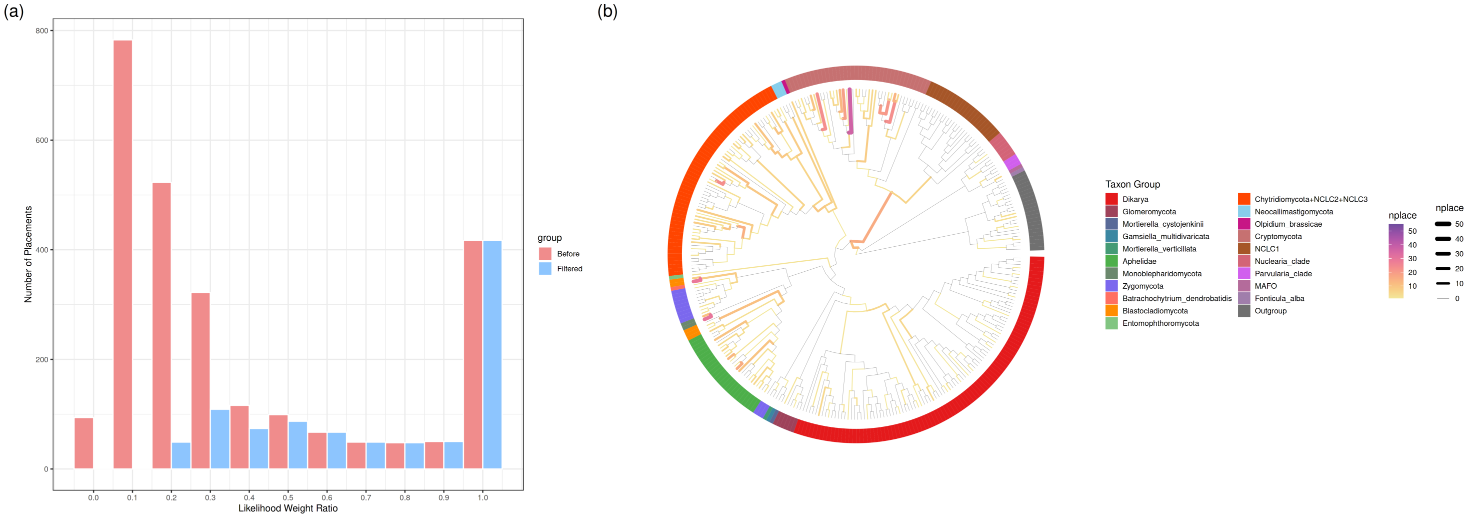
Supplemental File of

Phylogenetic placement visualization with treeio-ggtree method

0.1 Favorable placement filtration after parsing jplace file

```r
# Required packages
library(treeio)
library(ggtree)
library(jsonlite)
library(dplyr)
library(ggtreeExtra)
library(RColorBrewer)
library(colorspace)
library(ggplot2)
library(aplot)

# Read jplace file
jtree <- jsonlite::fromJSON("../exampledata/Holomycota/HolomycotaV4_alignedtrim.jplace")

# Convert jplace to phylo object
phylo <- treeio:::jplace_treetext_to_phylo(jtree$tree)

# Extract placement information from jplace object
placements <- treeio:::extract.placement(jtree, phylo)

# Filter placements, selecting the maximum like_weight_ratio for each sequence
filtered_placements <- dplyr::group_by(placements, .data$name) %>%
    filter(.data$like_weight_ratio == max(.data$like_weight_ratio))

# Create a data frame to store the group and corresponding likelihood weight ratios
dat <- data.frame(
    group = c(rep("Before", length(placements$like_weight_ratio)), rep("Filtered", length(filtered_placements$l
    likelihood_weight_ratio = c(placements$like_weight_ratio, filtered_placements$like_weight_ratio)
)

# Plot the distribution of likelihood weight ratios using a histogram with ggplot2
p1 <- ggplot(data = dat, aes(x = likelihood_weight_ratio)) +
    geom_histogram(data = dat, aes(x = likelihood_weight_ratio, fill = group, ..count..), position = position_d
    scale_fill_manual(values = c("#f08c8c", "#8dc5fe")) +
    labs(y = "Number of Placements", x = "Likelihood Weight Ratio") +
    scale_x_continuous(breaks = c(seq(0, 1, 0.1))) +
    theme_bw()

# Convert phylo object to treedata object
tree1 <- treeio::as.treedata(phylo)

# Convert treedata to tibble
td <- dplyr::as_tibble(tree1)

# Calculate the number of placements per node and merge with original data
tree1@data <- dplyr::group_by(filtered_placements, .data$node) %>%
