

portal phylogenies.Rmd

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Add an intro to the newick format

A newick file is a text file that demonstrates a representation for a phylogenetic tree. This text file allows the easy accessibility and reading of the tree by the computer. An inner node is represented by a pair of paranthesis, a tip is represented by names or character stringgs, a lineage is represented by a comma which also allwos separation of the nodes and tups, and, finally, the semicolon is representative of the end of the tre; therefore, multiple semicolons in a newick file may represent multiple trees. This is useful as image files for the data are not able to be read by a cimputer, so a text file, such as the nwick file, is necessary for the computer to easily read the file

The package ‘ape’

```
library(ape)
```

To read a newick tree from a local file:

```
portal_tree <- read.tree("../data-raw/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 a newick from a 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

```
surveys <- read.csv("../data-raw/surveys.csv")
class(portal_tree)
```

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

```
length(portal_tree)
```

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

```
length(surveys)
```

```
## [1] 9
```

```
colnames(surveys)
```

```
## [1] "record_id"      "month"          "day"            "year"
## [5] "plot_id"        "species_id"     "sex"            "hindfoot_length"
## [9] "weight"
```

```
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"         "Poecetes_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"
```

```
portal_tree[[3]]
```

```
## [1] "Amniota"
## [2] "Mammalia"
## [3] "'Theria (subclass in Deuterostomia)'"
## [4] "'Eutheria (in Deuterostomia)'"
## [5] "Boreoeutheria"
## [6] "Euarchontoglires"
## [7] "mrcaott42ott30082"
## [8] "Glires"
## [9] "mrcaott42ott29157"
## [10] "Rodentia"
## [11] "mrcaott42ott10477"
## [12] "mrcaott42ott38834"
## [13] "mrcaott42ott48903"
## [14] "mrcaott42ott254702"
## [15] "Myomorpha"
## [16] "Muroidea"
## [17] "mrcaott42ott45197"
## [18] "mrcaott42ott55942"
## [19] "mrcaott42ott102"
## [20] "mrcaott102ott739"
## [21] "Cricetidae"
## [22] "mrcaott739ott15637"
## [23] "mrcaott739ott119008"
## [24] "mrcaott739ott38053"
## [25] "mrcaott38053ott39197"
## [26] "Sigmodon"
## [27] "mrcaott39197ott1067882"
## [28] "mrcaott39197ott1067867"
```

[29] "mrcaott39197ott208424"
 ## [30] "mrcaott39197ott208422"
 ## [31] "mrcaott208424ott576098"
 ## [32] "mrcaott208424ott1067878"
 ## [33] "mrcaott1067867ott1067876"
 ## [34] "Neotominae"
 ## [35] "mrcaott15637ott15642"
 ## [36] "Neotoma"
 ## [37] "mrcaott15638ott5266793"
 ## [38] "mrcaott15638ott83673"
 ## [39] "mrcaott83673ott169825"
 ## [40] "mrcaott169825ott690543"
 ## [41] "mrcaott169825ott381420"
 ## [42] "mrcaott18770ott5266794"
 ## [43] "mrcaott18770ott39171"
 ## [44] "mrcaott18770ott39181"
 ## [45] "mrcaott18770ott76407"
 ## [46] "mrcaott18770ott427266"
 ## [47] "Onychomys"
 ## [48] "mrcaott427266ott1004147"
 ## [49] "mrcaott76407ott1024550"
 ## [50] "mrcaott76407ott138845"
 ## [51] "mrcaott76407ott319357"
 ## [52] "mrcaott76407ott373073"
 ## [53] "mrcaott76407ott576106"
 ## [54] "mrcaott76407ott259483"
 ## [55] "mrcaott259483ott1026151"
 ## [56] "mrcaott259483ott259485"
 ## [57] "mrcaott373073ott576104"
 ## [58] "mrcaott138845ott162838"
 ## [59] "mrcaott138845ott162828"
 ## [60] "mrcaott162828ott343211"
 ## [61] "mrcaott343211ott343214"
 ## [62] "mrcaott343214ott576102"
 ## [63] "mrcaott39181ott489149"
 ## [64] "Reithrodontomys"
 ## [65] "mrcaott39181ott208412"
 ## [66] "mrcaott39181ott222510"
 ## [67] "mrcaott208412ott208414"
 ## [68] "mrcaott208412ott208418"
 ## [69] "mrcaott208414ott208416"
 ## [70] "mrcaott208416ott222512"
 ## [71] "mrcaott208416ott770864"
 ## [72] "mrcaott208416ott732037"
 ## [73] "mrcaott39171ott91079"
 ## [74] "Baiomys"
 ## [75] "Castorimorpha"
 ## [76] "mrcaott48903ott80974"
 ## [77] "Heteromyidae"
 ## [78] "mrcaott48903ott190180"
 ## [79] "Perognathinae"
 ## [80] "Chaetodipus"
 ## [81] "mrcaott190180ott320777"
 ## [82] "mrcaott190180ott190184"

[83] "mrcaott190180ott374303"
 ## [84] "mrcaott374303ott764440"
 ## [85] "mrcaott764440ott1004162"
 ## [86] "mrcaott764440ott1004164"
 ## [87] "mrcaott320777ott764435"
 ## [88] "mrcaott427276ott1004150"
 ## [89] "Perognathus"
 ## [90] "mrcaott365546ott890372"
 ## [91] "mrcaott365546ott943065"
 ## [92] "mrcaott943065ott1004160"
 ## [93] "Dipodomyinae"
 ## [94] "Dipodomys"
 ## [95] "mrcaott168145ott241218"
 ## [96] "mrcaott168145ott241216"
 ## [97] "mrcaott168145ott276776"
 ## [98] "mrcaott276776ott844926"
 ## [99] "mrcaott241216ott540773"
 ## [100] "mrcaott540773ott645721"
 ## [101] "mrcaott241218ott748116"
 ## [102] "Sciuromorpha"
 ## [103] "mrcaott10477ott829369"
 ## [104] "Sciuridae"
 ## [105] "mrcaott10477ott43435"
 ## [106] "mrcaott10477ott97818"
 ## [107] "mrcaott10477ott259084"
 ## [108] "mrcaott10477ott152097"
 ## [109] "Marmotini"
 ## [110] "mrcaott10477ott902084"
 ## [111] "mrcaott10477ott359117"
 ## [112] "mrcaott10477ott208064"
 ## [113] "mrcaott10477ott136299"
 ## [114] "mrcaott136299ott141507"
 ## [115] "mrcaott136299ott141525"
 ## [116] "mrcaott141525ott508655"
 ## [117] "mrcaott141525ott580345"
 ## [118] "Xerospermophilus"
 ## [119] "mrcaott141525ott508648"
 ## [120] "mrcaott782266ott833672"
 ## [121] "mrcaott359117ott580339"
 ## [122] "Ammospermophilus"
 ## [123] "mrcaott580339ott632597"
 ## [124] "mrcaott580339ott580350"
 ## [125] "Lagomorpha"
 ## [126] "Leporidae"
 ## [127] "Sylvilagus"
 ## [128] "Sauropsida"
 ## [129] "Sauria"
 ## [130] "mrcaott246ott4128455"
 ## [131] "mrcaott246ott4127082"
 ## [132] "mrcaott246ott4129629"
 ## [133] "mrcaott246ott4142716"
 ## [134] "mrcaott246ott4126667"
 ## [135] "mrcaott246ott1662"
 ## [136] "mrcaott246ott2982"

[137] "mrcaott246ott31216"
