

Buildingtrees_week 4

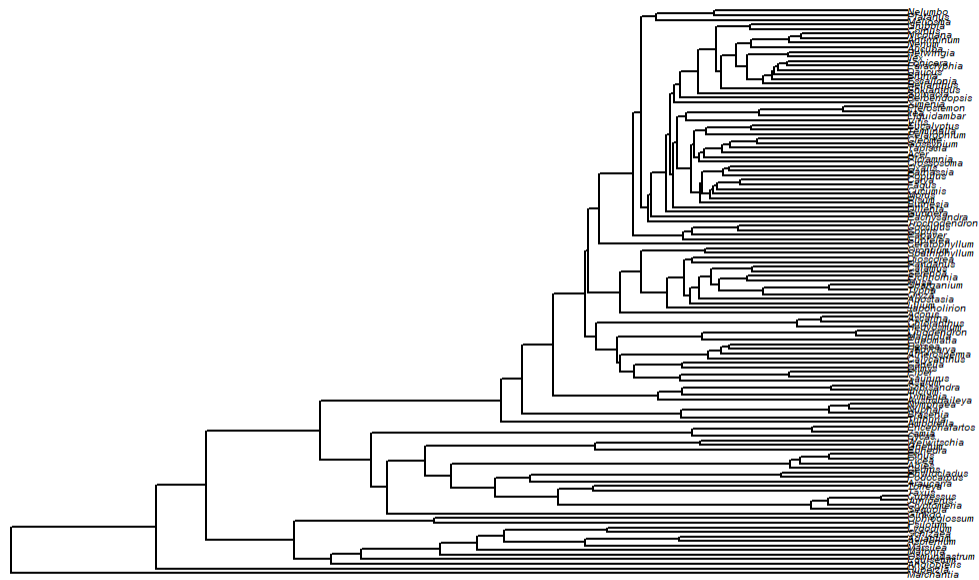
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1/29/2020

Downloading the phybase package `install.packages("devtools")` `library("devtools")`
`install_github("bomeara/phybase")`

Getting a tree from Open Tree of Life and a recent plant tree from Beaulieu et al.

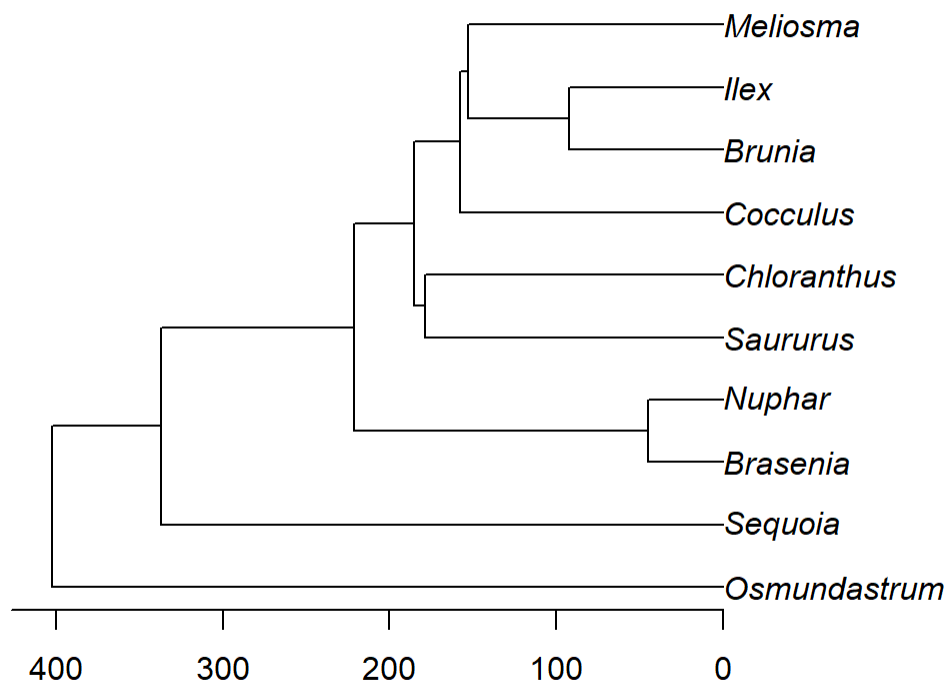
```
library(rotl)
library(ape)
phy <- get_study_tree("ot_485", "tree1")
plot(phy, cex=0.3)
```



