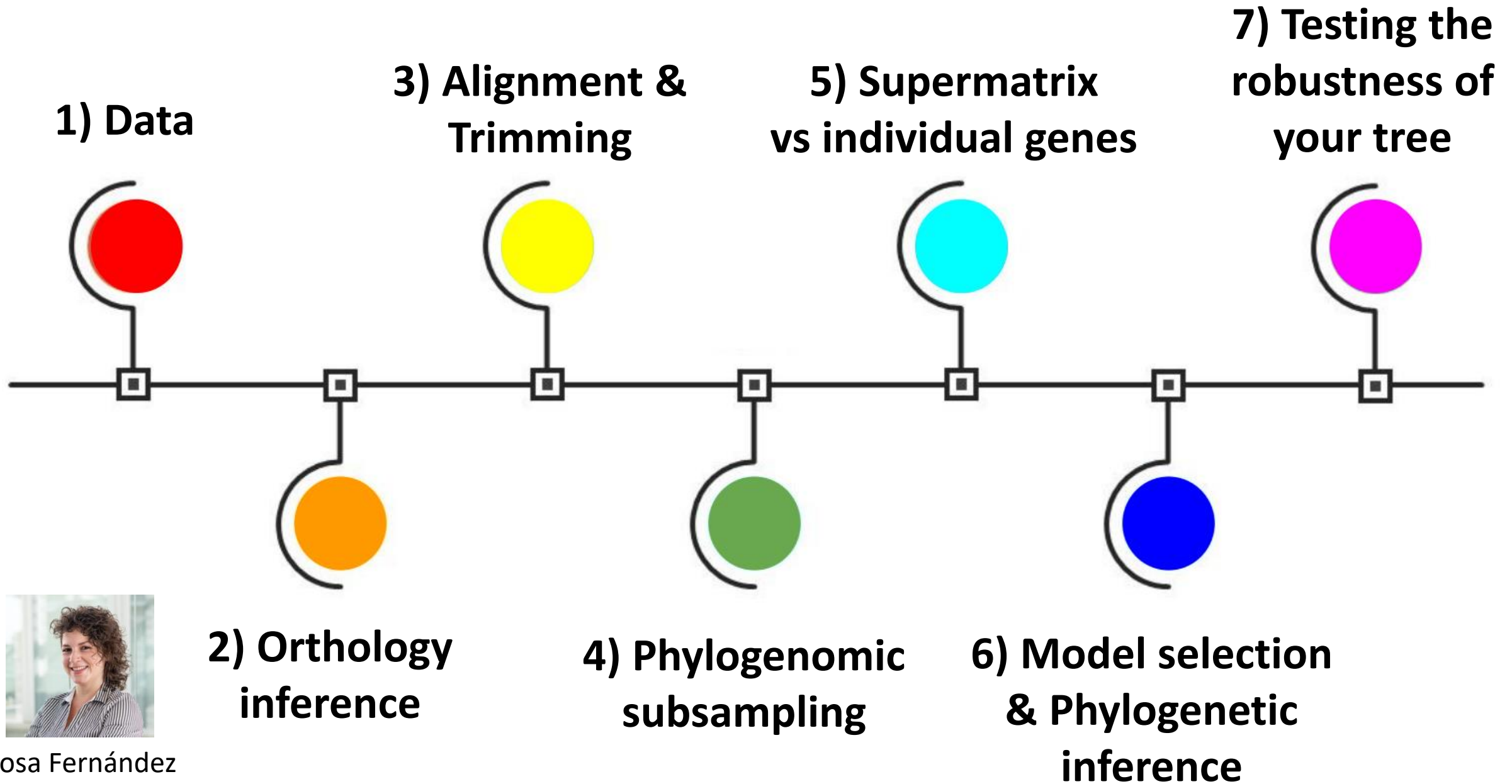


Summary of the Phylogenomics Workshop





Rosa Fernández
(23rd January)

1) Data

Source

Genomes

Transcriptomes

UCEs

RADseq

Metagenomics



Rosa Fernández (23rd January)

1)

Data

Source

Genomes
Transcriptomes

UCEs

RADseq

Metagenomics

Exonic protein-coding sequences



Rosa Fernández (23rd January)



Jacob L Steenwyk -> Gene trees challenge
(single copy orthologs + orthoSNAP)



Jordi Paps
(29th January)



Lisa Pokorný
(31st January)

1) Data

Source

Genomes

Transcriptomes

UCEs

RADseq

Metagenomics



Rosa Fernández (23rd January)



Exonic protein-coding sequences

Introns

Other non-coding elements

Retroelements



Toni Gabaldon
(30th January)



Erin Molloy
(26th January)



Lisa Pokorny
(31st January)

1) Data

Source

Genomes
Transcriptomes
UCEs
RADseq
Metagenomics



Matt Christmas (26th January)
Aoife McLysaght (27th January)



Erin Molloy (26th January)
Matt Christmas (26th January)
Lisa Pokorny (31st January)