 ## [138] "mrcaott246ott4947920"
 ## [139] "mrcaott246ott4127428"
 ## [140] "mrcaott246ott4126230"
 ## [141] "mrcaott246ott4127421"
 ## [142] "mrcaott246ott664349"
 ## [143] "mrcaott246ott4126505"
 ## [144] "mrcaott246ott4127015"
 ## [145] "mrcaott246ott4129653"
 ## [146] "mrcaott246ott4127541"
 ## [147] "mrcaott246ott4946623"
 ## [148] "mrcaott246ott4126482"
 ## [149] "mrcaott246ott4128105"
 ## [150] "mrcaott246ott4127288"
 ## [151] "mrcaott246ott4132146"
 ## [152] "mrcaott246ott3602822"
 ## [153] "mrcaott246ott4143599"
 ## [154] "mrcaott246ott3600976"
 ## [155] "mrcaott246ott4132107"
 ## [156] "Aves"
 ## [157] "Neognathae"
 ## [158] "mrcaott246ott5481"
 ## [159] "mrcaott246ott5021"
 ## [160] "mrcaott246ott7145"
 ## [161] "mrcaott246ott5272"
 ## [162] "mrcaott246ott928360"
 ## [163] "mrcaott246ott1858"
 ## [164] "mrcaott246ott2907"
 ## [165] "mrcaott246ott3600042"
 ## [166] "mrcaott246ott47588"
 ## [167] "mrcaott246ott7113"
 ## [168] "Passeriformes"
 ## [169] "mrcaott246ott3212"
 ## [170] "mrcaott246ott428578"
 ## [171] "mrcaott246ott44866"
 ## [172] "mrcaott246ott5929"
 ## [173] "mrcaott246ott32658"
 ## [174] "mrcaott246ott4820"
 ## [175] "mrcaott246ott22325"
 ## [176] "mrcaott246ott176461"
 ## [177] "mrcaott246ott10351"
 ## [178] "mrcaott246ott1488"
 ## [179] "mrcaott246ott3364"
 ## [180] "mrcaott246ott5934"
 ## [181] "mrcaott246ott1566"
 ## [182] "mrcaott246ott3599436"
 ## [183] "mrcaott246ott25638"
 ## [184] "mrcaott246ott157232"
 ## [185] "mrcaott246ott18313"
 ## [186] "Troglodytinae"
 ## [187] "mrcaott18313ott87938"
 ## [188] "Campylorhynchus"
 ## [189] "mrcaott87938ott800237"
 ## [190] "mrcaott3364ott73828"

[191] "mrcaott3364ott4083"
 ## [192] "mrcaott4083ott35042"
 ## [193] "mrcaott4083ott370807"
 ## [194] "mrcaott4083ott469177"
 ## [195] "mrcaott4083ott4088"
 ## [196] "mrcaott4088ott95302"
 ## [197] "mrcaott4088ott9416"
 ## [198] "mrcaott4088ott8371"
 ## [199] "mrcaott4088ott6366"
 ## [200] "mrcaott4088ott5616"
 ## [201] "mrcaott5616ott5620"
 ## [202] "mrcaott5616ott28339"
 ## [203] "mrcaott5616ott6023"
 ## [204] "mrcaott5616ott6024"
 ## [205] "mrcaott6024ott6025"
 ## [206] "mrcaott6024ott603334"
 ## [207] "mrcaott6023ott243614"
 ## [208] "mrcaott6023ott101225"
 ## [209] "mrcaott6023ott125079"
 ## [210] "mrcaott6023ott261498"
 ## [211] "mrcaott6023ott97318"
 ## [212] "mrcaott6023ott262696"
 ## [213] "mrcaott6023ott1027553"
 ## [214] "mrcaott6023ott97315"
 ## [215] "mrcaott97315ott463018"
 ## [216] "Kieneria"
 ## [217] "mrcaott97318ott408447"
 ## [218] "Pipilo"
 ## [219] "mrcaott261498ott292639"
 ## [220] "mrcaott261498ott934463"
 ## [221] "mrcaott261498ott292635"
 ## [222] "mrcaott292635ott765407"
 ## [223] "Poecetes"
 ## [224] "mrcaott125079ott463026"
 ## [225] "mrcaott125079ott765405"
 ## [226] "'Zonotrichia (genus in domain Eukaryota)'"
 ## [227] "mrcaott125079ott265547"
 ## [228] "mrcaott125079ott265554"
 ## [229] "mrcaott243614ott292646"
 ## [230] "Spizella"
 ## [231] "mrcaott243614ott989506"
 ## [232] "mrcaott243614ott463036"
 ## [233] "mrcaott243614ott989508"
 ## [234] "mrcaott243614ott567431"
 ## [235] "mrcaott243614ott463034"
 ## [236] "mrcaott292646ott890355"
 ## [237] "mrcaott292646ott630695"
 ## [238] "Amphispiza"
 ## [239] "mrcaott890355ott948123"
 ## [240] "Calamospiza"
 ## [241] "mrcaott5021ott17146"
 ## [242] "mrcaott17146ott57819"
 ## [243] "Columbiformes"
 ## [244] "mrcaott17146ott45505"

[245] "mrcaott45505ott50388"
 ## [246] "mrcaott50388ott120585"
 ## [247] "mrcaott120585ott189782"
 ## [248] "mrcaott120585ott244142"
 ## [249] "mrcaott120585ott183576"
 ## [250] "Zenaida"
 ## [251] "mrcaott183576ott329066"
 ## [252] "mrcaott183576ott329068"
 ## [253] "Galloanserae"
 ## [254] "Galliformes"
 ## [255] "mrcaott4765ott6520194"
 ## [256] "mrcaott4765ott109888"
 ## [257] "mrcaott4765ott75785"
 ## [258] "mrcaott4765ott104461"
 ## [259] "mrcaott4765ott151684"
 ## [260] "mrcaott204719ott554512"
 ## [261] "Odontophoridae"
 ## [262] "mrcaott204719ott329467"
 ## [263] "mrcaott204719ott5860929"
 ## [264] "mrcaott204719ott3596007"
 ## [265] "mrcaott204719ott3596012"
 ## [266] "mrcaott204719ott5860945"
 ## [267] "Callipepla"
 ## [268] "mrcaott204719ott5860923"
 ## [269] "mrcaott1662ott4947157"
 ## [270] "Lepidosauria"
 ## [271] "'Squamata (order in Deuterostomia)'"
 ## [272] "Bifurcata"
 ## [273] "Unidentata"
 ## [274] "Episquamata"
 ## [275] "mrcaott1662ott2417"
 ## [276] "mrcaott1662ott4126044"
 ## [277] "Serpentes"
 ## [278] "mrcaott1662ott20148"
 ## [279] "mrcaott1662ott4126085"
 ## [280] "mrcaott1662ott35603"
 ## [281] "mrcaott1662ott16254"
 ## [282] "mrcaott1662ott106872"
 ## [283] "mrcaott1662ott215727"
 ## [284] "mrcaott1662ott6519"
 ## [285] "Viperidae"
 ## [286] "mrcaott6519ott705289"
 ## [287] "Crotalinae"
 ## [288] "mrcaott6519ott26866"
 ## [289] "mrcaott6519ott6535"
 ## [290] "mrcaott6519ott11126"
 ## [291] "mrcaott6519ott27081"
 ## [292] "mrcaott6519ott125357"
 ## [293] "mrcaott6519ott130701"
 ## [294] "Crotalus"
 ## [295] "mrcaott6519ott21537"
 ## [296] "mrcaott21537ott27076"
 ## [297] "mrcaott27076ott373874"
 ## [298] "mrcaott27076ott29217"


