

# ggtreeExtra: Compact visualization of richly annotated phylogenetic data

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## 1 The purpose of development and overview

Integrating and visualizing associated data with a phylogenetic tree can help to find biological patterns and generate new hypotheses by interpreting the data in the evolutionary text. The associated data sets are heterogeneous (*e.g.* abundance of species, gene expression, taxonomy information of species, type and number of target genes and sampling information). Several tools have been developed to integrate and display associated data on a phylogenetic tree. However, only a few annotation layers and tree layouts are supported and most of the tools are designed for specific domains (Tab. S1). Here, we developed *ggtreeExtra* as an universal tool to annotate multi-dimensional data on the external panels of a phylogenetic tree (Fig. S1). It can link *ggtree* (Yu et al. 2017) and **geom** functions defined in *ggplot2* (Wickham 2016) or other *ggplot2* extensions. It supports most of the tree layouts defined in *ggtree* (Yu et al. 2017) before passing it to *ggtreeExtra* (Fig. S1). The *ggtreeExtra* package was developed based on the grammar of graphic (Wilkinson 2012) implemented in the *ggplot2* (Wickham 2016) package. Users can easily map variables (*e.g.* abundance of species, length of genome or sampling location) of associated data to aesthetic attributes (*e.g.* size, color and shape) for visualizing external geometric objects (*e.g.* bar, point or box plot) with a phylogenetic tree using *ggtreeExtra*. The details (such as the actual mapping of visual values, figure legends and plot appearance) of the graphic can be adjusted by corresponding *scale* or *theme* functions defined in *ggplot2* (Wickham 2016) (Fig. S1). Compared to other tools, *ggtreeExtra* supports more layouts and geometric layers for phylogenetic tree annotation. Making it more universal to handle data from different disciplines (Tab. S1 and Fig. S2).

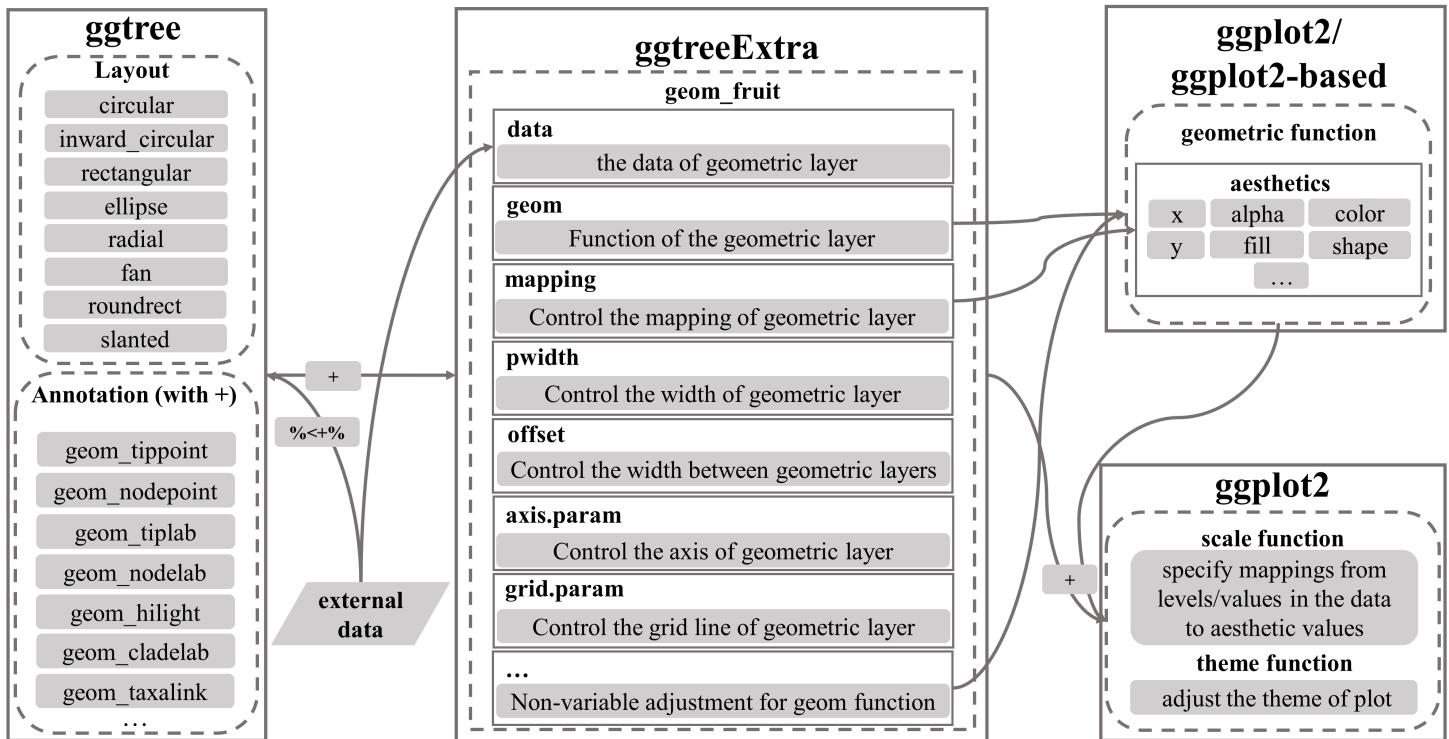


Fig. S1: Overview of the design of *ggtreeExtra* package.

Table S1: Comparing features in ggTreeExtra and other tools

Tool	Platform	Supported layouts for tree annotation <sup>1</sup>	Annotation layers	Layer combination <sup>2</sup>	Layer operation	Has a grammar	User interface
ggTreeExtra	R package	circular, inward circular, rectangular, slanted, ellipse, round rectangular, radial	Heat map, scatter, simple bar, patter bar, stacked bar, dodged bar, box, pattern box, violin, dot intervals plot, density plot, line plot, pie, image plot, insert plot	Yes	add modify delete	Yes	programming and command line
GraPhlAn	Python package	circular	Heat map, scatter, simple bar	Yes	add	No	command line with configure file
ETE3	Python package	rectangular	Heat map, scatter, simple bar, stacked bar, box, pie, image plot	Yes	add	No	programming and command line
iTOL	Web tool	circular, rectangular, slanted, ellipse, inward circular	Heat map, scatter, simple bar, stacked bar, dodged bar, box, pie, image plot	Yes	add	No	interactive (mouse click with configure file)
Micromreact	Web tool	circular, rectangular	Heat map, scatter	Yes	add	No	interactive (mouse click and command line with configure file)
Evolview	Web tool	circular, rectangular, slanted, round rectangular	Heat map, scatter, simple bar, stacked bar	Yes	add	No	interactive (mouse click with configure file)

<sup>1</sup> tree annotation: tree and data graphic alignment;

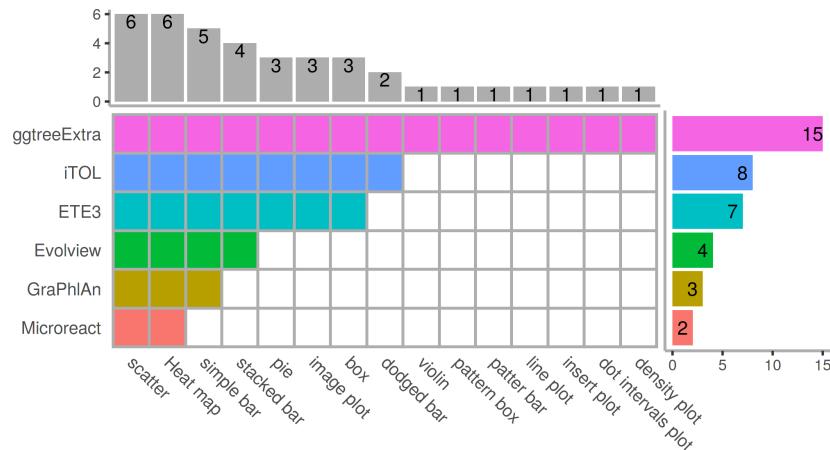
<sup>2</sup> Layer combination: whether layers listed in the 'Annotation layers' column can be combined freely.


Fig. S2: Visualization methods for tree annotation supported by different software tools.

## 2 Geometric layers supported by *geom\_fruit* of *ggtreeExtra*

The *ggtreeExtra* package is designed to link *ggtree* (Yu et al. 2017) and **geom** functions defined in *ggplot2* (Wickham 2016) and other *ggplot2* extension packages (Fig. S1). The *ggtreeExtra* package implemented a layer function, *geom\_fruit*, which can internally reorder associated data based on the structure of a phylogenetic tree, visualize the data using specific geometric layer function with user provided aesthetic mapping and non-variable setting and the graphic layer will be displayed on the external panel (right hand side for rectangular layout and outer ring for circular layout). Here is the list of the geometric layer functions which work seamlessly with the *geom\_fruit* function (Tab. S2). Each geometric layer function has its own unique geometric attributes (Tab. S2). Users can choose appropriate geometric layer functions according the type of the input data. The variables of the data can be mapped to visual attributes of the corresponding geometric layer function. For example, if user want to view the distribution and uncertainty (continuous data) of associated data in different groups (such as the gene expression or species abundance in different samples), several methods, including box, violin and density plot, can be used to display them (Fig. S3). For simple numeric data (e.g. length of genome, abundance of species), they can be visualized with simple (pattern) bar plot or grouped (pattern) bar plot. Specifically, pattern bar plot is efficient to visualize count data for different groups in grayscale (Fig. S4). Non-variable of aesthetic setting is also supported. With the development of the *ggplot2* community, *ggtreeExtra* supports more geometric layers compare other tools (Tab. S1 and Fig. S2). Until now, *ggtreeExtra* can integrate heat map, scatter plot, simple (grouped) (pattern) bar plot, simple (grouped) (pattern) box plot, violin, dot intervals plot, density plot, pie, image plot, insert plot (Tab. S1 and Fig. S2). Even though other tools might support similar graphic layers, *ggtreeExtra* is more powerful and flexible since it inherits all the features of the geometric functions. For example, *iTOL* (Letunic and Bork 2019), *Evolview* (Subramanian et al. 2019) and *ggtreeExtra* all support displaying image plot on the phylogenetic tree, but only *ggtreeExtra* supports mapping variable to color and scale the images (Fig. S5.B). In addition, subplots that describe statistical information of taxa can be embeded as inset in *ggtreeExtra* (Fig. S5.A). The data that used to generate Fig. S5.B is from Fig.1 of (Song et al. 2020) and it is available on github<sup>1</sup>. As the *ggplot2* (Wickham 2016) community keeps expanding, there will be more *geom* functions implemented in either *ggplot2* (Wickham 2016) or other extensions and *geom\_fruit* will gain more power to present data in future.

