

Phylogeny tree

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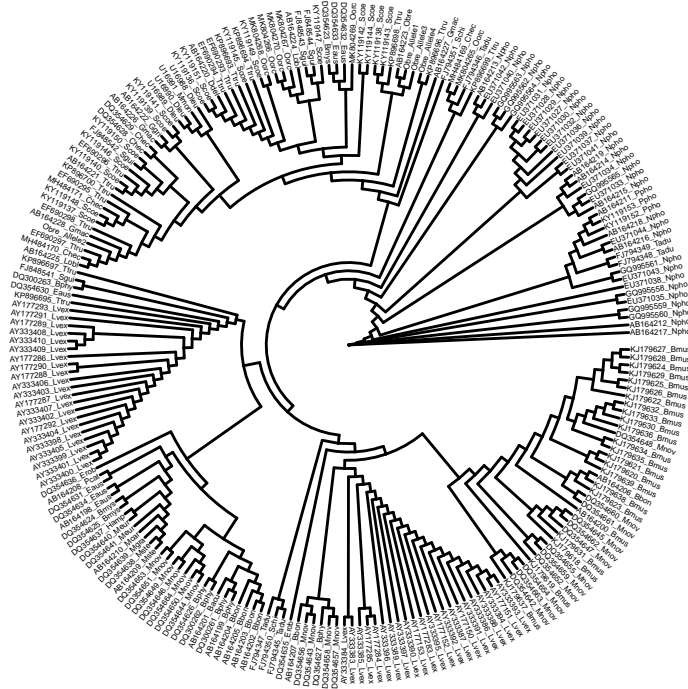
```
library(tidyverse)
library(openintro)
library(ggtree)
library(ape)
```

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

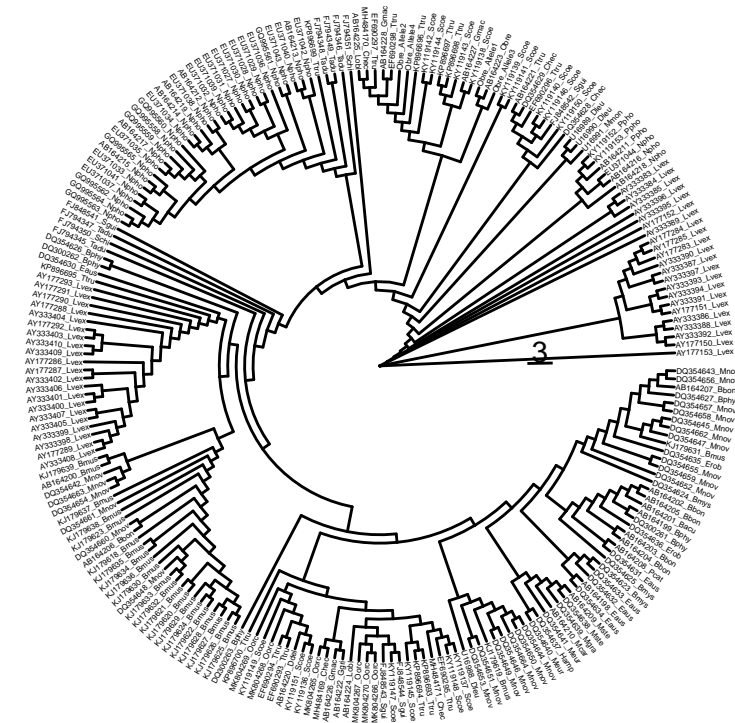
```
tree2 <- ladderize(tree2, right = F)
```

```
# 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") +  
  geom_treescale()
```

```
tree_3
```

Bootstrap tree – Comparing DQB Alleles of Irrawaddy dolphins to Alleles of cetaceans



```
# 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, branch.length='none', layout='circular') +  
  geom_tiplab(size = 1)
```

```
tree_5
```

