# PTRscripts Vignette

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Load the two necessary libraries for almost everything:	
library(PTRscripts) library(tidyverse)	

### General scripts

### Adding leading zeros

### Create empty tibble

```
<dbl> <dbl> <dbl> <dbl>
#>
   1
              NA
        NA
                    NA
#> 2
        NA
              NA
#> 3
              NA
        NA
                   NA
#> 4
              NA
        NA
                   NA
#> 5
        NA
              NA
                    NA
#> 6
        NA
              NA
                    NA
#> 7
              NA
        NA
                    NA
#> 8
        NA
              NA
                   NA
#> 9
              NA
        NA
                    NA
#> 10
        NA
              NA
                    NA
\# empty tibble with 100 rows and factor columns
empty_tibble(nrow = 10,
            names = c("col1", "col2", "col3"),
            type = "factor")
#> # A tibble: 10 x 3
     col1 col2 col3
#>
     <fct> <fct> <fct>
#> 1 <NA> <NA> <NA>
#> 2 <NA>
           <NA>
                 <NA>
                <NA>
#> 3 <NA>
           <NA>
#> 4 <NA> <NA> <NA>
#> 5 <NA> <NA> <NA>
#> 6 <NA>
           <NA> <NA>
#> 7 <NA> <NA> <NA>
#> 8 <NA> <NA> <NA>
#> 9 <NA> <NA> <NA>
#> 10 <NA> <NA> <NA>
```

#### Show loop progress in percent

```
n = 100
for(i in 1:n){
  print_progress(i, n)
}
#> 1%... 2%... 3%... 4%... 5%... 6%... 7%... 8%... 9%... 10%... 11%... 12%... 13%... 14%... 15%... 16%
```

## Phylogeny scripts

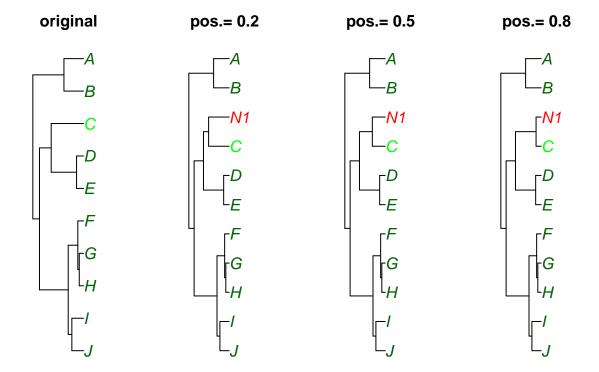
#### Adding tips to trees

```
#library(ape)
#library(phytools)
set.seed(1)
tree <- phytools::pbtree(n=10,scale=1)

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

#### Adding single tips

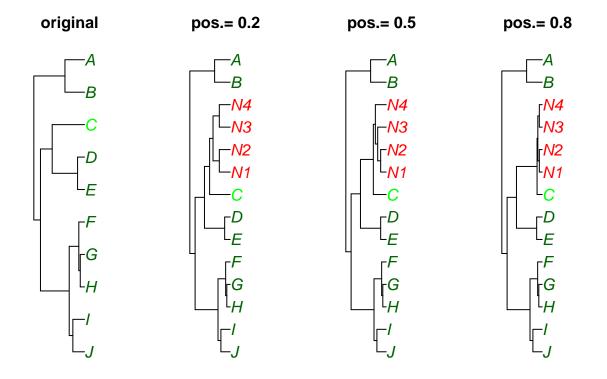
```
# library(tibble)
par(mfrow=c(1,4))
tip_colors_orig <- tibble::tibble(tip = tree$tip.label, color = NA) %>%
  mutate(color = case_when(grepl("^N", tip) ~ "red",
                           tip == "C" ~ "green",
                           TRUE ~ "darkgreen"))
ape::plot.phylo(tree,
                mar=c(0.1,0.1,1.1,0.1),
                cex=1.5,
                tip.color = tip_colors_orig$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,</pre>
                                 tip = "C",
                                 new_tips = "N1",
                                 position = i)
  # get colors
  tip_colors <- tibble::tibble(tip = tree_new1$tip.label, color = NA) %>%
    mutate(color = case_when(grepl("^N", tip) ~ "red",
                             tip == "C" ~ "green",
                             TRUE ~ "darkgreen"))
  ape::plot.phylo(tree_new1,
                  mar=c(0.1,0.1,1.1,0.1),
                  cex=1.5,
                  tip.color = tip_colors$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"
```



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

#### Adding multiple tips

```
par(mfrow=c(1,4))
ape::plot.phylo(tree,
                mar=c(0.1,0.1,1.1,0.1),
                cex=1.5,
                tip.color = tip_colors_orig$color)
title(main = paste0("original"), cex.main=1.5)
i=.5
for(i in c(.2,.5,.8)){ # c(.1,.25,.5,.75,.9)
  tree_new1 <- add_cherry_to_tip(tree = tree,</pre>
                                 tip = "C",
                                 new_tips = c("N1", "N2", "N3", "N4"),
                                 position = i)
  # get colors
  tip_colors <- tibble::tibble(tip = tree_new1$tip.label, color = NA) %>%
    mutate(color = case_when(grepl("^N", tip) ~ "red",
                             tip == "C" ~ "green",
                             TRUE ~ "darkgreen"))
  ape::plot.phylo(tree_new1,
```



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