

# Microbial Ecology Analysis Report

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## 1. Alpha Diversity Analysis

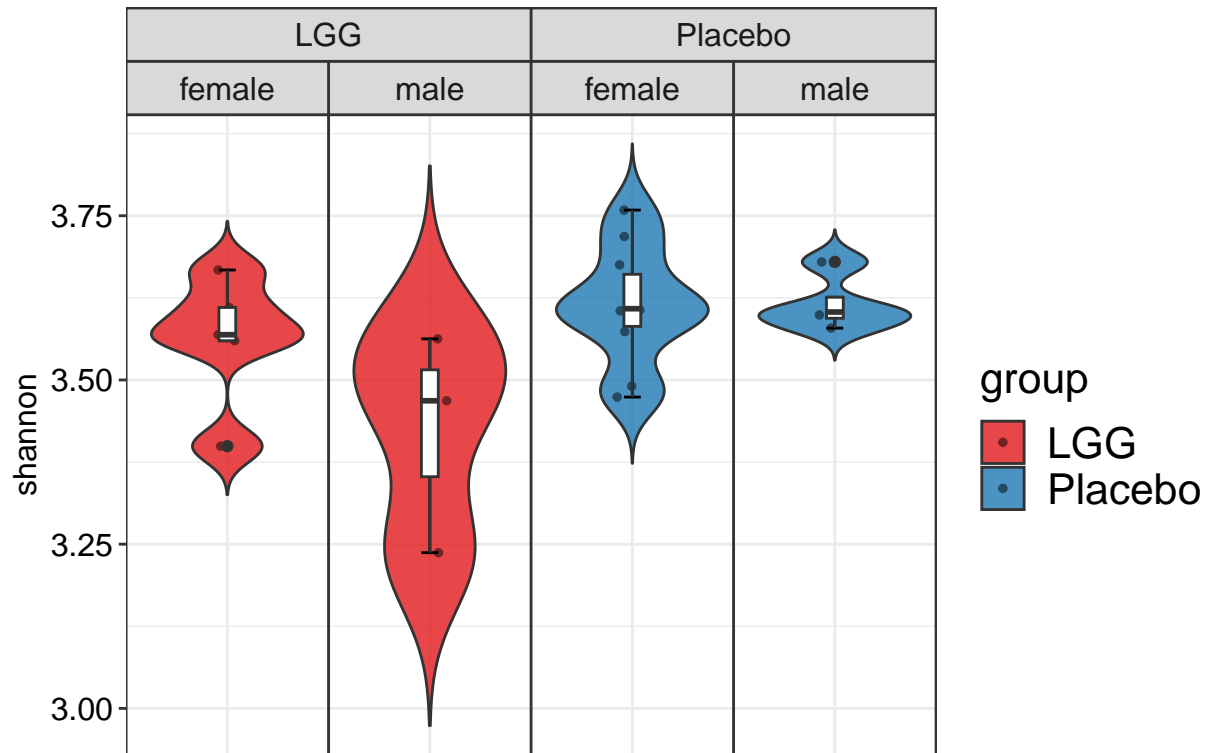
### 1.1 Alpha Diversity Boxplots

```
alpha_boxplot_results <- generate_alpha_boxplot_single(data.obj = data.obj,  
                                                       alpha.obj = alpha.obj,  
                                                       alpha.name = alpha.name,  
                                                       subject.var = subject.var,  
                                                       time.var = time.var,  
                                                       t.level = t.level,  
                                                       group.var = group.var,  
                                                       strata.var = strata.var,  
                                                       base.size = base.size,  
                                                       theme.choice = theme.choice,  
                                                       custom.theme = custom.theme,  
                                                       palette = palette,  
                                                       pdf = pdf,  
                                                       file.ann = file.ann,  
                                                       pdf.wid = pdf.wid,  
                                                       pdf.hei = pdf.hei)
```

```
alpha_boxplot_results
```

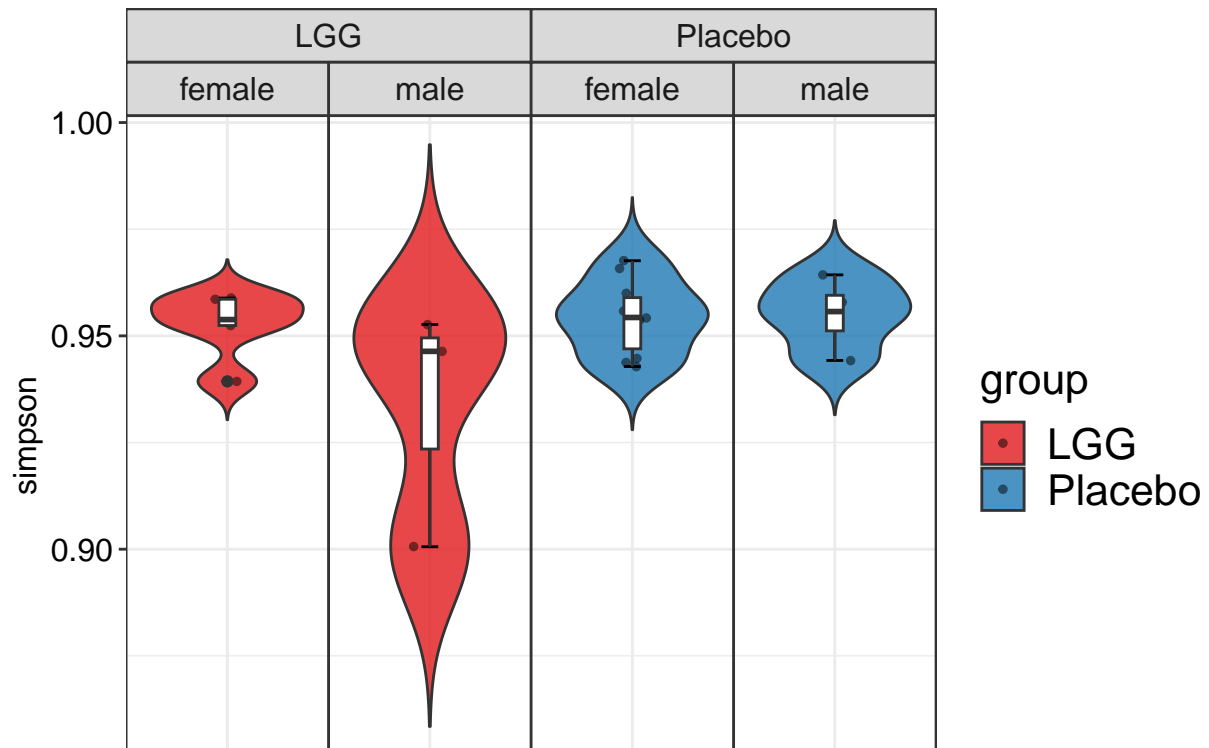
```
## [[1]]
```

time = 1



##  
## [[2]]

time = 1



## 1.2 Alpha Diversity Test Results

```
alpha_test_results <- generate_alpha_test_single(data.obj = data.obj,  
                                                  alpha.obj = alpha.obj,  
                                                  time.var = time.var,  
                                                  t.level = t.level,  
                                                  alpha.name = alpha.name,  
                                                  group.var = group.var,  
                                                  adj.vars = adj.vars)
```

### shannon Index

| term         | Estimate | Std.Error | Statistic | P.Value   |
|--------------|----------|-----------|-----------|-----------|
| (Intercept)  | 3.531    | 0.03964   | 89.09     | 2.234e-26 |
| sexmale      | -0.05447 | 0.04633   | -1.176    | 0.2542    |
| groupPlacebo | 0.09928  | 0.04486   | 2.213     | 0.03931   |

#### shannon Index Analysis

The variable (Intercept) has a statistically significant impact on the shannon diversity index with an estimate of 3.53.

The variable sexmale does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.05.

The variable groupPlacebo has a statistically significant impact on the shannon diversity index with an estimate of 0.1.

### simpson Index

| term         | Estimate  | Std.Error | Statistic | P.Value   |
|--------------|-----------|-----------|-----------|-----------|
| (Intercept)  | 0.9481    | 0.005097  | 186       | 1.911e-32 |
| sexmale      | -0.007223 | 0.005957  | -1.213    | 0.2401    |
| groupPlacebo | 0.008501  | 0.005768  | 1.474     | 0.1569    |

#### simpson Index Analysis

The variable (Intercept) has a statistically significant impact on the simpson diversity index with an estimate of 0.95.

