Traits and trees

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Analyzing trees and traits

In this example we are going to explore whether domesticated ungulates are closer to each other in trait values than they are in evolutionary relatedness. Only some ungulates have ever been domesticated, and there are indications that the succesful ones have been domesticated multiple times (cows, pigs), whereas others have been failures. Apparently there are combinations of trait values among ungulates that determine whether domestication can ever succeed, and only some of them have the right combination (Jared Diamond's Anna Karenina argument). Thus, average pairwise distance among domesticated ungulates clustered by Gower distance should be shorter than everage pairwise evolutionary distance.

To assess this, we are going to build on the occurrences/trees tutorial. First, we need a tree for the Ungulates.

```r
library(taxize)
library(DBI)
```

```
## Warning: package 'DBI' was built under R version 3.4.4
```

```r
library(ape)
source('../R/expand_taxon.R')

# 'ungulates' is a common name, not an accepted higher taxon.
# So what accepted taxa fall under this name?
ungulates <- unique(comm2sci("Ungulates",db="itis")$Ungulates)

# locations of data files
db_file <- '../data/sql/tgd.db'
msw3_file <- '../data/taxa/msw3-all.csv'
supertree_file <- '../data/phylogeny/Bininda-emonds_2007_mammals.tsv'

# we need the tree_id of the msw3_file
db <- dbConnect(RSQLite::SQLite(), db_file)
query <- 'select tree_id from trees where tree_name="%s"'
tree_id <- dbGetQuery(db, sprintf(query, msw3_file))$tree_id

# iterate over the top level 'ungulates' and expand them to species
names <- list()
for ( name in ungulates ) {

    # the actual call to the file we sourced above
    expanded <- expand.taxon(
        db_file     = db_file,
        taxon_name  = toupper(name),
        db          = db,
        tree_id     = tree_id,
        taxon_level = 'SPECIES'
    )

    # post process to get a flat list
```

```
    nnames <- length(expanded)
    expanded_names <- vector(mode="list", length=nnames)
    for ( i in 1:nnames ) {
        expanded_names[[i]] <- expanded[[i]]$taxon_name
    }
    names <- c(names,expanded_names)
}

# now switch to the mammal supertree and extract its subtree
source('../R/make_phylo.R')
tree_id <- dbGetQuery(db, sprintf(query, supertree_file))$tree_id
tree <- make.phylo(db_file, tree_id, names)
plot(tree, show.tip.label=F)
axisPhylo(side = 1)
```