```

## [299] "mrcaott29217ott123878"
## [300] "mrcaott29217ott600067"
## [301] "mrcaott29217ott29219"
## [302] "mrcaott2417ott97368"
## [303] "mrcaott2417ott4124528"
## [304] "Iguania"
## [305] "mrcaott3089ott4125746"
## [306] "mrcaott3089ott4125739"
## [307] "mrcaott3089ott9418"
## [308] "mrcaott3089ott53412"
## [309] "mrcaott3089ott6523"
## [310] "mrcaott3089ott15148"
## [311] "Phrynosomatidae"
## [312] "Phrynosomatinae"
## [313] "mrcaott47621ott160827"
## [314] "mrcaott47621ott47629"
## [315] "Sceloporus"
## [316] "mrcaott47621ott47622"
## [317] "mrcaott47622ott342572"
## [318] "mrcaott47622ott47623"
## [319] "mrcaott47623ott51605"
## [320] "mrcaott51605ott265513"
## [321] "mrcaott51605ott795086"
## [322] "mrcaott51605ott656094"
## [323] "mrcaott51605ott51946"
## [324] "mrcaott51605ott57949"
## [325] "mrcaott51605ott624292"
## [326] "mrcaott51605ott96965"
## [327] "mrcaott51605ott917784"
## [328] "mrcaott51605ott608985"
## [329] "mrcaott51605ott917788"
## [330] "mrcaott51605ott80380"
## [331] "mrcaott80380ott265537"
## [332] "Crotaphytinae"
## [333] "'Gambelia (genus in Opisthokonta)'"
## [334] "mrcaott4987ott10058"
## [335] "mrcaott4987ott41163"
## [336] "mrcaott41163ott236051"
## [337] "mrcaott41163ott973821"
## [338] "mrcaott41163ott164954"
## [339] "mrcaott41163ott661799"
## [340] "mrcaott41163ott227429"
## [341] "mrcaott41163ott153490"
## [342] "mrcaott41163ott153486"
## [343] "Aspidoscelis"
## [344] "mrcaott348427ott498244"
## [345] "Aspidoscelis_tigris_group"

```

```
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 (i
## $ tip.label : chr [1:43] "Sigmodon_ochrognathus" "Sigmodon_hispidus" "Sigmodon_fulviventer" "Neotoma
## - 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
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## [77,] 110 111
## [78,] 111 11
## [79,] 110 112
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## [81,] 113 114
## [82,] 114 115
## [83,] 115 12
## [84,] 86 116
## [85,] 116 117
## [86,] 117 13
## [87,] 56 118
## [88,] 118 119
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## [97,] 127 14
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## [103,] 123 131
## [104,] 131 17
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## [110,] 120 136
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## [113,] 138 139
## [114,] 139 140
## [115,] 140 141
## [116,] 141 19
## [117,] 139 142
## [118,] 142 143
## [119,] 143 20

```

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## [120,] 138 144
## [121,] 144 21
## [122,] 54 145
## [123,] 145 146
## [124,] 146 147
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## [142,] 163 23
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## [146,] 166 167
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## [152,] 44 171
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## [168,] 186 187
## [169,] 187 188
## [170,] 188 189
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## [173,] 191 192

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## [174,] 192 193
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## [224,] 241 242
## [225,] 242 243
## [226,] 243 244
## [227,] 244 245