The variable sexmale does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.01.

The variable groupPlacebo does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is 0.01.

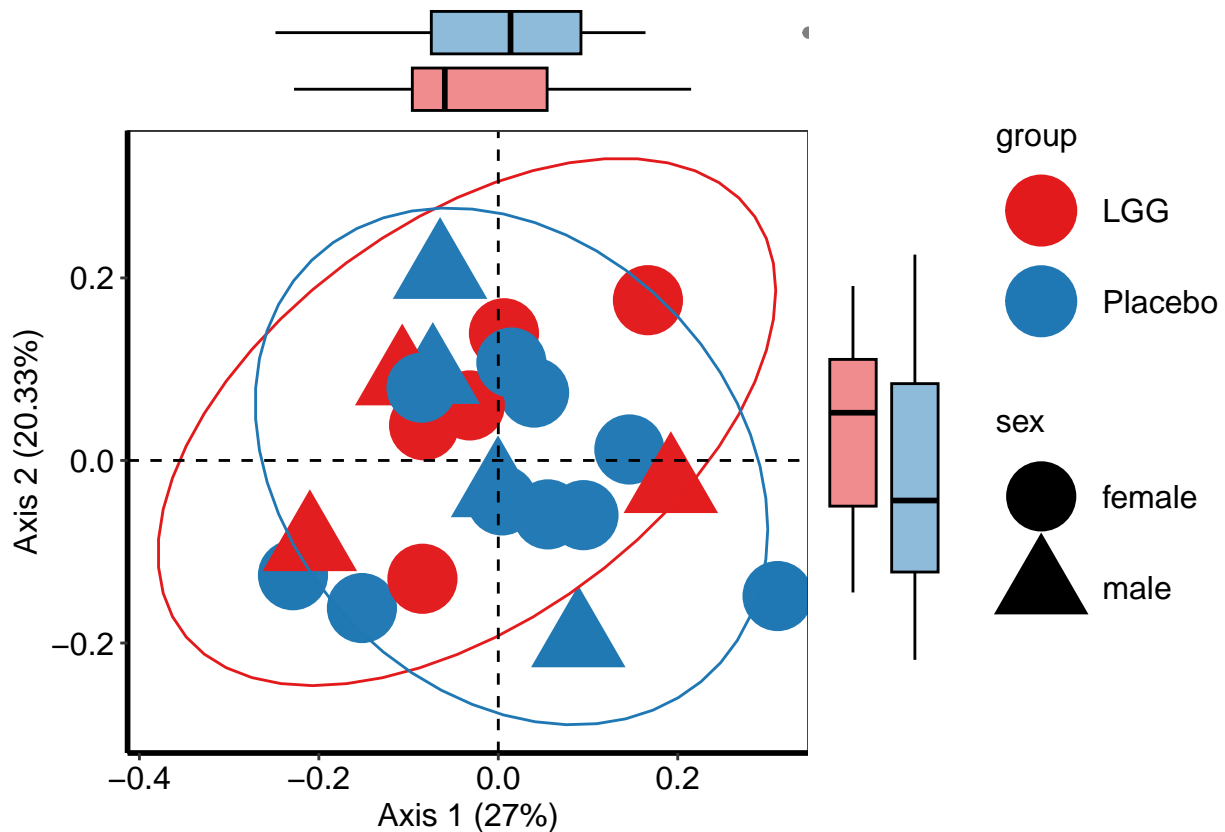
## 2. Beta Diversity Analysis

## 2.1 Beta Diversity Ordination

```
beta_ordination_results <- generate_beta_ordination_single(data.obj = data.obj,
  dist.obj = dist.obj,
  pc.obj = NULL,
  subject.var = subject.var,
  time.var = time.var,
  t.level = t.level,
  group.var = group.var,
  strata.var = strata.var,
  dist.name = dist.name,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei)
```

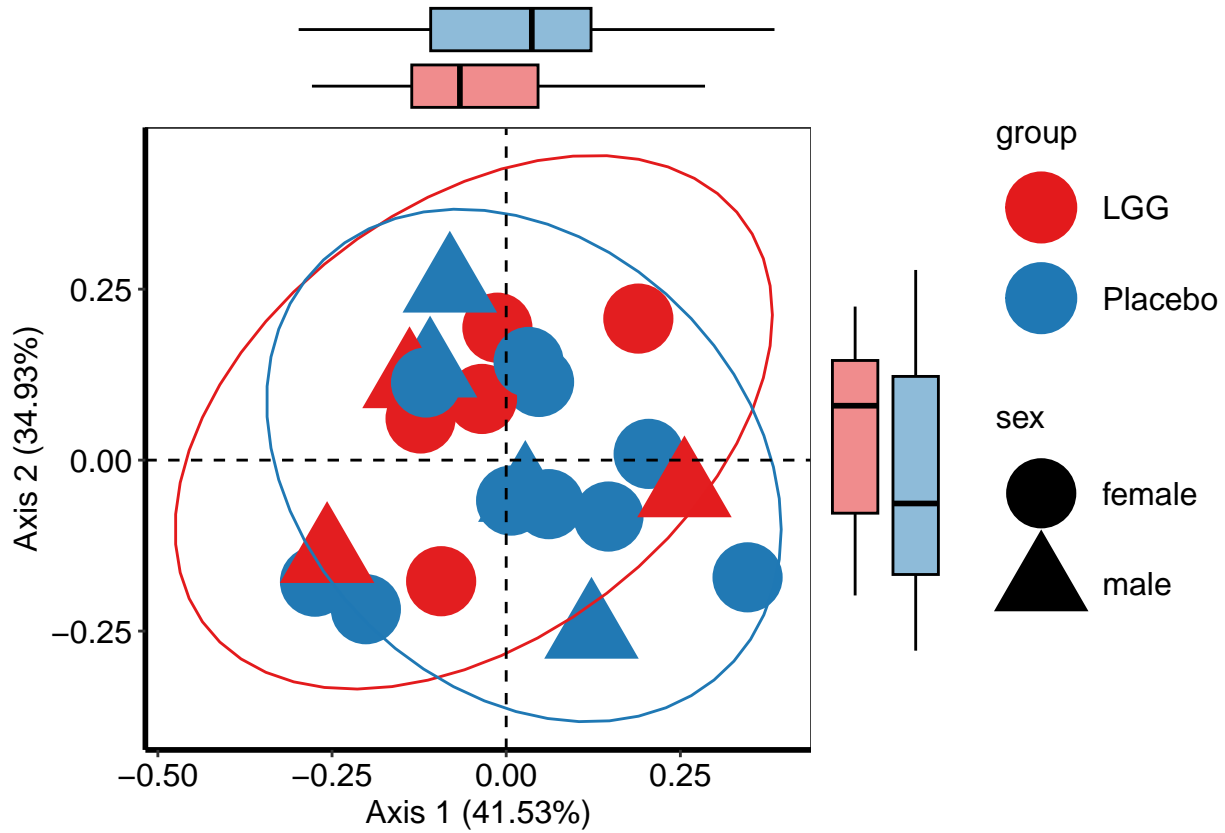
beta\_ordination\_results

## [[1]]



##

## [[2]]



## 2.2 Beta Diversity Test Results

```
beta_test_results <- generate_beta_test_single(data.obj = data.obj,
  dist.obj = dist.obj,
  time.var = time.var,
  t.level = t.level,
  group.var = group.var,
  adj.vars = adj.vars,
  dist.name = dist.name)
```

## P-Tab Results

| Term  | D1.p.value | D2.p.value | omni.p.value |
|-------|------------|------------|--------------|
| sex   | 0.785      | 0.832      | 0.809        |
| group | 0.787      | 0.839      | 0.814        |

### Beta Diversity PERMANOVA Analysis for Variable: sex

The variable sex does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable sex does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

The variable sex does not appear to have a statistically significant effect on the beta diversity according to the omnibus PERMANOVA test.

### Beta Diversity PERMANOVA Analysis for Variable: group

The variable group does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable group does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

The variable group does not appear to have a statistically significant effect on the beta diversity according to the omnibus PERMANOVA test.

