

# Phylogenetic\_H1

Sedreh

9/15/2019

```
library(ape)
library(ggplot2)
library(ggtree)
```

```
#1-reads the file https://www.jasondavies.com/tree-of-life/life.txt to the "tree1" object
tree1 = read.tree(file = "/home/sedreh/Desktop/life.txt", text = NULL, tree.names = NULL, skip = 0,
  comment.char = "", keep.multi = FALSE)
tree1
```

```
##
## Phylogenetic tree with 191 tips and 190 internal nodes.
##
## Tip labels:
## Escherichia_coli_EDL933, Escherichia_coli_0157_H7, Escherichia_coli_06, Escherichia_coli_K12, Shigella_flexneri_2a_2457T, Shigella_flexneri_2a_301, ...
## Node labels:
## , Bacteria, 66, 74, 98, 82, ...
##
## Rooted; includes branch lengths.
```

```
str(tree1)
```

```
## List of 5
## $ edge      : int [1:380, 1:2] 192 193 194 195 196 197 198 199 200 201 ...
## $ edge.length: num [1:380] 1.3496 0.0265 0.0347 0.0555 0.0443 ...
## $ Nnode      : int 190
## $ node.label : chr [1:190] "" "Bacteria" "66" "74" ...
## $ tip.label  : chr [1:191] "Escherichia_coli_EDL933" "Escherichia_coli_0157_H7" "Escherichia_coli_06" "Escherichia_coli_K12" ...
## - attr(*, "class")= chr "phylo"
## - attr(*, "order")= chr "cladewise"
```

```
#2-draws this tree using the standard function from the ape package;
plot(tree1, main="Phylogenetic Tree of life")
```

[illegible]

```
## png
## 2
```

```
## png
## 2
```

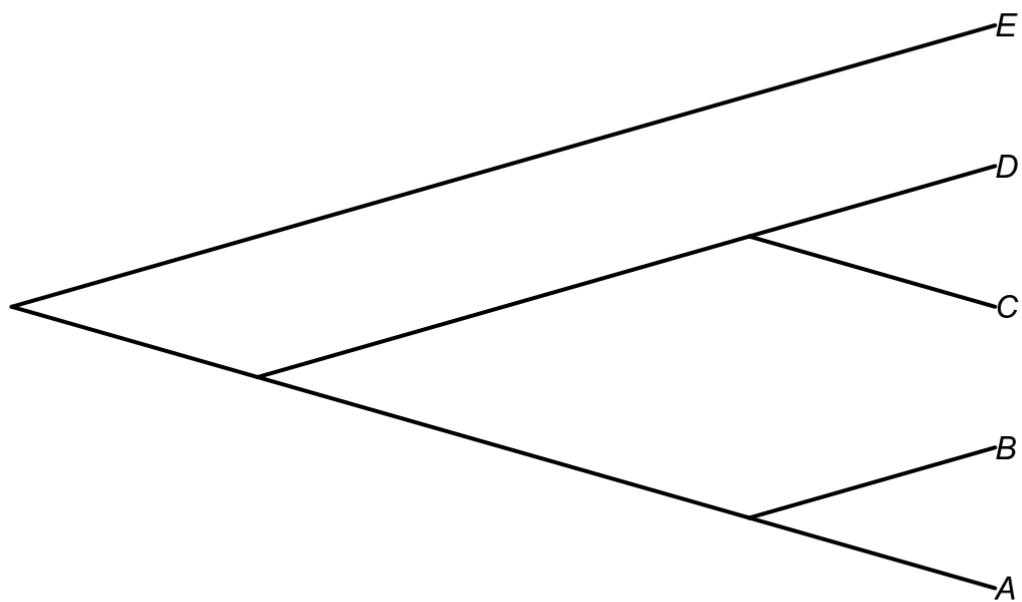
2/11

Phylogenetic tree of the 16S rRNA gene sequences of the bacterial community in the rumen of the yak. The tree is rooted on the left and branches out to the right. The sequences are labeled with their accession numbers. The tree shows a high degree of similarity between the sequences, with many branches having a bootstrap value of 100. The sequences are grouped into several clusters, including a large cluster of sequences from the genus *Mycoplasma*, a cluster of sequences from the genus *Streptococcus*, and a cluster of sequences from the genus *Lactobacillus*. The tree also shows a few sequences from other genera, such as *Clostridium* and *Bacteroides*.

```
##
## Phylogenetic tree with 5 tips and 4 internal nodes.
##
## Tip labels:
## [1] "A" "B" "C" "D" "E"
##
## Rooted; no branch lengths.
```

```
#6-draws this second tree using the standard function from the ape package and saves
in raster (png) and vector formats (svg or pdf);

plot(tree2, type = "cladogram", edge.width = 2)
```



