

# ggtreeExtra: Compact visualization of richly annotated phylogenetic data

Shuangbin Xu, Zehan Dai, Pingfan Guo, Xiaocong Fu, Shanshan Liu, Lang Zhou, Wenli Tang, Tingze Feng, Meijun Chen, Li Zhan and Guangchuang Yu\*

\*correspondence: guangchuangyu@gmail.com, gcyu1@smu.edu.cn

## 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 a 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 chart, 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).

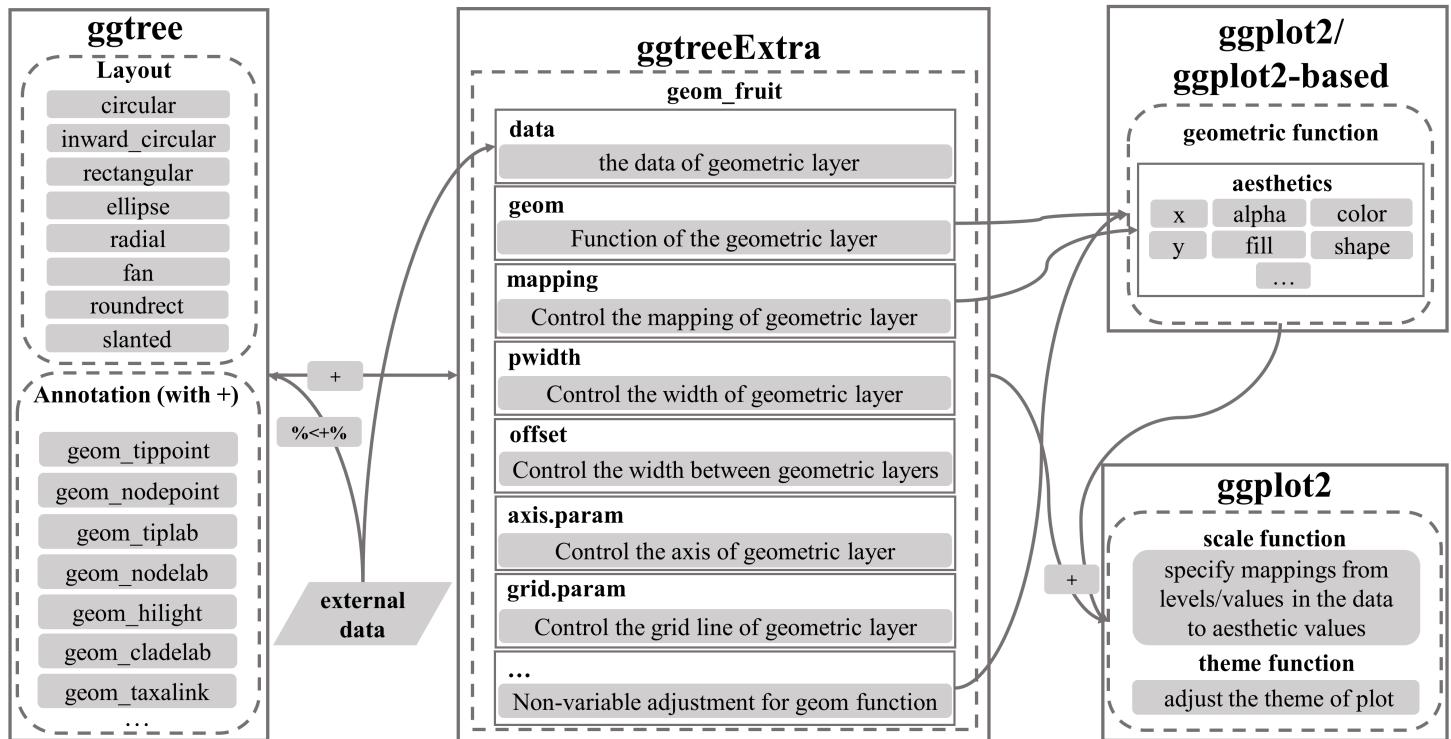


Fig. S1: Overview of the design of *ggtreeExtra* package.

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 plot, simple bar chart, patter bar, stacked bar chart, dodged bar chart, boxplot, pattern boxplot, violin, dot intervals plot, density plot, line plot, pie chart, image plot, inset plot	Yes	add, modify, delete	Yes	programming and command line
GraPhlAn	Python package	circular	Heat map, scatter plot, simple bar chart	Yes	add	No	command line with configure file
ETE3	Python package	rectangular	Heat map, scatter plot, simple bar chart, stacked bar chart, boxplot, pie chart, image plot, protein domain, MSA <sup>3</sup>	Yes	add	No	programming and command line
iTOL	Web tool	circular, rectangular, slanted, ellipse, inward circular	Heat map, scatter plot, simple bar chart, stacked bar chart, dodged bar chart, boxplot, line plot, pie chart, image plot, protein domain, MSA	Yes	add	No	interactive (mouse click with configure file)
Microreact	Web tool	circular, rectangular	Heat map, scatter plot	Yes	add	No	interactive (mouse click and command line with configure file)
Evolview	Web tool	circular, rectangular, slanted, round rectangular	Heat map, scatter plot, simple bar chart, stacked bar chart, protein domain	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;

<sup>3</sup> MSA: multiple sequence alignments

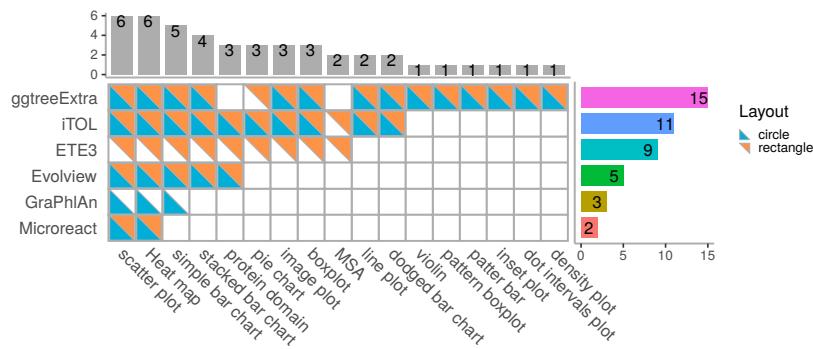


Fig. S2: Visualization methods for tree annotation supported by different software tools. Note: circle: circular, inward circular, radial; rectangle: rectangular, slanted, ellipse, round rectangular.

## 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).

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
ggimage	geom_image	alpha, color, fill	creates slab, point and interval meta-geom
	geom_phylopic	alpha, color, fill	visualizes image files
ggpattern	geom_bar_pattern	pattern_alpha, pattern_color, pattern_fill	queries image files from phylopic database and visualizes them
	geom_boxplot_pattern	pattern_alpha, pattern_color, pattern_fill	draws bar charts with support for pattern fills
	geom_col_pattern	pattern_alpha, pattern_color, pattern_fill	draws box and whiskers plot with support for pattern fills
	geom_tile_pattern	pattern_alpha, pattern_color, pattern_fill	draws bar charts using 'stat_identity()' with support for pattern fills
ggplot2	geom_bar	pattern_alpha, pattern_color, pattern_fill	draws rectangle by using the center of the tile and its size with support for pattern fills
	geom_boxplot	alpha, color, fill	draws bar charts
	geom_col	alpha, color, fill	draws box and whiskers plot
	geom_label	alpha, color, fill, size	draws bar charts using 'stat_identity()'
	geom_point	alpha, color, fill, shape, size	draws a rectangle behind the text
	geom_raster	alpha, fill	creates scatterplots
	geom_text	color, size	a high performance special case for all the tiles are the same size
ggpmisc	geom_tile	alpha, color, fill	adds text to the plot
	geom_plot	vp.width, vp.height	adds rectangle by using the center of the tile and its size
ggrepel	geom_table	size	ggplot objects as insets to the base ggplot, using syntax similar to that of 'geom_label'
	geom_text_repel	color, size	adds a textual table directly to the ggplot, using syntax similar to that of 'geom_label'
ggridges	geom_label_repel	alpha, color, fill, size	adds text to the plot. The text labels repel away from each other and away from the data points
	geom_density_ridges	alpha, fill	draws a rectangle underneath the text. The text labels repel away from each other and away from the data points
	geom_density_ridges2	alpha, fill	arranges multiple density plots in a staggered fashion
	geom_ridgeline	alpha, color, fill	arranges multiple density plots in a staggered fashion
ggstance	geom_ridgeline_gradient	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_barh	alpha, color, fill	works just like 'geom_ridgeline' except that the 'fill' aesthetic can vary along the x axis
	geom_boxploth	alpha, color, fill	horizontal version of 'geom_bar()'
ggstar	geom_colh	alpha, color, fill	horizontal version of 'geom_boxplot()'
	geom_star	alpha, color, fill, size, starshape	horizontal version of 'geom_col()'
ggsymbol	geom_symbol	alpha, color, fill, size, symbolshape	creates scatterplots
ggtext	geom_richtext	alpha, color, fill, size, fontface	creates scatterplots
scatterpie	geom_scatterpie	alpha, color, fill	draws text labels similar to 'ggplot2::geom_label()', but formatted using basic markdown/html

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 plot, 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.

