

portal-phylogenies.Rmd

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2022-10-25

add intro to ape

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

```
library(ape)
portal_tree <- read.tree(file = "../raw_data/portal-tree.tre")
portal_tree
```

```
##
## Phylogenetic tree with 43 tips and 345 internal nodes.
##
## Tip labels:
##   Sigmodon_ochrognathus, Sigmodon_hispidus, Sigmodon_fulviventer, Neotoma_albigula, Onychomys_leucogaster
## Node labels:
##   Amniota, Mammalia, 'Theria (subclass in Deuterostomia)', 'Eutheria (in Deuterostomia)', Boreoeutheria
##
## Rooted; no branch lengths.
```

read tre from url

```
small_tree <- read.tree(file = "http://ape-package.ird.fr/APER/APER2/primfive.tre")
small_tree
```

```
##
## Phylogenetic tree with 5 tips and 4 internal nodes.
##
## Tip labels:
##   Homo, Pongo, Macaca, Ateles, Galago
##
## Rooted; includes branch lengths.
```

the structure of a tree in R

```
class(portal_tree)
```

```
## [1] "phylo"
```

```
length(portal_tree)
```

```
## [1] 4
```

```
colnames(portal_tree)
```

```
## NULL
```

```
names(portal_tree)
```

```
## [1] "edge"      "Nnode"      "node.label" "tip.label"
```

```
portal_tree$Nnode
```

```
## [1] 345
```

```
portal_tree["tip.label"]
```

```
## $tip.label
```

```
## [1] "Sigmodon_ochrognathus"      "Sigmodon_hispidus"
## [3] "Sigmodon_fulviventer"      "Neotoma_albigula"
## [5] "Onychomys_leucogaster"      "Onychomys_torridus"
## [7] "Peromyscus_maniculatus"     "Peromyscus_leucopus"
## [9] "Peromyscus_eremicus"       "Reithrodontomys_fulvescens"
## [11] "Reithrodontomys_montanus"   "Reithrodontomys_megalotis"
## [13] "Baiomys_taylori"           "Chaetodipus_intermedius"
## [15] "Chaetodipus_penicillatus"   "Chaetodipus_baileyi"
## [17] "Chaetodipus_hispidus"       "Perognathus_flavus"
## [19] "Dipodomys_ordii"           "Dipodomys_merriami"
## [21] "Dipodomys_spectabilis"      "Xerospermophilus_spilosoma"
## [23] "Xerospermophilus_tereticaudus" "Ammospermophilus_harrisii"
## [25] "Sylvilagus_audubonii"       "Campylorhynchus_brunneicapillus"
## [27] "Ammodramus_savannarum"      "Kieneria_fusca"
## [29] "Pipilo_chlorurus"           "Pooecetes_gramineus"
## [31] "Zonotrichia_leucophrys"     "Spizella_breweri"
## [33] "Amphispiza_bilineata"       "Calamospiza_melanocorys"
## [35] "Zenaida_macroura"           "Callipepla_squamata"
## [37] "Crotalus_viridis"           "Crotalus_scutulatus"
## [39] "Sceloporus_undulatus"        "Sceloporus_clarkii"
## [41] "Gambelia_sila"              "Aspidoscelis_uniparens"
## [43] "Aspidoscelis_tigris"
```

```
head(portal_tree[[3]])
```

```
## [1] "Amniota"
## [2] "Mammalia"
## [3] "'Theria (subclass in Deuterostomia)'"
## [4] "'Eutheria (in Deuterostomia)'"
## [5] "Boreoeutheria"
## [6] "Euarchontoglires"
```

```
summary(portal_tree)
```

```
##
## Phylogenetic tree: portal_tree
##
##   Number of tips: 43
##   Number of nodes: 345
##   No branch lengths.
##   No root edge.
##   First ten tip labels: Sigmodon_ochrognathus
##                        Sigmodon_hispidus
##                        Sigmodon_fulviventer
##                        Neotoma_albigula
##                        Onychomys_leucogaster
##                        Onychomys_torridus
##                        Peromyscus_maniculatus
##                        Peromyscus_leucopus
##                        Peromyscus_eremicus
##                        Reithrodontomys_fulvescens
##   First ten node labels: Amniota
##                        Mammalia
##                        'Theria (subclass in Deuterostomia)'
##                        'Eutheria (in Deuterostomia)'
##                        Boreoeutheria
##                        Euarchontoglires
##                        mrcaott42ott30082
##                        Glires
##                        mrcaott42ott29157
##                        Rodentia
```

```
str(portal_tree)
```

```
## List of 4
## $ edge      : int [1:387, 1:2] 44 45 46 47 48 49 50 51 52 53 ...
## $ Nnode     : int 345
## $ node.label: chr [1:345] "Amniota" "Mammalia" "'Theria (subclass in Deuterostomia)'" "'Eutheria (in Deuterostomia)'"
## $ tip.label : chr [1:43] "Sigmodon_ochrognathus" "Sigmodon_hispidus" "Sigmodon_fulviventer" "Neotoma_albigula"
## - attr(*, "class")= chr "phylo"
## - attr(*, "order")= chr "cladewise"
```

```
class(portal_tree$edge)
```

```
## [1] "matrix" "array"
```

```
portal_tree$edge
```

```
##      [,1] [,2]
## [1,]  44  45
## [2,]  45  46
## [3,]  46  47
## [4,]  47  48
```

