

# Read, Visualize, Manipulate, and Export Trees

Jose Eduardo Meireles

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## Setup

### Install packages

If you do not already have these three packages installed, simply run:

```
install.packages("ape")      # work horse of phylogenetic stuff in R
install.packages("phytools") # lots of functionality for analyses and viz
install.packages("rotl")     # interface with open tree of life
```

### Load packages

```
library("ape")
library("phytools")
library("rotl")
```

## Reading Trees

### Types of tree file

There are two major file formats for trees – **Newick** (extension .tre) and **Nexus** (extension .nex).

**Newick** is simply a parenthetical statement. For example ((A, B), C) says that A and B are sister to each other and they, as a group, are sister to C. Usually, branch length information is also written in the file.

1. Go to our `basics_phylo_in_R` R project, then to the `data` folder, and open the `mock_tree.tre` file using your text editor. Try to understand the file.

**Nexus** encodes the newick tree inside it, but can include a lot more information, such as DNA sequences, morphology, or ecological data. Open the `poecilanthe.nex` file with your text editor and find where the tree is.

## Importing trees from a file

Now let's read the `mock_tree.tre` and the `poecilanthe.nex` into R. Here's how you do it:

```
mock_tree = read.tree("data/mock_tree.tre")
poecilanthe = read.nexus("data/poecilanthe.nex")
```

These objects are known as “phylo” objects. You can get a summary of a phylo object just by typing its name.

```
mock_tree
```

```
##
## Phylogenetic tree with 3 tips and 2 internal nodes.
##
## Tip labels:
## [1] "A" "B" "C"
##
## Rooted; includes branch lengths.
```

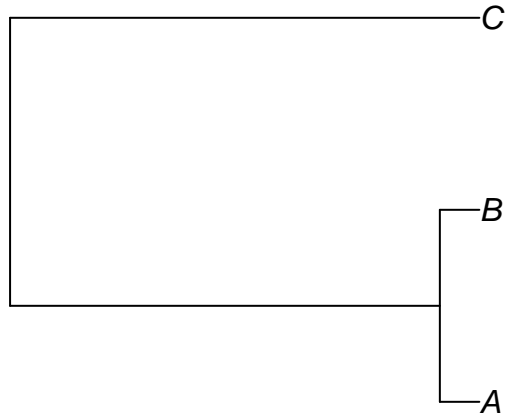
```
poecilanthe
```

```
##
## Phylogenetic tree with 35 tips and 34 internal nodes.
##
## Tip labels:
## Brongniartia_amosana, Brongniartia_inconstans, Brongniartia_peninsularis, Clathrotropis_nitida, C.
##
## Rooted; includes branch lengths.
```

## Plotting a tree

The best way to explore a tree is to plot it out.

```
plot(mock_tree)
```



You can display that tree in many different ways. Look at the help function for plotting trees in `ape` `?plot.phylo` for more info. Here are a few examples:

```

par(mfrow = c(2, 2), mar = c(1,1,1,1), oma = c(3,3,3,3))

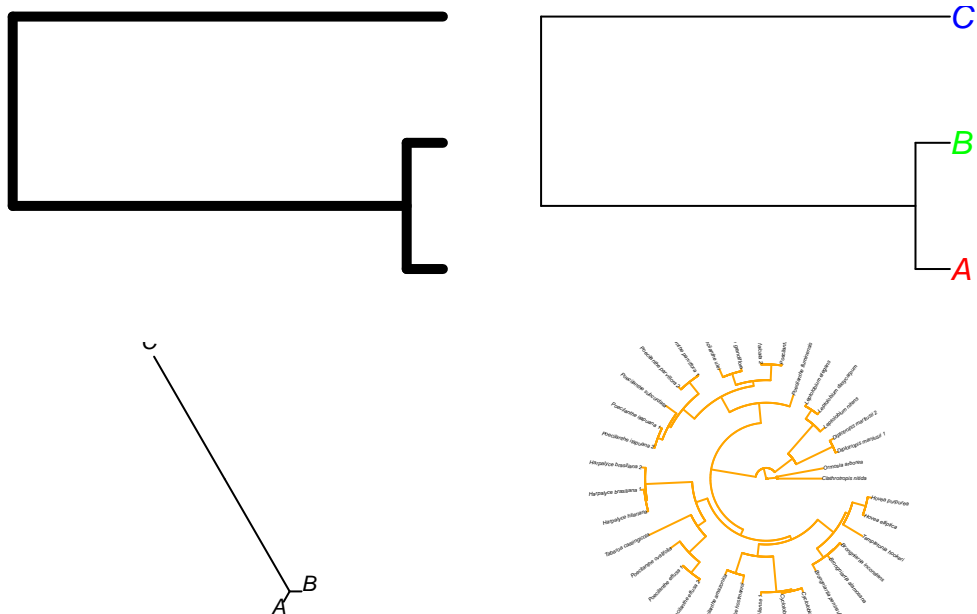
## No tip labels. Thicker branches
plot(mock_tree, show.tip.label = FALSE, edge.width = 5)

## Color tip labels and increase font size
plot(mock_tree, tip.color = c("red", "green", "blue"), cex = 1.2)

## Unrooted tree
plot(mock_tree, type = "unrooted")

## Circular tree. Color branches
plot(poecilanthe, type = "fan", cex = 0.2, edge.color = "orange")