Here to demonstrate the usages of *ggtreeExtra* with other *ggplot2*-based packages, we provided several examples, including density plot with *ggridges* (Fig. S3A and C), boxplot with *ggplot2* (Fig. S3B and D) and *ggpattern* (Figure S4C and D), bar chart with *ggpattern* (Fig. S4A and B), subplot with *ggpmisc* (Fig. S5A) and silhouette image with *ggimage* (Fig. S5B). These examples also illustrate the design of the *ggtreeExtra* package (Fig. S1). The *ggtreeExtra* package supports the grammar of graphic syntax and allows employing geometric layers defined in the *ggplot2* community to visualize phylogenetic data with a tree. 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, inset 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 and advantages of the geometric functions developed by the community. For example, *iTOL* (Letunic and Bork 2019), *ETE3* (Huerta-Cepas, Serra, and Bork 2016) and *ggtreeExtra* all support displaying image plot on the phylogenetic tree, but

only *ggtreeExtra* supports mapping variable to color and scale the images (Fig. S5B<sup>1</sup>). In addition, *ggtreeExtra* supports several visualization methods that cannot be found elsewhere. For example, subplots that describe statistical information of taxa can be embeded as insets in *ggtreeExtra* (Fig. S5A) to annotate corresponding taxa. 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.

## 2.1 Visualizing distribution of species abundance

Species phylogenetic tree and abundance in each samples are often common. To view the distribution of species abundance with phylogenetic tree, here, a microbiome data provided in *phyloseq* package (McMurdie and Holmes 2013), density plot and box plot are used to display the abundance data (continuous data) via specified *geom* i.e. *geom\_density\_ridge* and *geom\_boxplot*. The abundance data (i.e. *melt\_simple*) is a data frame require by *geom\_density\_ridges* and *geom\_boxplot*. It has a column (i.e. *OTU*) contained tip labels of phylogenetic tree, another column (i.e. *val*) contained abundance of the species. The data frame was imported by the *data* argument of *geom\_fruit* function. Then the column (i.e. *OTU*) contained tip labels was assigned to the *y* axis in *aes*. The column (i.e. *val*) contained corresponding abundance was assigned to the *x* axis in *aes*. Then the phylum (i.e. *Phylum*) information which is in the *ggtree* object was assigned to the *fill* aesthetic to color the density ridge plot and box plot in *aes*. 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(ggplot2)
library(ggtreeExtra)
library(patchwork)
library(gggridges)
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(
    mapping=aes(color = Phylum),
    show.legend = FALSE,
    size=0.6
  )

p1 <- p +
  geom_fruit(
    data = melt_simple,
    geom = geom_density_ridges,
    mapping = aes(
      y = OTU,
```

---

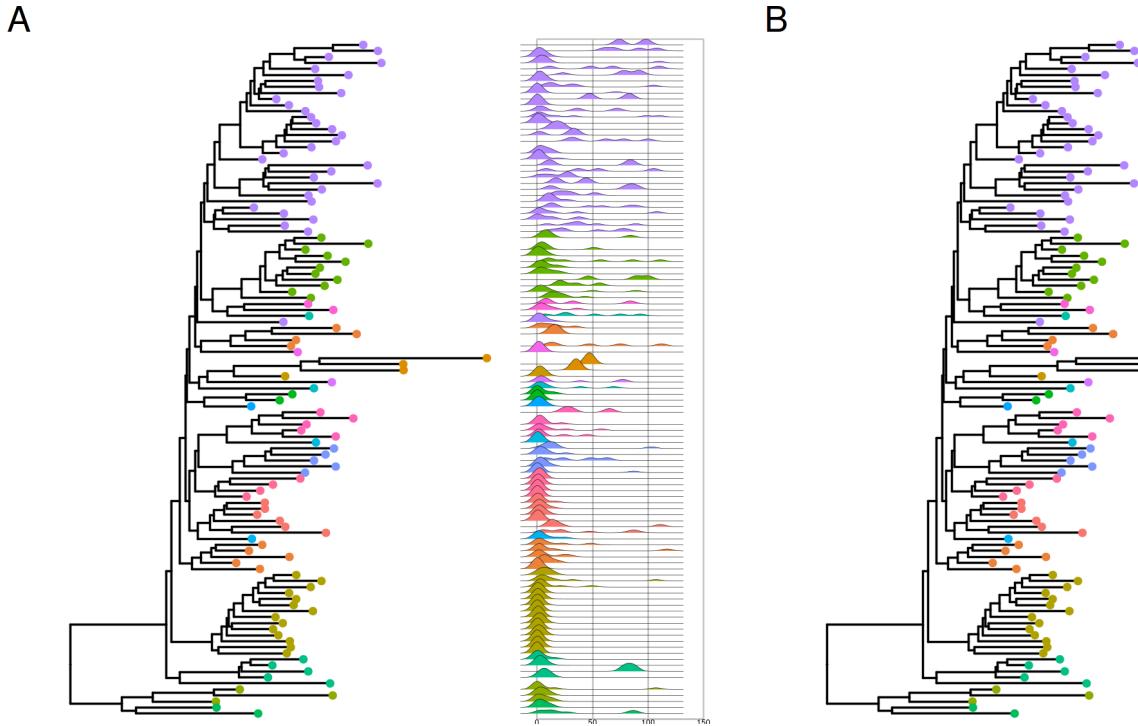
<sup>1</sup>The data that used to generate Fig. S5B is from Fig.1 of (Song et al. 2020) and it is available on [https://github.com/tanaes/tetrapod\\_microbiome\\_analysis](https://github.com/tanaes/tetrapod_microbiome_analysis)

```

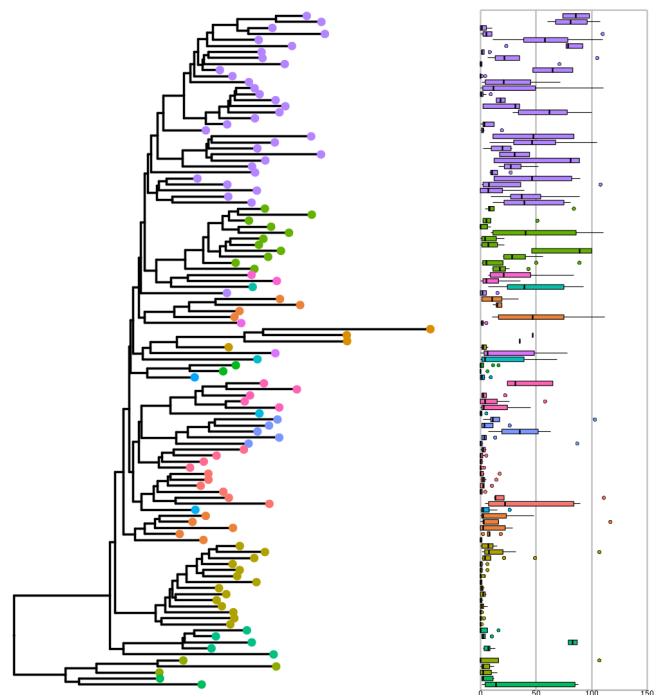
        x = val,
        fill = Phylum
    ),
    offset = 0.12,
    pwidth = 0.4,
    lwd = .05,
    axis.params = list(
        axis = "x",
        text.size = 1,
        hjust = 0.5,
        vjust = 1
    ),
    grid.params = list(),
    show.legend = FALSE
)

