

HM_4

Sedreh

10/4/2019

```
library(seqinr)
library(phangorn)
```

```
## Loading required package: ape
```

```
##
```

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

```
## The following objects are masked from 'package:seqinr':
```

```
##
```

```
##      as.alignment, consensus
```

```
myseqs <- read.alignment("/home/sedreh/ITM0/semester3/Molecular_phylogenetic/homework_4/data/SUP35_aln.1
```

```
distance_matrix <- dist.alignment(myseqs, matrix = "identity" )
distance_matrix
```

```
##                                     SUP35_K1a_AB039749
## SUP35_Agos_ATCC_10895_NM_211584          0.49823537
## SUP35_Scer_74-D694_GCA_001578265.1      0.52121398
## SUP35_Sbou_unique28_CM003560            0.52070373
## SUP35_Scer_beer078_CM005938             0.51995991
## SUP35_Spar_A12_Liti                     0.51865774
## SUP35_Smik_IF01815T_30                  0.51247074
## SUP35_Sarb_H-6_chrXIII_CM001575         0.51865774
## SUP35_Skud_IF01802T_36                  0.52246539
## SUP35_Seub_CBS12357_chr_II_IV_DF968535  0.51525863
##                                     SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1      0.52635461
## SUP35_Sbou_unique28_CM003560            0.52583527
## SUP35_Scer_beer078_CM005938             0.52749048
## SUP35_Spar_A12_Liti                     0.52427415
## SUP35_Smik_IF01815T_30                  0.52061334
## SUP35_Sarb_H-6_chrXIII_CM001575         0.53357235
## SUP35_Skud_IF01802T_36                  0.53503423
## SUP35_Seub_CBS12357_chr_II_IV_DF968535  0.53666043
##                                     SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560            0.03119673
## SUP35_Scer_beer078_CM005938             0.05002502
## SUP35_Spar_A12_Liti                     0.25989945
## SUP35_Smik_IF01815T_30                  0.34345855
## SUP35_Sarb_H-6_chrXIII_CM001575         0.37114027
## SUP35_Skud_IF01802T_36                  0.37497951
## SUP35_Seub_CBS12357_chr_II_IV_DF968535  0.39402784
##                                     SUP35_Sbou_unique28_CM003560
## SUP35_Agos_ATCC_10895_NM_211584
```

```

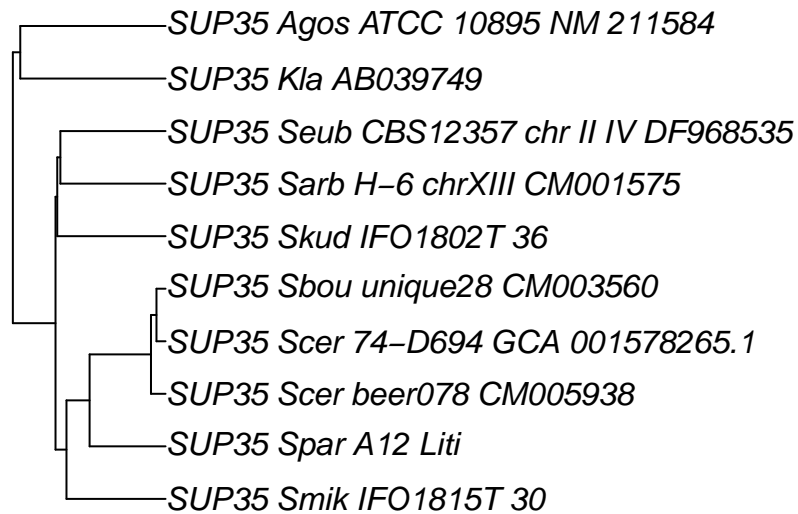
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938 0.05002502
## SUP35_Spar_A12_Liti 0.25989945
## SUP35_Smik_IF01815T_30 0.34345855
## SUP35_Sarb_H-6_chrXIII_CM001575 0.37114027
## SUP35_Skud_IF01802T_36 0.37628835
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.39402784
## SUP35_Scer_beer078_CM005938
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938
## SUP35_Spar_A12_Liti 0.26168560
## SUP35_Smik_IF01815T_30 0.34252190
## SUP35_Sarb_H-6_chrXIII_CM001575 0.37171828
## SUP35_Skud_IF01802T_36 0.37296065
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.39188650
## SUP35_Spar_A12_Liti
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938
## SUP35_Spar_A12_Liti
## SUP35_Smik_IF01815T_30 0.32964182
## SUP35_Sarb_H-6_chrXIII_CM001575 0.35837323
## SUP35_Skud_IF01802T_36 0.37234805
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.38447036
## SUP35_Smik_IF01815T_30
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938
## SUP35_Spar_A12_Liti
## SUP35_Smik_IF01815T_30
## SUP35_Sarb_H-6_chrXIII_CM001575 0.36245351
## SUP35_Skud_IF01802T_36 0.37954068
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.38575837
## SUP35_Sarb_H-6_chrXIII_CM001575
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938
## SUP35_Spar_A12_Liti
## SUP35_Smik_IF01815T_30
## SUP35_Sarb_H-6_chrXIII_CM001575
## SUP35_Skud_IF01802T_36 0.37129923
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.36076862
## SUP35_Skud_IF01802T_36
## SUP35_Agos_ATCC_10895_NM_211584
## SUP35_Scer_74-D694_GCA_001578265.1
## SUP35_Sbou_unique28_CM003560
## SUP35_Scer_beer078_CM005938
## SUP35_Spar_A12_Liti

