

## Phylogenetic placement visualization with treeio-ggtree method

## 0.1 Utility to explore the placement uncertainty

```
# Required packages
library(ggplot2)
library(treeio)
library(ggtree)
library(jsonlite)
library(dplyr)
library(reshape2)
library(ggtreeExtra)
library(aplot)
library(patchwork)

# Read jplace
jtree <- fromJSON("../exampledata/subtree/pplacer_Amt_subtree.jplace")
phylo <- treeio::jplace_treetext_to_phylo(jtree$tree)
placements <- treeio::extract.placement(jtree, phylo)
seq_name <- "saltern1"
sgplacement <- group_by(placements, .data$name) %>%
  filter(.data$name == seq_name)

tree1 <- as.treedata(phylo)
tree2 <- left_join(tree1, sgplacement, by="node")
p1 <- ggtree(tree2, layout = "circular", aes(color=like_weight_ratio)) +
  scale_color_continuous_sequential(palette = "Sunset", limits = c(0, 1)) +
  ggtitle(seq_name)

Amt_tiplabel <- read.csv(file = "../exampledata/subtree/Amt_tiplabel.csv",
  header = TRUE)
head(Amt_tiplabel)
```

```
##   node      tiplabel      Group
## 1     1 Asterochloris Trebouxiphyceae
## 2     2 Asterochloris Trebouxiphyceae
## 3     3      Coccomyxa Trebouxiphyceae
## 4     4 Stichococcus Trebouxiphyceae
## 5     5      Galdieria      Cyanidiales
## 6     6      Galdieria      Cyanidiales
```

```
taxon_groups <- c("Trebouxiphyceae", "Cyanidiales", "Non-Cyanidiales",
  "Chlamydomonadales", "Tetraselmis ssp.", "Pyramimonas ssp.",
  "Nephroselmis pyriformis CCMP717", "Bathycoccus ssp.",
  "Ostreococcus", "Mantoniella ssp.", "Micromonas ssp.",
  "Embryophyta")
Amt_tiplabel$Group <- factor(Amt_tiplabel$Group, levels=taxon_groups)
cols <- c("#FFC125", "#87CEFA", "#7B68EE", "#191970", "#800080",
  "#9ACD32", "#D15FEE", "#FFC0CB", "#EE6A50", "#8DEEEE",
  "#006400", "#800000", "#B0171F")

p2 <- p1<+>% Amt_tiplabel +
  geom_fruit(
    geom = geom_tile,
```

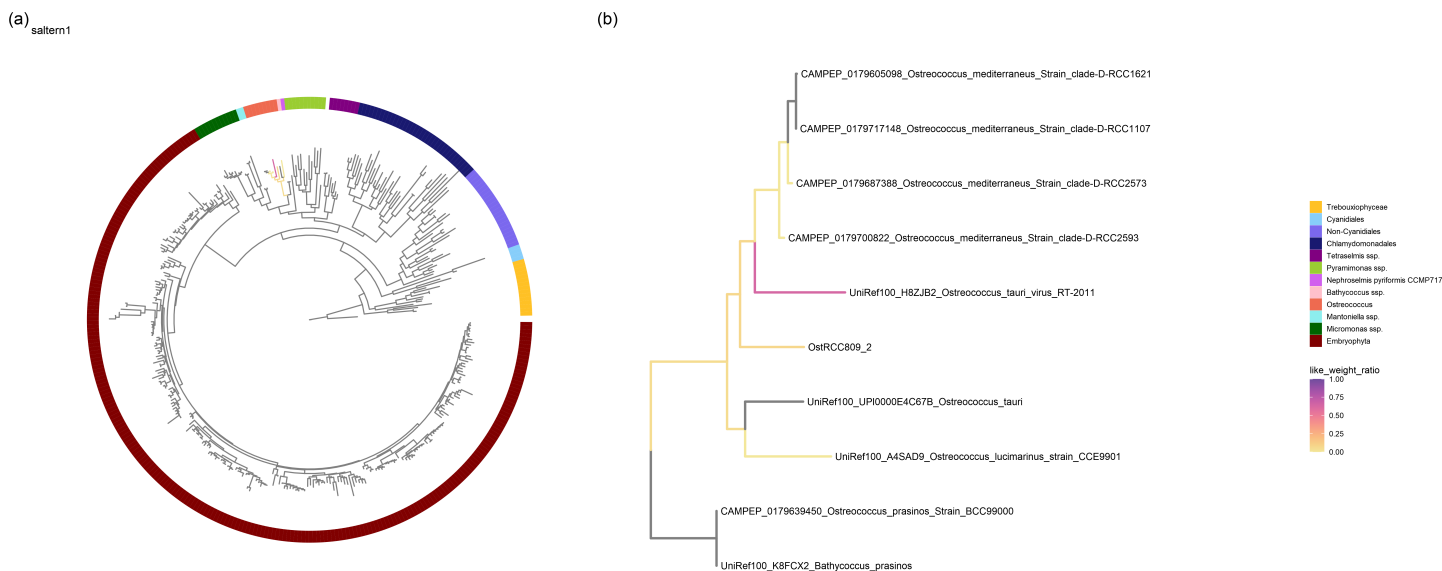
```

    mapping = aes(fill = Group),
    width = 0.2,
    offset = 0.01
  ) +
  scale_fill_manual(
    name = "",
    values = cols,
    guide = guide_legend(
      keywidth = 1,
      keyheight = 1,
      order = 3
    ),
    na.translate = FALSE
  )

# viewClade(p1,659) # viewClade
tree3 <- tree_subset(tree2, node=657, levels_back=0)
p3 <- ggtree(tree3,layout = "rect",aes(color=like_weight_ratio),size=1) +
  scale_color_continuous_sequential(palette = "Sunset",limits =c(0, 1)) +
  geom_tiplab(size=4,color="black",offset = 0.01) + xlim(0,2)

plot_list(p2, p3, tag_levels = list(c('(a)', '(b)'), '1'), guides = 'collect',
  nrow = 1,tag_size = 20)

