UNDERSTANDING AND USING PHYLOGENETIC TREES IN YOUR RESEARCH

E Tuschhoff

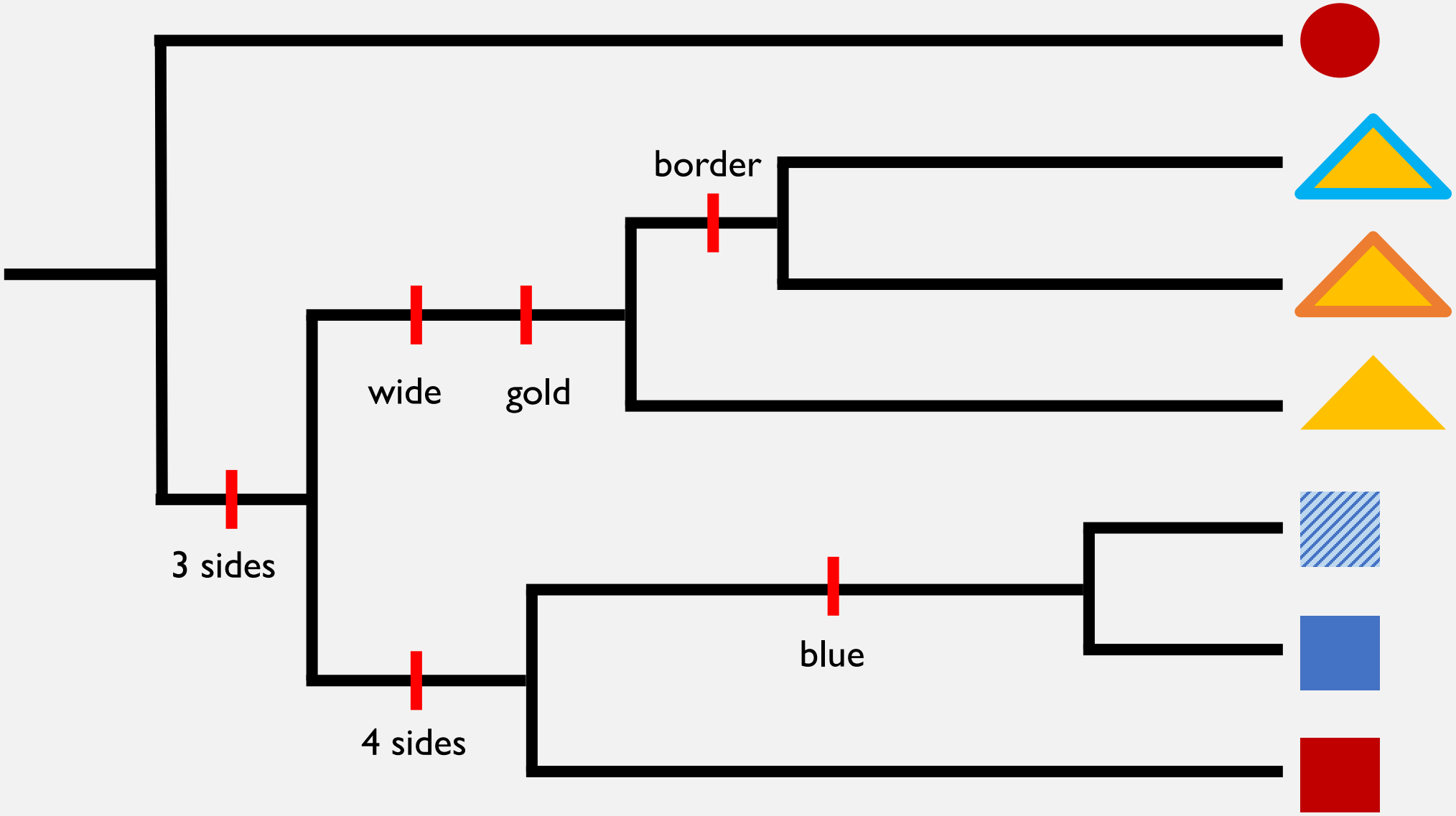
Wiens lab

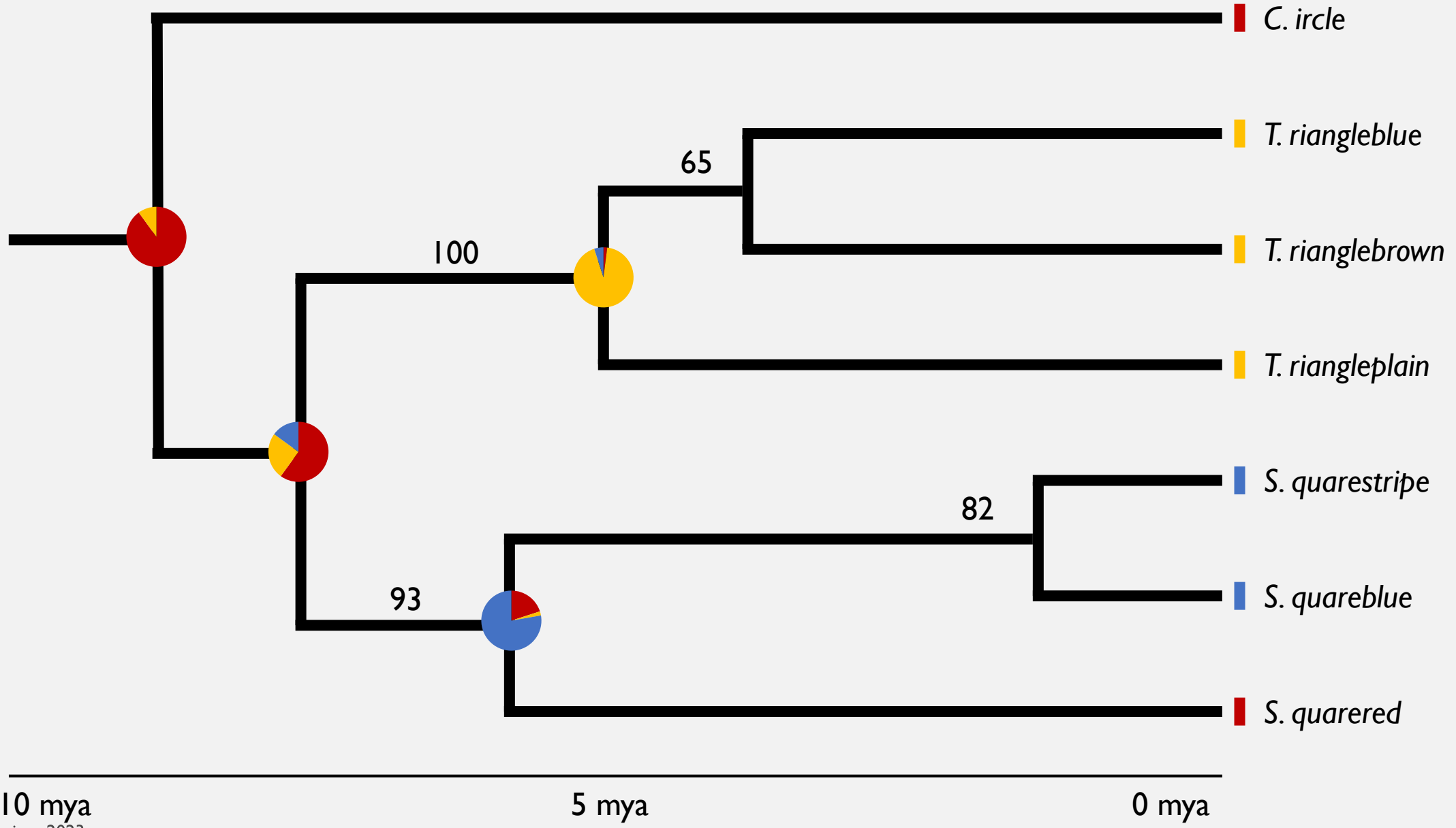
Tuesday Seminar 4/11

OUTLINE

1. What information is on trees?
2. Using trees in research
3. R coding overview

WHAT INFORMATION IS ON TREES?


border
wide
gold
3 sides
blue
4 sides


C. ircle
T. riangleblue
T. rianglebrown
T. riangleplain
S. quarestripe
S. quareblue
S. quarered
65
100
82
93
10 mya
5 mya
0 mya

WHAT INFORMATION IS ON TREES?