    dplyr::summarize(nplace = n()) %>%
    dplyr::full_join(td, by = 'node') %>%
    dplyr::mutate(nplace = ifelse(is.na(.data$nplace), 0, .data$nplace))

# Use ggtree to plot a circular tree, adjusting node color and size based on the number of placements
p2 <- ggtree::ggtree(tree1, layout = "circular", branch.length = "none", aes(color = nplace, size = nplace)) +
    colorspace::scale_color_continuous_sequential(palette = "Sunset", limits = c(1, 55)) +
    scale_size_continuous(range = c(0.1, 2), limits = c(0, 55),
        guide = guide_legend(reverse = TRUE)) +
    theme(
        legend.position = "right",
        legend.box = "horizontal",
        legend.box.just = "left"
    )

# Read group information from CSV file
V4_group <- read.csv(file = "../exampledata/Holomycota/V4_group.csv")

# Define color palette
cols <- c(
  "#E41A1C",
  "#9E425A",
  "#596A98",
  "#3B87A2",
  "#449B75",
  "#4DAF4A",
  "#6B886D",
  "#7B68EE",
  "#FF6F61",
  "#FF8C00",
  "#81c581",
  "#FF4500",
  "#87CEEB",
  "#C71585",
  "#C67171",
  "#A65628",
  "#D36477",
  "#D15FEE",
  "#B46B9B",
  "#A07EAB",
  "#707070"
)

# Get unique levels of the group and reverse the order
levels <- rev(unique(V4_group$group))

# Use ggtree and ggtreeExtra to draw the plot with group information
p3 <- p2 %<+% V4_group +
    ggtreeExtra::geom_fruit(
        geom = geom_tile,
        mapping = aes(fill = factor(group, levels = levels)),
        width = 2,
        offset = 0.1
    ) +
    scale_fill_manual(
        name = "Taxon Group",
        values = cols,
        guide = guide_legend(
            keywidth = 1,
            keyheight = 1,
            order = 3
        ),
        na.translate = FALSE
    )

# Combine p1 and p3 into a single plot and add labels
aplot::plot_list(p1, p3, tag_levels = list(c('(a)', '(b)', '(c)', '(d)'), '1'),
tag_size = 20)
```



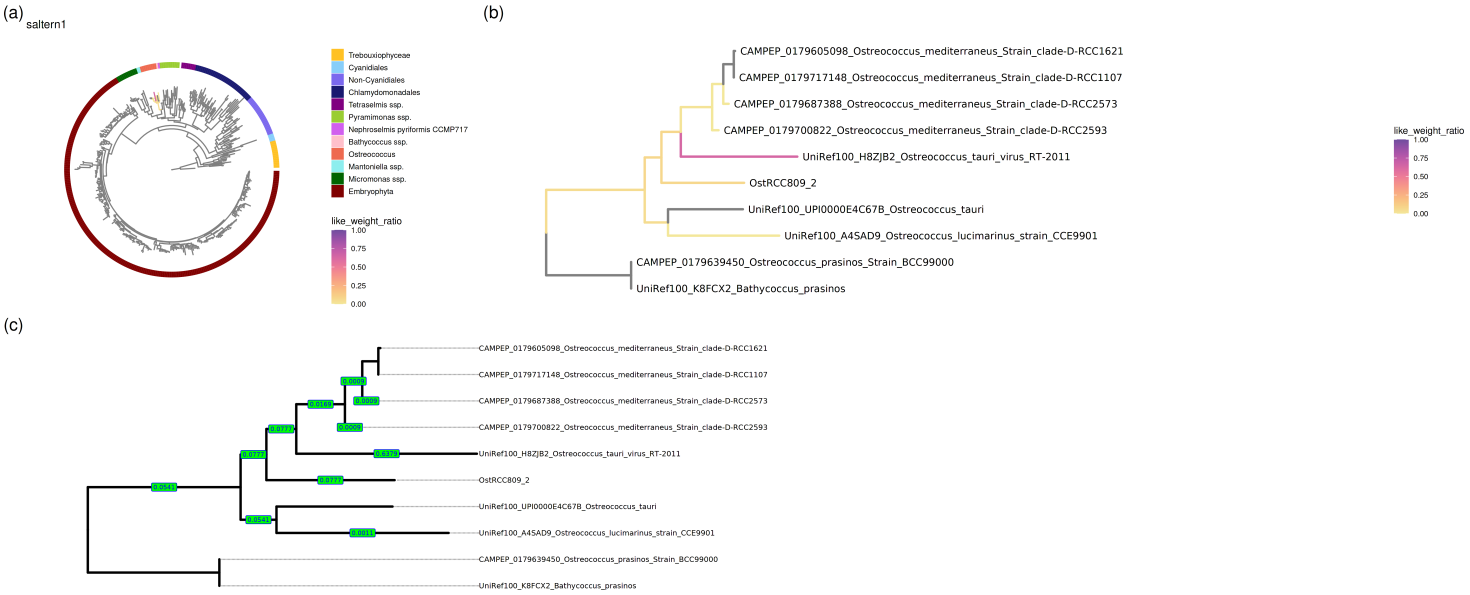
0.2 Utility to explore the placement uncertainty