##	[5,]	48	49
##	[6,]	49	50
##	[7,]	50	51
##	[8,]	51	52
##	[9,]	52	53
##	[10,]	53	54
##	[11,]	54	55
##	[12,]	55	56
##	[13,]	56	57
##	[14,]	57	58
##	[15,]	58	59
##	[16,]	59	60
##	[17,]	60	61
##	[18,]	61	62
##	[19,]	62	63
##	[20,]	63	64
##	[21,]	64	65
##	[22,]	65	66
##	[23,]	66	67
##	[24,]	67	68
##	[25,]	68	69
##	[26,]	69	70
##	[27,]	70	71
##	[28,]	71	72
##	[29,]	72	73
##	[30,]	73	1
##	[31,]	72	74
##	[32,]	74	75
##	[33,]	75	2
##	[34,]	71	76
##	[35,]	76	3
##	[36,]	65	77
##	[37,]	77	78
##	[38,]	78	79
##	[39,]	79	80
##	[40,]	80	81
##	[41,]	81	82
##	[42,]	82	83
##	[43,]	83	84
##	[44,]	84	4
##	[45,]	77	85
##	[46,]	85	86
##	[47,]	86	87
##	[48,]	87	88
##	[49,]	88	89
##	[50,]	89	90
##	[51,]	90	91
##	[52,]	91	5
##	[53,]	90	6
##	[54,]	88	92
##	[55,]	92	93
##	[56,]	93	94
##	[57,]	94	95
##	[58,]	95	96

##	[59,]	96	97
##	[60,]	97	98
##	[61,]	98	99
##	[62,]	99	7
##	[63,]	95	100
##	[64,]	100	8
##	[65,]	93	101
##	[66,]	101	102
##	[67,]	102	103
##	[68,]	103	104
##	[69,]	104	105
##	[70,]	105	9
##	[71,]	87	106
##	[72,]	106	107
##	[73,]	107	108
##	[74,]	108	109
##	[75,]	109	10
##	[76,]	108	110
##	[77,]	110	111
##	[78,]	111	11
##	[79,]	110	112
##	[80,]	112	113
##	[81,]	113	114
##	[82,]	114	115
##	[83,]	115	12
##	[84,]	86	116
##	[85,]	116	117
##	[86,]	117	13
##	[87,]	56	118
##	[88,]	118	119
##	[89,]	119	120
##	[90,]	120	121
##	[91,]	121	122
##	[92,]	122	123
##	[93,]	123	124
##	[94,]	124	125
##	[95,]	125	126
##	[96,]	126	127
##	[97,]	127	14
##	[98,]	127	128
##	[99,]	128	129
##	[100,]	129	15
##	[101,]	124	130
##	[102,]	130	16
##	[103,]	123	131
##	[104,]	131	17
##	[105,]	122	132
##	[106,]	132	133
##	[107,]	133	134
##	[108,]	134	135
##	[109,]	135	18
##	[110,]	120	136
##	[111,]	136	137
##	[112,]	137	138

```

## [113,] 138 139
## [114,] 139 140
## [115,] 140 141
## [116,] 141 19
## [117,] 139 142
## [118,] 142 143
## [119,] 143 20
## [120,] 138 144
## [121,] 144 21
## [122,] 54 145
## [123,] 145 146
## [124,] 146 147
## [125,] 147 148
## [126,] 148 149
## [127,] 149 150
## [128,] 150 151
## [129,] 151 152
## [130,] 152 153
## [131,] 153 154
## [132,] 154 155
## [133,] 155 156
## [134,] 156 157
## [135,] 157 158
## [136,] 158 159
## [137,] 159 160
## [138,] 160 161
## [139,] 161 162
## [140,] 162 22
## [141,] 161 163
## [142,] 163 23
## [143,] 154 164
## [144,] 164 165
## [145,] 165 166
## [146,] 166 167
## [147,] 167 24
## [148,] 52 168
## [149,] 168 169
## [150,] 169 170
## [151,] 170 25
## [152,] 44 171
## [153,] 171 172
## [154,] 172 173
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## [158,] 176 177
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## [160,] 178 179
## [161,] 179 180
## [162,] 180 181
## [163,] 181 182
## [164,] 182 183
## [165,] 183 184
## [166,] 184 185