### AOV-Tab Results

| Variable  | DF | Sum_Sq | Mean_Sq | F_Statistic | R_Squared | P_Value | Distance |
|-----------|----|--------|---------|-------------|-----------|---------|----------|
| sex       | 1  | 0.043  | 0.043   | 0.644       | 0.032     | 0.785   | BC       |
| group     | 1  | 0.042  | 0.042   | 0.621       | 0.031     | 0.787   | BC       |
| Residuals | 19 | 1.277  | 0.067   | NA          | 0.938     | NA      | BC       |
| Total     | 21 | 1.362  | NA      | NA          | 1         | NA      | BC       |
| sex       | 1  | 0.099  | 0.099   | 0.707       | 0.035     | 0.832   | Jaccard  |
| group     | 1  | 0.094  | 0.094   | 0.668       | 0.033     | 0.839   | Jaccard  |
| Residuals | 19 | 2.669  | 0.14    | NA          | 0.933     | NA      | Jaccard  |
| Total     | 21 | 2.862  | NA      | NA          | 1         | NA      | Jaccard  |

### sex Variable Analysis

The variable sex does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable sex does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

### group Variable Analysis

The variable group does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable group does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

### Residuals Variable Analysis

```
## Warning: NAs introduced by coercion
```

```
## Warning: NAs introduced by coercion
```

### Total Variable Analysis

```
## Warning: NAs introduced by coercion
```

```
## Warning: NAs introduced by coercion
```

## 3. Taxonomic Feature Analysis

### 3.1 Taxa Barplot

```
taxa_barplot_results <- generate_taxa_barplot_single(data.obj = data.obj,  
                                                    subject.var = subject.var,  
                                                    time.var = time.var,
```

```

t.level = t.level,
group.var = group.var,
strata.var = strata.var,
feature.level = feature.level,
feature.dat.type = feature.dat.type,
feature.number = feature.number,
base.size = base.size,
theme.choice = theme.choice,
custom.theme = custom.theme,
palette = NULL,
pdf = pdf,
file.ann = file.ann,
pdf.wid = pdf.wid,
pdf.hei = pdf.hei)

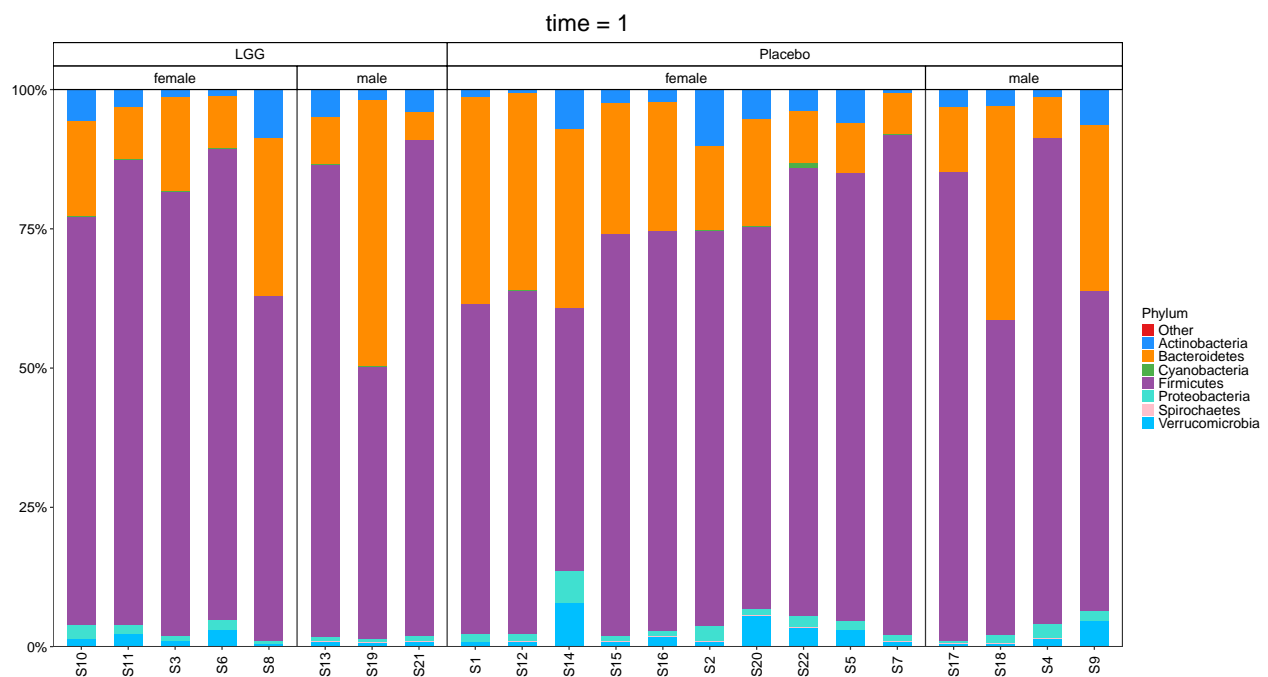
taxa_barplot_results

