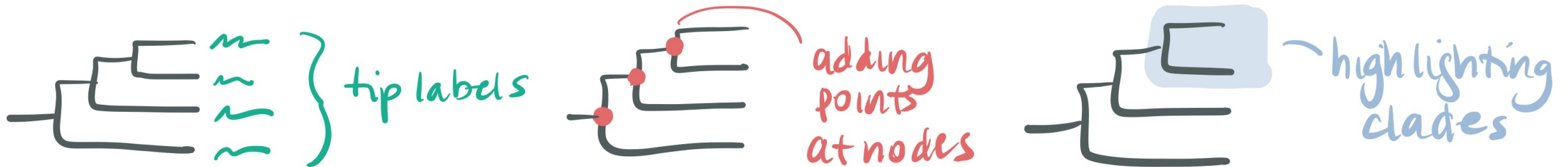# Data visualization in R
ggtree package

ggtree package

- ggtree is a package that uses the exact same syntax and **aesthetic mapping** as *ggplot2* except for phylogenetic trees

- Reads in a tree as class **phylo** object (*ape* package)

- A few examples of phylogenetic tree aesthetics:

Basically, any aesthetic modification you'd make in FigTree, you can make with *ggtree*

Can do complex aesthetic mapping
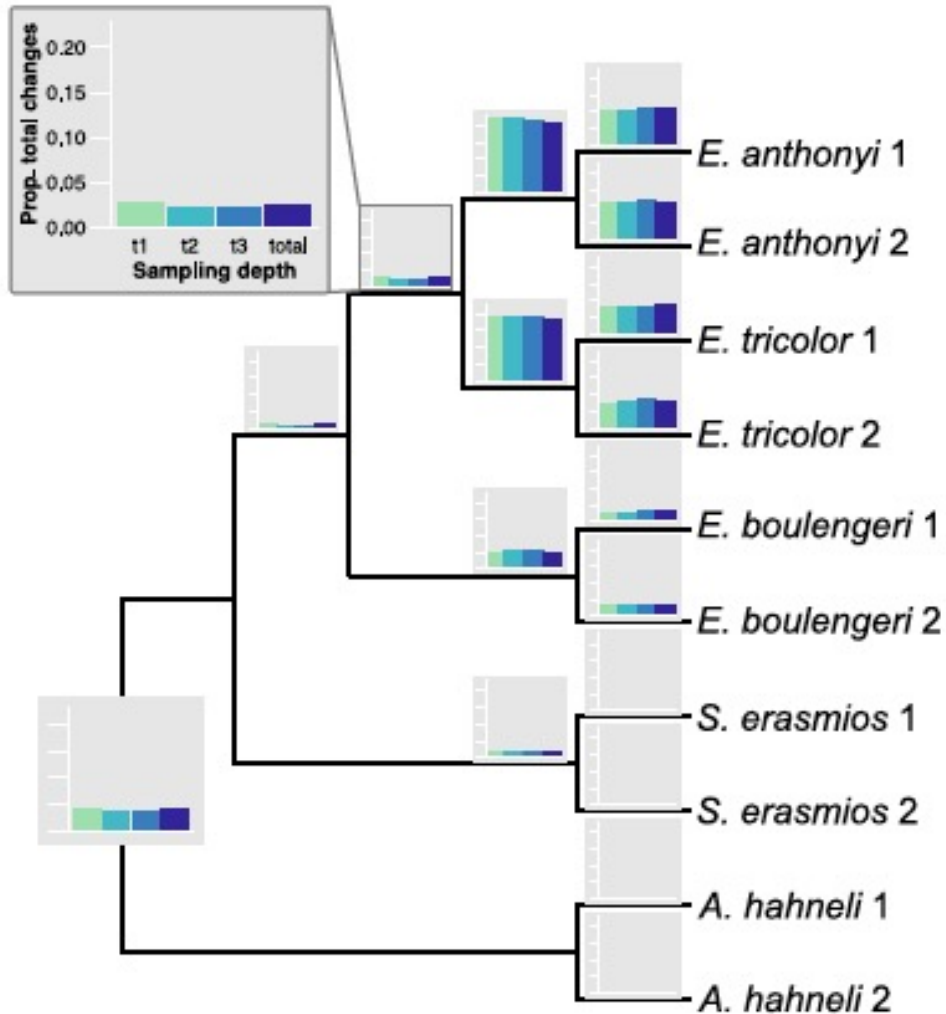

```
p.epi <-
  ggtree(epi, size=1.5) %<+%
  epilabs +
  coord_cartesian(xlim = c(0,5.5), clip="off") +
  geom_tiplab(aes(label=paste0('italic(', genera, ')~italic(', species, ')~', e_numbers)),
  parse=T, size=5) +
  theme(plot.margin=unit(c(2,3,.75,1.5),"cm")) # top, right, bottom, left
p.epi <-
  p.epi %>%
  flip(15, 16)

p.epi +
    ggplot(df, aes(x = type, y = value, fill = StateChange)) +
    geom_bar(aes(alpha = type), stat = "identity", position = 'stack') +
    theme(strip.background = element_blank(),
        aspect.ratio = 1,
        axis.ticks.x = element_blank(),
        axis.title = element_blank(),
        axis.ticks.y = element_line(color="white", size=0.75),
        axis.line.y = element_line(color="white", size=0.75),
        axis.line.x = element_line(color="white", size=0.75),
        axis.ticks.length = unit(0.2,"cm"),
        legend.position='none',
        axis.text = element_blank(),
        plot.background = element_rect(fill = "#e6e6e6"),
        plot.margin = margin(1,1,-1.5,1,"mm")) + # t, r, b, l
    scale_x_discrete(expand = c(0,0)) +
    scale_y_continuous(expand = c(0,0), limits=ylim) +
    scale_fill_manual(values = c("0 <=> 1"="#91d5de", "1 ==> 0"="#eaae37", "1 <=>
0"="#b4674e", "0 ==> 1"="#2e8289")) +
    scale_alpha_manual(values = c(1, 0.4))
```