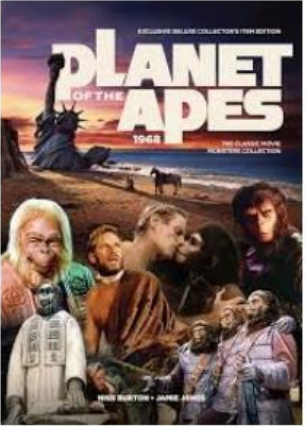


Gytis Dudas (30th January)
Ania Karnkowska (2nd February)



Rosa Fernández (23rd January)

1) Data



Taxon sampling



Marina Marcet-Houben
(24th January)



Antonis Rokas
(29th January)



Rosa Fernández
(23rd January)



Jordi Paps
(29th January)

Data quality



Rosa Fernández
(23rd January)

BUSCO

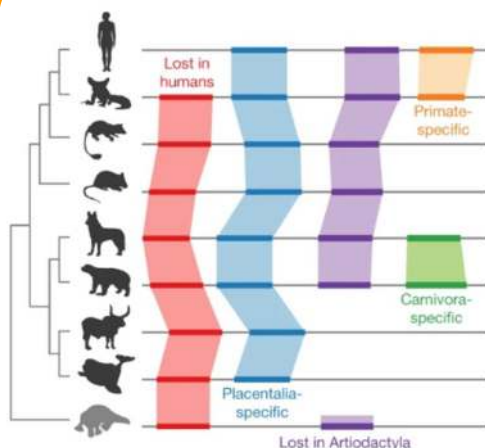


Jordi Paps
(29th January)

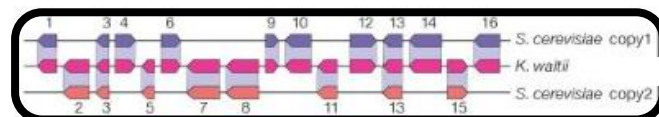
2) Orthology inference



Marina Marcet-Houben (24th January)



Whole genome alignment



Syntenic information

Aoife McLysaght
(27th January)



Matt Christmas
(26th January)

De novo inference

BLAST

Basic Local Alignment Search Tool



diamond

OrthoFinder 2

SwiftOrtho

Oma browser
orthologous matrix



Best reciprocal hits

Pre-calculated orthologs



Oma OrthoDB
browser

OrthoMCL DB
Ortholog Groups of Protein Sequences
Release 6.19
28 Nov 2023



InParanoidB 9
Protein and Domain Ortholog Groups



FungiDB

<https://fungidb.org/>



PLAZA

bioinformatics.psb.ugent.be/plaza/

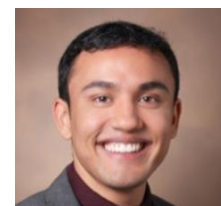
Tree-based methods

OrthoSNAP

Lisa Pokorny
(31st January)

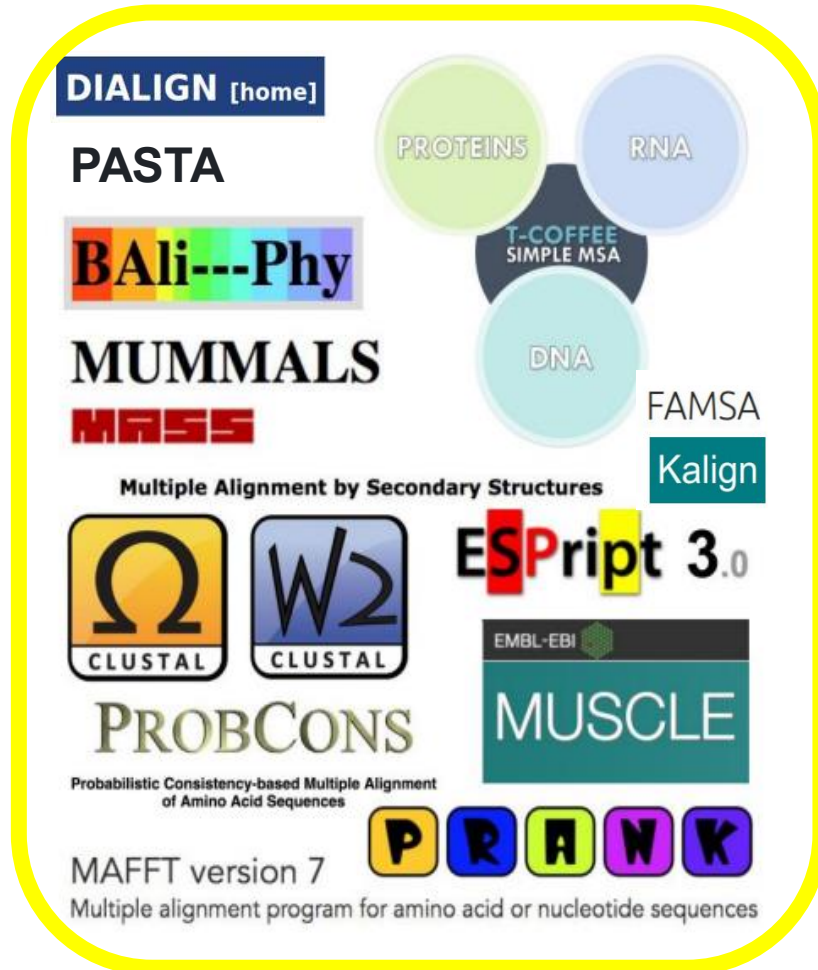


Jacob L Steenwyk
(24th January)



