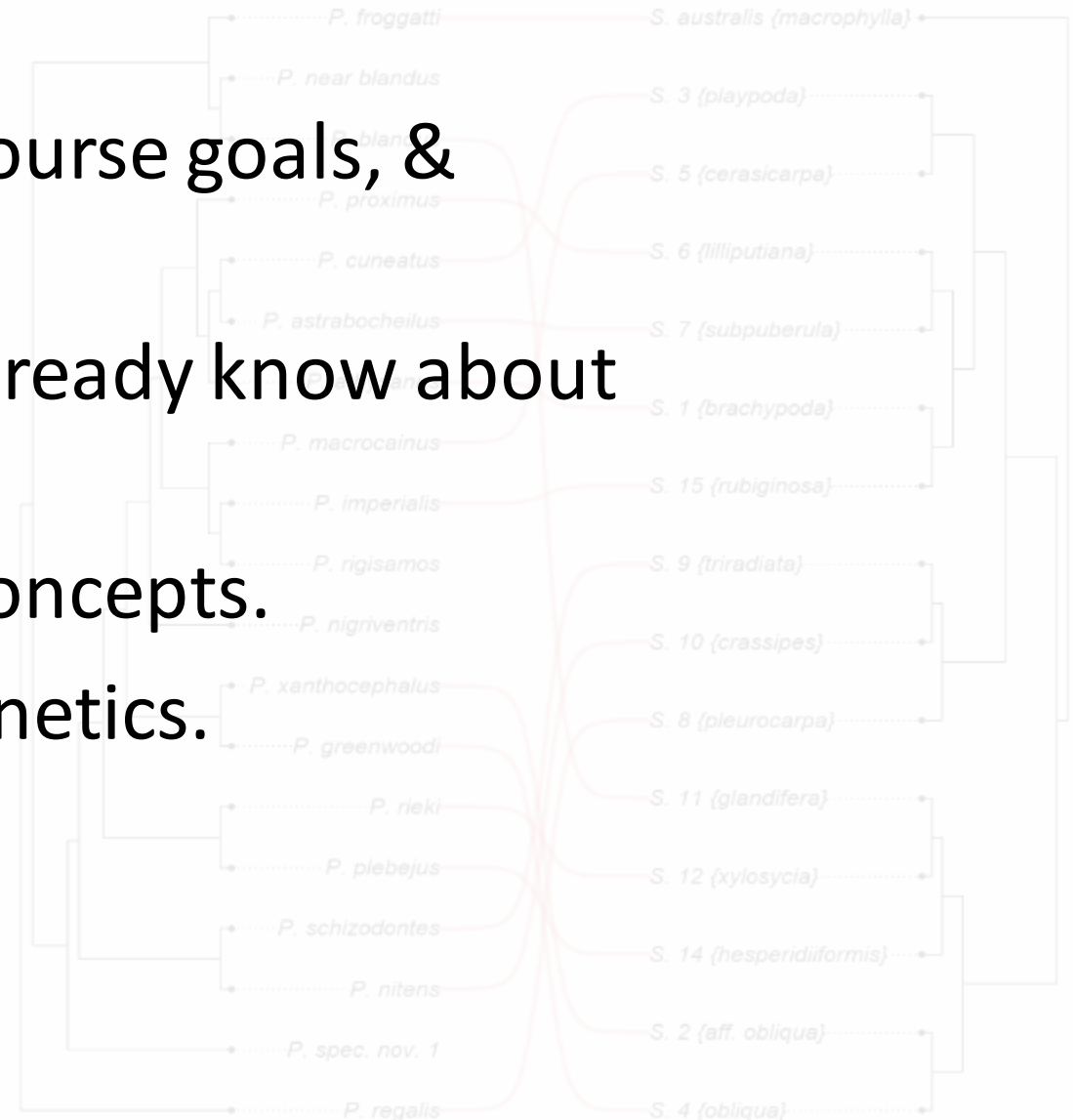


# Schedule

1. Class information, syllabus, course goals, & evaluation.
2. Tree drawing – what do we already know about phylogenies?
3. Basic phylogenetic terms & concepts.
4. Introduction to R for phylogenetics.



```
1 library(
2 data(wasp
3 data(wasp
4 ## creat
5 wasp.cop
6 asso
7 ## plot
8 plot(wasp
9 lin
10 0.2
11 par(mar=
12
```

12.1 (Top Level)

Console Terminal

```
R 4.2.2 -- /
PIACTOIR: X00_
```

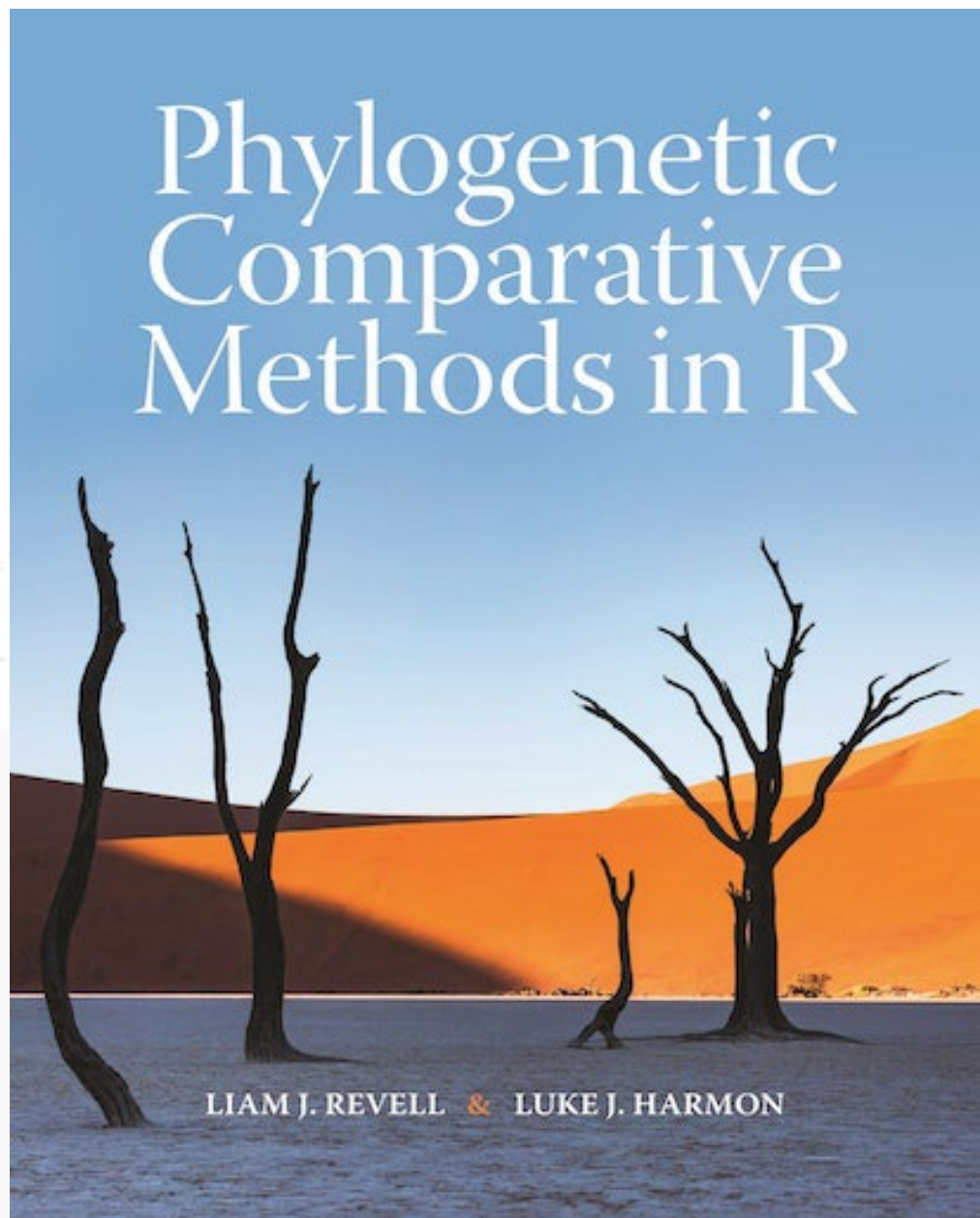
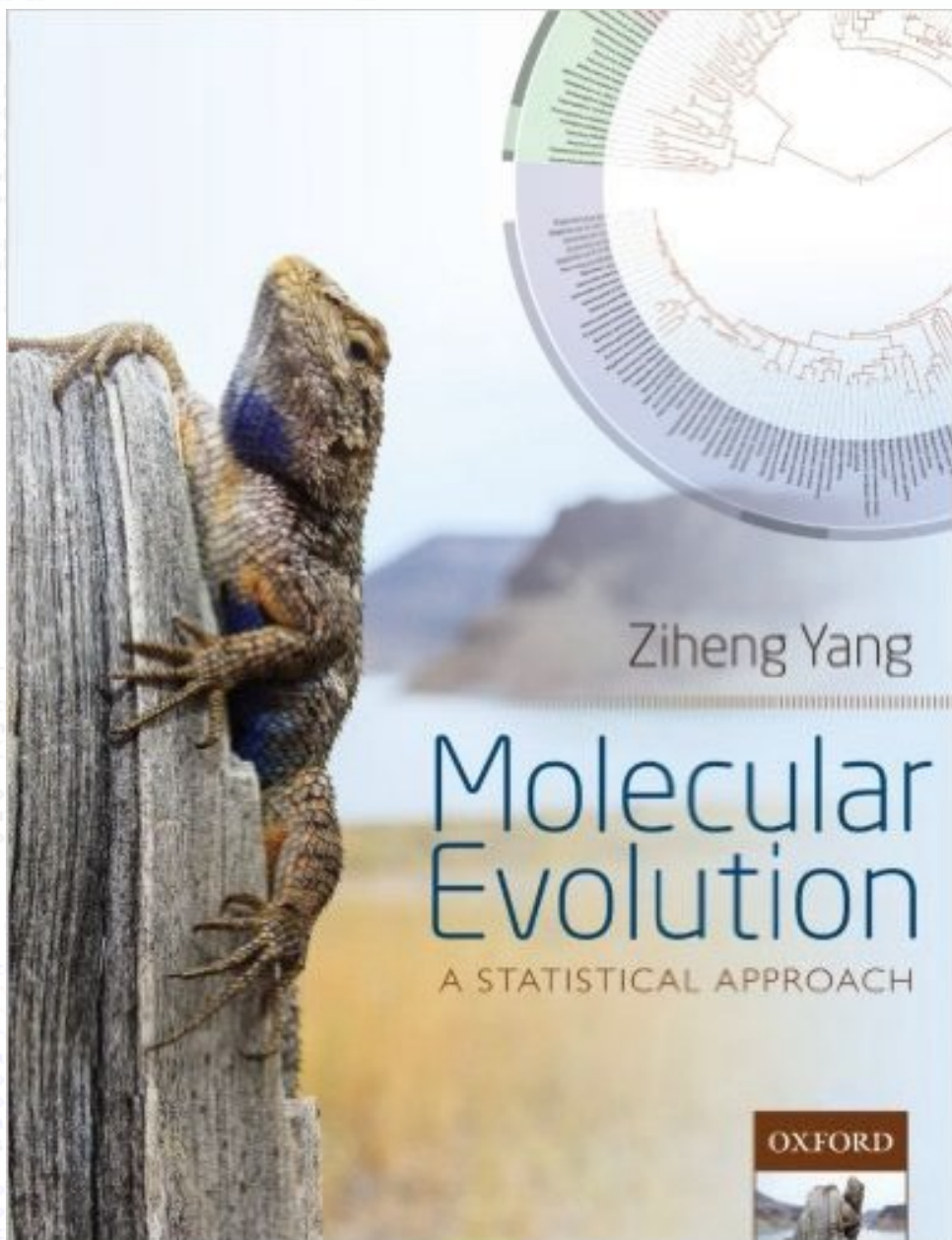
R is free soft  
You are welcom  
Type 'license()

R is a collabor  
Type 'contribu  
'citation()' o

Type 'demo()  
'help.start()  
Type 'q()' to

```
> library(phyt
Loading requir
Loading requir
> data(wasp.tr
> data(wasp.da
> ## create co
> wasp.cophylo
+ assoc-wa
Rotating nodes
Done.
```

```
> ## plot co-p
> plot(wasp.co
+ link.lti
+ 0.25))
> par(mar=c(5.1,4.1,4.1,2.1))
>
```

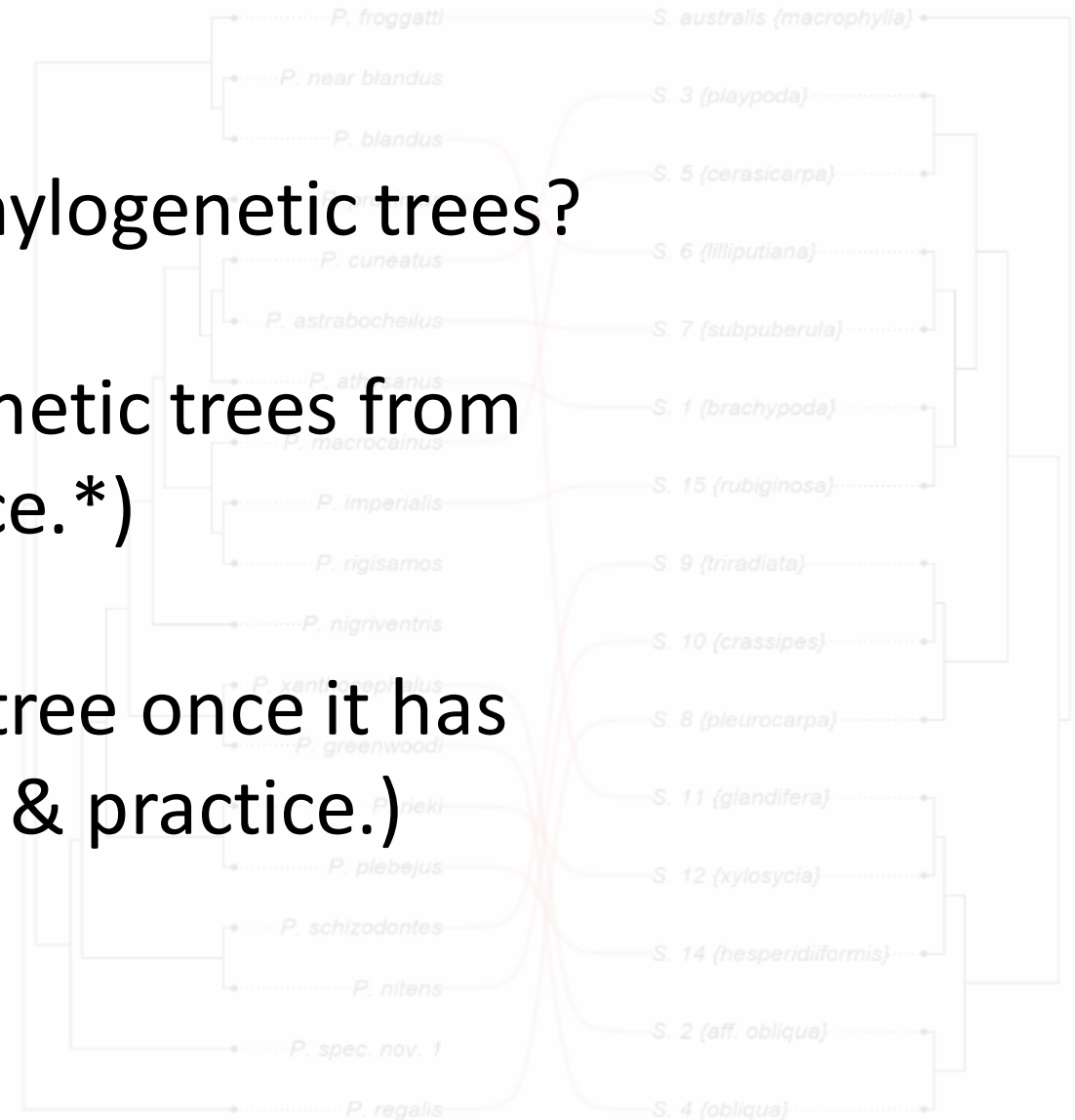


# Course goals:

1) Why do we care about phylogenetic trees?

2) How do we infer phylogenetic trees from data? (In theory & practice.\*)

3) What do we do with our tree once it has been inferred? (In theory & practice.)