Phylo objects

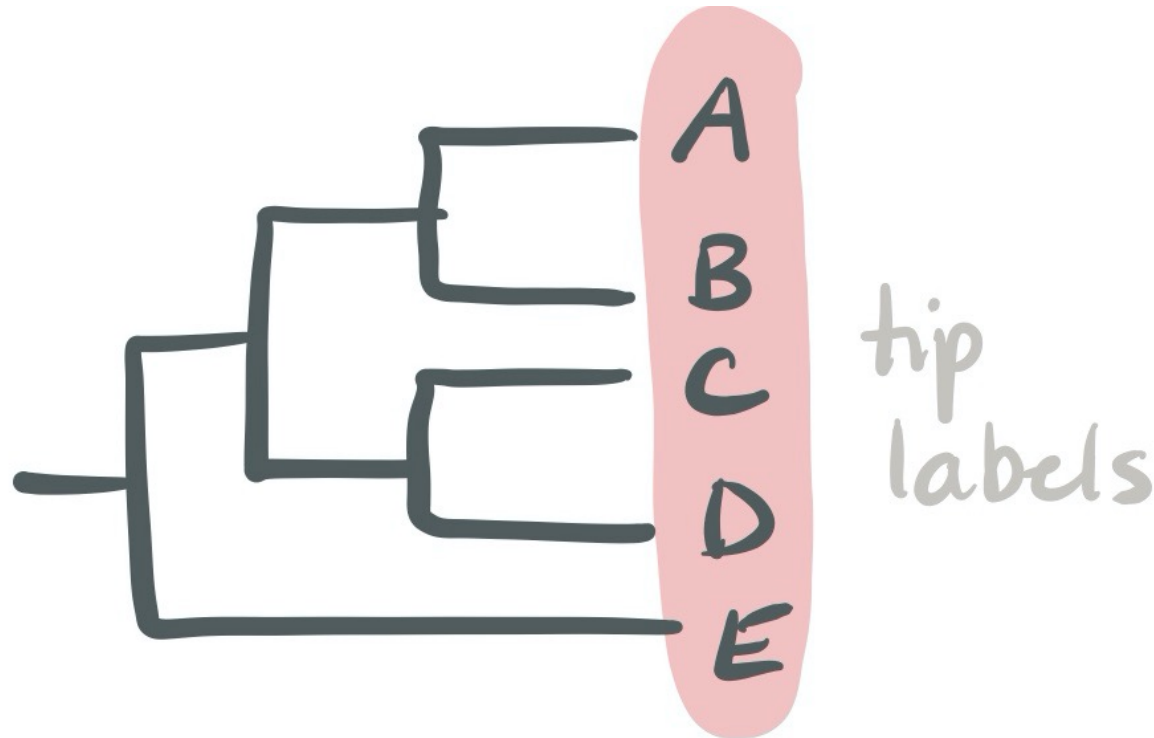- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

