

# 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 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).

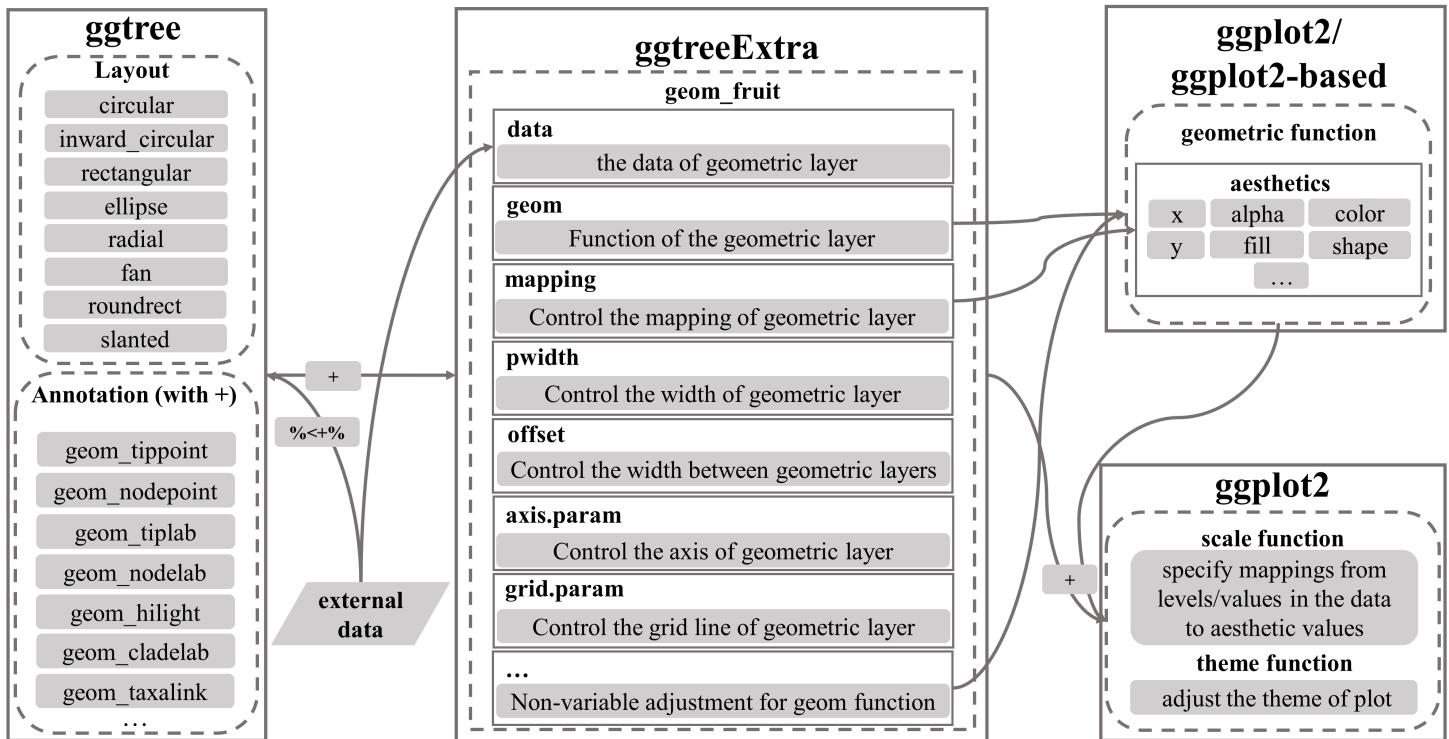


Fig. S1: Overview of the design of *ggtreeExtra* package.

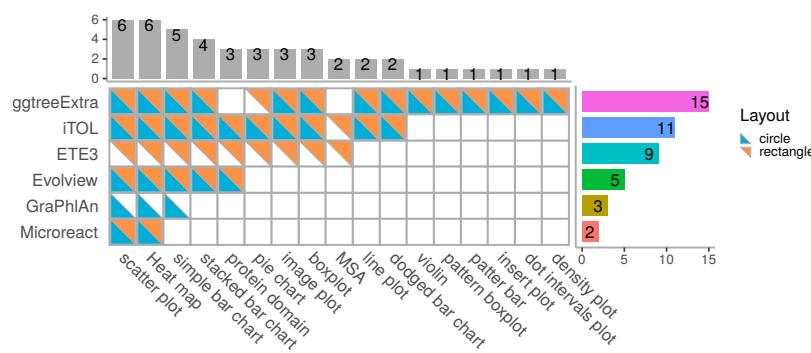
Table S1: Comparing features in ggtreeExtra and other tools