3) Alignment & Trimming

Alignment

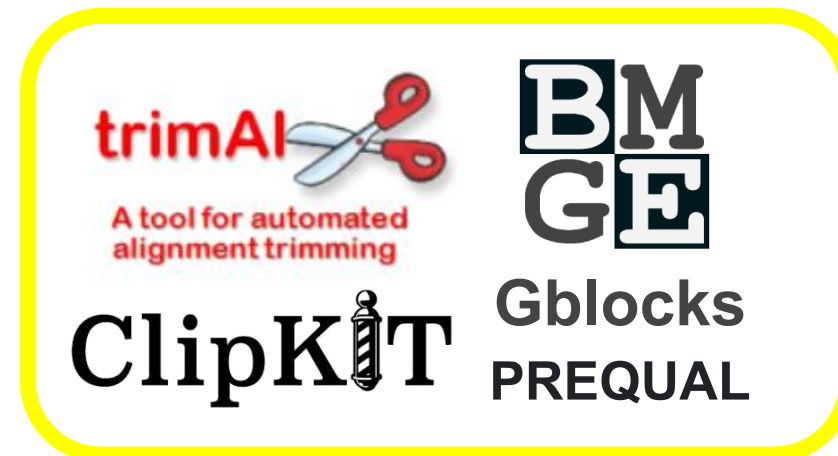


Oleksiy M. Kozlov (27th January)



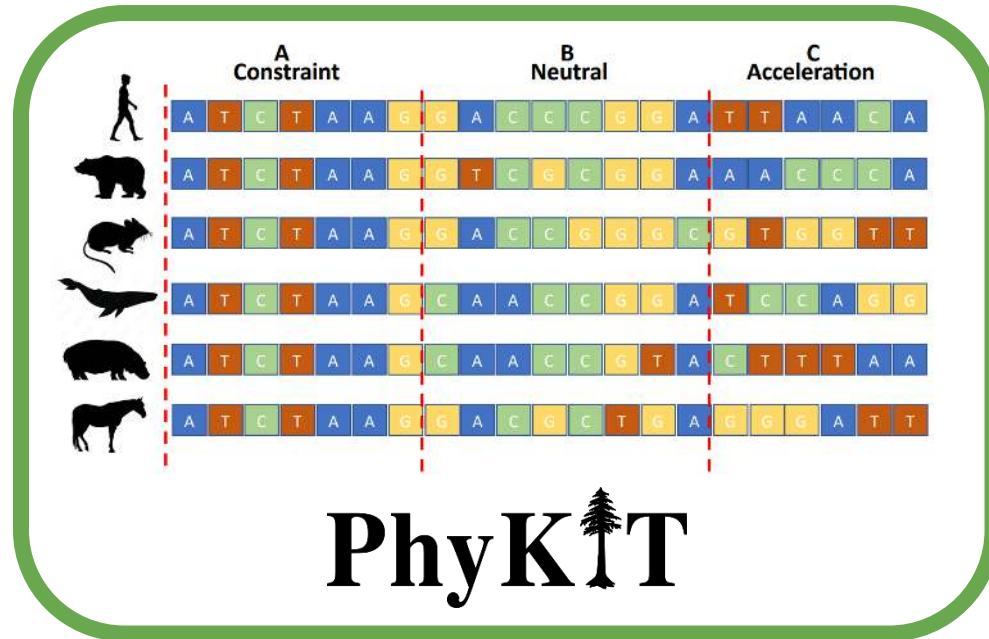
Marina Marcet-Houben & Jacob L Steenwyk (23rd January)

Trimming



4) Phylogenomic subsampling

At the level of sites



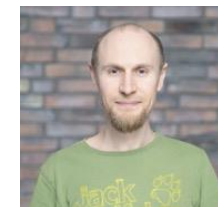
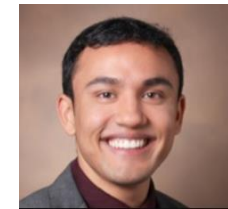
At the level of genes

genesortR

Jacob L Steenwyk (23rd January)

Matt Christmas (26th January)

Antonis Rokas & Jacob L Steenwyk
(29th January)



Oleksiy M. Kozlov (27th January)

Lisa Pokorny
(31st January)



5) Supermatrix vs individual genes



Antonis Rokas &
Jacob L Steenwyk
(29th January)

Gene tree $\neq$ species tree

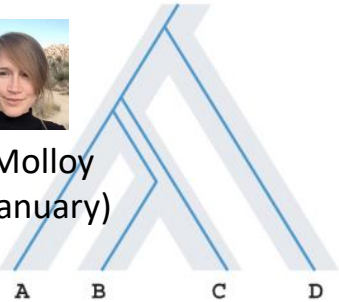


Marina Marcet-
Houben
(24th January)

