

Tree from Open Tree

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Stats

Insect- 1 million named species Mammals - 5k named species Flowering plants - 200k named species

Read a newick tree from 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 and will not be ready

```
tree <- read.tree(file = "../Data-raw/BunnyTData.tre")
```

Now plot the tree

```
plot(tree, cex= 0.5)
```

```
## Warning in plot.phylo(tree, cex = 0.5): 1 branch length(s) NA(s): branch  
## lengths ignored in the plot
```

```
mtext(text = "Oryctolagus cuniculus OpenTree 2017")
```

Oryctolagus cuniculus OpenTree 2017