Table S2: List of geometric layers supported by 'geom\_fruit()'

Package	Geom layer	Visual characteristic	Description
ggdist	geom_dots	alpha, color, fill, size, shape	creates dotplots that automatically determines a bin width that ensures the plot fits within the available space
	geom_dotsinterval	alpha, color, fill, size, shape	creates dots, intervals, and quantile dotplots
	geom_pointinterval	alpha, color, fill, size, shape	creates point and multiple uncertainty interval
	geom_slab	alpha, color, fill	creates slab geom
	geom_slabinterval	alpha, color, fill	creates slab, point and interval meta-geom
ggimage	geom_image	alpha, color, size	visualizes image files
	geom_phylopic	alpha, color, size	queries image files from phylopic database and visualizes them
ggpattern	geom_bar_pattern	pattern_alpha, pattern_color, pattern_fill	draws bar charts with support for pattern fills
	geom_boxplot_pattern	pattern_alpha, alpha, color, fill	draws box and whiskers plot with support for pattern fills
	geom_col_pattern	pattern_alpha, pattern_color, pattern_fill	draws bar charts using 'stat_identity()' with support for pattern fills
	geom_tile_pattern	pattern_alpha, pattern_color, pattern_fill	draws rectangle by using the center of the tile and its size with support for pattern fills
	geom_bar	alpha, color, fill	draws bar charts
ggplot2	geom_boxplot	alpha, color, fill	draws box and whiskers plot
	geom_col	alpha, color, fill	draws bar charts using 'stat_identity()'
	geom_label	alpha, color, fill, size	draws a rectangle behind the text
	geom_point	alpha, color, fill, shape, size	creates scatterplots
	geom_raster	alpha, fill	a high performance special case for all the tiles are the same size
	geom_text	color, size	adds text to the plot
	geom_tile	alpha, color, fill	draws rectangle by using the center of the tile and its size
ggpmisc	geom_plot	vp.width, vp.height	ggplot objects an insets to the base ggplot, using syntax similar to that of 'geom_label'
	geom_table	size	adds a textual table directly to the ggplot, using syntax similar to that of 'geom_label'
ggrepel	geom_text_repel	color, size	adds text to the plot. The text labels repel away from each other and away from the data points
	geom_label_repel	alpha, color, fill, size	draws a rectangle underneath the text. The text labels repel away from each other and away from the data points
ggridges	geom_density_ridges	alpha, fill	arranges multiple density plots in a staggered fashion
	geom_density_ridges2	alpha, fill	arranges multiple density plots in a staggered fashion
	geom_ridgeline	alpha, color, fill	plots the sum of the 'y' and 'height' aesthetics versus 'x', filling the area between 'y' and 'y + height' with a color
	geom_ridgeline_gradient	color, fill	works just like 'geom_ridgeline' except that the 'fill' aesthetic can vary along the x axis
gstance	geom_barh	alpha, color, fill	horizontal version of 'geom_bar()'
	geom_boxploth	alpha, color, fill	horizontal version of 'geom_boxplot()'
	geom_colh	alpha, color, fill	horizontal version of 'geom_col()'
ggstar	geom_star	alpha, color, fill, size, starshape	creates scatterplots
ggsymbol	geom_symbol	alpha, color, fill, size, symbolshape	creates scatterplots
scatterpie	geom_scatterpie	alpha, color, fill	creates scatter pie plot

<sup>1</sup>[https://github.com/tanaes/tetrapod\\_microbiome\\_analysis](https://github.com/tanaes/tetrapod_microbiome_analysis)

```

library(ggtree)
library(ggplot2)
library(ggtreeExtra)
library(patchwork)
library(ggridges)
library(phyloseq)

set.seed(1024)
data("GlobalPatterns")
GP <- GlobalPatterns
GP <- prune_taxa(taxa_sums(GP) > 1000, GP)
sample_data(GP)$human <- get_variable(GP, "SampleType") %in%
  c("Feces", "Skin")
mergedGP <- merge_samples(GP, "SampleType")
mergedGP <- rarefy_even_depth(mergedGP, rngseed=1024)
mergedGP <- tax_glom(mergedGP, "Order")
melt_simple <- psmelt(mergedGP) %>%
  dplyr::filter(Abundance < 120) %>%
  dplyr::select(OTU, val=Abundance)

p <- ggtree(mergedGP, size = 0.3) +
  geom_tippoint(aes(color = Phylum), show.legend = FALSE, size=0.6)

p1 <- p +
  geom_fruit(
    data = melt_simple,
    geom = geom_density_ridges,
    mapping = aes(y = OTU, x = val, fill = Phylum),
    offset = 0.12,
    pwidth = 0.4,
    lwd = .05,
    axis.params = list(
      axis = "x",
      text.size = 1,
      hjust = 0.5,
      vjust = 1
    ),
    grid.params = list(),
    show.legend = FALSE
  )

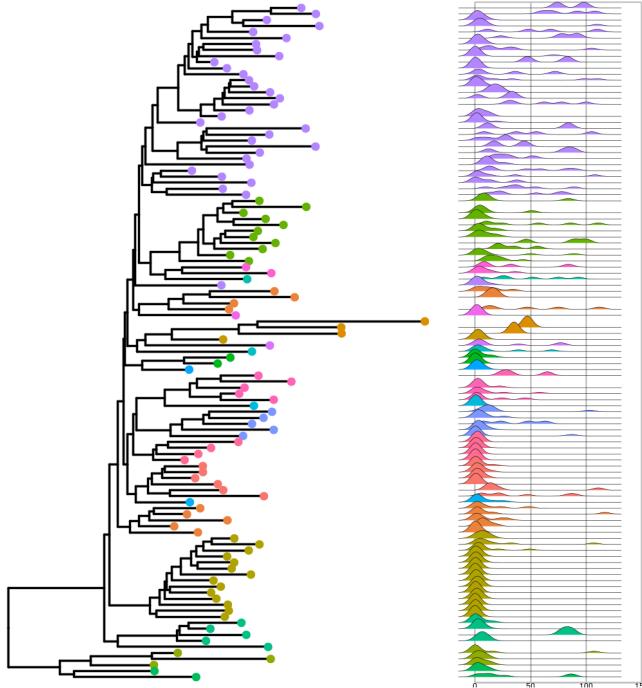
p2 <- p +
  geom_fruit(
    data = melt_simple,
    geom = geom_boxplot,
    mapping = aes(y = OTU, x = val, fill = Phylum),
    offset = 0.12,
    pwidth = 0.4,
    size = 0.1,
    outlier.size = 0.4,
    outlier.stroke = 0.06,
    outlier.shape = 21,
    axis.params = list(
      axis = "x",
      text.size = 1,
      hjust = 0.5,
      vjust = 1
    ),
    grid.params = list(),
    show.legend = FALSE
  )

```

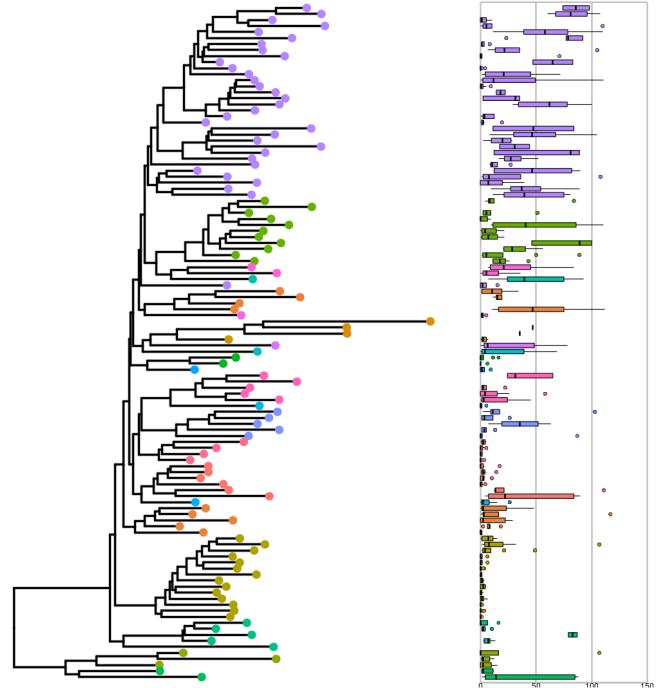
)

```
p3 <- p1 + layout_circular()
p4 <- p2 + layout_circular()
(p1 + p2)/(p3 + p4) + plot_annotation(tag_levels = 'A')
```

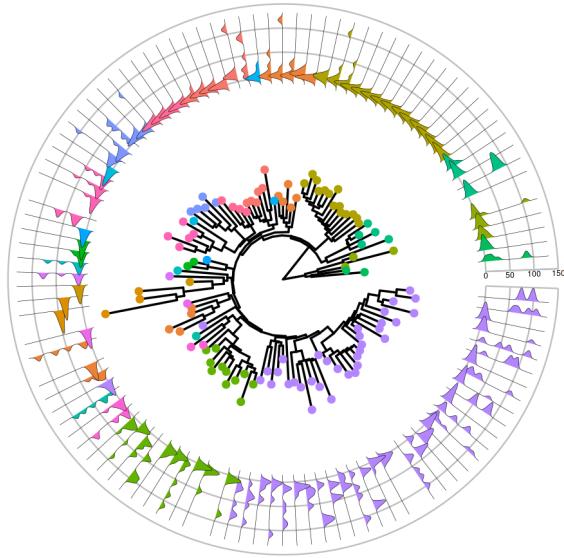
A



B



C



D

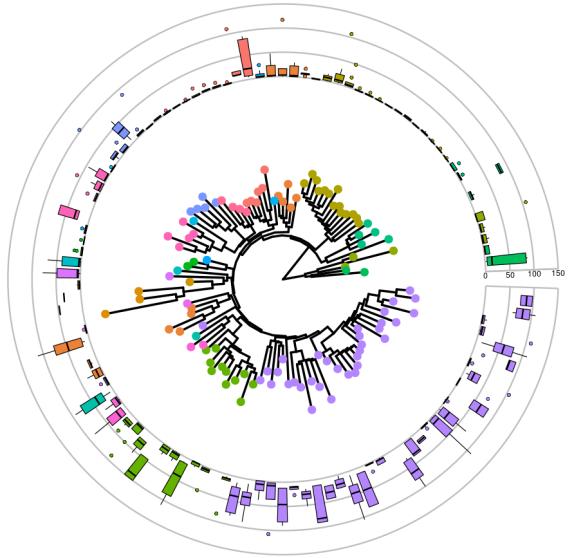


Fig. S3: This example demonstrates using *ggtreeExtra* with *geom\_density\_ridges* layer from the *ggridges* package (Wilke 2020) and *geom\_boxplot* layer from the *ggplot2* package (Wickham 2016). The associated data (*i.e.*, *melt\_simple*) was imported by the *data* argument of the *geom\_fruit* function. The data has a column (*i.e.*, *OTU*) that contains tip labels which was mapped to the *y* axis. The *val* column contains the abundance of the species (continuous data) was mapped to the *x* axis and the *phylum* column contains phylum information of the species (categorical data) was mapped to the *fill* aesthetic to color the desity ridge plot and boxplot. This dataset has been visualized by *facet\_plot* function from *ggtree* (Fig.1. of (Yu et al. 2018)). However, it only supports rectangular layout (A) while *ggtreeExtra* supports more layouts and allows transformation between different layouts. In this example, subplot C and D were transformed from A and B.

```

library(ggtree)
library(ggtreeExtra)
library(ggpattern)
library(ggplot2)
library(patchwork)

set.seed(1024)
tr <- rtree(20)
dat <- tibble::tribble(
  ~value, ~group,
  abs(rnorm(5, 10, sd = 3)), "A",
  abs(rnorm(3, 12, sd = 2)), "B",
  abs(rnorm(5, 9, sd = 3)), "C",
  abs(rnorm(7, 6, sd = 2)), "D"
) %>% tidyverse::unnest(value)
dat$id <- tr$tip.label
dt <- tibble::tribble(
  ~value, ~class,
  abs(rnorm(40, 10, sd = 3)), "A",
  abs(rnorm(24, 12, sd = 2)), "B",
  abs(rnorm(40, 9, sd = 3)), "C",
  abs(rnorm(56, 6, sd = 2)), "D"
) %>% tidyverse::unnest(value)
dt$id <- c(rep(tr$tip.label[1:5], 8), rep(tr$tip.label[6:8], 8),
           rep(tr$tip.label[9:13], 8), rep(tr$tip.label[14:20], 8))
      )

p1 <- ggtree(tr, size=0.2, branch.length="none")
p2 <- ggtree(tr, size=0.2, layout="slanted", branch.length="none")
p3 <- ggtree(tr, size=0.2, layout="fan", open.angle=180, branch.length="none")
p4 <- ggtree(tr, size=0.2, layout="fan", open.angle=180, branch.length="none")

p1 <- p1 +
  geom_fruit(
    data=dat,
    geom=geom_bar_pattern,
    mapping=aes(y=id, x=value, pattern=group, pattern_angle=group),
    width=0.6, stat="identity",
    pwidth = 0.6, pattern_spacing =0.01,
    pattern_size = 0.1, pattern_density = 0.4,
    fill = "grey", pattern_fill="grey35",
    position=position_identityx(),
    axis.params=list(axis="x", text.size=1.2, hjust=0.5, vjust=0.5)
  ) + theme(legend.key.size = unit(0.3, 'cm'))

p2 <- p2 +
  geom_fruit(
    data=dat,
    geom=geom_bar_pattern,
    mapping=aes(y=id, x=value, pattern=group, pattern_fill=group),
    width=0.6, stat="identity",
    pwidth = 0.6, pattern_spacing =0.01,
    pattern_size = 0.1, pattern_density = 0.4,
    fill = "grey",
    position=position_identityx(),
    axis.params=list(axis="x",text.size=1.2, hjust=0.5, vjust=0.5)
  ) + theme(legend.key.size = unit(0.3, 'cm'))

p3 <- p3 +
  geom_fruit(