Lineage sorting



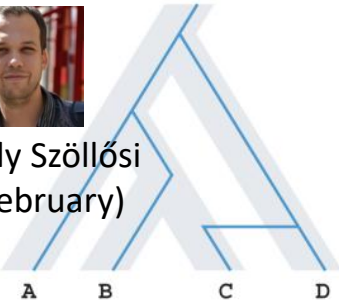
Erin Molloy
(25th January)



Horizontal transfer



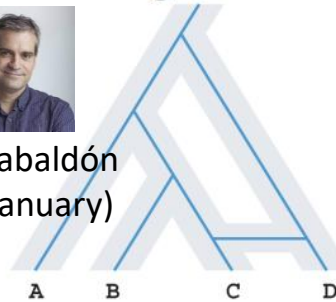
Gergely Szöllősi
(1st February)



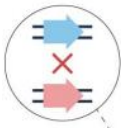
**Hybridization /
Introgression**



Toni Gabaldón
(30th January)



Recombination

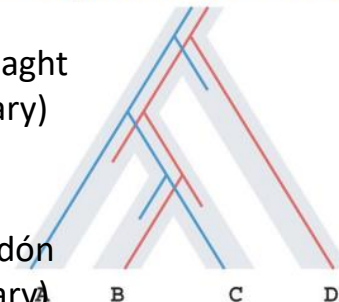


Aoife McLysaght
(27th January)

Duplication & Loss



Toni Gabaldón
(30th January)

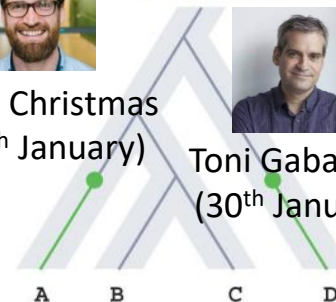


Matt Christmas
(26th January)

Selection



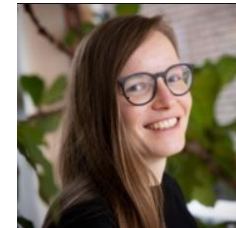
Toni Gabaldón
(30th January)



**Concatenation
+
partitioning**

vs coalescence

PhyKIT



Jacob L Steenwyk &
Karin Steffen (24th January)



Erin Molloy
(25th-26th January)



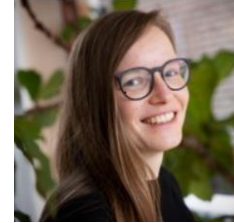
Oleksiy M. Kozlov (25th January)

6)

Model selection & phylogenetic inference

Model selection

Olivier Gascuel
(25th January)



Jacob L Steenwyk &
Karin Steffen (24th January)

Phylogenetic inference

Maximum Likelihood

Coalescence

Bayesian Inference

Oleksiy M. Kozlov
(25th January)



Olivier Gascuel
(25th January)



Jacob L Steenwyk
& Karin Steffen
(24th January)



RAxML-NG



IQ-TREE

PhyML

FastTree

Gene tree summary methods for unrooted trees

e.g. [BUCKy](#) (-pop), [NJst](#) / [USTAR](#) / [ASTRID](#), [ASTRAL](#) / [ASTER](#), [TREE-QMC](#), [wQFM](#)

Gene tree summary methods for rooted trees

e.g. [MDC](#), [STEM](#), [MP-EST](#)

Site-based methods

e.g. [SNAPP](#), [SVDQuartets](#), [CASTER](#)

Bayesian co-estimation methods (co-estimate gene trees & species tree)

e.g. [*BEAST](#), [StarBEAST2](#)

Also see methods based on population allele frequencies

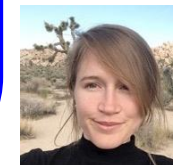
e.g. [PoMo](#), implemented in [RevBayes](#)



PhyloBayes



Gytis Dudas (30th January)



Erin Molloy (25th-26th January)

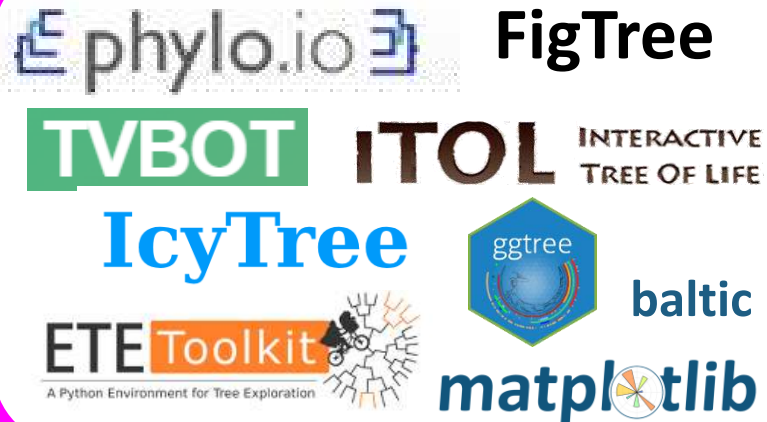


Edu Ocaña-Pallarès (30th January)

7)