```

```

## [[1]]
## [[1]][[1]]

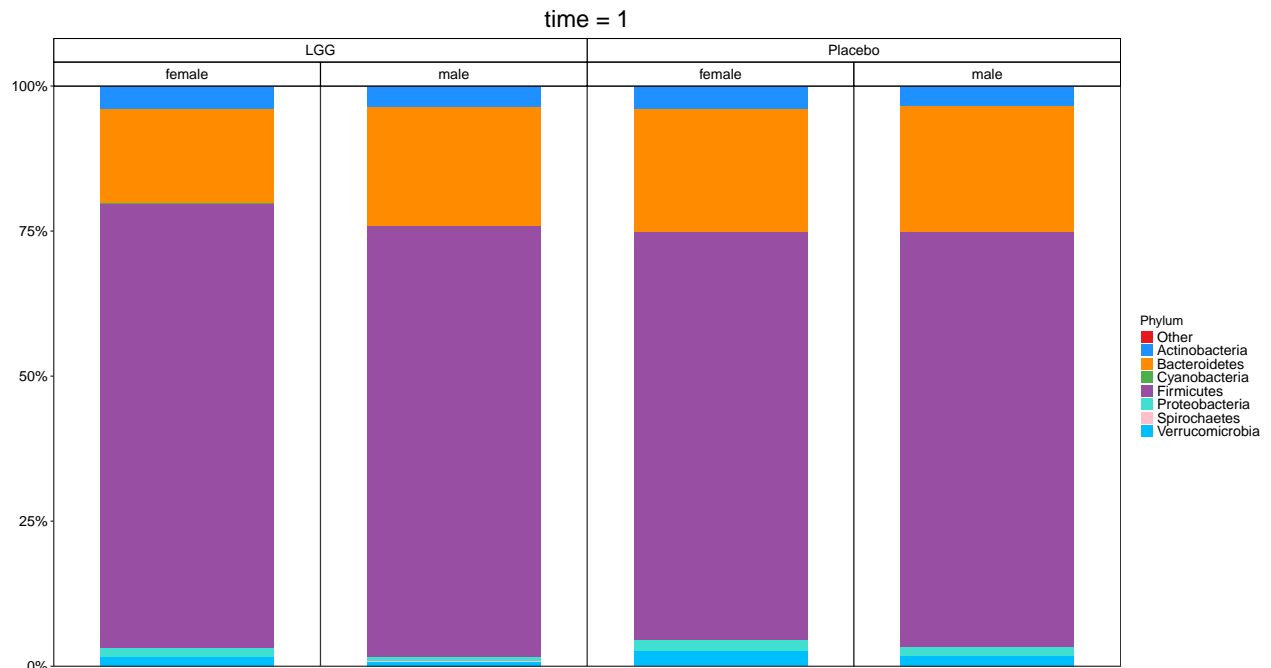
```



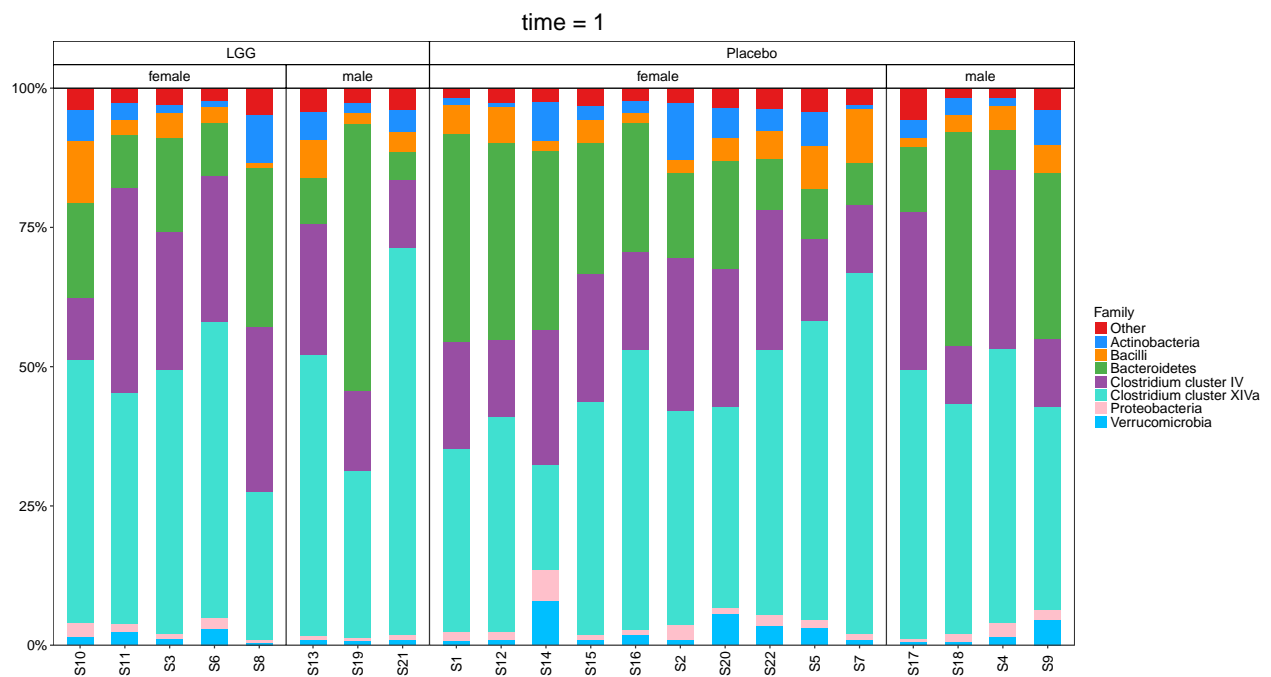
```

##
## [[1]][[2]]

```

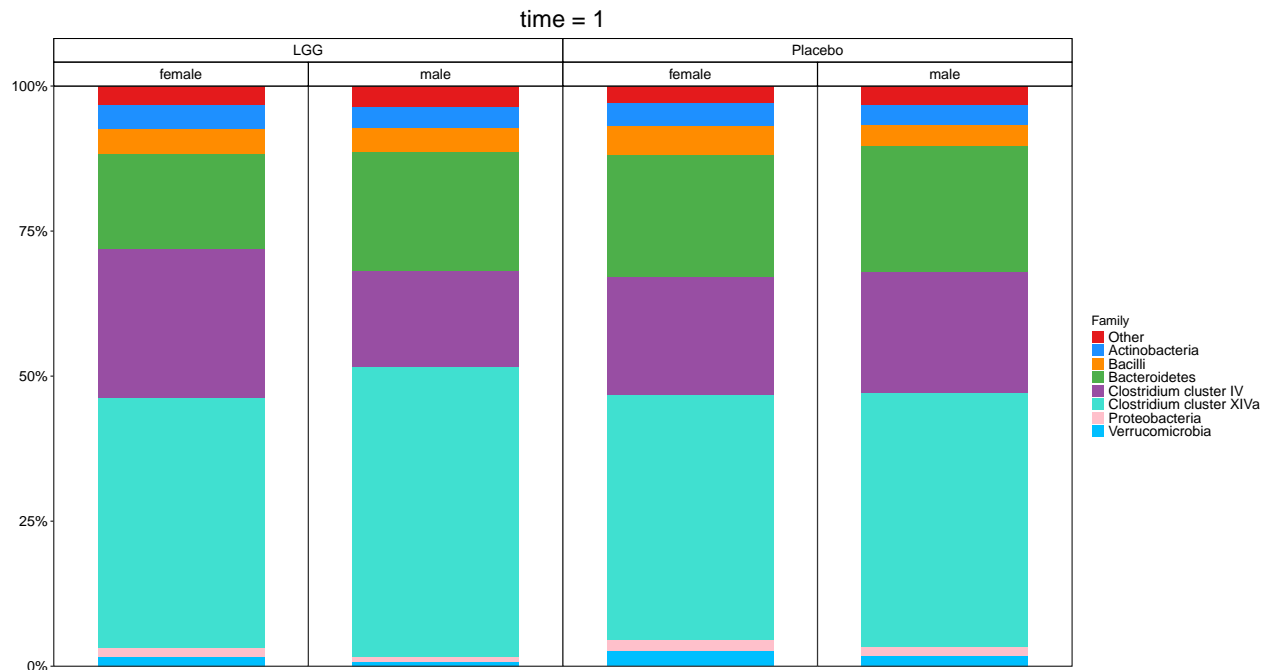


```
##
##
## [[2]]
## [[2]][[1]]
```



```
##
## [[2]][[2]]
```