```

```

data=dt,
geom=geom_boxplot_pattern,
mapping=aes(y=id, x=value, pattern=class, pattern_angle = class),
size=0.1, outlier.shape=NA,
pwidth=0.5, pattern_size = 0.1,
pattern_density = 0.4, pattern_spacing =0.01,
fill = "grey", pattern_fill="grey35",
position=position_dodge(),
grid.params=list(),
axis.params=list(axis="x", text.size=1.2, hjust=0.5, vjust=1)
) + theme(legend.key.size = unit(0.35, 'cm'))

p4 <- p4 +
  geom_fruit(
    data=dt,
    geom=geom_boxplot_pattern,
    mapping=aes(y = id, x = value, pattern = class, pattern_fill = class),
    size = 0.1, outlier.shape = NA,
    pwidth = 0.5, pattern_size = 0.1,
    pattern_density = 0.4, pattern_spacing = 0.01,
    fill = "grey",
    position = position_dodge(),
    grid.params = list(),
    axis.params = list(axis="x", text.size=1.2, hjust=0.5, vjust=1)
  ) + theme(legend.key.size = unit(0.35, 'cm'))

(p1 + p2)/(p3 + p4) + plot_annotation(tag_levels = 'A')

```

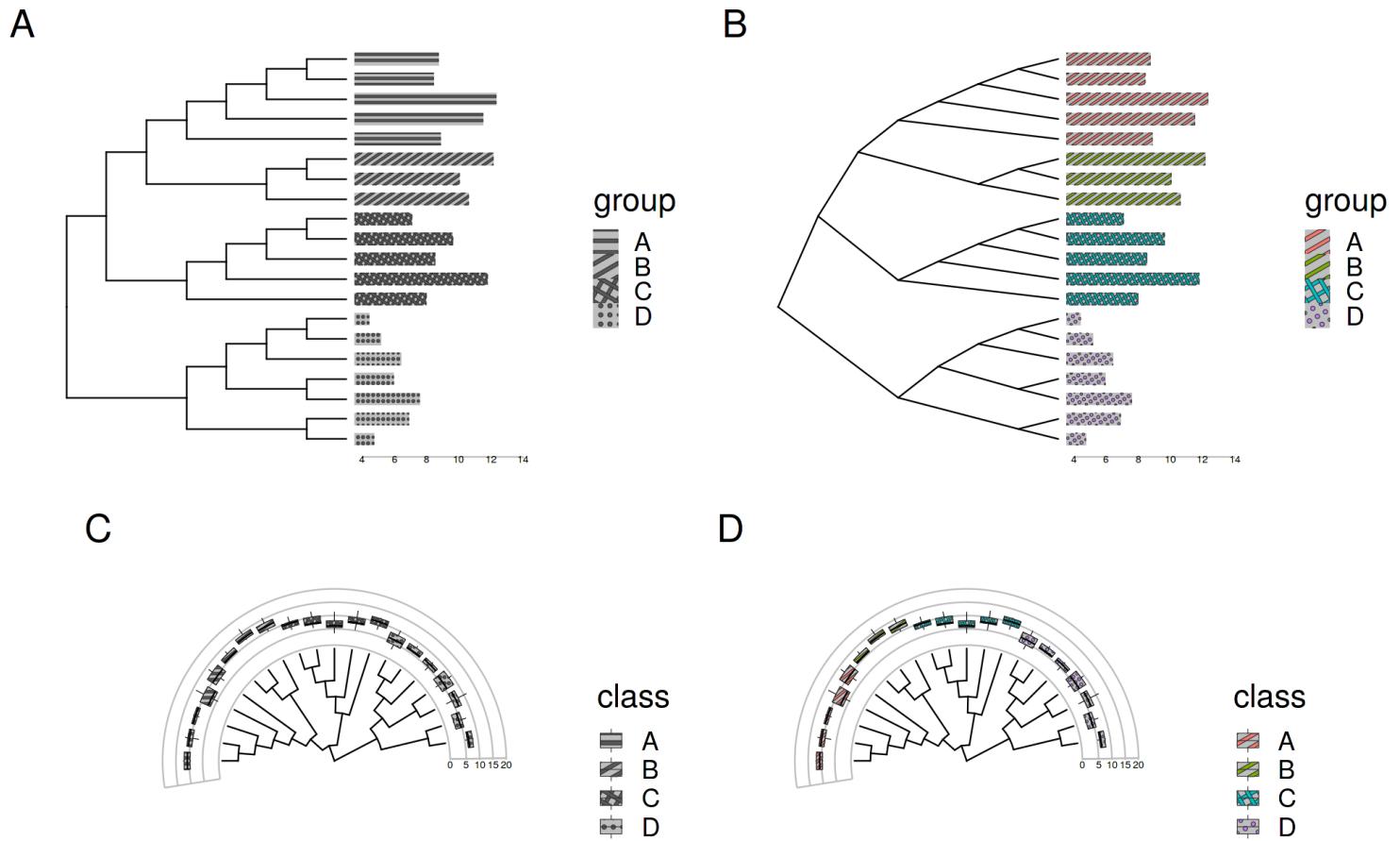


Fig. S4: This example demonstrates using *ggtreeExtra* with *geom\_bar\_pattern* and *geom\_boxplot\_pattern* layers from the *ggpattern* package (FC 2020). Different tree layouts including rectangular (A), slanted (B) and fan (C and D) layouts are all supported in *ggtreeExtra*.

```

library(ggtreeExtra)
library(ggtree)
library(treeio)
library(tidytree)
library(ggnewscale)
library(ggpmisc)
library(ggplot2)
library(ggimage)
library(patchwork)

set.seed(1024)
tr <- rtree(30)

dat1 <- data.frame(value=c(abs(rnorm(10, 3)),abs(rnorm(10, 5))), group=c(rep("A",10),rep("B",10)))
dat2 <- data.frame(value=c(abs(rnorm(15, 6)), abs(rnorm(15, 3))), group=c(rep("A",15),rep("B",15)))

subp1 <- ggplot(dat1) +
  geom_boxplot(aes(x=group, y=value, fill=group),
               size=0.1, outlier.size = 0.1, show.legend=F) +
  theme_bw() +
  theme(legend.key.size = unit(1, 'mm'),
        plot.background = element_rect(fill=NA, color=NA),
        panel.border = element_rect(size=0.1),
        legend.title = element_text(size=3.6),
        legend.text = element_text(size=3.2),
        axis.ticks = element_line(size=0.1),
        axis.text = element_text(size=2.8),
        axis.title = element_text(size=3))

subp2 <- ggplot(dat2) +
  geom_boxplot(aes(x=group, y=value, fill=group),
               size=0.1, outlier.size = 0.1, show.legend=F) +
  theme_bw() +
  theme(legend.key.size = unit(1, 'mm'),
        plot.background = element_rect(fill=NA, color=NA),
        panel.border = element_rect(size=0.1),
        legend.title = element_text(size=3.6),
        legend.text = element_text(size=3.2),
        axis.ticks = element_line(size=0.1),
        axis.text = element_text(size=2.8),
        axis.title = element_text(size=3))

dt <- tibble::tibble(id=c("t14", "t2"), plot=list(subp1, subp2))

p1 <- ggtree(tr,
              layout="fan",
              open.angle=0
            ) +
  geom_tiplab(align=T, size=2)

p2 <- p1 +
  geom_fruit(
    data=dt,
    geom=geom_plot,
    mapping=aes(
      y=id,
      label=plot
    ),
    offset=0.4,
    position=position_identityx(),

```

```

        vjust=0.4,
        hjust=0.7,
        vp.width=0.18,
        vp.height=0.22
    )

## subplot B
tr <- read.tree("../data/VertebrateGutMicrobiomes/annotated_host_tree.tre")
corda <- read.csv("../data/VertebrateGutMicrobiomes/mantel.jaccard.pearson.csv")
corda$r <- abs(corda$r)
barda <- read.csv("../data/VertebrateGutMicrobiomes/data_diet_bar.csv", check.names=F)
barda <- reshape2::melt(barda, id.vars="ID", variable.name="Diet", value.name="mete")
barda$Diet <- factor(barda$Diet, levels=c("Fruit", "Invertebrates",
                                             "Nectar", "Plants", "Scavenging",
                                             "Seeds", "Meat (Ectotherms)",
                                             "Meat (Endotherms)",
                                             "Meat (Fish)", "Meat (Unknown)"))

cladeda <- read.csv("../data/VertebrateGutMicrobiomes/data_clade_class.csv", check.names=F)
cladeda$id <- nodeid(tr, cladeda$id)
cladeda$class <- factor(cladeda$class, levels=c("Amphibia", "Chelonia", "Lepidosauria",
                                                 "Crocodylomorpha", "Aves", "Mammalia"))

flightda <- read.csv("../data/VertebrateGutMicrobiomes/data_flight_bar.csv")

phylopicda <- read.csv("../data/VertebrateGutMicrobiomes/data_phylopic_uid.csv")
phylopicda$class <- factor(phylopicda$class, levels=c("Amphibia", "Chelonia", "Lepidosauria",
                                                       "Aves", "Mammalia"))

fig <- ggtree(tr, layout="fan", open.angle=5)

fig <- fig %<+% corda
fig$data$width <- ifelse(is.na(fig$data$r), 0.1, 0.4)
r <- NULL
fig <- fig +
  aes(color=r, size=I(width)) +
  scale_colour_viridis_c(
    name="Mantel Correlation",
    option="C",
    guide=guide_colorbar(
      barheight = 0.35,
      barwidth = 3.8,
      order = 4,
      title.position = "top",
      label.position = "bottom",
      direction = "horizontal"
    )
  )
fig1 <- fig +
  geom_fruit(
    data=barda,
    geom=geom_bar,
    mapping=aes(x=mete, y=ID, fill=Diet),
    orientation="y",
    stat="identity",
    colour=NA,
    pwidth=0.25,
    offset=0.008
  ) +
  scale_fill_manual(
    values=c("#a6cee3", "#cab2d6",