Testing the robustness of your tree

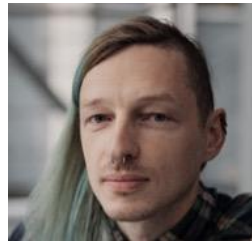
Tree visualization



Michał Karlicki &
Edu Ocaña-Pallarès
(24th January)



Gytis Dudas
(30th January)



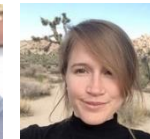
Support

Olivier Gascuel (25th January)

Erin Molloy (25th-26th January)

Oleksiy M. Kozlov (25th January)

Antonis Rokas & Jacob L Steenwyk (29th January)



Phylogenetic bootstrap support

Ultrafast bootstrap

Transfer bootstrap expectation

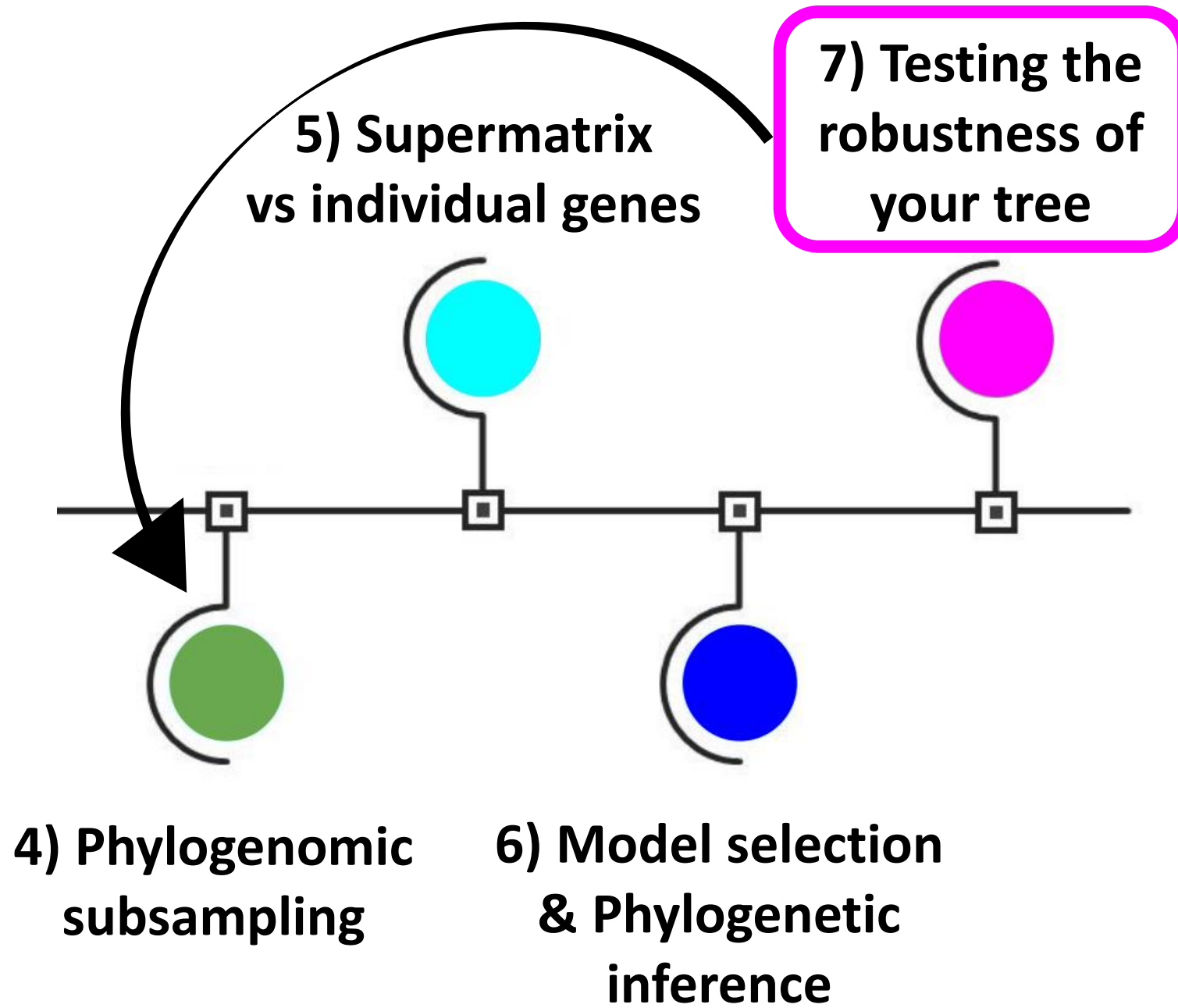
GSF (Gene Support Frequency) // gene concordance factor (gCF)