Relationships

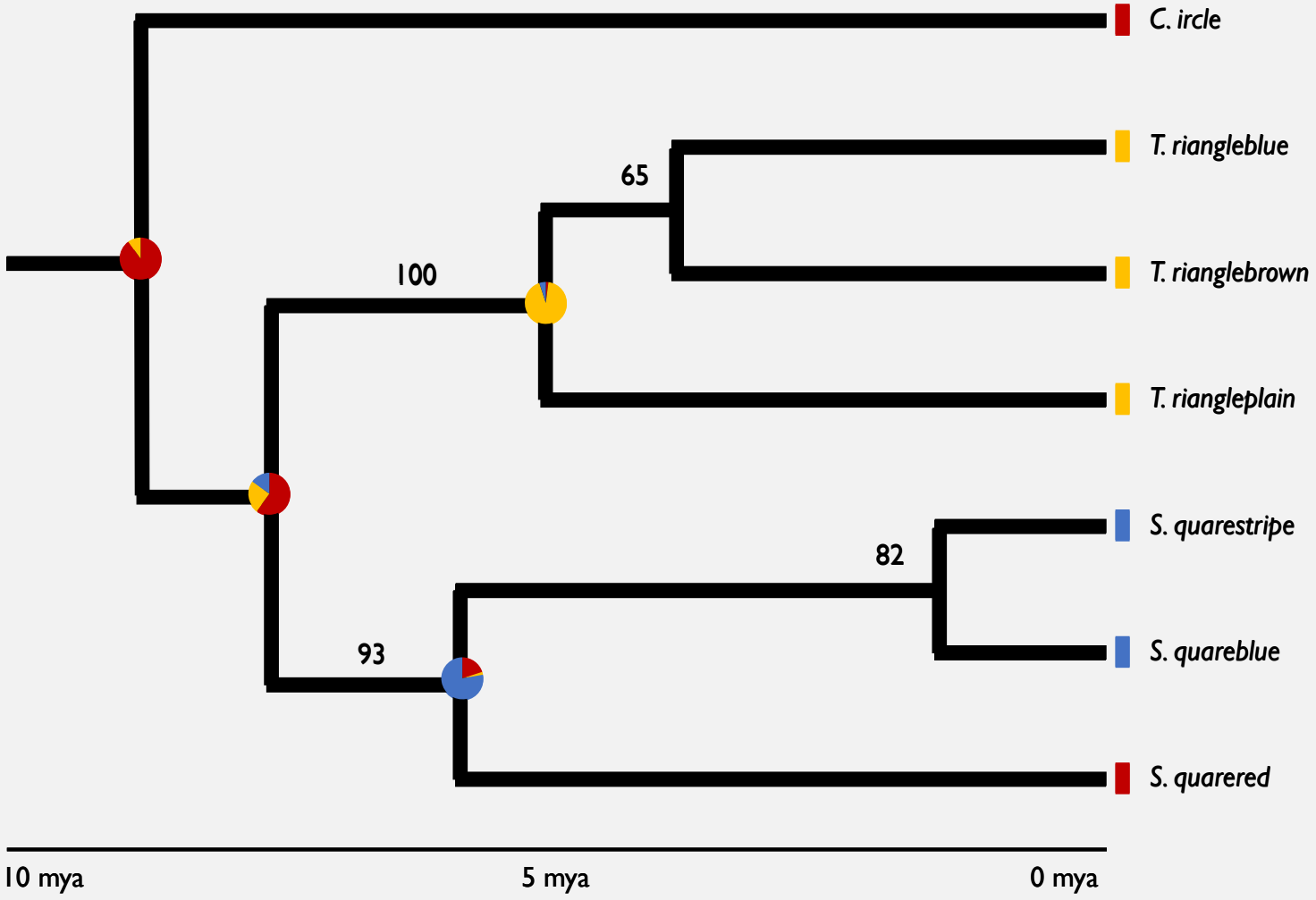
Traits

Taxonomic labels

Time

Ancestral reconstructions

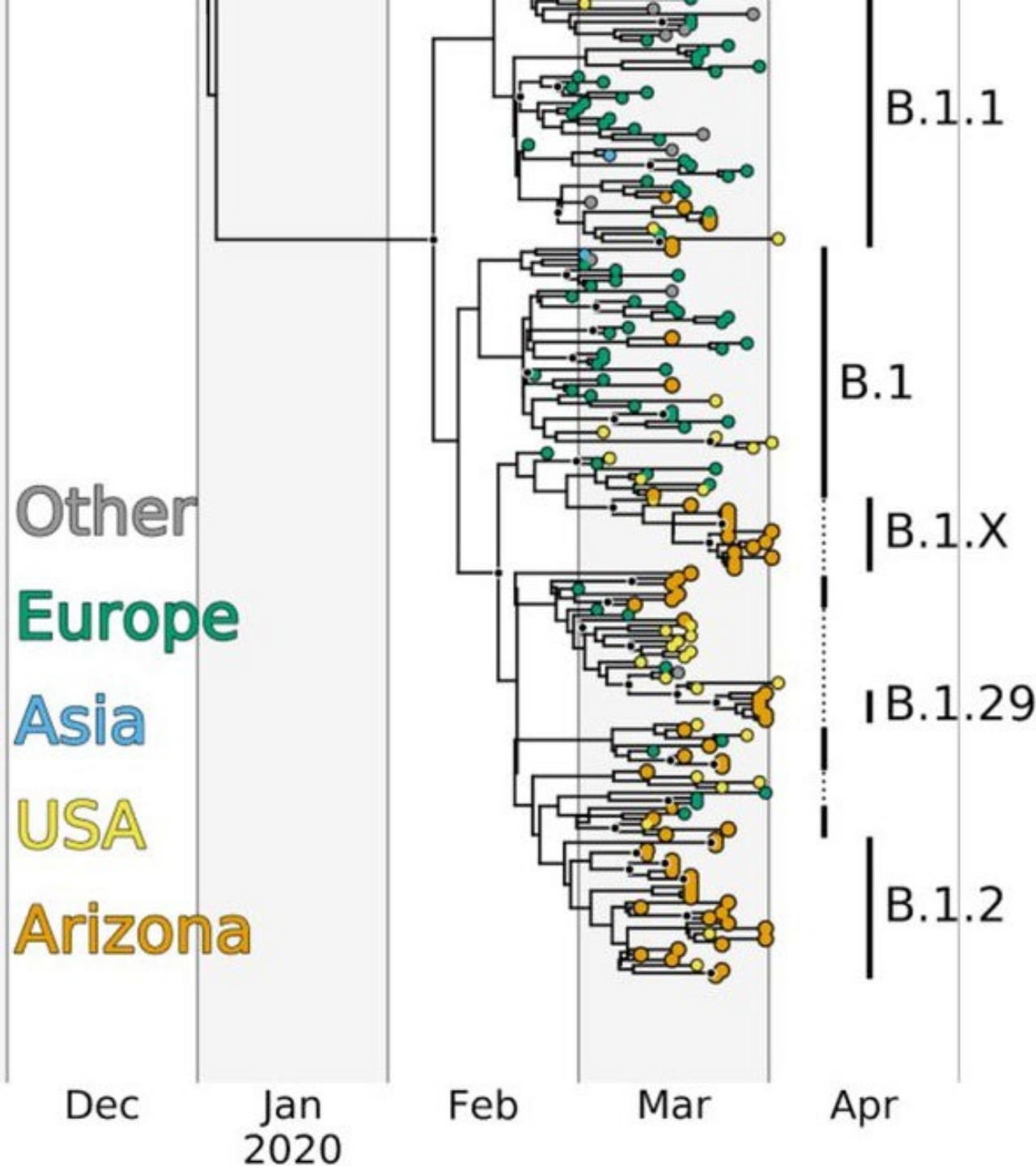
Confidence



WAYS TO USE TREES

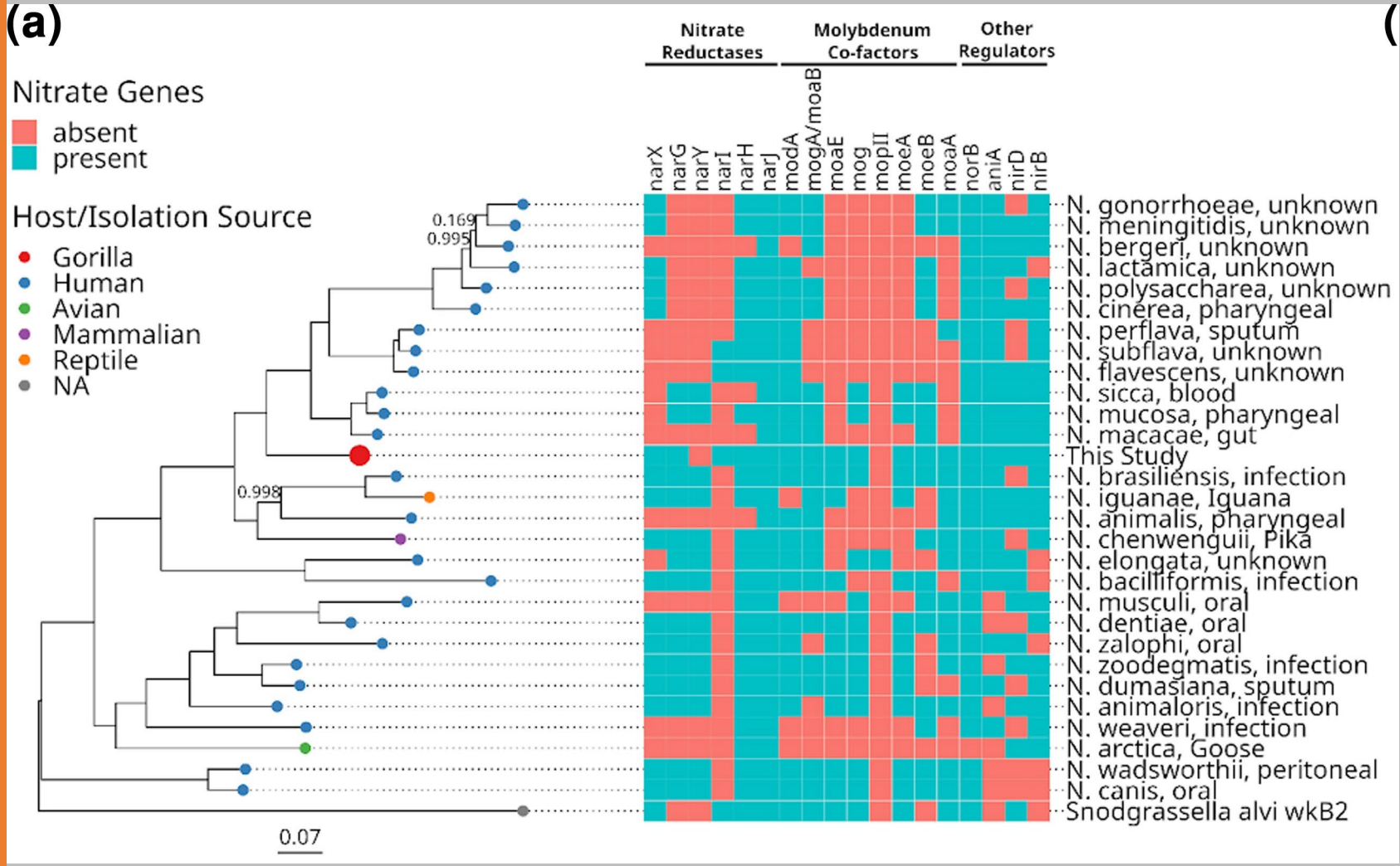
DISEASE DYNAMICS

Ladner et al. 2020



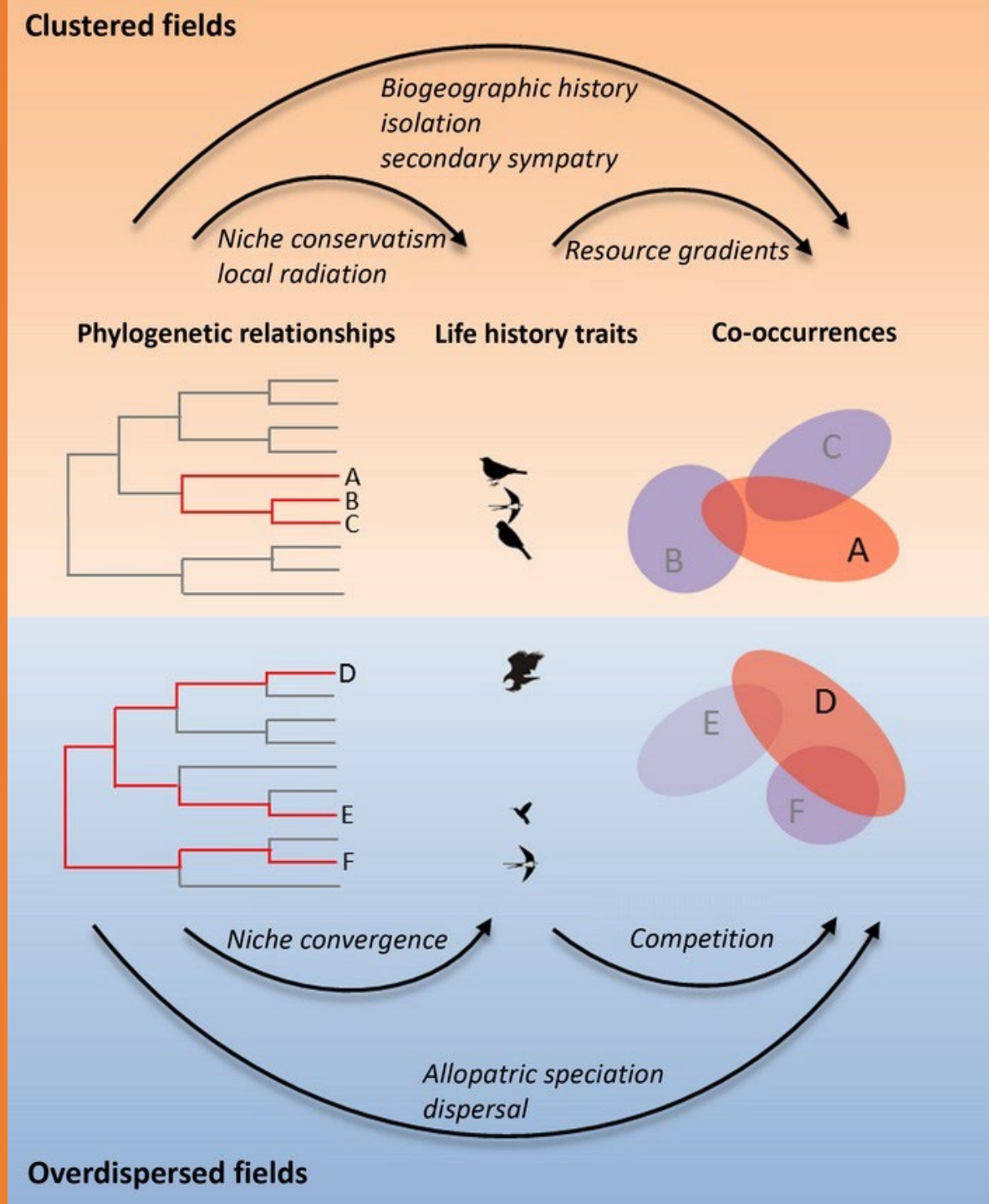
MICRO BIOMES

Moraitou et al. 2022



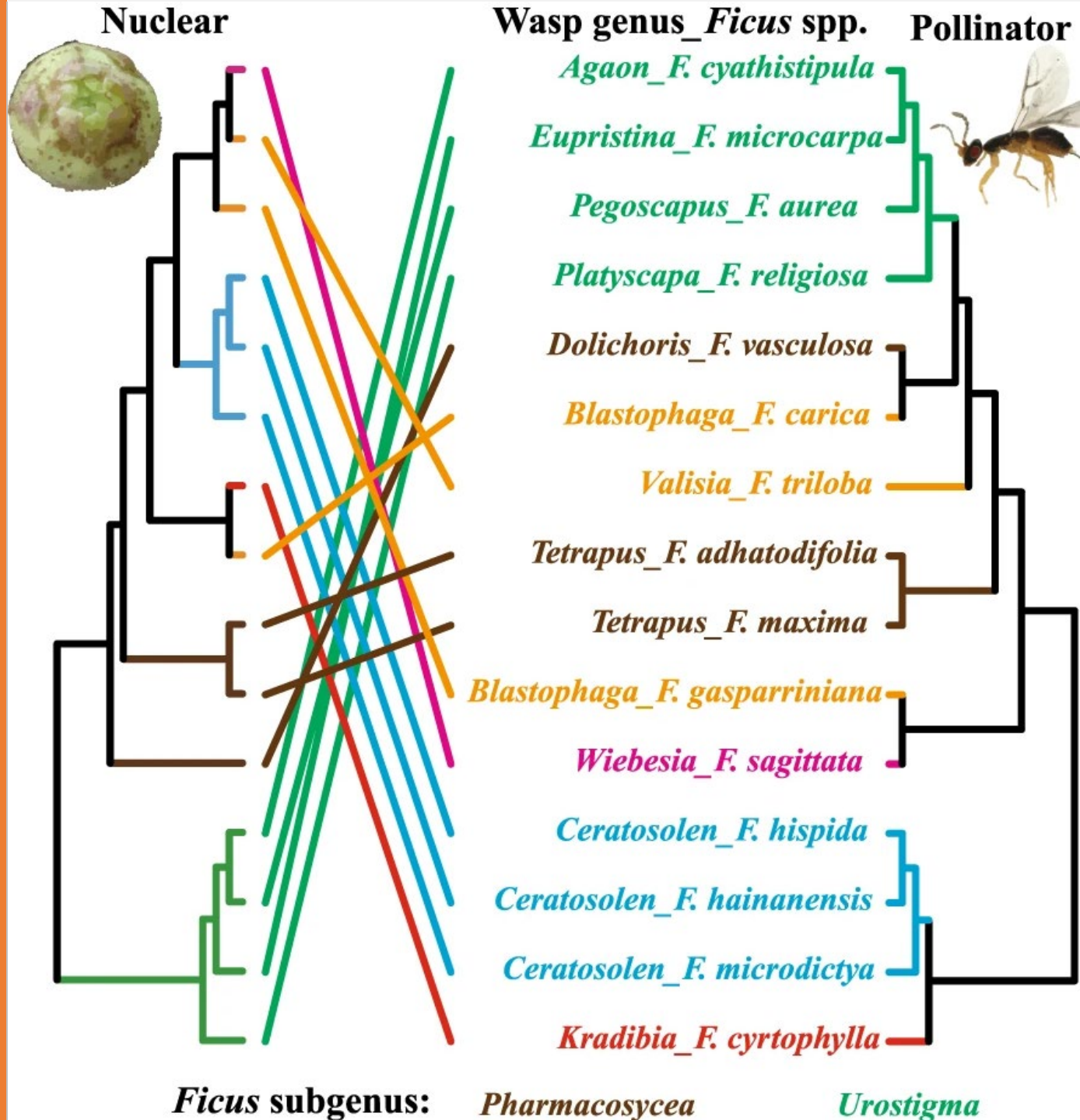