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

# Read jplace file containing tree data
jtree <- jsonlite::fromJSON("../exampledata/subtree/pplacer_Amt_subtree.jplace")

# Convert jplace  to phylo object
phylo <- treeio:::jplace_treetext_to_phylo(jtree$tree)

# Extract placement information from the jplace object
placements <- treeio:::extract.placement(jtree, phylo)

# Specify the sequence name of interest
seq_name <- "saltern1"

# Filter placements to keep only those matching the specified sequence name
sgplacement <- dplyr::group_by(placements, .data$name) %>%
    dplyr::filter(.data$name == seq_name)

# Convert phylo object to treedata format
tree1 <- treeio::as.treedata(phylo)

# Join filtered placements with the tree data by node
tree2 <- dplyr::left_join(tree1, sgplacement, by = "node")

# Plot a circular tree using ggtree, colored by likelihood weight ratio
p1 <- ggtree::ggtree(tree2, layout = "circular", aes(color = like_weight_ratio)) +
    colorspace::scale_color_continuous_sequential(palette = "Sunset", limits = c(0, 1)) +
    ggtitle(seq_name)

# Read taxon label data from CSV file
Amt_tiplabel <- read.csv(file = "../exampledata/subtree/Amt_tiplabel.csv", header = TRUE)
```

```r
# Display the first few rows of the taxon label data
head(Amt_tiplabel)
```

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

```r
# Define the taxon groups for categorization
taxon_groups <- c("Trebouxiophyceae", "Cyanidiales", "Non-Cyanidiales",
                  "Chlamydomonadales", "Tetraselmis ssp.", "Pyramimonas ssp.",
                  "Nephroselmis pyriformis CCMP717", "Bathycoccus ssp.",
                  "Ostreococcus", "Mantoniella ssp.", "Micromonas ssp.",
                  "Embryophyta")

# Convert Group column to a factor with specified levels
Amt_tiplabel$Group <- factor(Amt_tiplabel$Group, levels = taxon_groups)

# Define color palette for the groups
cols <- c("#FFC125", "#87CEFA", "#7B68EE", "#191970", "#800080",
          "#9ACD32", "#D15FEE", "#FFC0CB", "#EE6A50", "#8DEEEE",
          "#006400", "#800000", "#B0171F")

# Add group information to the tree plot p1
p2 <- p1 %<+% Amt_tiplabel +
    ggtreeExtra::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
    )

# Note: viewClade is not applicable for circular trees
# Create a subset of the tree for a specific node
tree3 <- tidytree::tree_subset(tree2, node = 657, levels_back = 0)

# Plot the subsetted tree using a rectangular layout, colored by likelihood weight ratio
p3 <- ggtree::ggtree(tree3, layout = "rect", aes(color = like_weight_ratio), size = 1) +
    colorspace::scale_color_continuous_sequential(palette = "Sunset", limits = c(0, 1)) +
    geom_tiplab(size = 4, color = "black", offset = 0.01) +
    xlim(0, 2)