```

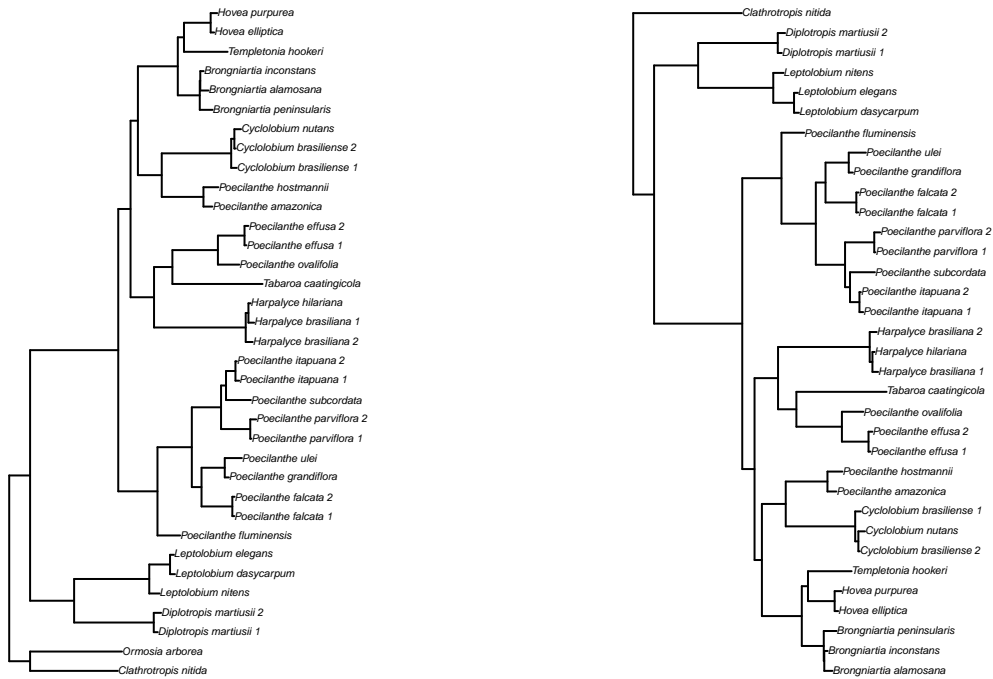


## Manipulating a tree

You can change your tree in many different ways. A common thing to do is to drop an unwanted tip. Another one is to ladderize the tree.

```
poecilanthe_mod = drop.tip(poecilanthe, "Ormosia_arborea")
poecilanthe_mod = ladderize(poecilanthe_mod)

par(mfrow = c(1, 2), mar = c(2,2,2,2))
plot(poecilanthe, cex = 0.3)
plot(poecilanthe_mod, cex = 0.3)
```



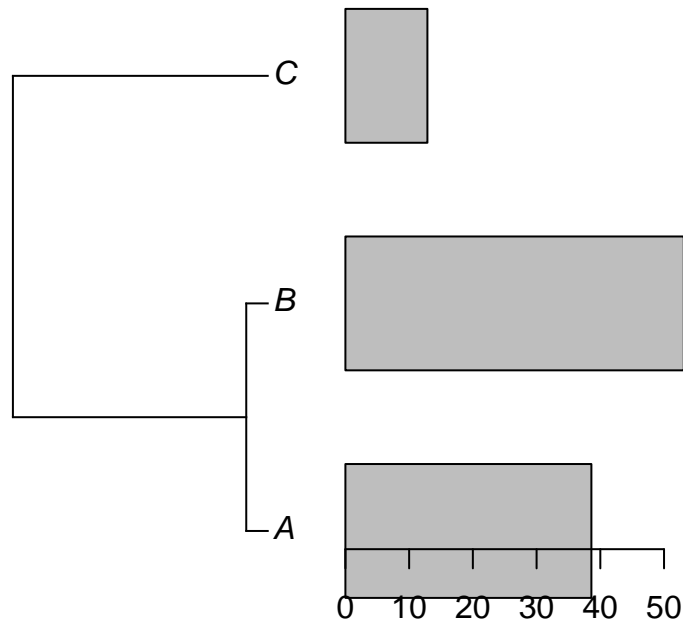
## Trees and Data

We can also display data along with phylogenies, be the data gene expression, body size, or whatever else.