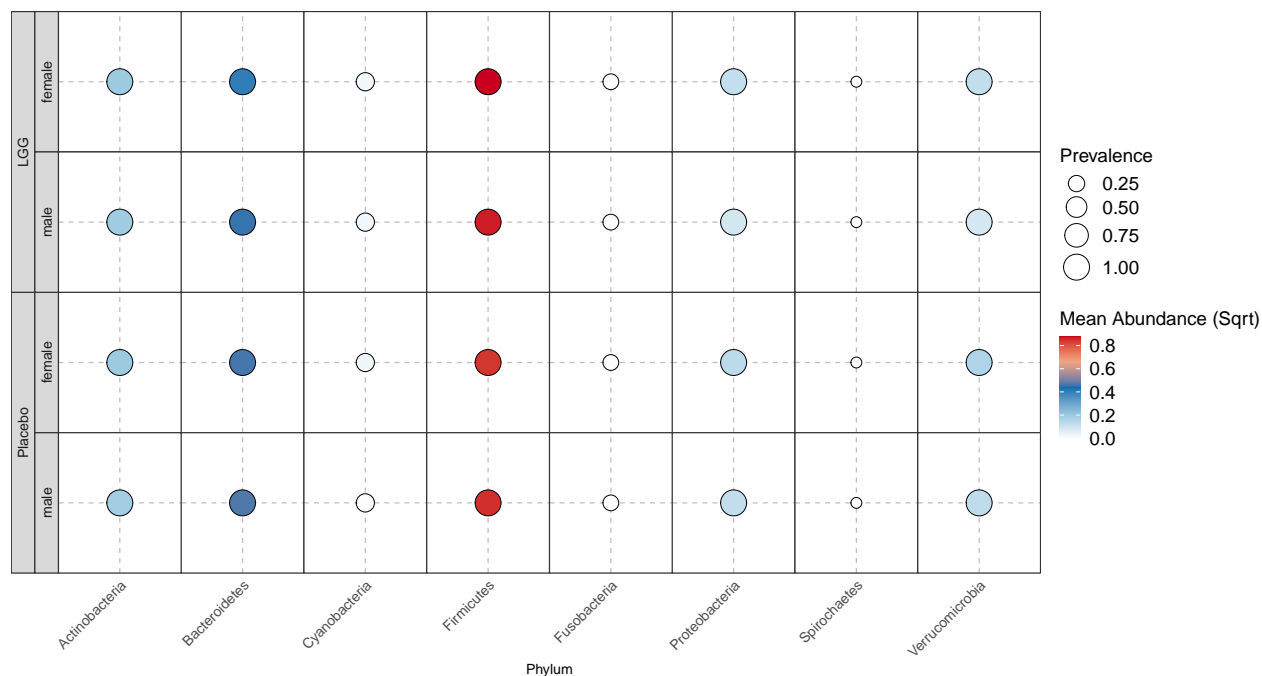


### 3.2 Taxa Dotplot

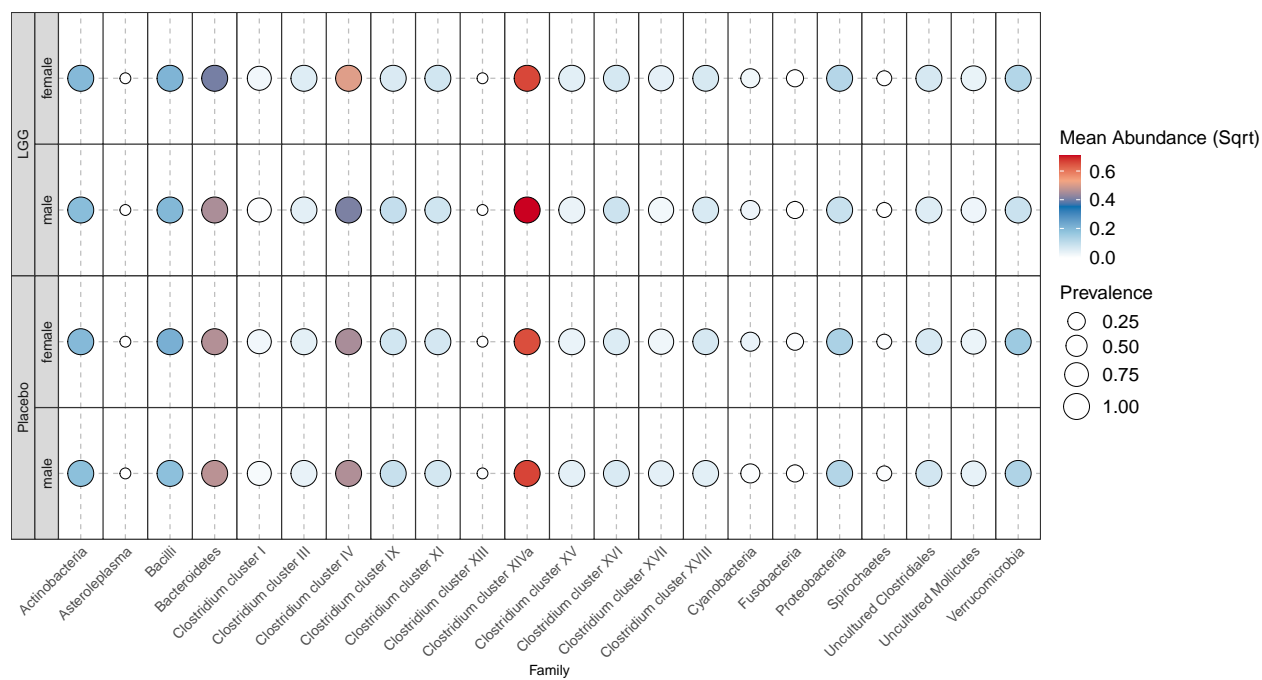
```
taxa_dotplot_results <- generate_taxa_dotplot_single(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t.level,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  features.plot = features.plot,
  top.k.plot = top.k.plot,
  top.k.func = top.k.func,
  prev.filter = prev.filter,
  abund.filter = abund.filter,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei)
```

taxa\_dotplot\_results

## [[1]]



```
##
## [[2]]
```



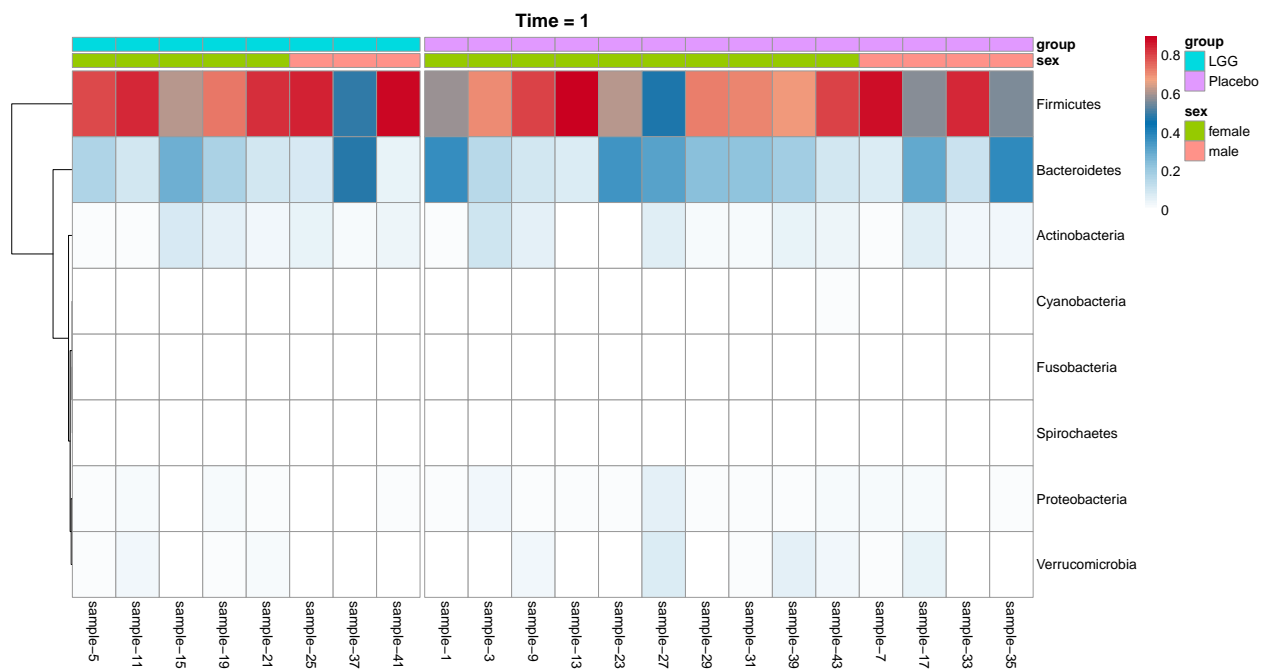
### 3.3 Taxa Heatmap

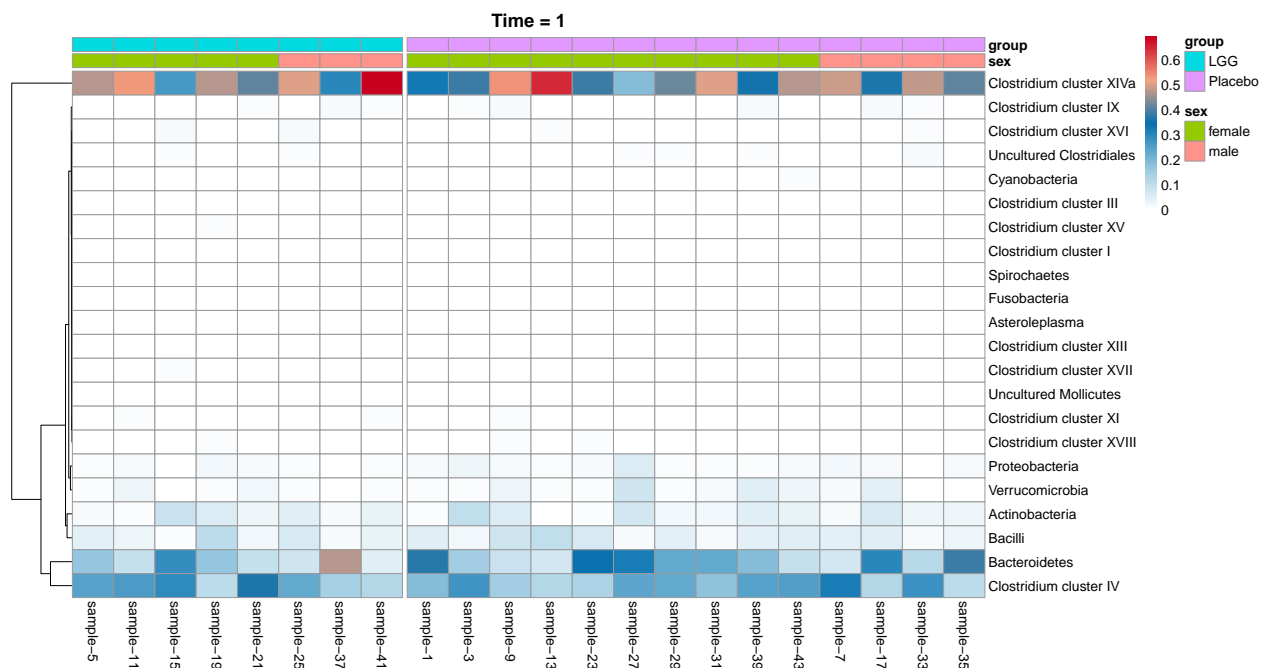
```
taxa_heatmap_results <- generate_taxa_heatmap_single(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t.level = t.level,
  group.var = group.var,
  strata.var = strata.var,
```

```

feature.level = feature.level,
feature.dat.type = feature.dat.type,
features.plot = features.plot,
top.k.plot = top.k.plot,
top.k.func = top.k.func,
prev.filter = prev.filter,
abund.filter = abund.filter,
base.size = base.size,
palette = NULL,
cluster.cols = NULL,
cluster.rows = NULL,
pdf = pdf,
file.ann = file.ann,
pdf.wid = pdf.wid,
pdf.hei = pdf.hei)