```

```
## SUP35_Smik_IFO1815T_30
## SUP35_Sarb_H-6_chrXIII_CM001575
## SUP35_Skud_IFO1802T_36
## SUP35_Seub_CBS12357_chr_II_IV_DF968535 0.37150631

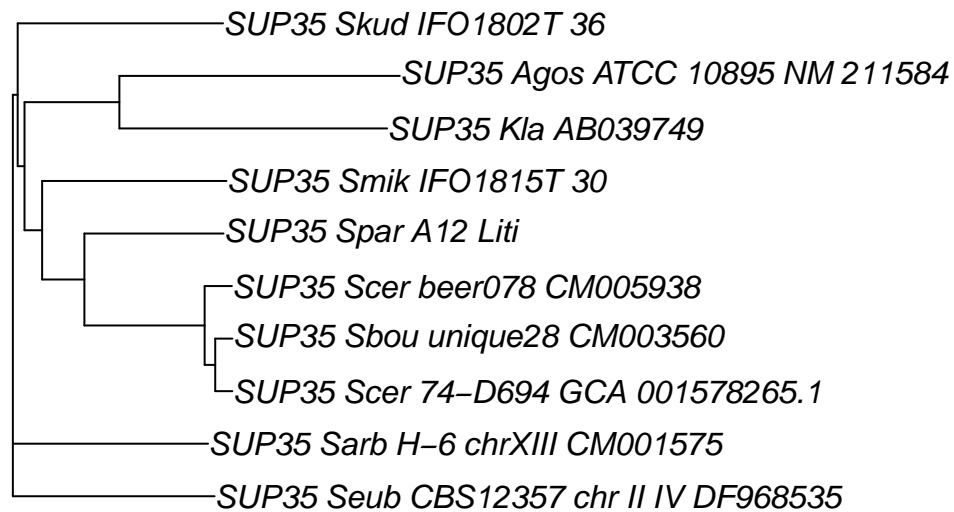
SUP35_aln_UPGMA <- upgma(distance_matrix)
SUP35_aln_NJ <- NJ(distance_matrix)
plot(SUP35_aln_UPGMA, main="UPGMA")
```

UPGMA



```
plot(SUP35_aln_NJ, main="NJ")
```

NJ



I used jmodeltest and Found Best-fit model TIM3+F+I+G4.

```
#fasta to Phylip conversion code
```

```
fastaobject<-seqinr::read.fasta("/home/sedreh/ITMO/semester3/Molecular_phylogenetic/homework_4/data/SUP  
ape::write.dna(fastaobject, "phyfile.phy", nbc=1,colsep=" ", colw=1000000)
```