In general, what we need is a vector or a matrix with the numerical data and the names of the tips. Here are two examples:

```
par(mfrow = c(1, 2), mar = c(5,5,5,5))
body_size = c("A" = 38.6, "B" = 53.1, "C" = 12.87)

plotTree.barplot(mock_tree, body_size)
```



## Stealing a tree

Let's try to find trees that actually interest you. You can try to find a tree file for a specific study in <https://www.treebase.org/>.

Another way of getting a tree is downloading it from the OpenTreeOfLife project.

## Getting a tree from Open Tree of Life

```
library("rotl")
```

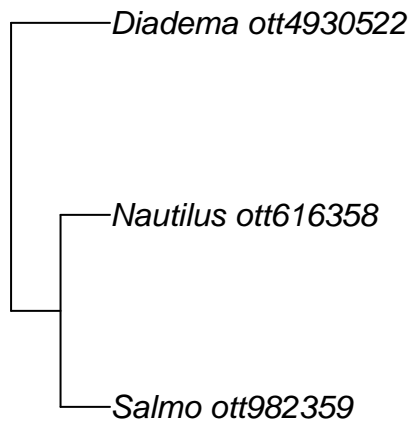
```
taxa_raw    = c("Salmo", "Diadema", "Nautilus")
taxa_clean  = tnrs_match_names(taxa_raw)
dudus_tree  = tol_induced_subtree(ott_ids = taxa_clean$ott_id)
```

```
## Progress [-----] 0/68 ( 0) ?sProgress [=====]
```

```
## Warning in collapse_singles(tr, show_progress): Dropping singleton nodes
## with labels: Holozoa ott5246131, mrcaott42ott34294, Metazoa ott691846,
## mrcaott42ott3989, mrcaott42ott570365, mrcaott42ott150, Bilateria
## ott117569, Deuterostomia ott147604, Chordata ott125642, mrcaott42ott658,
## Craniata (subphylum in Deuterostomia) ott947318, Vertebrata (subphylum in
## Deuterostomia) ott801601, Gnathostomata (superclass in phylum Chordata)
## ott278114, Teleostomi ott114656, Euteleostomi ott114654, Actinopterygii
## ott773483, Actinopteri ott285821, Neopterygii ott471203, Teleostei ott212201,
## Osteoglossocephalai ott5506109, Clupeocephala ott285819, Euteleosteomorpha
## ott5517919, mrcaott274ott392, mrcaott274ott595, Protacanthopterygii ott1024043,
## mrcaott274ott3887, mrcaott3887ott9371, Salmoniformes ott216171, Salmonidae
## ott739933, mrcaott3887ott28511, Salmoninae ott936925, mrcaott31485ott79094,
```

```
## Protostomia ott189832, mrcaott49ott6612, Lophotrochozoa ott155737,
## mrcaott56ott519, mrcaott56ott5497, Mollusca ott802117, mrcaott56ott1881,
## mrcaott1881ott102410, Cephalopoda ott7368, Nautiloidea ott854446, Nautilida
## ott854452, Nautilidae ott616361, Nucletmycea ott5246132, Fungi ott352914,
## mrcaott109ott3465, mrcaott109ott67172, mrcaott109ott1423, mrcaott109ott9352,
## h2007-2 ott5576447, h2007-1 ott5584405, Dikarya ott656316, Ascomycota
## ott439373, mrcaott235ott3445, saccharomyceta ott1098854, Pezizomycotina
## ott971709, mrcaott235ott428, mrcaott235ott6545, mrcaott235ott3264,
## mrcaott235ott1190, mrcaott235ott1320, mrcaott1320ott8438, mrcaott1320ott372181,
## mrcaott1320ott33787, mrcaott1320ott689966, Pleosporales ott18194, Diademaceae
## ott614335
```

```
plot(dudus_tree)
```



## Steal a tree on your own!

1. Pick a group of interest (Oaks, Mammals, whatever)
2. Download a phylogeny for Using the Open Tree of Life interface
3. Explore the tree
4. Make a figure out of it