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')

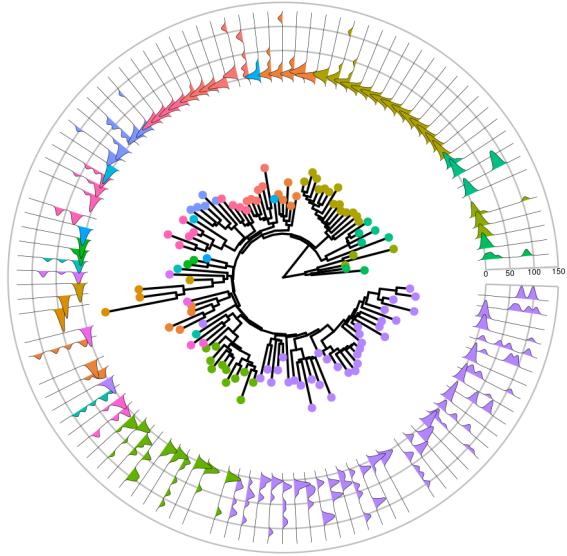
```



**A**

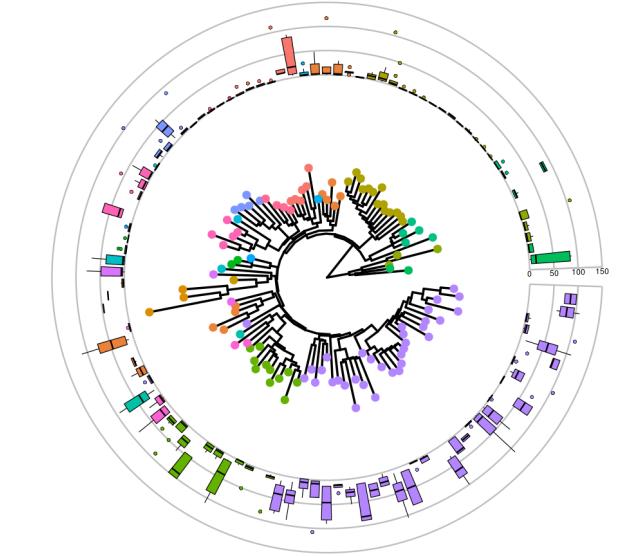


**B**



**C**

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 density ridge plot and box plot. 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.



**D**

## 2.2 Versatile bar and box plots by filling with colors and patterns

Although the above example is for a specific field, the method is general and can be applied in other fields. In this session, we generated two data frames (associated data) randomly. Each of them contains three columns, which have both a column (*i.e.* `id`) contained tip labels, a column (*i.e.* `value`) contained numerical data (continuous data), and a column (*i.e.* `group`) contained grouped data (discrete data). The two data frame are required by `geom_bar_pattern` and `geom_boxplot_pattern` of

*gppattern* respectively. The phylogenetic tree is also generated randomly, it was import to a *ggtree* graphic object using *ggtree* with different layouts. Then one of data frames (*i.e.* *dat*) was import by the *data* argument of *geom\_fruit* function, the *geom* argument was specified to *geom\_col\_pattern*, the column *i.e.* *id* contained tip labels was assigned to *y* axis in *aes*, the column *i.e.* *value* was assigned to *x* axis in *aes*, the column *i.e.* *group* was assigned to *pattern* and *pattern\_angle* (to generate more patterns when group is more than three) in *aes*. Next, the attributes of the layer was adjusted with non-variable of aesthetic setting (such as *width* to control the width of bar chart, *pattern\_fill* to control the color of pattern in bar chart etc.). For another data frame *i.e.* *dt*, it is required by *geom\_boxplot\_pattern*, it also imported by *data* argument of *geom\_fruit*, the *geom* argument was specified to *geom\_boxplot\_pattern* of *gppattern* package (FC 2020), then the column *i.e.* *id* contained tip labels was also assigned to *y* axis in *aes*, the column *i.e.* *value* was also assigned to *x* axis in *aes*, the column *i.e.* *group* was also assigned to *pattern* and *pattern\_angle* in *aes*. Again, the attributes of the layer was adjusted with non-variable of aesthetic setting.

```

library(ggtree)
library(ggtreeExtra)
library(gppattern)
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"
) %>% tidyr::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"
) %>% tidyr::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_col_pattern,
    mapping=aes(y=id, x=value, pattern=group, pattern_angle=group),
    width=0.6,
    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=1)
  ) +
  theme(legend.key.size = unit(0.3, 'cm'))

```

```

p2 <- p2 +
  geom_fruit(
    data=dat,
    geom=geom_col_pattern,
    mapping=aes(y=id, x=value, pattern=group, pattern_fill=group),
    width=0.6,
    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=1)
) +
  theme(legend.key.size = unit(0.3, 'cm'))

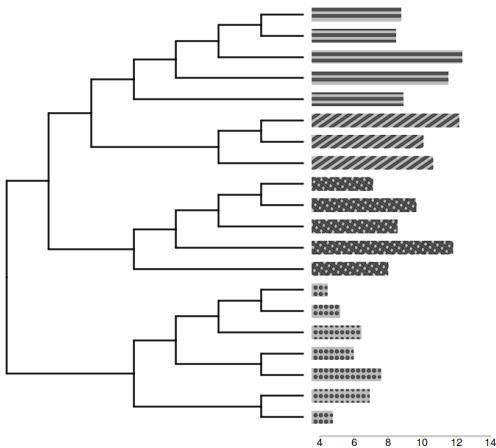
p3 <- p3 +
  geom_fruit(
    data=dt,
    geom=geom_boxplot_pattern,
    mapping=aes(y=id, x=value, pattern=class, pattern_angle = class),
    size=0.1,
    outlier.shape=NA,
    pwidth=0.5,
    pattern_size = 0.1,
    pattern_density = 0.4,
    pattern_spacing =0.01,
    fill = "grey",
    pattern_fill="grey35",
    position=position_dodgex(),
    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'))