Internode certainty

Tree certainty

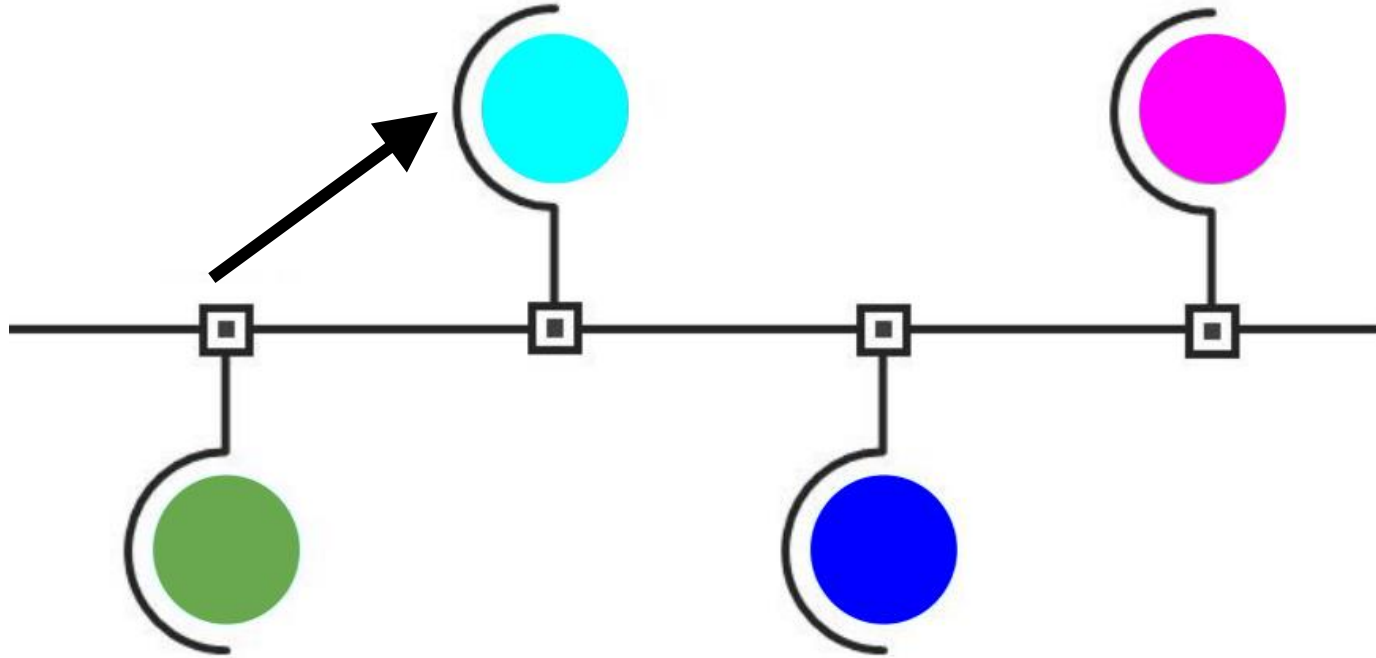
...