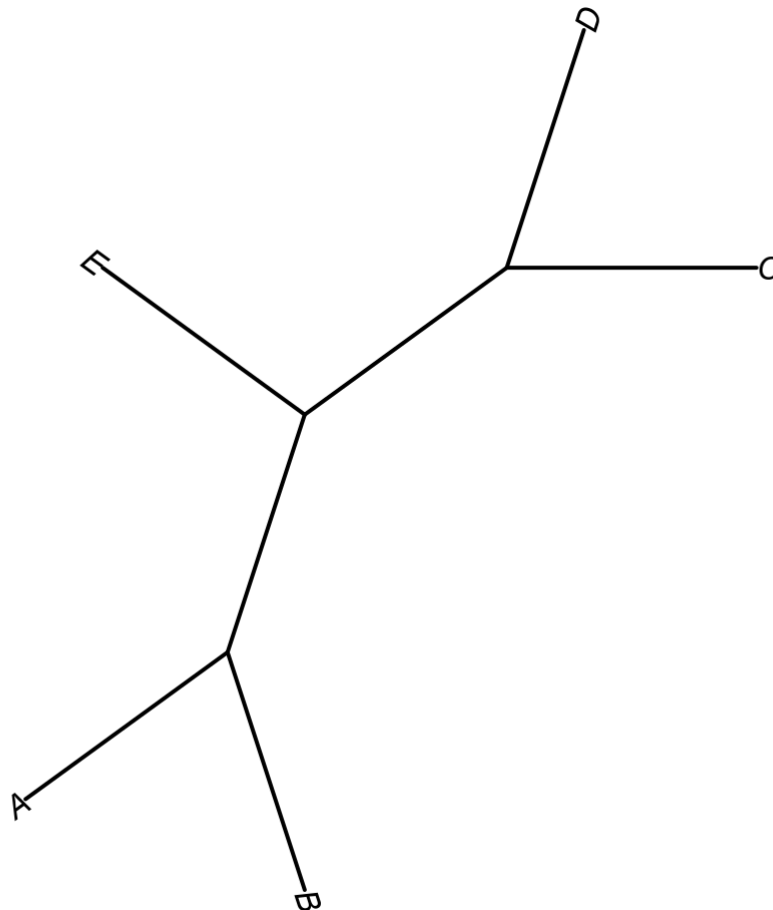
```
#saves tree2 in raster format (png)
png(filename="tree2.png")
plot(tree2)
dev.off()
```

```
## png
## 2
```

```
# save tree2 in vector (svg or pdf) format
svg(filename="tree2.svg")
plot(tree2)
dev.off()
```

```
## png
## 2
```

```
#7-draws "tree2" unrooted or circular ;
plot(unroot(tree2),type="unrooted", no.margin=TRUE,lab4ut="axial",
     edge.width=2)
```



```
#8-draws "tree1" so that the labels can be read (at least reduce the font);  
label <- plot(tree1,           # object with the tree information  
  font = 0.1,           # makes font bold  
  edge.width = 0.5,     # makes thicker lines  
  cex = 0.5,           # increase font size a little  
  main = "Phylogenetic Tree_of_life")
```

Phylogenetic tree showing the relationships between 100 bacterial strains. The tree is rooted on the left and branches out to the right. The strains are labeled with their names and accession numbers. The labels are color-coded: green for Proteobacteria, blue for Bacteroidetes, red for Firmicutes, and purple for Actinobacteria. The tree shows a high degree of genetic diversity, with many strains having unique accession numbers.

label

```
## $type
## [1] "phylogram"
##
## $use.edge.length
## [1] TRUE
##
## $node.pos
## [1] 1
##
## $node.depth
## [1] 1
##
## $show.tip.label
## [1] TRUE
##
## $show.node.label
## [1] FALSE
##
## $font
## [1] 0.1
##
## $cex
## [1] 0.5
##
## $adj
## [1] 0
##
## $srt
## [1] 0
##
## $no.margin
## [1] FALSE
##
## $label.offset
## [1] 0
##
## $x.lim
## [1] 0.000000 3.232527
##
## $y.lim
## [1] 1 191
##
## $direction
## [1] "rightwards"
##
## $tip.color
## [1] "black"
##
## $Ntip
## [1] 191
##
## $Nnode
## [1] 190
##
## $root.time
## NULL
##
```