Simplifying by dropping some taxa

```
library(geiger)
```

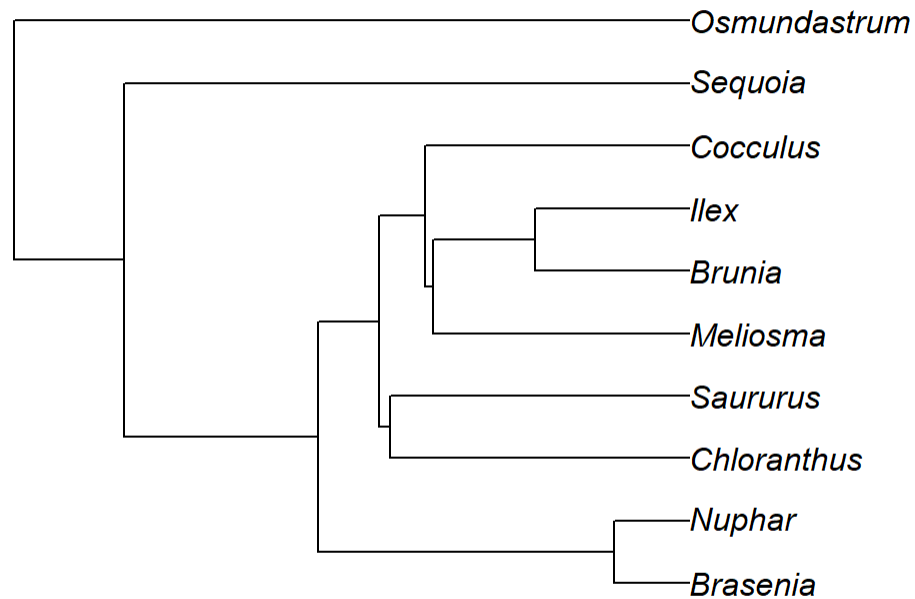
```
## Registered S3 method overwritten by 'geiger':
##   method      from
##   unique.multiPhylo ape
phy <- drop.random(phy, Ntip(phy) - 10)
plot(phy)
axisPhylo()
```



Simulating gene trees on this tree

```
library(phybase)
## Loading required package: Matrix
##
## Attaching package: 'phybase'
## The following objects are masked from 'package:ape':
##
##   node.height, write.dna
```

```
gene.tree <- phybase::sim.coaltree.phylo(phy, pop.size=1e-12)
plot(gene.tree)
```