Incongruence



**5) Supermatrix
vs individual genes**

**7) Testing the
robustness of
your tree**

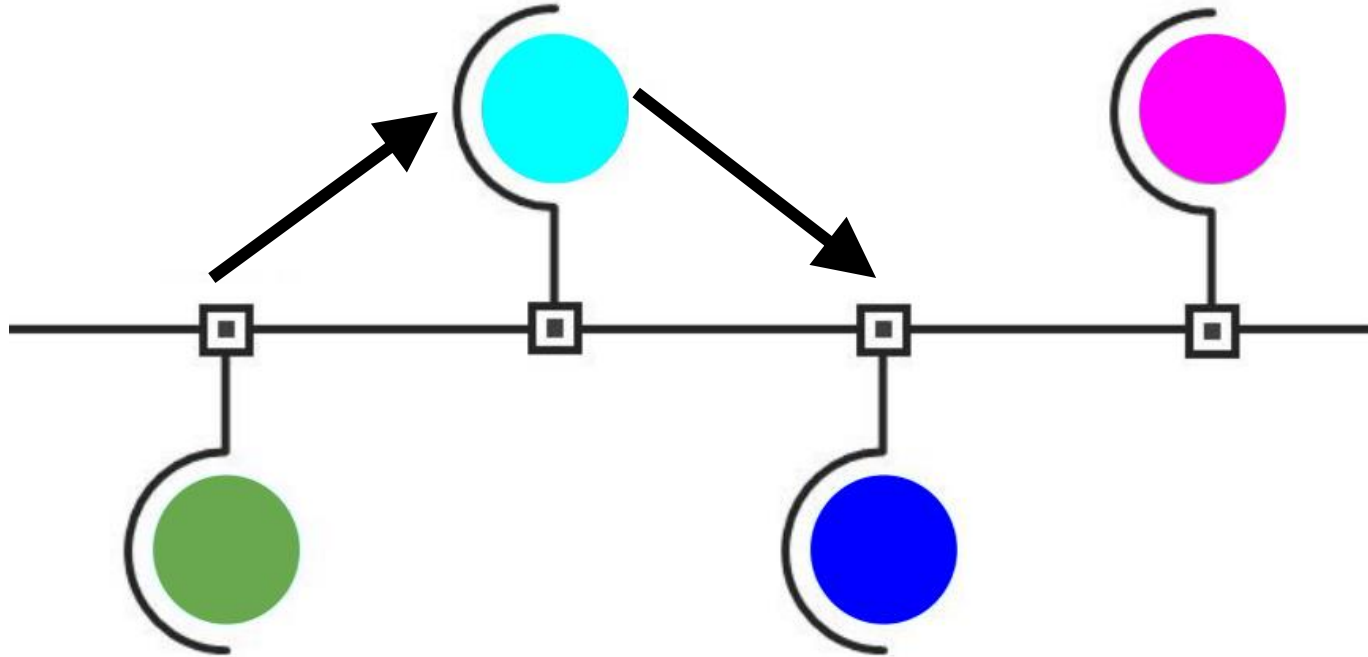


**4) Phylogenomic
subsampling**

**6) Model selection
& Phylogenetic
inference**

**5) Supermatrix
vs individual genes**

**7) Testing the
robustness of
your tree**

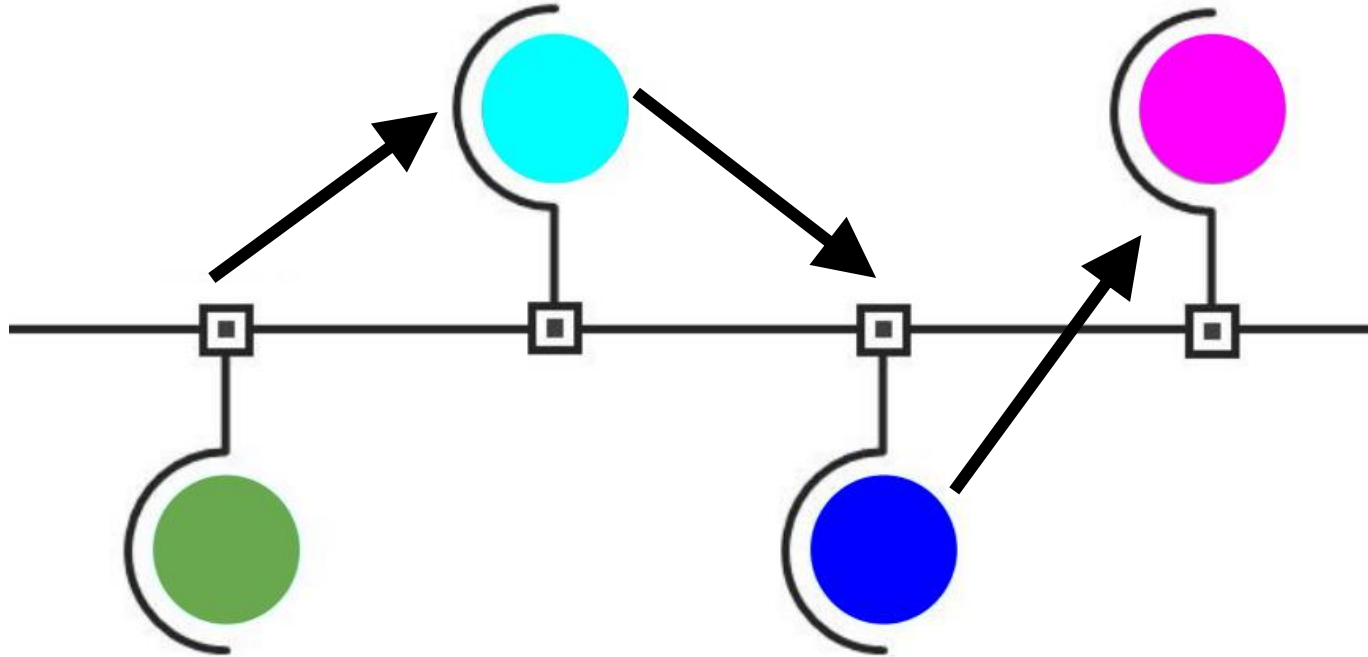


**4) Phylogenomic
subsampling**

**6) Model selection
& Phylogenetic
inference**

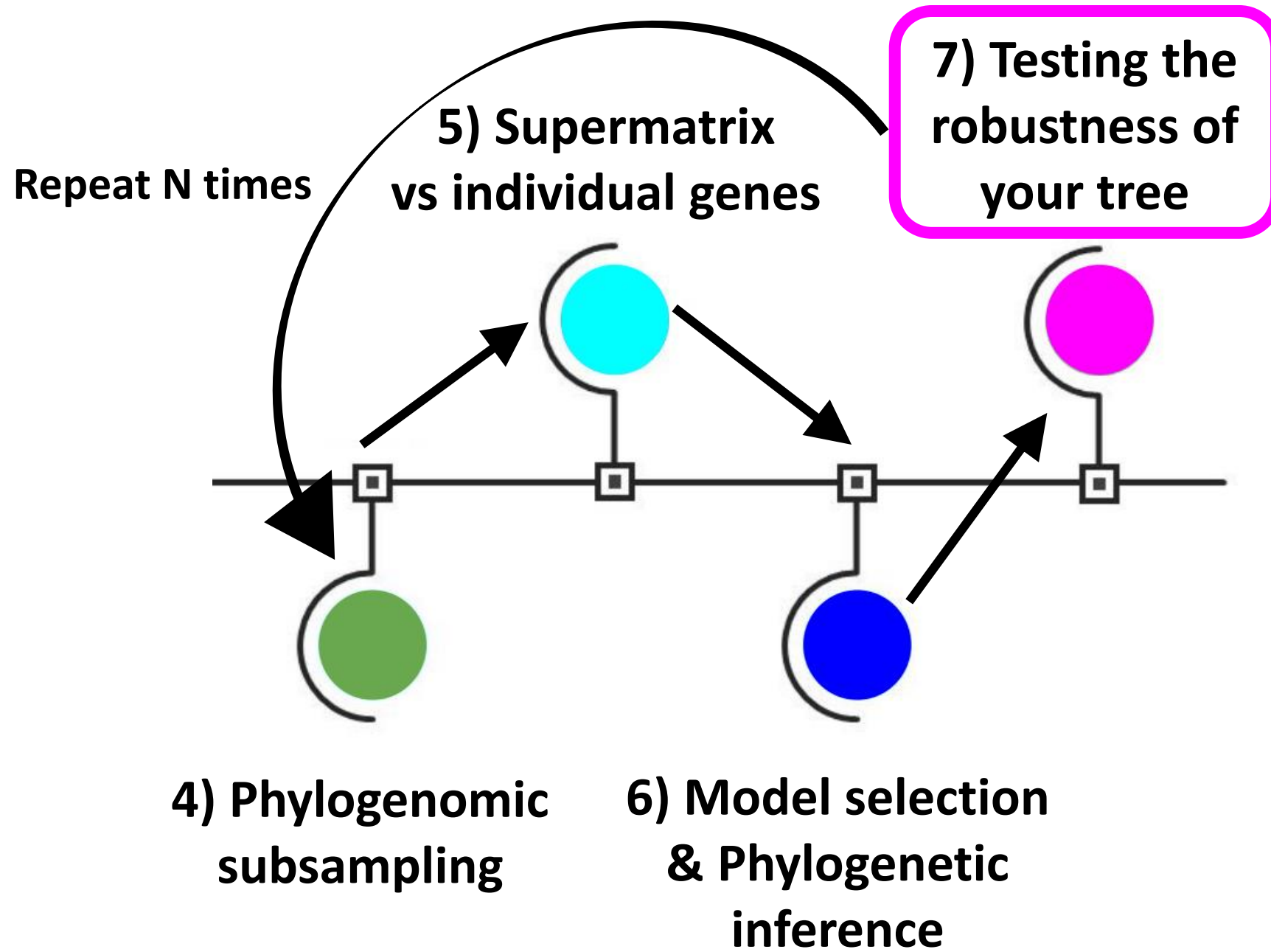
**5) Supermatrix
vs individual genes**