```





### 3.4 Taxa Test

```
taxa_test_results <- generate_taxa_test_single(data.obj = data.obj,
                                              time.var = time.var,
                                              t.level = t.level,
                                              group.var = group.var,
                                              adj.vars = adj.vars,
                                              prev.filter = prev.filter,
                                              abund.filter = abund.filter,
                                              feature.level = feature.level,
                                              feature.dat.type = feature.dat.type,
                                              ...)
```

```
## For proportion and other data types, posterior sampling will not be performed!
## The data has 22 samples and 8 features will be tested!
## On average, 1 outlier counts will be replaced for each feature!
## Permutation testing ...
## .....
## Completed!
## For proportion and other data types, posterior sampling will not be performed!
## The data has 22 samples and 21 features will be tested!
## On average, 1 outlier counts will be replaced for each feature!
## Permutation testing ...
## .....
## Completed!
## ## Taxa Test Results
```

- Phylum:

Table 5: Table continues below

| Variable        | Group   | R.Squared | F.Statistic | Estimate             |
|-----------------|---------|-----------|-------------|----------------------|
| Actinobacteria  | Placebo | 0.008281  | 1.622       | 0.0371656495862313   |
| Actinobacteria  | LGG     | 0.008281  | 1.622       | 0.0371656495862313   |
| Bacteroidetes   | Placebo | 3.171e-05 | 0.007819    | -0.00522944015520488 |
| Bacteroidetes   | LGG     | 3.171e-05 | 0.007819    | -0.00522944015520488 |
| Cyanobacteria   | Placebo | 0.007035  | 0.215       | -0.00426210232386587 |
| Cyanobacteria   | LGG     | 0.007035  | 0.215       | -0.00426210232386587 |
| Firmicutes      | Placebo | 1.488e-08 | 3.721e-05   | -0.00021666603778836 |
| Firmicutes      | LGG     | 1.488e-08 | 3.721e-05   | -0.00021666603778836 |
| Fusobacteria    | Placebo | 0.004317  | 0.102       | 0.000446912815084747 |
| Fusobacteria    | LGG     | 0.004317  | 0.102       | 0.000446912815084747 |
| Proteobacteria  | Placebo | 0.009319  | 3.424       | -0.0250120304262438  |
| Proteobacteria  | LGG     | 0.009319  | 3.424       | -0.0250120304262438  |
| Spirochaetes    | Placebo | 0.0612    | 1.45        | -0.00213813810466464 |
| Spirochaetes    | LGG     | 0.0612    | 1.45        | -0.00213813810466464 |
| Verrucomicrobia | Placebo | 0.002485  | 0.3079      | -0.0142760721608877  |
| Verrucomicrobia | LGG     | 0.002485  | 0.3079      | -0.0142760721608877  |

Table 6: Table continues below

| P.Value | Adjusted.P.Value | Mean.Proportion | Mean.Prevalence | SD.Abundance |
|---------|------------------|-----------------|-----------------|--------------|
| 0.24    | 0.7104           | 0.03858         | 1               | 0.02768      |
| 0.24    | 0.7104           | 0.03887         | 1               | 0.02551      |
| 0.96    | 0.9874           | 0.2133          | 1               | 0.1164       |
| 0.96    | 0.9874           | 0.1783          | 1               | 0.1418       |
| 0.61    | 0.9815           | 0.0008715       | 0.2857          | 0.002676     |
| 0.61    | 0.9815           | 0.0006973       | 0.5             | 0.0009465    |
| 0.98    | 0.9874           | 0.7056          | 1               | 0.129        |
| 0.98    | 0.9874           | 0.7568          | 1               | 0.1375       |
| 0.76    | 0.9815           | 2.213e-05       | 0.2143          | 5.433e-05    |
| 0.76    | 0.9815           | 0               | 0               | 0            |
| 0.09    | 0.5354           | 0.01829         | 1               | 0.01254      |
| 0.09    | 0.5354           | 0.01256         | 1               | 0.006984     |
| 0.32    | 0.7104           | 2.993e-05       | 0.2143          | 6.179e-05    |
| 0.32    | 0.7104           | 0               | 0               | 0            |
| 0.64    | 0.9815           | 0.02332         | 1               | 0.0224       |
| 0.64    | 0.9815           | 0.01274         | 1               | 0.008737     |

---

SD.Prevalence

---

0  
0  
0  
0  
0.4688  
0.5345  
0  
0  
0.4258

| SD.Prevalence |
|---------------|
| 0             |
| 0             |
| 0             |
| 0.4258        |
| 0             |
| 0             |
| 0             |

- **Family:**

Table 8: Table continues below

| Variable                  | Group   | R.Squared | F.Statistic |
|---------------------------|---------|-----------|-------------|
| Actinobacteria            | Placebo | 0.008281  | 1.622       |
| Actinobacteria            | LGG     | 0.008281  | 1.622       |
| Bacilli                   | Placebo | 0.007595  | 2.078       |
| Bacilli                   | LGG     | 0.007595  | 2.078       |
| Bacteroidetes             | Placebo | 3.171e-05 | 0.007819    |
| Bacteroidetes             | LGG     | 3.171e-05 | 0.007819    |
| Clostridium cluster I     | Placebo | 0.03478   | 1.937       |
| Clostridium cluster I     | LGG     | 0.03478   | 1.937       |
| Clostridium cluster III   | Placebo | 0.0009978 | 0.3254      |
| Clostridium cluster III   | LGG     | 0.0009978 | 0.3254      |
| Clostridium cluster IV    | Placebo | 0.0005453 | 0.3611      |
| Clostridium cluster IV    | LGG     | 0.0005453 | 0.3611      |
| Clostridium cluster IX    | Placebo | 0.02899   | 5.118       |
| Clostridium cluster IX    | LGG     | 0.02899   | 5.118       |
| Clostridium cluster XI    | Placebo | 0.0002079 | 0.2086      |
| Clostridium cluster XI    | LGG     | 0.0002079 | 0.2086      |
| Clostridium cluster XIII  | Placebo | 0.02201   | 0.4589      |
| Clostridium cluster XIII  | LGG     | 0.02201   | 0.4589      |
| Clostridium cluster XIVa  | Placebo | 3.245e-05 | 0.03652     |
| Clostridium cluster XIVa  | LGG     | 3.245e-05 | 0.03652     |
| Clostridium cluster XV    | Placebo | 0.00284   | 0.4938      |
| Clostridium cluster XV    | LGG     | 0.00284   | 0.4938      |
| Clostridium cluster XVI   | Placebo | 0.001252  | 0.1505      |
| Clostridium cluster XVI   | LGG     | 0.001252  | 0.1505      |
| Clostridium cluster XVII  | Placebo | 0.00913   | 0.6283      |
| Clostridium cluster XVII  | LGG     | 0.00913   | 0.6283      |
| Clostridium cluster XVIII | Placebo | 0.0008333 | 0.1064      |
| Clostridium cluster XVIII | LGG     | 0.0008333 | 0.1064      |
| Cyanobacteria             | Placebo | 0.007035  | 0.215       |
| Cyanobacteria             | LGG     | 0.007035  | 0.215       |
| Fusobacteria              | Placebo | 0.004317  | 0.102       |
| Fusobacteria              | LGG     | 0.004317  | 0.102       |
| Proteobacteria            | Placebo | 0.009319  | 3.424       |
| Proteobacteria            | LGG     | 0.009319  | 3.424       |
| Spirochaetes              | Placebo | 0.0612    | 1.45        |
| Spirochaetes              | LGG     | 0.0612    | 1.45        |
| Uncultured Clostridiales  | Placebo | 4.582e-05 | 0.004194    |
| Uncultured Clostridiales  | LGG     | 4.582e-05 | 0.004194    |

| Variable              | Group   | R.Squared | F.Statistic |
|-----------------------|---------|-----------|-------------|
| Uncultured Mollicutes | Placebo | 0.008615  | 0.4431      |
| Uncultured Mollicutes | LGG     | 0.008615  | 0.4431      |
| Verrucomicrobia       | Placebo | 0.002485  | 0.3079      |
| Verrucomicrobia       | LGG     | 0.002485  | 0.3079      |