```

##	[228,]	245	246
##	[229,]	246	247
##	[230,]	247	248
##	[231,]	248	249
##	[232,]	249	27
##	[233,]	246	250
##	[234,]	250	251
##	[235,]	251	252
##	[236,]	252	253
##	[237,]	253	254
##	[238,]	254	255
##	[239,]	255	256
##	[240,]	256	257
##	[241,]	257	258
##	[242,]	258	259
##	[243,]	259	28
##	[244,]	254	260
##	[245,]	260	261
##	[246,]	261	29
##	[247,]	253	262
##	[248,]	262	263
##	[249,]	263	264
##	[250,]	264	265
##	[251,]	265	266
##	[252,]	266	30
##	[253,]	252	267
##	[254,]	267	268
##	[255,]	268	269
##	[256,]	269	270
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##	[262,]	274	275
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##	[264,]	276	277
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##	[267,]	272	279
##	[268,]	279	280
##	[269,]	280	281
##	[270,]	281	33
##	[271,]	279	282
##	[272,]	282	283
##	[273,]	283	34
##	[274,]	202	284
##	[275,]	284	285
##	[276,]	285	286
##	[277,]	286	287
##	[278,]	287	288
##	[279,]	288	289
##	[280,]	289	290
##	[281,]	290	291

```

## [282,] 291 292
## [283,] 292 293
## [284,] 293 294
## [285,] 294 295
## [286,] 295 35
## [287,] 200 296
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## [329,] 336 337
## [330,] 337 338
## [331,] 338 339
## [332,] 339 340
## [333,] 340 341
## [334,] 341 342
## [335,] 342 343

```



```

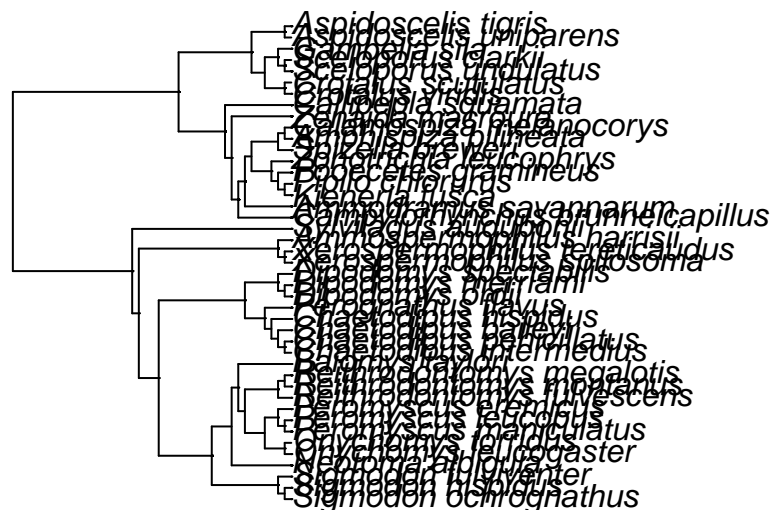
## [336,] 343 344
## [337,] 344 37
## [338,] 343 38
## [339,] 318 345
## [340,] 345 346
## [341,] 346 347
## [342,] 347 348
## [343,] 348 349
## [344,] 349 350
## [345,] 350 351
## [346,] 351 352
## [347,] 352 353
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## [349,] 354 355
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## [352,] 357 358
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## [361,] 366 367
## [362,] 367 368
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## [366,] 371 372
## [367,] 372 373
## [368,] 373 374
## [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

```

```
str(surveys)
```

```
## 'data.frame': 35549 obs. of 9 variables:
## $ record_id : int 1 2 3 4 5 6 7 8 9 10 ...
## $ month : int 7 7 7 7 7 7 7 7 7 7 ...
## $ day : int 16 16 16 16 16 16 16 16 16 16 ...
## $ year : int 1977 1977 1977 1977 1977 1977 1977 1977 1977 1977 ...
## $ plot_id : int 2 3 2 7 3 1 2 1 1 6 ...
## $ species_id : chr "NL" "NL" "DM" "DM" ...
## $ sex : chr "M" "M" "F" "M" ...
## $ hindfoot_length: int 32 33 37 36 35 14 NA 37 34 20 ...
## $ weight : int NA NA NA NA NA NA NA NA NA NA ...
```

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



An extension of ggplot for phylogenetic visualization: `ggtree` To install packages from the Bioconductor repo, we need a CRAN package called BiocManager