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, insert 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). 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 chart, 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')

```

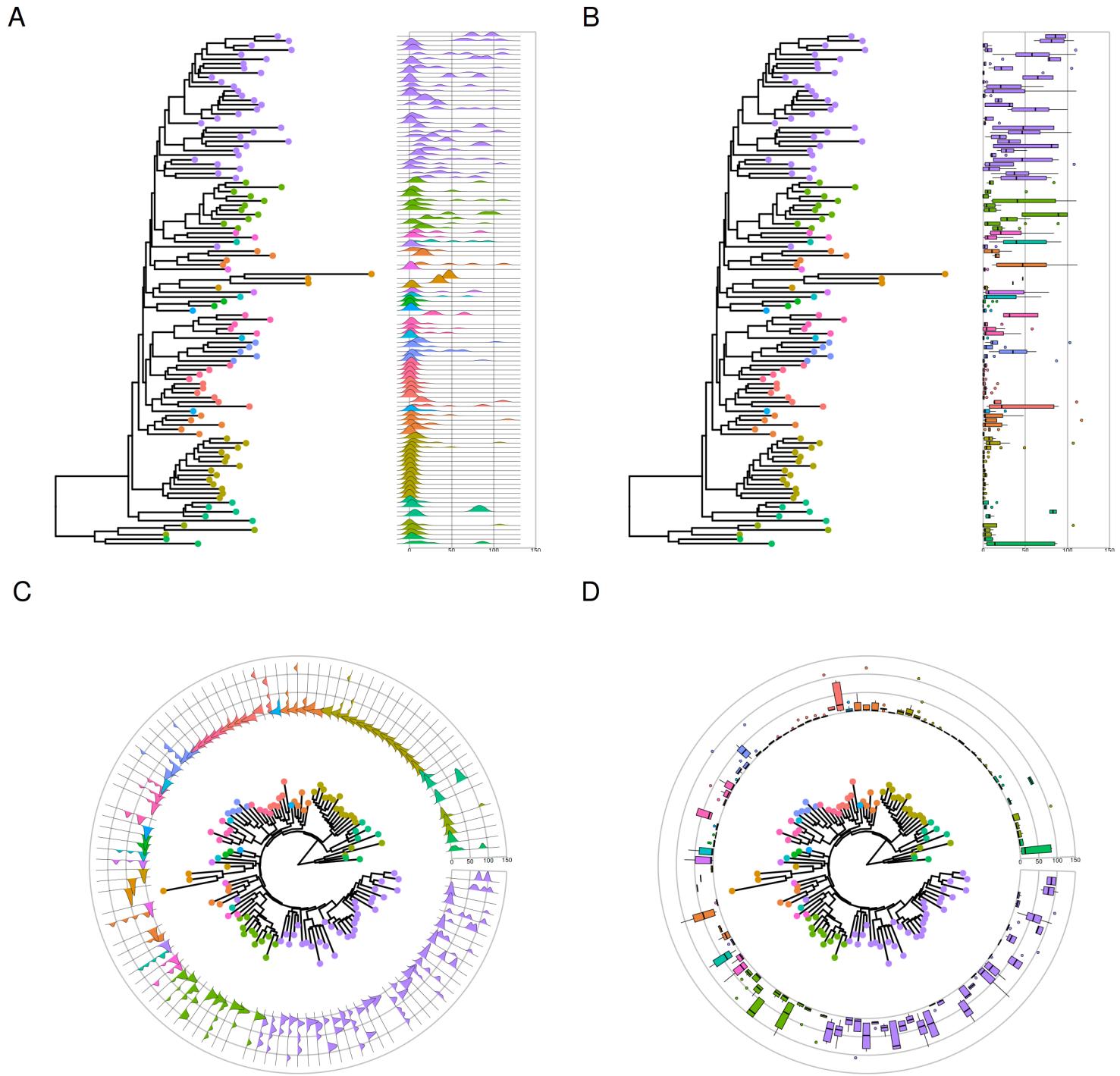


Fig. S3: This example demonstrates using `ggtreeExtra` with `geom_density_ridges` layer from the `ggridges` package (Wilke 2020) and `geom_boxplot` layer from the `ggplot2` package (Wickham 2016). The associated data (*i.e.*, `melt_simple`) was imported by the `data` argument of the `geom_fruit` function. 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 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')