```

##	[167,]	185	186
##	[168,]	186	187
##	[169,]	187	188
##	[170,]	188	189
##	[171,]	189	190
##	[172,]	190	191
##	[173,]	191	192
##	[174,]	192	193
##	[175,]	193	194
##	[176,]	194	195
##	[177,]	195	196
##	[178,]	196	197
##	[179,]	197	198
##	[180,]	198	199
##	[181,]	199	200
##	[182,]	200	201
##	[183,]	201	202
##	[184,]	202	203
##	[185,]	203	204
##	[186,]	204	205
##	[187,]	205	206
##	[188,]	206	207
##	[189,]	207	208
##	[190,]	208	209
##	[191,]	209	210
##	[192,]	210	211
##	[193,]	211	212
##	[194,]	212	213
##	[195,]	213	214
##	[196,]	214	215
##	[197,]	215	216
##	[198,]	216	217
##	[199,]	217	218
##	[200,]	218	219
##	[201,]	219	220
##	[202,]	220	221
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##	[204,]	222	223
##	[205,]	223	224
##	[206,]	224	225
##	[207,]	225	226
##	[208,]	226	227
##	[209,]	227	228
##	[210,]	228	229
##	[211,]	229	230
##	[212,]	230	231
##	[213,]	231	232
##	[214,]	232	26
##	[215,]	222	233
##	[216,]	233	234
##	[217,]	234	235
##	[218,]	235	236
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##	[220,]	237	238

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## [221,] 238 239
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## [266,] 278 32
## [267,] 272 279
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## [270,] 281 33
## [271,] 279 282
## [272,] 282 283
## [273,] 283 34
## [274,] 202 284

```



```

## [275,] 284 285
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## [304,] 178 312
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## [326,] 333 334
## [327,] 334 335
## [328,] 335 336

```

```

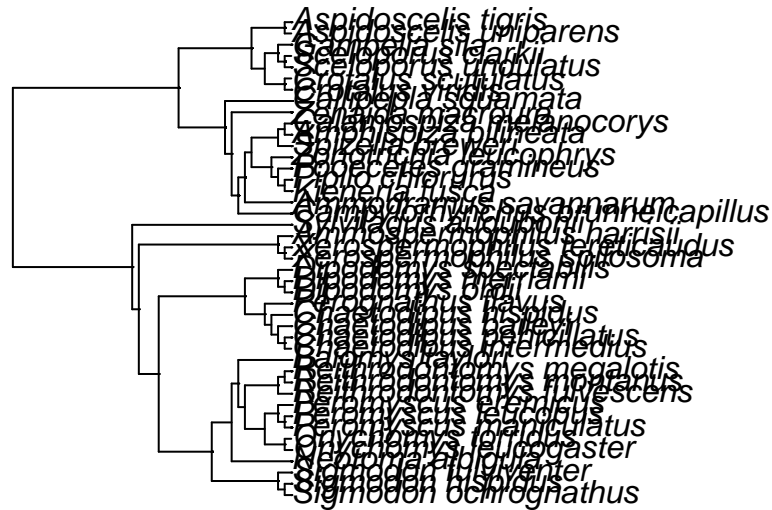
## [329,] 336 337
## [330,] 337 338
## [331,] 338 339
## [332,] 339 340
## [333,] 340 341
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## [335,] 342 343
## [336,] 343 344
## [337,] 344 37
## [338,] 343 38
## [339,] 318 345
## [340,] 345 346
## [341,] 346 347
## [342,] 347 348
## [343,] 348 349
## [344,] 349 350
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## [362,] 367 368
## [363,] 368 369
## [364,] 369 370
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## [369,] 374 39
## [370,] 368 40
## [371,] 351 375
## [372,] 375 376
## [373,] 376 41
## [374,] 317 377
## [375,] 377 378
## [376,] 378 379
## [377,] 379 380
## [378,] 380 381
## [379,] 381 382
## [380,] 382 383
## [381,] 383 384
## [382,] 384 385

```