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

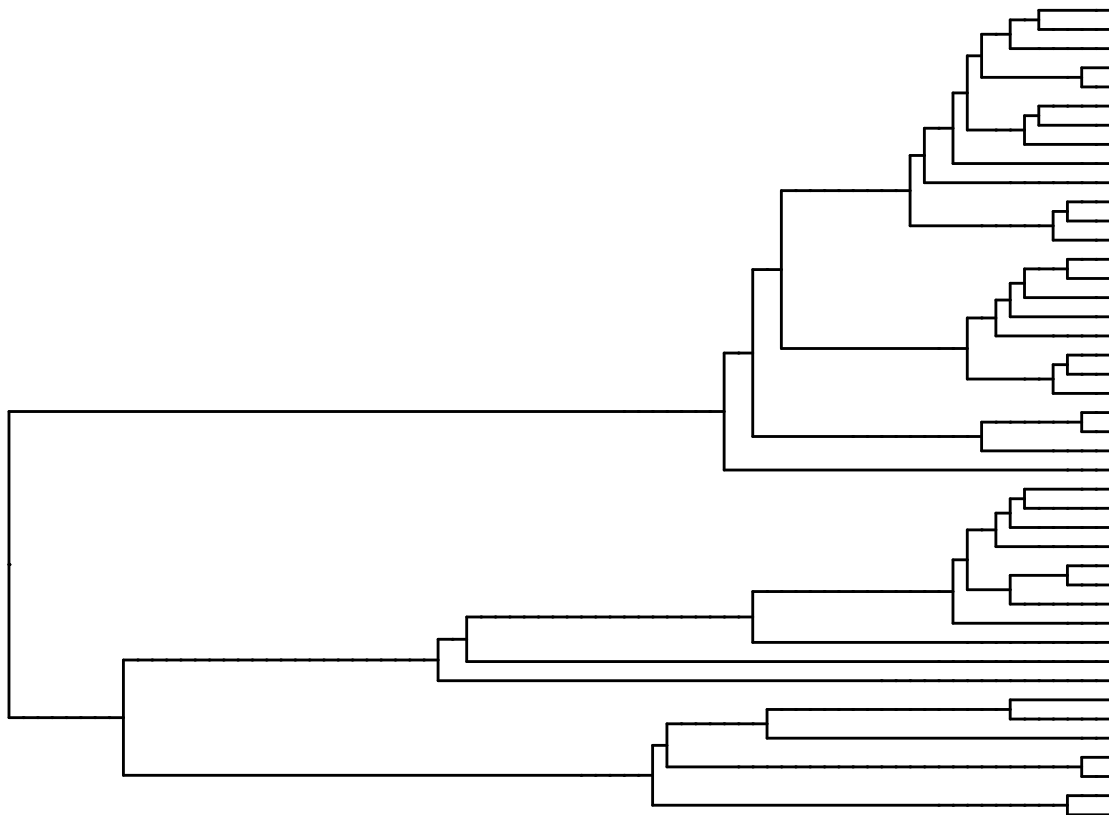
```
## ggtree v3.4.4 For help: https://yulab-smu.top/treedata-book/
##
## If you use the ggtree package suite in published research, please cite
```

```
## 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
##
## 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
##
## Guangchuang Yu. Data Integration, Manipulation and Visualization of
## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022,
## doi:10.1201/9781003279242

##
## Attaching package: 'ggtree'

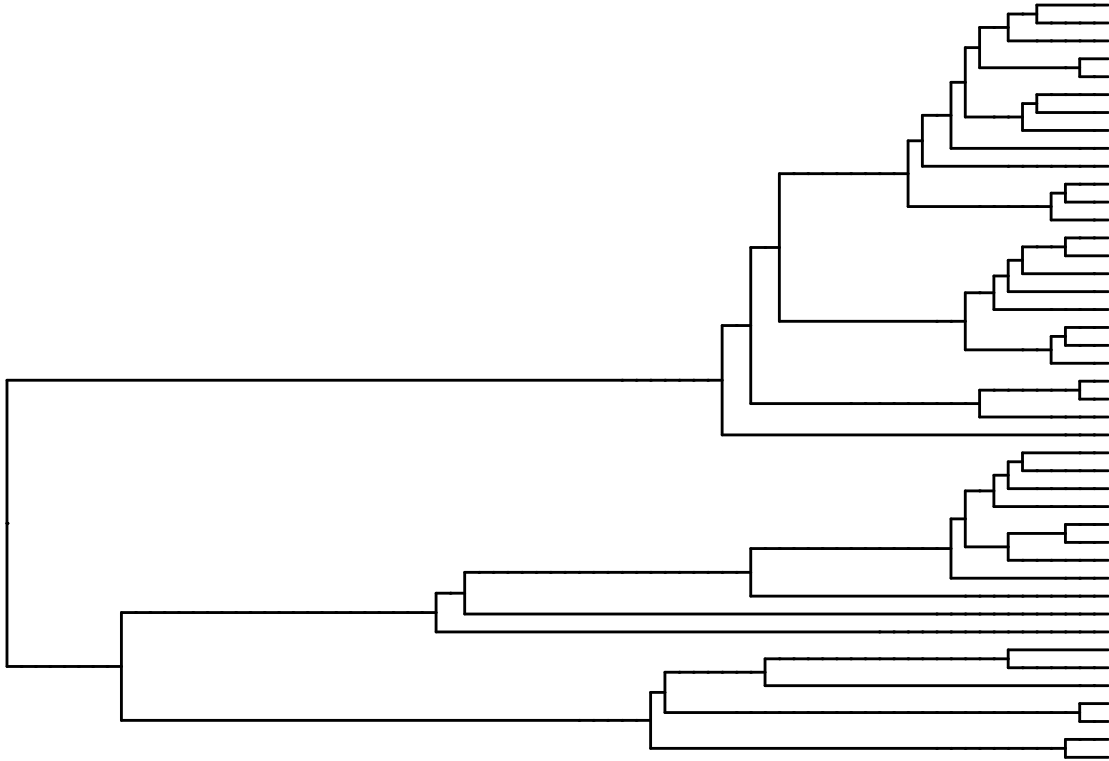
## The following object is masked from 'package:ape':
##
## rotate
```

```
ggtree(portal_tree)
```



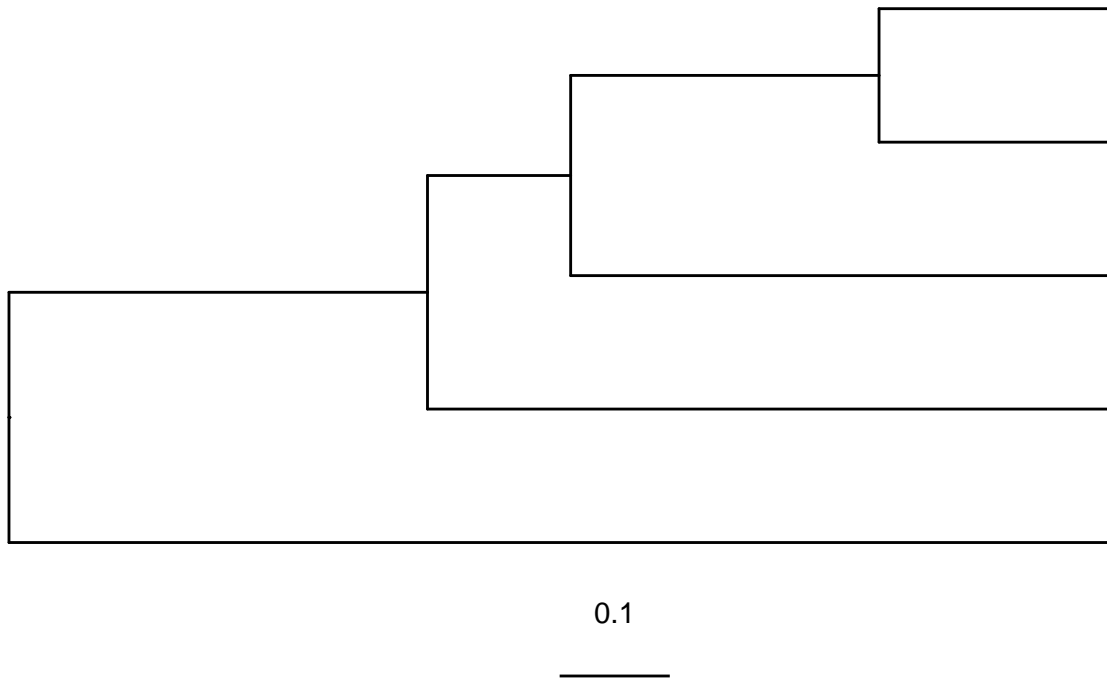
This is equivalent to:

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



Plot the small tree of five species of primates and include a scale what is the difference between the portal and the small tree

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



```
class(small_tree)
```

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

```
length(small_tree) # gives the number of
```

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

```
names(small_tree)
```

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

```
small_tree$Nnode
```

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

```
small_tree["tip.label"]
```

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

```
## [1] "Homo"  "Pongo" "Macaca" "Ateles" "Galago"
```

```
head(small_tree[[3]])
```

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

```
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.
```

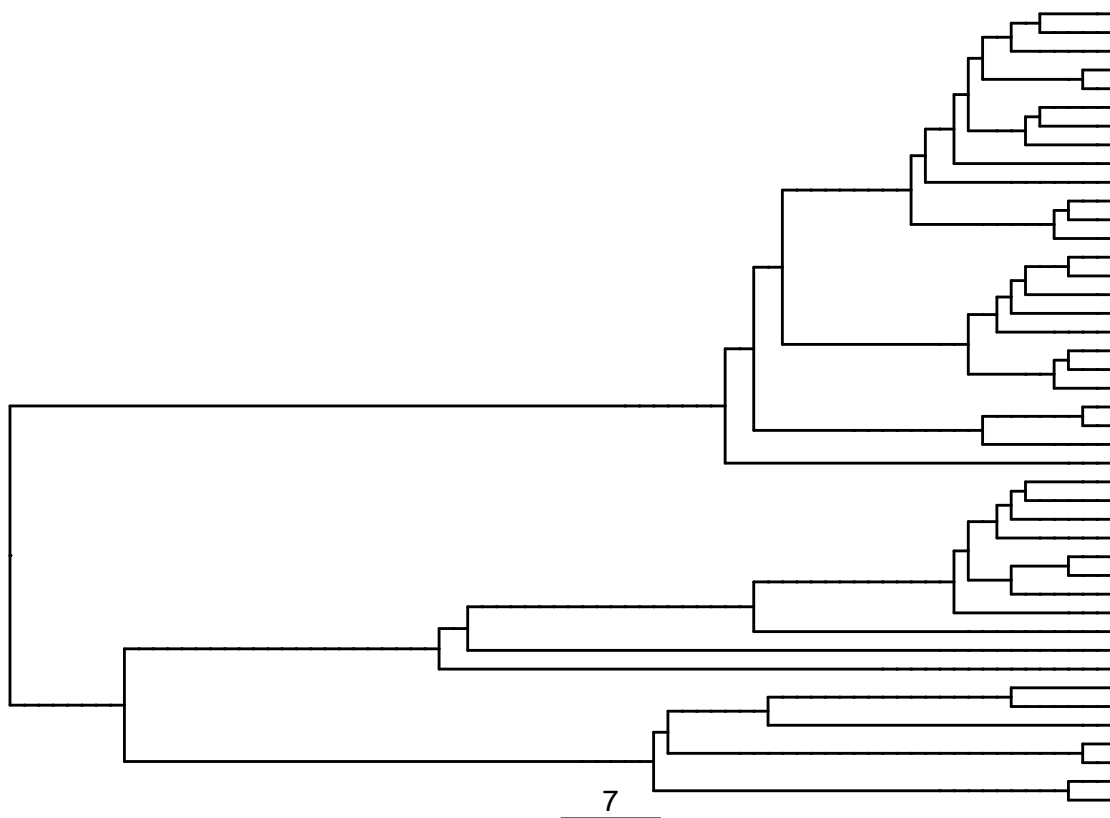
```
str(small_tree) # $ to access elements
```

```
## 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"
```

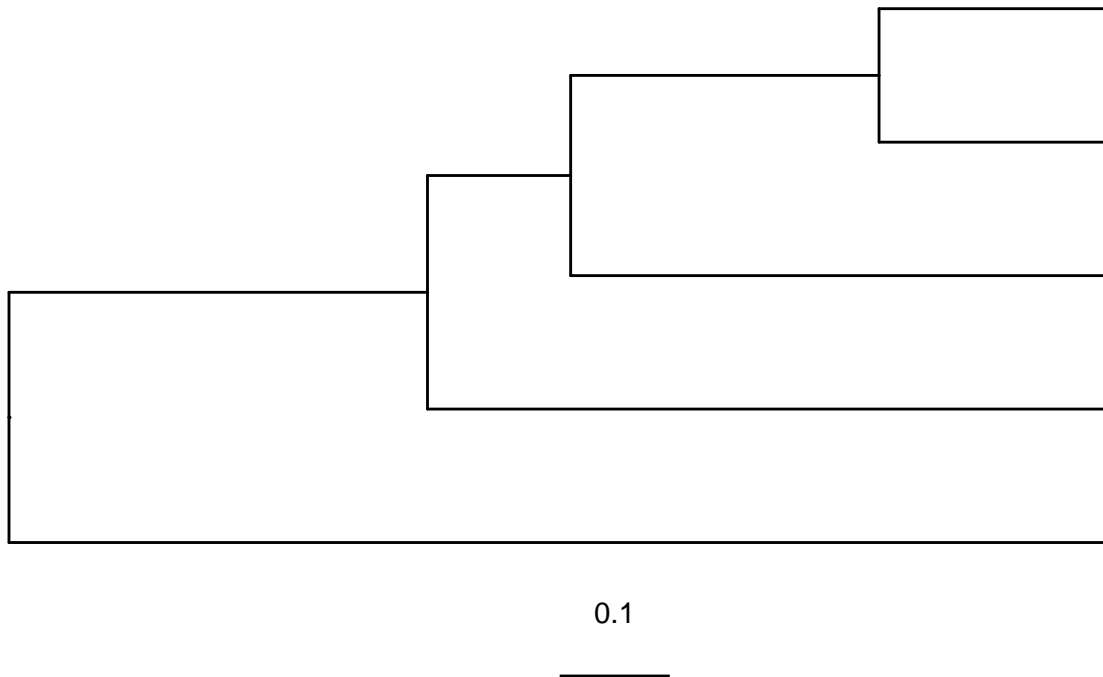
```
head(small_tree$edge)
```

```
##      [,1] [,2]
## [1,]    6    7
## [2,]    7    8
## [3,]    8    9
## [4,]    9    1
## [5,]    9    2
## [6,]    8    3
```

```
ggtree(portal_tree) +
  geom_treescale()
```



