BI-PHYLO-Balan

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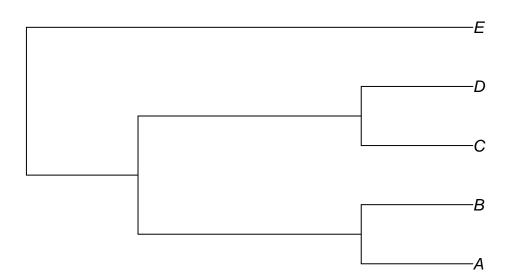
2023-02-05

1. Reads a tree in Newick format (((A,B),(C,D)),E); into object called simpletree

```
simpletree <- read.tree(text = "(((A,B), (C,D)), E);") #newick</pre>
```

2. draws a simpletree using a standard function from the ape package;

plot.phylo(simpletree)



3. saves this tree in raster (png) and vector (svg or pdf) format (one of these pictures must be inserted into the report);

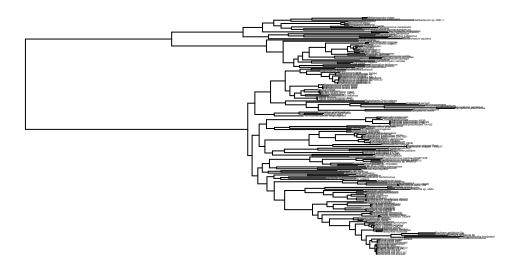
```
png("simpletree.png")
svg("simpletree.svg", width = 4, height = 4)
```

4. reads the file https://www.jasondavies.com/tree-of-life/life.txt into an object treeoflife (possible by saving to a file, but better directly in R);

```
treeoflife <- read.tree("https://www.jasondavies.com/tree-of-life/life.txt")</pre>
```

5. draws tree oflife using a standard function from the ape package and save this tree in your favorite format

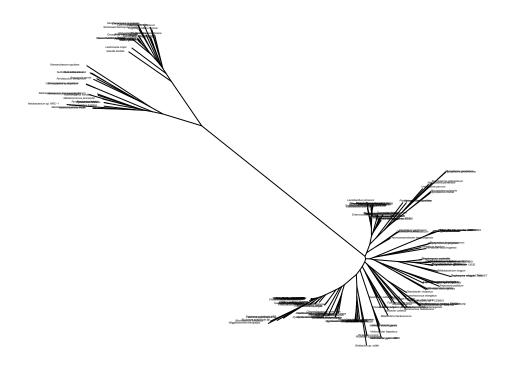
```
plot.phylo(treeoflife, cex = 0.2)
```



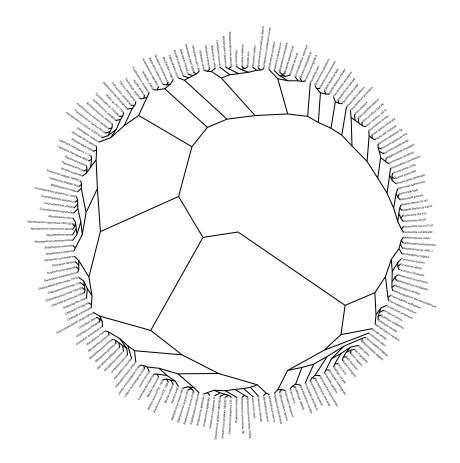
```
png(filename = "treeOfLife.png", width = 20, height = 20, units = "cm", res = 600)
```

6. draws treeoflife unrooted or circular (these are two different lines of code)

```
plot.phylo(treeoflife, type = "unrooted", no.margin = T, cex = 0.2)
```



plot.phylo(treeoflife, type = "radial", cex = 0.2)



7. draws treeoflife using ggtree with minimal settings;