```
## [383,] 385 386
## [384,] 386 42
## [385,] 386 387
## [386,] 387 388
## [387,] 388 43
```

plotting phylogenetic trees

```
plot.phylo(x = portal_tree)
```



an extension of phylogenetic visualization: ggtree to install packages from bioconductor we need a CRAN package called biocmanager

```
install.packages("BiocManager")
install("ggtree")
```

```
library(BiocManager)
library(ggtree)
```

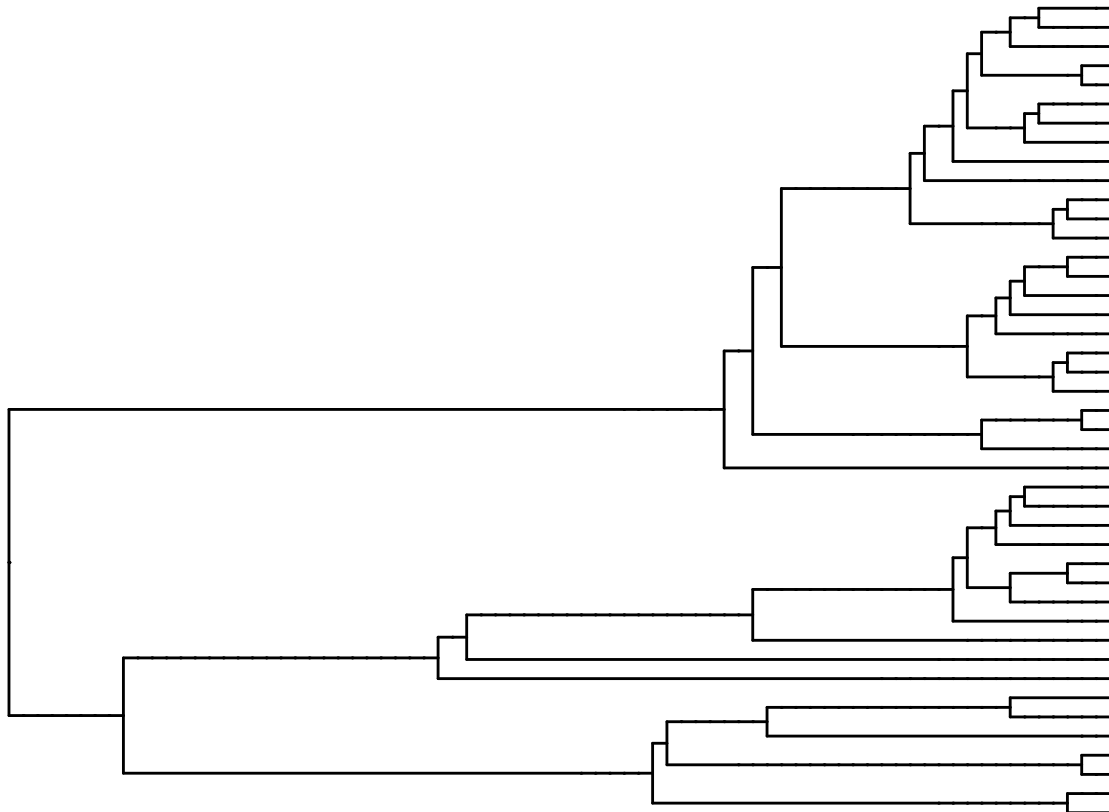
```
## ggtree v3.4.4 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
## the appropriate paper(s):
```

```
##
## 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
##
## 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
##
## Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods
## for mapping and visualizing associated data on phylogeny using ggtree.
## Molecular Biology and Evolution. 2018, 35(12):3041-3043.
## doi:10.1093/molbev/msy194