```

```

        "#1f78b4", "#33a02c",
        "#6a3d9a", "#b2df8a",
        "#fb9a99", "#e31a1c",
        "#ff7f00", "#fdbf6f"),
    guide=guide_legend(keywidth=0.3, keyheight=0.3, order=1)
)
fig2 <- fig1 +
  new_scale_colour() +
  geom_cladelab(
    data=cladeda,
    mapping=aes(node=id, label=class, colour=class),
    textcolour=NA,
    barsize=3,
    extend=0.2,
    offset=105) +
  scale_colour_manual(
    name="Host Class",
    values=c("#b2df8a", "#33a02c", "#fb9a99",
             "#e31a1c", "#EACB47", "#6a3d9a"),
    guide=guide_legend(
      keywidth=0.3,
      keyheight=0.3,
      order=2,
      override.aes=list(size=1.5, alpha=1)))
)
fig3 <- fig2 +
  new_scale_fill() +
  geom_fruit(
    data=flightda,
    geom=geom_tile,
    mapping=aes(y=ID, fill=flight),
    size=0,
    width=14,
    offset=0.15,
    pwidth=0.4,
  ) +
  scale_fill_manual(
    name="Flight Status",
    values=c("black", "white"),
    guide=guide_legend(keywidth=0.3, keyheight=0.3, order=3,
                       override.aes=list(color="black", size=0.3))
  )
)
fig4 <- fig3 +
  new_scale_colour() +
  geom_fruit(
    data=phylopicda,
    geom=geom_phylopic,
    mapping=aes(y=taxa, image=uid, color=class),
    size=0.035,
    offset=0.16,
    alpha=0.8,
    position=position_identityx()
  ) +
  scale_colour_manual(
    values=c("#b2df8a", "#33a02c", "#fb9a99",
             "#EACB47", "#6a3d9a"),
    guide="none"
  ) +
  theme(
    legend.background=element_rect(fill=NA),

```

```

        legend.title=element_text(size=7),
        legend.text=element_text(size=5),
        legend.spacing.y = unit(0.02, "cm")
    )
p2 + fig4 + plot_annotation(tag_levels = 'A')

```

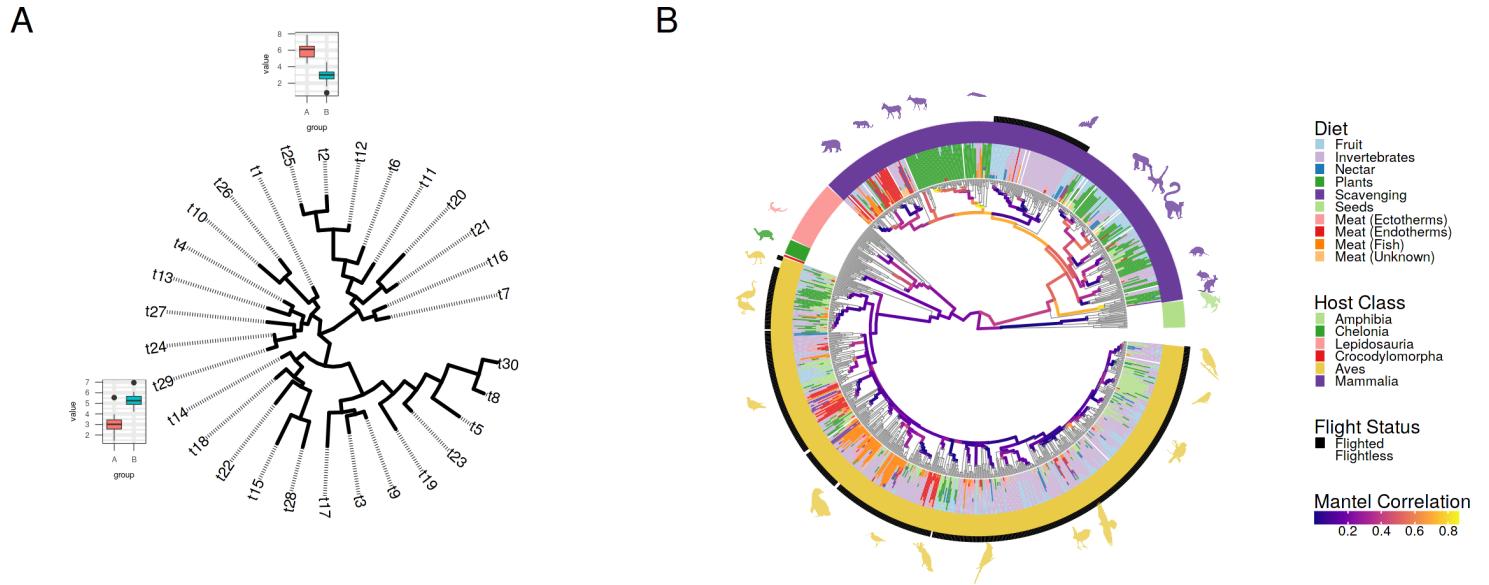


Fig. S5: Using subplots and images as insets on a phylogenetic tree in *ggtreeExtra*. Subplots can be a *ggplot* object that generated by *ggplot2* or its extensions that summarizes taxon-specific information (Fig. S5.A). Taxon information can be used color or scale the size of silhouette images (Fig. S5.B). The host tree of Fig. S5.B was obtained from TimeTree (Kumar et al. 2017), the branch colour represents the Mantel Pearson correlation of gut microbiome, the stack bar chart represents the diet composition of the host, the inner ring represents the host taxonomic class, the middle ring represents flight status, and some representative species are also displayed in the outermost circle (Fig. S5.B).

### 3 Examples of mapping and visualizing associated data on circular layout tree

*ggtreeExtra* can integrate many geometric layers by linking *geom* function defined in *ggplot2* (Wickham 2016) or *ggplot2*-extension packages (Tab. S1, S2 and Fig. S2). This is the basis for *ggtreeExtra* to be used for the annotation of phylogenetic tree. Two examples have been presented (Fig. S3 and S4) to show how to use *ggtreeExtra* to map simple associated data to phylogenetic tree by linking *geom* funtions. For the multiple associated data sets, circular layout is an efficient way to visualize multi-dimensional data sets, since it can reduce space and make the graph more compact. *ggtreeExtra* support annotation of multiple layouts of tree (Fig. S3, S4, S2 and Tab. S1), including circular layout. Furthermore, the associated data can be imported with the *data* parameter of *geom\_fruit* (Fig. S3 and S4), it can also be integrated to tree data (*ggtree* graphic object) with %<+% of *ggtree* (Yu et al. 2018), before passing it to *geom\_fruit* (Fig. S1), or the tree data from output of the *treeio*, which can parse different file formats as well as the outputs of commonly used software (Wang et al. 2020), can also be visualized by *ggtreeExtra*. Therefore, *ggtreeExtra* supports evolutionary statistics inferred by commonly used software, such as *BEAST* (Drummond and Rambaut 2007), *RAXML* (Stamatakis 2014), *HyPhy* (Pond, Frost, and Muse 2005), *PAML* (Yang 2007), *ASTRAL* (Mirarab and Warnow 2015), *pplacer* (Matsen, Kodner, and Armbrust 2010), *RevBayes* (Höhna et al. 2016), *PHYLOGOG* (Boussau et al. 2013) and *EPA* (Berger, Krompass, and Stamatakis 2011) to be visualized by *ggtreeExtra*. The variables (e.g. abundance of species, length of genome, sampling location) of associated data can be mapped to the attributes of outer geometric objects (e.g. bar, point, boxplot) of circular phylogenetic tree (Fig. S1 and S3), since *ggtreeExtra* was developed based on grammar of graphic (Wilkinson 2012). Here, we present several examples to elucidate how to map and display the associated data on the outer rings of circular phylogenetic trees using *ggtreeExtra*. More examples can be found on the *chapter10* of online book<sup>2</sup>.

<sup>2</sup><http://yulab-smu.top/treedata-book>

### 3.1 Data supported by *ggtreeExtra*

*ggtreeExtra* is designed to work with *ggtree* (Yu et al. 2017) and *treeio* (Wang et al. 2020), it supports visualization of the tree data parsed by *treeio* (Wang et al. 2020), any data frame that contains a column of tip labels can also be imported with *data* parameter of *geom\_fruit* (Fig. S3). Or the data frame that contains a column of tip labels can also be integrated into *ggtree* graphic object using `%<+%` operator (Yu et al. 2018), before passing it to *geom\_fruit*. So *ggtreeExtra* can be used to annotate evolutionary statistics inferred by commonly used software, and It is possible to display the evolutionary statistics with phylogeny-associated data (such as traits, metadata) using *ggtreeExtra* (Fig. S6). These features are not available in other tools. We reproduce Figure 3.3 of (Smith and Wrighton 2019) to show how to integrate the associated data to tree data using `%<+%` and visualize it. And the source data is available at this repository<sup>3</sup>. The associated data sets contain the information of Ecosystem type, sequencing type and sample treatment method (all categorical data). The first column of external data is tip labels (the element of the column must be unique). The tree was built using *RAxML* (Stamatakis 2014), it is parsed to tree data using *read.raxml* of *treeio* (Wang et al. 2020), contained bootstrap information. The tree data was visualized with *ggtree* (Yu et al. 2017). Then the associated data sets was imported *ggtree* graphic object using `%<+%`, *geom\_fruit* can extract the tree data integrated automatically, and the attributes of data can be mapped using related attributes of geometry layers. The *y* of *aes* can be ignored. Here we used heat map to display the associated data sets (categorical data). The external ring heat maps represent the different types in corresponding categories (the type of Ecosystem was mapped to the color of innermost ring heat map, the type of sequencing was mapped to the color of middle ring heat map, the type of sample treatment was mapped to the color of outermost ring heat map) (Fig. S6). In addition, compared with other tools, no restriction of data types should be visualized in *geom\_fruit* of *ggtreeExtra*. It depends on the data types of various geometric functions (Tab. S2). For example, The multiple density plots is not supported by other tools, but *ggtreeExtra* supports it by linking *geom\_density\_ridges* of *ggridges* (Wilke 2020) (the data types of *geom\_density\_ridges* should be provided) (Fig. S3.A and S3.C). The *ggplot* graphic object (one type of image plot) is also not supported by other tools, but *ggtreeExtra* also supports it by linking *geom\_plot* of *gppmisc* (Aphalo 2020), only we provides the data types of *geom\_plot* (Fig. S5.A). Therefore. As the *geom* of *ggplot2* (Wickham 2016) or other extensions will be updated and developed, so *ggtreeExtra* will be also more powerful to present associated data in the future.

```
library(ggtreeExtra)
library(ggtree)
library(treeio)
library(ggplot2)
library(ggnewscale)
library(tidytree)
tr <- read.raxml("../data/Methanotroph/Methanotroph_rpS3_Modified_Alignment_RAxML")
# Optional, Root the tree to the archaea sequences
treeda <- root(tr, node=1402, edgelabel=TRUE)
root <- rootnode(treeda)
# read associated data
df <- read.csv("../data/Methanotroph/metadata.csv")
# reset the levels of columns to reproduce the order of original figure.
df$Specific.Ecosystem <- factor(df$Specific.Ecosystem,
                                 levels=c("Agriculture", "Alkaline/Hypersaline",
                                         "Contaminated/Wastewater", "Endosymbiont",
                                         "Freshwater", "Forest", "Geothermal",
                                         "Marine", "Natural Seep", "Peat",
                                         "Permafrost", "Wetland", "Unknown"))
df$MetaType <- factor(df$MetaType,
                       levels=c("Metatranscriptome", "Metagenome",
                               "Single-amplified genome", "Fosmid", NA))
df$Treatment <- factor(df$Treatment, levels=c("Native", "Enrichment", "Isolate", "Unknown"))

p <- ggtree(treeda, layout="fan", open.angle=30)
print(as.treedata(p))

## 'treedata' S4 object'.
##
## ...@ phylo:
## Phylogenetic tree with 727 tips and 726 internal nodes.
##
## Tip labels:
```