SPECIES CO-OCCURRENCE

Barnagaud et al. 2014



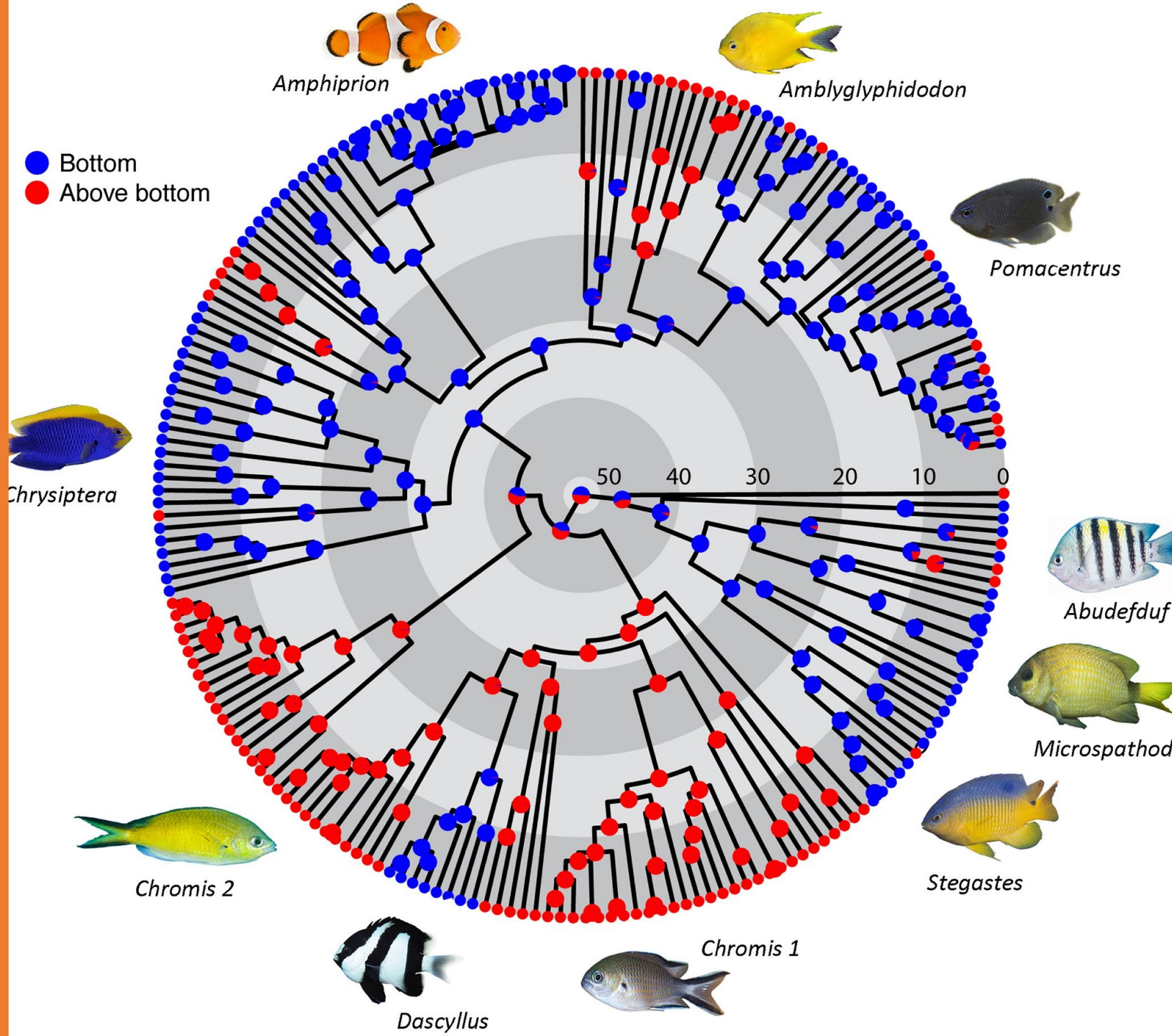
COEVOLUTION

Wang et al. 2021



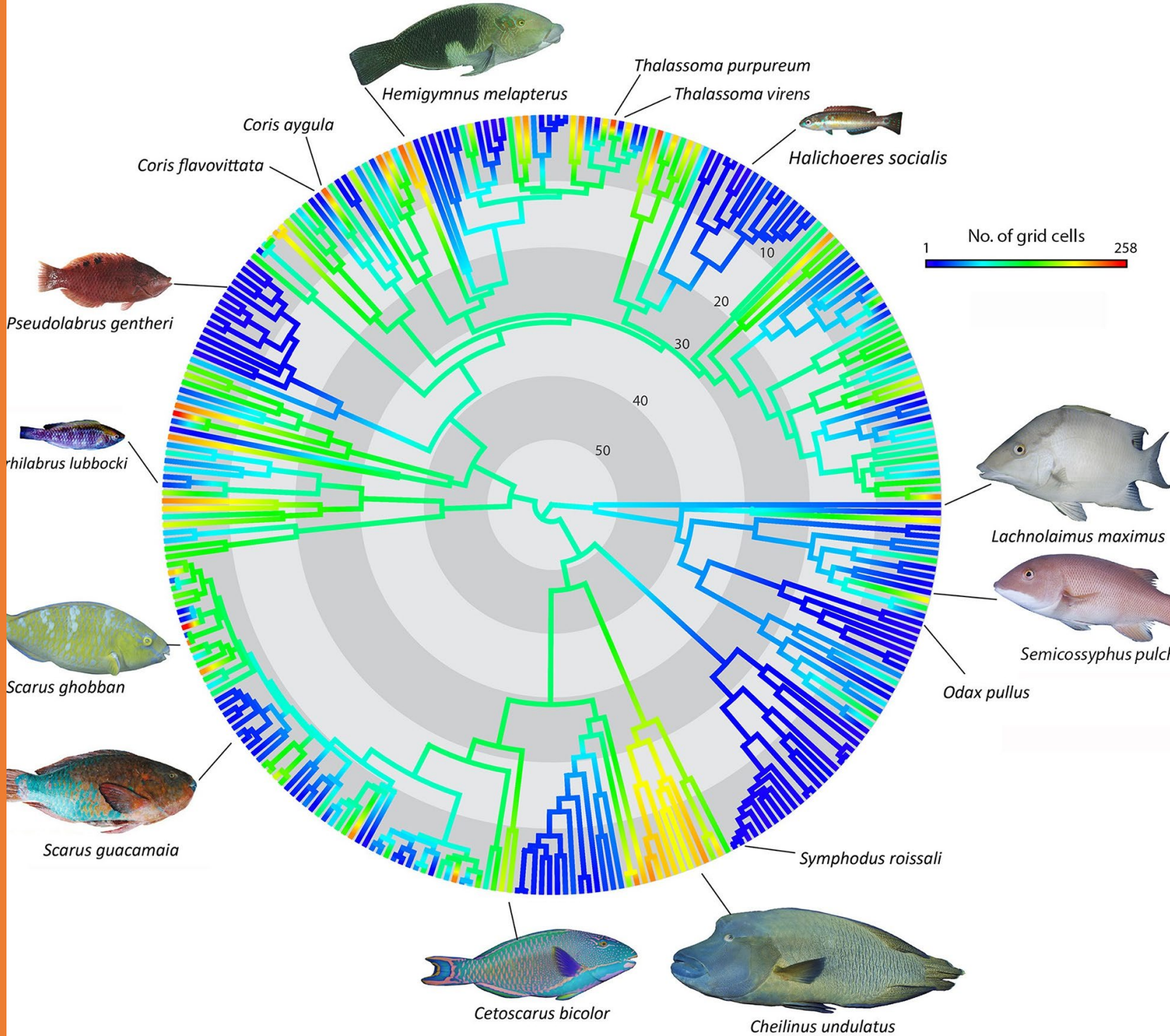
FUNCTIONAL TRAITS

Floeter et al. 2017



FUNCTIONAL TRAITS

Floeter et al. 2017



USING TREES IN RESEARCH

CREATING TREES DE NOVO

- Relationships between organisms are unknown
- Use a variety of traits