# Introduction to phylogenetic terms & concepts

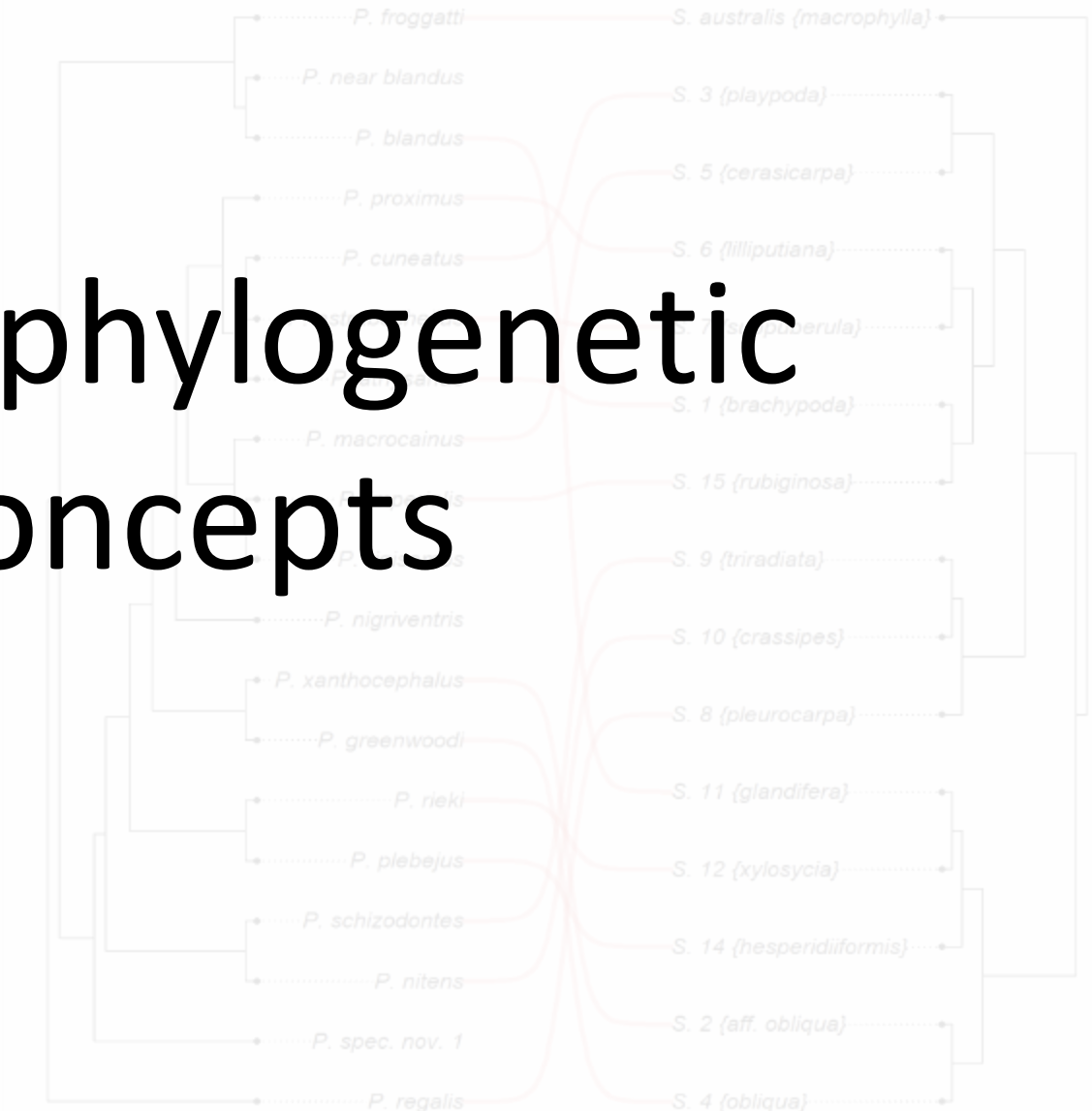
```
1 library(phytools)
2 data(wasp.trees)
3 data(wasp.data)
4 ## create co-phylogenetic object
5 wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.trees[[2]],
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7 ## plot co-phylogenies
8 plot(wasp.cophylo,link.type="curved",link.lwd=4,
9   link.lty="solid",link.col=make.transparent("red",
10     0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12
```