<sup>3</sup>[https://github.com/TheWrightonLab/Methanotroph\\_rpS3Analyses\\_SmithWrighton2018](https://github.com/TheWrightonLab/Methanotroph_rpS3Analyses_SmithWrighton2018)

```

## 3300019787==Ga0182031_12339262, 3300014838==Ga0182030_1009273110, gb_PLVF01000413_pos14750To15429=Methylloc
## Node labels:
## Root, NA, NA, NA, NA, NA, ...
##
## Rooted; includes branch lengths.
##
## with the following features available:
## 'bootstrap'.

p <- rotate_tree(p, 90)
p1 <- p +
  geom_treescale(x=0.2, y=727*6/11, width=1, offset=20) +
  geom_point2(aes(subset = !isTip & node != root,
                  fill = cut(bootstrap, c(0, 70, 90, 100), right = F)),
               shape=21, size=1.2, stroke=0.3) +
  scale_fill_manual(values = c("black", "grey", "white"),
                    name = "Bootstrap (BP)",
                    breaks = c('[90,100)', '[70,90)', '[0,70)'),
                    labels = expression(BP >= 90, 70<=BP*<90', BP<70),
                    guide=guide_legend(keywidth=0.5, keyheight=0.6,
                                       override.aes=list(size=2.5, stroke=0.3),
                                       order=1)
  )
# we can use %<+% to integrate the external datasets to tree structure.
# and the y can not be specified in geom_fruit.
p2 <- p1 %<+% df +
  new_scale_fill() +
  geom_fruit(
    geom=geom_tile,
    mapping=aes(fill=Specific.Ecosystem),
    offset=0.13,
    width=0.35,
    axis.params=list(
      axis="x", text="Ecosystem",
      text.angle=0, hjust=0, text.size=3,
      family="Times", fontface="bold"
    )
  ) +
  scale_fill_manual(
    values=c("green3", "turquoise", "maroon", "orchid",
            "deepskyblue", "forestgreen", "salmon", "cadetblue3",
            "slategray4", "yellowgreen", "gray90", "chocolate2",
            "yellow"),
    guide=guide_legend(title="Ecosystem", keywidth=0.5, keyheight=0.5, order=4),
    na.translate=FALSE
  )
)

p3 <- p2 +
  new_scale_fill() +
  geom_fruit(
    geom=geom_tile,
    mapping=aes(fill=MetaType),
    offset=0.13,
    width=0.35,
    axis.params=list(
      axis="x", text="Sequencing Type",
      text.angle=0, hjust=0, text.size=3,
      family="Times", fontface="bold"
    )
  ) +
  scale_fill_manual(

```

```

values=c("red", "black", "dodgerblue", "gray50"),
guide=guide_legend(title="Sequencing Type", keywidth=0.5, keyheight=0.5, order=3),
na.translate=FALSE
)

p4 <- p3 +
  new_scale_fill() +
  geom_fruit(
    geom=geom_tile,
    mapping=aes(fill=Treatment),
    offset=0.13,
    width=0.35,
    axis.params=list(
      axis="x", text="Sample Treatment",
      text.angle=0, hjust=0,
      text.size=3, family="Times", fontface="bold"
    )
  ) +
  scale_fill_manual(
    values=c("red", "gray50", "black", "yellow"),
    guide=guide_legend(title="Sample Treatment", keywidth=0.5, keyheight=0.5, order=2),
    na.translate=FALSE
  ) +
  theme(
    legend.background=element_rect(fill=NA), # the background of legend.
    legend.title=element_text(size=9, family="Times", face="bold"),
    legend.text=element_text(size=7, family="Times"), # the text size of legend.
    legend.spacing.y = unit(0.02, "cm"),
    legend.margin=margin(0.1, 0.9, 0.1, -0.9, unit="cm"), # t, r, b, l, cm
    legend.box.margin=margin(0.1, 0.9, 0.1, -0.9, unit="cm"),
    plot.margin = unit(c(-1.2, -1.2, -1.2, 0.1), "cm")
  )

# optional
cladeda <- data.frame(nodeid = c(793, 791, 1384, 1394, 1440, 1405),
                       label = c("Gammaproteobacteria", "Alphaproteobacteria",
                                 "Ca.Methylomirabilis", "Methylacidiphilae",
                                 "ANME-1", "ANME-2"),
                       horizontal = c(FALSE, FALSE, TRUE, TRUE, TRUE, TRUE),
                       hjust = c(0.5, 0.5, 0, 0, 0, 0))

p5 <- p4 +
  geom_cladelab(
    data = cladeda,
    mapping = aes(
      node=nodeid,
      label=label,
      horizontal=horizontal,
      hjust=hjust
    ),
    angle = "auto",
    offset = 1.4,
    align = T,
    fontsize = 2,
    barsize = 1,
    family = "Times",
    fontface="bold",
    offset.text = 0.1
  )
p5

```

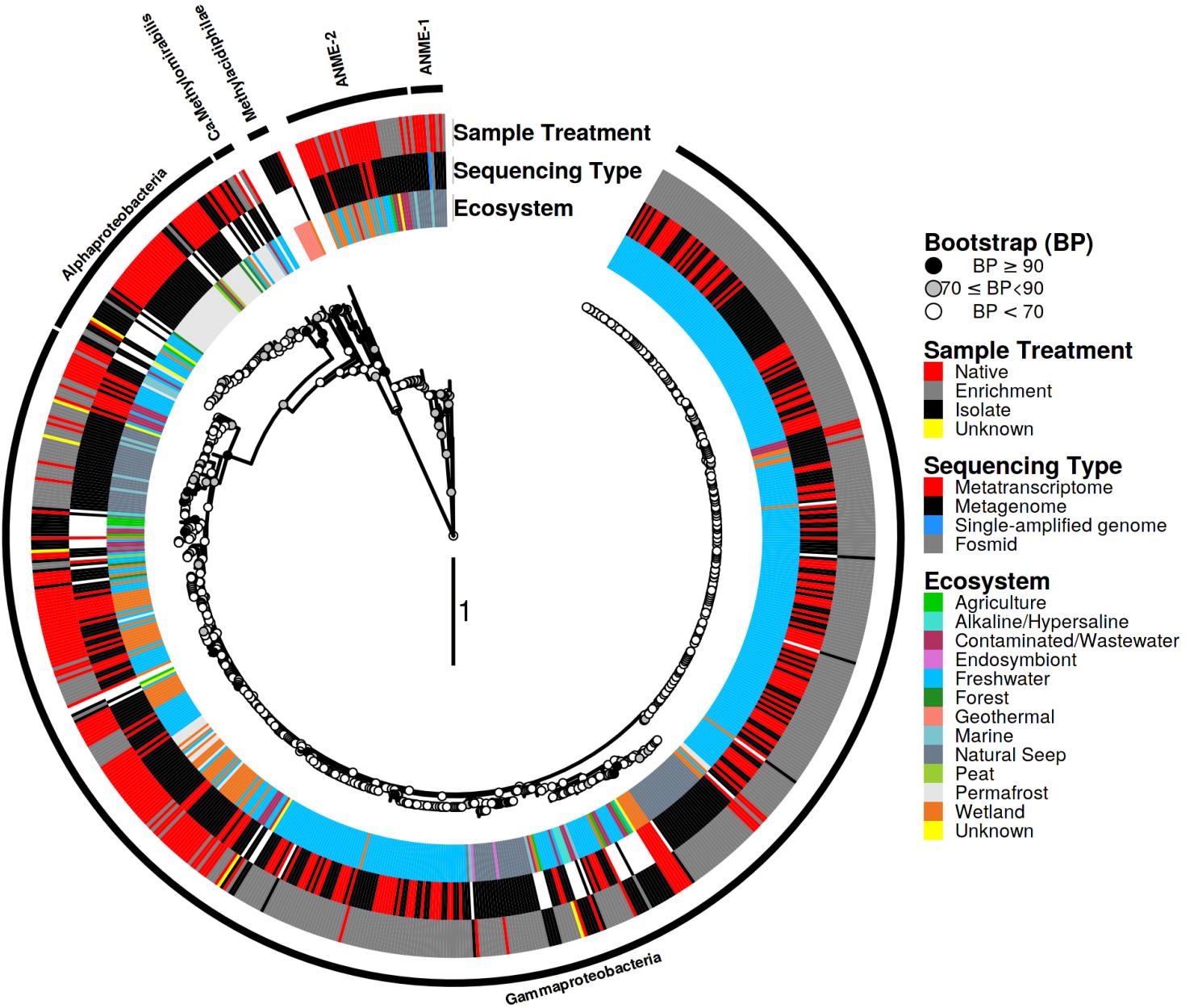


Fig. S6: Phylogeny of methanotroph ribosomal protein S39 (rpS3) genes from Figure 3.3 (Smith and Wrighton 2019). The external ring of circular tree is built with the associated data sets integrated to tree data using `%<+%`. This example also demonstrates it is possible to display the evolutionary statistics (bootstrap) with phylogeny-associated data (such as traits, metadata) using `ggtreeExtra`.

### 3.2 Displaying multiple associated data to circular phylogenetic tree using grammar of graphic

*ggtreeExtra* is developed based on grammar of graphic (Wilkinson 2012) implemented in the *ggplot2* (Wickham 2016) package. The variables of associated data sets can be mapped to the attributes of geometric layers, the graphic can be displayed with provided aesthetic mapping and non-variable setting. And users can specify their own set of mappings from levels or values in the data to aesthetic values using the corresponding *scale* function defined in *ggplot2* or *ggplot2-based* packages (Fig. S1). They do not need providing configure file which mixes associated data and the profiler of graphic (configure file is needed by many other tools (Tab. S1)), so no restriction of data types should be used in *geom\_fruit* of *ggtreeExtra* (see 3.1). Some examples used grammar of graphic (Wilkinson 2012) has been provided in the above description (Fig. S3, S4, S5 and S6). Here, we reproduce Fig.2 of (Morgan, Segata, and Huttenhower 2013) to show how to display multiple associated data to circular phylogenetic tree using *ggtreeExtra* again. The data sets are provided by GraPhlAn (Asnicar et al. 2015), but they were mixed with the profiler of graphic for GraPhlAn (Asnicar et al. 2015). We has extracted and saved them as the data frames for corresponding geometric layer functions. These data sets contain the relative abundance of bacteria (continuous data) at different body sites (categorical data). The associated data sets were imported with *data* parameter of *geom\_fruit*

