Gut microbiome of termites — Mikaelyan et al. 2015

Point 5

The goal is to compute Shannon's diversity index for the gut community associated with each species. First, we connect to the database:

```
library(RSQLite)
```

```
## Loading required package: DBI
```

```
sqlite <- dbDriver("SQLite")
con <- dbConnect(sqlite, "../data/Mikaelyan2015.db")
```

Make sure that we can see the tables:

```
print(dbListTables(con))
```

```
## [1] "tNumber" "tOTU"    "tSpp"
```

Now we run a query to extract the name of the species and the corresponding ID:

```
res <- dbSendQuery(con, "SELECT * FROM tSpp;")
# store the results
tSpp <- dbFetch(res, n = -1)
# print the table
head(tSpp)
```

```
##   IDSpp                   Spp
## 1     1 Amitermes_meridionalis
## 2     2    Apicotermes_trestus
## 3     3       Atlantitermes_sp
## 4     4         Cornitermes_sp
## 5     5          Cubitermes_sp
## 6     6  Cubitermes_ugandensis
```

Now we create a dataframe, and for each species, we calculate the Shannon's index of diversity using the package `vegan`:

```
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.0-10
```

```
div_termites <- data.frame()
for (i in 1:dim(tSpp)[1]){
  SpName <- tSpp[i,]$Spp
  SpID <- tSpp[i,]$IDSpp
  # Select all the Num > 0 for that Species ID from table tNumber
  res <-  dbSendQuery(con,
                      paste("SELECT Num FROM tNumber WHERE Num>0 AND IDSpp=", SpID, ";"))
  my_freq <- dbFetch(res, n = -1)
  # add to the database
  div_termites <- rbind(div_termites,
                        data.frame(Species = SpName,
                                   Diversity = diversity(my_freq, index = "shannon")))
}
# print the results
div_termites
```

```
##                          Species Diversity
## 1         Amitermes_meridionalis  4.065947
## 2            Apicotermes_trestus  5.499537
## 3               Atlantitermes_sp  6.925475
## 4                 Cornitermes_sp  6.661177
## 5                  Cubitermes_sp  7.708297
## 6           Cubitermes_ugandensis  5.051364
## 7                 Macrotermes_sp  4.543402
## 8        Macrotermes_subhyalinus  3.463195
## 9         Microcerotermes_parvus  5.335292
## 10            Microcerotermes_sp  4.240155
## 11         Nasutitermes_corniger  3.475954
## 12    Nasutitermes_takasagoensis  3.763673
## 13 Nasutitermitinae_Unclassified  7.265237
## 14                Neocapritermes  7.641412
## 15               Odontotermes_sp  4.882004
## 16                Ophiotermes_sp  4.724733
## 17                Proboscitermes  7.199716
## 18                 Termes_hospes  7.206910
## 19             Trinervitermes_sp  3.907873
```

Close the connection to the database:

```
# clean results
dbClearResult(con)
```

```
## [1] TRUE
```

```
dbDisconnect(con)
```

```
## [1] TRUE
```