##
## Attaching package: 'ggtree'

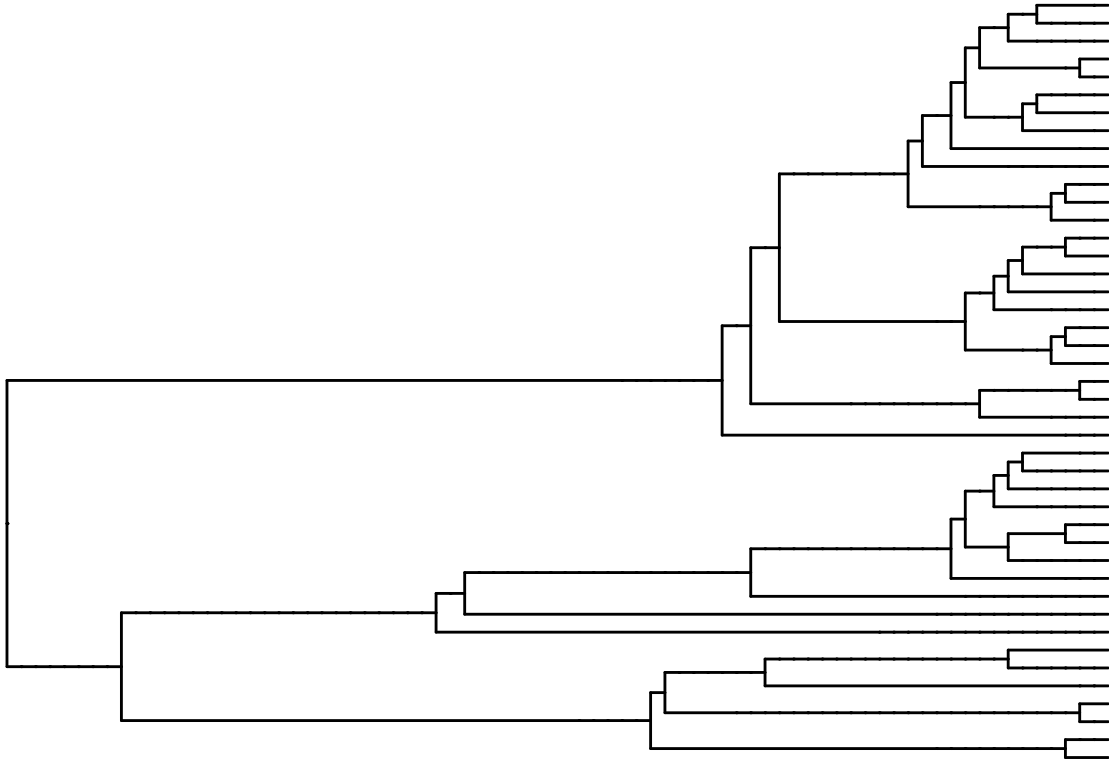
## The following object is masked from 'package:ape':
##
##      rotate
```

```
ggtree(portal_tree)
```



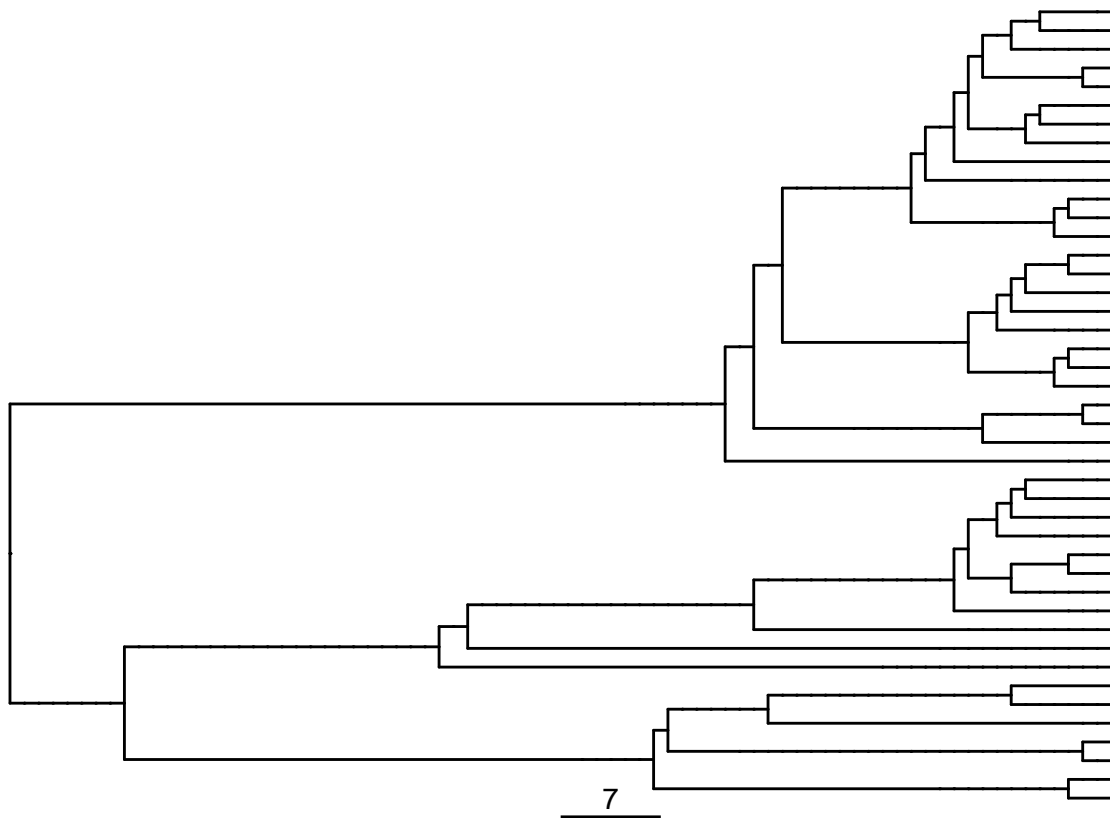
```
# this is equivalent to:
```