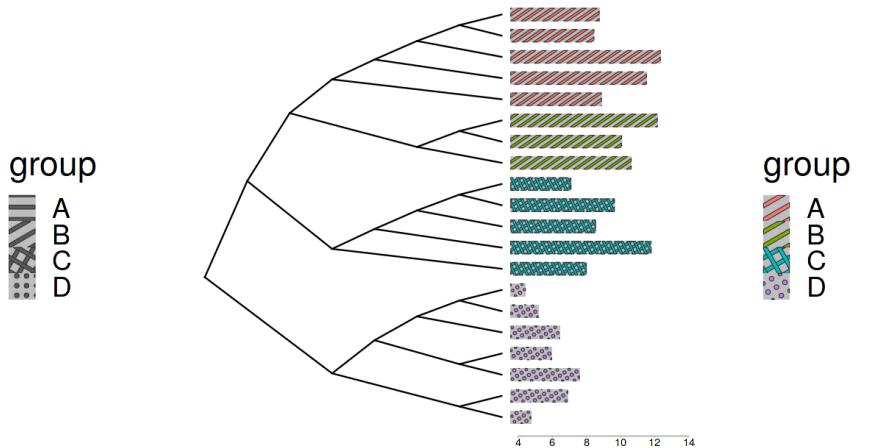
(p1 + p2)/(p3 + p4) + plot_annotation(tag_levels = 'A')

```

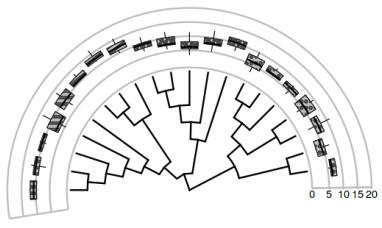
A



B

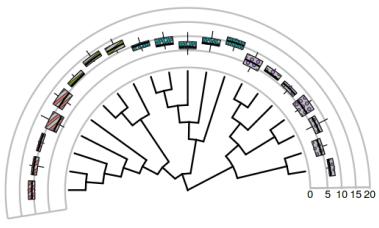


C



group  
 — A  
 — B  
 — C  
 — D

D



group  
 — A  
 — B  
 — C  
 — D

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

## 2.3 Taxon-specific graphical information

Supporting adding taxon-specific graphical information on the outside of phylogenetic tree is one of the important features of *ggtreeExtra*. Although iTOL (Letunic and Bork 2019), and ETE3 (Huerta-Cepas, Serra, and Bork 2016) also support this, *ggtreeExtra* is more powerful and flexible.

First, the subplots that describe statistical information of taxa can be embedded as insets in *ggtreeExtra* (Fig. S5A) to annotate corresponding taxa by linking *geom\_plot* of *ggpmisc* package (Aphalo 2020). Here, a phylogenetic tree was generated by random. Two subplots (*i.e.* *subp1* and *subp2*) that describes statistical information of two tips (*i.e.* *t2* and *t14*) was built by *ggplot2* (Wickham 2016), next, the subplots and tip labels was save a *tibble* object (*i.e.* *dt*) required by *geom\_plot*. Then the data was also import by *data* argument of *geom\_fruit*, and the *geom* was specified to *geom\_plot*, the tip labels column (*i.e.* *id*) was assigned to *y* axis in *aes*, the column (*i.e.* *plot*) contained subplots was assigned to *label* in *aes*.

Second, the local or online images files such as those deposited on phylopic database<sup>2</sup> are also supported labeling on the outside of phylogenetic tree by *ggtreeExtra*. It also supports mapping variables of associated data to color and scale the images (Fig. S5B<sup>3</sup>). The images layer can also combined with other layers (Fig. S5B). In this example, the bar chart, clade label and heat map was firstly added one by one, then the images layer was added in the outermost ring. We will describe the combination of layers in the next following section in detail. Here, we focus on how to add images in the outer ring. Firstly, a data frame *i.e.* *phylopeda* required by *geom\_phylopic* of *ggimage* and contained three columns (one column *i.e.* *taxa* contains some tip labels, one column *i.e.* *uid* contains image id of phylopic database, one column *i.e.* *class* contains the taxonomy information) was built. Then it was also imported by *data* argument of *geom\_fruit*, *geom* was specified to *geom\_phylopic*. Next, the *taxa* column was assigned to *y* axis in *aes*, *uid* was assigned to *image* in *aes*, *class* was assigned to *color* in *aes* (this can color the images).

<sup>2</sup><http://phylopic.org/>

<sup>3</sup>The data that used to generate Fig. S5B is from Fig.1 of (Song et al. 2020) and it is available on [https://github.com/tanaes/tetrapod\\_microbiome\\_analysis](https://github.com/tanaes/tetrapod_microbiome_analysis)

```

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)

# Optional for color branches.
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"
    )
  )
# Bar chart in the innermost ring
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)
)
# Clade label in the inner ring
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)))
)
# Clade in the middle ring
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))
  )
# Silhouettes image in the outermost ring
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",

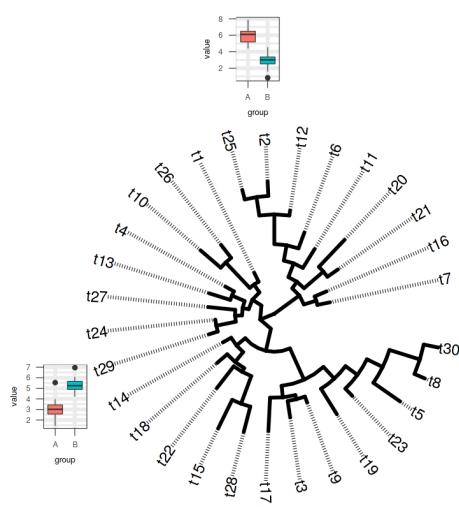
```

```

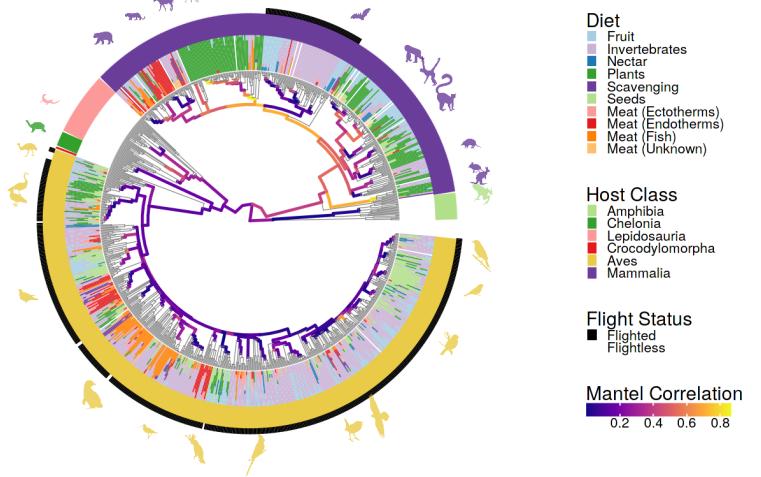
      "#EACB47", "#6a3d9a"),
      guide="none"
    ) +
  theme(
    legend.background=element_rect(fill=NA),
    legend.title=element_text(size=7),
    legend.text=element_text(size=5),
    legend.spacing.y = unit(0.02, "cm")
  )
p2 + fig4 + plot_annotation(tag_levels = 'A')

```

A



B



**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 (A). Taxon information can be used color or scale the size of silhouette images (B). The host tree (B) was obtained from TimeTree (Kumar et al. 2017). The branch colour represents the Mantel Pearson correlation of gut microbiome. The first ring uses stack bar chart to represent the diet composition of the host. The second ring represents the host taxonomic class and the third ring represents flight status. Some of the representative species are displayed in the outermost ring and colored by taxonomic class (B).

### 3 Mapping and visualizing associated data using the *ggtreeExtra* package

The *ggtreeExtra* package allows different geometric layers defined in *ggplot2* (Wickham 2016) or *ggplot2*-extension packages (Tab. S1, S2 and Fig. S2) to be integrated on a phylogenetic tree. The combination of these geometric layers allows a number of associated data sets to be visualized with a tree side by side (Fig. S3 and S4). The *ggtreeExtra* package supports tree annotation for multiple tree layouts (Fig. S3, S4, S2 and Tab. S1), including rectangular and circular layouts. Circular layout is an efficient way to visualize multi-dimensional data sets, since it can reduce space and make the graph more compact.

The associated data can be imported with the *data* parameter of the *geom\_fruit* function (Fig. S3 and S4). The *geom\_fruit* function can utilize tree data integrated to the *ggtree* graphic object by the %<+>% operator (Yu et al. 2018) defined in the *ggtree* package (Fig. S1). In addition, tree data parsed by the *treeio* package (Wang et al. 2020) can also be used in *ggtreeExtra*.

The *ggtreeExtra* package was developed based on the grammar of graphic (Wilkinson 2012). It allows users mapping variables (*e.g.* abundance of species, length of genome, sampling location) of the associated data to the visual attributes (*e.g.* color, size, shape) of the geometric objects (*e.g.* bar chart, point, boxplot) on rectangular or circular phylogenetic tree (Fig. S1). Users are freely to combine different geometric layers to create complex tree annotation. We present many examples to elucidate how to use *ggtree* and *ggtreeExtra* to visualize data on phylogenetic trees in the online book<sup>4</sup>.

<sup>4</sup><http://yulab-smu.top/treedata-book>

### 3.1 Data importation

The *ggtreeExtra* is a sub-package of the *ggtree* package suite and it works seamlessly with *ggtree* (Yu et al. 2017), *treeio* (Wang et al. 2020) and *tidytree*. Tree data parsed by *treeio* (Wang et al. 2020) can be used directly in *ggtreeExtra*. This allows 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), *PHYLODOG* (Boussau et al. 2013) and *EPA* (Berger, Krompass, and Stamatakis 2011), to be incorporated and visualized with *ggtreeExtra*. Any data frame that contains a column of tip labels can be integrated into a *ggtree* graphic object using `%<+%` operator (Yu et al. 2018) and can be imported directly in the *geom\_fruit* via the *data* parameter. Consequently, *ggtreeExtra* supports visualizing evolutionary statistics inferred by commonly used software tools (via the *treeio* package) and external associated data (*e.g.* experimental or clinical data) (Fig. S6). These unique features ensure that *ggtreeExtra* supports more diverse sources of data compare to other tools.

In previous examples (Figure S3-5), we have demonstrated the usage of importing external data directly in *geom\_fruit*. Here, we reproduce Figure 3.3 (also served as the book cover) of (Smith and Wrighton 2019)<sup>5</sup> to show how to use internal data stored in a tree object and integrate external associated data to a tree using the `%<+%` operator and visualize the in *ggtreeExtra*. The tree was built using *RAXML* (Stamatakis 2014) and was parsed by the *read.raxml* function provided by the *treeio* package (Wang et al. 2020). Clade support (*i.e.*, bootstrap values) will be parsed and stored in the output tree object. The tree was visualized by *ggtree* (Yu et al. 2017). There are associated data sets that contain the information of Ecosystem type, sequencing type and sample treatment method (all categorical data). The first column of external data should be tip labels and the element of the column must be unique, so that the data can be linked to the *ggtree* graphic object using the `%<+%` operator. The *geom\_fruit* function is able to utilize internal tree data from the tree object (either parsed by *treeio* or integrated by *ggtree*). The variable of the data can be mapped to related attributes of the geometry layer. In this case of using internal data, the *y* aesthetic mapping can be ignored. Here we used heat map to visualize categorical data. The external ring heat maps represent different types of corresponding categories (*i.e.*, the types of Ecosystem were mapped to the color of the innermost ring heat map, the types of sequencing methods were mapped to the color of the middle ring heat map and the types of sample treatment were mapped to the color of outermost ring heat map) (Fig. S6).

Comparing with other tools, there is no restriction of data types in *geom\_fruit* of the *ggtreeExtra* package. It depends on the data types required by corresponding geometric functions (Tab. S2). For example, visualizing distribution of species abundance (numerical data with unequal lengths) with a tree is not supported by other tools. Such data can be visualized as density plots using *geom\_density\_ridges* (Wilke 2020) in *ggtreeExtra* (Fig. S3A and C). Even *ggplot* graphic objects (a complex data structure produced by *ggplot2*) can be served as taxon-specific data and can be used in *ggtreeExtra* via the *geom\_plot* layer provided by the *ggpmisc* package (Aphalo 2020). As long as a data type is supported by a geometric layer that works with *ggtreeExtra* (Tab. S2), it is supported by *ggtreeExtra*. Since there will more *ggplot2* extensions developed in the future, more data types will be supported and the applications of *ggtreeExtra* in multi-discipline areas will also be expanded.

