

Phylogenetic Analysis

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Topics to be addressed - Survey Result



Phylogenetic Inference Methods

Neighbour-joining

Maximum likelihood

Maximum parsimony

Bayesian inference

R packages:

Phybase, Ape, **Phangorn** (<https://cran.r-project.org/web/packages/phangorn/index.html>)

```
install.packages("ape")
install.packages("phangorn")
library(phangorn)
setwd("your/target/work/directory/")
mycop16S = read.phyDat("mycop16S.phy", format = "phylip", type = "DNA")
dm = dist.ml(mycop16S, model="F81")
tree = NJ(dm)
plot(tree)
fitNJ = pml(tree, mycop16S, model="F81", k=4, inv=.15) # replace .15 on inv parameter by the average (%) of invariable sites (identical residues) that is present in your alignment
fit = optim.pml(fitNJ, rearrangement = "stochastic", optInv=TRUE, optGamma=TRUE) # "NNI" (nearest neighbor interchange) rearrangement is faster than "stochastic", but the latter gives better trees
bs = bootstrap.pml(fit, bs=1000, optNni=TRUE, multicore = TRUE, mc.cores=4)
plotBS(fit$tree, bs, type = "phylo", bs.col = "red", bs.adj = 1.2, p = 25)
add.scale.bar(cex = 0.7, font = 2, ask = TRUE)

### To export your phylogram with bootstraps in a format which is viewable by other programs (e.g. figtree):
# Assign a variable to the plotBS function
tempBS = plotBS(fit$tree, bs, type = "phylo", bs.col = "red", bs.adj = 1.2, p = 25)
write.tree(tempBS, file = "mycop16S-phangorn.tree")
```

Other tools/packages (non-R):

MEGA, BayesPhylogenies, PAML, PhyML, Phyx, **Phylip** (<http://evolution.gs.washington.edu/phylip/phylip.html>)

On the attempt of reproducing the same R code above with Phylip, one would need to run the following executables:

\$ seqboot # Setting 1000 replicates

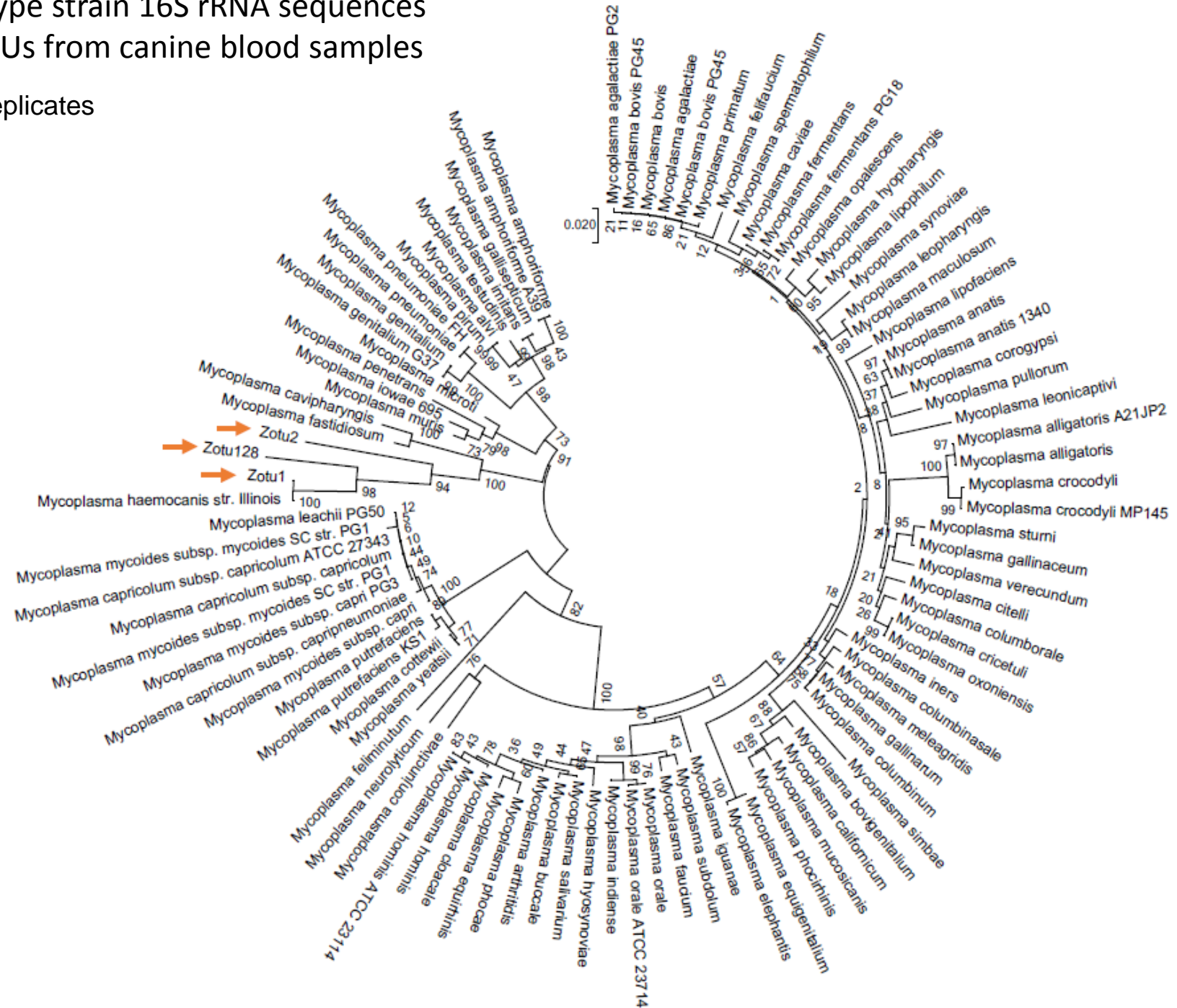
\$ dnadist

\$ neighbor

\$ consense

NJ tree of Mycoplasmatacea type strain 16S rRNA sequences (SILVA-NR99 db) plus novel OTUs from canine blood samples

-> 1000 bootstrapped alignment replicates



Bring your issues on!