

Final Project

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```
require(phytools)
```

```
Loading required package: phytools
```

```
Loading required package: ape
```

```
Loading required package: maps
```

```
packageVersion("phytools")
```

```
[1] '2.3.0'
```

```
library(ggtree)
```

```
ggtree v3.14.0 Learn more at https://yulab-smu.top/contribution-tree-data/
```

```
Please cite:
```

```
Guangchuang Yu. Using ggtree to visualize data on tree-like structures.  
Current Protocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
```

```
Attaching package: 'ggtree'
```

```
The following object is masked from 'package:ape':
```

```
rotate
```

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    3.5.1      v tibble     3.2.1
v lubridate  1.9.3      v tidyr      1.3.1
v purrr      1.0.2
```

```
-- Conflicts ----- tidyverse_conflicts() --
x tidyr::expand() masks ggtree::expand()
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
x purrr::map()     masks maps::map()
x dplyr::where()   masks ape::where()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(ape)
```

Making the Tree

```
tr<-ladderize(read.nexus("Vert.tree.nex"))
tr$tip.label
```

[1] "Ciona"	"Eptatretus"	"Scleropages"	"Ictalurus"
[5] "Danio"	"Salmo"	"Takifugu"	"Poecilia"
[9] "Labrus"	"Amphiprion"	"Callorhinchus"	"Latimeria"
[13] "Pogona"	"Anolis"	"Chelonoidis"	"Crocodylus"
[17] "Struthio"	"Gallus"	"Vombatus"	"Loxodonta"
[21] "Dasypus"	"Balaenoptera"	"Vicugna"	"Rhinolophus"
[25] "Zalophus"	"Ailuropoda"	"Lynx"	"Otolemur"
[29] "Gorilla"	"Pan"	"Homo"	"Spermophilus"

```
tree<-root(tr, outgroup="Eptatretus")
tree<-tr

ggtree(tree)+
  geom_tiplab()
```