```
ggplot(portal_tree, aes(x, y)) +  
  geom_tree() +  
  theme_tree()
```



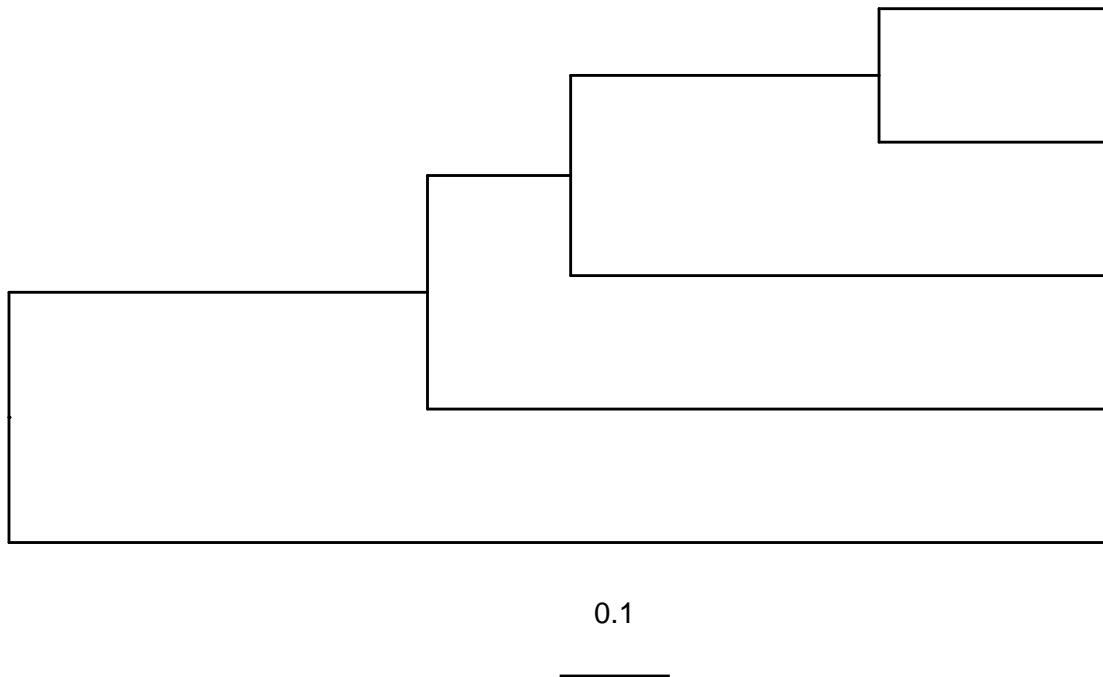
add a scale with the function `geom_treescalc()`

```
ggtree(portal_tree) +  
  geom_treescalc()
```



exercise: plot the small tree of five species of primates and include a scale what is the difference in structure between the two trees?