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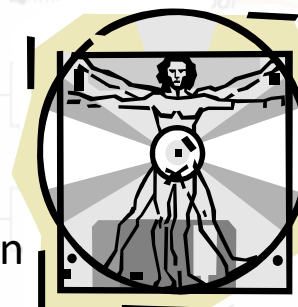
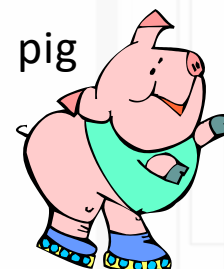
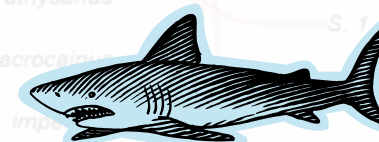
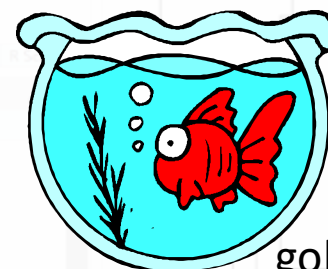
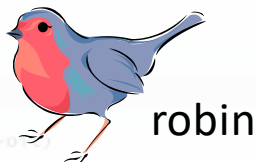
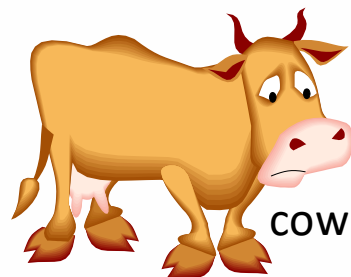
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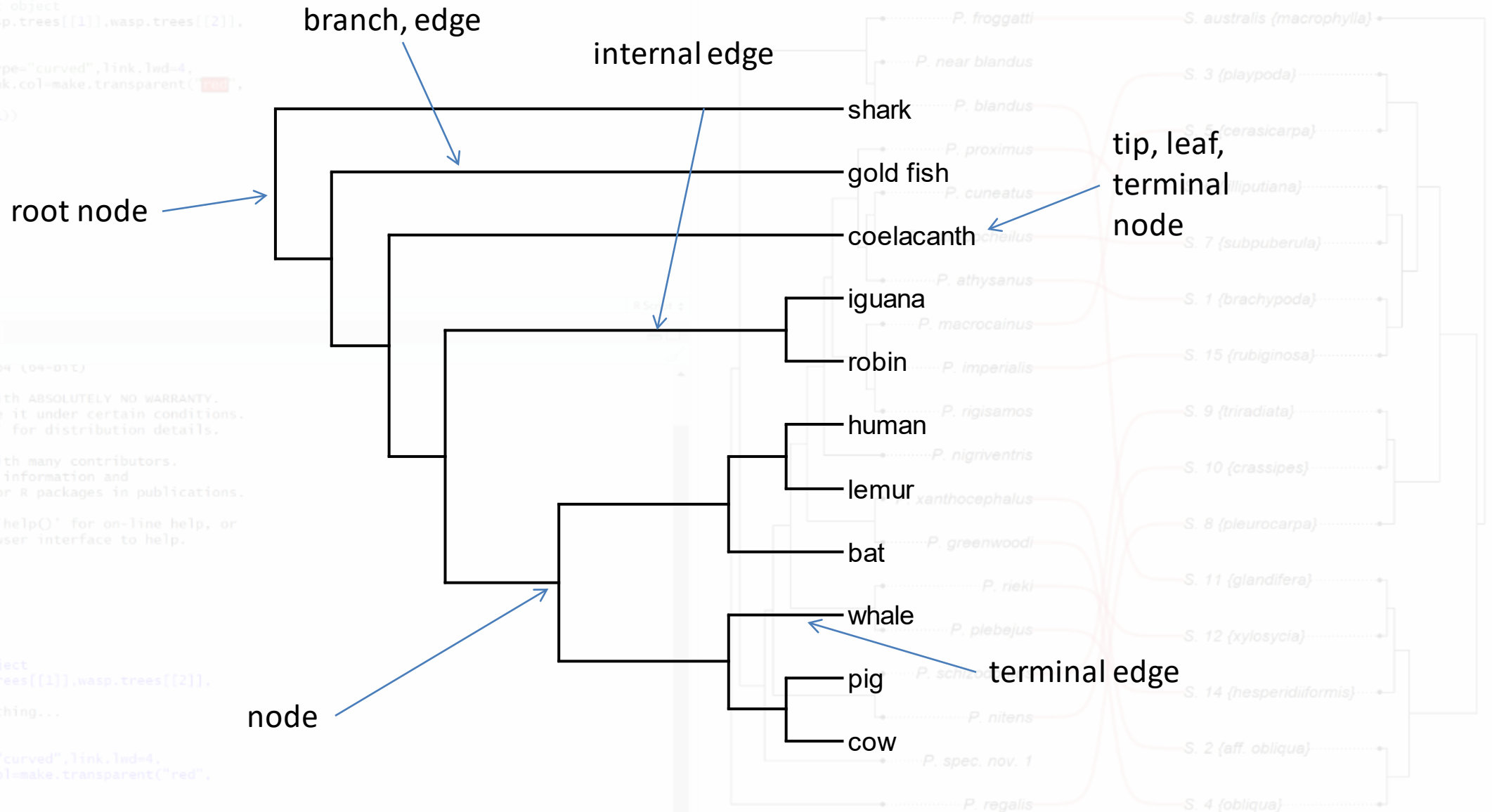
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Loading required package: ape
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> data(wasp.data)
> ## create co-phylogenetic object
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Rotating nodes to optimize matching...
Done.
> ## plot co-phylogenies
> plot(wasp.cophylo,link.type="curved",link.lwd=4,
+   link.lty="solid",link.col=make.transparent("red",
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> par(mar=c(5.1,4.1,4.1,2.1))
>
```





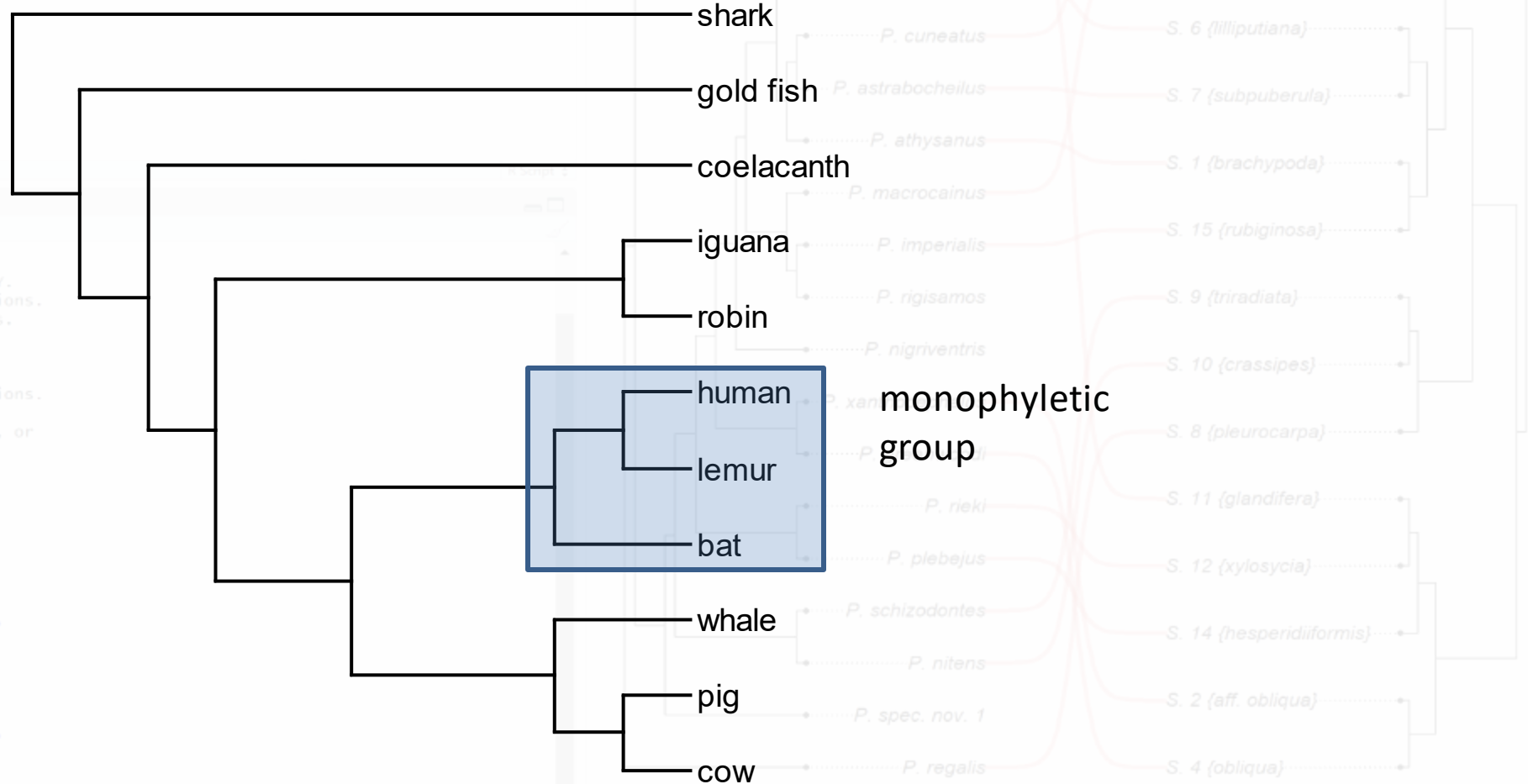


# Parts of a tree



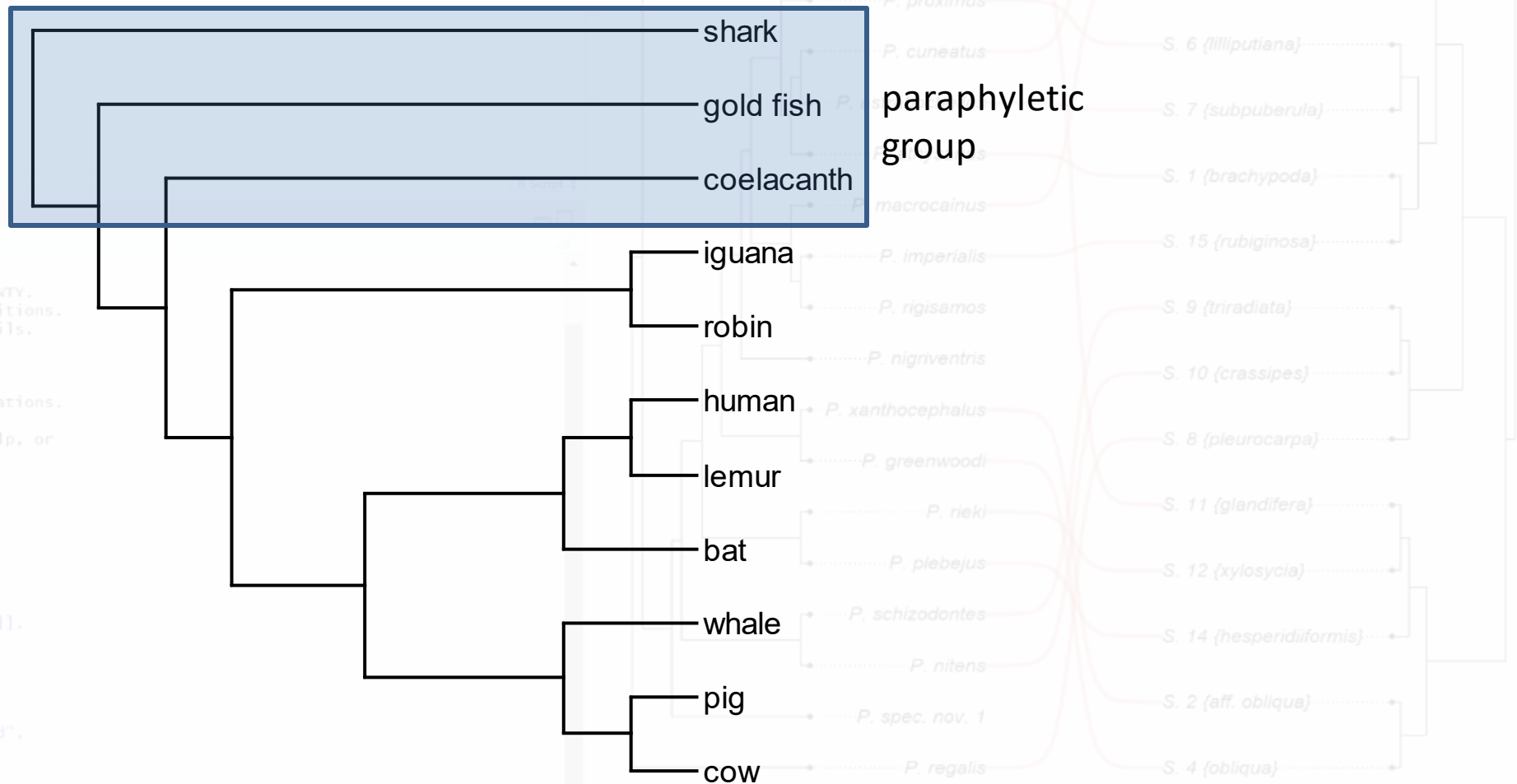
# Types of “groupings” on a phylogeny

A **monophyletic group** is a phylogenetic group that includes an ancestor & all of its descendants.



# Types of “groupings” on a phylogeny

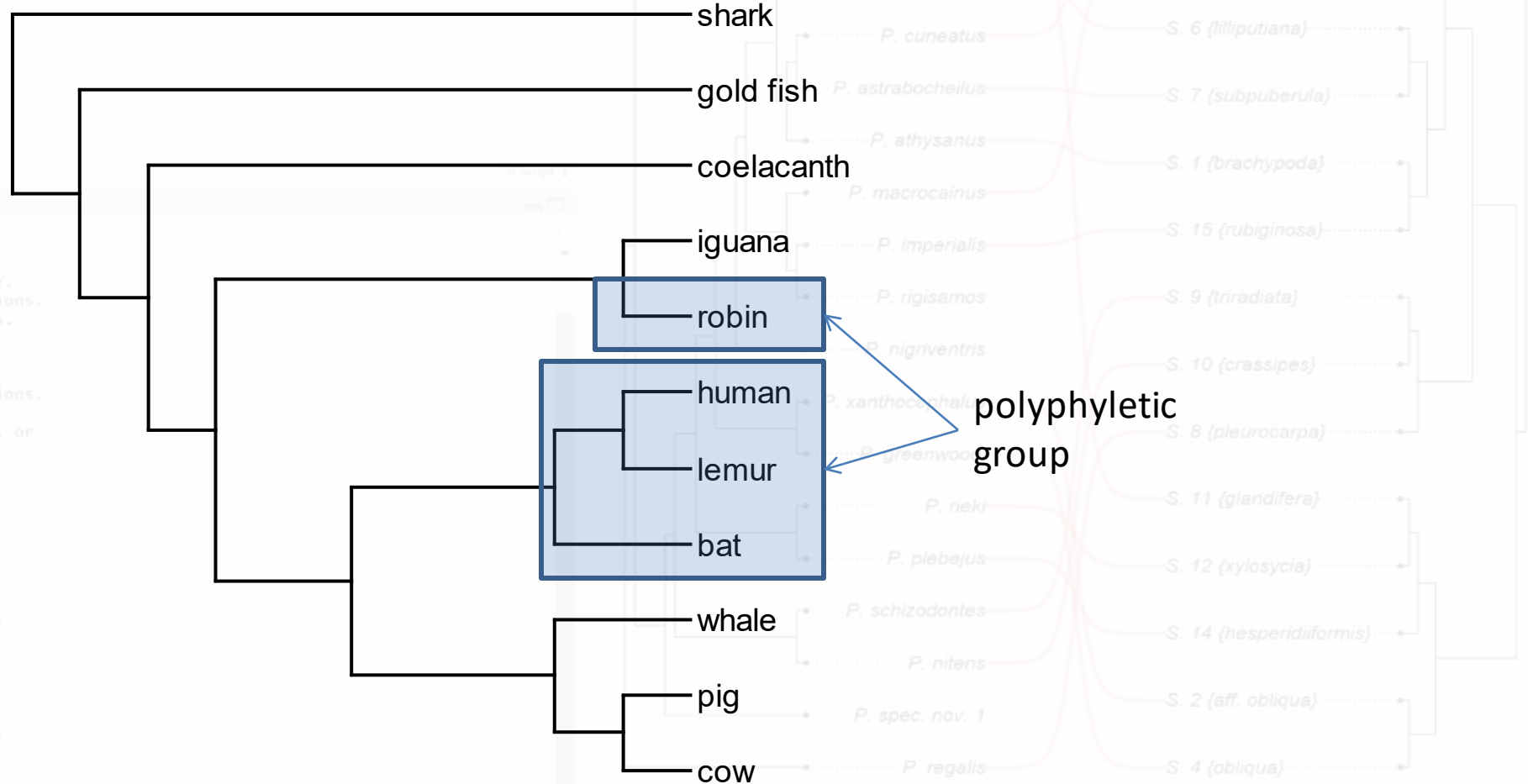
A **paraphyletic group** is a phylogenetic group that includes an ancestor & some, but not all, of its descendants.





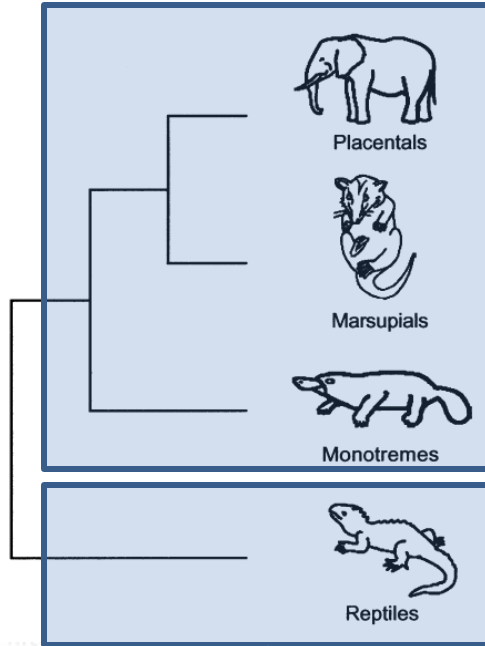
# Types of “groupings” on a phylogeny

A **polyphyletic group** is a phylogenetic group that does not include the common ancestor.



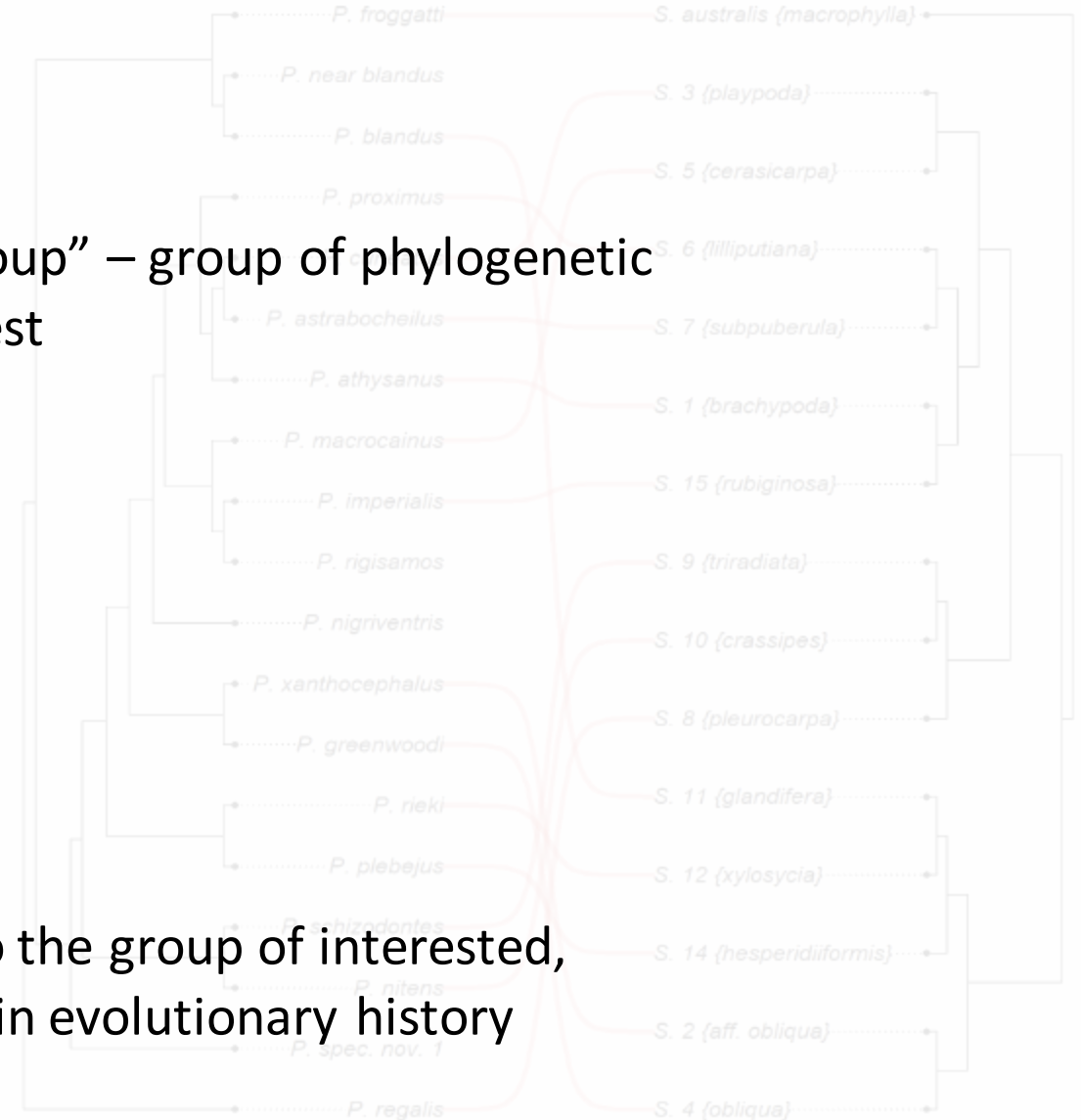
# Ingroup vs. outgroup

A



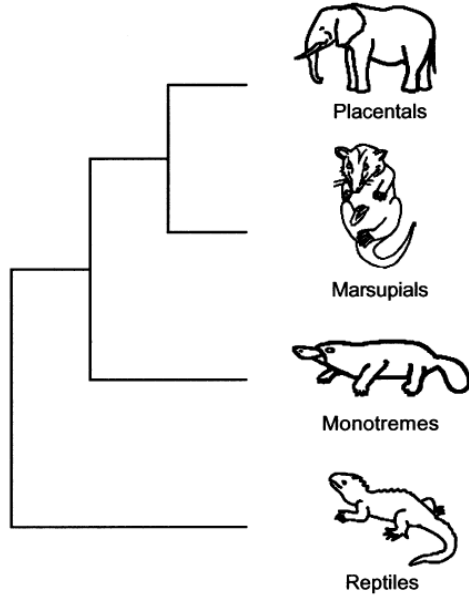
“ingroup” – group of phylogenetic interest

“outgroup” – taxon related to the group of interested, but that branched off earlier in evolutionary history

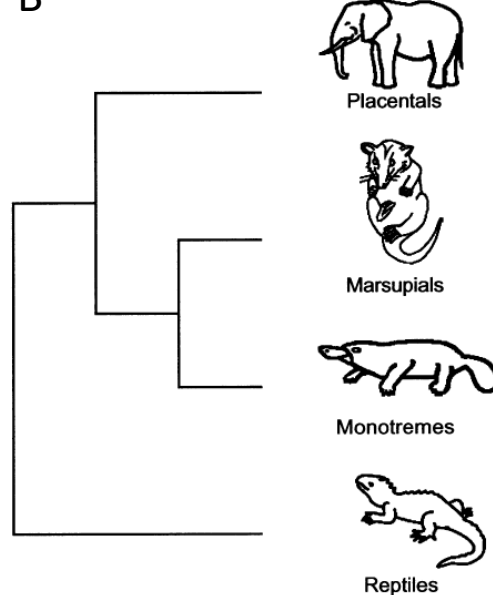


# Bifurcating trees & polytomies

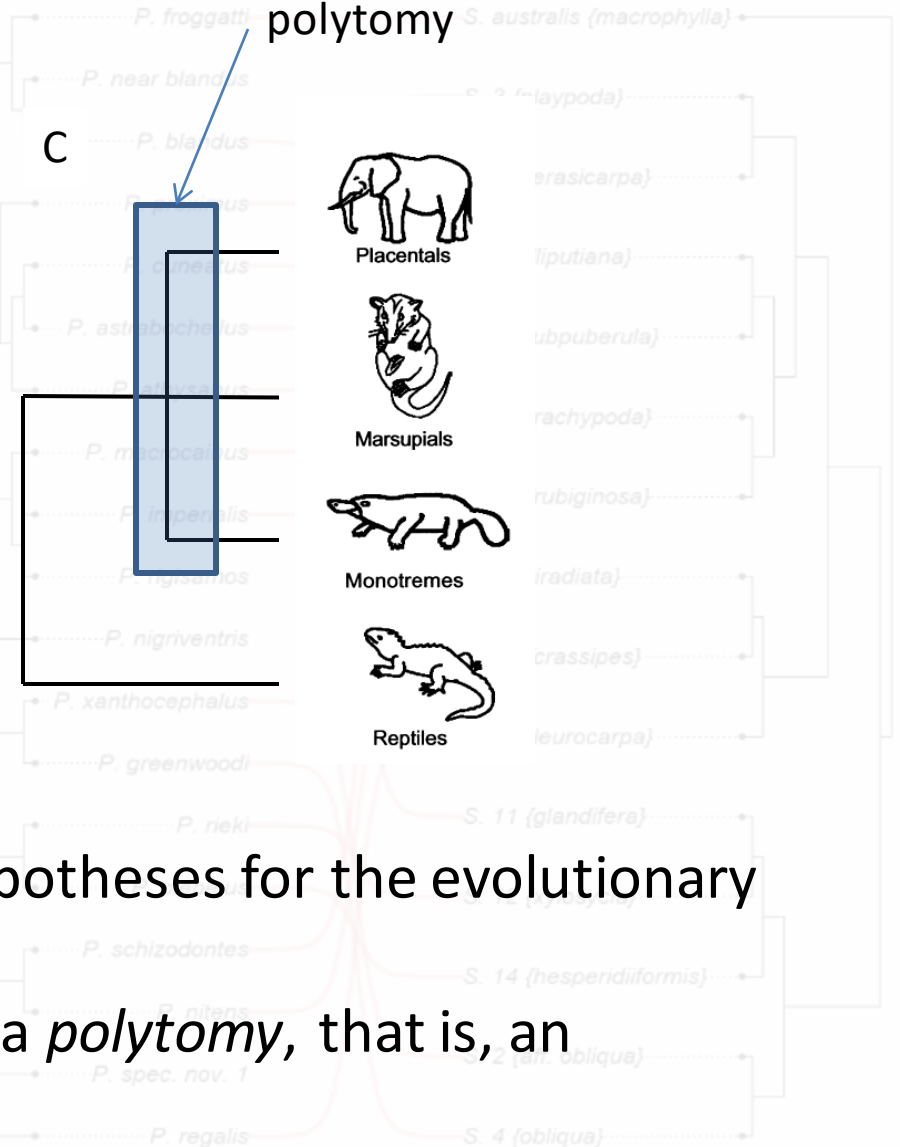
A



B



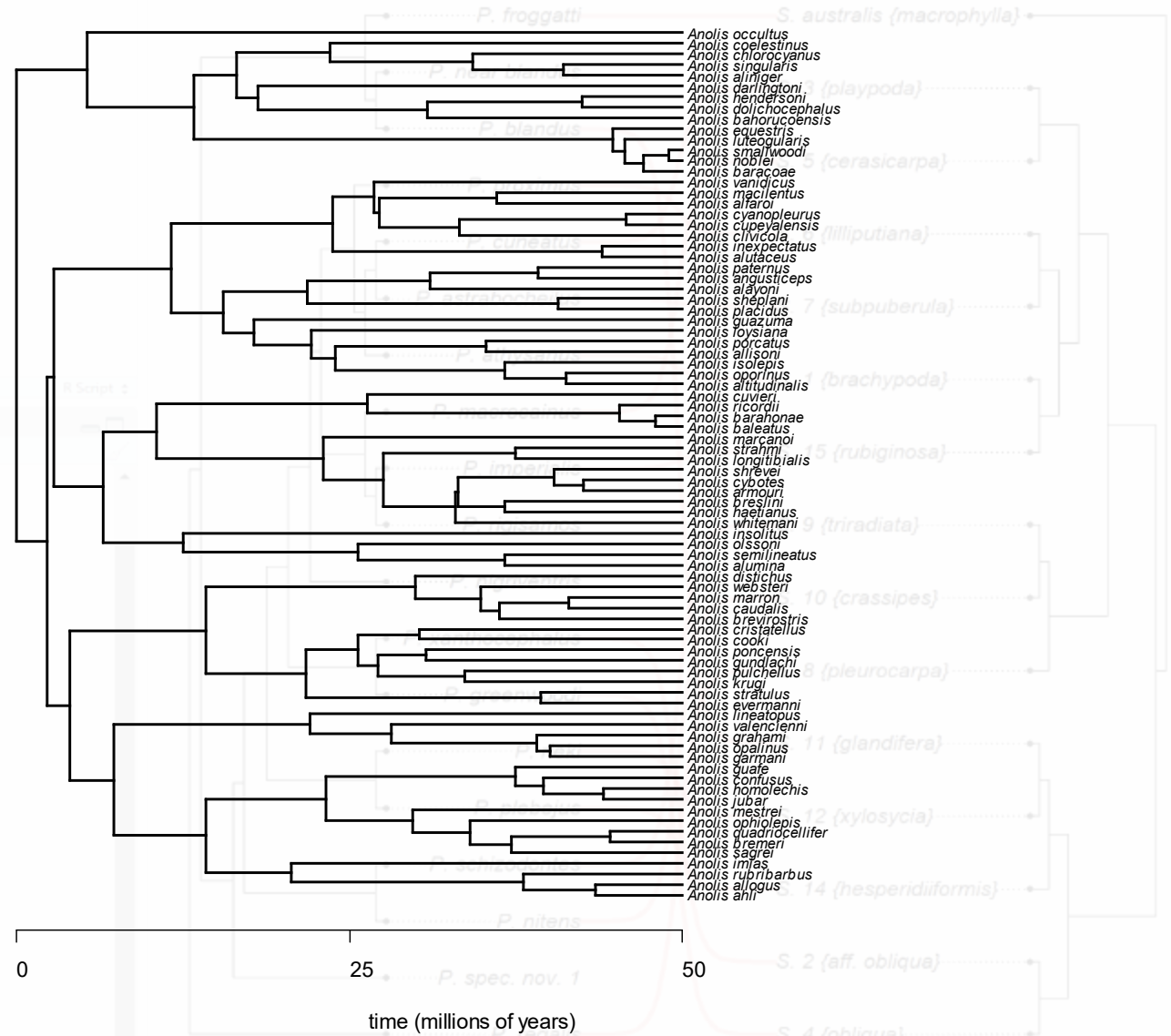
C



1. Often, there is evidence in support of alternative hypotheses for the evolutionary relationships among taxa.
2. One way to represent this uncertainty is by drawing a *polytomy*, that is, an internal node with more than two descendants.

