

Phylogeny tree

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

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

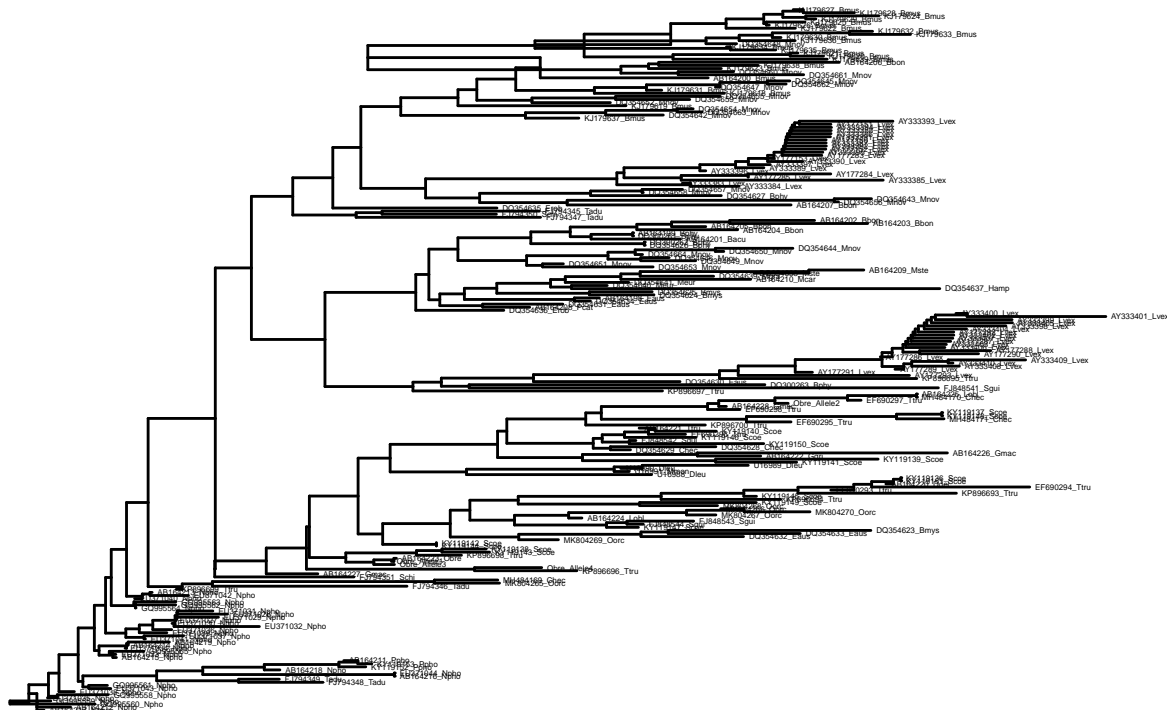
```
# Ladderizing the tree (Neighborjoining tree)
tree <- ladderize(tree, right = F)
```

```
# Importing NJ tree from CIPRES using IQ Tool
tree_1 <- ggtree(tree) +
  geom_tiplab(size = 1) +
  ggtitle(
    "Neighbor-joining tree -
    Comparing DQB Alleles of Irrawaddy dolphins
    to DQB Alleles of cetaceans ")
```

```
## ! 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.
```

```
tree_1
```

Neighbor-joining tree – Comparing DQB Alleles of Irrawaddy dolphins to DQB Alleles of cetaceans



```
# 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, branch.length='none', layout='circular') +  
  geom_tiplab(size = 1) +  
  ggtitle("Bootstrap tree - Comparing DQB Alleles of Irrawaddy dolphins to DQB  
  Alleles of cetaceans")
```

tree_3

A circular phylogenetic tree showing the relationships between various bacterial strains. The tree is rooted at the top and branches outwards. Strains are labeled with names like AY177281, AY177282, etc., and are grouped into clusters. The tree is colored with a gradient from blue to red.

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

tree_5
```