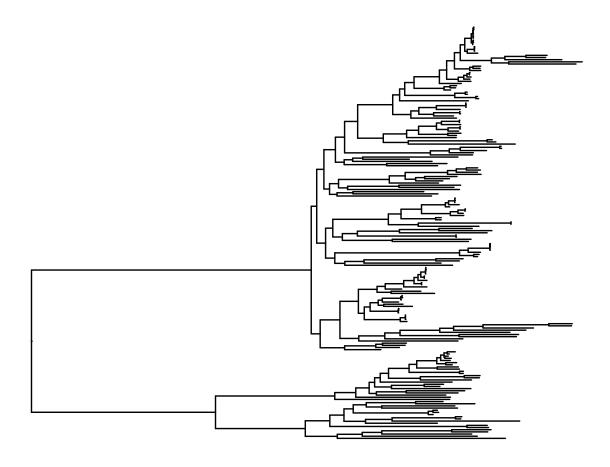
library(ggtree)

```
## ggtree v3.7.1.002 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.
## ggtree: an R package for visualization and annotation of phylogenetic
## trees with their covariates and other associated data. Methods in
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628
##
## LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR
## Jones, T Bradley, H Zhu, Y Guan, Y Jiang, G Yu. treeio: an R package
## for phylogenetic tree input and output with richly annotated and
## associated data. Molecular Biology and Evolution. 2020, 37(2):599-603.
## doi: 10.1093/molbev/msz240
##
## S Xu, Z Dai, P Guo, X Fu, S Liu, L Zhou, W Tang, T Feng, M Chen, L
## Zhan, T Wu, E Hu, Y Jiang, X Bo, G Yu. ggtreeExtra: Compact
## visualization of richly annotated phylogenetic data. Molecular Biology
## and Evolution. 2021, 38(9):4039-4042. doi: 10.1093/molbev/msab166
```

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

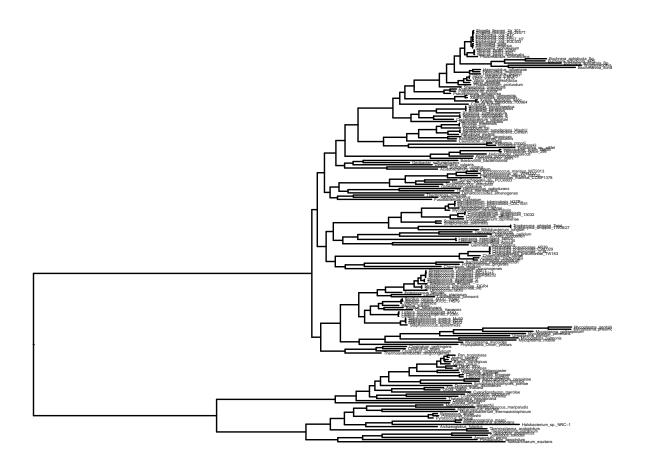
## The following object is masked from 'package:ape':
##
## rotate
```

ggtree(treeoflife)



8. draws treeoflife using ggtree so that the inscriptions are readable (the picture must be inserted into the report);

```
ggtree(treeoflife) + geom_tiplab(size = 1)
```



9. draws treeoflife in a circle with readable inscriptions (picture in the report);

```
ggtree(treeoflife) + layout_circular() + geom_tiplab(size = 2)
```

- ## Scale for y is already present.
- ## Adding another scale for y, which will replace the existing scale.



10. draws treeoflife with an additional selection of some part of your choice (a picture in the report).

```
ggtree(treeoflife) + layout_circular() + geom_tiplab2(size = 2) +
  geom_hilight(node = 198, fill = "gold") + #piece markering
  geom_cladelabel(node = 198, label = "Here", fontsize = 2, offset = 1)
## Scale for y is already present.
## Adding another scale for y, which will replace the existing scale.
## Warning: The following aesthetics were dropped during statistical transformation: node,
## parent
## i This can happen when ggplot fails to infer the correct grouping structure in
     the data.
## i Did you forget to specify a 'group' aesthetic or to convert a numerical
     variable into a factor?
## The following aesthetics were dropped during statistical transformation: node,
## parent
## i This can happen when ggplot fails to infer the correct grouping structure in
## i Did you forget to specify a 'group' aesthetic or to convert a numerical
     variable into a factor?
```