# Branch lengths

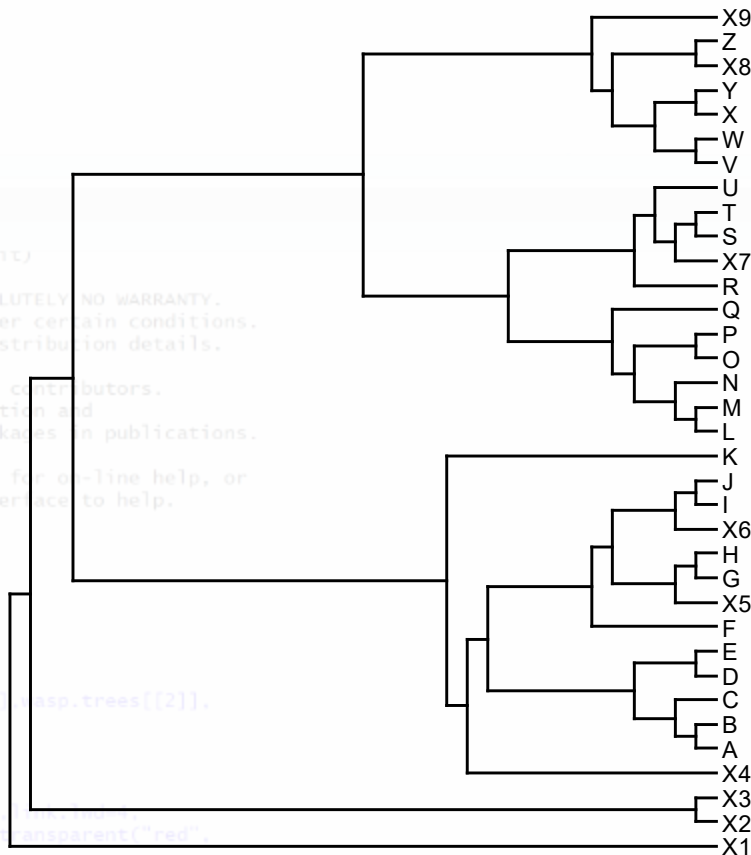
The **lengths** of plotted edges can be used to convey information about the amount of time that has elapsed since the root of the tree; or the amount of evolutionary change along each edge.



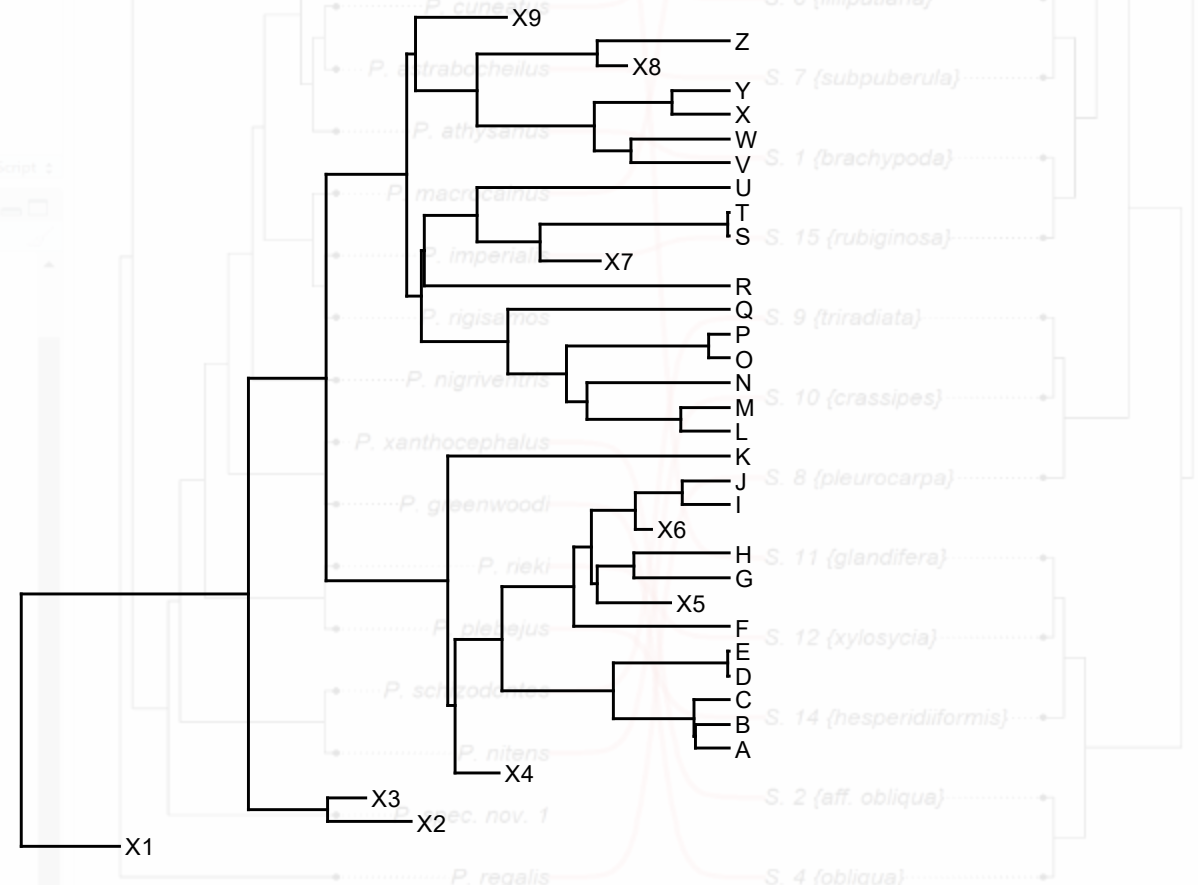
# Topology vs. topology & branch lengths

The **topology** of the tree refers to the relationships of taxa *only*.

a) topology only



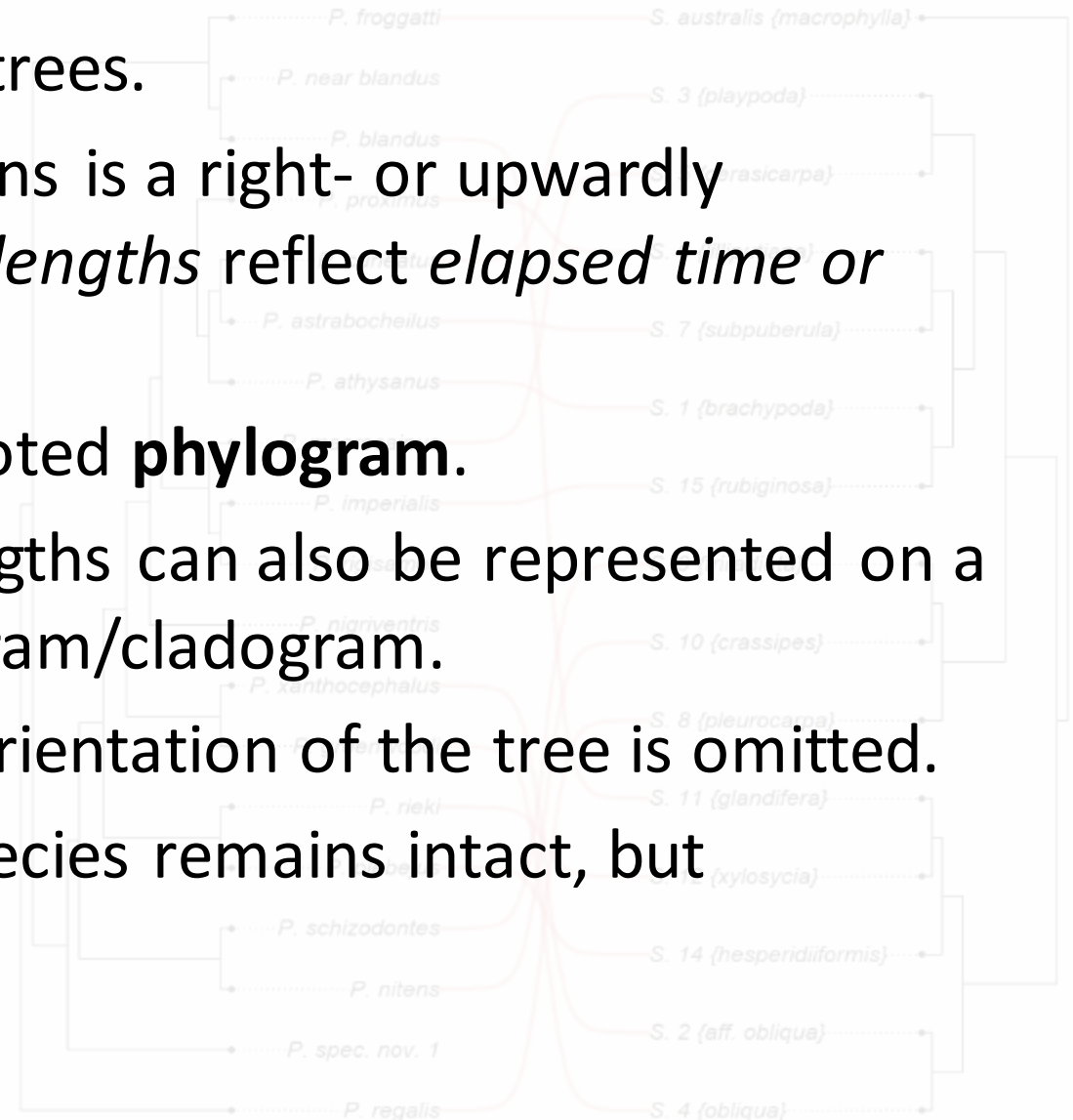
b) topology & branch lengths





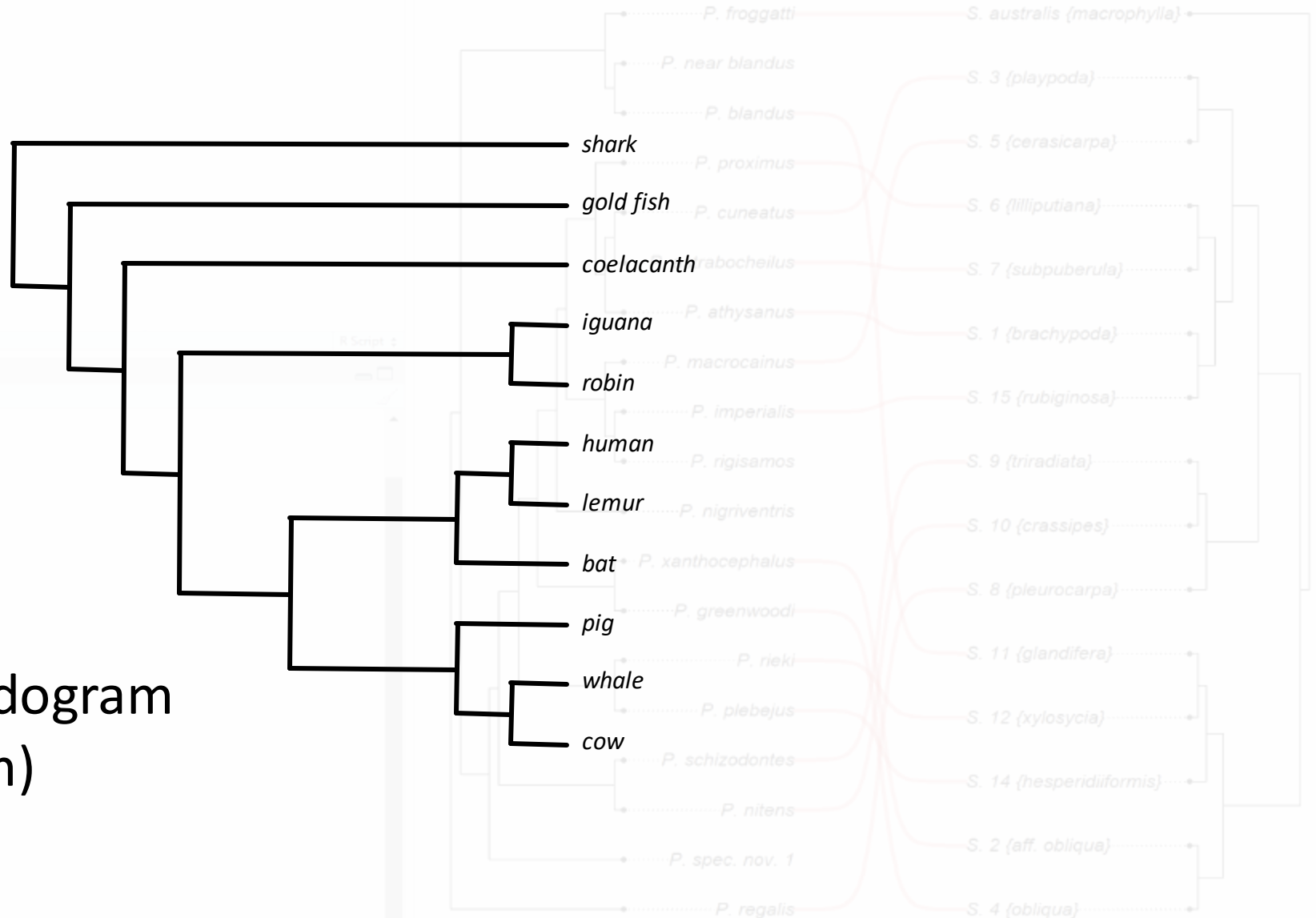
# Drawing trees

- There are many different ways to draw trees.
- One of the most common representations is a right- or upwardly oriented *square graph* in which *branch lengths* reflect *elapsed time* or *amount of change*.
- This is called a rectangular or square rooted **phylogram**.
- **Topology** (relationships) and branch lengths can also be represented on a *slanted* (sometime “triangular”) phylogram/cladogram.
- Finally, for some purposes the **root** or orientation of the tree is omitted.
- In this case, the relationships among species remains intact, but *monophyly* cannot be directly inferred.



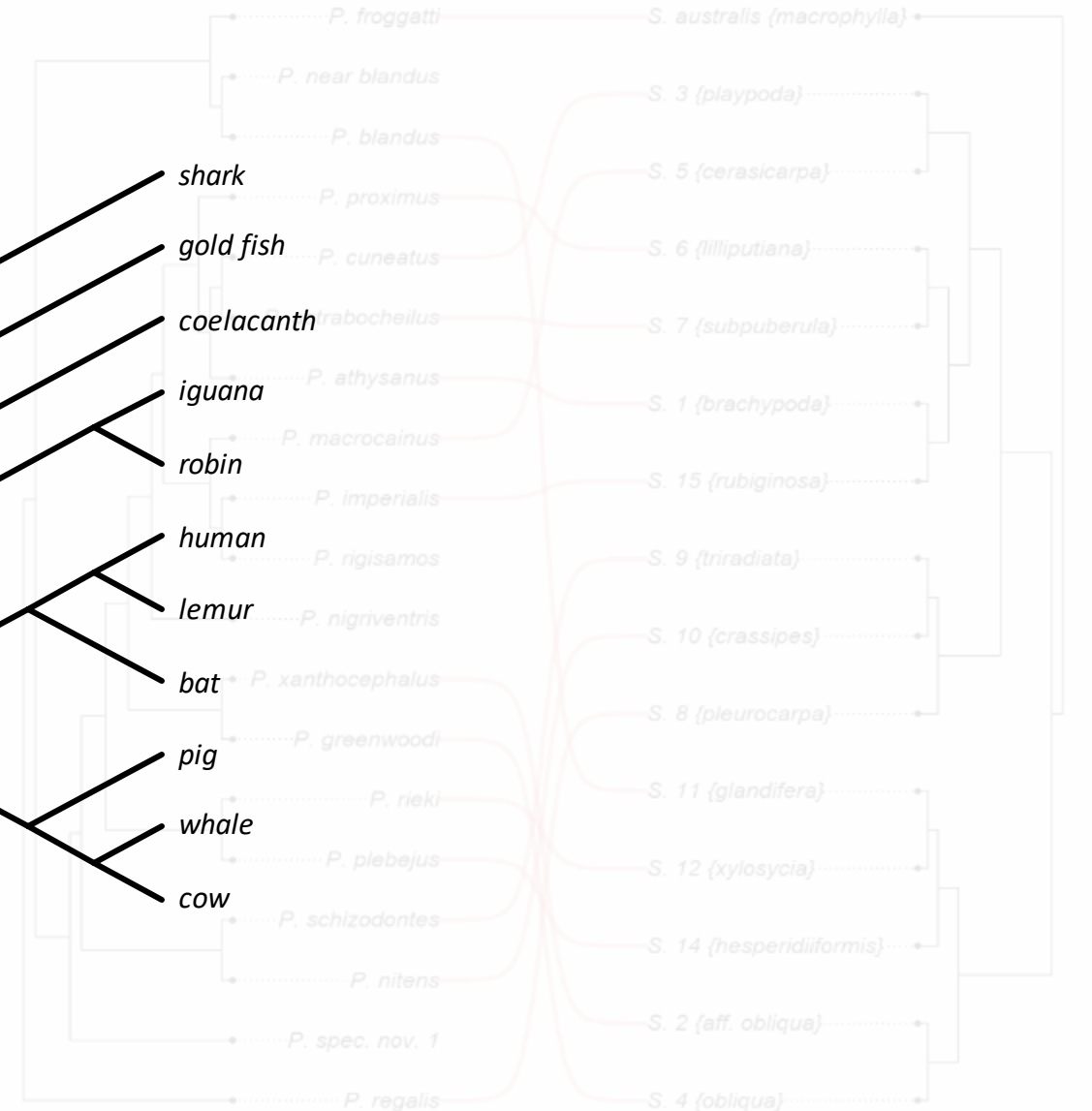
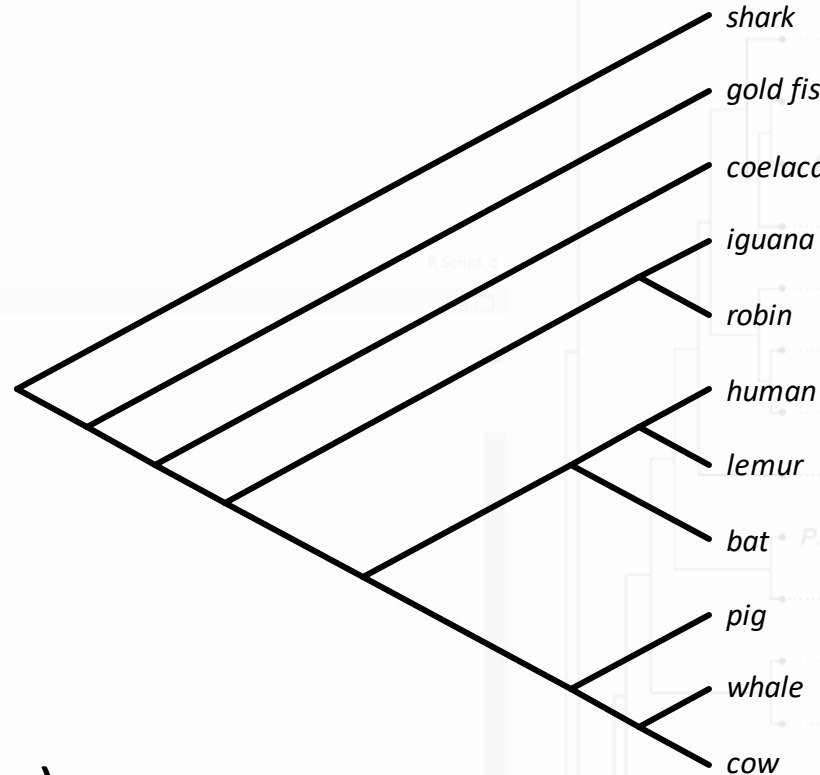
# Square cladogram

rooted square cladogram  
(square phylogram)



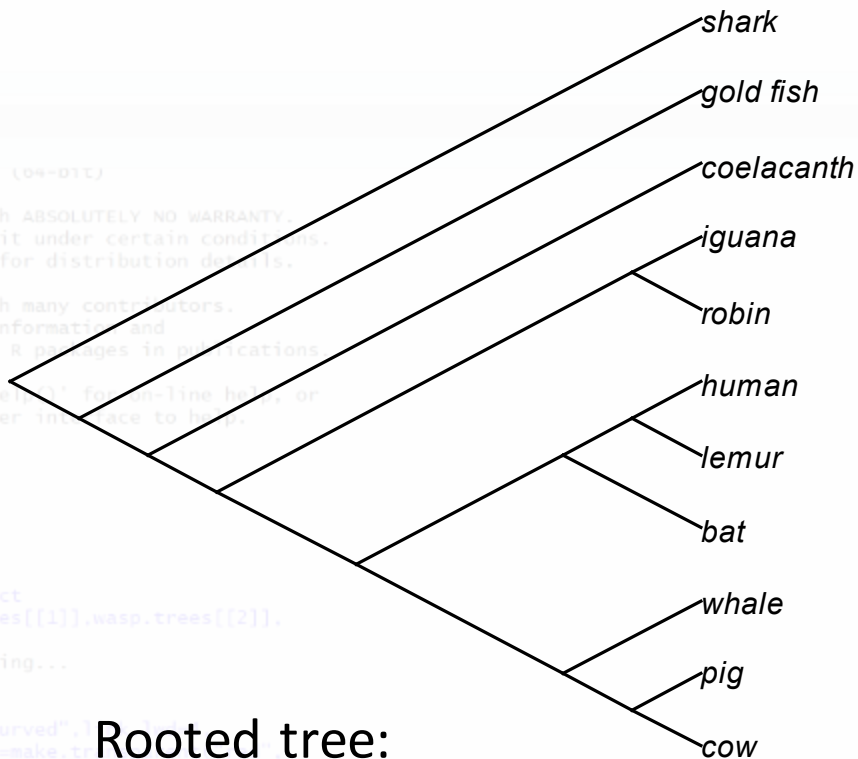
# Slanted cladogram

rooted cladogram  
(slanted cladogram)

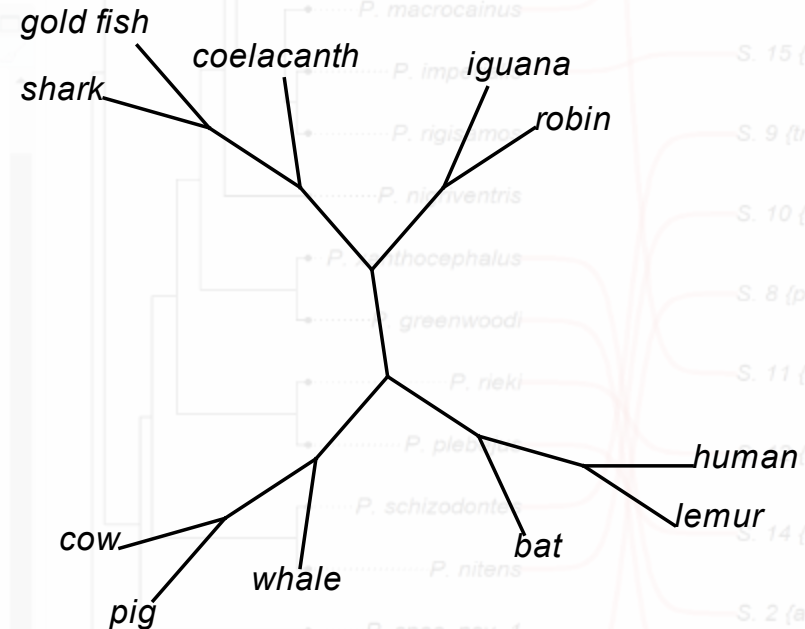


# Rooting

A **rooted** phylogeny is a phylogenetic tree in which the ordering of the nodes in any path from the deepest node in the tree implies a temporal sequence of ancestor-descendant relationships along that path.



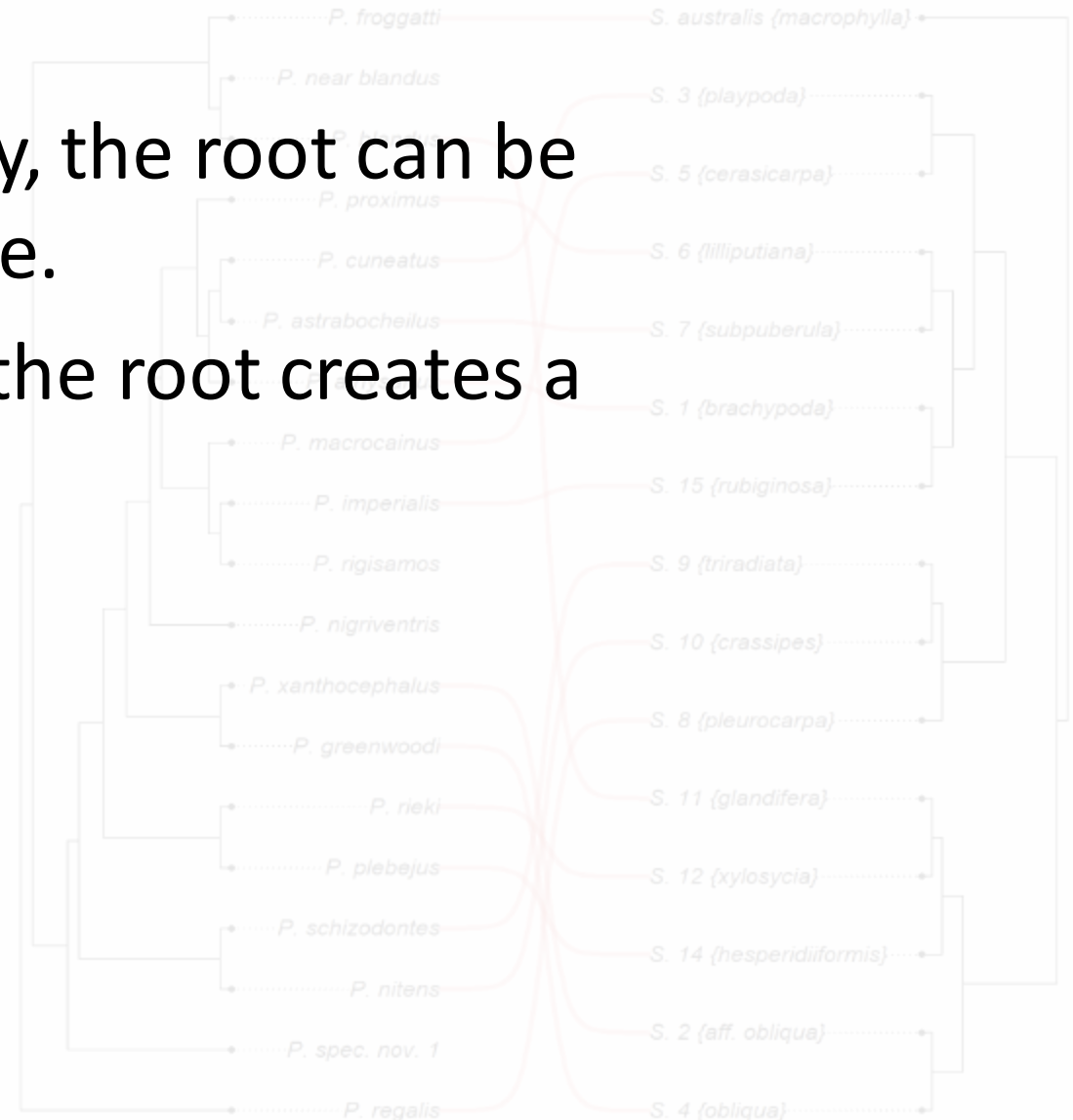
Rooted tree:



Unrooted tree:

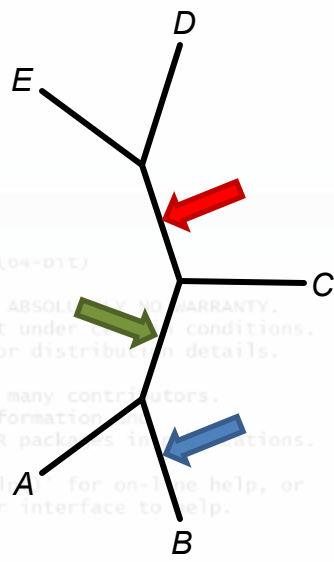
# Rooted vs. unrooted trees

- Given an unrooted phylogeny, the root can be placed on any branch or node.
- Each different placement of the root creates a different rooted phylogeny.



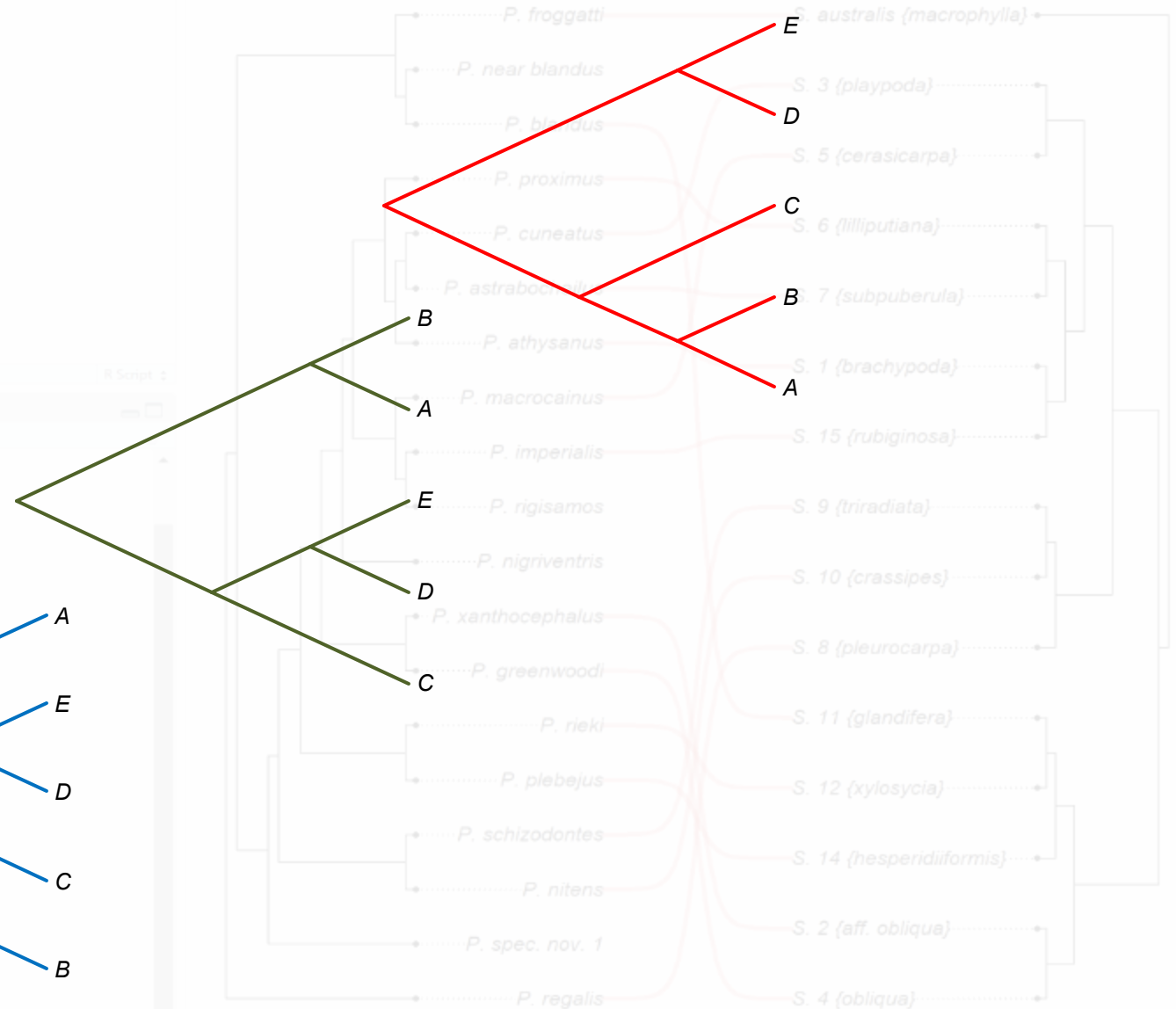
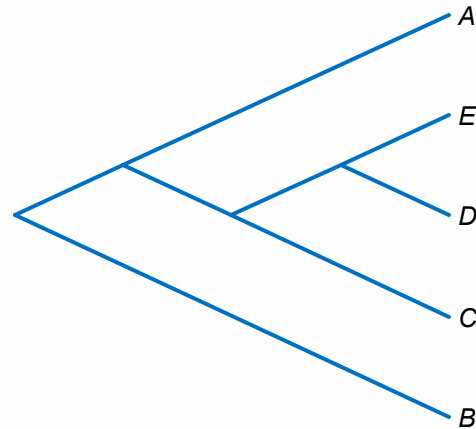
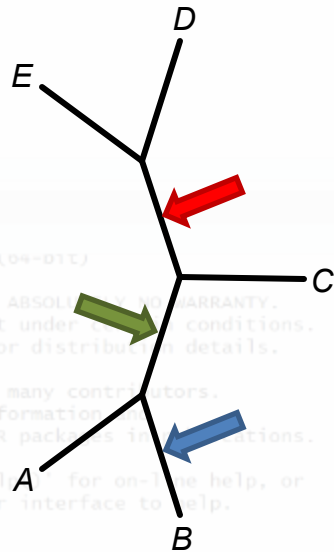


# Phylogenetic tree rooting



# Phylogenetic tree rooting