Table 9: Table continues below

| Estimate              | P.Value | Adjusted.P.Value | Mean.Proportion |
|-----------------------|---------|------------------|-----------------|
| 0.0371656495862313    | 0.28    | 0.8956           | 0.03858         |
| 0.0371656495862313    | 0.28    | 0.8956           | 0.03887         |
| -0.0380311099488204   | 0.21    | 0.8956           | 0.04462         |
| -0.0380311099488204   | 0.21    | 0.8956           | 0.04312         |
| -0.00522944015520488  | 0.95    | 0.949            | 0.2133          |
| -0.00522944015520488  | 0.95    | 0.949            | 0.1783          |
| -0.00778505857179085  | 0.18    | 0.8956           | 0.0004309       |
| -0.00778505857179085  | 0.18    | 0.8956           | 0.0003633       |
| 0.00307464254072209   | 0.61    | 0.8984           | 0.001921        |
| 0.00307464254072209   | 0.61    | 0.8984           | 0.002703        |
| 0.022308499587939     | 0.53    | 0.8984           | 0.2038          |
| 0.022308499587939     | 0.53    | 0.8984           | 0.2228          |
| 0.0284837310780048    | 0.07    | 0.6768           | 0.006706        |
| 0.0284837310780048    | 0.07    | 0.6768           | 0.006017        |
| 0.00223243108522325   | 0.64    | 0.8984           | 0.005256        |
| 0.00223243108522325   | 0.64    | 0.8984           | 0.005965        |
| 0.000419187792751176  | 0.71    | 0.8984           | 7.779e-06       |
| 0.000419187792751176  | 0.71    | 0.8984           | 0               |
| -0.00785830208245519  | 0.86    | 0.9484           | 0.4268          |
| -0.00785830208245519  | 0.86    | 0.9484           | 0.4572          |
| -0.00433160436417467  | 0.48    | 0.8984           | 0.001428        |
| -0.00433160436417467  | 0.48    | 0.8984           | 0.001955        |
| 0.00485366929249193   | 0.7     | 0.8984           | 0.003553        |
| 0.00485366929249193   | 0.7     | 0.8984           | 0.005731        |
| 0.00668670952996451   | 0.48    | 0.8984           | 0.001052        |
| 0.00668670952996451   | 0.48    | 0.8984           | 0.00137         |
| -0.00387419196078766  | 0.77    | 0.8984           | 0.004027        |
| -0.00387419196078766  | 0.77    | 0.8984           | 0.004411        |
| -0.00426210232386587  | 0.62    | 0.8984           | 0.0008715       |
| -0.00426210232386587  | 0.62    | 0.8984           | 0.0006973       |
| 0.000446912815084747  | 0.75    | 0.8984           | 2.213e-05       |
| 0.000446912815084747  | 0.75    | 0.8984           | 0               |
| -0.0250120304262438   | 0.11    | 0.7879           | 0.01829         |
| -0.0250120304262438   | 0.11    | 0.7879           | 0.01256         |
| -0.00213813810466464  | 0.44    | 0.8956           | 2.993e-05       |
| -0.00213813810466464  | 0.44    | 0.8956           | 0               |
| -0.000912135473189165 | 0.96    | 0.949            | 0.004694        |
| -0.000912135473189165 | 0.96    | 0.949            | 0.004054        |
| -0.00648233320320809  | 0.51    | 0.8984           | 0.001222        |
| -0.00648233320320809  | 0.51    | 0.8984           | 0.001134        |
| -0.0142760721608877   | 0.6     | 0.8984           | 0.02332         |
| -0.0142760721608877   | 0.6     | 0.8984           | 0.01274         |

| Mean.Prevalence | SD.Abandance | SD.Prevalence |
|-----------------|--------------|---------------|
| 1               | 0.02768      | 0             |
| 1               | 0.02551      | 0             |
| 1               | 0.02371      | 0             |
| 1               | 0.03268      | 0             |
| 1               | 0.1164       | 0             |
| 1               | 0.1418       | 0             |
| 0.8571          | 0.0005898    | 0.3631        |
| 0.625           | 0.0004214    | 0.5175        |
| 1               | 0.0009628    | 0             |
| 1               | 0.001215     | 0             |
| 1               | 0.06958      | 0             |
| 1               | 0.09082      | 0             |
| 1               | 0.005046     | 0             |
| 1               | 0.005356     | 0             |
| 1               | 0.001698     | 0             |
| 1               | 0.001659     | 0             |
| 0.07143         | 2.91e-05     | 0.2673        |
| 0               | 0            | 0             |
| 1               | 0.109        | 0             |
| 1               | 0.1352       | 0             |
| 1               | 0.001012     | 0             |
| 1               | 0.002454     | 0             |
| 1               | 0.00294      | 0             |
| 1               | 0.006604     | 0             |
| 1               | 0.001502     | 0             |
| 1               | 0.002487     | 0             |
| 0.9286          | 0.002957     | 0.2673        |
| 1               | 0.002947     | 0             |
| 0.2857          | 0.002676     | 0.4688        |
| 0.5             | 0.0009465    | 0.5345        |
| 0.2143          | 5.433e-05    | 0.4258        |
| 0               | 0            | 0             |
| 1               | 0.01254      | 0             |
| 1               | 0.006984     | 0             |
| 0.2143          | 6.179e-05    | 0.4258        |
| 0               | 0            | 0             |
| 1               | 0.005238     | 0             |
| 1               | 0.003825     | 0             |
| 0.7857          | 0.001711     | 0.4258        |
| 0.75            | 0.001318     | 0.4629        |
| 1               | 0.0224       | 0             |
| 1               | 0.008737     | 0             |

### 3.5 Taxa Boxplot for Significant Taxa

```

significant_taxa <- taxa_test_results$Taxa[taxa_test_results$Adjusted.P.Value < 1]

taxa_boxplot_results <- generate_taxa_boxplot_single(data.obj = data.obj,
                                                    subject.var = subject.var,
                                                    time.var = time.var,
                                                    t.level = t.level,