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



```
names(small_tree)
```

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

- a difference in number of tips (43 vs 5)
- an edge length in 'small_tree', but it has no node labels

```
small_tree$edge.length
```

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

```
small_tree$node.label
```

```
## NULL
```

```
portal_tree$node.label
```

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



```

## [7] "mrcaott42ott30082"
## [8] "Glires"
## [9] "mrcaott42ott29157"
## [10] "Rodentia"
## [11] "mrcaott42ott10477"
## [12] "mrcaott42ott38834"
## [13] "mrcaott42ott48903"
## [14] "mrcaott42ott254702"
## [15] "Myomorpha"
## [16] "Muroidea"
## [17] "mrcaott42ott45197"
## [18] "mrcaott42ott55942"
## [19] "mrcaott42ott102"
## [20] "mrcaott102ott739"
## [21] "Cricetidae"
## [22] "mrcaott739ott15637"
## [23] "mrcaott739ott119008"
## [24] "mrcaott739ott38053"
## [25] "mrcaott38053ott39197"
## [26] "Sigmodon"
## [27] "mrcaott39197ott1067882"
## [28] "mrcaott39197ott1067867"
## [29] "mrcaott39197ott208424"
## [30] "mrcaott39197ott208422"
## [31] "mrcaott208424ott576098"
## [32] "mrcaott208424ott1067878"
## [33] "mrcaott1067867ott1067876"
## [34] "Neotominae"
## [35] "mrcaott15637ott15642"
## [36] "Neotoma"
## [37] "mrcaott15638ott5266793"
## [38] "mrcaott15638ott83673"
## [39] "mrcaott83673ott169825"
## [40] "mrcaott169825ott690543"
## [41] "mrcaott169825ott381420"
## [42] "mrcaott18770ott5266794"
## [43] "mrcaott18770ott39171"
## [44] "mrcaott18770ott39181"
## [45] "mrcaott18770ott76407"
## [46] "mrcaott18770ott427266"
## [47] "Onychomys"
## [48] "mrcaott427266ott1004147"
## [49] "mrcaott76407ott1024550"
## [50] "mrcaott76407ott138845"
## [51] "mrcaott76407ott319357"
## [52] "mrcaott76407ott373073"
## [53] "mrcaott76407ott576106"
## [54] "mrcaott76407ott259483"
## [55] "mrcaott259483ott1026151"
## [56] "mrcaott259483ott259485"
## [57] "mrcaott373073ott576104"
## [58] "mrcaott138845ott162838"
## [59] "mrcaott138845ott162828"
## [60] "mrcaott162828ott343211"

```

[61] "mrcaott343211ott343214"
 ## [62] "mrcaott343214ott576102"
 ## [63] "mrcaott39181ott489149"
 ## [64] "Reithrodontomys"
 ## [65] "mrcaott39181ott208412"
 ## [66] "mrcaott39181ott222510"
 ## [67] "mrcaott208412ott208414"
 ## [68] "mrcaott208412ott208418"
 ## [69] "mrcaott208414ott208416"
 ## [70] "mrcaott208416ott222512"
 ## [71] "mrcaott208416ott770864"
 ## [72] "mrcaott208416ott732037"
 ## [73] "mrcaott39171ott91079"
 ## [74] "Baiomys"
 ## [75] "Castorimorpha"
 ## [76] "mrcaott48903ott80974"
 ## [77] "Heteromyidae"
 ## [78] "mrcaott48903ott190180"
 ## [79] "Perognathinae"
 ## [80] "Chaetodipus"
 ## [81] "mrcaott190180ott320777"
 ## [82] "mrcaott190180ott190184"
 ## [83] "mrcaott190180ott374303"
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 ## [87] "mrcaott320777ott764435"
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 ## [89] "Perognathus"
 ## [90] "mrcaott365546ott890372"
 ## [91] "mrcaott365546ott943065"
 ## [92] "mrcaott943065ott1004160"
 ## [93] "Dipodomyinae"
 ## [94] "Dipodomys"
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 ## [101] "mrcaott241218ott748116"
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 ## [104] "Sciuridae"
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 ## [106] "mrcaott10477ott97818"
 ## [107] "mrcaott10477ott259084"
 ## [108] "mrcaott10477ott152097"
 ## [109] "Marmotini"
 ## [110] "mrcaott10477ott902084"
 ## [111] "mrcaott10477ott359117"
 ## [112] "mrcaott10477ott208064"
 ## [113] "mrcaott10477ott136299"
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[115] "mrcaott136299ott141525"
 ## [116] "mrcaott141525ott508655"
 ## [117] "mrcaott141525ott580345"
 ## [118] "Xerospermophilus"
 ## [119] "mrcaott141525ott508648"
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 ## [121] "mrcaott359117ott580339"
 ## [122] "Ammospermophilus"
 ## [123] "mrcaott580339ott632597"
 ## [124] "mrcaott580339ott580350"
 ## [125] "Lagomorpha"
 ## [126] "Leporidae"
 ## [127] "Sylvilagus"
 ## [128] "Sauropsida"
 ## [129] "Sauria"
 ## [130] "mrcaott246ott4128455"
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 ## [132] "mrcaott246ott4129629"
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 ## [135] "mrcaott246ott1662"
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 ## [154] "mrcaott246ott3600976"
 ## [155] "mrcaott246ott4132107"
 ## [156] "Aves"
 ## [157] "Neognathae"
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 ## [176] "mrcaott246ott176461"
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 ## [183] "mrcaott246ott25638"
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 ## [185] "mrcaott246ott18313"
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 ## [188] "Campylorhynchus"
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[223] "Poecetes"
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 ## [225] "mrcaott125079ott765405"
 ## [226] "'Zonotrichia (genus in domain Eukaryota)'"
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 ## [229] "mrcaott243614ott292646"
 ## [230] "Spizella"
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 ## [250] "Zenaida"
 ## [251] "mrcaott183576ott329066"
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 ## [253] "Galloanserae"
 ## [254] "Galliformes"
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 ## [256] "mrcaott4765ott109888"
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 ## [265] "mrcaott204719ott3596012"
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 ## [268] "mrcaott204719ott5860923"
 ## [269] "mrcaott1662ott4947157"
 ## [270] "Lepidosauria"
 ## [271] "'Squamata (order in Deuterostomia)'"
 ## [272] "Bifurcata"
 ## [273] "Unidentata"
 ## [274] "Episquamata"
 ## [275] "mrcaott1662ott2417"
 ## [276] "mrcaott1662ott4126044"