```
1 library(phytools)
2 data(wasp.trees)
3 data(wasp.data)
4 ## create co-phylogenetic object
5 wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.trees[[2]],
6   assoc=wasp.data)
7 ## plot co-phylogenies
8 plot(wasp.cophylo,link.type="curved",link.lwd=4,
9   link.lty="solid",link.col=make.transparent("red",
10   0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12
```



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3 data(wasp.data)
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8 plot(wasp.cophylo,link.type="curved",link.l
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10   0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12
```

12:1 (Top Level) z

Console Terminal Background Jobs

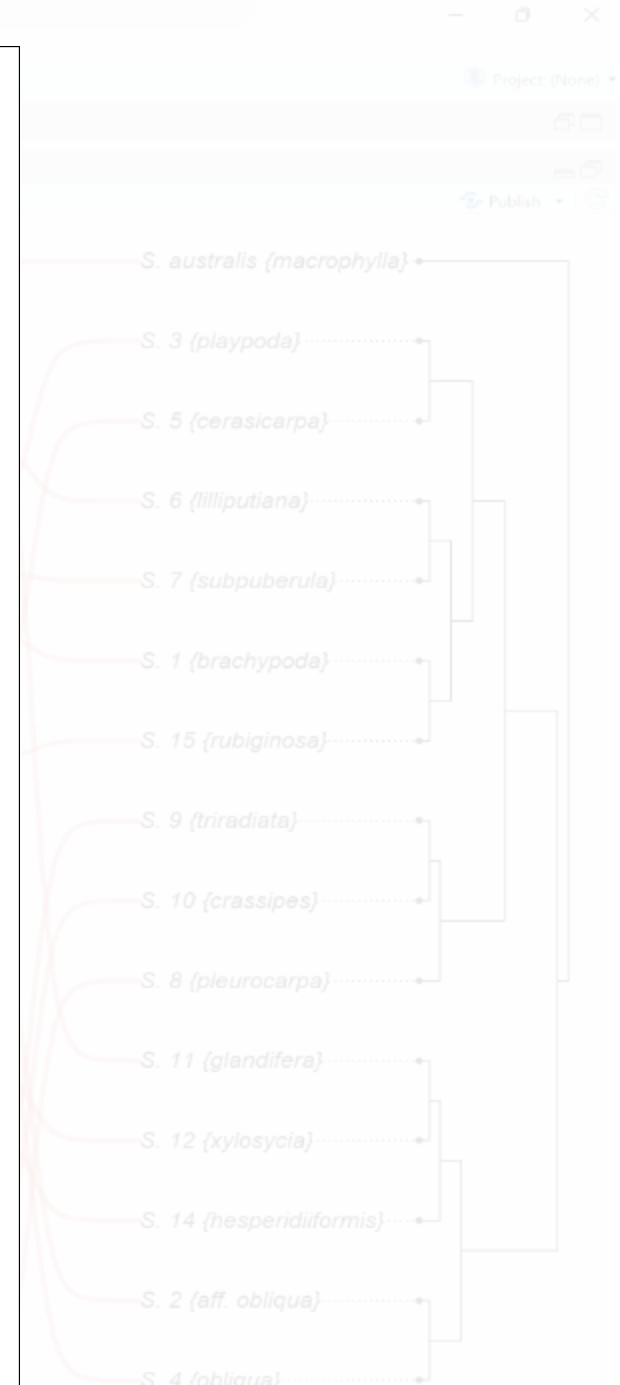
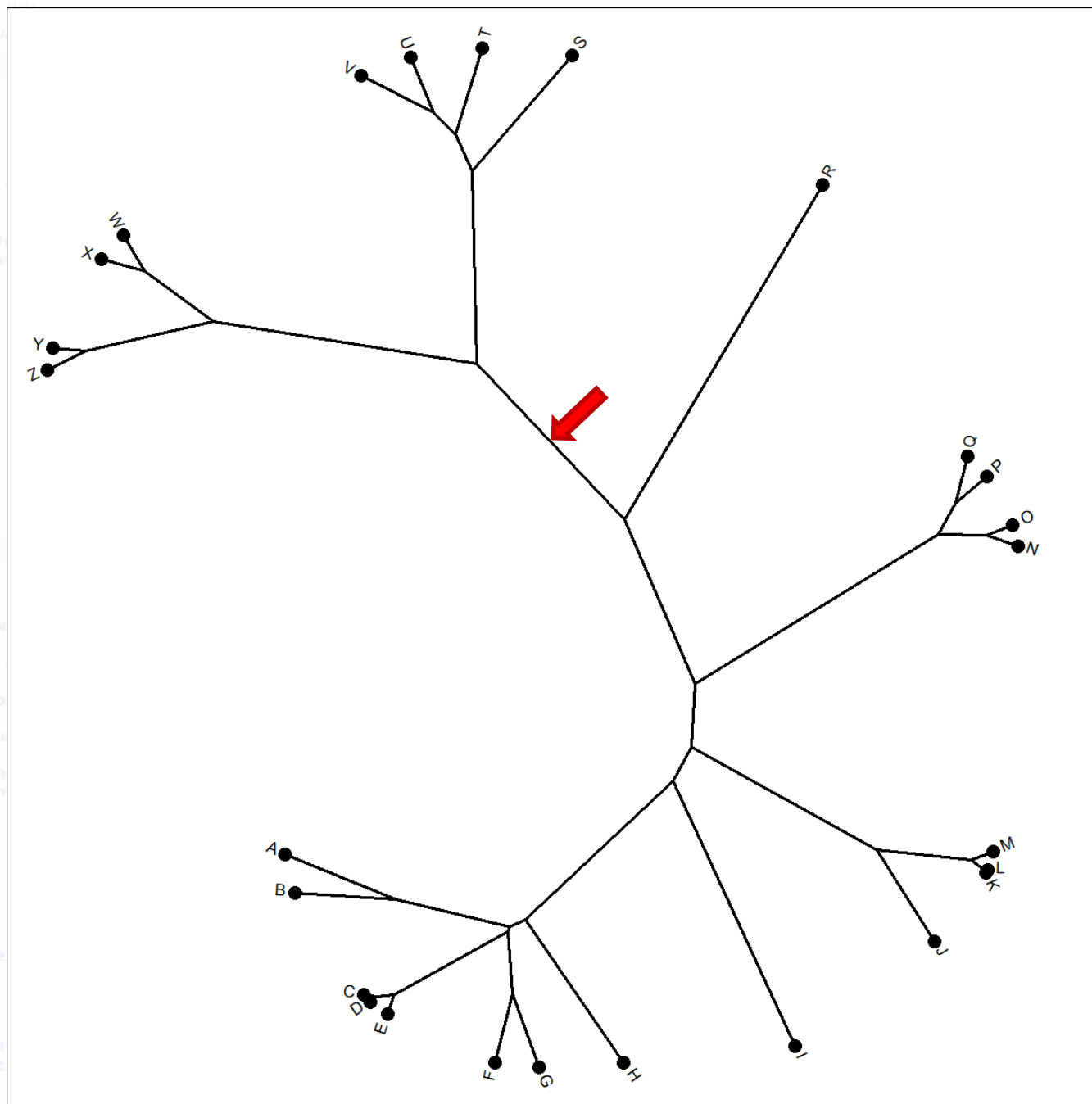
```
R 4.2.2 ~ /
PLATFORM: x86_64-w64-mingw32/x64 (64-bit)
```