  Let's take a simple example: 5 taxa and *no* branch lengths
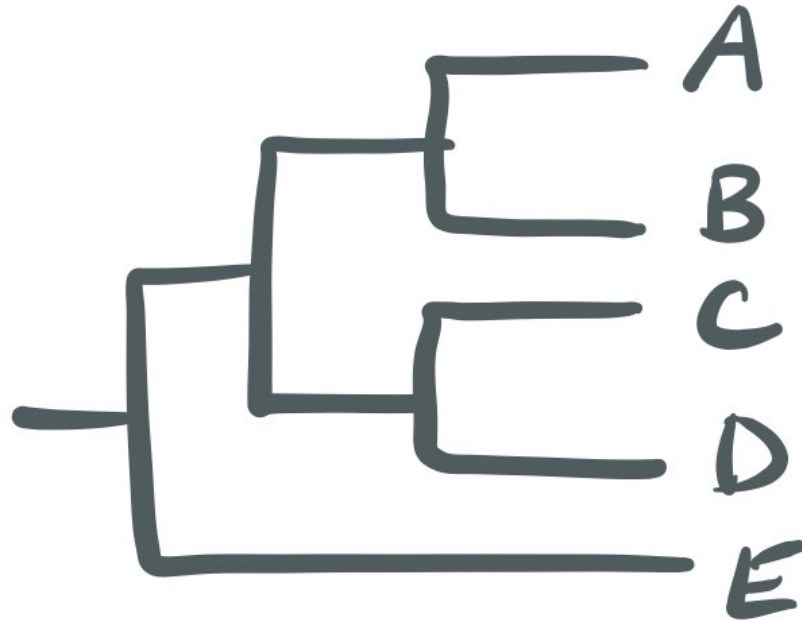
What is the **bare minimum** amount of information needed to make this tree?

Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

You can access parts of a phylo object (or a data frame) using the $ symbol
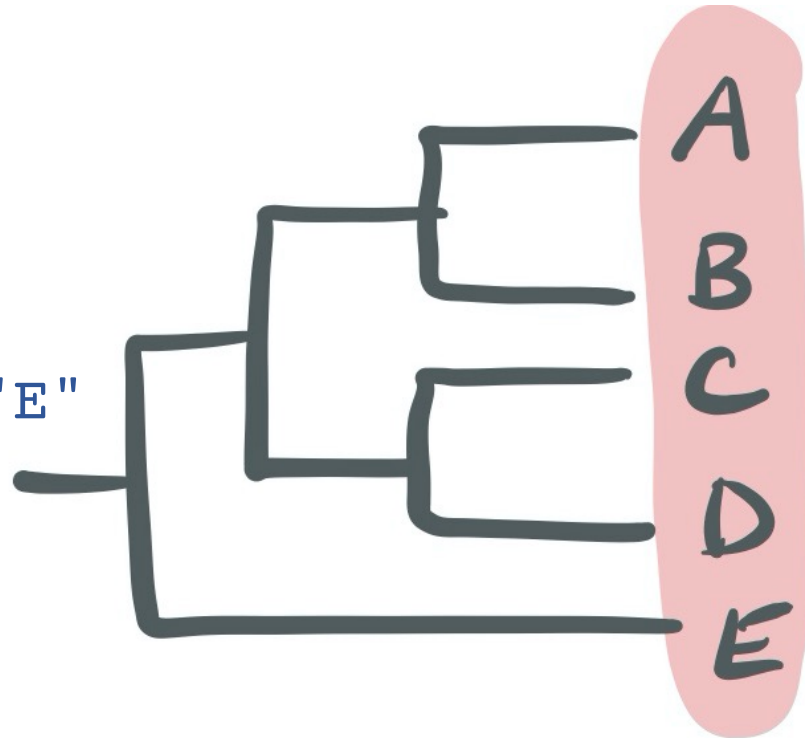
Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R:

```
tree$tip.label
```