This tree probably looks very similar to the initial tree

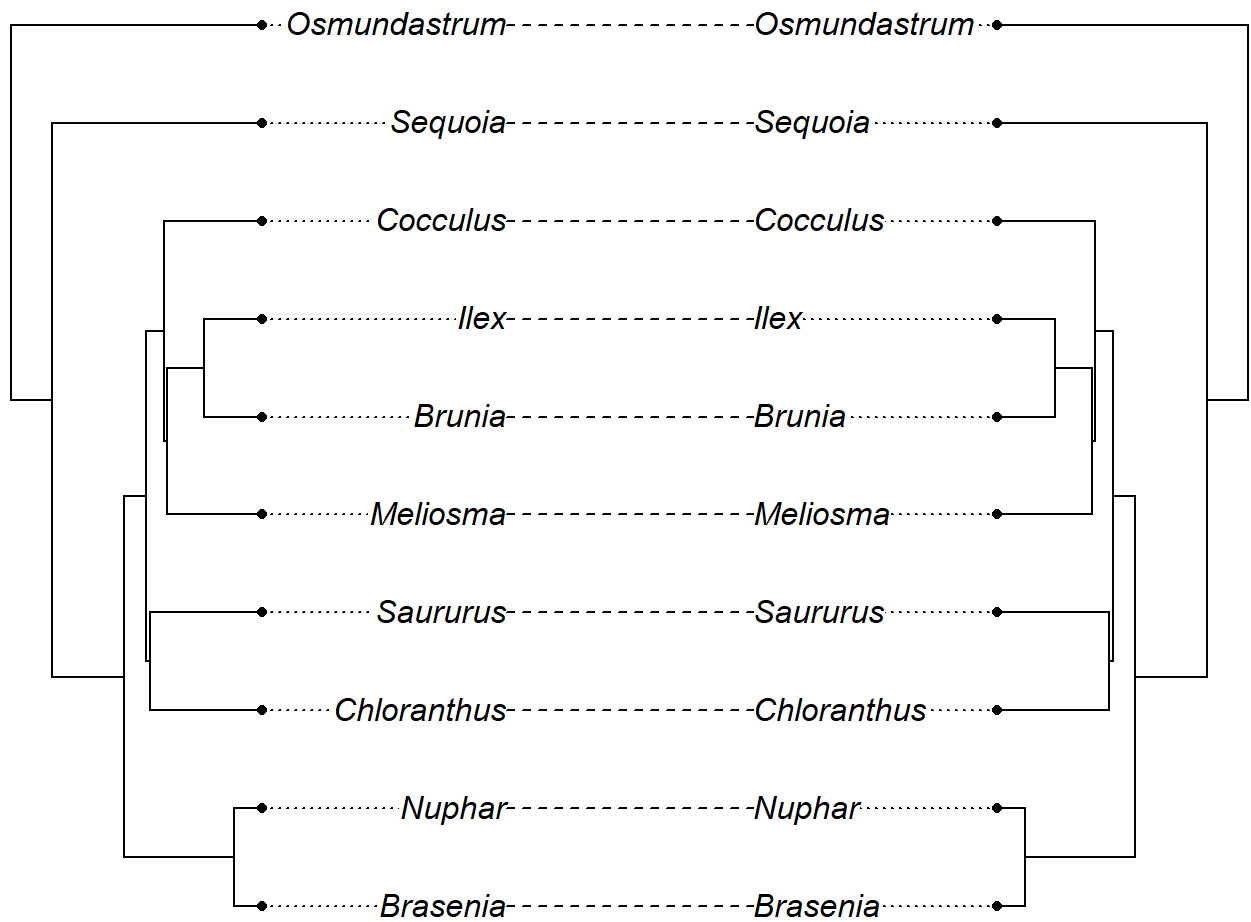
```
library(phytools)

## Loading required package: maps

