

# PTRscripts Vignette

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## Installation

```
install_github("Peter-T-Ruehr/misc_R_scripts")
```

Load the two necessary libraries for almost everything:

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

## General scripts

### Adding leading zeros

```
# add leading zeros to numbers
add_leading_zeros(numbers = c(1, 2, 3),
                  length = 4)
#> [1] "0001" "0002" "0003"

# add leading zeros to characters
add_leading_zeros(numbers = c("01", "2", "003"),
                  length = 4)
#> [1] "0001" "0002" "0003"
```

### Create empty tibble

```
# empty tibble with zero rows and character columns
empty_tibble(nrow = 0,
             names = c("col1", "col2", "col3"),
             type = "character")
#> # A tibble: 0 x 3
#> #   i 3 variables: col1 <chr>, col2 <chr>, col3 <chr>
```

```

# empty tibble with three rows and numeric columns
empty_tibble(nrow = 3,
              names = c("col1", "col2", "col3"),
              type = "number")

#> # A tibble: 3 x 3
#>   col1 col2 col3
#>   <dbl> <dbl> <dbl>
#> 1    NA    NA    NA
#> 2    NA    NA    NA
#> 3    NA    NA    NA

# empty tibble with five rows and factor columns
empty_tibble(nrow = 5,
              names = c("col1", "col2", "col3"),
              type = "factor")

#> # A tibble: 5 x 3
#>   col1 col2 col3
#>   <fct> <fct> <fct>
#> 1 <NA> <NA> <NA>
#> 2 <NA> <NA> <NA>
#> 3 <NA> <NA> <NA>
#> 4 <NA> <NA> <NA>
#> 5 <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)

```

### 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,
                                tip = "C",
                                new_tips = "N1",
                                position = i)

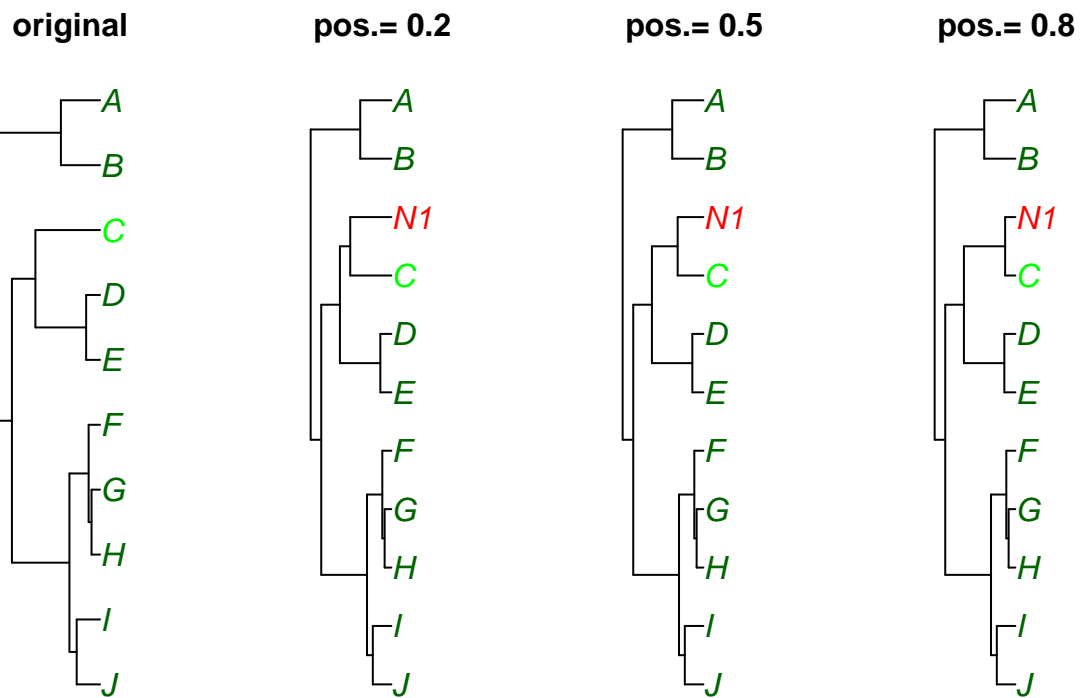
  # get colors
  tip_colors <- tibble::tibble(tip = tree_new1$tip.label, color = NA) %>%
    mutate(color = case_when(grepl("^N", tip) ~ "red",
                             tip == "C" ~ "green",
                             TRUE ~ "darkgreen"))

  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,
    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"))

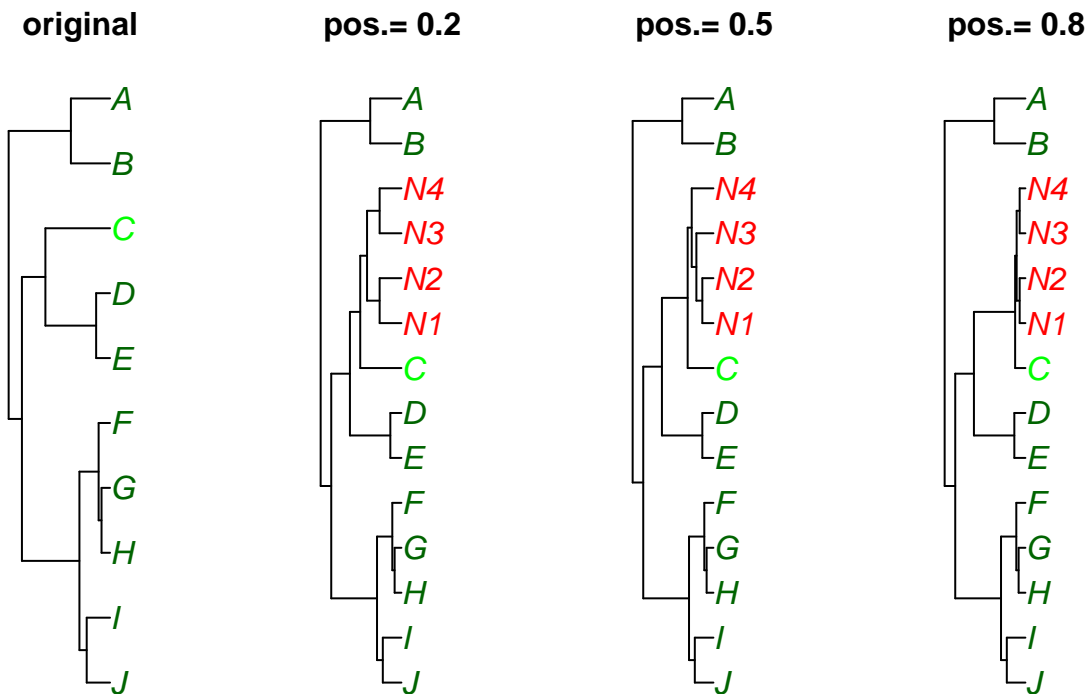
  ape::plot.phylo(tree_new1,
```

```

        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"

```



```

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

```