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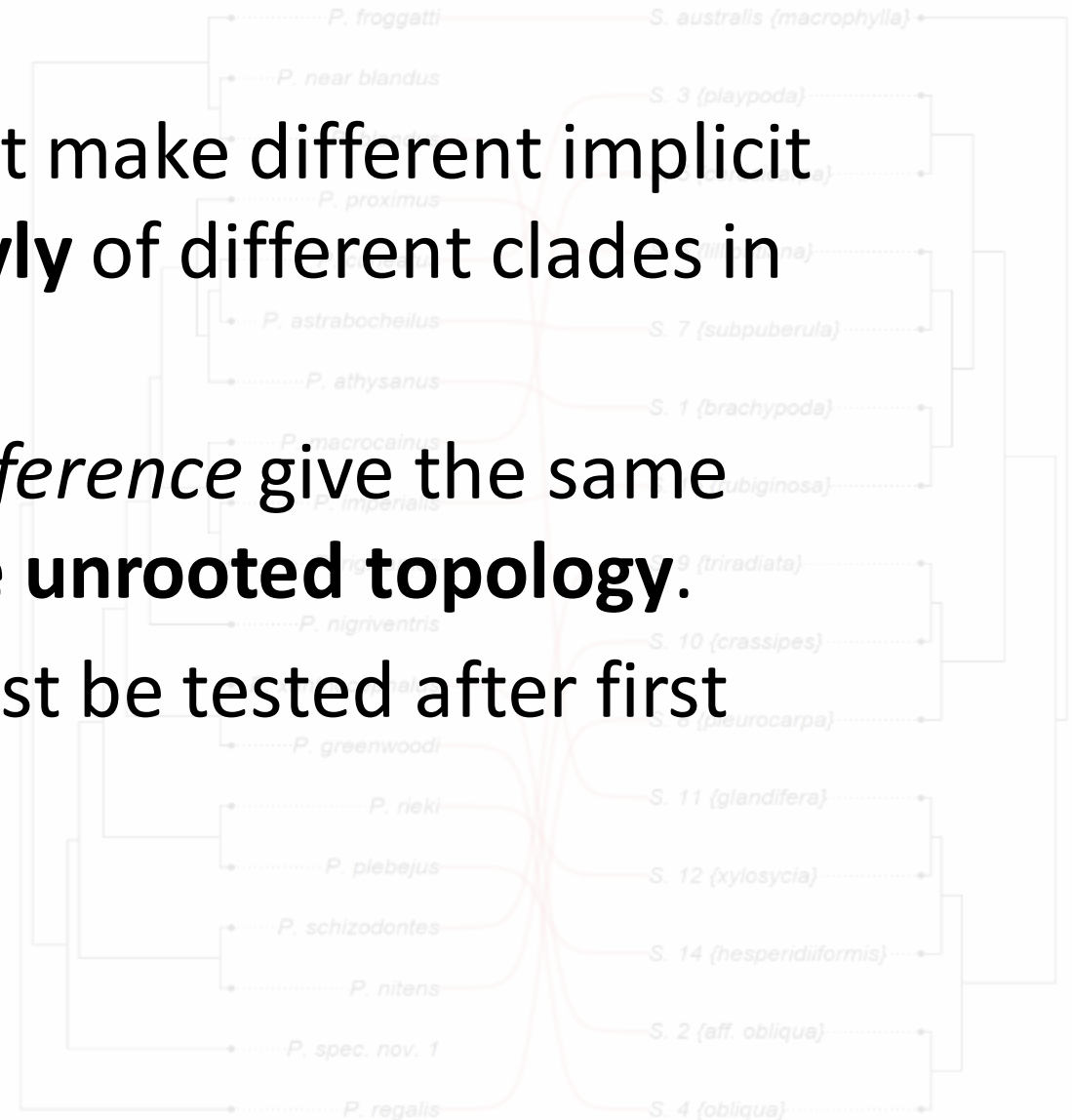
Type 'demo()' for some demos, 'help()' for on-line help, or  
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Rotating nodes to optimize matching...
Done.
> ## plot co-phylogenies
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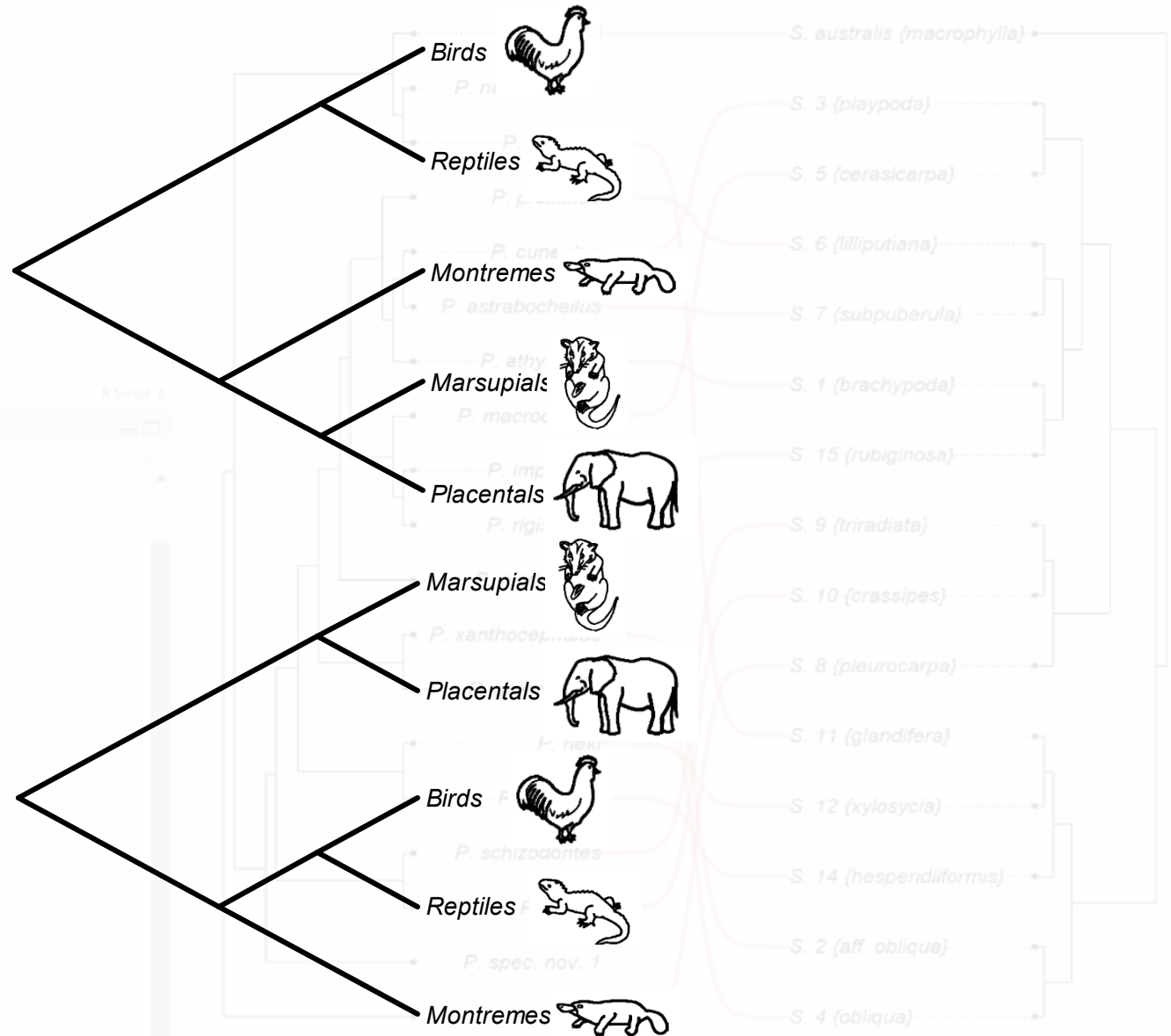
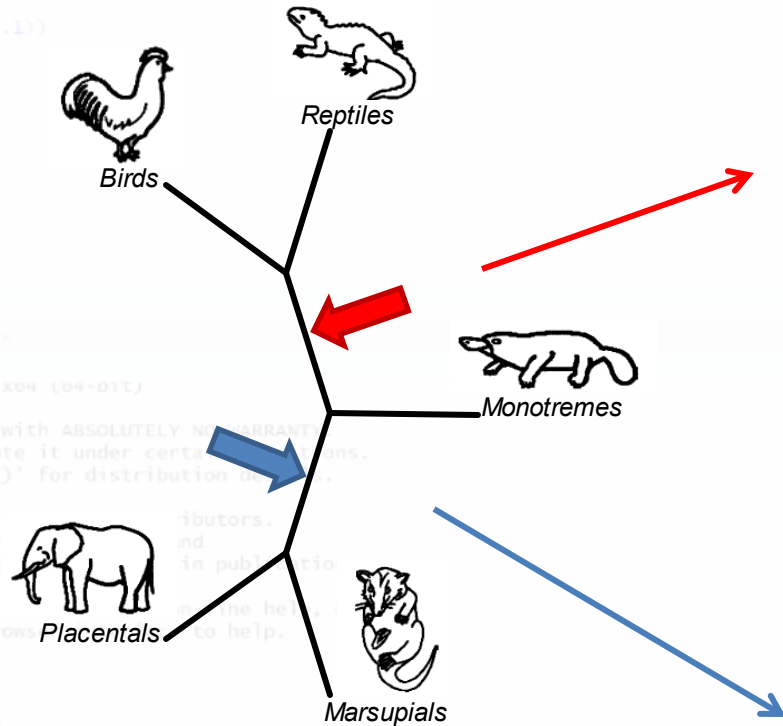


# Rooted vs. unrooted trees

- Different placements of the root make different implicit statements about the **monophyly** of different clades in our tree. **Why?**
- Most methods for phylogeny *inference* give the same score to any tree with the **same unrooted topology**.
- This means that monophyly must be tested after first rooting the tree.



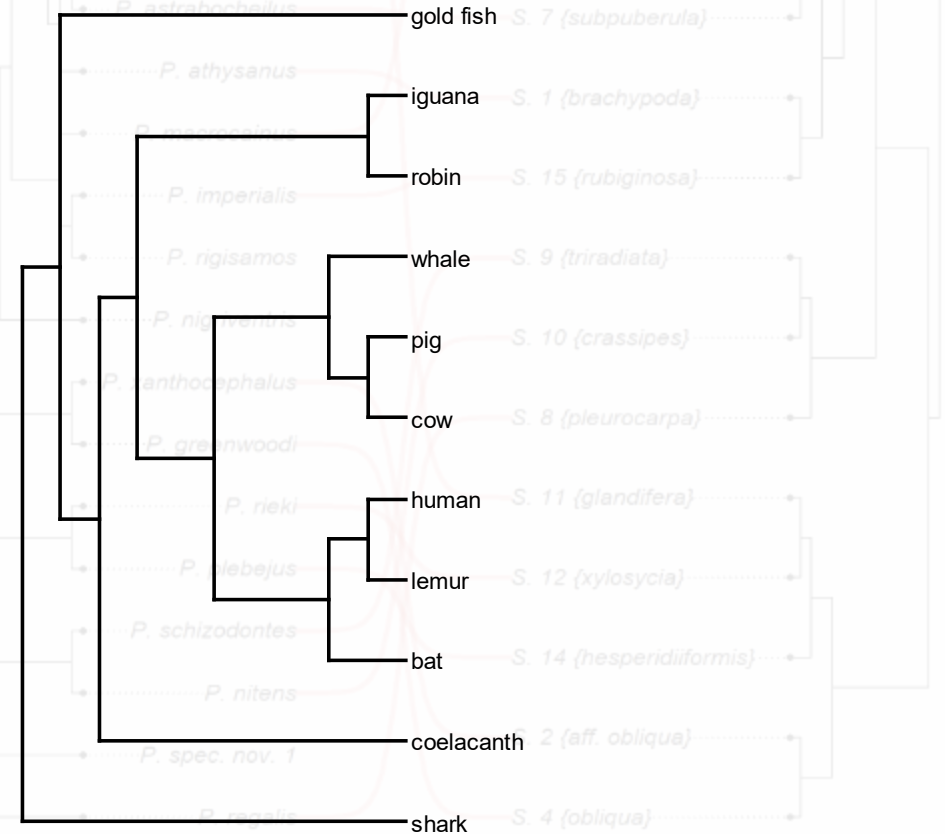
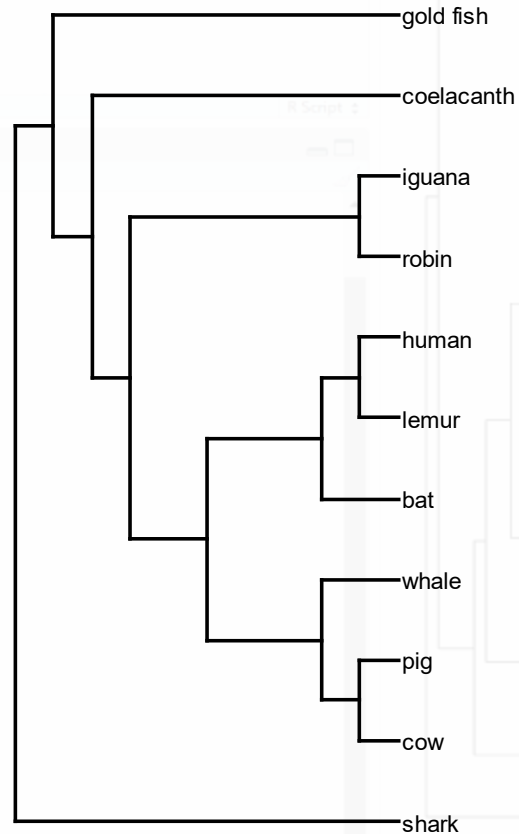
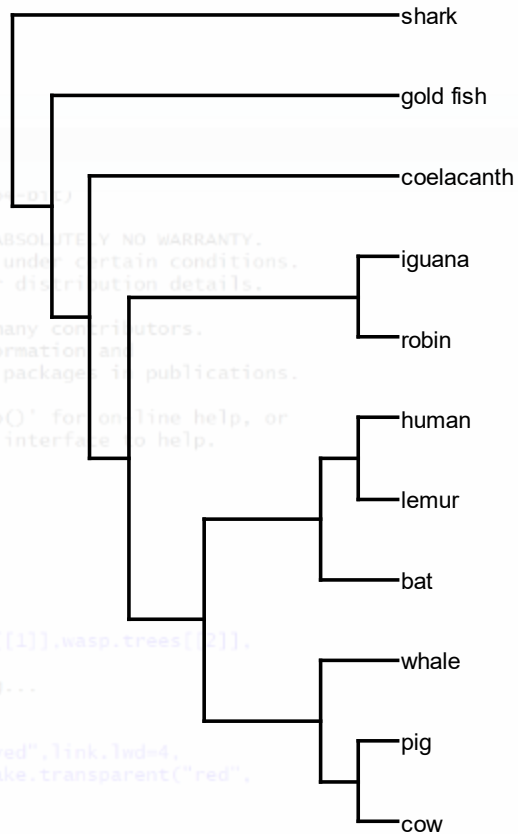
# Rooting & monophyly





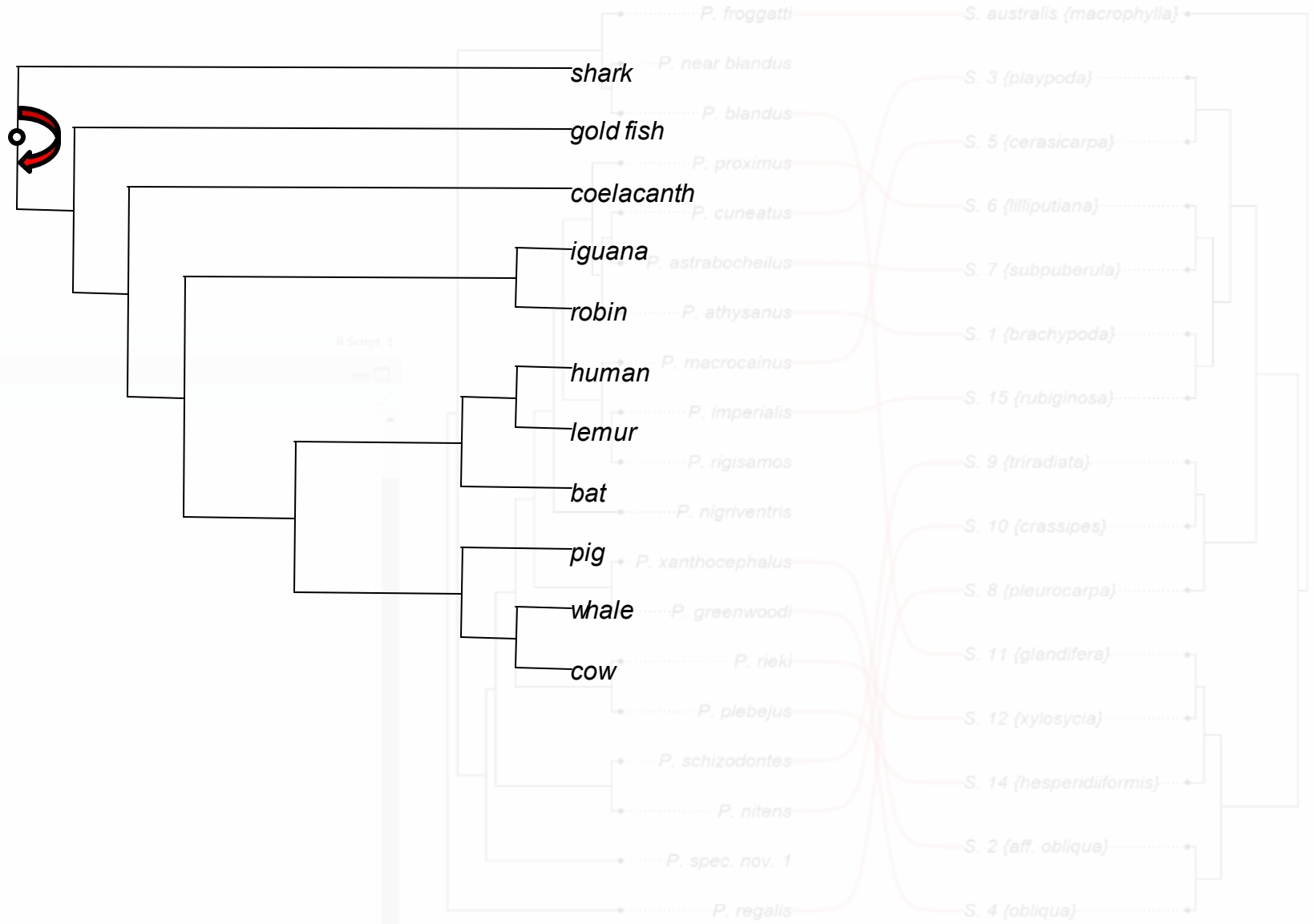
# Node rotation

The **rotation** of nodes in the tree is *arbitrary*. That means that we can always swap the position of two subtrees descended from a common ancestor without changing the tree.



