Phylogeny tree

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

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

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

```r
# 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
```
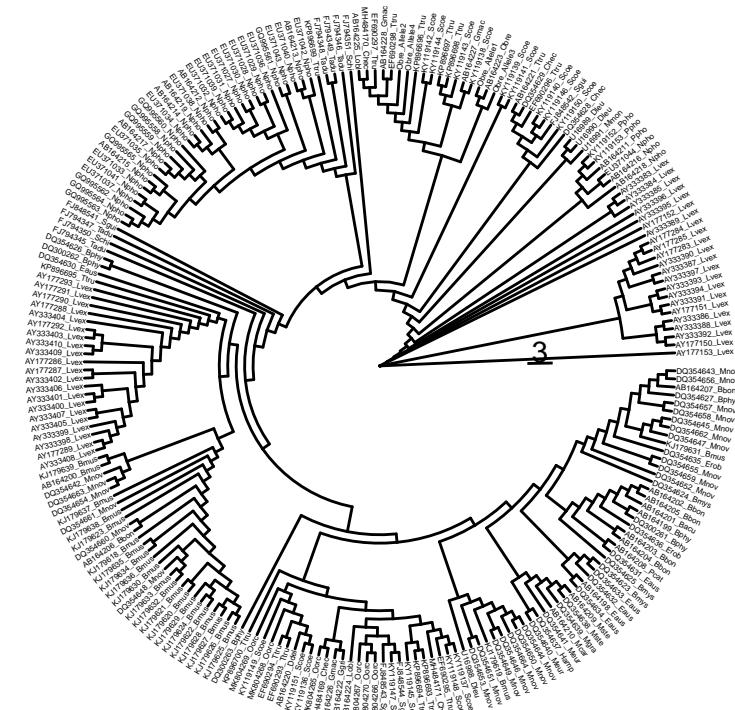
Neighbor–joining tree – Comparing DQB Alleles of Irrawaddy dolphins to DQB Alleles of cetaceans


```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, 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
DQB Alleles of cetaceans


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


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


# Importing ML tree from CIPRES using IQ Tool
tree_5 <- ggtree(tree4, branch.length='none', layout='circular') +
  geom_tiplab(size = 1) +
  ggtitle("Maximum Likelihood tree – Comparing DQB Alleles of Irrawaddy
                  dolphins to DQB Alleles of cetaceans") +
  geom_treescale()

tree_5
```

Maximum Likelihood tree – Comparing DQB Alleles of Irrawaddy dolphins to DQB Alleles of cetaceans