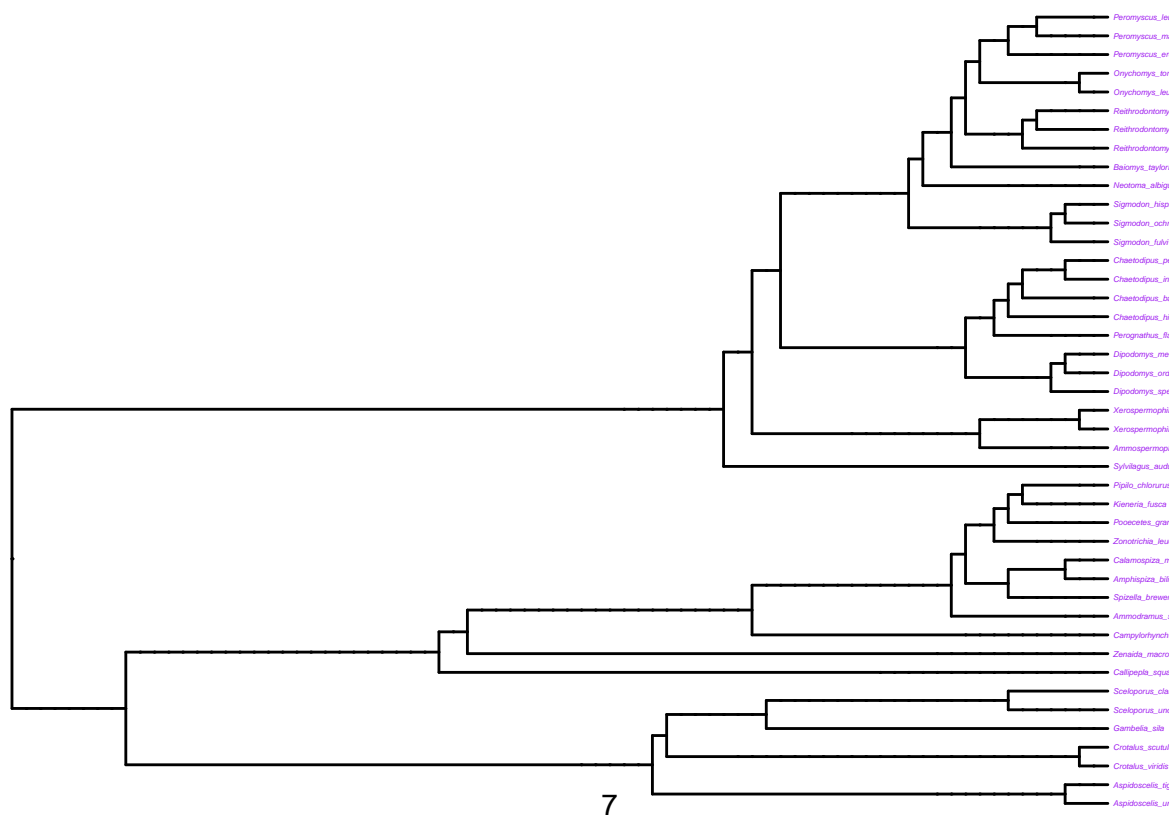
[277] "Serpentes"
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 ## [293] "mrcaott6519ott130701"
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 ## [296] "mrcaott21537ott27076"
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 ## [302] "mrcaott2417ott97368"
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 ## [329] "mrcaott51605ott917788"
 ## [330] "mrcaott51605ott80380"

```
## [331] "mrcaott80380ott265537"
## [332] "Crotaphytinae"
## [333] "'Gambelia (genus in Opisthokonta)'"
## [334] "mrcaott4987ott10058"
## [335] "mrcaott4987ott41163"
## [336] "mrcaott41163ott236051"
## [337] "mrcaott41163ott973821"
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## [342] "mrcaott41163ott153486"
## [343] "Aspidoscelis"
## [344] "mrcaott348427ott498244"
## [345] "Aspidoscelis_tigris_group"
```

Add tip labels and node labels

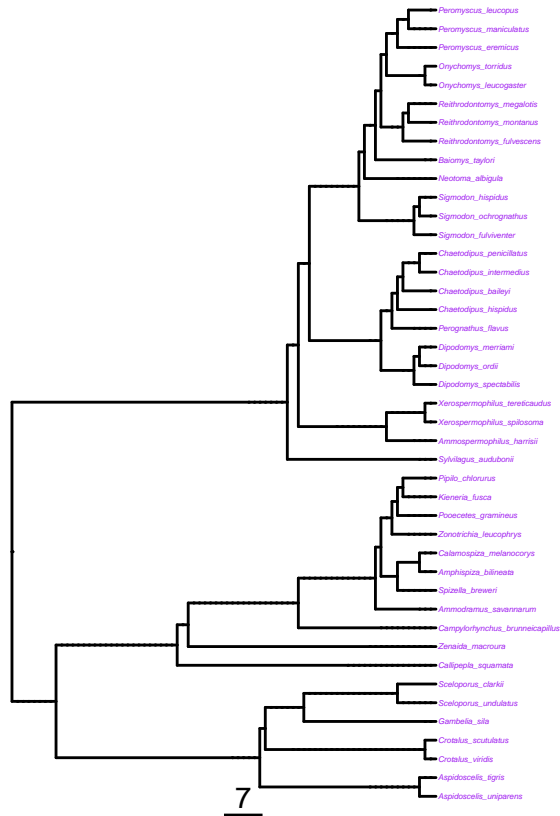
Because a plot is nothing with no labels:

```
ggtree(portal_tree) +  
  geom_treescale() +  
  geom_tiplab(size = 1, color = "purple", fontface = "italic")
```



Add a limit to the plot so we can see the labels fully:

```
ggtree(portal_tree) +
  geom_treescale() +
  geom_tiplab(size = 1, color = "purple", fontface = "italic") +
  xlim(NA, 200)
```



Do this for small_tree for homework

Get branch lengths

```
branching.times(small_tree)
```

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

```
ggtree(small_tree) +
  geom_treescale() +
  geom_tiplab(size = 4, color = "purple", fontface = "italic") +
  xlim(NA, 1.15)
```