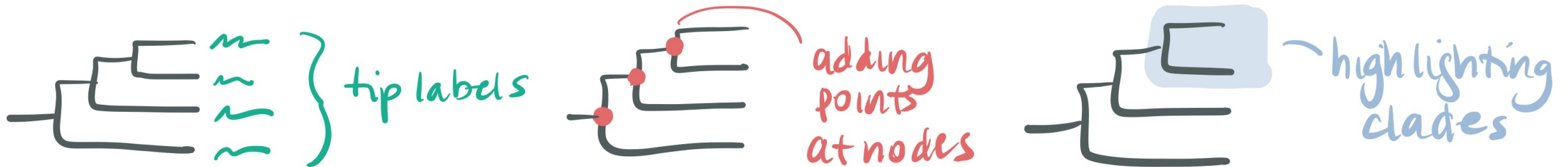


# Data visualization in R

## *ggtree* package

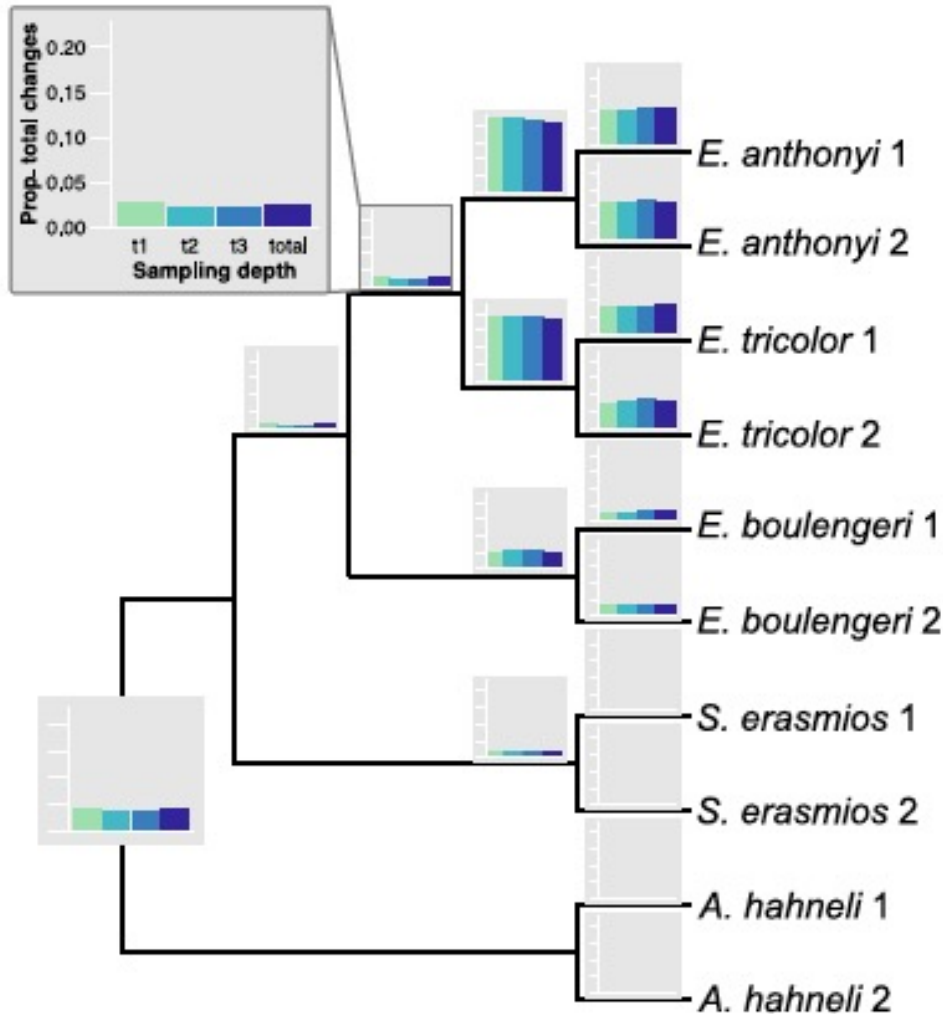
# *ggtree* package

- *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

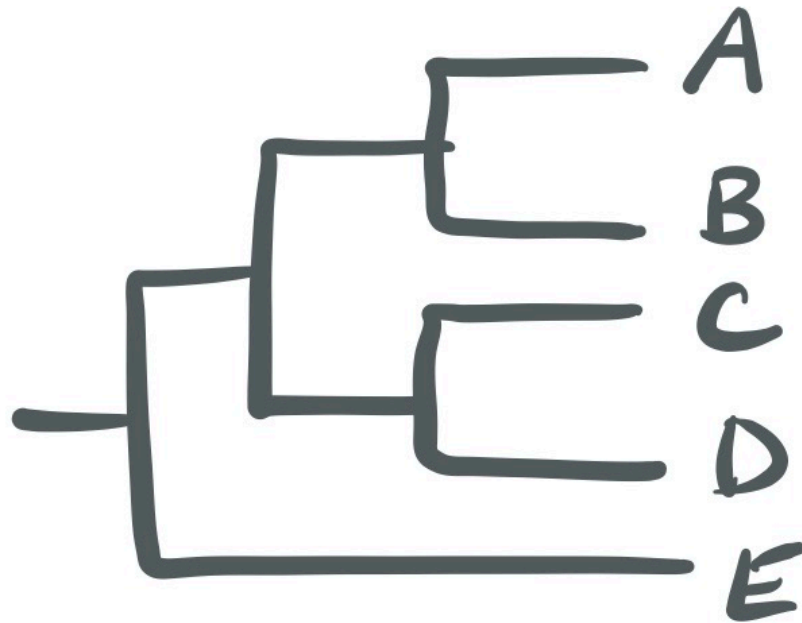


```
ggplot(df, aes(x = type, y = value, fill = StateChange)) +
  geom_bar(aes(alpha = type), stat = "identity", position = 'stack') +
  theme(strip.background = element_blank(),