```

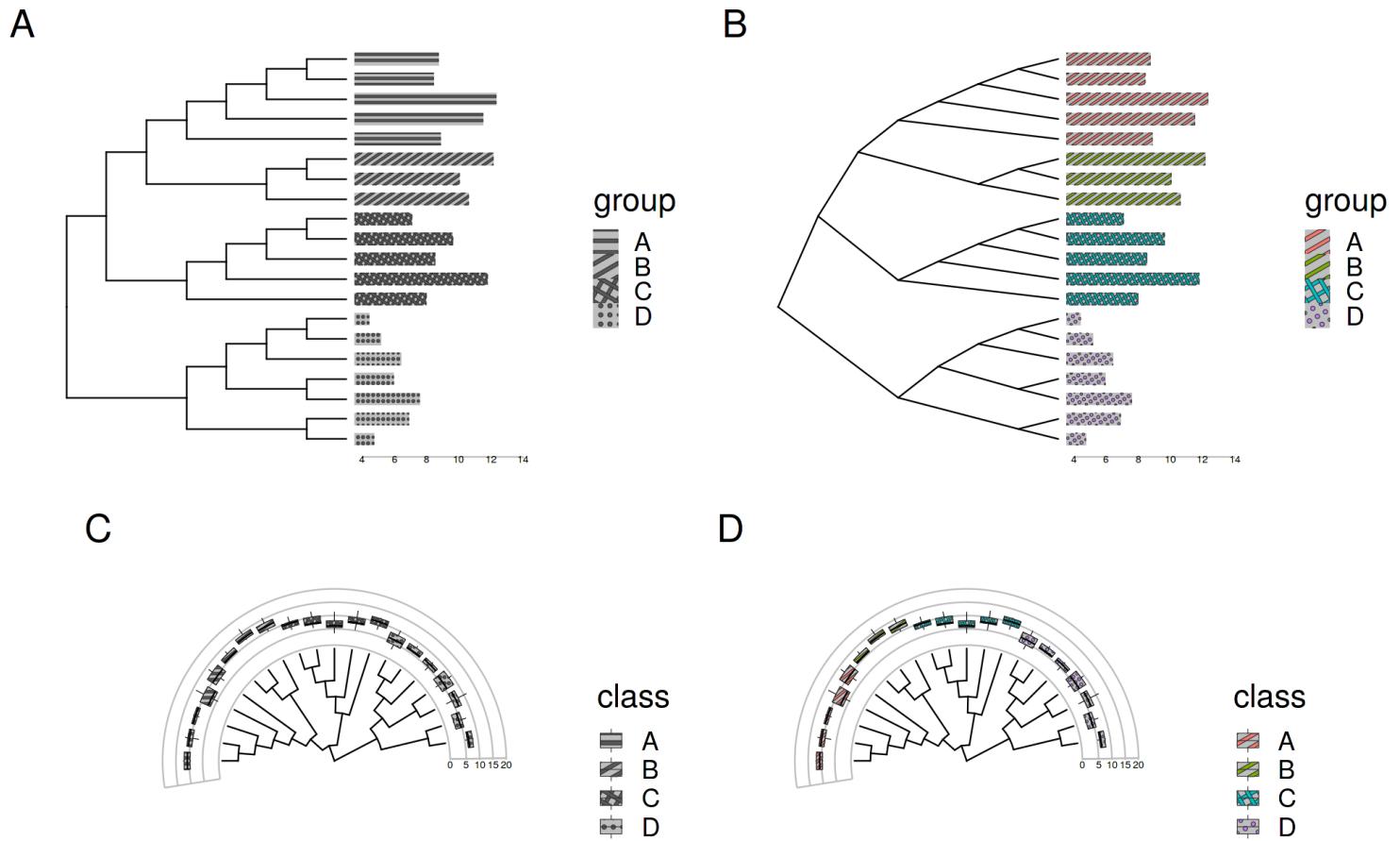


Fig. S4: This example demonstrates using *ggtreeExtra* with *geom\_bar\_pattern* and *geom\_boxplot\_pattern* layers from the *ggpattern* package (FC 2020). Different tree layouts including rectangular (A), slanted (B) and fan (C and D) layouts are all supported in *ggtreeExtra*.

```

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",