```
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"))
```

<sup>5</sup>the source data is available on [https://github.com/TheWrightonLab/Methanotroph\\_rpS3Analyses\\_SmithWrighton2018](https://github.com/TheWrightonLab/Methanotroph_rpS3Analyses_SmithWrighton2018)

```

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:
##   3300019787==Ga0182031_12339262, 3300014838==Ga0182030_1009273110, gb_PLVF01000413_pos14750To15429=Methyloc
## 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
)

```

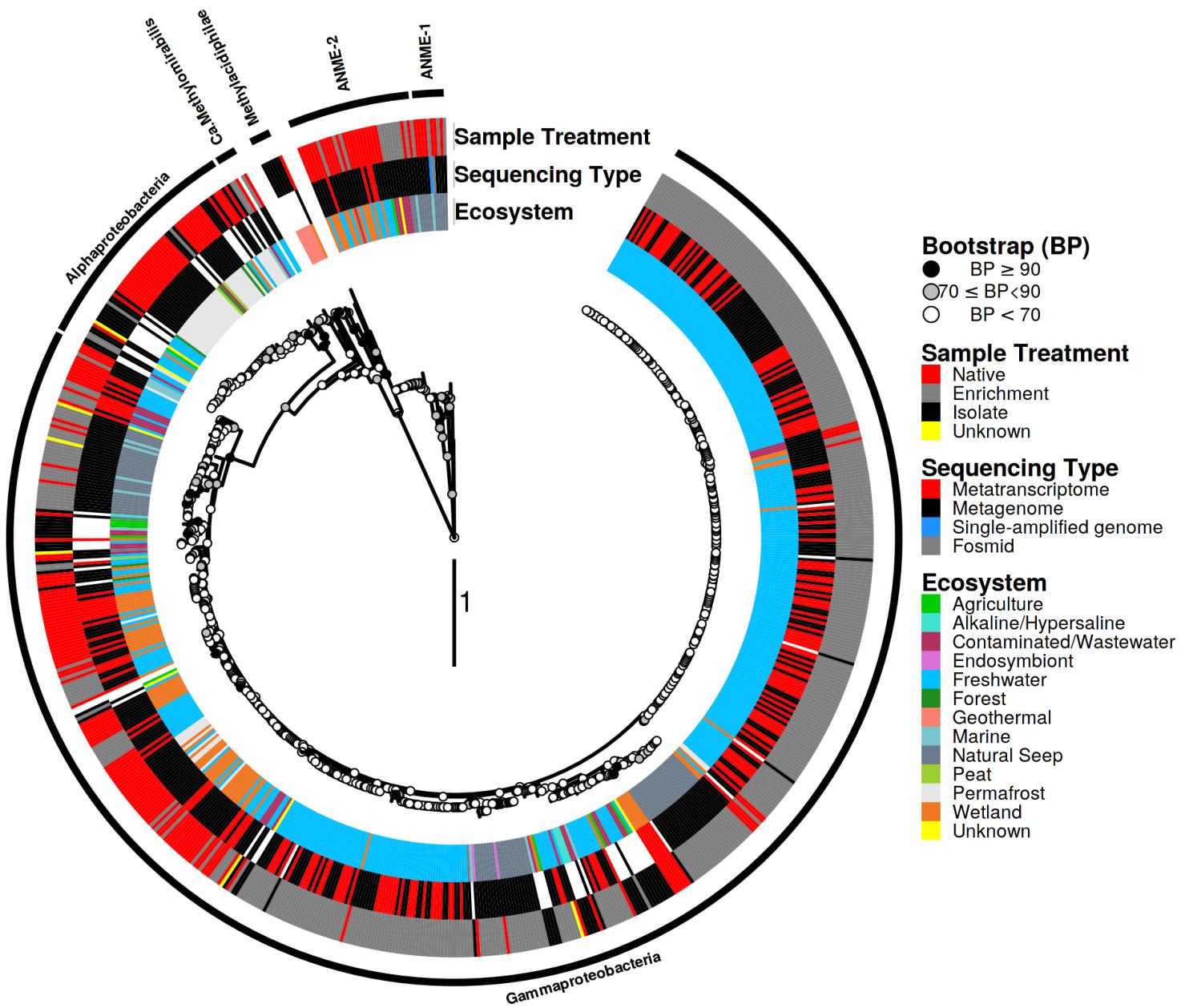


Fig. S6: Phylogeny of methanotroph ribosomal protein S39 (rpS3) genes from Figure 3.3 of (Smith and Wrighton 2019). Bootstrap value was parsed with the tree by the *read.raxml* function and other associated data sets were integrated to the tree via the %<+% operator. The *ggtreeExtra* can directly use these data sets to visualize data layers.

### 3.2 Displaying multiple associated data using a layered grammar of graphics

The *ggtreeExtra* supports the grammar of graphics (Wilkinson 2012) implemented in the *ggplot2* package (Wickham 2016) (Wickham 2016). In previous sessions, we have demonstrated the usages of aesthetic mapping, which allows user to map variables of associated data to visual characteristic at high level of abstraction (Fig. S3, S4, S5 and S6). Other tools (Tab. S1), such as GraPhlAn (Asnicar et al. 2015), relies on user to convert associated data to visual values (*e.g.* color, position) manually and data conversion may require. For example, the input for GraPhlAn is phyloxml which contains tree, visual values of associated data and configuration setting. Such data file is hard to prepare for ordinary users without programming expertise.

In this session, we emphasize another part of the grammar of graphics – the *ggplot2* layered graphics. Visualizing each layer is simple as we can specify aesthetic mapping and don't need to care about how data was converted to the actual visual values. Different layers can be progressively added to the plot to integrate different visualization methods for different data

sets and thus leading to a personalized and complex tree graphic. Here, as an example we reproduce Fig.2 of (Morgan, Segata, and Huttenhower 2013) to demonstrate how to combine different data graphic layers to a circular phylogenetic tree using *ggtreeExtra*. The data sets<sup>6</sup> contain the relative abundance of bacteria (continuous data) at different body sites (categorical data). The associated data sets were imported by the *data* parameter of the *geom\_fruit* function and displayed by corresponding geometric functions.

The tree was first visualized and annotated by *ggtree* with symbolic points to differentiate commensal microbes and potential pathogens (Fig. S7A), grey background to highlight different clades and the clades were labeled by corresponding names (Fig. S7B). Then a heat map was used to display the abundance of the microbes at different body sites. Heatmap cells are filled with different colors to represent different sampling sites and the transparency of the heatmap cells indicates corresponding abundance of the microbes (Fig. S7C). Finally, a stacked bar chart was employed to display relative abundance of the most abundant species at different body sites (Fig. S7D). The color of the bar chart represents different body sites and it is consistent with the color used in the heatmap. (Fig. S7A-D) were produced by adding multiple layers on the tree with a step-by-step solution. Source code for each layer is relatively simple and easy to follow. The combination of these layers eventually create a compact graphic that represents complex information from several data sets. The *ggtreeExtra* package works seamlessly with *ggtree*, a tree annotated by *ggtree* (Fig. S7A-B) can be used in *ggtreeExtra* to add data graphic layers on external panels and vice versa.