```



## 0.2 Merge placement information to the placement tree

### # Required packages

```

library(treeio)
library(ggtree)
library(ggplot2)
library(ggtreeExtra)
library(colorspace)
library(dplyr)
library(patchwork)

```

```

tree1 <- read.jplace(file = "../exampledata/Mitsi/rsbl20190182supp2.jplace")
tree2 <- read.tree(file = "../exampledata/Mitsi/rsbl20190182supp7.tre")
tree2 <- as.treedata(tree2)

p1 <- ggtree(tree1,layout = "circular",aes(color=nplace,size=nplace)) +
  scale_color_viridis_c(option="viridis",limit=c(0.1,120)) +
  scale_size_continuous(range=c(0, 2))

# Extract placement informations
pla <- get.placements(tree1)

# merge placement data onto best-hit tree
#pla$label <- unlist(lapply(pla$name,function(x){paste("QUERY_",x,sep = "_")}))
pla$label <- pla$name
pla2 <- select(pla,c("name","label", "likelihood","like_weight_ratio"))
tree3 <- as_tibble(tree2)
tree4 <- left_join(tree3,pla2,by="label",)

tree4$group <- gsub("_1","",tree4$label)
tree4$group <- gsub("_2","",tree4$group)
tree4$group <- lapply(tree4$group,function(x){unlist(strsplit(x,"_"))[c(2)]})
tree4$group <- gsub("Rhabditophora","Bothrioplana_semperi",tree4$group)
s_group <- c("Catenulida","Polycladida","Macrostomorpha","Prorhynchidae",
  "Proseriata","Rhabdocoela","Bothrioplana_semperi","Fecampiidae",
  "Tricladida","Prolecithophora","Monogenea","Trematoda","Cestoda")
otu_group <- unlist(list(tree4[grepl("^OTU.",tree4$group),"group"]))
all_group <- c(s_group,otu_group)
tree4[!(tree4$group %in% all_group),"group"] <- "Outgroup"
tree4[seq(193,201),"group"] <- "Prorhynchidae"
tree4[seq(249,252),"group"] <- "Fecampiidae"
tree4[seq(169,171),"group"] <- "Gnosonesimidae"
tree4[seq(119,121),"group"] <- "Clade 1"
tree4[seq(174,192),"group"] <- "Clade 2"
s_group2 <- c("Trematoda","Cestoda","Monogenea",
  "Prolecithophora","Tricladida","Fecampiidae",
  "Bothrioplana_semperi","Rhabdocoela","Proseriata","Prorhynchidae",
  "Clade 2","Gnosonesimidae","Macrostomorpha","Polycladida",
  "Clade 1","Catenulida","Outgroup")
tree4[is.na(tree4$label),"group"] <- NA
tree4$group <- factor(tree4$group, levels=s_group2)
tree4[is.na(tree4$like_weight_ratio),"like_weight_ratio"] <- 0

tree5 <- as.treedata(tree4)

# tree5 <- root(tree5,node=572)
p2<- ggtree(tree5,
  layout = "circular",
  # branch.length = "none",

) + geom_tree(
  aes(
    color=like_weight_ratio,
    size=like_weight_ratio
  )
) +
  # geom_tiplab(size=2,offset=0.02,align=TRUE) +
  scale_color_continuous_sequential(palette = "Sunset", limits=c(0.000001, 0.2)) +
  scale_size_continuous(range=c(0, 1.5)) +

```

```
geom_tiplab2(data=td_filter(like_weight_ratio > 0),align=TRUE,size=3,offset=0.1)

p3 <- scaleClade(p2,
  node=c(MRCA(tree5,"SA_OTU14871","SA_OTU158753")),
  scale=5)
p4 <- scaleClade(p3,
  node=c(MRCA(tree5,"SA_OTU22294","SA_OTU9482")),
  scale=5)

# Annotate Group Labels
#ggtree(tree5) + geom_text2(aes(x=branch,label=node))

p5 <- p4 +
  geom_fruit(geom = geom_tile,
    mapping = aes(fill = group),
    width = 0.1,
    offset = 0.01)

p5
```