# Set options to avoid scientific notation in plot labels
options(scipen = 200)

# Round the likelihood weight ratio values and convert them to character for labeling
tree3@extraInfo[, 5] <- tree3@extraInfo[, 5] |>
    as.vector() |>
    unlist() |>
    as.numeric() |>
    round(digits = 4) |>
    as.character()

# Plot the subsetted tree with additional labels and adjustments
p4 <- ggtree(tree3, layout = "rect", size = 1) +
    colorspace::scale_color_continuous_sequential(palette = "Sunset", limits = c(0, 1)) +
    geom_tiplab(size = 3, color = "black", align = TRUE, offset = 0) +
    xlim(0, 2) +
    geom_label2(aes(x = branch, label = like_weight_ratio), color = 'blue', fill = "green", size = 2.5)

# Combine the plots p2, p3, and p4 into a single multi-panel plot
aplot::plot_list(p2, p3, p4, ncol = 2, nrow = 2,
          tag_levels = list(c('(a)', '(b)', '(c)')),
          tag_size = 20, design = "ABBB\nABBB\nCCCC\nCCCC")
```

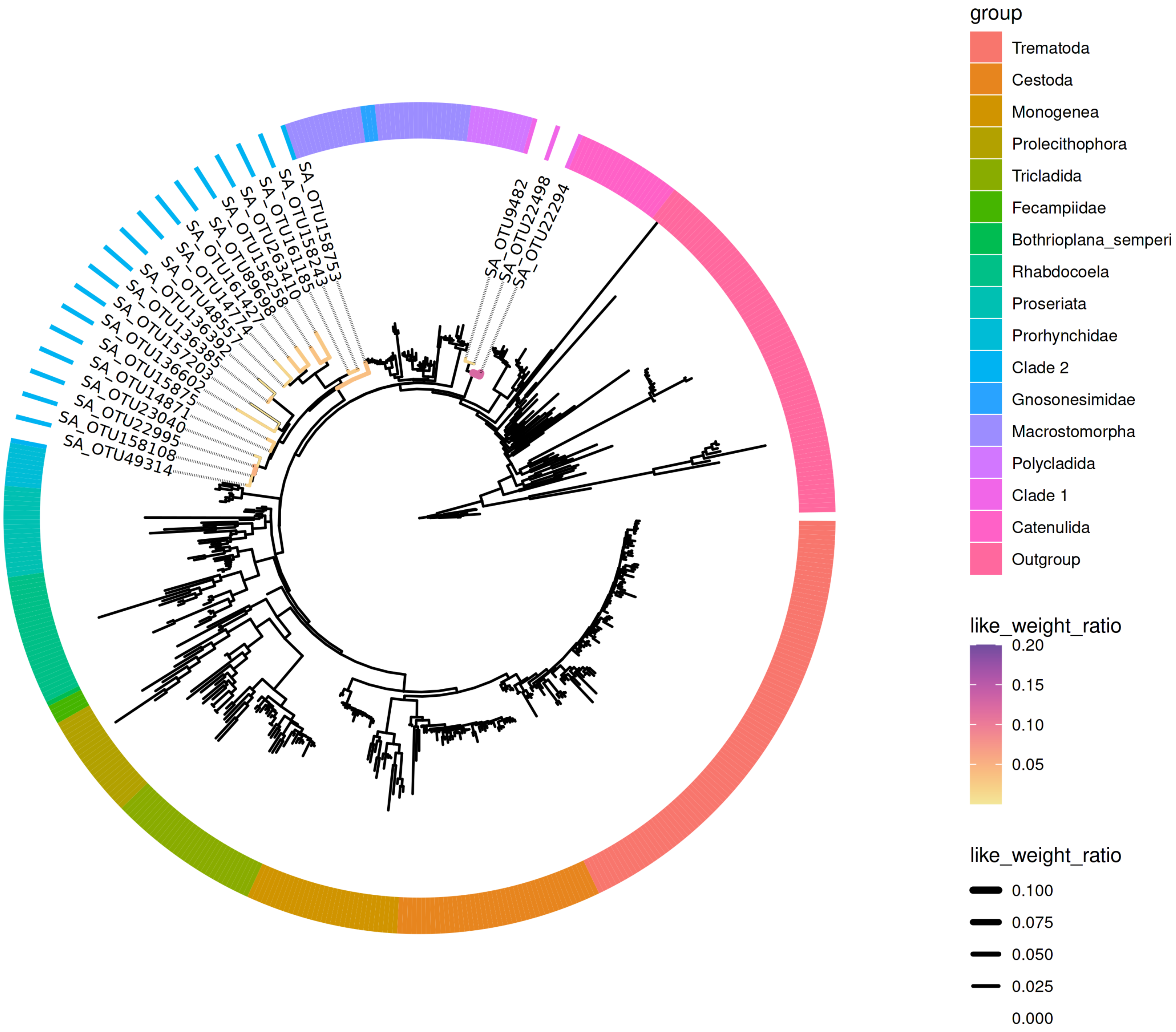

(a)
saltern1
Trebouxiophyceae
Cyanidiales
Non-Cyanidiales
Chlamydomonadales
Tetraselmis ssp.
Pyramimonas ssp.
Nephroselmis pyriformis CCMP717
Bathycoccus ssp.
Ostreococcus
Mantoniella ssp.
Micromonas ssp.
Embryophyta
like_weight_ratio
1.00
0.75
0.50
0.25
0.00
(b)
CAMPEP_0179605098_Ostreococcus_mediterraneus_Strain_clade-D-RCC1621
CAMPEP_0179717148_Ostreococcus_mediterraneus_Strain_clade-D-RCC1107
CAMPEP_0179687388_Ostreococcus_mediterraneus_Strain_clade-D-RCC2573
CAMPEP_0179700822_Ostreococcus_mediterraneus_Strain_clade-D-RCC2593
UniRef100_H8ZJB2_Ostreococcus_tauri_virus_RT-2011
OstRCC809_2
UniRef100_UPI0000E4C67B_Ostreococcus_tauri
UniRef100_A4SAD9_Ostreococcus_lucimarinus_strain_CCE9901