plot(cophylo(phy, gene.tree, cbind(sort(phy$tip.label), sort(gene.tree$tip.label))))

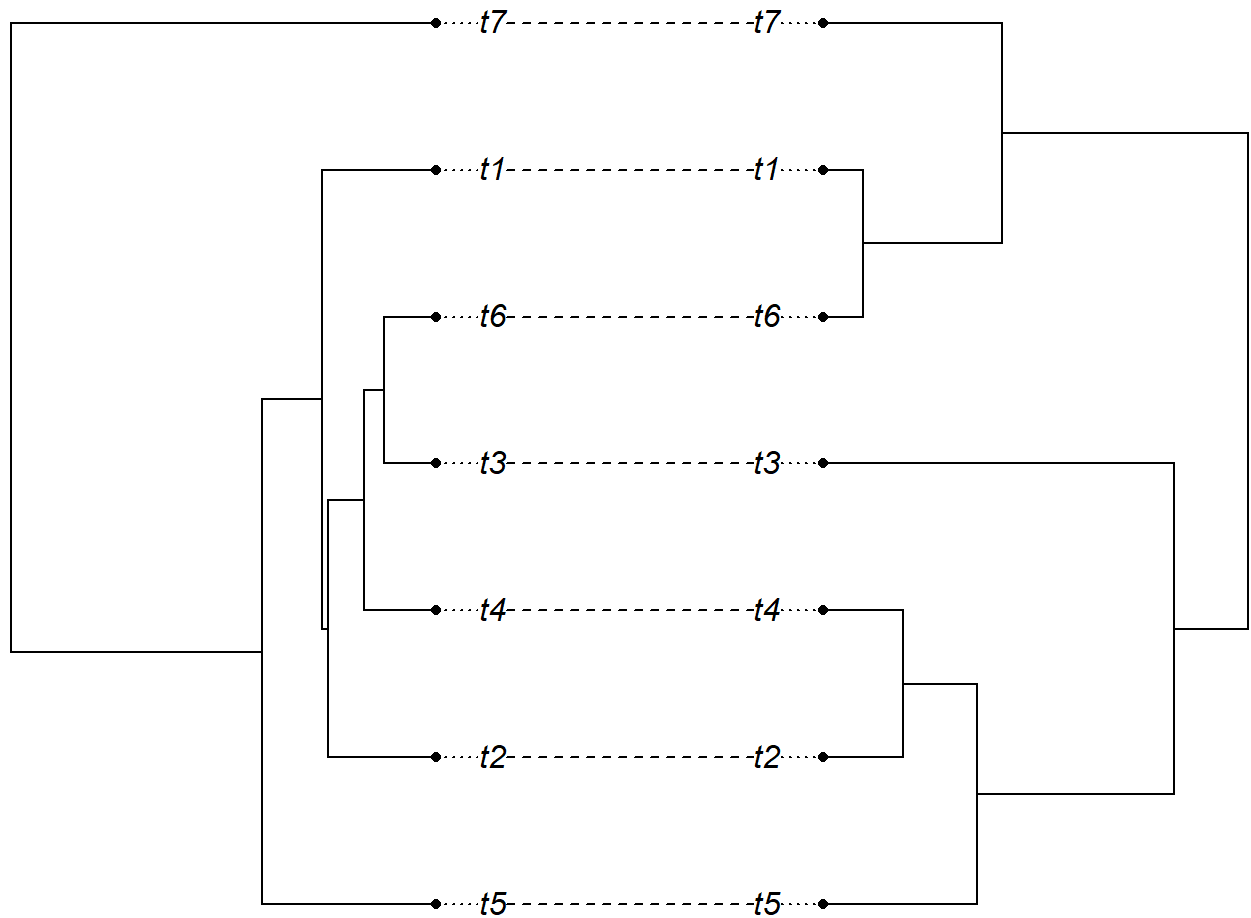
## Rotating nodes to optimize matching...

## Done.
```