```

```

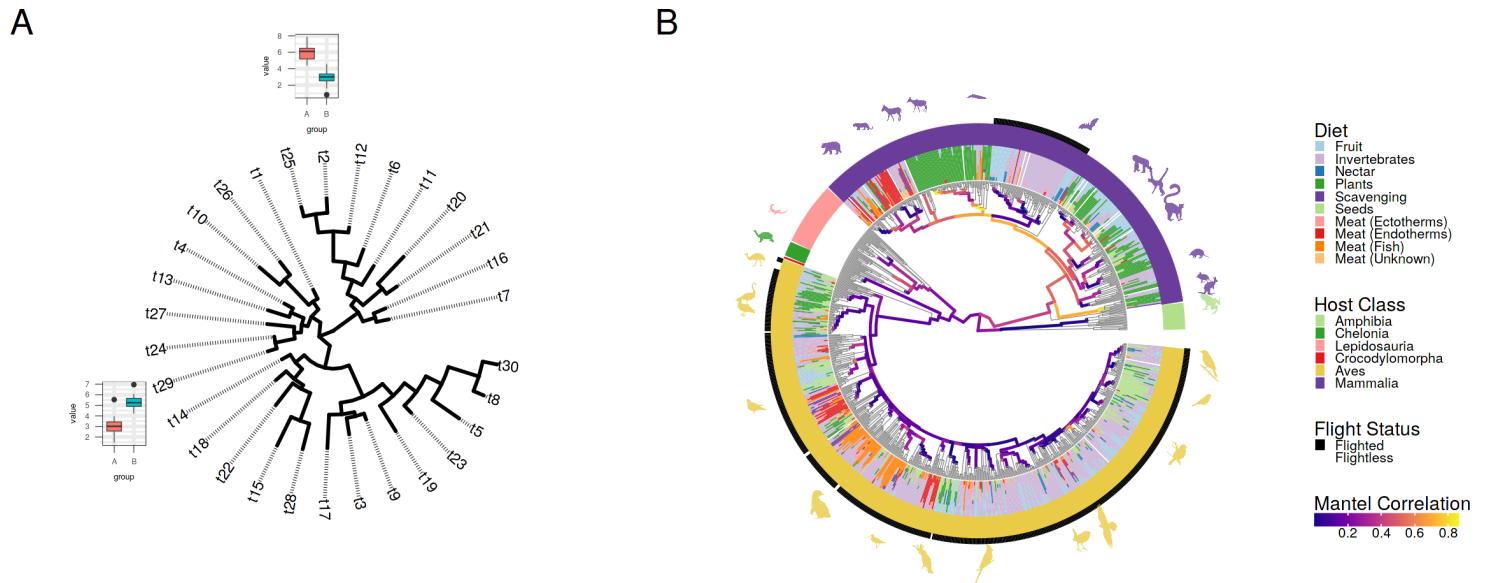
        "#1f78b4", "#33a02c",
        "#6a3d9a", "#b2df8a",
        "#fb9a99", "#e31a1c",
        "#ff7f00", "#fdbf6f"),
    guide=guide_legend(keywidth=0.3, keyheight=0.3, order=1)
)
fig2 <- fig1 +
  new_scale_colour() +
  geom_cladelab(
    data=cladeda,
    mapping=aes(node=id, label=class, colour=class),
    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 (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, 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>2</sup>.

#### 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*

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

(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>3</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. S3.A 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 *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 expanding.

```
library(ggteeExtra)
library(ggtee)
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 <- ggtee(treeda, layout="fan", open.angle=30)
print(as.treedata(p))

## 'treedata' S4 object'.
##
## ...@ phylo:
```

<sup>3</sup>the source data is available on [https://github.com/TheWrightonLab/Methanotroph\\_rpS3Analyses\\_SmithWrighton2018](https://github.com/TheWrightonLab/Methanotroph_rpS3Analyses_SmithWrighton2018)