```



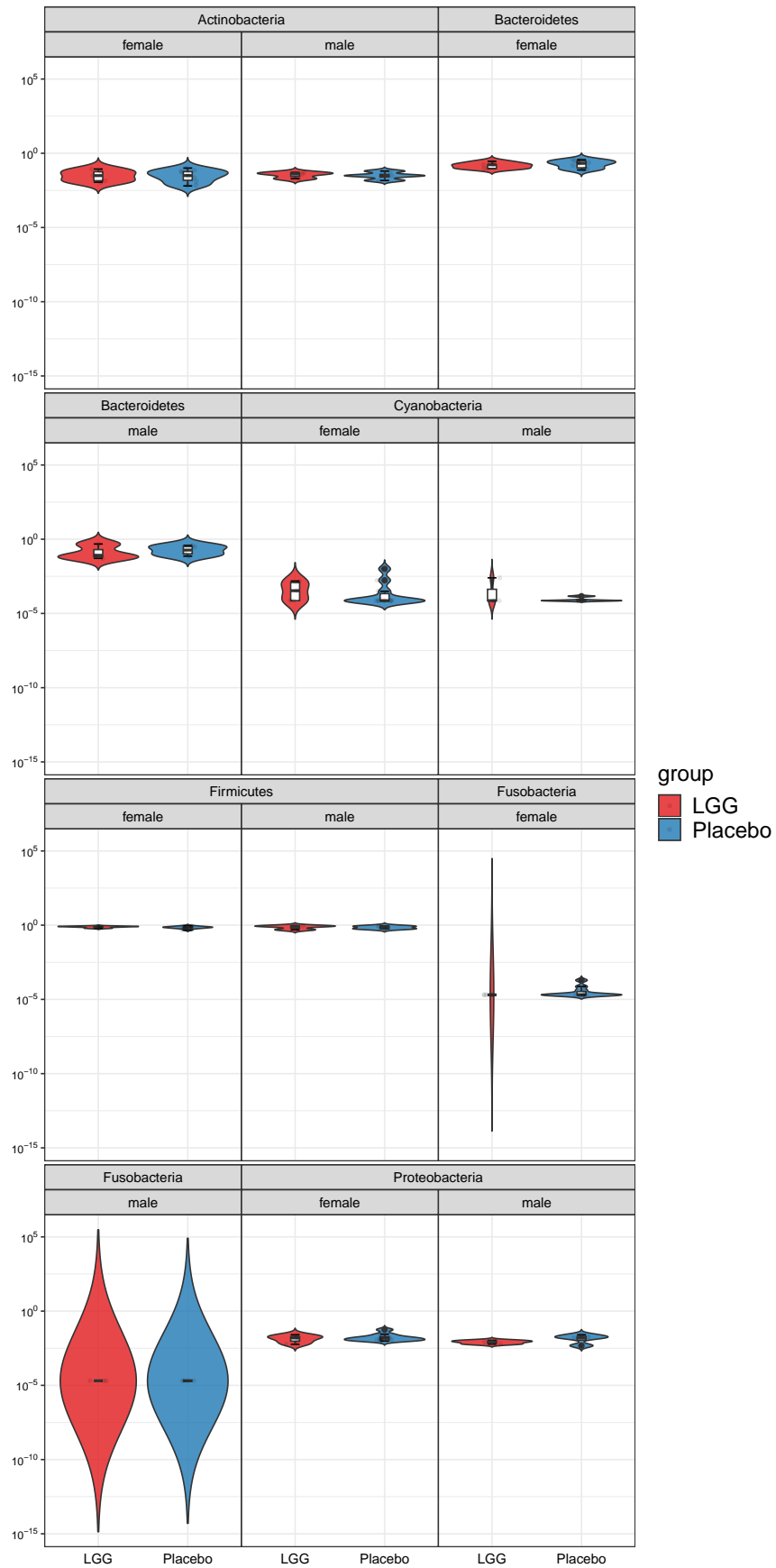
```

names(taxa_boxplot_results) <- feature.level
taxa_boxplot_results

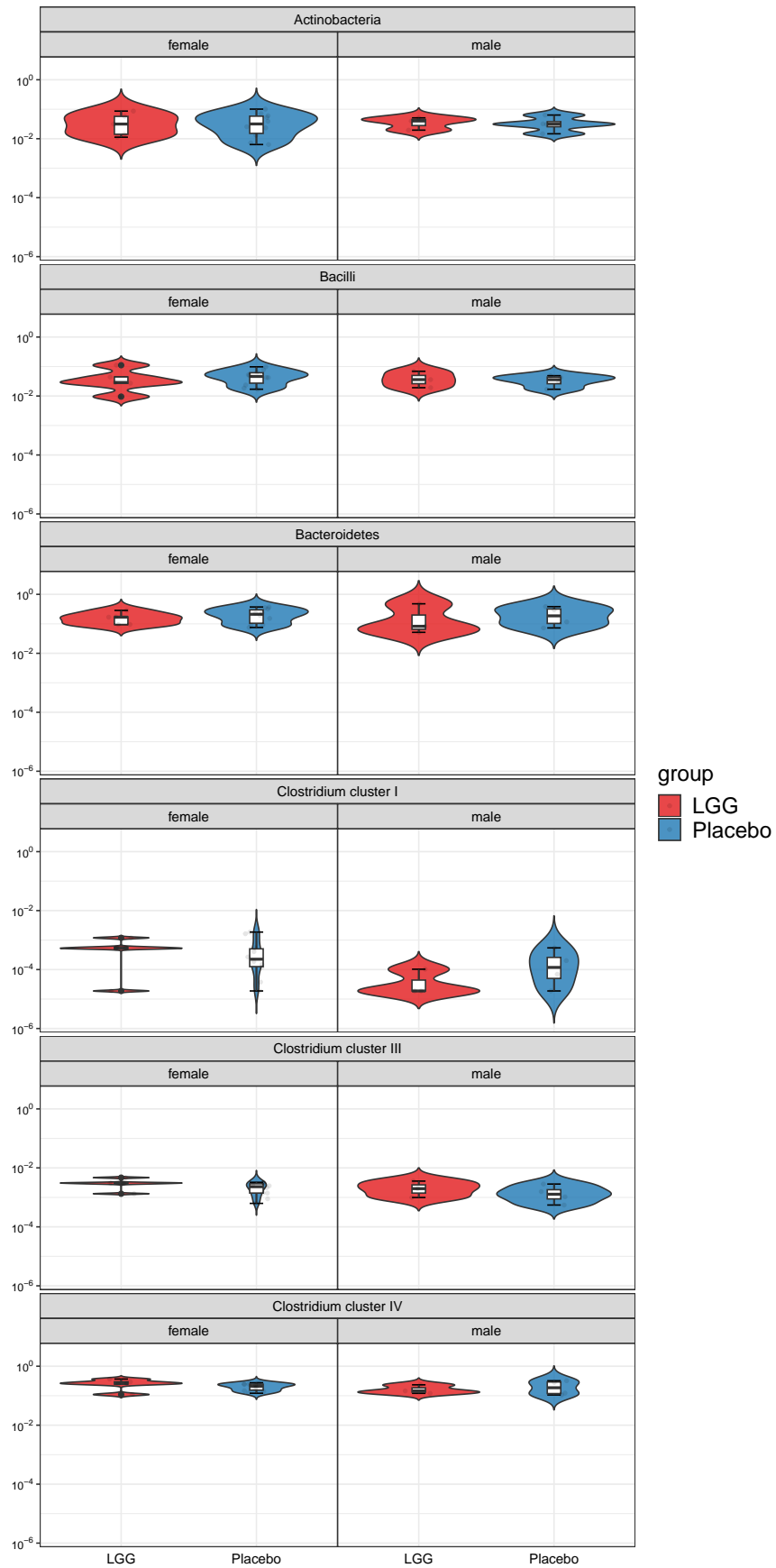
group.var = group.var,
strata.var = strata.var,
feature.level = feature.level,
feature.dat.type = feature.dat.type,
features.plot = significant_taxa,
top.k.plot = top.k.plot,
top.k.func = top.k.func,
Transform = Transform,
prev.filter = prev.filter,
abund.filter = abund.filter,
base.size = 10,
theme.choice = theme.choice,
custom.theme = custom.theme,
palette = palette,
pdf = pdf,
file.ann = file.ann,
pdf.wid = pdf.wid,
pdf.hei = pdf.hei)

## $Phylum

```



##  
## \$Family



```

taxa_indiv_boxplot_results <- generate_taxa_indiv_boxplot_single(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t.level = t.level,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  features.plot = significant_taxa,
  feature.dat.type = feature.dat.type,
  top.k.plot = top.k.plot,
  top.k.func = top.k.func,
  Transform = Transform,
  prev.filter = prev.filter,
  abund.filter = abund.filter,
  base.size = 10,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = TRUE,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei)

```

The boxplot results for individual taxa or features can be found in the current working directory. The relevant file is named: taxa\_indiv\_boxplot\_single\_subject\_subject\_time\_time\_feature\_level\_Phylum\_transform\_log\_prev\_filter\_0\_abund\_filter\_0\_group\_group\_strata\_sex\_Phylum.pdf. Please refer to this file for more detailed visualizations. The boxplot results for individual taxa or features can be found in the current working directory. The relevant file is named: taxa\_indiv\_boxplot\_single\_subject\_subject\_time\_time\_feature\_level\_Family\_transform\_log\_prev\_filter\_0\_abund\_filter\_0\_group\_group\_strata\_sex\_Family.pdf. Please refer to this file for more detailed visualizations.