and displayed with the corresponding geometric function. We used heat map to display the abundance of tip species by linking *geom\_tile* of *ggplot2* (Wickham 2016) (the abundance of species was mapped to the transparency of heat map using *alpha* aesthetic of *geom\_tile*, then *alpha* was specified the mapping from values in the data using *scale\_alpha\_continuous* defined in *ggplot2*). The different body sites was mapped to the color of heat map using *fill* aesthetic of *geom\_tile*, then the *fill* was specified the mapping from levels in the data using *scale\_fill\_manual* defined in *ggplot2*) (Fig. S7.C), and the most abundance of species (continuous data) at specific site was visualized with bar plot by linking *geom\_col* of *ggplot2* (the abundance of species was mapped to the length of bar plot using *x* aesthetic of *geom\_col*, the different body sites was mapped to the color of bar plot using *fill* aesthetic of *geom\_col*) (Fig. S7.D). The outer graphic layers can be aligned automatically according to the tip labels of phylogenetic tree (tip labels were mapped to *y* value). The tree annotated by *geom\_fruit* can also be annotated with other geometric layer functions provided by *ggtree* (Yu et al. 2017), *ggplot2* or *ggplot2*-based packages, such as *geom\_star* of *ggstar* (Xu 2020) (Fig. S7.A), *geom\_hilight* and *geom\_cladelab* of *ggtree* (Fig. S7.B). The layers and outer graphic layers can be added step-by-step with + symbol (Fig. S7). These features make it possible to display fully annotated tree with complex data panels that contains multiple graphic layers. More step-by-step instructions are also available at the vignette<sup>4</sup>.

```
library(ggtreeExtra)
library(ggtree)
library(treeio)
library(tidytree)
library(ggstar)
library(ggplot2)
library(ggnewscale)
library(patchwork)

tree <- read.tree("../data/HMP_tree/hmptree.nwk")
# the abundance and types of microbes
dat1 <- read.csv("../data/HMP_tree/tippoint_attr.csv")
# the abundance of microbes at different body sites.
dat2 <- read.csv("../data/HMP_tree/ringheatmap_attr.csv")
# the abundance of microbes at the body sites of greatest prevalence.
dat3 <- read.csv("../data/HMP_tree/barplot_attr.csv")
# adjust the order, it is optional.
dat2$Sites <- factor(dat2$Sites, levels=c("Stool (prevalence)", "Cheek (prevalence)",
                                             "Plaque (prevalence)", "Tongue (prevalence)",
                                             "Nose (prevalence)", "Vagina (prevalence)",
                                             "Skin (prevalence)"))
dat3$Sites <- factor(dat3$Sites, levels=c("Stool (prevalence)", "Cheek (prevalence)",
                                             "Plaque (prevalence)", "Tongue (prevalence)",
                                             "Nose (prevalence)", "Vagina (prevalence)",
                                             "Skin (prevalence)"))

# extract the clade label information. Because some nodes of tree are annotated to genera,
# which can be displayed with high light using ggtree.
# This is optional, since the node information are always not present.
nodeids <- nodeid(tree, tree$node.label[nchar(tree$node.label)>4])
nodedf <- data.frame(node=nodeids)
nodelab <- gsub("[\\\\.0-9]", "", tree$node.label[nchar(tree$node.label)>4])
# The layers of clade and hightlight (optional)
poslist <- c(1.6, 1.4, 1.6, 0.8, 0.1, 0.25, 1.6, 1.6, 1.2, 0.4,
            1.2, 1.8, 0.3, 0.8, 0.4, 0.3, 0.4, 0.4, 0.4, 0.6,
            0.3, 0.4, 0.3)
labdf <- data.frame(node=nodeids, label=nodelab, pos=poslist)
# The circular layout tree.
p <- ggtree(tree, layout="fan", size=0.15, open.angle=5)
# add tip points with geom_star of ggstar
p <- p %<+% dat1 +
  geom_star(
    mapping=aes(fill=Phylum, starshape=Type, size=Size),
    starstroke=0.05
  ) +
  scale_fill_manual(
```

<sup>4</sup><http://bioconductor.org/packages/release/bioc/vignettes/ggtreeExtra/inst/doc/ggtreeExtra.html>

```

values=c("#FFC125", "#87CEFA", "#7B68EE", "#808080", "#800080",
        "#9ACD32", "#D15FEE", "#FFC0CB", "#EE6A50", "#8DEEEE",
        "#006400", "#800000", "#B0171F", "#191970"),
guide=guide_legend(keywidth = 0.5, keyheight = 0.5, order=1,
override.aes=list(starshape=15)),
na.translate=FALSE) +
scale_starshape_manual(
  values=c(15, 1),
  guide=guide_legend(keywidth = 0.5, keyheight = 0.5, order=2),
  na.translate=FALSE
) +
scale_size_continuous(
  range = c(0.5, 1.5),
  guide = guide_legend(keywidth = 0.5, keyheight = 0.5, order=3,
  override.aes=list(starshape=15))
) +
new_scale_fill() +
theme(legend.position="none")
# optional for highlight and clade labels
p1 <- p +
  geom_hilight(data=nodedf, mapping=aes(node=node),
               extendto=6.8, alpha=0.3, fill="grey",
               color="grey50", size=0.05
  ) +
  geom_cladelab(data=labdf,
                 mapping=aes(node=node, label=label, offset.text=pos),
                 barsize=NA, fontsize=0.7, angle="auto",
                 hjust=0.5, horizontal=FALSE, fontface="italic"
  )
# using geom_fruit to add outer layers
p2 <- p1 +
  geom_fruit(
    data=dat2,
    geom=geom_tile,
    mapping=aes(y=ID, x=Sites, alpha=Abundance, fill=Sites),
    color = "grey50",
    offset = 0.04,
    size = 0.02
  )+
  scale_alpha_continuous(
    range=c(0, 1),
    guide=guide_legend(keywidth = 0.3, keyheight = 0.3, order=5)
  ) +
  scale_fill_manual(
    values=c("#0000FF", "#FFA500", "#FF0000", "#800000",
            "#006400", "#800080", "#696969"),
    guide=guide_legend(keywidth = 0.3, keyheight = 0.3, order=4)
  ) + theme(legend.position="none")

p3 <- p2 +
  geom_fruit(
    data=dat3,
    geom=geom_col,
    mapping=aes(y=ID, x=HigherAbundance, fill=Sites),
    pwidth=0.38,
    orientation="y",
    position=position_stackx(),
  )+
  geom_treescale(fontsize=1.2, linesize=0.3, x=4.9, y=0.1) +
  theme(legend.position="none")

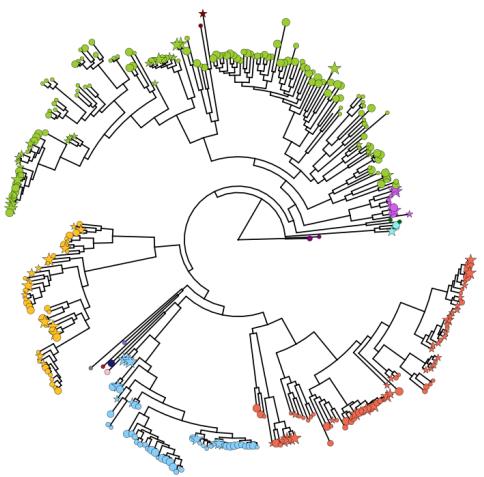
```

```

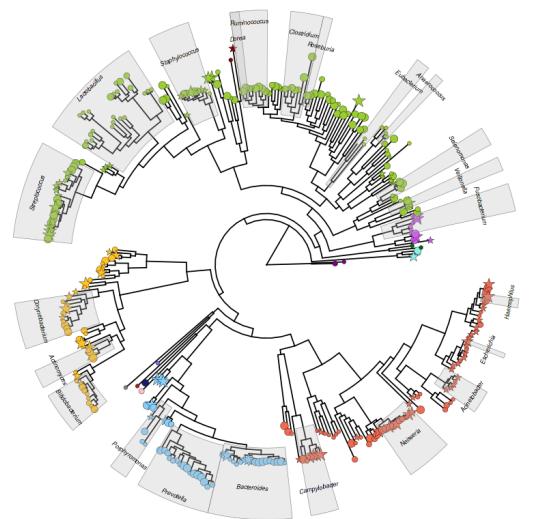
p4 <- (p + p1 + plot_layout(width=c(3.4,4)))/ (p2 + p3 + plot_layout(width=c(3.4,4))) +
  plot_layout(heights=c(3,4)) + plot_annotation(tag_levels = 'A')
p4

```

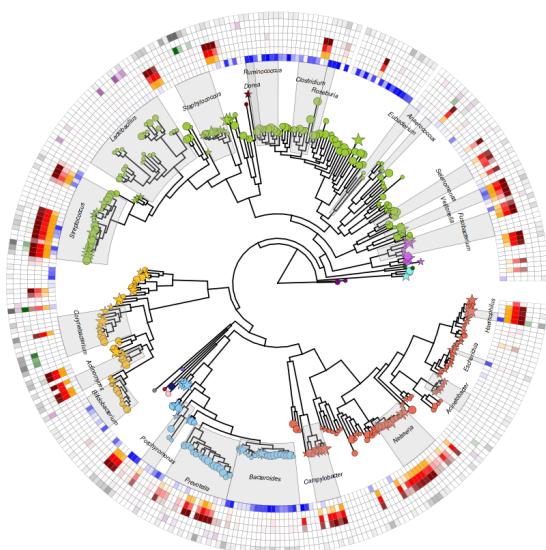
A



B



C



D

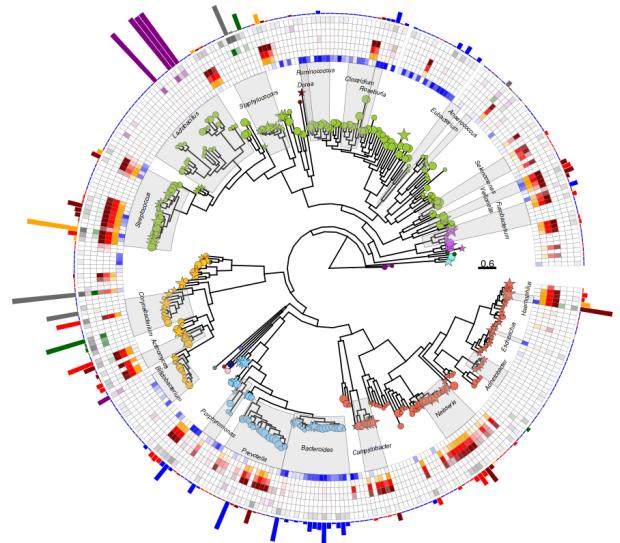


Fig. S7: The abundance of microbes at different sites of human. The shape of tip labels indicated the commensal microbes or potential pathogens. The transparency of heat map indicates the abundance of microbes, and colors of heat map indicate the different sites of human. The bar plot indicates the relative abundance at body site of the most abundance. Fig. S7.A contains the tree layer and tip point layer; Fig. S7.B is from Fig. S7.A added high light layer and clade label layer; Fig. S7.C is from Fig. S7.B added a heatmap layer; Fig. S7.D is from Fig. S7.C added a bar chart layer. This example shows the abilities of annotate phylogenetic tree through grammar of graphic using ggtree and ggtreeExtra.