        aspect.ratio = 1,
        axis.ticks.x = element_blank(),
        axis.title = element_blank(),
        axis.ticks.y = 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

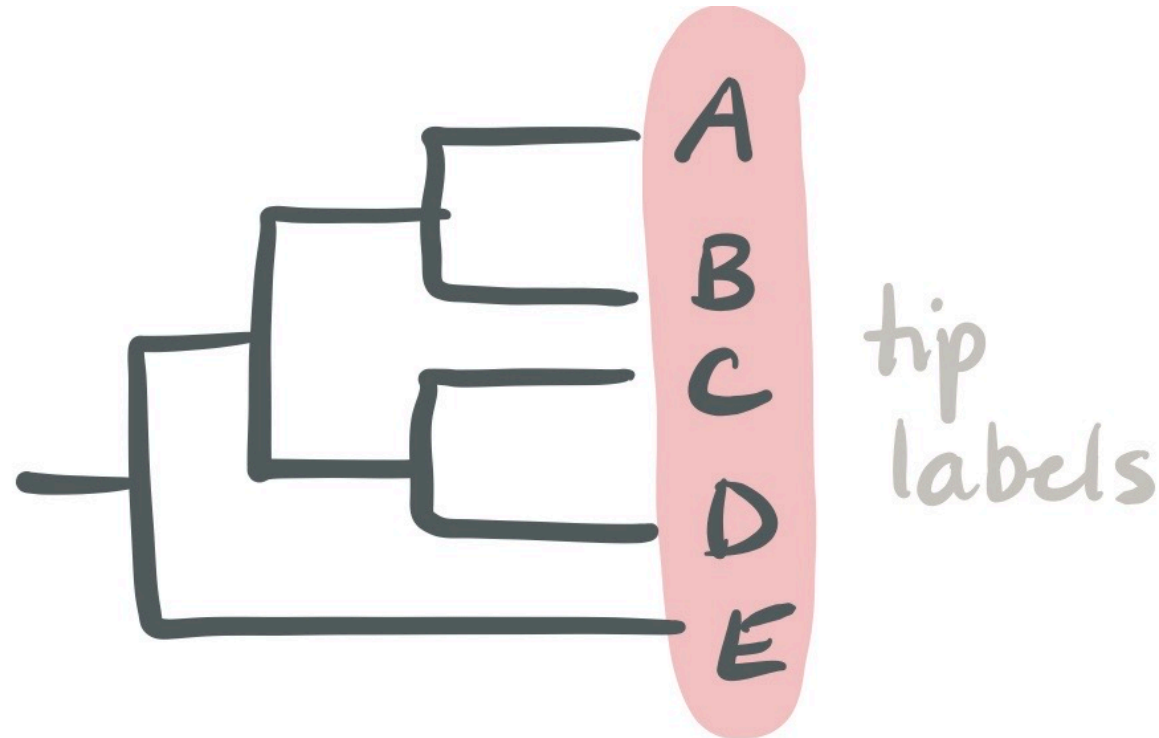
Let's take a simple example: 5 taxa and *no* branch lengths



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

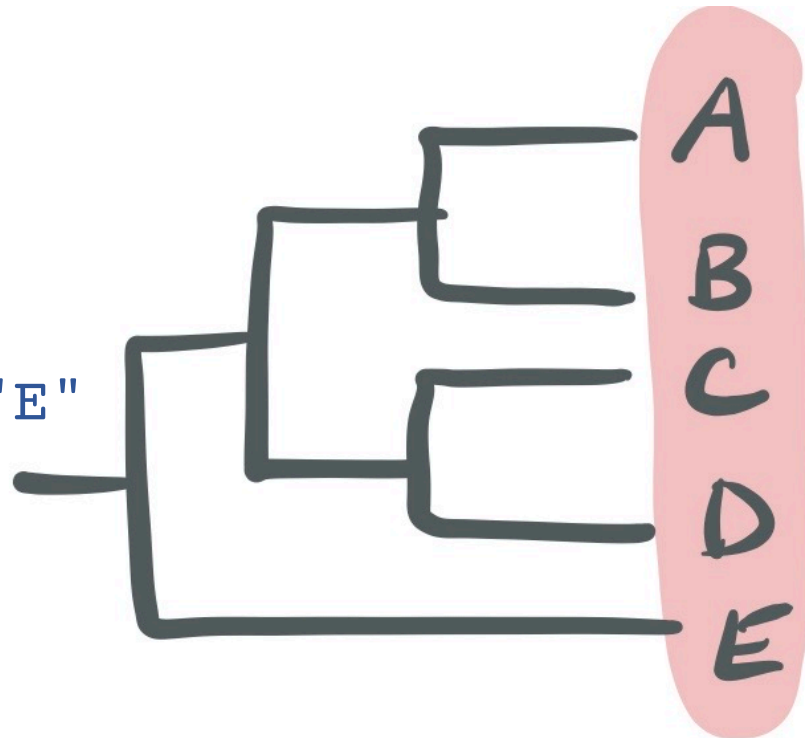
- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R:

```
tree$tip.label
```

R output:

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



tip  
labels

```
tip.label
```

# Phylo objects

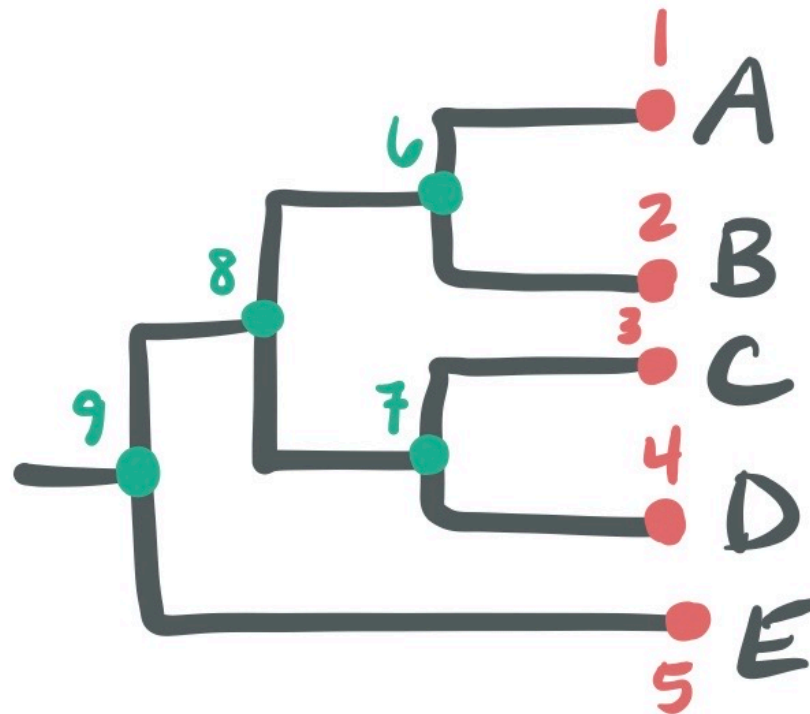
- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R:

```
tree$Nnode
```

R output:

```
[1] 4
```



*n* internal nodes = 4

Nnode

# Phylo objects

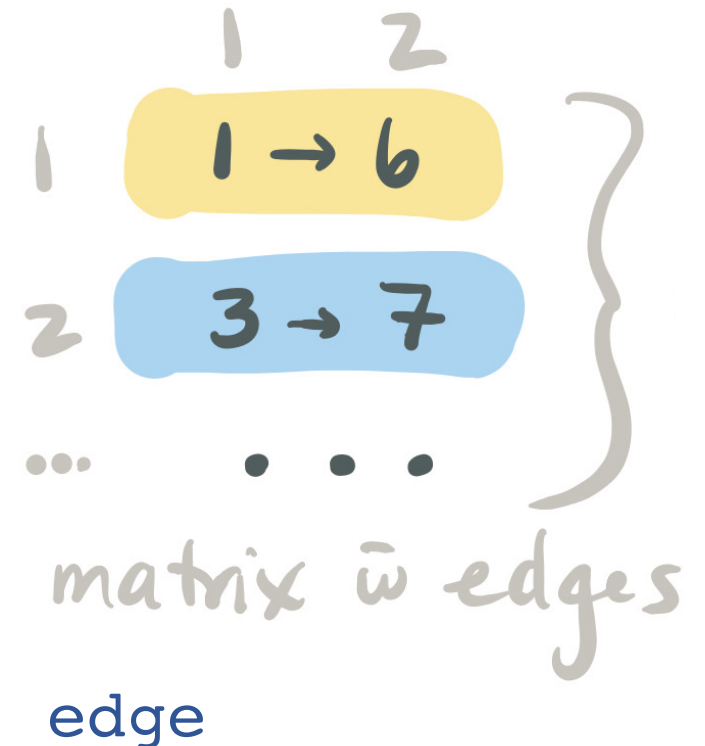
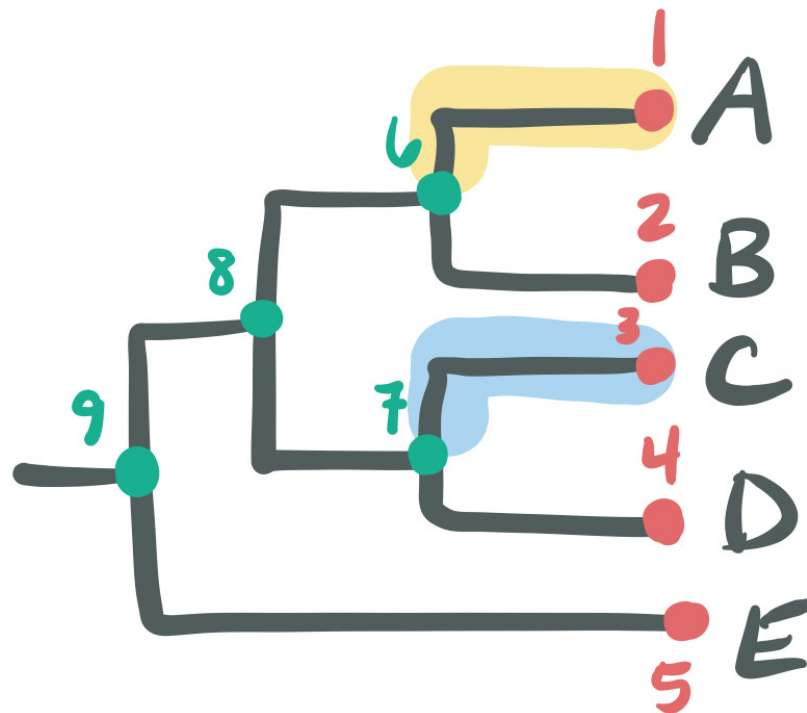
- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

Code to enter into R

`tree$edge`

R output:

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