R output:

```
[1] "A" "B" "C" "D" "E"
```
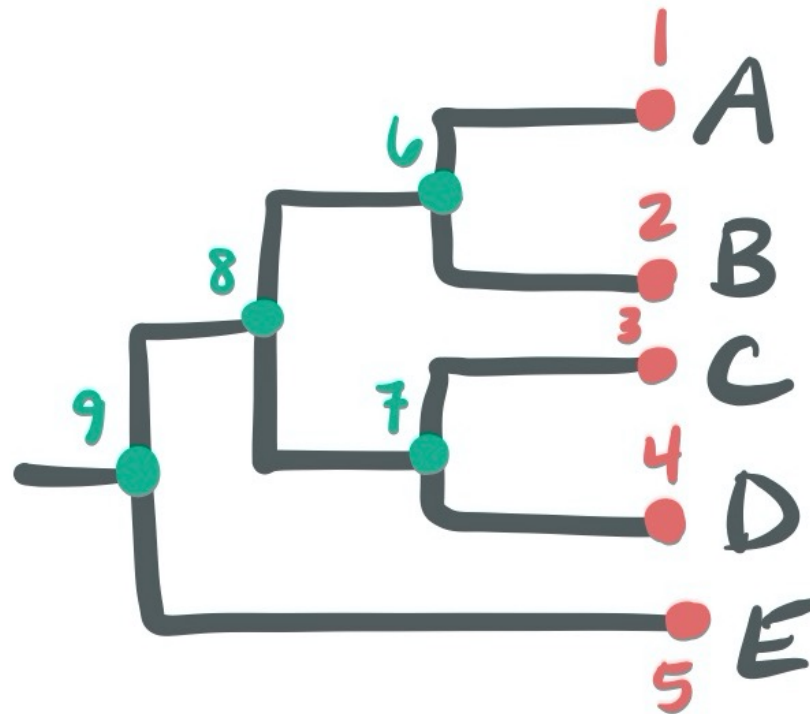

tip labels

`tip.label`

Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R:

```
tree$Nnode
```

R output:

```
[1] 4
```


n internal nodes = 4
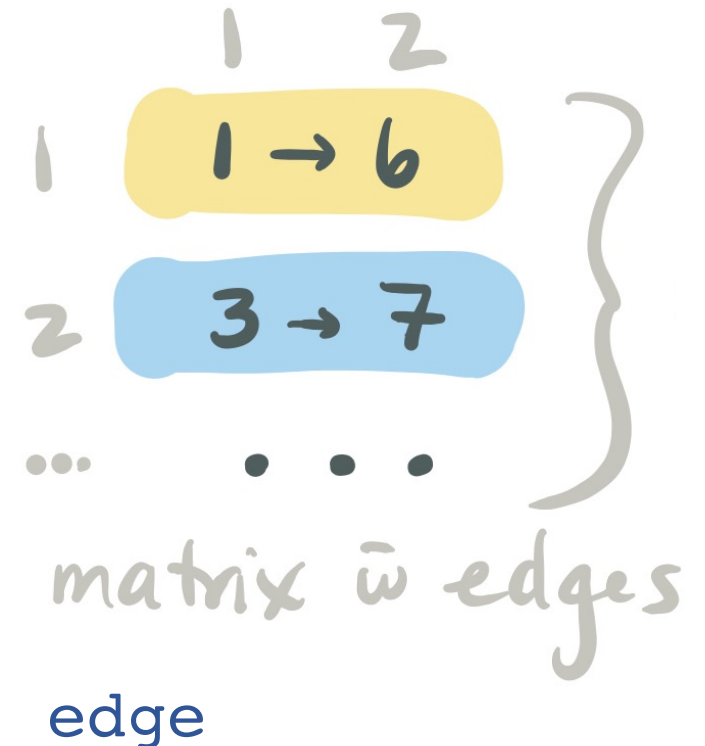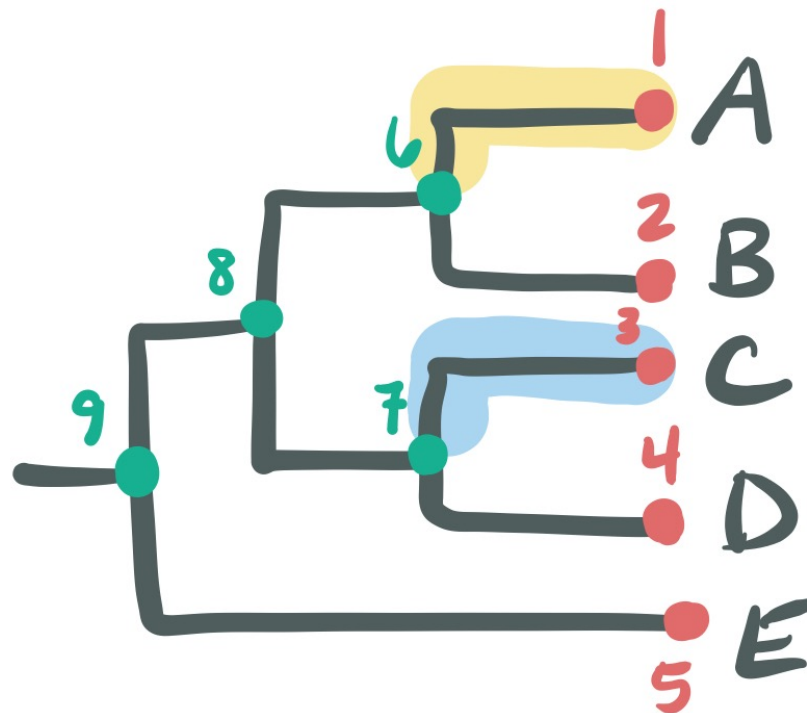
Nnode

Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R

```
tree$edge
```

R output:

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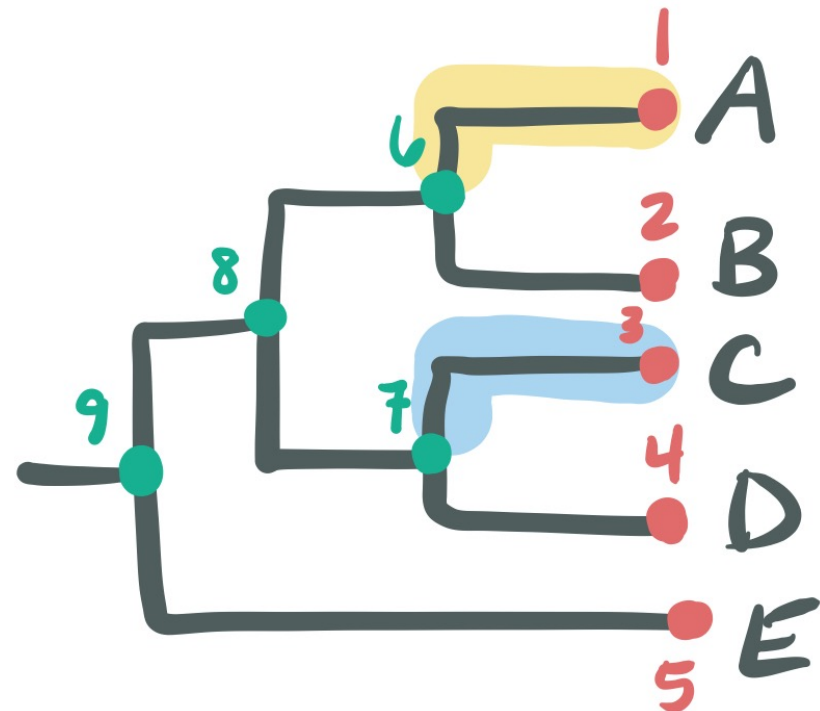

edge

Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Simplest phylo object requires **3 parts:**

edges (connections between nodes)
node numbers
tip labels

Phylo objects

- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

edges (connections between nodes)
node numbers
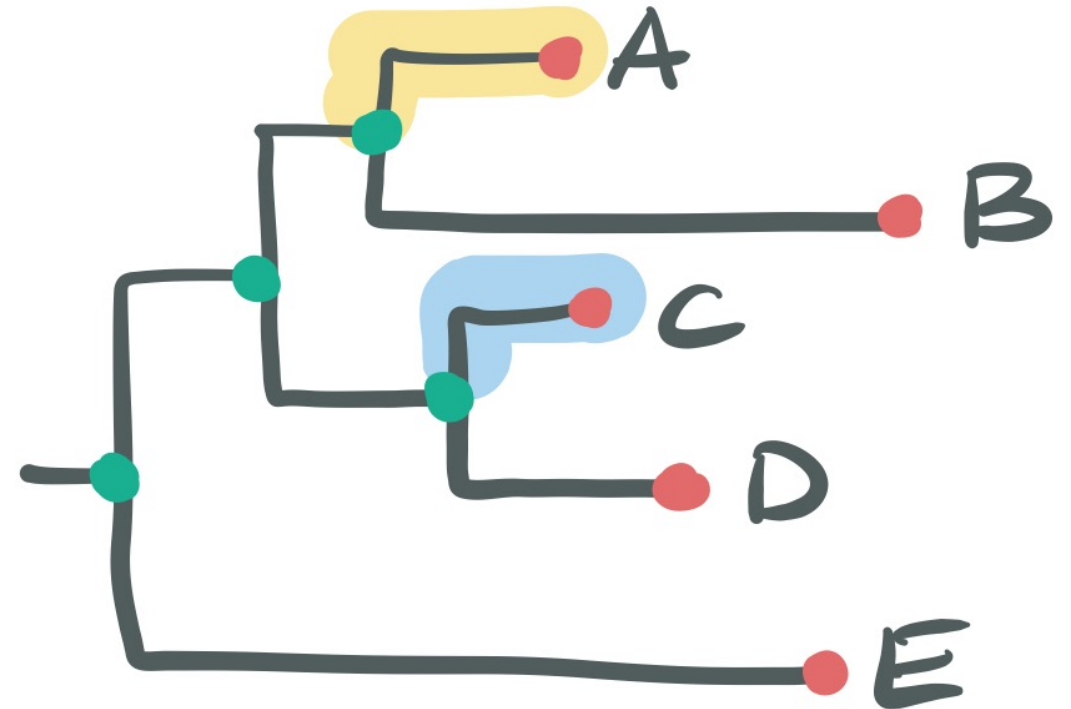tip labels
branch lengths: `edge.length`
`tree$edge.length`
`[1] 0.1 0.5 0.4 0.3 ...`
support values: `node.labels`
`tree$node.labels`
`[1] 100 98 99 96 ...`