# Node rotation

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1 library(phytools)
2 data(wasp.trees)
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5 wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.trees[[2]],
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12.1 (Top Level) z

Console Terminal Background Jobs

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PLATFORM: x86\_64-w64-mingw32/x64 (64-bit)

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Loading required package: ape
Loading required package: maps
> data(wasp.trees)
> data(wasp.data)
> ## create co-phylogenetic object
> wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.trees[[2]],
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Rotating nodes to optimize matching...
Done.
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+   link.lty="solid",link.col=make.transparent("red",
+     0.25))
> par(mar=c(5.1,4.1,4.1,2.1))
>
```

Phylogenetic tree of the genus *Pseudoceros* showing relationships between various species and their corresponding *S.* species. The tree is rooted on the left and branches out to the right. Species names are listed on the left, and their corresponding *S.* species are listed on the right. Red curved arrows indicate specific relationships or groupings. A red circle highlights a specific node in the tree.

Species on the left (Pseudoceros):

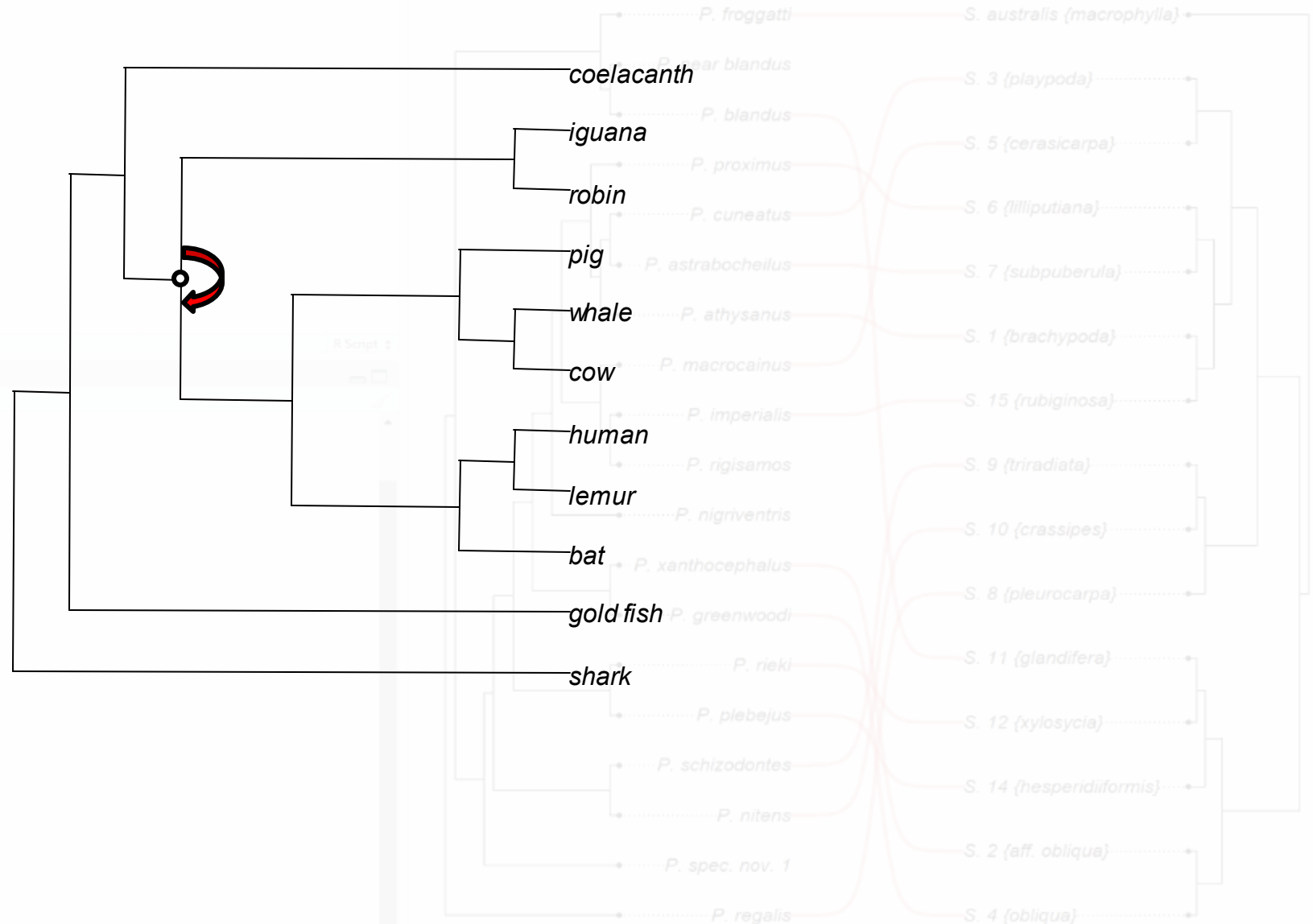
- P. froggatti*
- P. near blandus*
- P. blandus*
- P. proximus*
- P. cuneatus*
- P. astrabocheilus*
- P. athysanus*
- P. macrocainus*
- P. imperialis*
- P. rigisamos*
- P. nigriventris*
- P. xanthocephalus*
- P. greenwoodi*
- P. rieki*
- P. plebejus*
- P. schizodontes*
- P. nitens*
- P. spec. nov. 1*
- P. regalis*

Species on the right (*S.* species):

- S. australis (microphylla)*
- S. 3 (playpoda)*
- S. 5 (cerasicarpa)*
- S. 6 (lilliputiana)*
- S. 7 (subpuberula)*
- S. 1 (brachypoda)*
- S. 15 (rubiginosa)*
- S. 9 (triradiata)*
- S. 10 (crassipes)*
- S. 8 (pleurocarpa)*
- S. 11 (glandifera)*
- S. 12 (xylosycia)*
- S. 14 (hesperidiiformis)*
- S. 2 (aff. obliqua)*
- S. 4 (obliqua)*

# Node rotation

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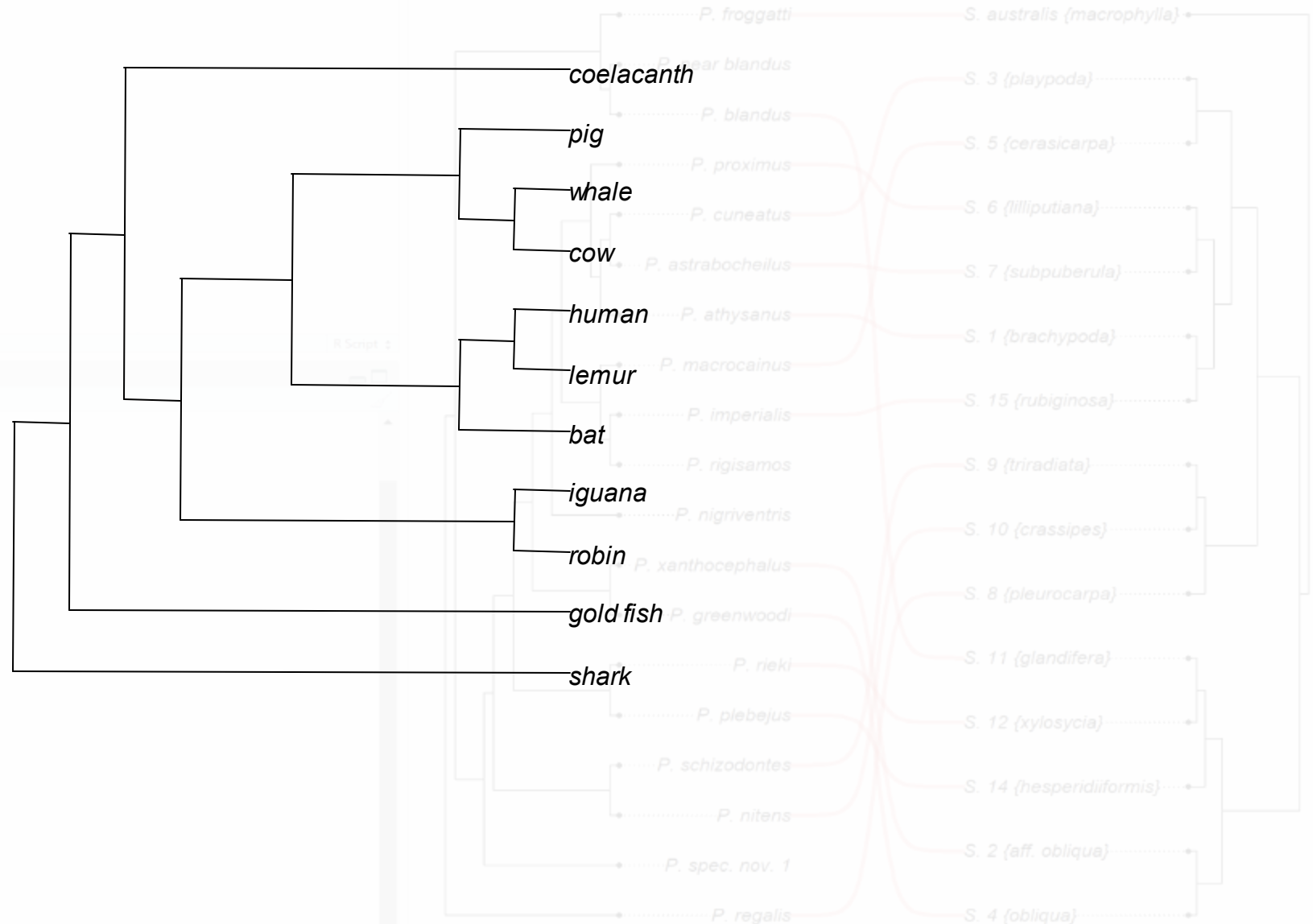
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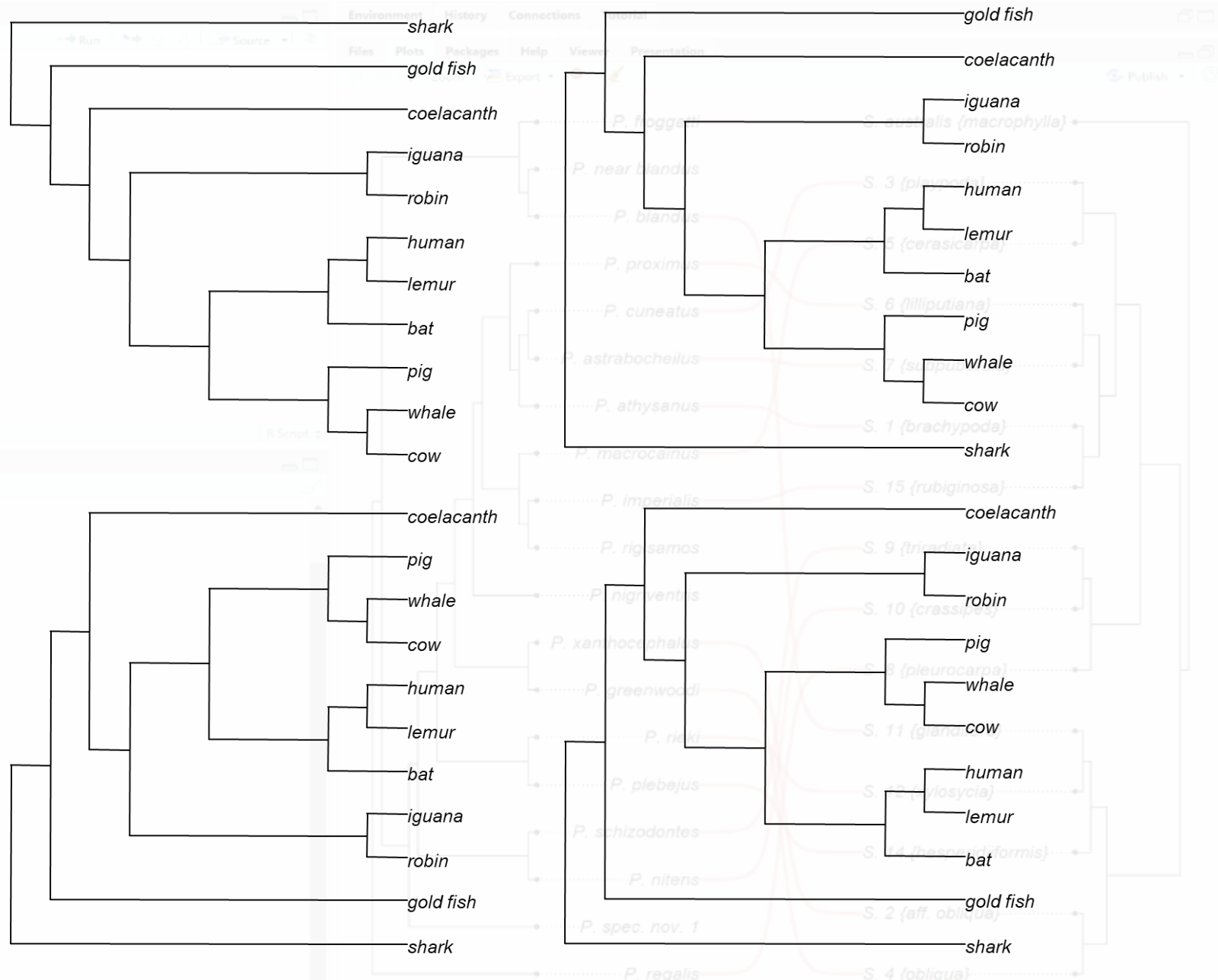
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8 plot(wasp.cophylo,link.type="curved",link.lwd=4,
9   link.lty="solid",link.col=make.transparent("red",
10   0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12 |
```





All of these  
graphs show the  
*same* tree!!



```
1 library(phytools)
2 data(wasp.trees)
3 data(wasp.data)
4 ## create co-phylogenetic object
5 wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.data)
6 assoc=wasp.data)
7 ## plot co-phylogenies
8 plot(wasp.cophylo,link.type="curved",link.lwd=
9       link.lty="solid",link.col=make.transp
10       0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12
```

12.1 (Top Level) z

Console Terminal Background Jobs

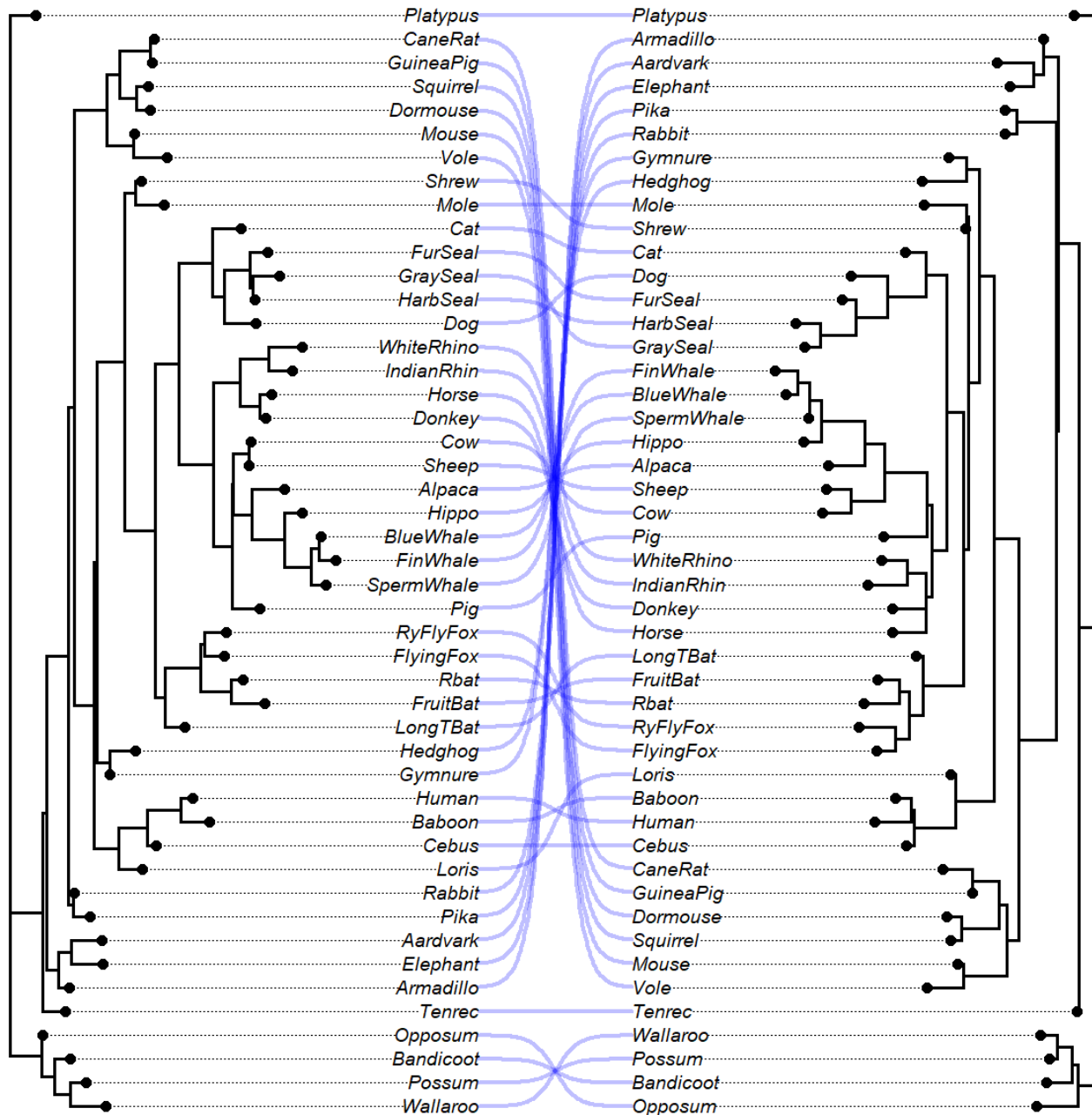
R422 ~/R  
PLATFORM: x86\_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY. You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors. Type 'contributors()' for more information and 'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or 'help.start()' for an HTML browser interface to help. Type 'q()' to quit R.

```
> library(phytools)
Loading required package: ape
Loading required package: maps
> data(wasp.trees)
> data(wasp.data)
> ## create co-phylogenetic object
> wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.data)
+ assoc=wasp.data)
Rotating nodes to optimize matching...
Done.
> ## plot co-phylogenies
> plot(wasp.cophylo,link.type="curved",link.lwd=
+       link.lty="solid",link.col=make.transp
+       0.25))
> par(mar=c(5.1,4.1,4.1,2.1))
>
```



```
1 library(phytools)
2 data(wasp.trees)
3 data(wasp.data)
4 ## create co-phylogenetic object
5 wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.data)
6 assoc=wasp.data)
7 ## plot co-phylogenies
8 plot(wasp.cophylo,link.type="curved",link.lwd=
9 link.lty="solid",link.col=make.transp
10 0.25))
11 par(mar=c(5.1,4.1,4.1,2.1))
12
```