```
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])
nodeiddf <- 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
```

<sup>6</sup>extracted from phyloxml file downloaded from <https://github.com/biobakery/graphlan/tree/master/examples>

```

) +
scale_fill_manual(
  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 high light 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"
  )
# Heat map, using geom_fruit to link geom_tile
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")
# Bar chart, using geom_fruit to link geom_col
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(),
  )+

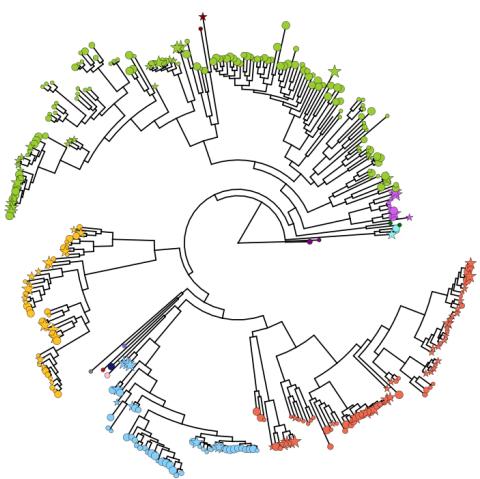
```

```

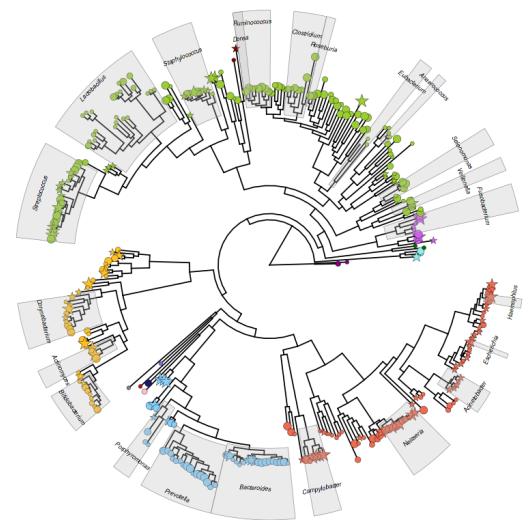
geom_treescale(fontsize=1.2, linesize=0.3, x=4.9, y=0.1) +
theme(legend.position="none")
p4 <- (p + p1 + plot_layout(width=c(3.4,4)))/ (p2 + p3 + plot_layout(width=c(3.4,4))) +
plot_layout(heights=c(3,4)) + plot_annotation(tag_levels = 'A')
p4

```

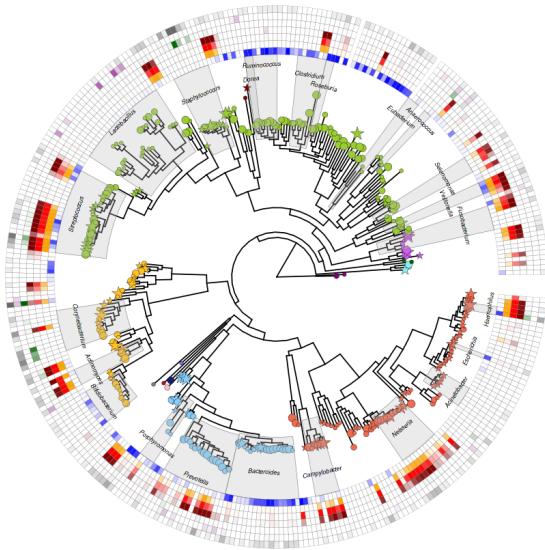
A



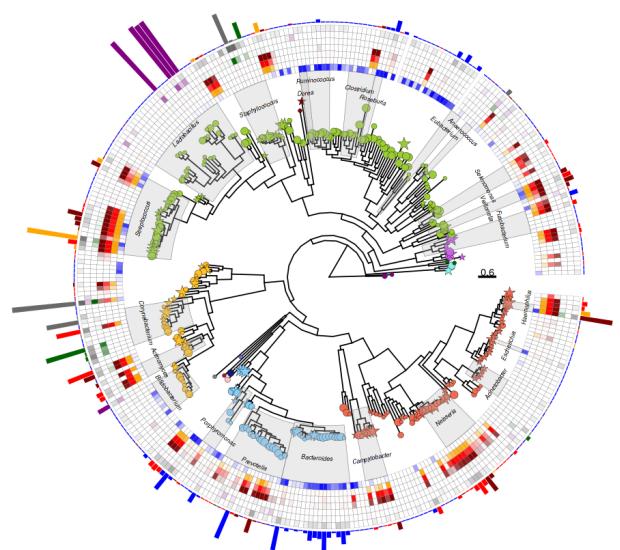
B



C



D



**Fig. S7: The abundance of microbes at different sites of human.** The shapes of symbolic points on the tips indicate the commensal microbes or potential pathogens (A). Clades were highlighted with grey background and labeled by clade name using *ggtree* (B). A heat map layer represent different body sites the transparency of the colors indicates the abundance of microbes (C). The bar chart visualizes relative abundance of the most abundant species at different body sites (D). Different graphic layers were added to the tree progressively to create the final figure (D).

### 3.3 Example of complex tree annotations

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.

```

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

tree <- read.tree("../data/kegg/kegg.nwk")
# The attributes of tip point
dt1 <- read.csv("../data/kegg/tippoint_attr.csv")
# The attributes of first ring
dt2 <- read.csv("../data/kegg/firstring_attr.csv")
# The attributes of second ring
dt3 <- read.csv("../data/kegg/secondring_attr.csv")
# The attrihutes of bar plot
dt4 <- read.csv("../data/kegg/barplot_attr.csv")

#reorder the Phyla column
dt1$Phyla <- factor(dt1$Phyla, levels=c("Actinobacteria", "Aquificae", "Bacteroidetes",
                                             "Chlamydiae", "Chlorobi", "Chloroflexi", "Crenarchaeota",
                                             "Cyanobacteria", "Euryarchaeota", "Firmicutes", "Proteobacteria",
                                             "Spirochaetes", "Tenericutes", "Thermi", "Thermotogae", "Other"))

# reorder the Type2 column
dt3$Type2 <- factor(dt3$Type2, levels=c("FA synth init", "FA synth elong",
                                           "acyl-CoA synth", "beta-Oxidation",
                                           "Ketone biosynth"))

dt4$Phyla <- factor(dt4$Phyla, levels=c("Actinobacteria", "Aquificae", "Bacteroidetes",
                                             "Chlamydiae", "Chlorobi", "Chloroflexi", "Crenarchaeota",
                                             "Cyanobacteria", "Euryarchaeota", "Firmicutes", "Proteobacteria",
                                             "Spirochaetes", "Tenericutes", "Thermi", "Thermotogae", "Other"))

# extract node label for the clade layers
nodelab <- tree$node.label[nchar(tree$node.label)>0]
nodeids <- nodeid(tree, nodelab)