### 3.3 Annotating phylogenetic tree fully with multiple associated data

Since *ggtreeExtra* supports annotation of multiple layouts tree (tree and geometric layers alignment) (Tab. S1 and Fig. S2, S3, S4). It can also link *ggtree* (Yu et al. 2017) and geometric layer functions defined in *ggplot2* (Wickham 2016) or *ggplot2*-based packages based on grammar of graphic (Tab. S2 in 2 and Fig. S7 in 3.2). The annotation layers on the outer of phylogenetic tree can be combined freely. So it can be easily used to visualize complex and high-dimensional associated data on the outer of phylogenetic tree including the tree containing thousands of tips. Here, we reproduce Fig 2 of (Asnicar et al. 2015). The phylogenetic tree also was built using a part of 3737 microbes (Segata et al. 2013). The associated data sets have also been extracted from configure file and saved as the data frame types for corresponding geometric layer functions. They contain present or not (discrete data) and type (discrete data) of target gene, the type (discrete data) and capability (continuous data) of fatty acid metabolism, and the length of microbes genome. The present or not of different target gene was visualized with first inner heat map (the type of target gene was mapped to color of heat map, and the subtype of target gene was mapped to the x value(take on numerical values)). The type and capability of fatty acid metabolism was also visualized with middle heat map (the type was mapped to color of heat map, the capability of fatty acid metabolism was mapped to the transparency of heat map). The length of genome was displayed with bar chart (the length of genome was mapped to length of bar, the phylum information of genome was mapped to the color of bar). (Fig. S8). Notably, the same colors of Proteobacteria and Spirochaetes were found in the original configure file (Asnicar et al. 2015). We tried to separate the tips from Proteobacteria and Spirochaetes. Unfortunately, They can not be separated since the phylum information of tips was replaced color code. So the color of Proteobacteria and Spirochaetes is also identical in Fig. S8. This show that providing configure file mixed associated data and profiler of graphic layer is tedious and error-prone since the profiler of graphic layer (*e.g.* color or size) should be consistent for the same information.

```

  0.8, 1, 0.6, 0.6, 0.4, 0.3, 0, 0.4, 0.1, 0.25,
  0.2, 0.3, 0.8, 0.8, 0.8, 0.6, 2.4)
# optional for clade layers
cladelabels <- mapply(function(x, y, z){geom_cladelabel(node=x, label=y, barsize=NA, extend=0.3,
                                                     offset.text=z, fontsize=1.2, angle="auto",
                                                     hjust=0.5, horizontal=FALSE, fontface="italic")},
                        nodeids, nodelab, textex, SIMPLIFY=FALSE)

# high light layers
fills <- c("#808080", "#808080", "#808080", "#808080",
          "#191970", "#87CEFA", "#FFC125", "#B0171F", "#B0171F",
          "#B0171F", "#B0171F", "#B0171F", "#B0171F", "#B0171F",
          "#B0171F", "#B0171F", "#B0171F", "#B0171F", "#B0171F",
          "#B0171F", "#B0171F", "#9ACD32", "#9ACD32", "#9ACD32",
          "#006400", "#800000")

# optional for hight light
highlights <- mapply(function(x, y){geom_hilight(node=x, extendto=5.8, alpha=0.3,
                                                   fill=y, color=y, size=0.05)},
                      nodeids, fills, SIMPLIFY=FALSE)

# to reproduce the original figures, we use the same colors.
# uses can custom set it.
colors <- c("#9ACD32", "#EE6A50", "#87CEFA", "#FFC125", "#D15FEE", "#8DEEEE", "#800000",
            "#006400", "#800080", "#808080", "#B0171F", "#B0171F", "#191970", "#7B68EE",
            "#00CD00", "Black")
p1 <- ggtree(
  tree,
  layout="circular",
  size=0.1
)
# Optional for hight clade
p1 <- p1 +
  highlights

p2 <- p1 +
  geom_fruit(
    data=dt1,
    geom=geom_point,
    mapping=aes(
      y=ID,
      fill=Phyla
    ),
    shape=21,
    size=1.2,
    stroke=0.05,
    position="identity",
    show.legend=FALSE
  )+
  scale_fill_manual(values=colors)
# Optional for clade label
p2 <- p2 +
  cladelabels +
  new_scale_fill()

p3 <- p2 +
  geom_fruit(
    data=dt2,
    geom=geom_tile,
    mapping=aes(
      y=ID,

```

```

        x=ring,
        fill=Type1
    ),
    offset=-0.02,
    pwidth=0.14,
    addbrink=TRUE
) +
scale_fill_manual(
    name="ATP synthesis",
    values=c("#339933", "#dfac03"),
    guide=guide_legend(keywidth=0.5, keyheight=0.5, order=1)
) +
new_scale_fill()

p4 <- p3 +
geom_fruit(
    data=dt3,
    geom=geom_tile,
    mapping=aes(
        y=ID,
        alpha=Abundance,
        x=Type2,
        fill=Type2
    ),
    offset=0.001,
    pwidth=0.18
) +
scale_fill_manual(
    name="Fatty Acid metabolism",
    values=c("#b22222", "#005500", "#0000be", "#9f1f9f", "#793a07"),
    guide=guide_legend(keywidth=0.5, keyheight=0.5, order=2)
) +
scale_alpha_continuous(
    range=c(0, 0.4),
    guide=guide_legend(keywidth=0.5, keyheight=0.5, order=3)
) +
new_scale_fill()

p5 <- p4 +
geom_fruit(data=dt4,
    geom=geom_bar,
    mapping=aes(
        y=ID,
        x=Length,
        fill=Phyla
    ),
    stat="identity",
    orientation="y",
    pwidth=0.3,
    position=position_dodgex()) +
scale_fill_manual(
    values=colors,
    guide=guide_legend(keywidth=0.5, keyheight=0.5, order=4)
) +
geom_treescale(fontsize=1.2, linesize=0.3) +
theme(
    legend.position=c(0.95, 0.5),
    legend.background=element_rect(fill=NA),
    legend.title=element_text(size=7),
    legend.text=element_text(size=6),
    legend.spacing.y = unit(0.02, "cm"))

```

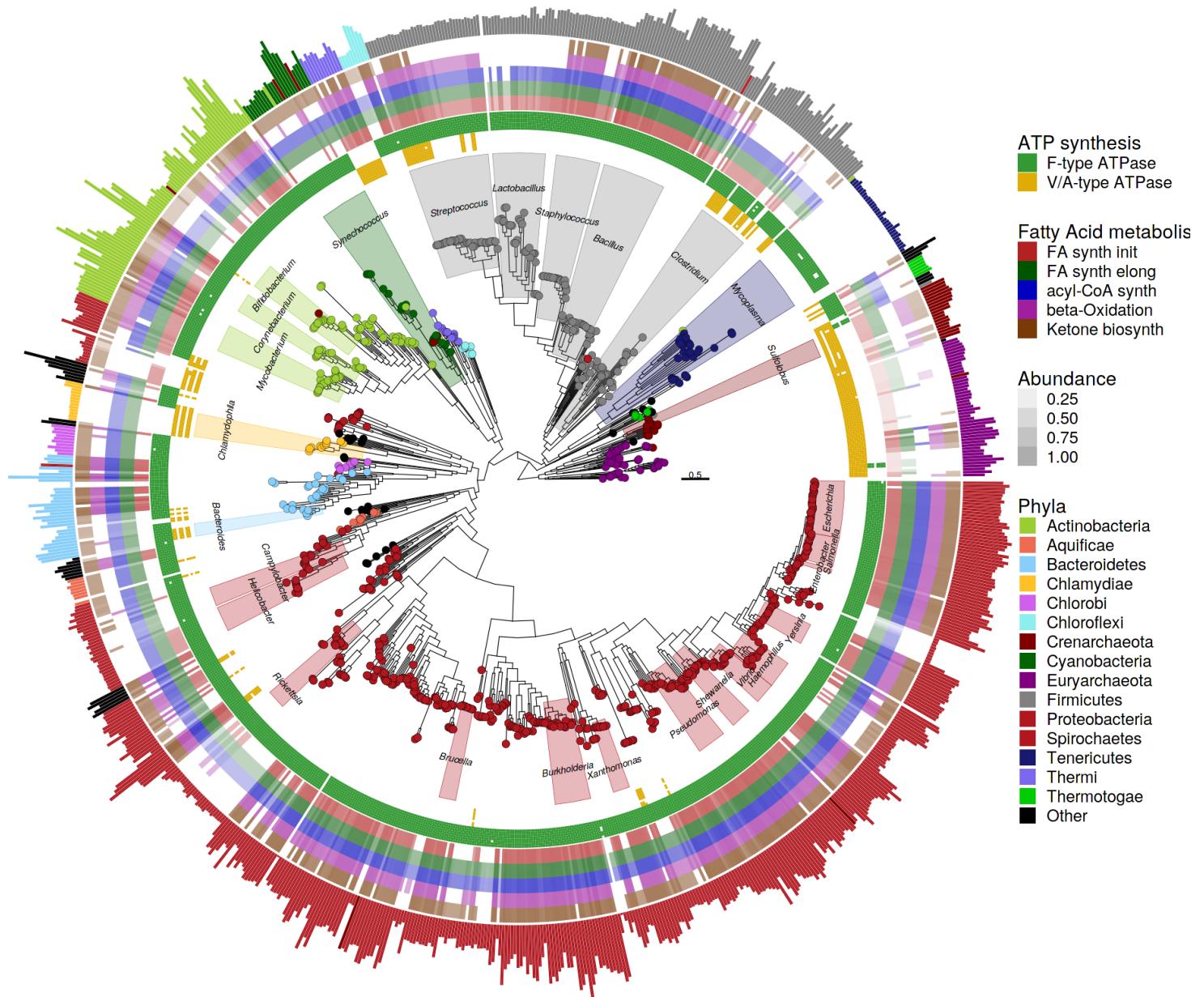


Fig. S8: The phylogenetic tree built using in (Segata et al. 2013) using 963 microbial genomes (a part of 3737 microbes (Segata et al. 2013)). The first and second ring heat map were built with discrete data, it represents the presence or absence of each module, the other heat map rings were created with continuous data, the transparency represents the capability of fatty acid metabolism, the different colors represent the types of fatty acid metabolism. The length of bar represents the genome length of corresponding microbes. This example demonstrates the *Annotation layers* (Tab. S1) can be combined freely using *ggtreeExtra*.

### 3.4 Annotating associated data to the phylogenetic tree combined chord diagram

As the mentioned above, *ggtreeExtra* can link *ggtree* (Yu et al. 2017) and geometric layer functions defined *ggplot2* (Wickham 2016) or other *ggplot2* extension packages (Tab. S2). It also developed based on grammar of graphic (Fig. S7). The geometric layers of *ggtree* (Yu et al. 2017) and *ggplot2* or other *ggplot2* extension packages can be combined freely using *ggtreeExtra* (Fig. S8), and the layers can be added, deleted or modified. *ggtreeExtra* is more flexible and universal than other tools, since it can also integrate more geometric layers and support more layouts for tree annotation (Tab. S1 and Fig. S2). These features allow *ggtreeExtra* to better explore phylogenetic patterns behind multi-dimensional data. For example, the Fig.1b and Fig.2 of (Helfrich et al. 2018) show the directional interactions and the biosynthetic potential of isolates from *Arabidopsis* leaf microbiome in phylogenetic tree using GraPhlAn (Asnicar et al. 2015). However, because GraPhlAn (Asnicar et al.

2015) is not general, it only support annotation of circular layout tree and support few geometric layers, some phylogenetic patterns behind multi-dimensional data were not be found easily. Here, we can use *ggtree* and *ggtreeExtra* to combine the total information of Fig.1b and Fig.2 of (Helfrich et al. 2018). In details, the interactions of isolates are visualized with chord diagram using *geom\_taxalink* of *ggtree* (Yu et al. 2017). The biosynthetic potential of isolates are displayed with heat map by linking *geom\_tile* of *ggplot2* (Wickham 2016) (the number of target gene (continuous data) was mapped to the transparency of heat map, the type of target gene (discrete data) was mapped to the x value and color of heat map). The number of interactions of inhibitions or sensitivities per strain is displayed with stacked bar by linking *geom\_bar* of *ggplot2* (Wickham 2016) (the number of interactions (continuous data) was mapped to the x value (length) of bar plot, and the type of interactions (discrete data) was mapped to the color of bar plot.). We found some strains from Firmicutes and from Grammaproteobacteria have more inhibitor interactions. However, many strains from Alphaproteobacteria and Betaproteobacteria prefer the interaction of sensitivity. In addition, These strains that prefer the interactions of sensitivity might be have more BGCs (biosynthesis gene clusters) from ribosomally synthesized and post-translationally modified peptide (*RiPP*). Notably, other tools do not support annotation of phylogenetic tree combined chord diagram to show relationship data, such as correlation data of species or genes, horizontal gene transfer and syntenic linkage. However, *ggtreeExtra* support this feature (Fig. S9), because of its unique design (Fig. S1). This proves *ggtreeExtra* is more powerful and universal than other tools again.

```

library(ggtree)
library(ggteeExtra)
library(ggplot2)
library(MicrobiotaProcess)
library(ggstar)
library(ggnewscale)
library(grid)

alltax <- read.csv("../data/Arabidopsis_leaf_microbiome/all_stain_taxonomy.csv")
linktab <- read.csv("../data/Arabidopsis_leaf_microbiome/Interaction_link_tab.csv")
weighttab <- read.csv("../data/Arabidopsis_leaf_microbiome/Interaction_weight.csv")
tippoint <- read.csv("../data/Arabidopsis_leaf_microbiome/stain_tippoint.csv")
BGCsda <- read.csv("../data/Arabidopsis_leaf_microbiome/BGCs_heatmap.csv")

tippoint$Taxa <- factor(tippoint$Taxa,
                         levels=c("Actinobacteria",
                                  "Bacteroidetes",
                                  "Firmicutes",
                                  "Deinococcus-Thermus",
                                  "Alphaproteobacteria",
                                  "Betaproteobacteria",
                                  "Gammaproteobacteria"
                         )
)
tippoint$names <- gsub("s_Leaf","",tippoint$Isolation)

BGCsda$BGCs <- factor(BGCsda$BGCs,
                       levels=c("modular.PKS",
                               "modular.PKS.NRPS.hybrid",
                               "non_modular.PKS", "NRPS",
                               "RiPP",
                               "Quorum.sensing",
                               "terpene",
                               "other"
                       )
)
BGCsda$Count <- log10(BGCsda$Count+1)
BGCsda$Count <- ifelse(BGCsda$Count==0, NA, BGCsda$Count)

trda <- convert_to_treedata(alltax)
p <- ggtree(trda, layout="inward_circular", size=0.2, xlim=c(18,NA))
p <- p %<+% tippoint

p1 <- p +
  geom_tippoint(