```
ggtree(small_tree) +  
  geom_treescale()
```



- A difference in number of tips (43 vs 5) - our small_tree does not have node.label as opposed to the portal trees but it does include branch lengths through the edge.length element as shown by the tree above

```
names(small_tree)
```

```
## [1] "edge"          "edge.length" "Nnode"        "tip.label"
```

```
summary(small_tree)
```

```
##
## Phylogenetic tree: small_tree
##
##   Number of tips: 5
##   Number of nodes: 4
##   Branch lengths:
##     mean: 0.415
##     variance: 0.08208571
##     distribution summary:
##   Min. 1st Qu.  Median 3rd Qu.    Max.
## 0.1300 0.2100 0.3300 0.5225 1.0000
## No root edge.
## Tip labels: Homo
##             Pongo
##             Macaca
##             Ateles
##             Galago
```

```
## No node labels.
```

```
str(small_tree)
```

```
## List of 4
## $ edge      : int [1:8, 1:2] 6 7 8 9 9 8 7 6 7 8 ...
## $ edge.length: num [1:8] 0.38 0.13 0.28 0.21 0.21 0.49 0.62 1
## $ Nnode      : int 4
## $ tip.label   : chr [1:5] "Homo" "Pongo" "Macaca" "Ateles" ...
## - attr(*, "class")= chr "phylo"
## - attr(*, "order")= chr "cladewise"
```

```
class(small_tree$edge.length)
```

```
## [1] "numeric"
```

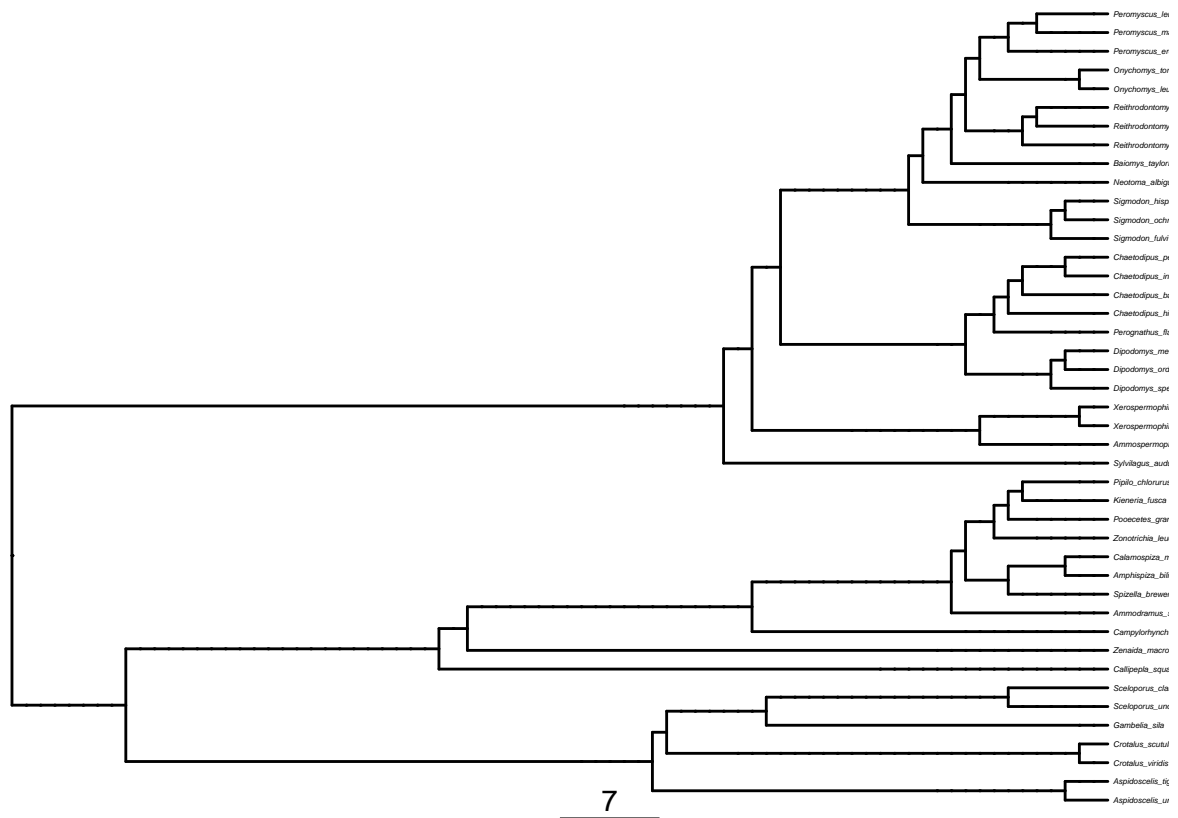
```
small_tree$edge.length
```