# the position of clade label

```

```

textex <- c(1.0, 0.4, 0.2, 1.4, 1.4, 0.4, 1.4, 0.4, 0.4,
          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", "#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"))
```

p5

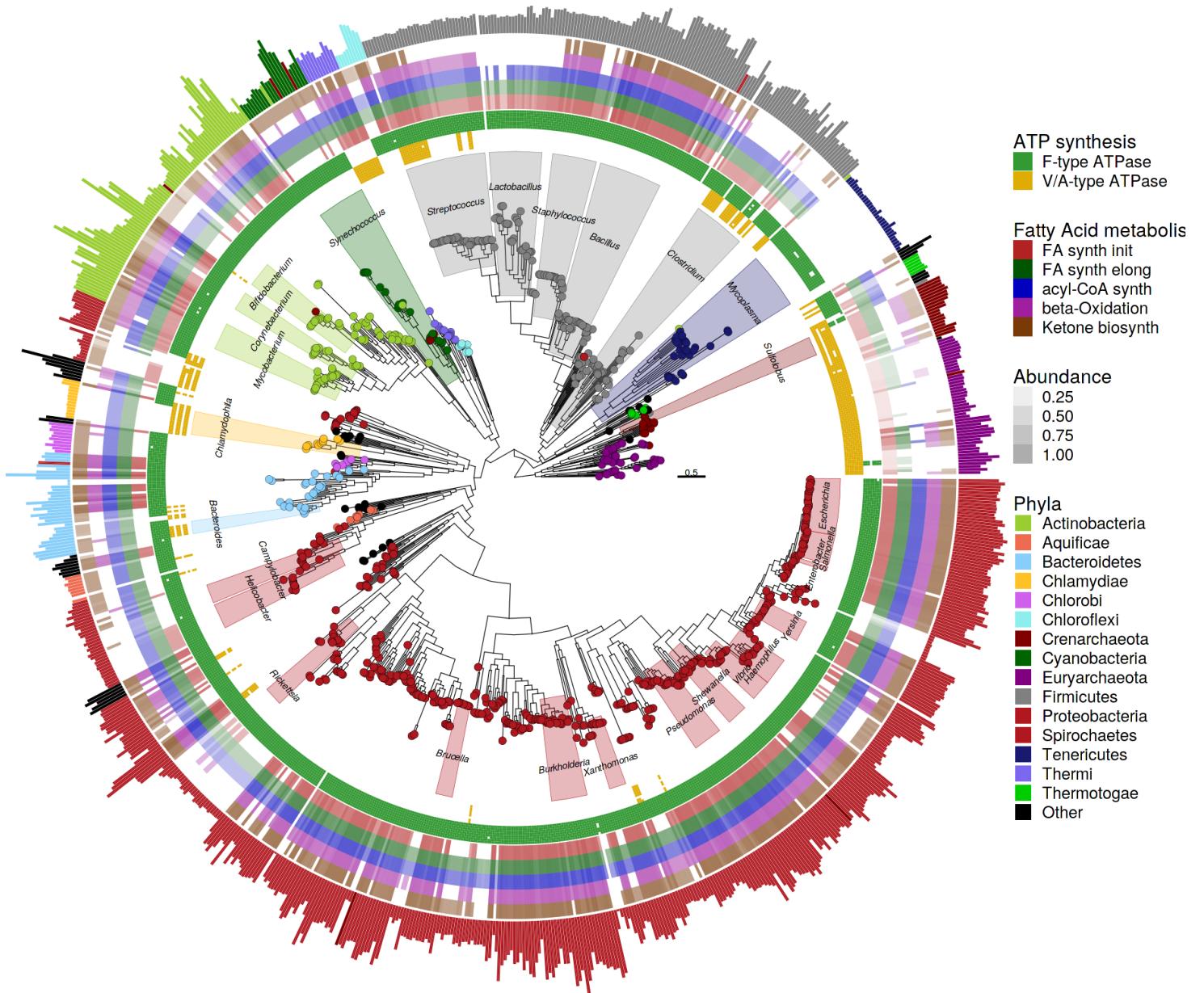


Fig. S8: The phylogenetic tree built using in (Segata et al. 2013) using 963 microbial genomes (a part of 3737 microbes (Segata et al. 2013)). The first and second ring heat map were built with discrete data, it represents the presence or absence of each module, the other heat map rings were created 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 Complex tree annotations combined with 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

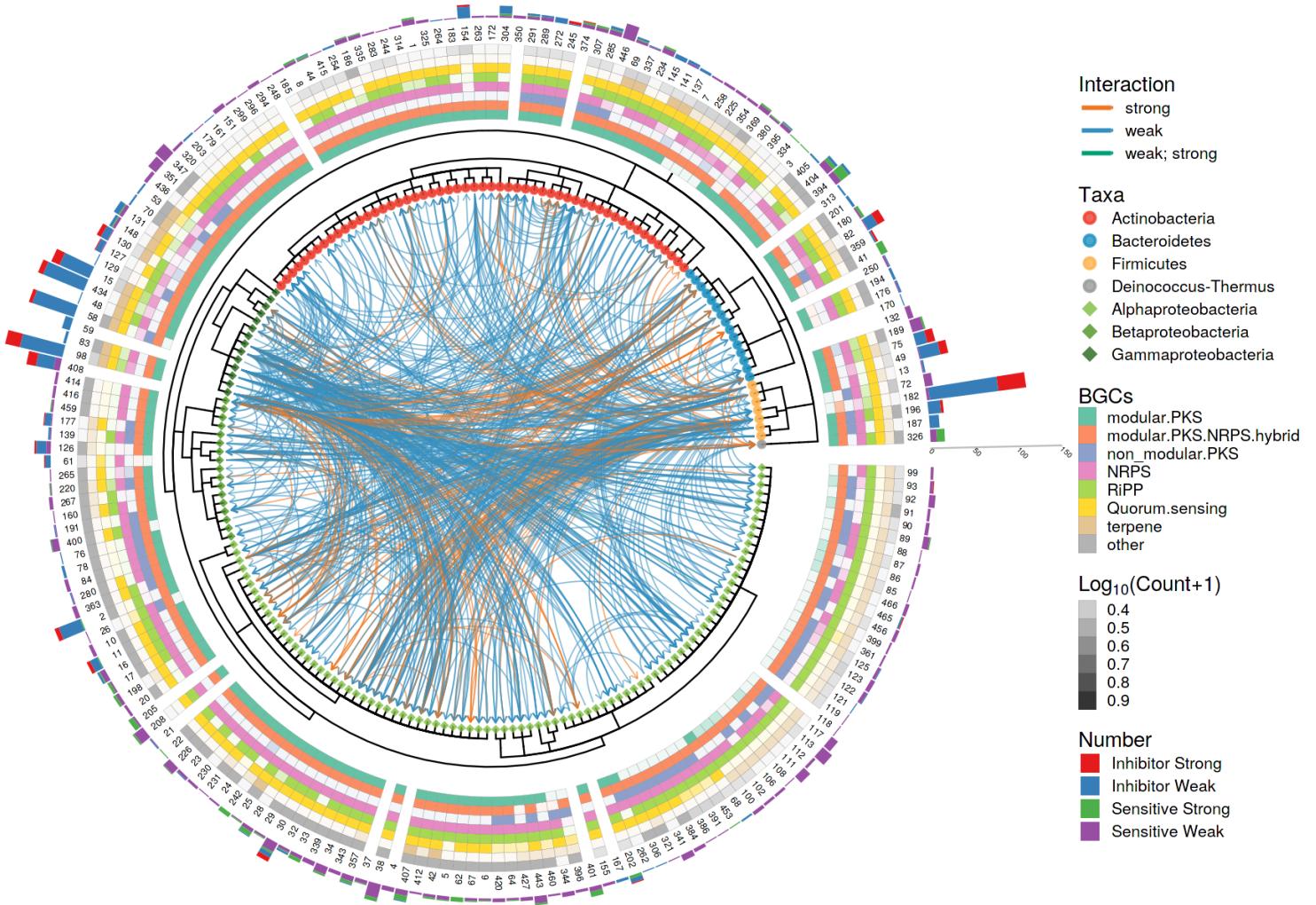


Fig. S9: **Illustration of representing multi-dimensional data sets on inward circular phylogenetic tree with chord diagram incorporated to display inter-relationships.** The inward circular layout tree reflects the evolutionary relationships among isolates from *Arabidopsis* leaf microbiome (Bai et 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* can work seamlessly with *ggtree*, which will make *ggtreeExtra* more powerful. The phylogenetic tree can be annotated (high light, clade label, branch color, etc.) by *ggtree*, before or after passing to *geom\_fruit* of *ggtreeExtra*. For example, *ggtreeExtra* 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 many 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>7</sup>.

## References

- Aphalo, Pedro J. 2020. *Ggpmisc: Miscellaneous Extensions to 'Ggplot2'*. <https://CRAN.R-project.org/package=ggpmisc>.
- Asnicar, Francesco, George Weingart, Timothy L Tickle, Curtis Huttenhower, and Nicola Segata. 2015. “Compact Graphical Representation of Phylogenetic Data and Metadata with Graphlan.” *PeerJ* 3: e1029. <https://doi.org/10.7717/peerj.1029>.
- Bai, Yang, Daniel B Müller, Girish Srinivas, Ruben Garrido-Oter, Eva Potthoff, Matthias Rott, Nina Dombrowski, et al. 2015. “Functional Overlap of the Arabidopsis Leaf and Root Microbiota.” *Nature* 528 (7582): 364–69. <https://doi.org/10.1038/nature16192>.
- Berger, Simon A., Denis Krompass, and Alexandros Stamatakis. 2011. “Performance, Accuracy, and Web Server for Evolutionary Placement of Short Sequence Reads under Maximum Likelihood.” *Systematic Biology* 60 (3): 291–302. <https://doi.org/10.1093/sysbio/syr010>.
- Boussau, Bastien, Gergely J. Szöllősi, Laurent Duret, Manolo Gouy, Eric Tannier, and Vincent Daubin. 2013. “Genome-Scale Coestimation of Species and Gene Trees.” *Genome Research* 23 (2): 323–30. <https://doi.org/10.1101/gr.141978.112>.
- Drummond, Alexei J, and Andrew Rambaut. 2007. “BEAST: Bayesian Evolutionary Analysis by Sampling Trees.” *BMC Evolutionary Biology* 7 (1): 1–8. <https://doi.org/10.1186/1471-2148-7-214>.
- FC, Mike. 2020. *Ggpattern: Geoms with Patterns*.
- Helfrich, Eric J. N., Christine M. Vogel, Reiko Ueoka, Martin Schäfer, Florian Ryffel, Daniel B. Müller, Silke Probst, Markus Kreuzer, Jörn Piel, and Julia A. Vorholt. 2018. “Bipartite Interactions, Antibiotic Production and Biosynthetic Potential of the Arabidopsis Leaf Microbiome.” *Journal Article. Nature Microbiology* 3 (8): 909–19. <https://doi.org/10.1038/s41564-018-0200-0>.
- Höhna, Sebastian, Michael J. Landis, Tracy A. Heath, Bastien Boussau, Nicolas Lartillot, Brian R. Moore, John P. Huelsenbeck, and Fredrik Ronquist. 2016. “RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language.” *Systematic Biology* 65 (4): 726–36. <https://doi.org/10.1093/sysbio/syw021>.
- Huerta-Cepas, Jaime, François Serra, and Peer Bork. 2016. “ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data.” *Molecular Biology and Evolution* 33 (6): 1635–8. <https://doi.org/10.1093/molbev/msw046>.
- Kumar, Sudhir, Glen Stecher, Michael Suleski, and S. Blair Hedges. 2017. “TimeTree: A Resource for Timelines, Timetrees, and Divergence Times.” *Molecular Biology and Evolution* 34 (7): 1812–9. <https://doi.org/10.1093/molbev/msx116>.