Lack of coalescence of copies can occur any time there are short, fat branches

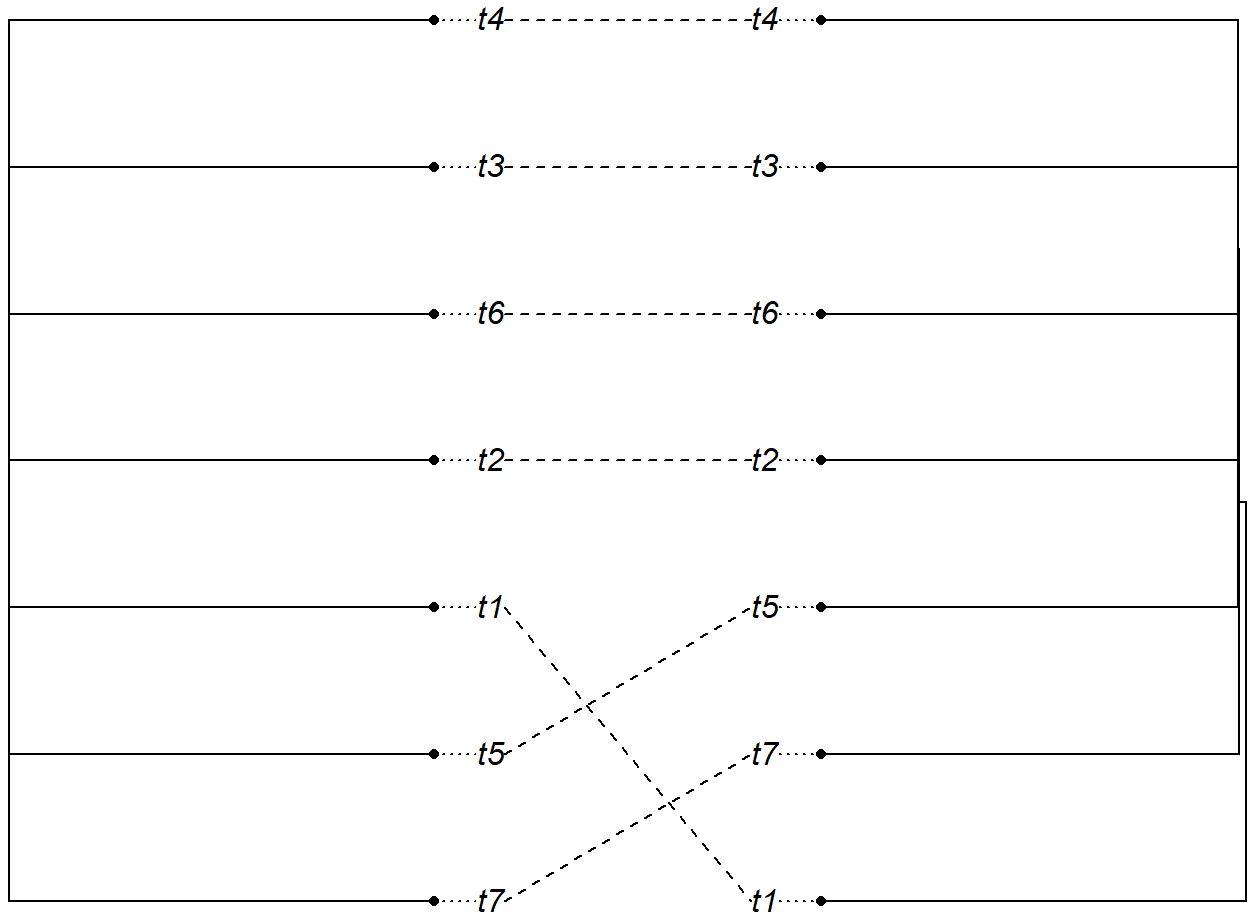
```
species.tree <- rcoal(7)
species.tree$edge.length <- species.tree$edge.length / (10*max(branching.times(species.tree)))
gene.tree <- phybase::sim.coaltree.phylo(species.tree)
plot(cophylo(species.tree, gene.tree, cbind(sort(species.tree$tip.label), sort(gene.tree$tip.label))))
## Rotating nodes to optimize matching...
## Done.
```



Lengthening the tips of the species tree

```
tip.rows <- which(species.tree$edge[,2]<=Ntip(species.tree))
species.tree2 <- species.tree
species.tree2$edge.length[tip.rows] <- 100 + species.tree2$edge.length[tip.ro
ws]
gene.tree2 <- phybase::sim.coaltree.phylo(species.tree2)
plot(cophylo(species.tree2, gene.tree2, cbind(sort(species.tree2$tip.label),
sort(gene.tree2$tip.label))))

## Rotating nodes to optimize matching...
## Done.
```



Plotting the cladogram

```
species.tree2.clado <- compute.brlen(species.tree2)
gene.tree2.clado <- compute.brlen(gene.tree2)

plot(cophylo(species.tree2.clado, gene.tree2.clado, cbind(sort(species.tree2.
clado$tip.label),

                                                                    sort(gene.tree2.cla
do$tip.label))))

## Rotating nodes to optimize matching...
## Done.
```

