DateLife Examples

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```
frin_ds <- datelife_search(input = "Fringilidae", get_spp_from_taxon = TRUE)</pre>
frin_dq <- make_datelife_query(input = "Pan", get_spp_from_taxon = TRUE)</pre>
frin_dr <- get_datelife_result(input = frin_dq)</pre>
datelife_result <- frin_dr
frin_phyloall <- summarize_datelife_result(datelife_query = frin_dq, datelife_result = frin_ds, summary</pre>
plot(frin_ds)
cet_ds <- datelife_search(input = "Cetacea", get_spp_from_taxon = TRUE)</pre>
cet_dq <- make_datelife_query(input = "Cetacea", get_spp_from_taxon = TRUE)</pre>
cet_dr <- get_datelife_result(input = cet_dq)</pre>
cet_phyloall <- summarize_datelife_result(datelife_result = cet_dr, summary_format = "phylo_all")</pre>
sapply(cet_phyloall, ape::is.binary)
plot_phylo_all(cet_phyloall)
cet_syntree <- get_otol_synthetic_tree(input = cet_dq)</pre>
ape::is.binary(cet_syntree)
ape::Ntip(cet_syntree)
names(cet_syntree)
head(cet_syntree$tip.label)
plot(cet_syntree)
# tree_from_taxonomy not working sometimes
# getting Error in open.connection(con, "rb") : HTTP error 503.
cet_taxtree <- tree_from_taxonomy(taxa = cet_dq$cleaned_names, sources = "NCBI")</pre>
cet_boldtree <- make_bold_otol_tree(input = cet_syntree)</pre>
# there are no sequences to construct a bold tree for cetacea
cet_allcal <- get_all_calibrations(input = cet_phyloall)</pre>
head(cet_allcal)
cet_cal <- use_all_calibrations(phy = cet_syntree, all_calibrations = cet_allcal)</pre>
cet_cal$phy
# will try using each phylo object to calibrate:
cet_allcallist <- lapply(cet_phyloall, get_all_calibrations)</pre>
length(cet_allcallist)
cet_allcallist[[1]]
cet_chronos <- lapply(cet_allcallist, function(x) use_all_calibrations(phy = cet_syntree, all_calibrati</pre>
names(cet_chronos)
cet chronos[1]
lapply(cet_chronos, "[", "phy") # they are all null
cet_chronos2 <- lapply(seq(cet_allcallist), function(i) use_all_calibrations(phy = cet_phyloall[[i]], a</pre>
sapply(cet_chronos2, "[", "phy") # the bininda emmonds and hedges are NULL
plot(cet_phyloall[[1]])
```