# ncbi-alignment

## 2024-12-06

```r
library(ape)
```

Read in the ncbi alignment and tree

```r
all_matched_names <- readRDS("/home/millerjared/blue_guralnick/millerjared/BoCP/outputs/ncbi_matched_na

poa_tree <- ape::read.tree("/home/millerjared/blue_guralnick/millerjared/BoCP/data/processed/tree-outpu
```

Redo tree labels

```r
# create a named vector to map IDs to names
id_to_name <- setNames(all_matched_names$ncbiMappedSpecies, all_matched_names$ncbiAcceptedNameUsageIDLe

# replace the IDs in tip.label with corresponding names
poa_tree$tip.label <- id_to_name[poa_tree$tip.label]
```

Plot tree

```r
plot.phylo(poa_tree, cex=0.4, label.offset = 0.0005, no.margin=TRUE)
```
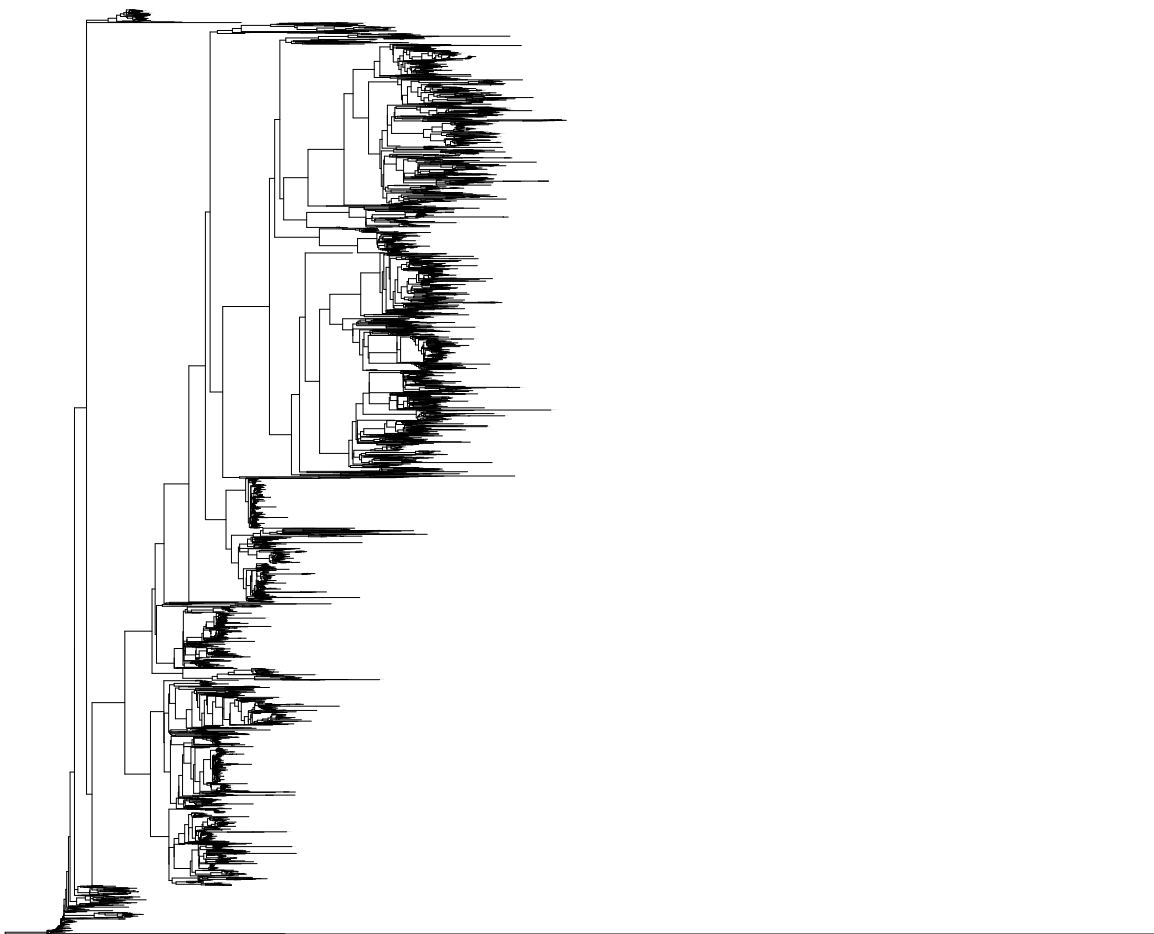
```
library(ggtree)
```

```
## Registered S3 methods overwritten by 'treeio':
##   method              from
##   MRCA.phylo          tidytree
##   MRCA.treedata       tidytree
##   Nnode.treedata      tidytree
##   Ntip.treedata       tidytree
##   ancestor.phylo      tidytree
##   ancestor.treedata   tidytree
##   child.phylo         tidytree
##   child.treedata      tidytree
##   full_join.phylo     tidytree
##   full_join.treedata  tidytree
##   groupClade.phylo    tidytree
##   groupClade.treedata tidytree
##   groupOTU.phylo      tidytree
##   groupOTU.treedata   tidytree
##   inner_join.phylo    tidytree
##   inner_join.treedata tidytree
##   is.rooted.treedata  tidytree
```

```
##    nodeid.phylo        tidytree
##    nodeid.treedata     tidytree
##    nodelab.phylo       tidytree
##    nodelab.treedata    tidytree
##    offspring.phylo     tidytree
##    offspring.treedata  tidytree
##    parent.phylo        tidytree
##    parent.treedata     tidytree
##    root.treedata       tidytree
##    rootnode.phylo      tidytree
##    sibling.phylo       tidytree
```

```
## ggtree v3.8.2 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
##
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.
## ggtree: an R package for visualization and annotation of phylogenetic
## trees with their covariates and other associated data. Methods in
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628
##
## Guangchuang Yu. Using ggtree to visualize data on tree-like structures.
## Current Protocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
##
## Guangchuang Yu.  Data Integration, Manipulation and Visualization of
## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022,
## doi:10.1201/9781003279242
```

```
##
## Attaching package: 'ggtree'
```

```
## The following object is masked from 'package:ape':
##
##      rotate
```

plot ggtree

```r
# Plot the tree with ggtree
p <- ggtree(poa_tree, layout="rectangular") +
    geom_tiplab(align=TRUE, linesize=.1, size = 1) +
   theme_tree2()# +  # Remove unnecessary plot elements
  # theme(plot.margin = margin(40, 40, 40, 40))  # Adjust margins
# Save the plot as an interactive HTML
ggsave("/home/millerjared/blue_guralnick/millerjared/BoCP/outputs/poaceae_tree_figure.svg", plot = p, d
```

Isolate missing names