12.1 (Top Level) z

Console Terminal Background Jobs

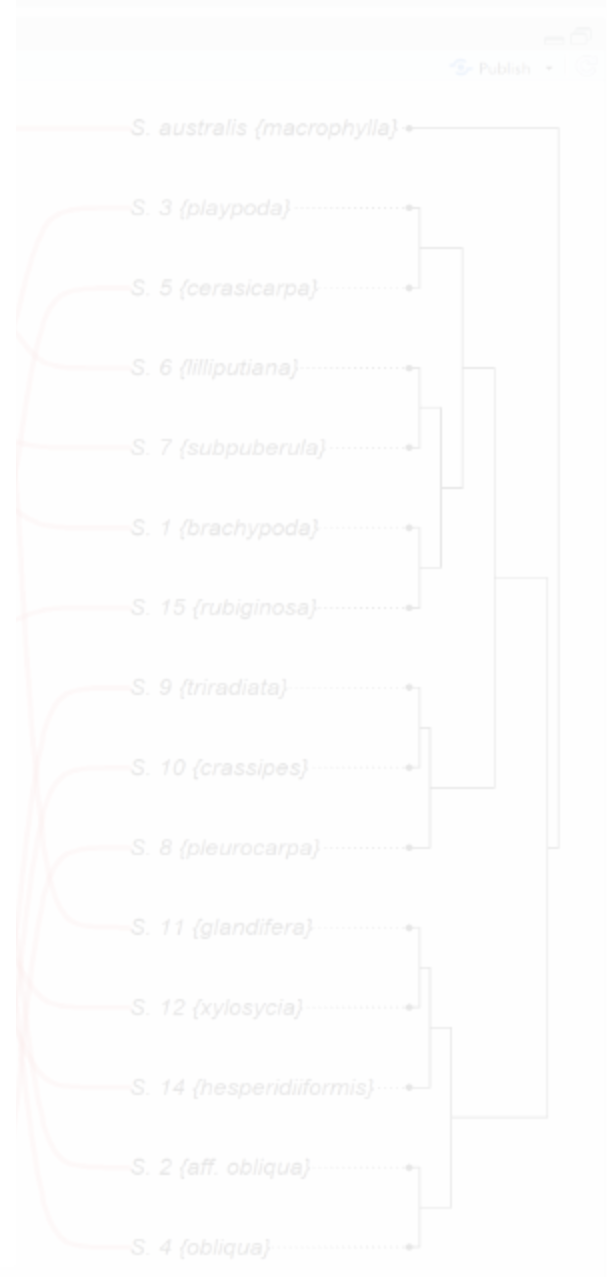
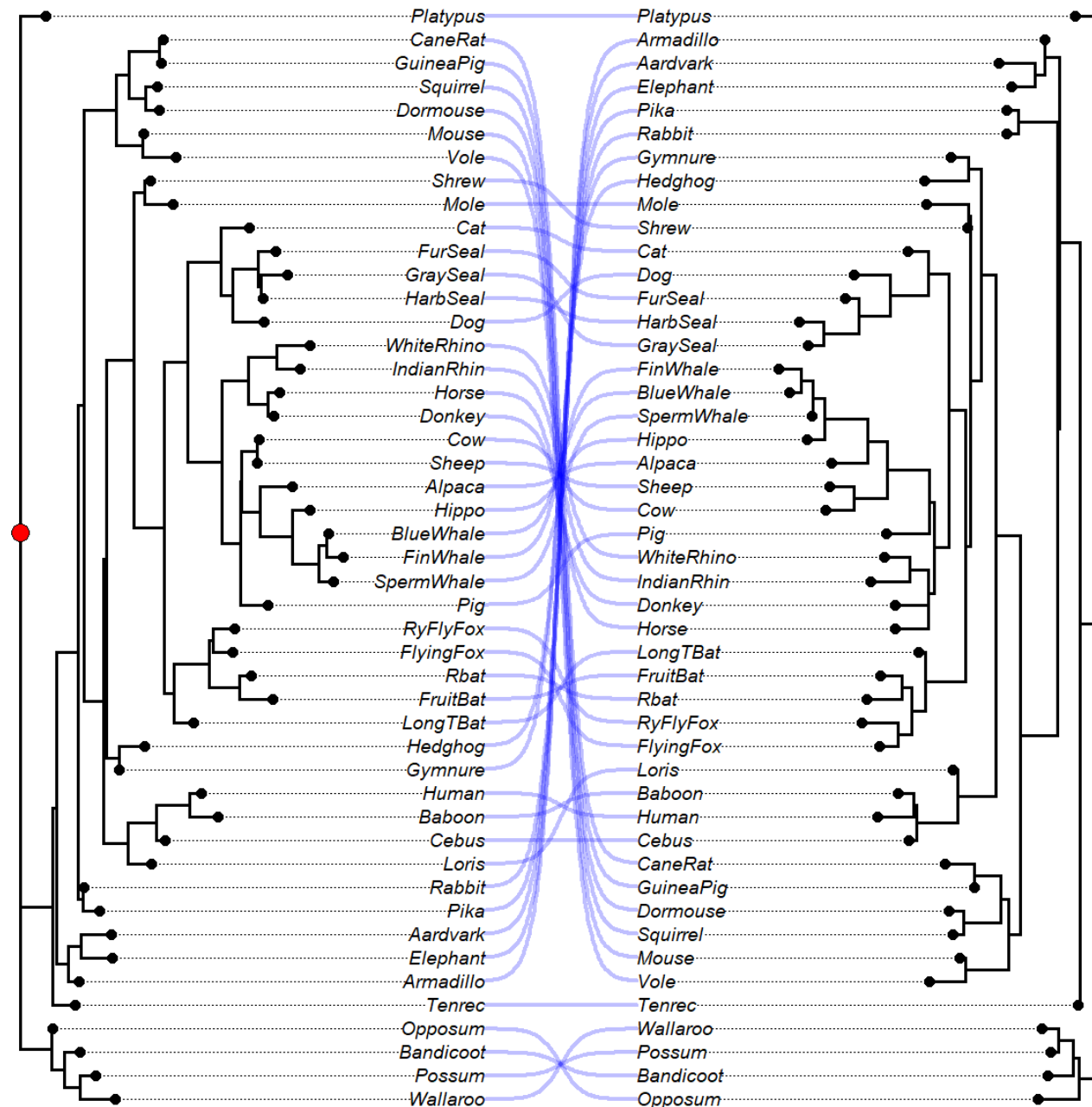
R422 ~/...  
PLATFORM: x86\_64-w64-mingw32/x64 (64-bit)

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'citation()' on how to cite R or R packages in publications.

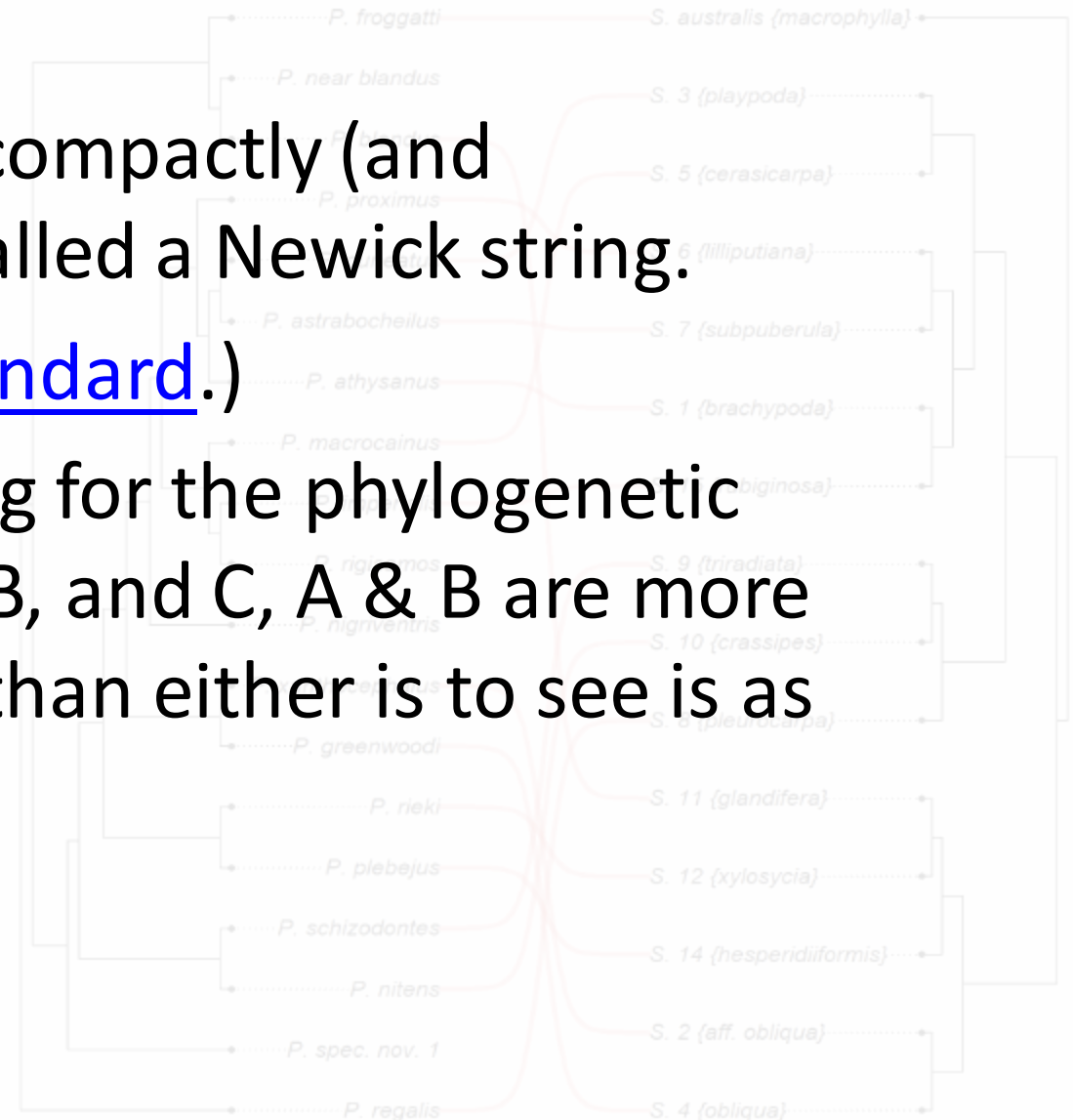
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.

```
> library(phytools)
Loading required package: ape
Loading required package: maps
> data(wasp.trees)
> data(wasp.data)
> ## create co-phylogenetic object
> wasp.cophylo<-cophylo(wasp.trees[[1]],wasp.data)
+ assoc=wasp.data)
Rotating nodes to optimize matching...
Done.
> ## plot co-phylogenies
> plot(wasp.cophylo,link.type="curved",link.lwd=
+ link.lty="solid",link.col=make.transp
+ 0.25))
> par(mar=c(5.1,4.1,4.1,2.1))
>
```



# The “Newick string”

- The tree can be represented compactly (and completely) in a line of text called a Newick string.
- (The source of the Newick [standard](#).)
- For instance, the Newick string for the phylogenetic hypothesis that of species A, B, and C, A & B are more closely related to each other than either is to see is as follows: ((A,B),C);







NEWICK'S

WELCOME ABOARD

# The “Newick string”

## “Newick” tree

```
(((((cow, whale), pig), (bat, (lemur, human))), (robin, iguana)), coelacanth), gold_fish), shark);
```



# $(((\text{Human}, \text{Chimp}), \text{Gorilla}), \text{Monkey});$

```
1 library(phytools)
2 data(wasp.trees)
3 data(wasp.data)
4 ## create co-phylog
5 wasp.cophylo<-cophy
6   assoc=wasp.data
7 ## plot co-phylogen
8 plot(wasp.cophylo, l
9       link.lty="solid",
10      0.25))
11 par(mar=c(5.1,4.1,4
12
```

12.1 (Top Level) z

Console Terminal Background

R 4.2.2 ~ /  
PIACTOTM: X00\_04-W04-MTNG

R is free software and co  
You are welcome to redist  
Type 'license()' or 'lice

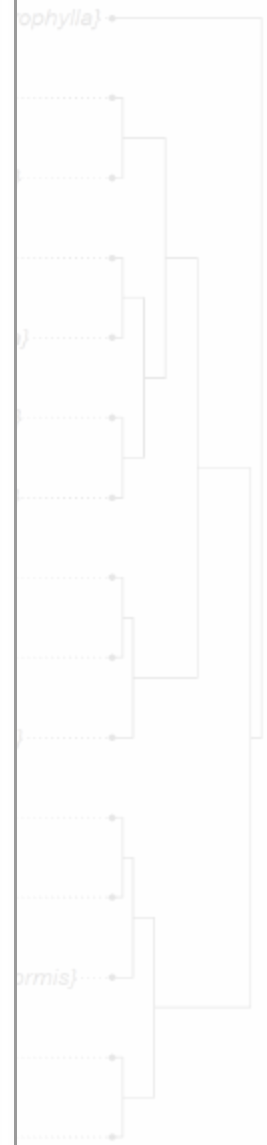
R is a collaborative proj  
Type 'contributors()' for  
'citation()' on how to ci

Type 'demo()' for some de  
'help.start()' for an HTM  
Type 'q()' to quit R.

```
> library(phytools)
Loading required package:
Loading required package:
> data(wasp.trees)
> data(wasp.data)
> ## create co-phylogen
> wasp.cophylo<-cophylo(
+   assoc=wasp.data)
Rotating nodes to optimiz
Done.
> ## plot co-phylogenies
> plot(wasp.cophylo, link
+       link.lty="solid", l
+       0.25))
> par(mar=c(5.1,4.1,4.1,2
>
```

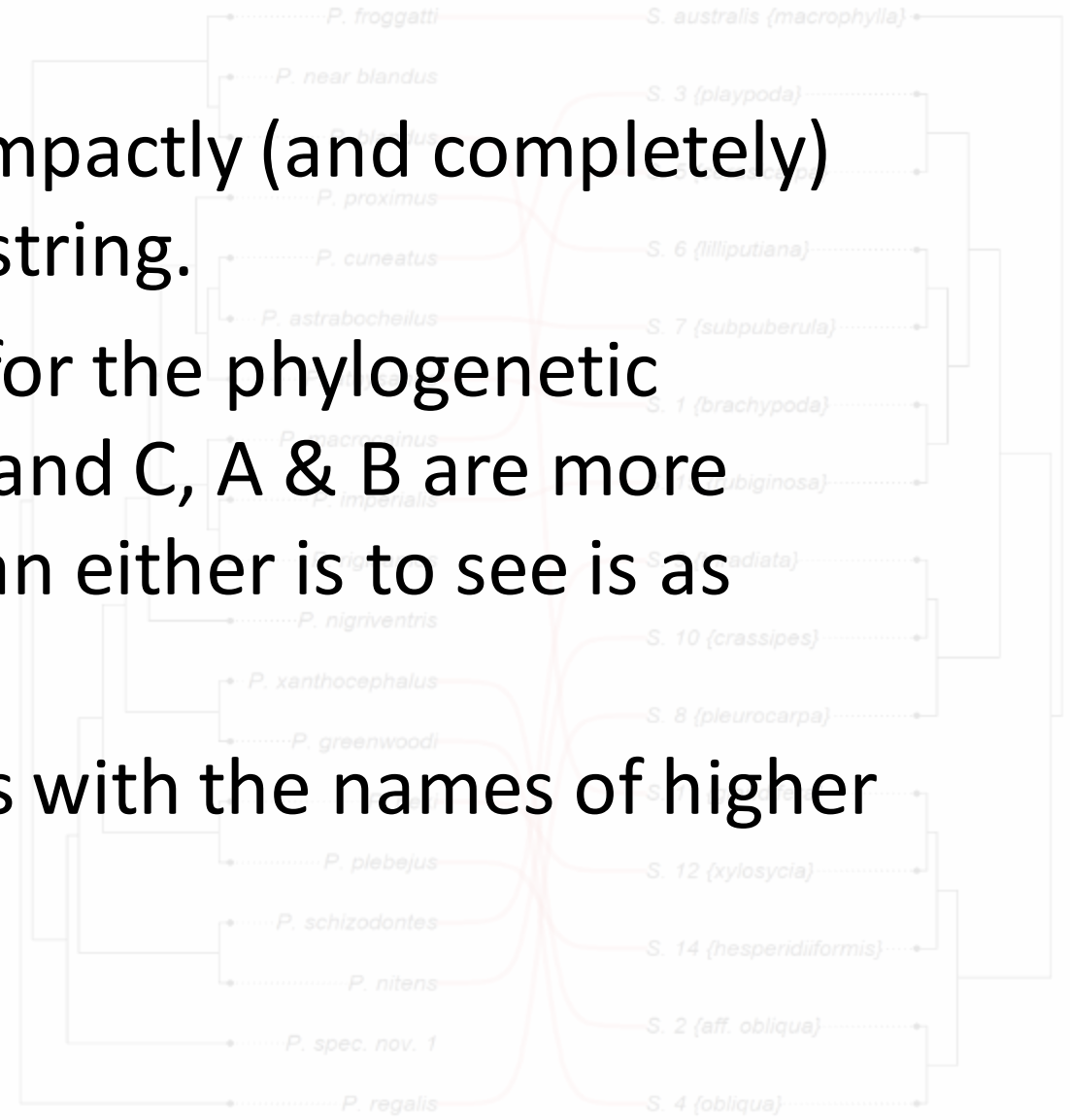


← root node

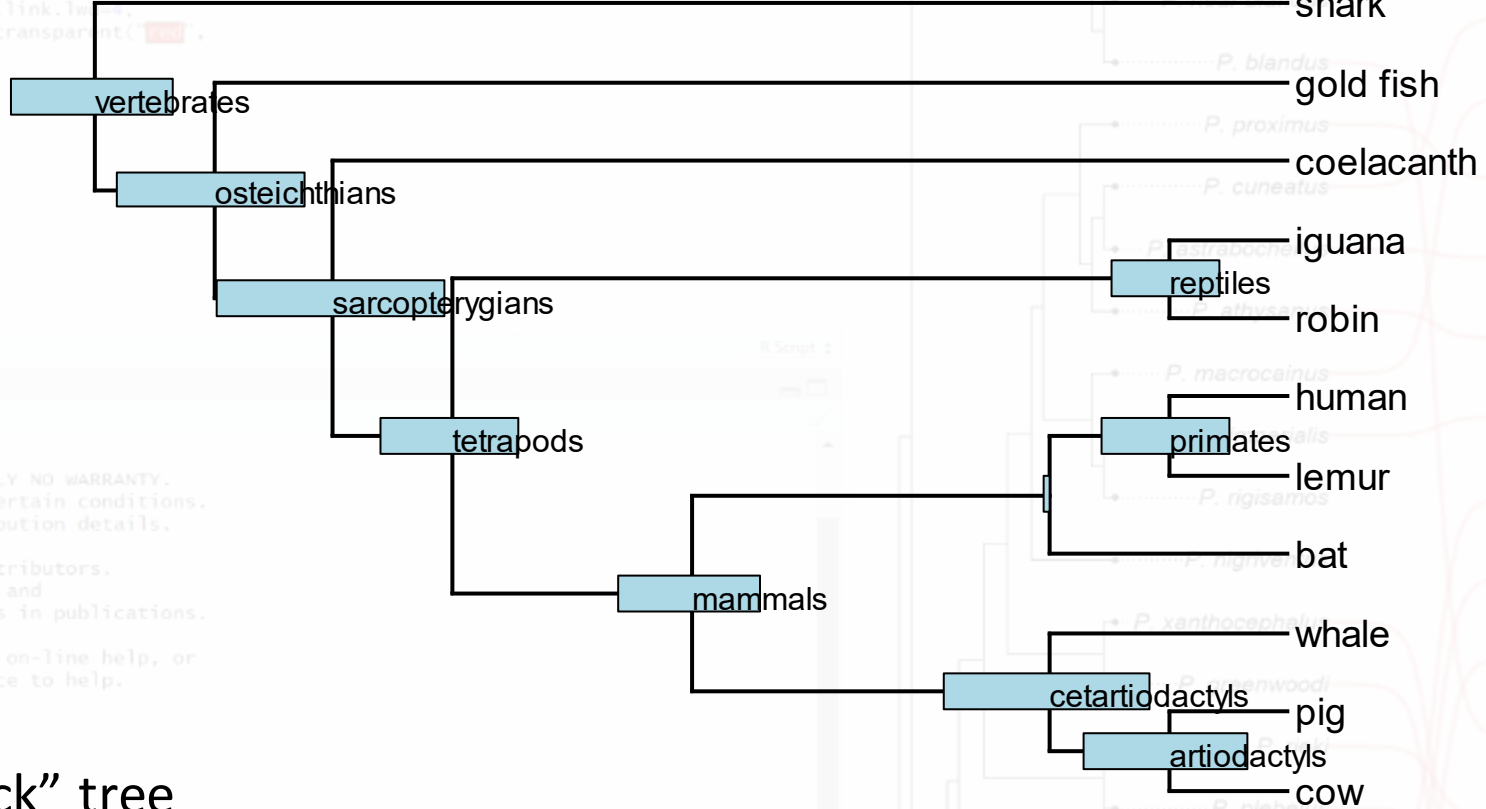


# The “Newick string”

- The tree can be represented compactly (and completely) in a line of text called a Newick string.
- For instance, the Newick string for the phylogenetic hypothesis that of species A, B, and C, A & B are more closely related to each other than either is to see is as follows: ((A,B),C);
- We can also label internal nodes with the names of higher taxa.



# The “Newick string”



“Newick” tree

((((((((cow, pig)artiodactyls, whale)cetartiodactyls, (bat, (lemur, human)primates))mammals, (robin, iguana)reptiles)tetrapods, coelacanth)sarcopterygians, gold\_fish)osteichthians, shark)vertebrates;

# What is ?

- R is simultaneously:
  - a **statistical software**.
  - a **scientific computing environment**.
  - a **programming language**.
- R is distributed *free* and *open source*.
- R requires that you enter commands into a command-line interface.
- The two main components of an R session are *objects* & *functions*.
- Objects are variables, data, and results that we have input, uploaded, or created in memory.
- Functions are special types of objects that take one or more *arguments*, and then *do* something (e.g., create a new object, make a visualization, or write a file).