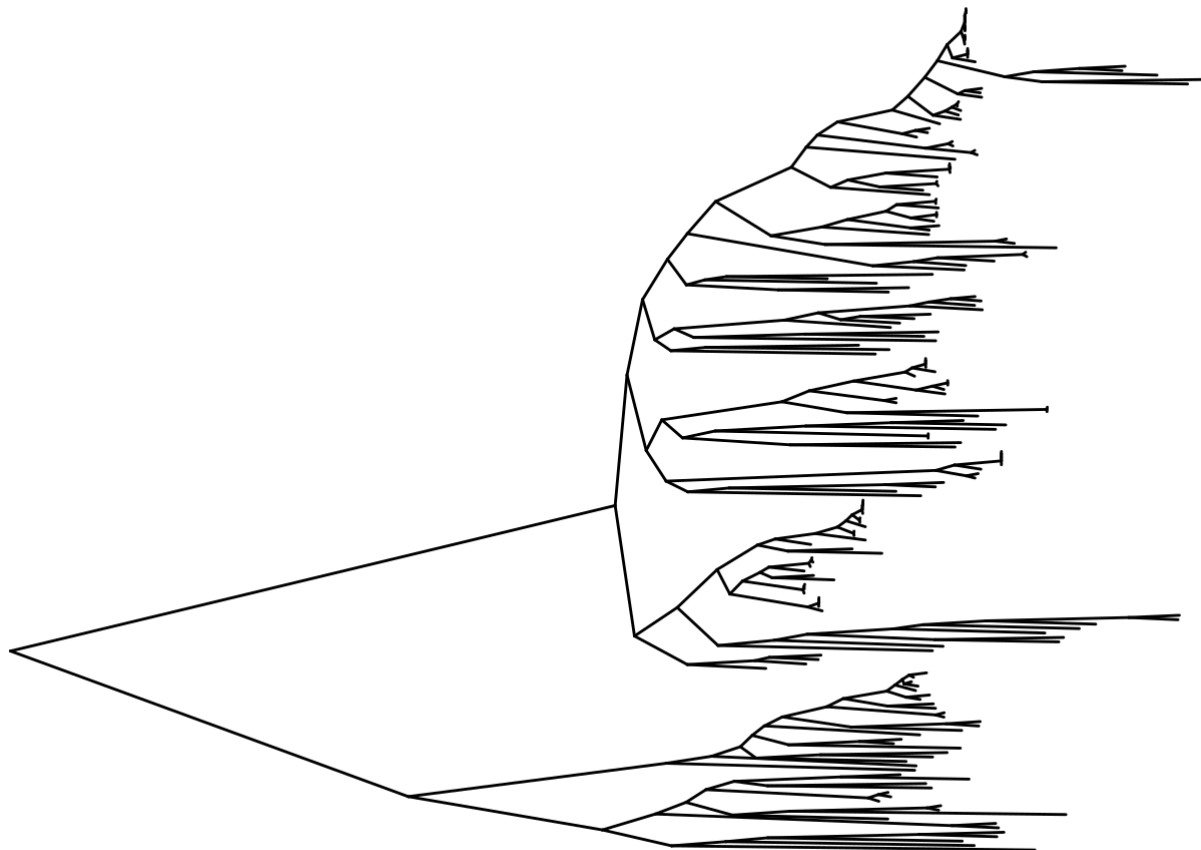
```
## $align.tip.label
## [1] FALSE
```

```
#png(filename="tree_label.png")

png(filename = "tree_label.png", res = 300,
     width = 8000, height = 8000)
plot(tree1)
dev.off()
```

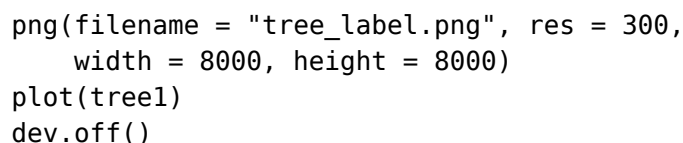
```
## png
## 2
```

```
#9- draws "tree1" with ggtree with minimal settings;
#ggtree(tree1) + geom_treescale()
p <- ggtree(tree1, layout='slanted')
p
```