```

## 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
```

p5

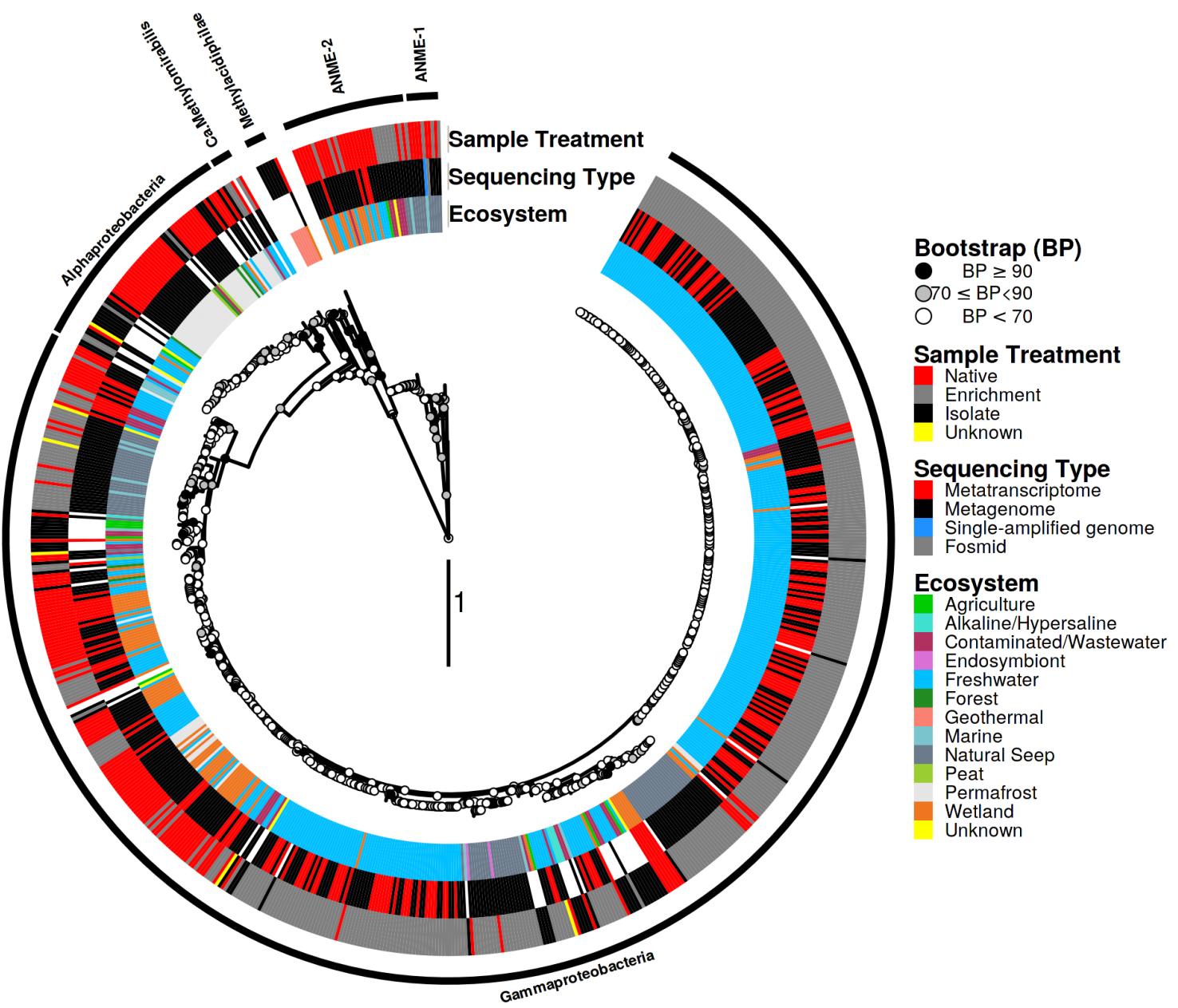


Fig. S6: Phylogeny of methanotroph ribosomal protein S39 (rpS3) genes from Figure 3.3 of (Smith and Wrighton 2019). Bootstrap value was parsed with the tree by the `read.raxml` function and other associated data sets were integrated to the tree via the `%<+%` operator. The `ggtreeExtra` can directly 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 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>4</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.

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>5</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.
```

<sup>4</sup>extracted from phyloxml file downloaded from <https://github.com/biobakery/graphlan/tree/master/examples>

<sup>5</sup><http://bioconductor.org/packages/release/bioc/vignettes/ggtreeExtra/inst/doc/ggtreeExtra.html>

```

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(
    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"
  )
# 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