# Phylo objects

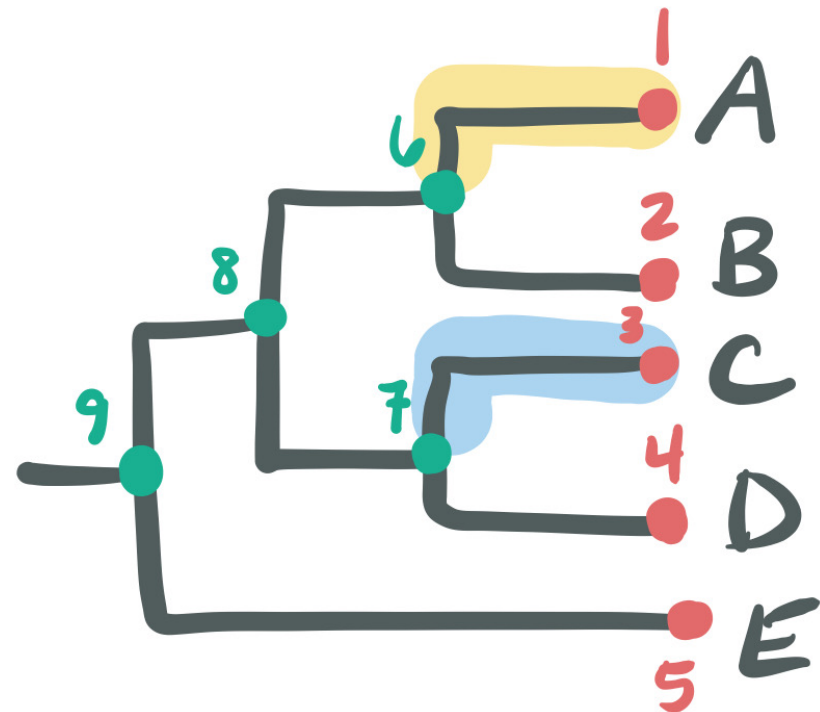
- A **phylo object** (*ape* package) is a standard R tree object and this is what *ggtree* also uses

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

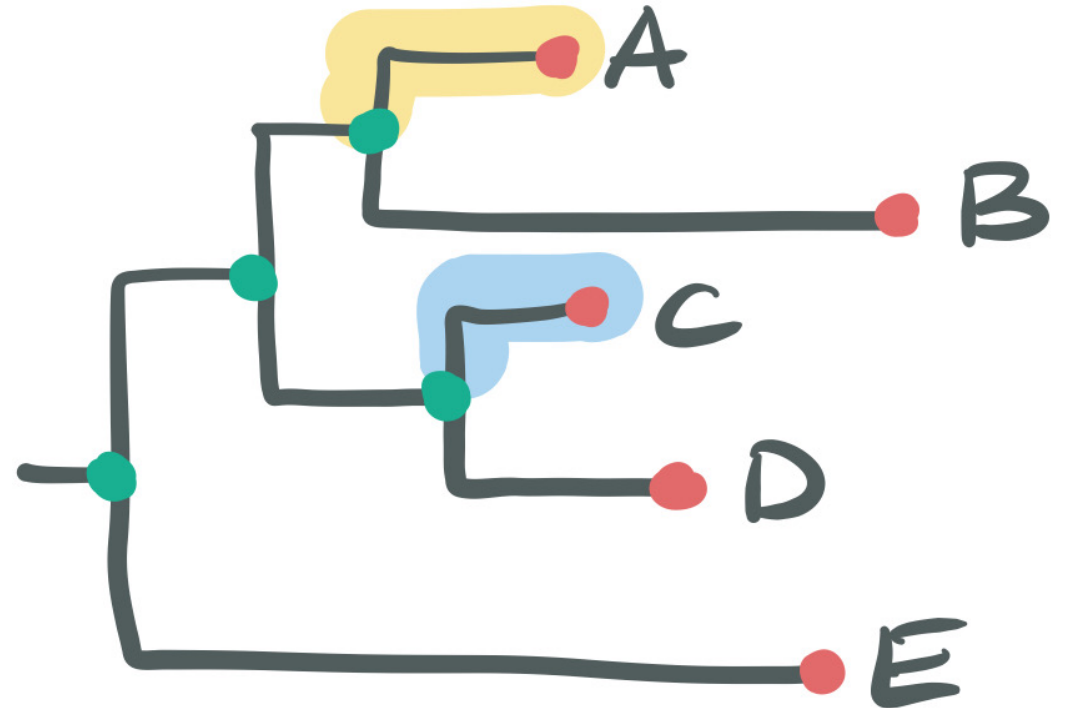
tip labels

branch lengths: `edge.length`