```
## [1] 0.38 0.13 0.28 0.21 0.21 0.49 0.62 1.00
```

add tip labels and node labels

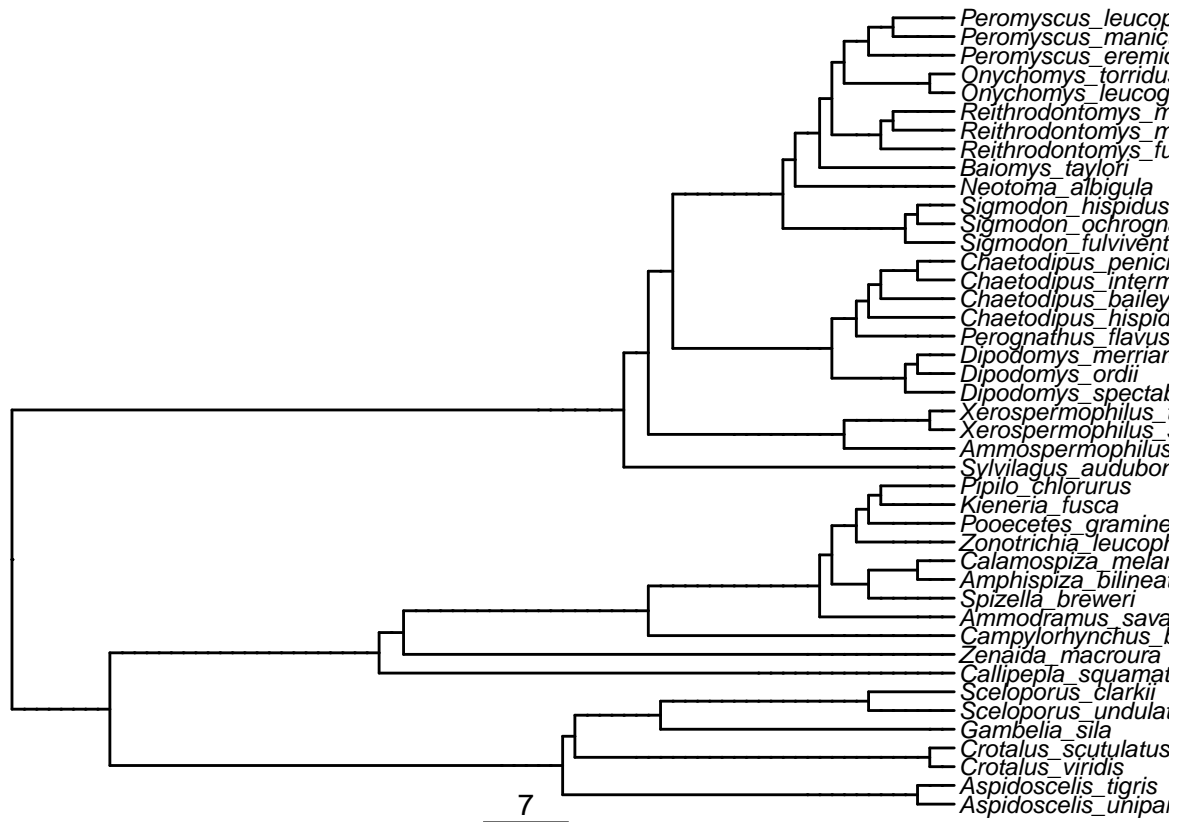
Because a plot is nothing without labels

```
ggtree(portal_tree) +
  geom_treescale() +
  geom_tiplab(size = 1, col = "cyan", fontface = "italic")
```

add a limit to the plot so we can see the labels

```
ggtree(portal_tree) +
  geom_treescale() +
  geom_tiplab(size = 3, col = "springgreen", fontface = "italic") +
  xlim(NA, 90)
```



```
#age of each node
branching.times(small_tree)
```

```
##      6      7      8      9
## 1.00 0.62 0.49 0.21
```

homework: make a plot for small_tree with scale, tip labels, and an appropriate, and an appropriate xlim size to display names fully