```

### 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.

```

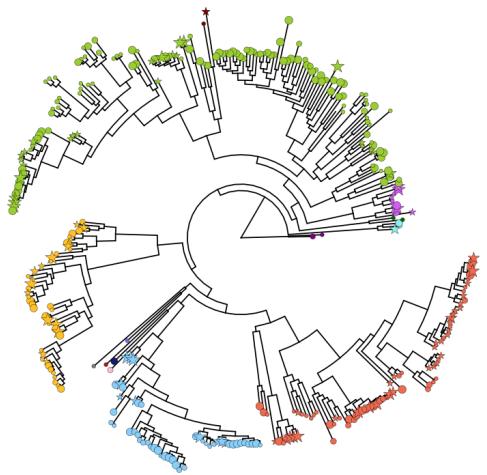
library(ggtreeExtra)
library(ggtree)
library(treeio)
library(tidytree)
library(ggstar)
library(ggplot2)
library(ggnewscale)

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")

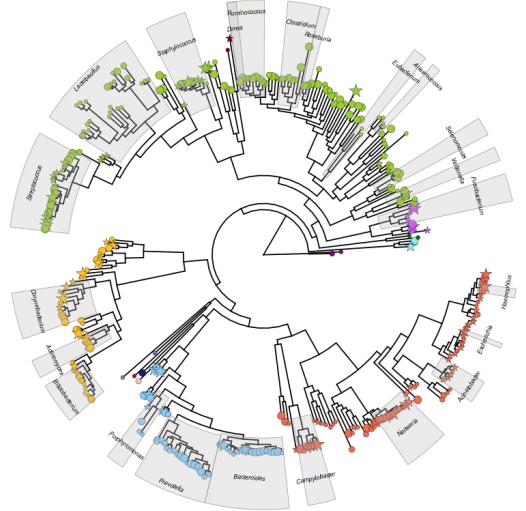
#reorder the Phyla column
dt1$Phyla <- factor(dt1$Phyla, levels=c("Actinobacteria", "Aquificae", "Bacteroidetes",
                                             "Chlamydiae", "Chlorobi", "Chloroflexi", "Crenarchaeota",
                                             "Cyanobacteria", "Euryarchaeota", "Firmicutes",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

```

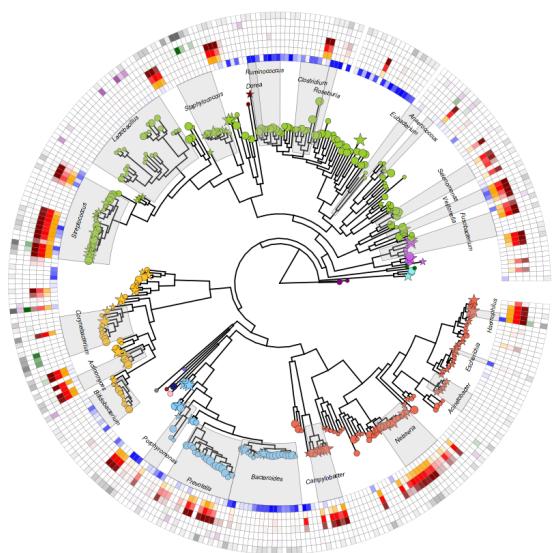
A



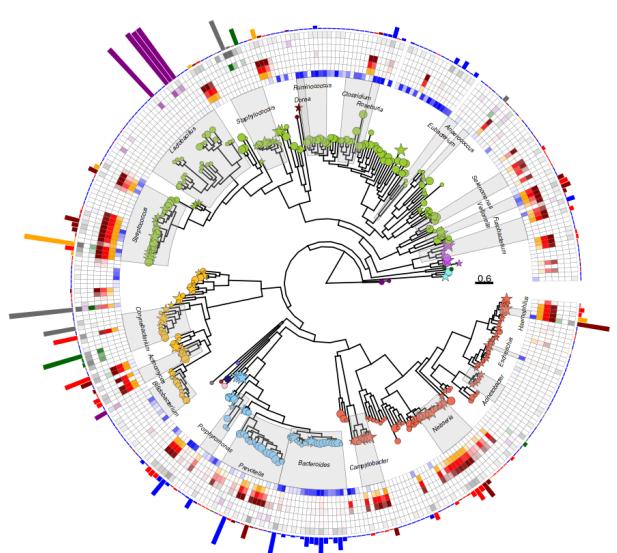
B



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).

```
# 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
nodeid <- tree$node.label[nchar(tree$node.label)>0]
nodeids <- nodeid(tree, nodeid)

# the position of clade label
textex <- c(1.0, 0.4, 0.2, 1.4, 1.4, 0.4, 1.4, 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){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, nodeid, 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"))