  - Morphology
  - Behavior
  - Genetics
- Incorporate fossils and molecular clocks for dating

USING EXISTING TREES

- Finding the right tree
  - Broadness
  - Detail
  - Current hypotheses

FROG EXAMPLE: QUESTION

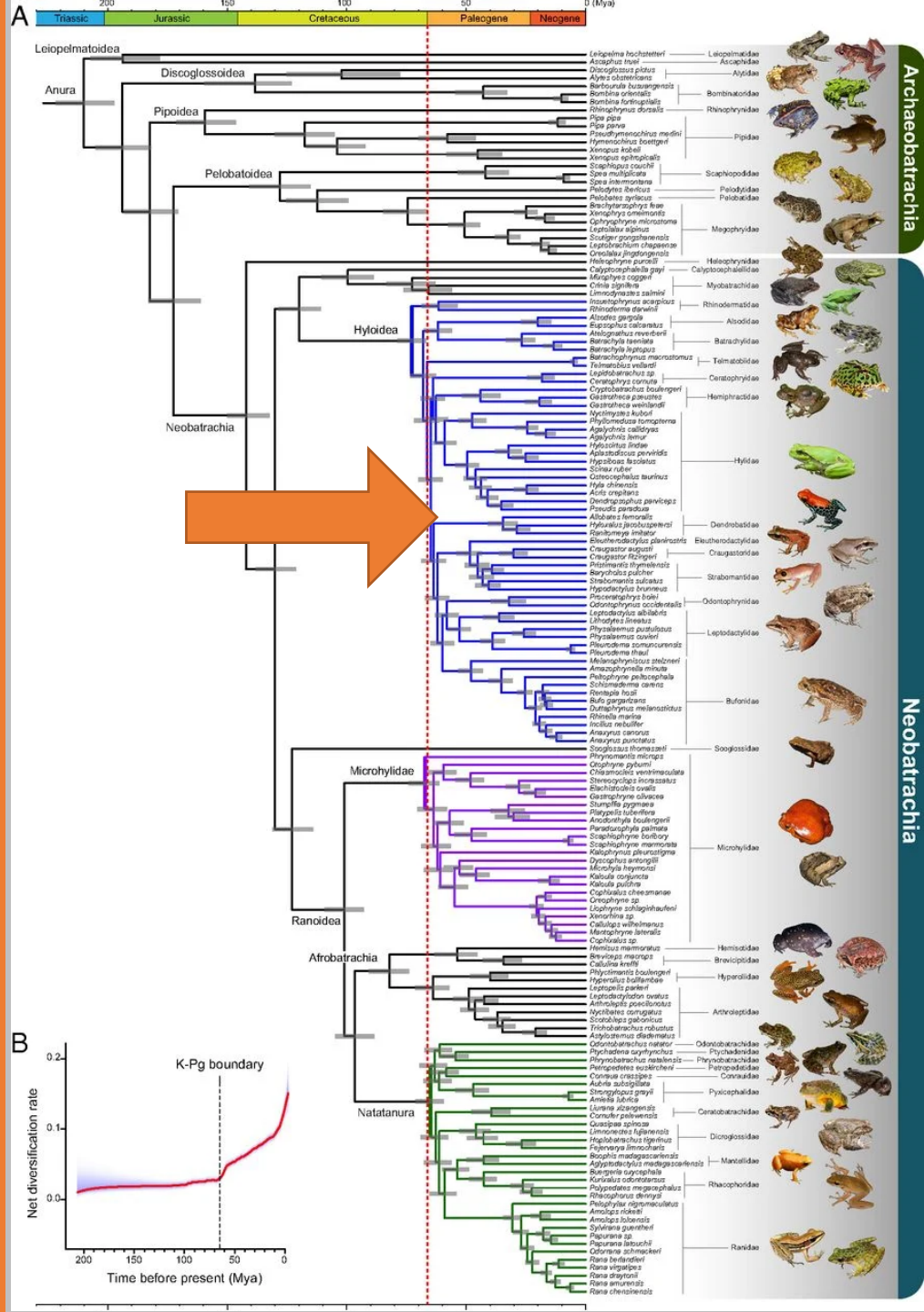
- Evolution of parental care in poison frogs
  - Broadness: Include all dendrobatid frogs
  - Detail: Tips represent species

