nexus_fie

Sedreh

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```r
library(seqinr)
library(ape)
```

```
##
## Attaching package: 'ape'

## The following objects are masked from 'package:seqinr':
##
##     as.alignment, consensus
```

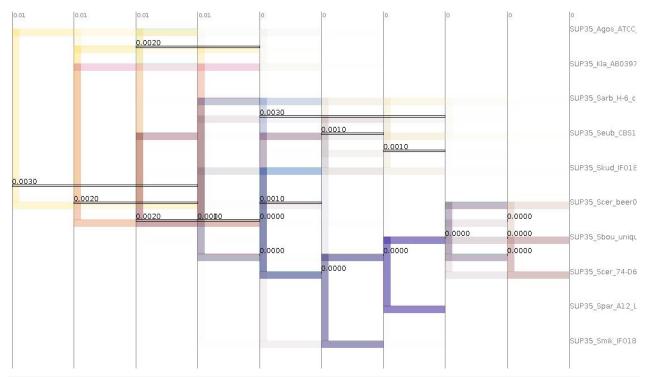We will save Raxml results as nexus trees because DensiTree supports nexus format.

A new list for final result was created. This list will contain every single bootstrap tree but rooted for 'SUP35_Kla_AB039749' for cleaner visualistaion.

then trees plotted beautifuly using DensiTree (As Mrinal advised it to me!) Both trees after rooting are almost the same(with partition, without parttion)

```r
tree_raxml <- read.tree('/home/sedreh/ITMO/semester3/Molecular_phylogenetic/homework_5/homework_5/RAXML

# Take each tree from trees, root them and supply as a nexus writable object
rooted_raxml_partitions_trees <- list()

for (i in seq(1,500,by=1)){
root_item <- root.phylo(tree_raxml[[i]], outgroup = c('SUP35_Kla_AB039749'))
rooted_raxml_partitions_trees <- c(rooted_raxml_partitions_trees, list(root_item))
}

name_raxml_500 <- "/home/sedreh/ITMO/semester3/Molecular_phylogenetic/homework_5/homework_5/RAXML/BOOTS

# write.nexus(rooted_raxml_partitions_trees, file = name_raxml_500)
```

Figure labels (right side, top to bottom): SUP35_Agos_ATCC, SUP35_Kla_AB0397, SUP35_Sarb_H-6_c, SUP35_Seub_CBS1, SUP35_Skud_IFO18, SUP35_Scer_beer0, SUP35_Sbou_uniqu, SUP35_Scer_74-D6, SUP35_Spar_A12_L, SUP35_Smik_IFO18

```
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rooted_raxml_partitions_trees <- c(rooted_raxml_partitions_trees, list(root_item))
}

name_raxml <- "/home/sedreh/ITMO/semester3/Molecular_phylogenetic/homework_5/homework_5/RAXML/PARTITION,

# write.nexus(rooted_raxml_partitions_trees, file = name_raxml)
```