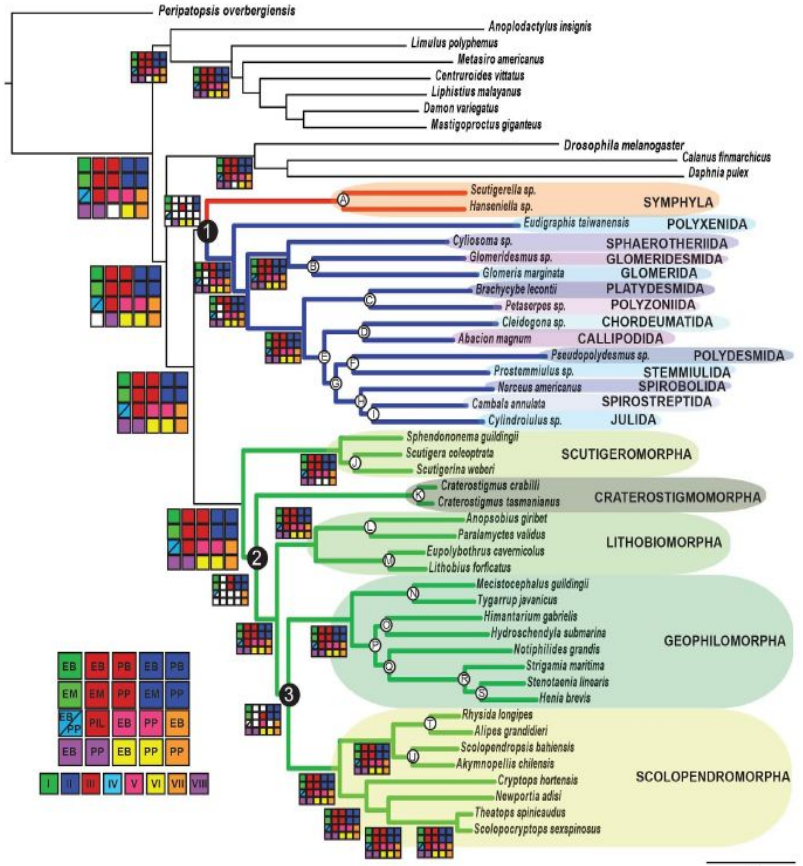

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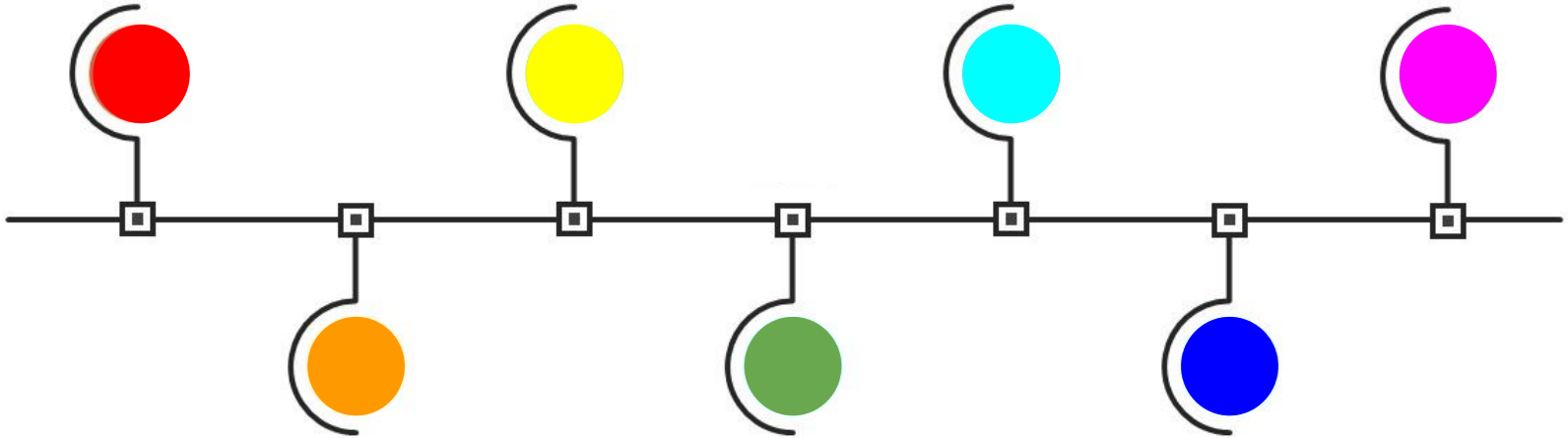
AND YOU, HOW IS **YOUR** PROJECT?



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QUIZ TIME