Phylogeny tree

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```r
library(tidyverse)
library(openintro)
library(ggtree)
library(ape)
```

```r
tree <- read.tree("../Data/output.bionj")
```

```r
# Ladderizing
tree <- ladderize(tree, right = F)
```

```r
# Importing tree from CIPRES using IQ Tool
tree_1 <- ggtree(tree) +
  geom_tiplab(size = 1)
```

```
## ! The tree contained negative edge lengths. If you want to ignore the edges,
## you can set `options(ignore.negative.edge=TRUE)`, then re-run ggtree.
```

```r
tree_1
```

```r
# reading contree output from CIPRES
tree2 <- read.tree("../Data/output.contree")


# Ladderizing
tree2 <- ladderize(tree2, right = F)


# Importing contree from CIPRES using IQ Tool
tree_3 <- ggtree(tree2) +
  geom_tiplab(size = 1)


tree_3
```
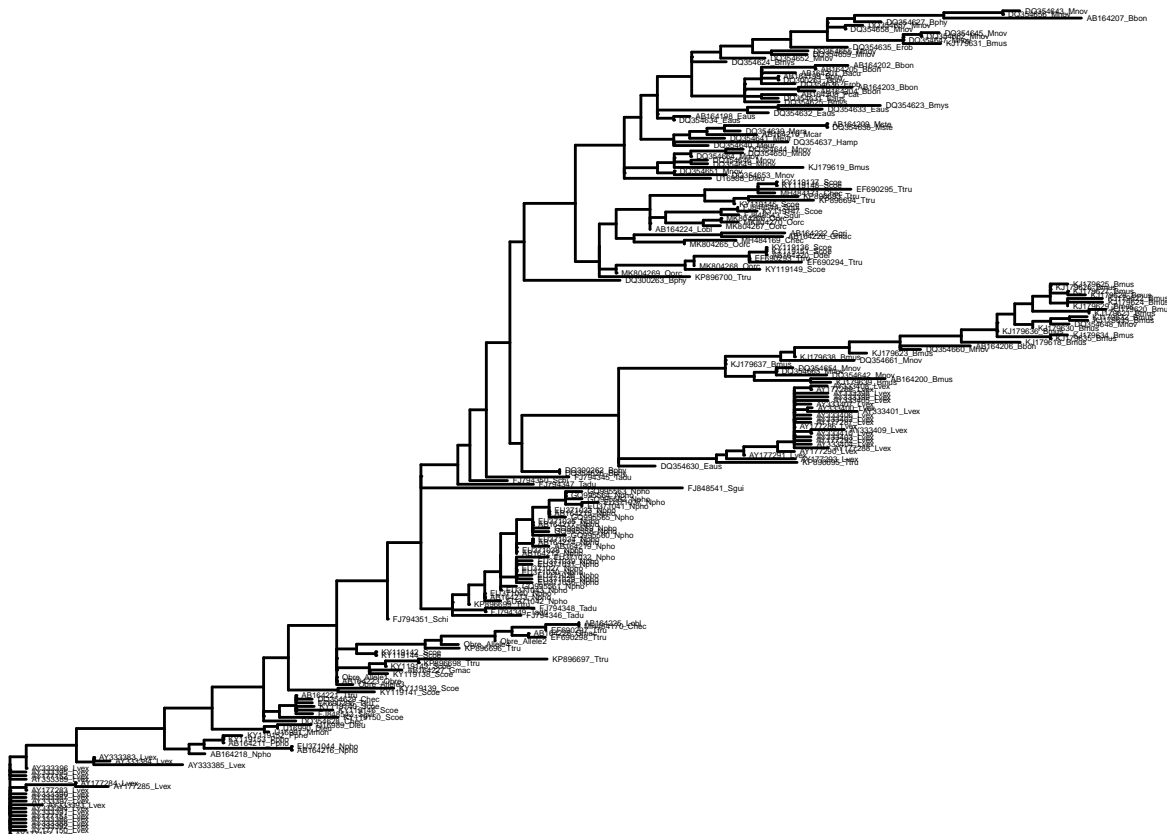
```r
# reading treefile output from CIPRES
tree4 <- read.tree("../Data/output.treefile")


# Ladderizing
tree4 <- ladderize(tree4, right = F)


# Importing contree from CIPRES using IQ Tool
tree_5 <- ggtree(tree4) +
  geom_tiplab(size = 1)


tree_5
```