CAMPEP_0179639450_Ostreococcus_prasinos_Strain_BCC99000
UniRef100_K8FCX2_Bathycoccus_prasinos
like_weight_ratio
1.00
0.75
0.50
0.25
0.00
(c)
CAMPEP_0179605098_Ostreococcus_mediterraneus_Strain_clade-D-RCC1621
CAMPEP_0179717148_Ostreococcus_mediterraneus_Strain_clade-D-RCC1107
0.0009
CAMPEP_0179687388_Ostreococcus_mediterraneus_Strain_clade-D-RCC2573
0.0169
0.0009
CAMPEP_0179700822_Ostreococcus_mediterraneus_Strain_clade-D-RCC2593
0.0777
0.0009
UniRef100_H8ZJB2_Ostreococcus_tauri_virus_RT-2011
0.0777
0.6379
OstRCC809_2
0.0541
0.0777
UniRef100_UPI0000E4C67B_Ostreococcus_tauri
0.0541
UniRef100_A4SAD9_Ostreococcus_lucimarinus_strain_CCE9901
0.0011
CAMPEP_0179639450_Ostreococcus_prasinos_Strain_BCC99000
UniRef100_K8FCX2_Bathycoccus_prasinos

0.3 Merge placement information to the placement tree

```
# Required packages

library(treeio)
library(ggtree)
library(ggplot2)
library(ggtreeExtra)
library(colorspace)
library(dplyr)
library(patchwork)
# Read jplace file containing placement data for the phylogenetic tree
tree1 <- treeio::read.jplace(file = "../exampledata/Mitsi/rsbl20190182supp2.jplace")

# Read Newick formatted tree file and convert to treedata format
tree2 <- ggtree::read.tree(file = "../exampledata/Mitsi/rsbl20190182supp7.tre")
tree2 <- treeio::as.treedata(tree2)

# Create a circular tree plot with color and linewidth based on number of placements
p1 <- ggtree::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 information from the jplace tree
```

```r
pla <- treeio::get.placements(tree1)

pla$label <- pla$name
pla2 <- dplyr::select(pla, c("name", "label", "likelihood", "like_weight_ratio"))

