

# PTRscripts Vignette

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Load the two necessary libraries for almost everything:

```
library(PTRscripts)
library(tidyverse)
```

## Phylogeny scripts

### Adding tips to trees

```
library(ape)
#> Warning: package 'ape' was built under R version 4.4.1
#>
#> Attaching package: 'ape'
#> The following object is masked from 'package:dplyr':
#>
#>     where

set.seed(1)
tree <- phytools::pbtrees(n=10,scale=1)

tree$tip.label <- LETTERS[ape::Ntip(tree):1]
# plot(tree)
```

### Adding single tips

```
par(mfrow=c(1,4))

tip_colors_orig <- tibble::tibble(tip = tree$tip.label, color = NA) %>%
  mutate(color = case_when(grepl("^N", tip) ~ "red",
                           tip == "C" ~ "green",
                           TRUE ~ "darkgreen"))

plot.phylo(tree,
  mar=c(0.1,0.1,1.1,0.1),
  cex=1.5,
  tip.color = tip_colors_orig$color)
title(main = paste0("original"), cex.main=1.5)
```

```

for(i in c(.2,.5,.8)){ # c(.1,.25,.5,.75,.9)
  tree_new1 <- add_cherry_to_tip(tree = tree,
                                tip = "C",
                                new_tips = "N1",
                                position = i)

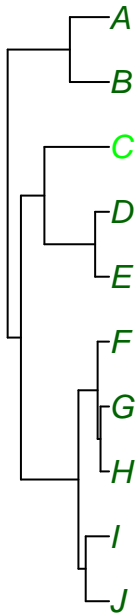
  # get colors
  tip_colors <- tibble::tibble(tip = tree_new1$tip.label, color = NA) %>%
    mutate(color = case_when(grepl("^N", tip) ~ "red",
                             tip == "C" ~ "green",
                             TRUE ~ "darkgreen"))

  plot.phylo(tree_new1,
             mar=c(0.1,0.1,1.1,0.1),
             cex=1.5,
             tip.color = tip_colors$color)

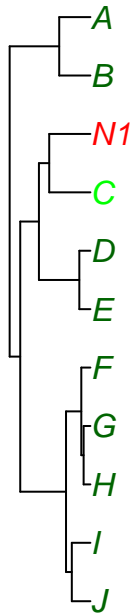
  title(main = paste0("pos.= ", i), cex.main=1.5)
}
#> [1] "Added the following 1 tip label(s):"
#> [1] "N1"
#> [1] "Added the following 1 tip label(s):"
#> [1] "N1"
#> [1] "Added the following 1 tip label(s):"
#> [1] "N1"

```

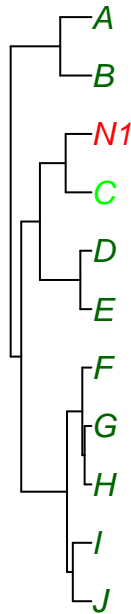
**original**



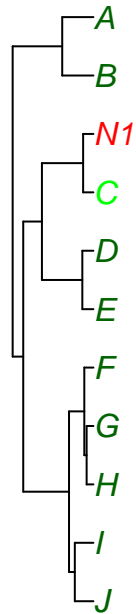
**pos.= 0.2**



**pos.= 0.5**



**pos.= 0.8**



```
par(mar=c(5.1,4.1,4.1,2.1))
```

### Adding multiple tips

```
par(mfrow=c(1,4))
plot.phylo(tree,
  mar=c(0.1,0.1,1.1,0.1),
  cex=1.5,
  tip.color = tip_colors_orig$color)
title(main = paste0("original"), cex.main=1.5)

i=.5
for(i in c(.2,.5,.8)){ # c(.1,.25,.5,.75,.9)
  tree_new1 <- add_cherry_to_tip(tree = tree,
    tip = "C",
    new_tips = c("N1", "N2", "N3", "N4"),
    position = i)

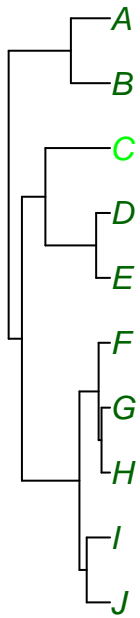
  # get colors
  tip_colors <- tibble::tibble(tip = tree_new1$tip.label, color = NA) %>%
    mutate(color = case_when(grepl("^N", tip) ~ "red",
      tip == "C" ~ "green",
      TRUE ~ "darkgreen"))

  plot.phylo(tree_new1,
    mar=c(0.1,0.1,1.1,0.1),
    cex=1.5,
    tip.color = tip_colors$color)

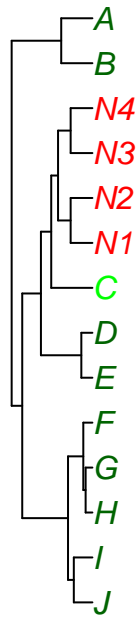
  title(main = paste0("pos.= ", i), cex.main=1.5)
}

#> [1] "Added the following 4 tip label(s):"
#> [1] "N1" "N2" "N3" "N4"
#> [1] "Added the following 4 tip label(s):"
#> [1] "N1" "N2" "N3" "N4"
#> [1] "Added the following 4 tip label(s):"
#> [1] "N1" "N2" "N3" "N4"
```

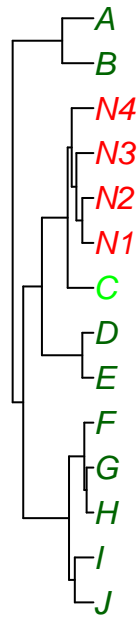
original



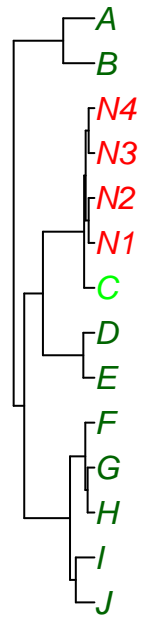
pos.= 0.2



pos.= 0.5



pos.= 0.8



```
par(mar=c(5.1,4.1,4.1,2.1))
```