

Microbial Ecology Analysis Report

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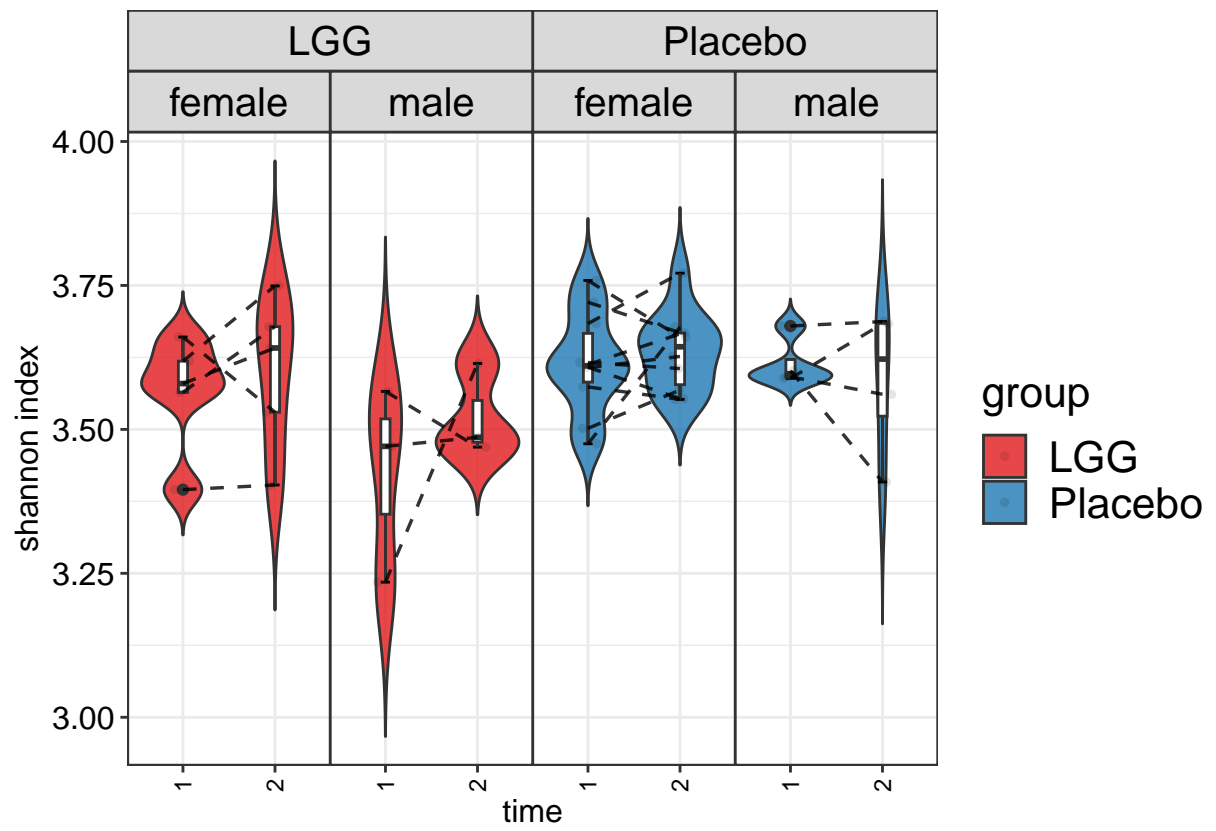
1. Alpha Diversity Analysis