# Convert tree2 to a tibble
tree3 <- dplyr::as_tibble(tree2)

# Merge the placement data (pla2) onto the tree data (tree3) using labels
tree4 <- dplyr::left_join(tree3, pla2, by = "label")

# Clean up group names by removing suffixes
tree4$group <- gsub("_1", "", tree4$label)
tree4$group <- gsub("_2", "", tree4$group)

# Extract the second element from the split group names
tree4$group <- lapply(tree4$group, function(x) { unlist(strsplit(x, "_"))[c(2)] })

# Rename specific groups for clarity
tree4$group <- gsub("Rhabditophora", "Bothrioplana_semperi", tree4$group)

# Define standard groups for categorization
s_group <- c("Catenulida", "Polycladida", "Macrostomorpha", "Prorhynchidae",
             "Proseriata", "Rhabdocoela", "Bothrioplana_semperi", "Fecampiidae",
             "Tricladida", "Prolecithophora", "Monogenea", "Trematoda", "Cestoda")

# Extract OTU groups from the data
otu_group <- unlist(list(tree4[grep("^OTU.", tree4$group), "group"]))
all_group <- c(s_group, otu_group)

# Assign "Outgroup" to other undefined groups
tree4[!(tree4$group %in% all_group), "group"] <- "Outgroup"

# Assign specific group names to certain row indices
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")

# Set groups that are NA to be NA
tree4[is.na(tree4$label), "group"] <- NA

# Convert the group column to a factor with specified levels
tree4$group <- factor(tree4$group, levels = s_group2)

# Assign a default value to NA likelihood weight ratios
tree4[is.na(tree4$like_weight_ratio), "like_weight_ratio"] <- 0

# Convert the modified tibble back to treedata format
tree5 <- treeio::as.treedata(tree4)

# Create a circular tree plot based on tree5 with specified aesthetics
```

```
p2 <- ggtree::ggtree(tree5, layout = "circular") +
    ggtree::geom_tree(
        aes(
            color = like_weight_ratio,  # Color branches based on likelihood weight ratio
            size = like_weight_ratio     # Size branches based on likelihood weight ratio
        )
    ) +
    colorspace::scale_color_continuous_sequential(palette = "Sunset", limits = c(0.000001, 0.2)) +  # Set color
    scale_size_continuous(range = c(0, 1.5), guide = guide_legend(reverse = TRUE)) +  # Scale size of branches
    ggtree::geom_tiplab2(data = td_filter(like_weight_ratio > 0), align = TRUE, size = 3, offset = 0.1)  # Labe

# Scale the clade for specific nodes
p3 <- ggtree::scaleClade(p2,
           node = c(MRCA(tree5, "SA_OTU14871", "SA_OTU158753")),
           scale = 5)

# Scale another clade for specific nodes
p4 <- ggtree::scaleClade(p3,
                 node = c(MRCA(tree5, "SA_OTU22294", "SA_OTU9482")),
                 scale = 5)

# Add a out-circle layer to the plot to represent group information with colored tiles
p5 <- p4 +
    ggtreeExtra::geom_fruit(geom = geom_tile,
               mapping = aes(fill = group),
               width = 0.1,
               offset = 0.01)

# Display the final plot
p5
```


SA_OTU158753
SA_OTU158243
SA_OTU161185
SA_OTU263410
SA_OTU158258
SA_OTU89698
SA_OTU161427
SA_OTU14774
SA_OTU48557
SA_OTU136392
SA_OTU136385
SA_OTU157203
SA_OTU136602
SA_OTU15875
SA_OTU14871
SA_OTU23040
SA_OTU22995
SA_OTU158108
SA_OTU49314
SA_OTU9482
SA_OTU22498
SA_OTU22294
group
Trematoda
Cestoda
Monogenea
Prolecithophora
Tricladida
Fecampiidae
Bothrioplana_semperi
Rhabdocoela
Proseriata
Prorhynchidae
Clade 2
Gnosonesimidae
Macrostomorpha
Polycladida
Clade 1
Catenulida
Outgroup
like_weight_ratio
0.20
0.15
0.10
0.05
like_weight_ratio
0.100
0.075
0.050
0.025
0.000