```

```

mapping=aes(
    color=Taxa,
    shape=Level
),
size=1,
alpha=0.8
) +
scale_color_manual(values=c("#EF3B2C", "#1D91C0", "#FEB24C", "grey60",
                            "#7FBC41", "#4D9221", "#276419"),
                    guide=guide_legend(
                        keywidth=0.5,
                        keyheight=0.5,
                        order=2,
                        override.aes=list(shape=c("Actinobacteria"=20,
                                                  "Bacteroidetes" =20,
                                                  "Firmicutes" =20,
                                                  "Deinococcus-Thermus" =20,
                                                  "Alphaproteobacteria" =18,
                                                  "Betaproteobacteria" =18,
                                                  "Gammaproteobacteria" =18
                                                ),
                        size=2
                      ),
na.translate=TRUE
)
) +
scale_shape_manual(values=c("Phylum"=20, "Class"=18), guide="none" )

p2 <- p1 +
  new_scale_color() +
  geom_taxalink(
    data=linktab,
    mapping=aes(
      taxa1=Inhibitor,
      taxa2=Sensitive,
      color=Interaction
    ),
    alpha=0.6,
    offset=0.1,
    size=0.15,
    ncp=10,
    hratio=1,
    arrow=grid::arrow(length = unit(0.005, "npc"))
  ) +
  scale_colour_manual(values=c("chocolate2", "#3690C0", "#009E73"),
                      guide=guide_legend(
                        keywidth=0.8, keyheight=0.5,
                        order=1, override.aes=list(alpha=1, size=0.5)
                      )
  )
)

p3 <- p2 +
  geom_fruit(
    data=BGCsda,
    geom=geom_tile,
    mapping=aes(
      y=Strain,
      x=BGCs,
      alpha=Count,
      fill=BGCs
    )
  )

```

```

),
offset=-0.9,
pwidth=1,
size=0.02,
color = "grey50"
) +
scale_alpha_continuous(range=c(0.1, 1),
                       name=bquote(paste(Log[10], "(",.("Count+1"), ")")),
                       guide=guide_legend(keywidth = 0.4, keyheight = 0.4, order=4)
) +
scale_fill_manual(
  values=c("#66C2A5", "#FC8D62", "#8DA0CB", "#E78AC3",
          "#A6D854", "#FFD92F", "#E5C494", "#B3B3B3"),
  guide=guide_legend(keywidth = 0.4, keyheight = 0.4, order=3)
)

p4 <- p3 +
  geom_tiplab(
    mapping=aes(
      label=names
    ),
    align=TRUE,
    size=1,
    linetype=NA,
    offset=7.8
  )

p5 <- p4 +
  new_scale_fill() +
  geom_fruit(
    data=weighttab,
    geom=geom_bar,
    mapping=aes(
      x=value,
      y=Strain,
      fill=Number
    ),
    stat="identity",
    orientation="y",
    offset=0.48,
    pwidth=2,
    axis.params=list(
      axis = "x",
      text.angle = -45,
      hjust = 0,
      vjust = 0.5,
      nbreak = 4
    )
  ) +
  scale_fill_manual(
    values=c("#E41A1C", "#377EB8", "#4DAF4A", "#984EA3"),
    guide=guide_legend(keywidth=0.5, keyheight=0.5, order=5)
) +
theme(
  legend.background=element_rect(fill=NA),
  legend.title=element_text(size=6.5),
  legend.text=element_text(size=5),
  legend.spacing.y = unit(0.02, "cm"),
  legend.margin=margin(0.1, 0.9, 0.1, -0.9, unit="cm"),
  legend.box.margin=margin(0.1, 0.9, 0.1, -0.9, unit="cm"),

```

```
plot.margin = unit(c(-1.2, -1.2, -1.2, 0.1), "cm")
```

p5

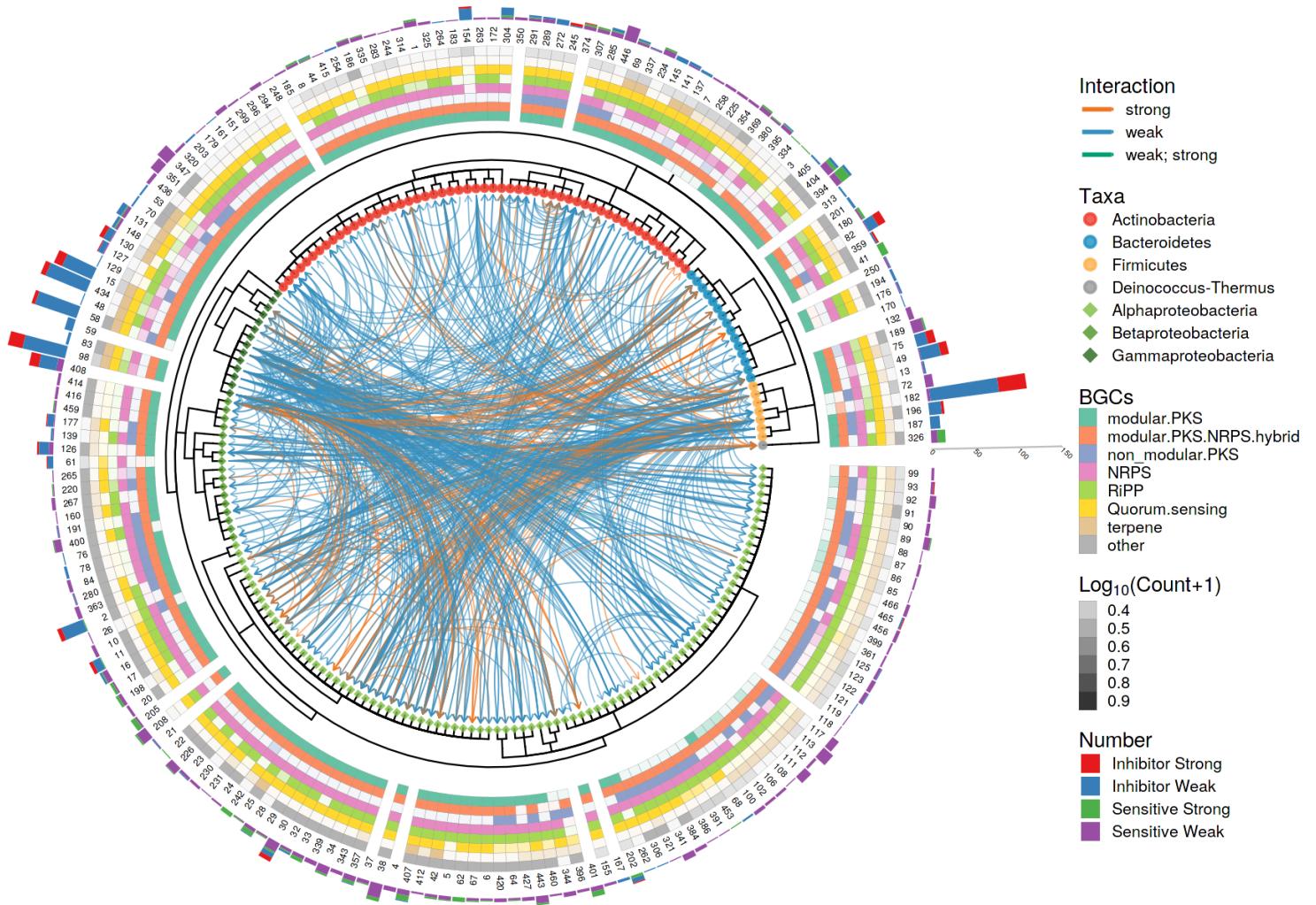


Fig. S9: Illustration of representing multi-dimensional data sets on inward circular phylogenetic tree with chord diagram incorporated to display inter-relationships. The inward circular layout tree reflects the evolutionary relationships among isolates from *Arabidopsis* leaf microbiome (Bai et al. 2015). In the center of the plot, the arcs connect isolates to show the inhibitory interactions, the arc arrows were meant to indicate directional inhibition and the colors of the arcs represent interaction strengths (*i.e.* weak or strong). The colors of symbolic points on tips indicate taxonomy annotation and circle points represent the phylum while square points represent the class from Proteobacteria. The heatmap on external ring displays the number of detected BGCs (biosynthesis gene clusters). The outermost ring use stacked bar chart to visualize the number of inhibitory and sensitivity interactions per strain.

## 4 Summary

There are some tools depending on python or other platform to annotate phylogenetic tree with associated data, but they are not general and still have some shortcomings. For example, they support less layouts and less geometric layers for tree annotation (tree and data graphic alignment) (Tab. S1 and Fig. S2). And many tools need user providing configure file mixed associated data and profiler of graphic, which make them tedious and error-prone since the profiler of graphic layer (*e.g.* color or size) should be consistent for the same information (Fig. S8 in 3.3). These features make these tools not universal. It is worth mentioning that *ggtree* has also provided *facet\_plot(geom\_facet)* to annotated phylogenetic tree with external data (Yu et al. 2018). This function is also a universal function with many unique features (Yu et al. 2018). But it can not work with circular layout tree, which is an efficient way to visualize multi-dimensional dataset and phylogenetic tree, since circular layout can reduce space and make the graph more compact. Fortunately, *geom\_fruit* of *ggtreeExtra* inherits the design concept of *facet\_plot (geom\_facet)* of *ggtree* (Yu et al. 2018) and supports more layouts for tree annotation (tree and data graphic

alignment), So *geom\_fruit* has also some features contained in *facet\_plot(geom\_facet)*. For example:

1. No restriction of input data types or how the data should be plotted in *geom\_fruit*, it depends on the data types of various geometric functions. (Tab. S2 and 3.1)
2. Associated data integrated by %<+% can also be used in “*geom\_fruit*”. (Fig. S6)
3. Combining different *geom* functions to visualize associated data is supported. (Fig. S8)
4. Supporting ggplot object subplot or image. (Fig. S5)
5. Supporting grammar of graphic. (Fig. S7)

In addition, the phylogenetic tree annotated by *ggtreeExtra* can also be converted to another layout tree (Fig. S3). Moreover, although other tools can also integrate similar geometric layer to *ggtreeExtra*, such as bar plot, box plot, *ggtreeExtra* is more powerful and flexible since it inherits the features of corresponding **geom** functions (Fig. S4 and S5). Furthermore, *ggtreeExtra* also supports annotation of phylogenetic combined chord diagram, which is an efficient way to display relationship data, such as correlation data of species or genes, horizontal gene transfer and syntenic linkage (Fig. S9). This feature is also not available in other tools. Therefore, the versatility of this package ensure its applications in different research areas such as population genetics, molecular epidemiology and microbiome.

**NOTE:** source code to produce this file can be obtained online<sup>5</sup>.

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<sup>5</sup><https://github.com/YuLab-SMU/plotting-tree-with-data-using-ggtreeExtra>

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