```

p5

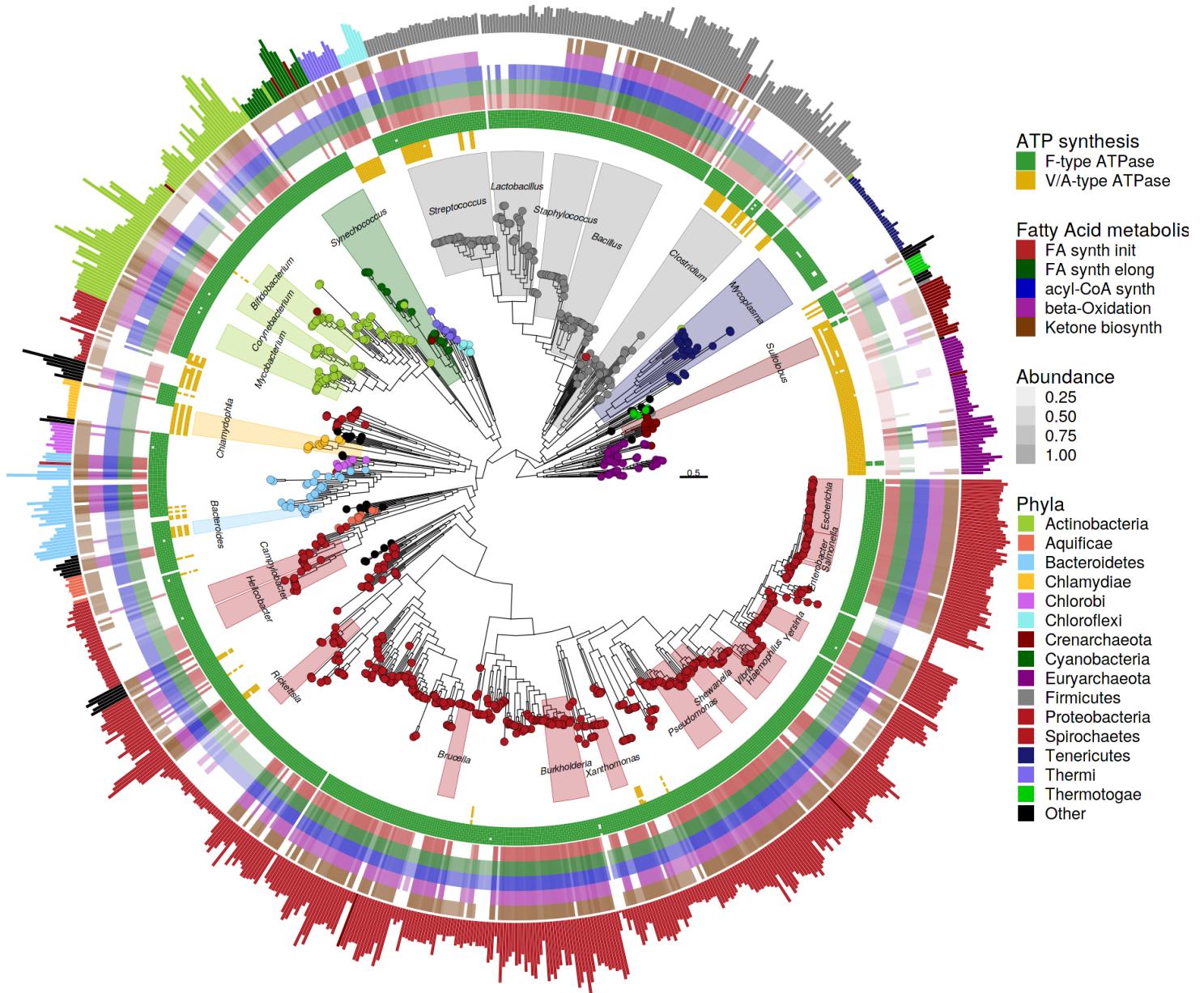


Fig. S8: The phylogenetic tree built using in (Segata et al. 2013) using 963 microbial genomes (a part of 3737 microbes (Segata et al. 2013)). The first and second ring heat map were built with discrete data, it represents the presence or absence of each module, the other heat map rings were created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