FROG EXAMPLE: STEPS

1. Find a paper with a useful tree
2. Find the tree file
3. Download tree file and use

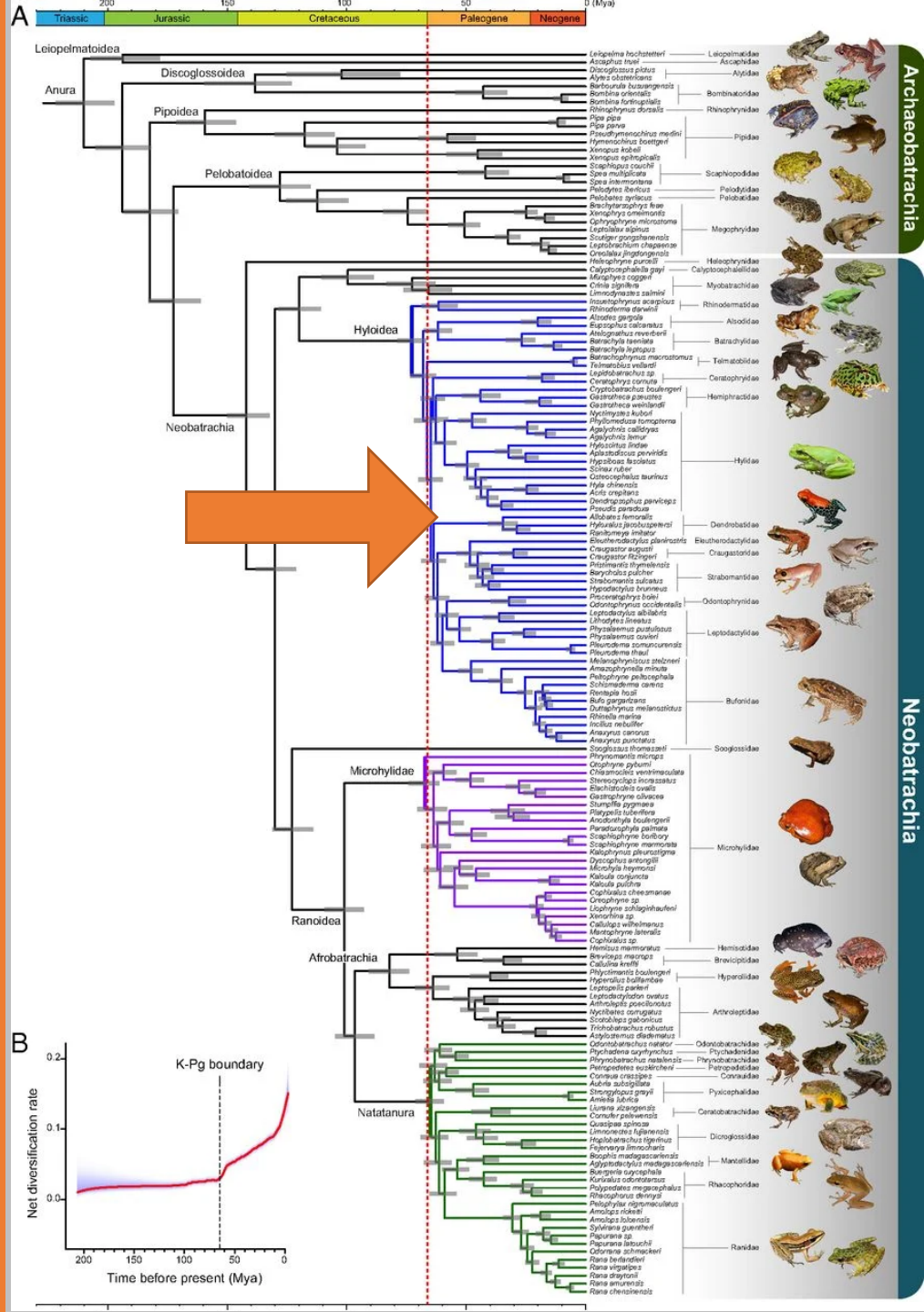
ALL FROGS

Feng et al. 2017



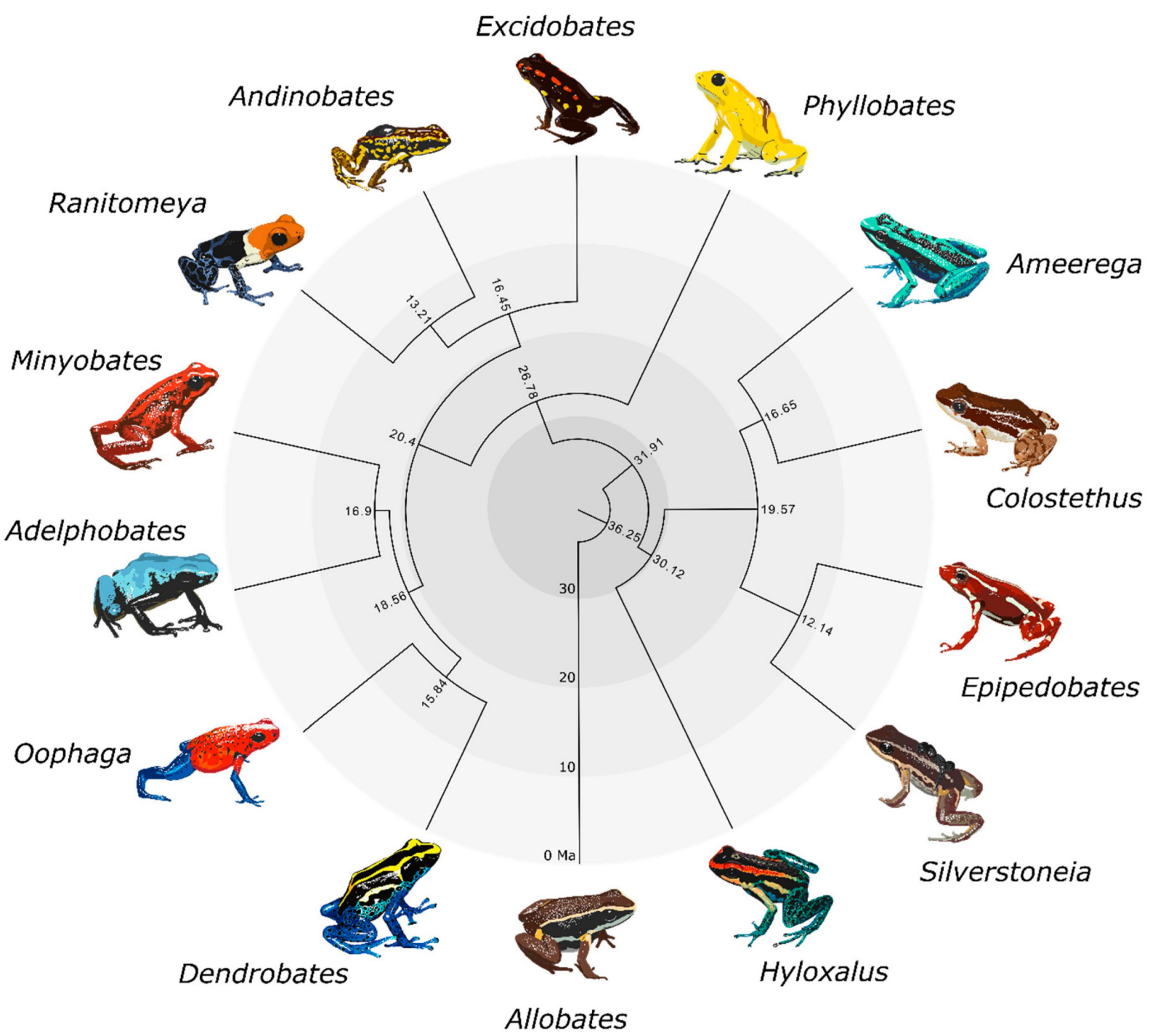
TOO BROAD

Feng et al. 2017



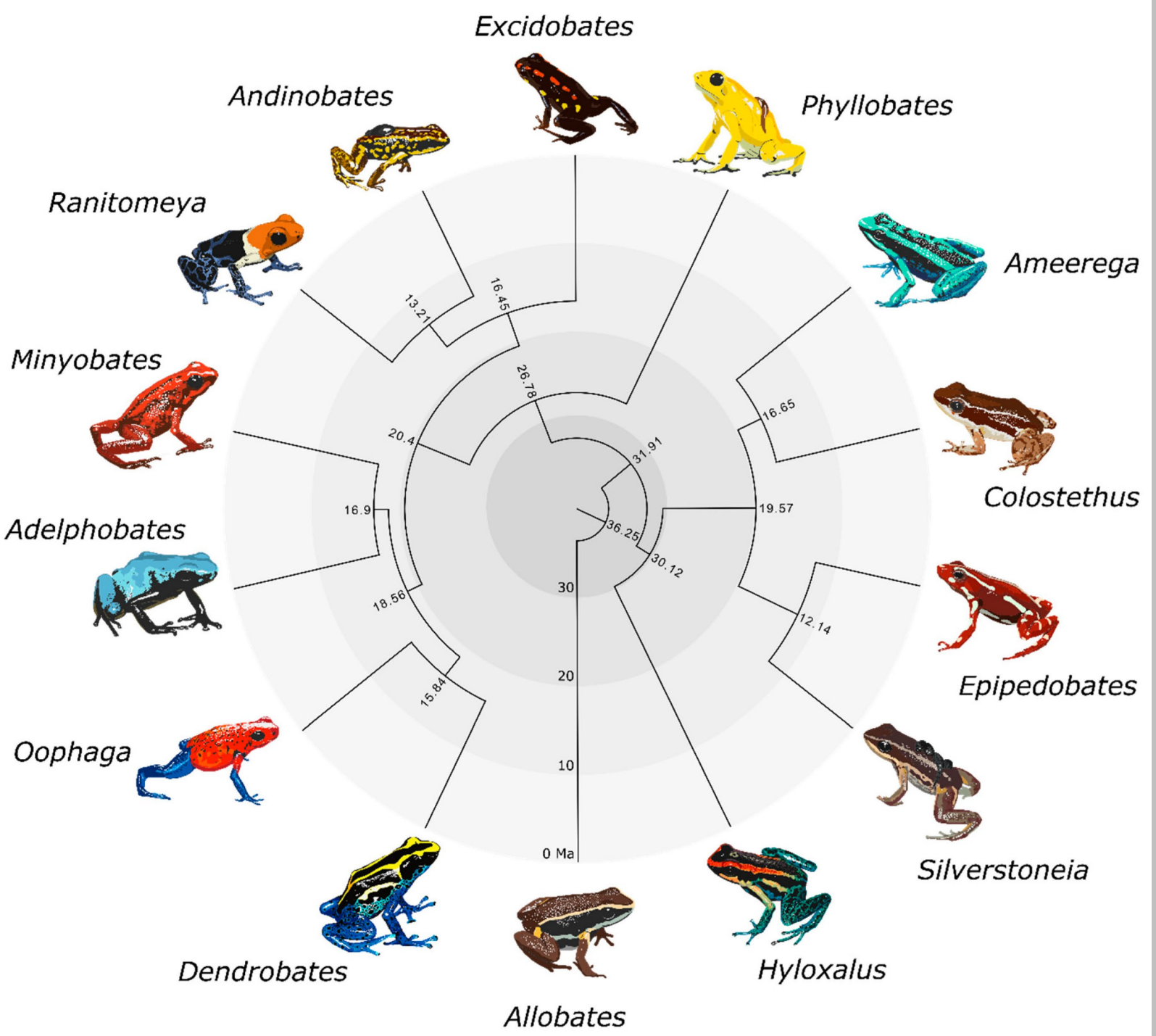
DENDROBATIDAE

Guillory et al. 2019



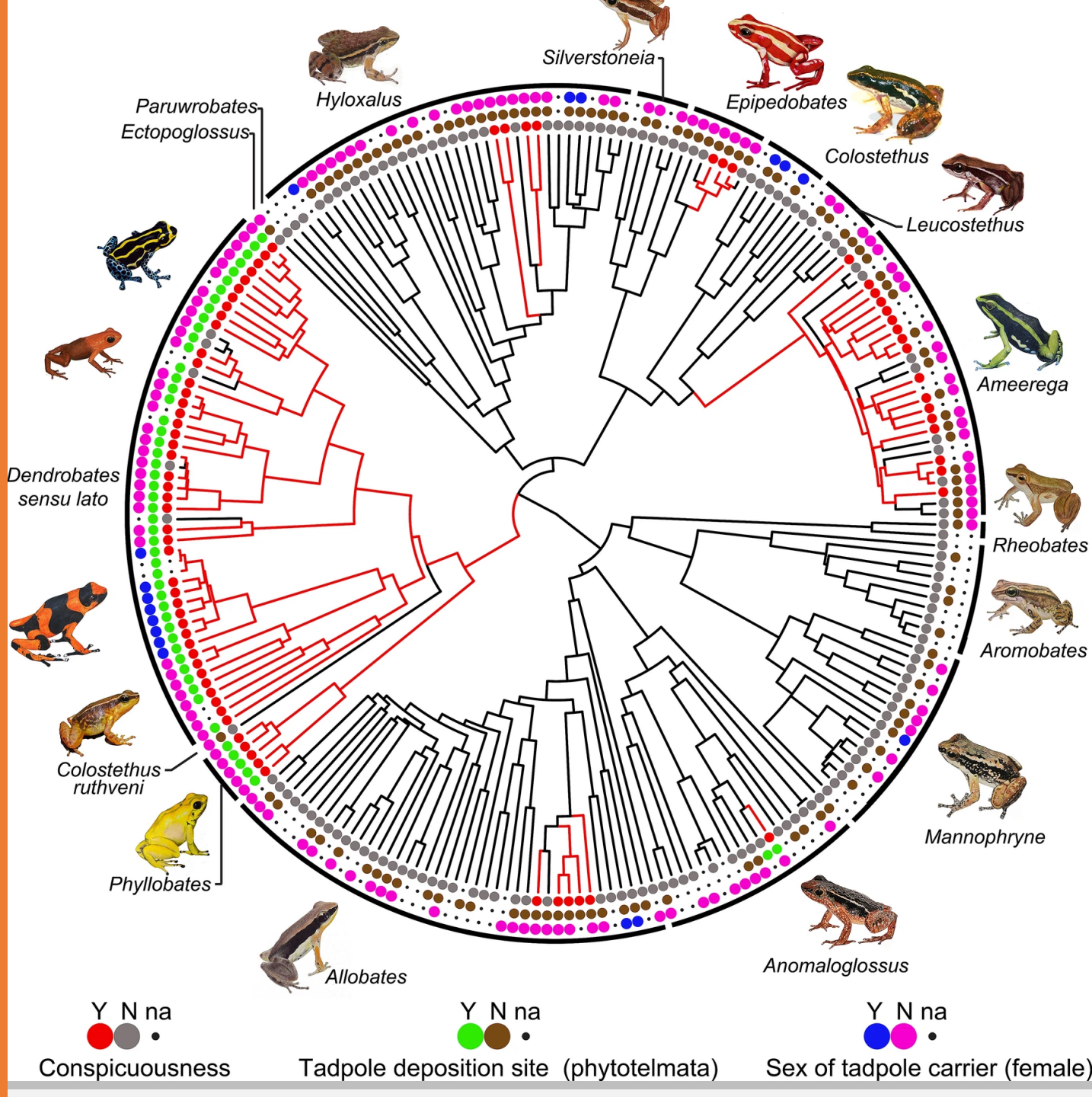
GOOD SCALE TIPS ARE GENERA

Guillory et al. 2019



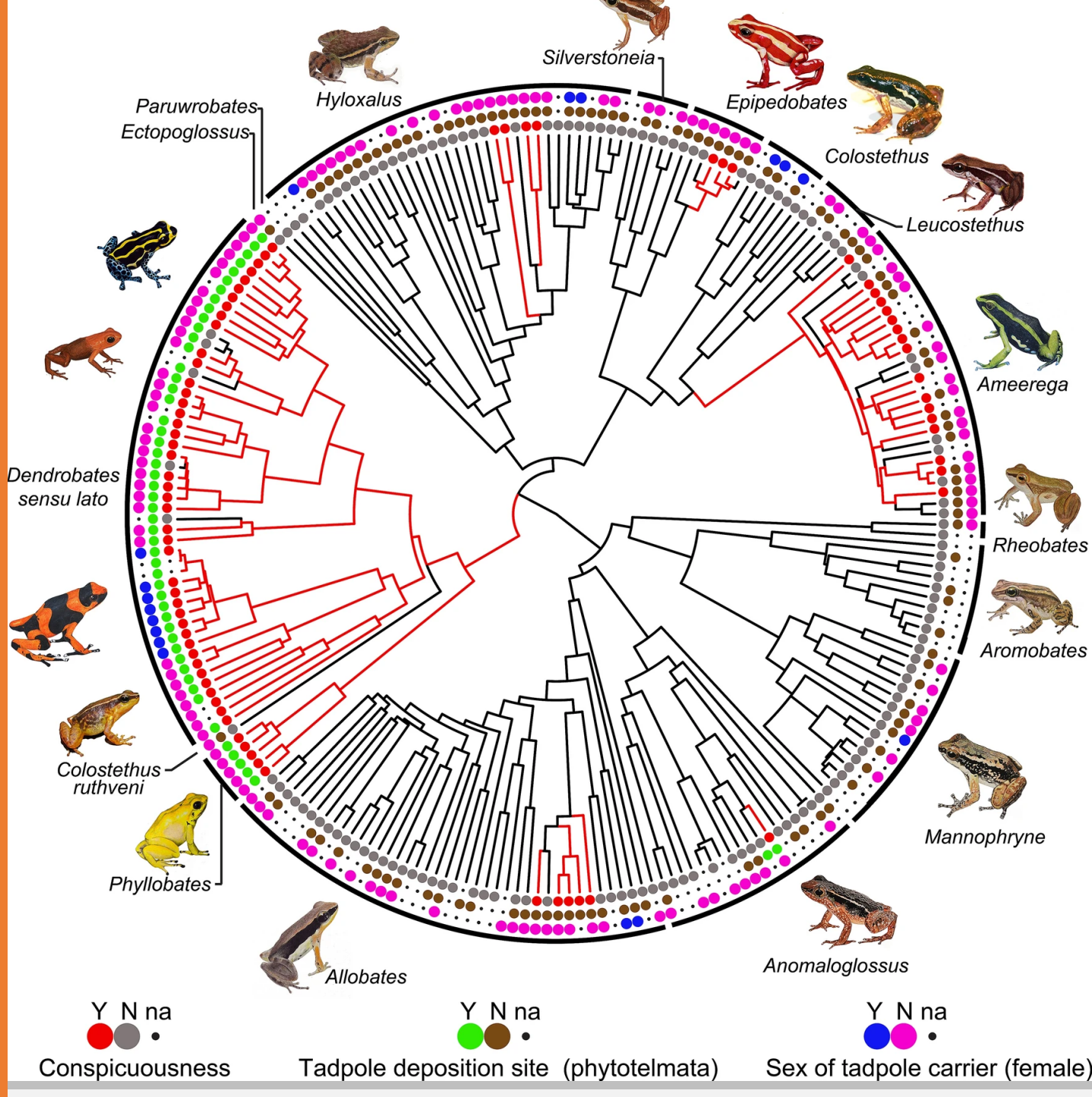
DENDROBATIDAE

Carvajal-Castro et al. 2021



GOOD SCALE TIPS ARE SPECIES

Carvajal-Castro et al. 2021



FROG EXAMPLE: STEPS

1. ~~Find a paper with a useful tree~~
   a. Carvajal-Castro et al. 2021
2. Find the tree file
3. Download tree file and use

FROG EXAMPLE: FIND TREE

- Read methods of Carvajal-Castro et al. 2021
- Did they make their own tree?
  - If yes, look in supplementary materials or data accessibility statement
  - If no, look at source paper

PHYLOGENETIC DATABASES

- Dryad: data repository with many trees
- Open Tree of Life: find supporting and conflicting studies for nodes
- MorphoBank: matrices of morphological characters and associated trees
- PhylomeDB: gene phylogenies
- DataOne: search across multiple databases

TREES IN R

TREE FORMATS

Newick:

