Wares Lab - University of Georgia

Metazoan Diversity

2005-2015

```r
# download packages rncl and rotl
#library(devtools)
#install_github("fmichonneau/rncl") # R interface to the Nexus Class Library
#install_github("fmichonneau/rotl") # Interface to Open Tree of Life API

# load libraries
library(rncl)
library(rotl)

# make string of metazoan taxa lab has worked on - microbes, fungi, plants, parasites excluded
# biogeography and multi-taxon studies have representative taxa

lab10orders <- c("Thoracica","Decapoda","Isopoda","Cladocera","Neogastropoda","Unionoidea",
                 "Mytiloidea","Ostreoidea","Galliformes","Rodentia","Clupeiformes","Cypriniformes",
                 "Perciformes","Forcipulatida","Scleractinia")

# match names of string with OTOL names
resolved_names <- tnrs_match_names(lab10orders)

# make tree
response <- tol_induced_subtree(ott_ids=as.numeric(resolved_names$ott_id), parser="phytools")
#nb if rgl package not installed correctly will not work, update X11 to XQuartz all good!

# simplify tip labels
v=strsplit(response$tip.label,split="_",fixed=TRUE)
for(i in 1:length(response$tip.label)){
  response$tip.label[i]<-v[[i]][1]
}

# plot tree

plot(response)
```
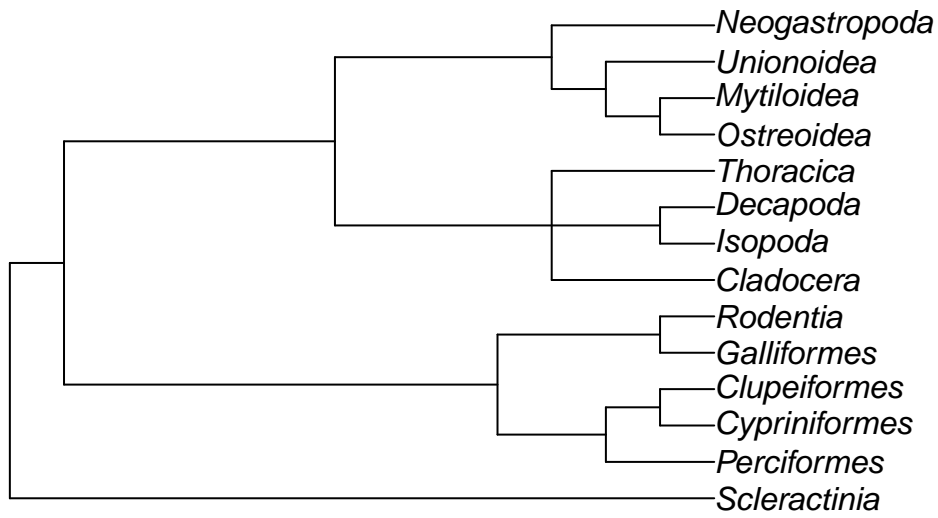
Neogastropoda
Unionoidea
Mytiloidea
Ostreoidea
Thoracica
Decapoda
Isopoda
Cladocera
Rodentia
Galliformes
Clupeiformes
Cypriniformes
Perciformes
Scleractinia

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