Phylo objects

tree

```
Phylogenetic tree with 5 tips and 4 internal nodes.

Tip labels:
  A, B, C, D, E
Node labels:
  100, 86, 98, 100

Rooted; includes branch lengths.
```
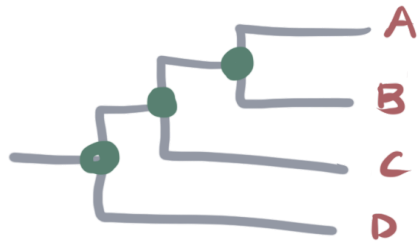
str(tree)

```
## List of 4
##     $ edge : int [1:38, 1:2] 21 22 23 24 24 23 25 26 27 27 ...
##     $ tip.label : chr [1:20] "t1" "t20" "t2" "t7" ...
##     $ edge.length: num [1:38] 0.0729 0.8743 0.1989 0.5346 0.1056 ...
##     $ Nnode : int 19
##     - attr(*, "class")= chr "phylo"
##     - attr(*, "order")= chr "cladewise"
```
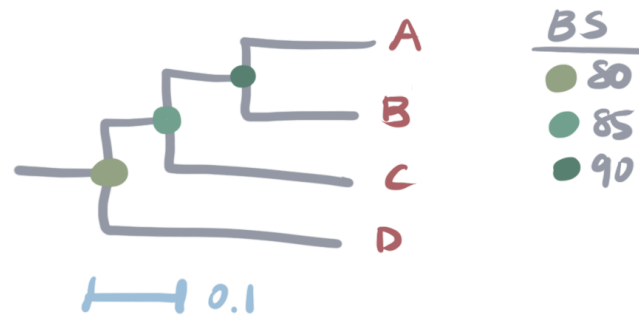
Let's build a tree!

ggtree (phylo object)
    + geom_tiplab( )

ggtree manual: http://yulab-smu.top/treedata-book/

Let's build a tree!


```
ggtree (phylo object)
    + geom_tiplab (size = 0.5)
    + geom_nodepoint ()
```

ggtree manual: http://yulab-smu.top/treedata-book/

Let's build a tree!


```
ggtree (phylo object)
    + geom_tiplab (size = 0.5)
    + geom_nodepoint (aes (color = bootstrap))
    + geom_treescale ()
```
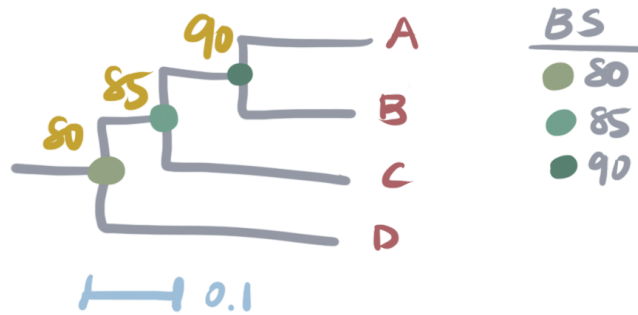
ggtree manual: http://yulab-smu.top/treedata-book/

Let's build a tree!


```
ggtree (phylo object)
        + geom_tiplab(size = 0.5)
        + geom_nodepoint(aes(color = bootstrap))
        + geom_treescale()
        + geom_text(aes(label = node))
```

ggtree manual: http://yulab-smu.top/treedata-book/