**7) Testing the
robustness of
your tree**



**4) Phylogenomic
subsampling**

**6) Model selection
& Phylogenetic
inference**



8) Post-tree building analyses



Hélène Morlon
(26th January)



Matt Christmas
(26th January)



Matt Christmas
(26th January)



Toni Gabaldon
(30th January)

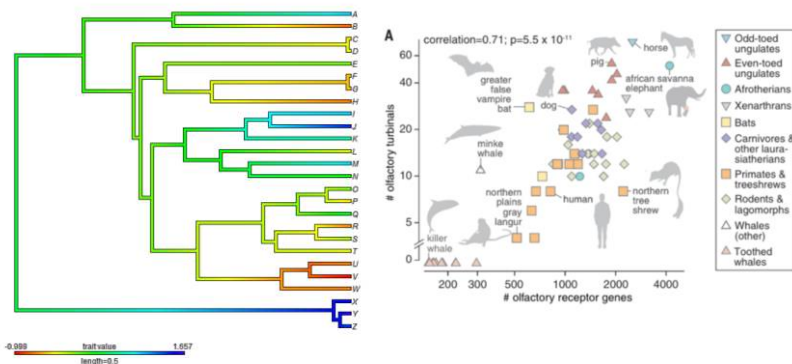


Antonis Rokas
(31th January)

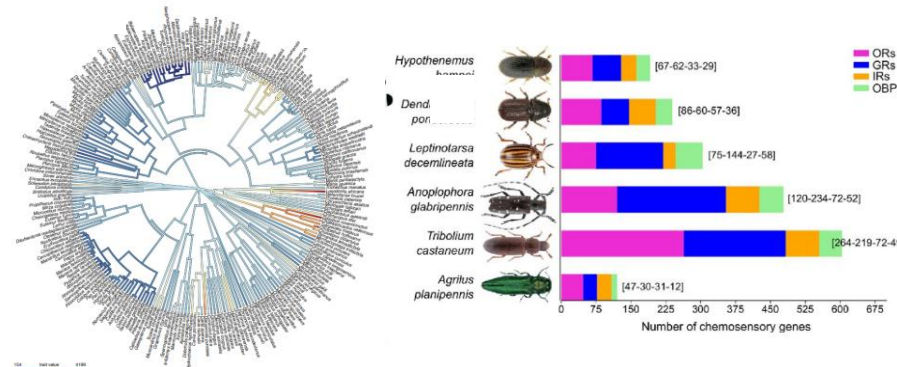


Lisa Pokorny
(31st January)

Trait evolution



Comparative genomics



Population Genomics

Museomics

Biogeography