Fall 2022 Course:

Data Science Research in Biology

Get research and writing credits, and *fulfill the culminating experience* for your major!

Goals

Learn to

➔ program in R and Python

➔ make reproducible science

Develop skills in

★ data science

★ creating academic websites

Contact

Are you *interested*?

Send an email to

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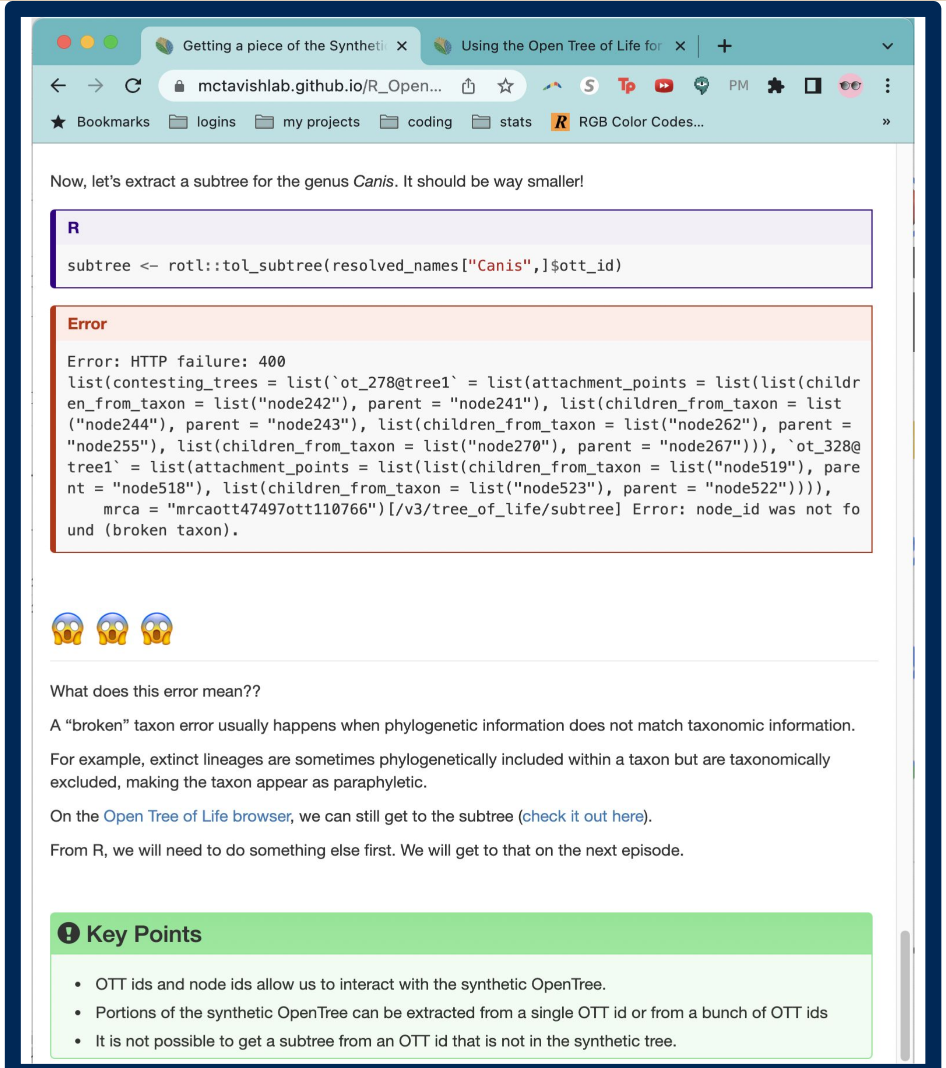
Visit mctavishlab.github.io/data-science-research



Now, let's extract a subtree for the genus *Canis*. It should be way smaller!

R

```
subtree <- rotl::tol_subtree(resolved_names["Canis",]$ott_id)
```

Error

```
Error: HTTP failure: 400
list(contesting_trees = list(`ot_278@tree1` = list(attachment_points = list(list(childr
en_from_taxon = list("node242"), parent = "node241"), list(children_from_taxon = list
("node244"), parent = "node243"), list(children_from_taxon = list("node262"), parent =
"node255"), list(children_from_taxon = list("node270"), parent = "node267"))), `ot_328@
tree1` = list(attachment_points = list(list(children_from_taxon = list("node519"), pare
nt = "node518"), list(children_from_taxon = list("node523"), parent = "node522")))),
    mrca = "mrcaott47497ott110766")[/v3/tree_of_life/subtree] Error: node_id was not fo
und (broken taxon).
```

😱 😱 😱

What does this error mean??

A "broken" taxon error usually happens when phylogenetic information does not match taxonomic information.

For example, extinct lineages are sometimes phylogenetically included within a taxon but are taxonomically excluded, making the taxon appear as paraphyletic.

On the Open Tree of Life browser, we can still get to the subtree (check it out here).

From R, we will need to do something else first. We will get to that on the next episode.

Key Points

- OTT ids and node ids allow us to interact with the synthetic OpenTree.
- Portions of the synthetic OpenTree can be extracted from a single OTT id or from a bunch of OTT ids
- It is not possible to get a subtree from an OTT id that is not in the synthetic tree.