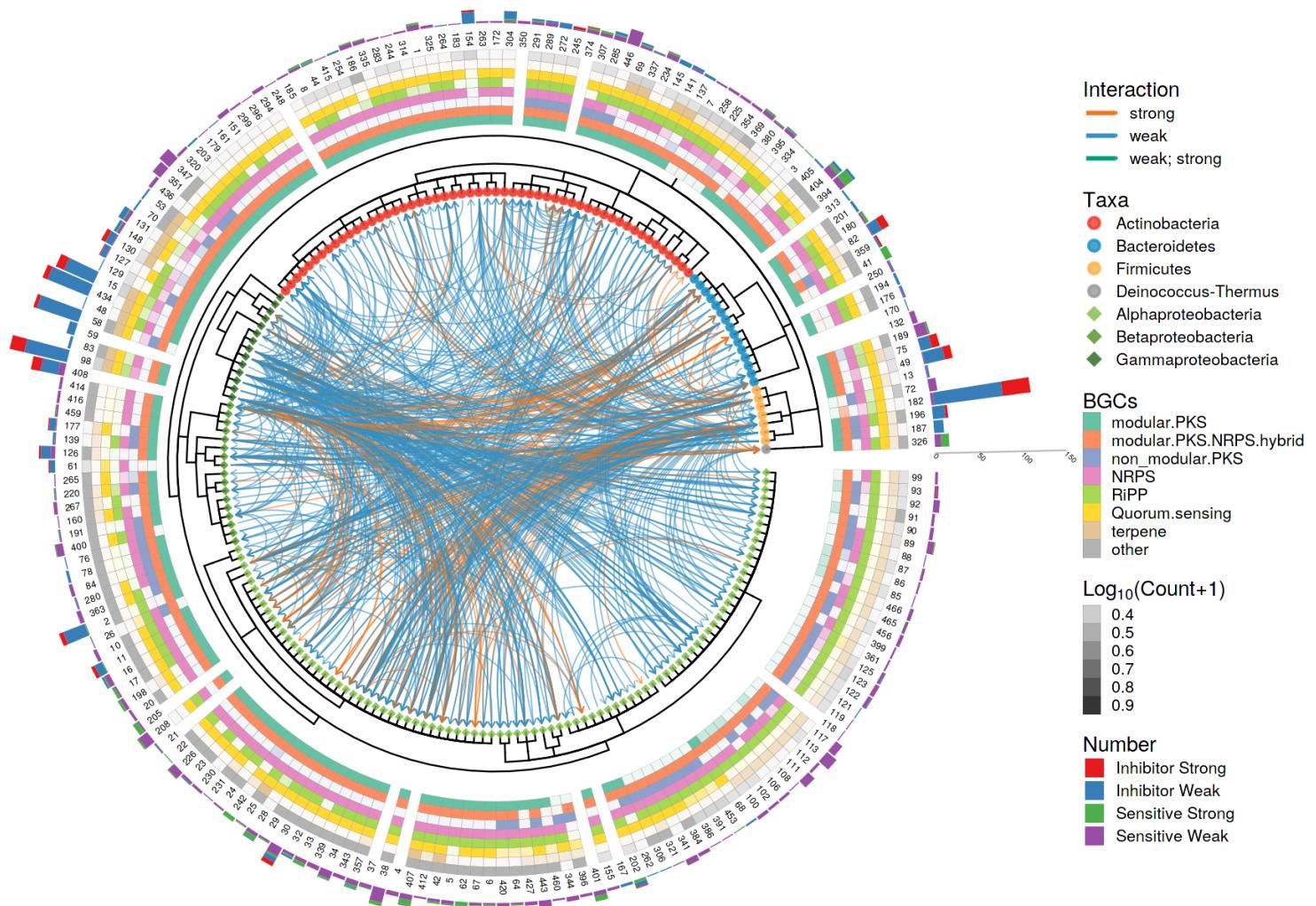


Fig. S9: Illustration of representing multi-dimensional data sets on inward circular phylogenetic tree with chord diagram incorporated to display inter-relationships. The inward circular layout tree reflects the evolutionary relationships among isolates from *Arabidopsis* leaf microbiome (Bai et al. 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>6</sup>.

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<sup>6</sup><https://github.com/YuLab-SMU/plotting-tree-with-data-using-ggtreeExtra>

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