```
In [16]: library("igraph")
         library("ggtree")
         library("phangorn")
         library("treeio")
         library("Biostrings")
```

```
Loading required package: BiocGenerics
Loading required package: parallel

Attaching package: 'BiocGenerics'

The following objects are masked from 'package:parallel':

    clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
    clusterExport, clusterMap, parApply, parCapply, parLapply,
    parLapplyLB, parRapply, parSapply, parSapplyLB

The following objects are masked from 'package:igraph':

    normalize, path, union

The following objects are masked from 'package:stats':

    IQR, mad, sd, var, xtabs

The following objects are masked from 'package:base':

    anyDuplicated, append, as.data.frame, basename, cbind, colnames,
    dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
    grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
    order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
    rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
    union, unique, unsplit, which, which.max, which.min

Loading required package: S4Vectors
Warning message:
"package 'S4Vectors' was built under R version 3.6.2"Loading required package:
stats4

Attaching package: 'S4Vectors'

The following object is masked from 'package:ggtree':

    expand

The following object is masked from 'package:base':

    expand.grid

Loading required package: IRanges
Warning message:
"package 'IRanges' was built under R version 3.6.2"
Attaching package: 'IRanges'

The following object is masked from 'package:ggtree':

    collapse

The following object is masked from 'package:grDevices':

    windows

Loading required package: XVector

Attaching package: 'Biostrings'

The following object is masked from 'package:treeio':

    mask

The following object is masked from 'package:ape':

    complement

The following object is masked from 'package:base':

    strsplit
```
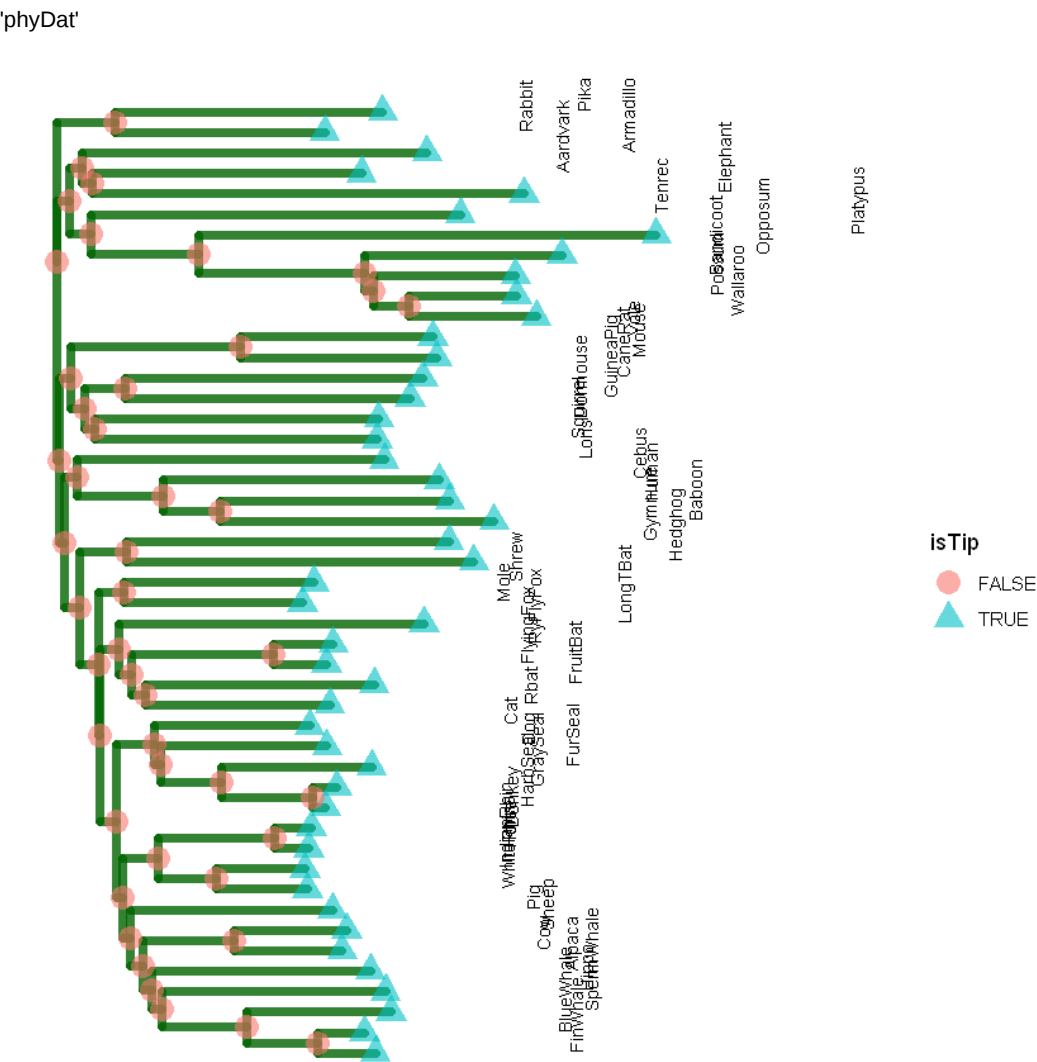
Визуализация дерева: стандартные данные (эксперимент):

```
In [68]: data(Laurasiatherian)
         tree <- nj(dist.ml(Laurasiatherian))
         ggtree(tree, lwd = 2, color = "darkgreen", alpha = 0.8, right = TRUE) +
             geom_tiplab(size = 3, angle = 90, offset = 0.05) +
             geom_point(aes(shape = isTip, color = isTip), size = 5, alpha = 0.6)
```

'phyDat'



Данные скачены по ссылке:

ftp://download.big.ac.cn/Genome/Viruses/Coronaviridae/genome/

```
In [137]: # fasta to DNAbin matrix
          names.list <- c("AB008939.cds.fasta", "AB008940.cds.fasta",
                  "AB086881.cds.fasta", "AB242262.cds.fasta",
                  "AB105373.cds.fasta", "AB086904.cds.fasta")
          n = length(names.list)
          data <- as.matrix(read.fasta(names.list[1]))
          for (i in seq(2,n)) {
              name <- names.list[i]
              data <- cbind(data, as.matrix(read.fasta(name)), fill.with.gaps = TRUE)
          }
          # DNAbin matrix to phyDat
          phy.data <- as.phyDat(data)
```

In [142]:
```
tree <- nj(dist.ml(phy.data))
ggtree(tree, lwd = 2, color = "darkgreen", alpha = 0.8, right = TRUE) +
  geom_tiplab(size = 3, angle = 0, offset = 0.05) +
  geom_point(aes(shape = isTip, color = isTip), size = 5, alpha = 0.6)
```

AB08

AB10

AB00

isTip

FALSE

TRUE

AB08

AB24

AB00