- Letunic, Ivica, and Peer Bork. 2019. “Interactive Tree of Life (iTOL) V4: Recent Updates and New Developments.” *Nucleic Acids Research* 47 (W1): W256–W259. <https://doi.org/10.1093/nar/gkz239>.

<sup>7</sup><https://github.com/YuLab-SMU/plotting-tree-with-data-using-ggtreeExtra>

- Matsen, Frederick A., Robin B Kodner, and E Virginia Armbrust. 2010. “Pplacer: Linear Time Maximum-Likelihood and Bayesian Phylogenetic Placement of Sequences onto a Fixed Reference Tree.” *BMC Bioinformatics* 11 (1): 538. <https://doi.org/10.1186/1471-2105-11-538>.
- McMurdie, Paul J., and Susan Holmes. 2013. “Phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data.” *PLoS ONE* 8 (4): e61217. <https://doi.org/10.1371/journal.pone.0061217>.
- Mirarab, Siavash, and Tandy Warnow. 2015. “ASTRAL-II: Coalescent-Based Species Tree Estimation with Many Hundreds of Taxa and Thousands of Genes.” *Bioinformatics (Oxford, England)* 31 (12): i44–52. <https://doi.org/10.1093/bioinformatics/btv234>.
- Morgan, Xochitl C., Nicola Segata, and Curtis Huttenhower. 2013. “Biodiversity and Functional Genomics in the Human Microbiome.” *Trends in Genetics* 29 (1): 51–58. <https://doi.org/10.1016/j.tig.2012.09.005>.
- Pond, Sergei L. Kosakovsky, Simon D. W. Frost, and Spencer V. Muse. 2005. “HyPhy: Hypothesis Testing Using Phylogenies.” *Bioinformatics* 21 (5): 676–79. <https://doi.org/10.1093/bioinformatics/bti079>.
- Segata, Nicola, Daniela Börnigen, Xochitl C. Morgan, and Curtis Huttenhower. 2013. “PhyloPhlAn Is a New Method for Improved Phylogenetic and Taxonomic Placement of Microbes.” Journal Article. *Nature Communications* 4 (1): 2304. <https://doi.org/10.1038/ncomms3304>.
- Smith, Garrett J, and Kelly C Wrighton. 2019. “Metagenomic Approaches Unearth Methanotroph Phylogenetic and Metabolic Diversity.” *Curr Issues Mol Biol* 33: 57–84. <https://doi.org/10.21775/9781912530045.03>.
- Song, Se Jin, Jon G. Sanders, Frédéric Delsuc, Jessica Metcalf, Katherine Amato, Michael W. Taylor, Florent Mazel, et al. 2020. “Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence Between Birds and Bats.” Edited by Joerg Graf. *mBio* 11 (1). <https://doi.org/10.1128/mBio.02901-19>.
- Stamatakis, Alexandros. 2014. “RAxML Version 8: A Tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies.” *Bioinformatics*, January, btu033. <https://doi.org/10.1093/bioinformatics/btu033>.
- Wang, Li-Gen, Tommy Tsan-Yuk Lam, Shuangbin Xu, Zehan Dai, Lang Zhou, Tingze Feng, Pingfan Guo, et al. 2020. “Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data.” *Molecular Biology and Evolution* 37 (2): 599–603. <https://doi.org/10.1093/molbev/msz240>.
- Wickham, Hadley. 2016. *Ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. <https://ggplot2.tidyverse.org>.
- Wilke, Claus O. 2020. *Ggridges: Ridgeline Plots in 'Ggplot2'*. <https://CRAN.R-project.org/package=ggridges>.
- Wilkinson, Leland. 2012. “The Grammar of Graphics.” In *Handbook of Computational Statistics: Concepts and Methods*, edited by James E. Gentle, Wolfgang Karl Härdle, and Yuichi Mori, 375–414. Berlin, Heidelberg: Springer Berlin Heidelberg. [https://doi.org/10.1007/978-3-642-21551-3\\_13](https://doi.org/10.1007/978-3-642-21551-3_13).
- Yang, Ziheng. 2007. “PAML 4: Phylogenetic Analysis by Maximum Likelihood.” *Molecular Biology and Evolution* 24 (8): 1586–91. <https://doi.org/10.1093/molbev/msm088>.
- Yu, Guangchuang, Tommy Tsan-Yuk Lam, Huachen Zhu, and Yi Guan. 2018. “Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using Ggtree.” *Molecular Biology and Evolution* 35 (2): 3041–3. <https://doi.org/10.1093/molbev/msy194>.
- Yu, Guangchuang, David Smith, Huachen Zhu, Yi Guan, and Tommy Tsan-Yuk Lam. 2017. “Ggtree: An R Package for Visualization and Annotation of Phylogenetic Trees with Their Covariates and Other Associated Data.” *Methods in Ecology and Evolution* 8 (1): 28–36. <https://doi.org/10.1111/2041-210X.12628>.