- Tips
- Sister taxa
- Branch lengths

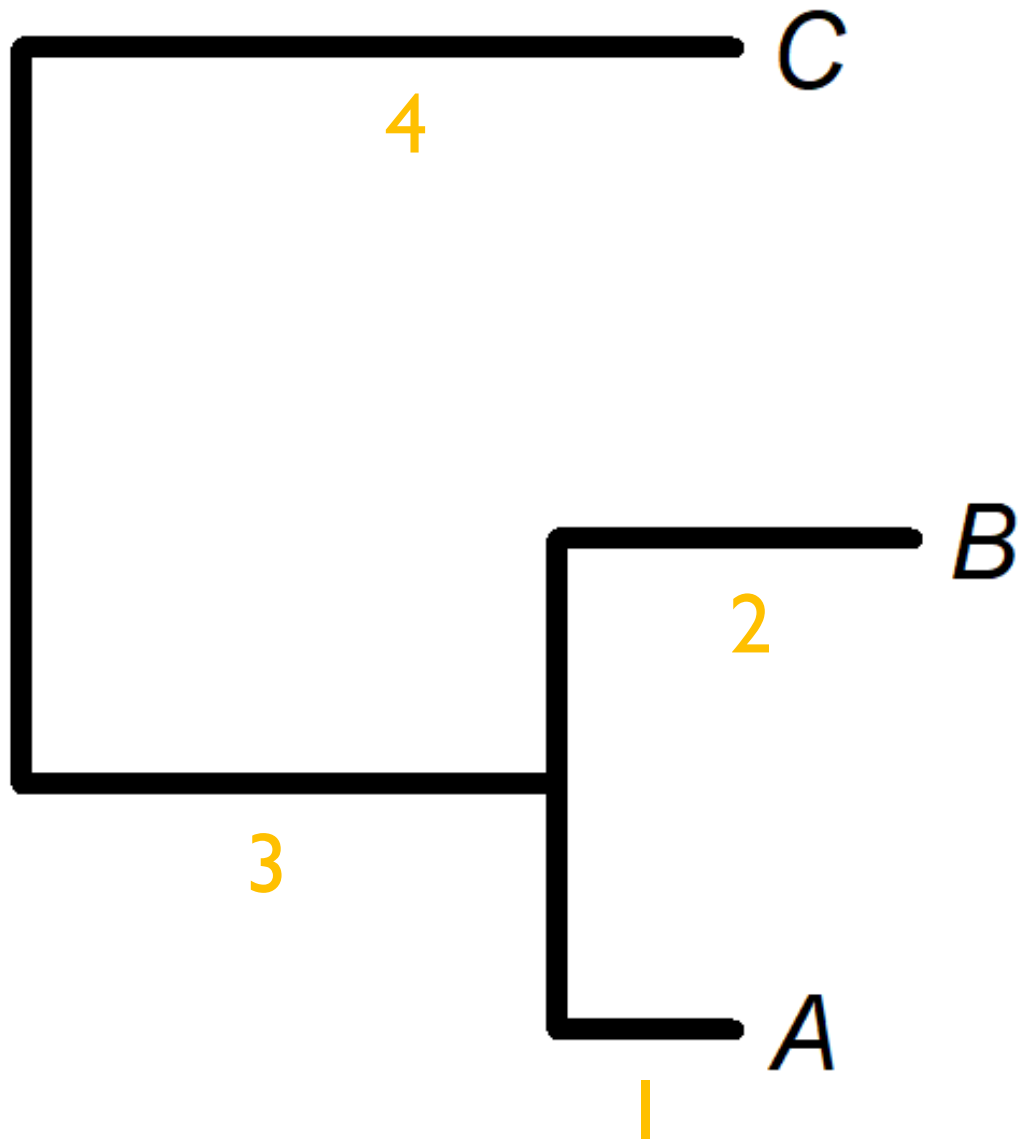
((A:1,B:2):3,C:4);

((A:1,B:2):3,C:4);

Tips

Sister taxa

Branch lengths



TREE FORMATS

- Phylip: includes multiple sequence alignments
- NEXUS: includes comments and additional information in blocks

PLOTTING A TREE IN R

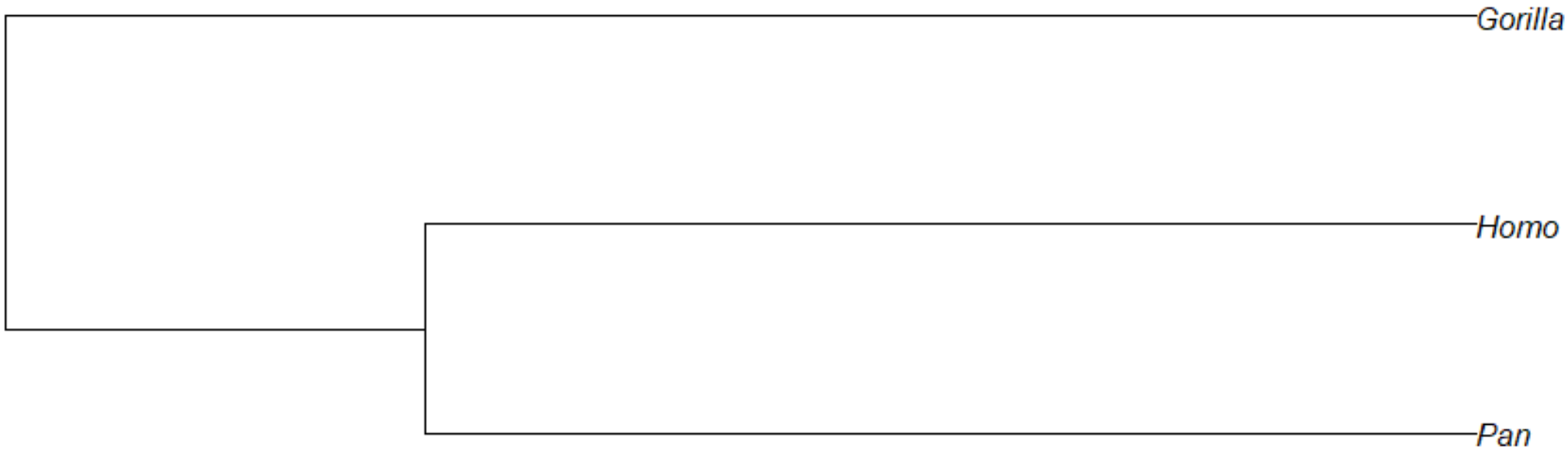
Package: ape

Functions:

