trees-opentree

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2023-04-20

```
install.packages("ape")
```

```
## Installing package into '/home/amercado44/R/x86_64-pc-linux-gnu-library/4.1'
## (as 'lib' is unspecified)
```

```
install.packages("rotl")
```

```
## Installing package into '/home/amercado44/R/x86_64-pc-linux-gnu-library/4.1'
## (as 'lib' is unspecified)
```

Insect - ~1 million named species Mammals - ~5 thousands species Flowering plants - ~200K named species

```
library("ape") # Analysis, Phylogenetics and Evolution R Package
library("rotl") #
```

Read a newick tree from the Open Tree of Life

The following function can only read trees in newick format. Make sure your file is a newick tree. If you got your tree from the Phylesystem repo, your tree is going to be in json format

```
tree <- read.tree(file = "../data-raw/subtree-node-ott247341-Canis-lupus.tre")
```

```
plot(tree, cex = 0.5)
mtext(text = "Canis Lupus OpenTree tree")
```

Canis Lupus OpenTree tree

Canis lupus orion ott7067596

Canis lupus variabilis ott5839539

Canis lupus arctos ott5340002

Canis lupus campestris ott4941916

Canis lupus lupaster ott987895

Canis lupus lycaon ott948004

Canis lupus lupus ott883675

Canis lupus signatus ott545727

Canis lupus labradorius ott531973

Canis lupus dingo ott380529

Canis lupus hodophilax ott318630

Canis lupus mogollonensis ott263524

Canis lupus familiaris ott247333

Canis lupus desertorum ott234374

Canis lupus hattai ott83897

Canis lupus laniger ott80830

Canis lupus baileyi ott67371

Canis lupus chanco ott47500

Canis lupus pallipes ott47497