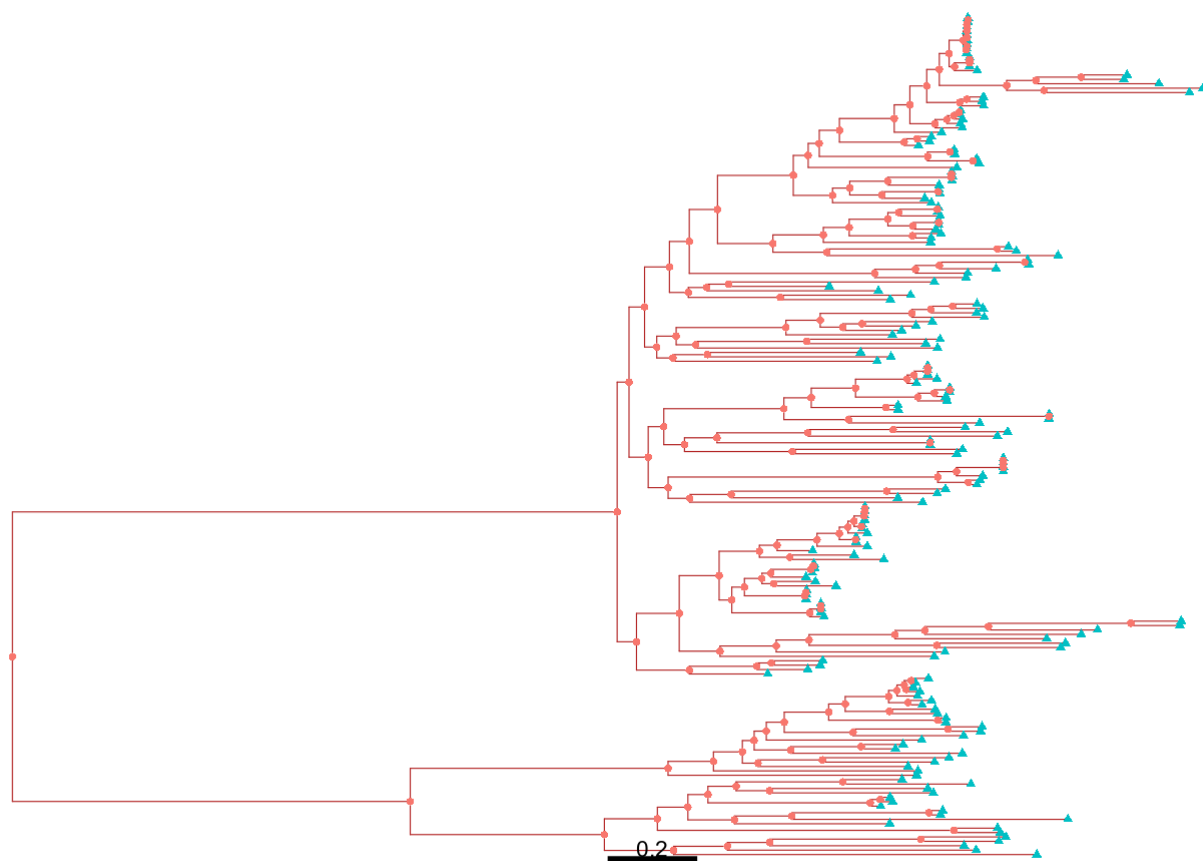
```
#some practice
label <- p+ geom_text2(aes(label = node, subset = !isTip), col = "red", size = 0.5,
                      hjust = -0.3) + geom_tiplab(size=3, color="purple")
label
```





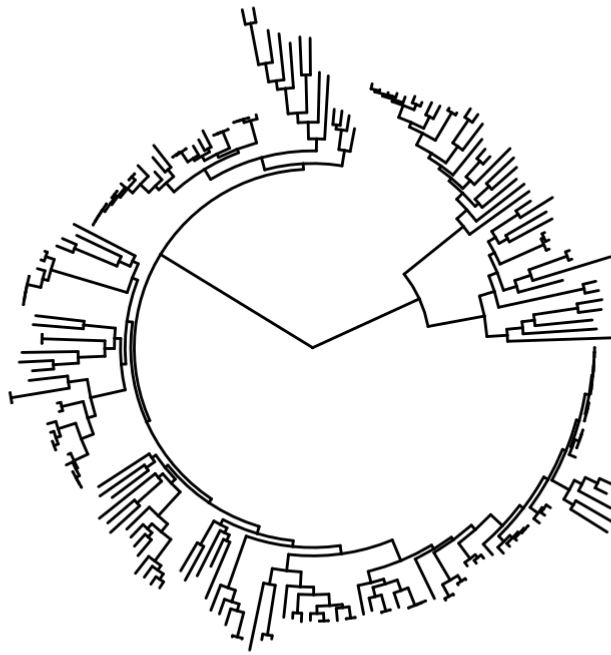
```
## png
## 2
```

9/11



```
# draws the "tree1" unrooted or circular with ggtree  
tree1_circular <- ggtree(tree1, layout="circular") + ggtitle("(Phylogram) circular layout")  
tree1_circular
```

## (Phylogram) circular layout



```
svg(filename = "tree1_circular")  
plot(tree1_circular)  
dev.off()
```

```
## png  
## 2
```