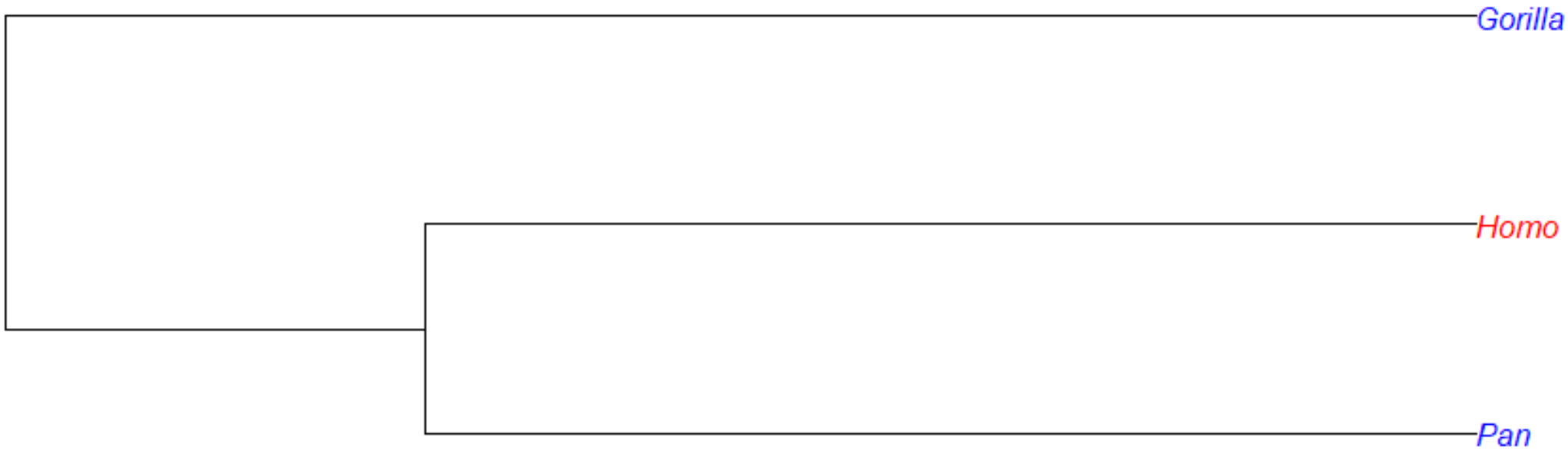
read.tree() for Newick trees

read.nexus() for NEXUS trees

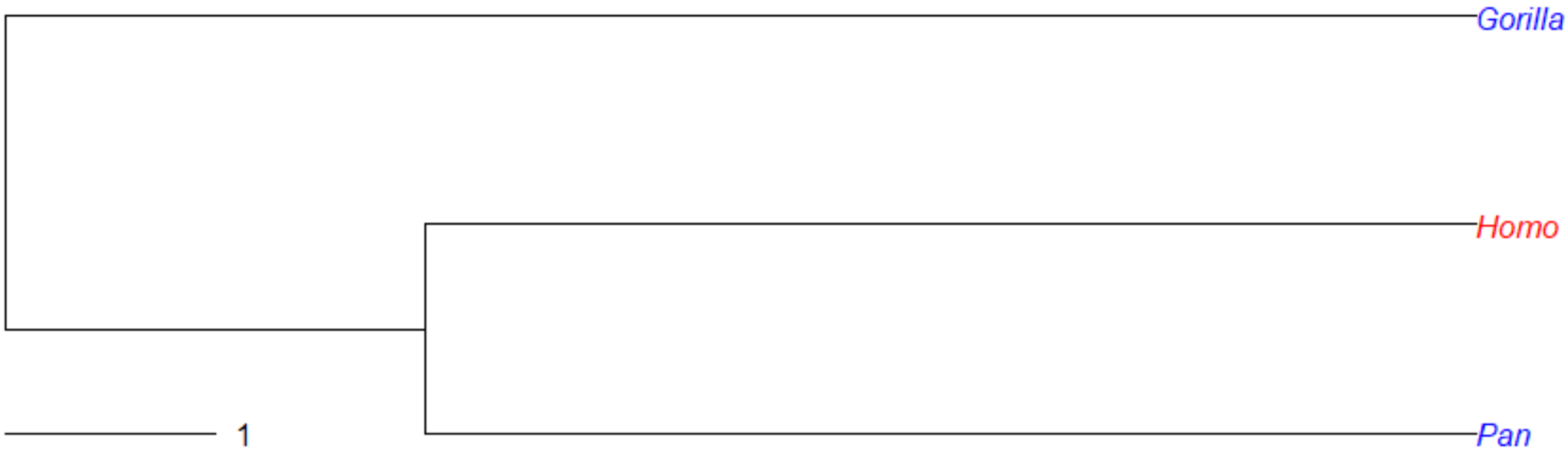
plot.phylo() draw and adjust appearance



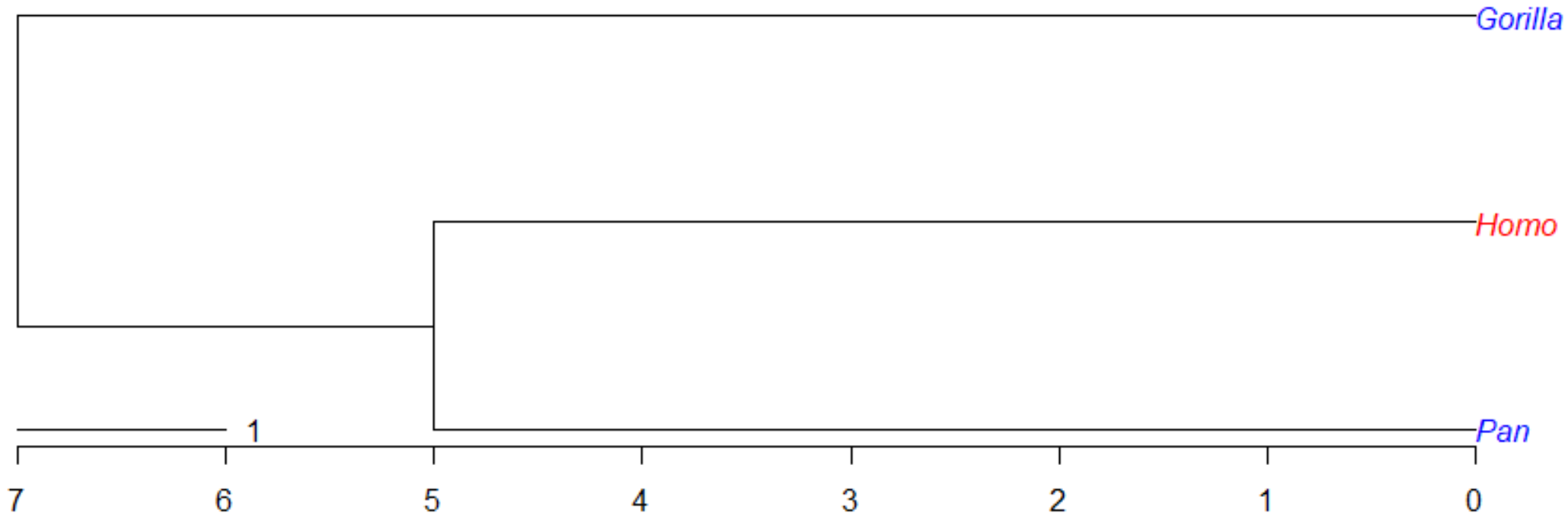

```
library(ape)
mytr <- read.tree(text = "((pan:5,homo:5):2,gorilla:7);")
plot.phylo(mytr)
```



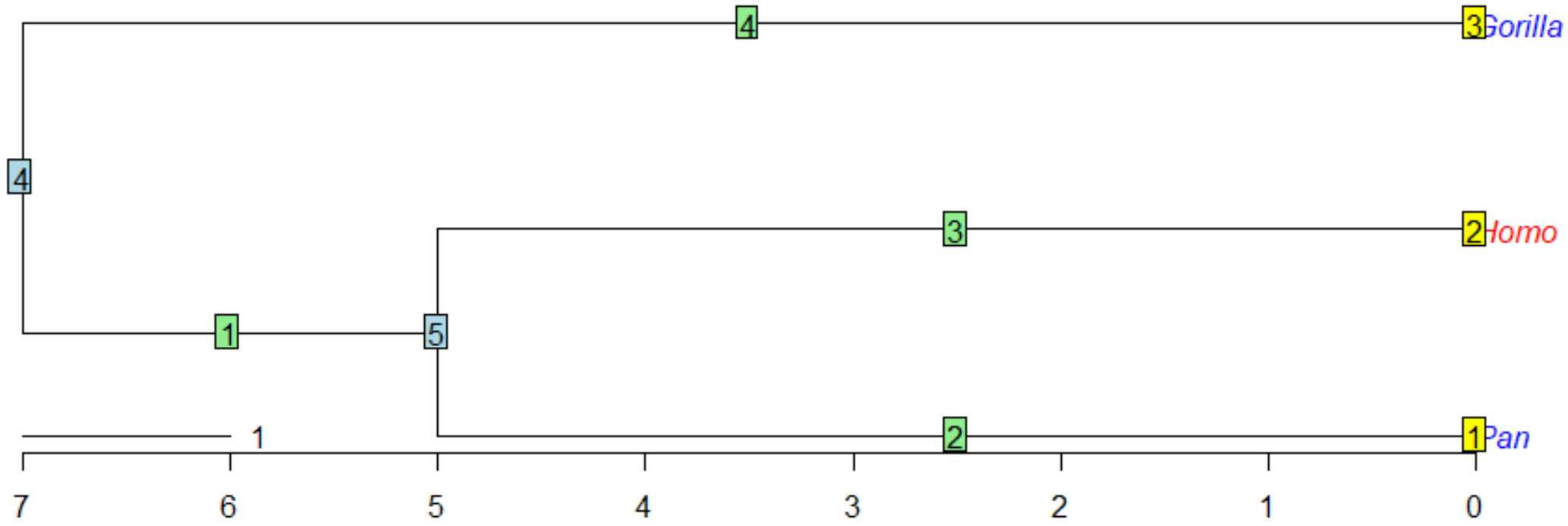

```
geo <- factor(c("Africa", "World", "Africa"))
mycol <- c("blue", "red")[geo]
plot.phylo(mytr, tip.color = mycol)
```



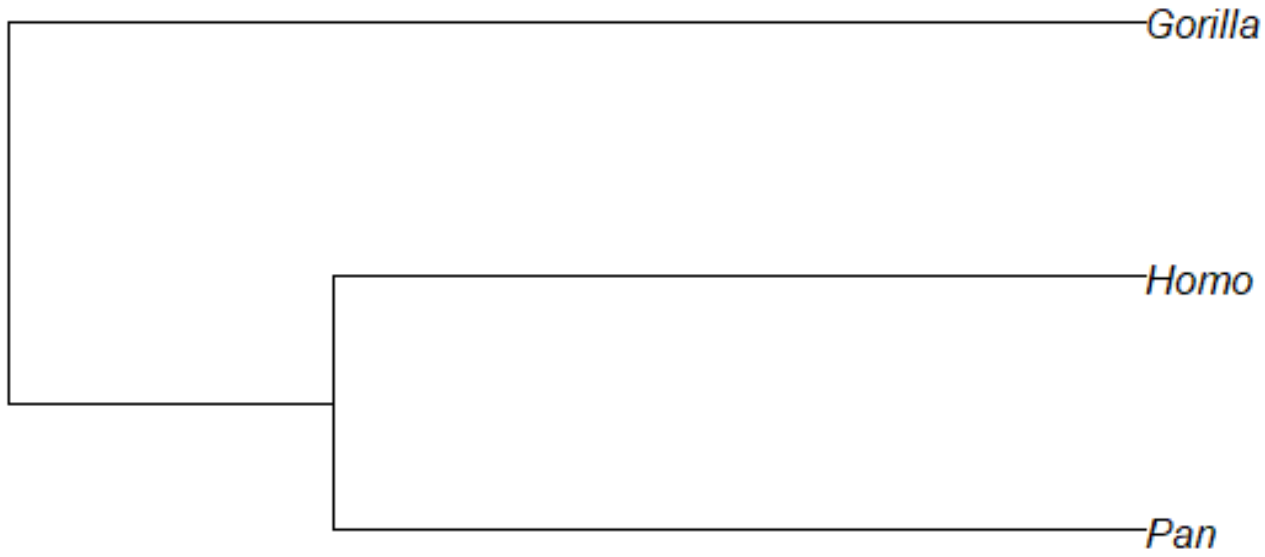

```
add.scale.bar()
```

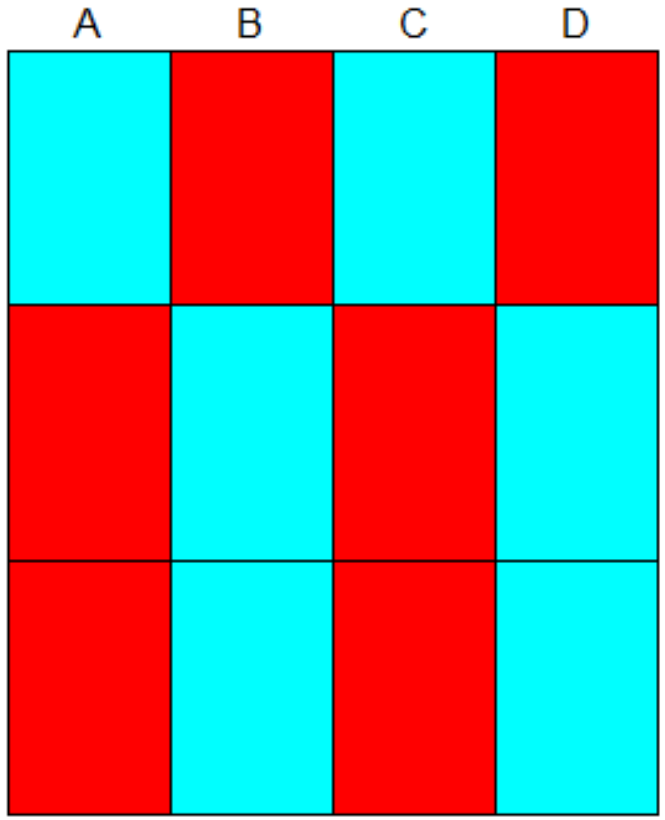


`axisPhylo()`




```
nodelabels()
tiplabels()
edgelabels()
```






```
plot.phylo(mytr,x.lim=12)
phydataplot(x, mytr, "m", offset = 2, width = 1)
```

ANSWERING QUESTIONS WITH PHYLOGENIES

- How fast are traits evolving?
- Are traits correlated with one another?
- What were the ancestral traits?

IMPORTANT PACKAGES

ape: Paradis et al. 2023

phangorn: Schliep et al. 2023

phytools: Revell 2023

RATES OF EVOLUTION

Package: geiger

Functions:

fitDiscrete() models vary by # of rates

fitContinuous() variety of models

fitContinuousMCMC() writes to BEAST-friendly text file

TRAIT CORRELATIONS

Package: caper

Function:

pgls() linear model for continuous traits

TRAIT CORRELATIONS

Package: phytools

Function:

fitPagel() direction of effect for binary traits

TRAIT RECONSTRUCTION

Package: ape

Function:

ace() continuous and discrete traits

TRAIT RECONSTRUCTION

Package: HiSSE

Function:

MarginReconHiSSE() probabilities of traits at nodes and tips

TRAIT RECONSTRUCTION

Package: phangorn

Function:

ancestral.pml() no probabilities

THANKS

- John Wiens
- Wiens lab
- Bronstein lab

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E Tuschhoff

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