```
[1] 0.1 0.5 0.4 0.3 ...
```

support values: `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)

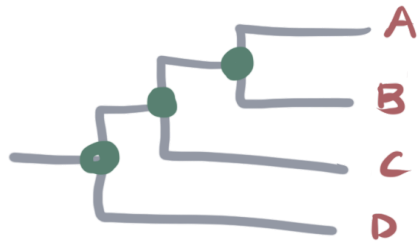
```
## List of 4
##      $ edge : int [1:38, 1:2] 21 22 23 24 24 23 25 26 27 27 ...
##      $ tip.label : chr [1:20] "t1" "t20" "t2" "t7" ...
##      $ edge.length: num [1:38] 0.0729 0.8743 0.1989 0.5346 0.1056 ...
##      $ Nnode : int 19
##      - attr(*, "class")= chr "phylo"
##      - attr(*, "order")=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

# Let's build a tree!



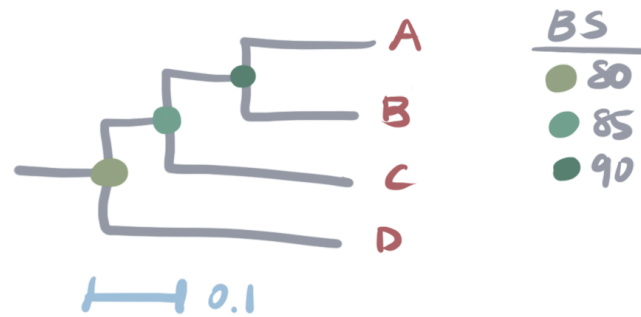
```
ggtree (phylo object)  
+ geom_tiplab( )
```

# Let's build a tree!



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

# Let's build a tree!



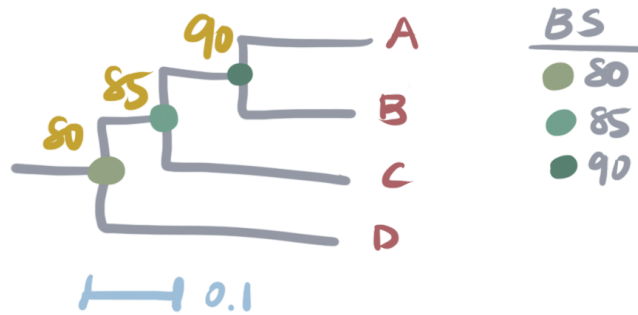
ggtree (phylo object)

+ geom\_tiplab (size = 0.5)

+ geom\_nodepoint (aes (color = bootstrap))

+ geom\_treescale ( )

# 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/>