1.1 Alpha Diversity Boxplots

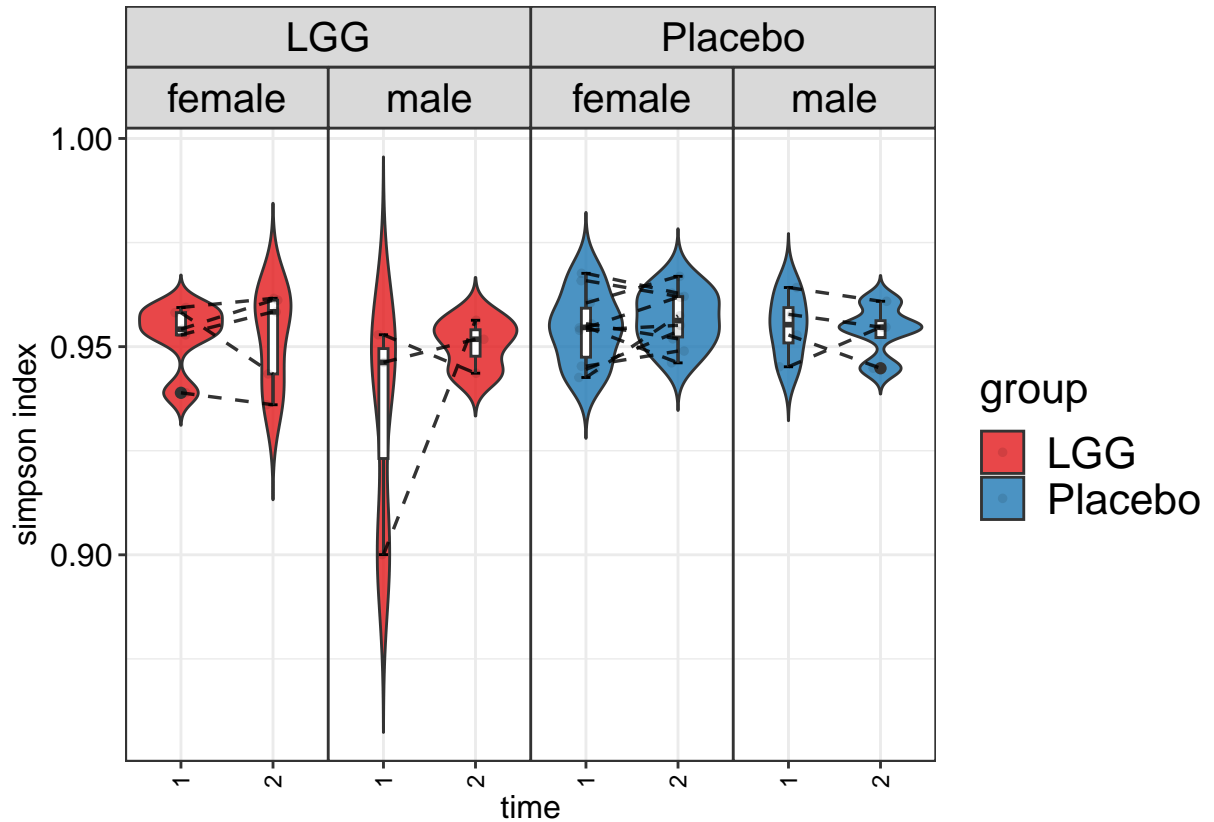
```
alpha_boxplot_results <- generate_alpha_boxplot_long(data.obj = data.obj,  
                                                    alpha.obj = alpha.obj,  
                                                    alpha.name = alpha.name,  
                                                    subject.var = subject.var,  
                                                    time.var = time.var,  
                                                    t0.level = change.base,  
                                                    ts.levels = NULL,  
                                                    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]]
```



[[2]]



1.2 Alpha Diversity Test Results

```
alpha_test_results <- generate_alpha_test_pair(data.obj = data.obj,
  alpha.obj = alpha.obj,
  time.var = time.var,
  alpha.name = alpha.name,
  subject.var = subject.var,
  group.var = group.var,
  adj.vars = adj.vars)
```

shannon Index

| Term | Estimate | Std.Error | Statistic | P.Value |
|-------------|----------|-----------|-----------|-----------|
| (Intercept) | 3.569 | 0.01796 | 198.7 | 5.438e-33 |
| time1 | -0.01388 | 0.01296 | -1.072 | 0.296 |
| sex1 | 0.02937 | 0.01757 | 1.671 | 0.111 |
| group1 | -0.03626 | 0.01701 | -2.131 | 0.04633 |

shannon Index Analysis

The variable (Intercept) has a statistically significant impact on the shannon diversity index with an estimate of 3.57.

The variable time1 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.01.

The variable sex1 does not appear to have a statistically significant effect on the shannon diversity index.

The estimate of its effect is 0.03.

The variable group1 has a statistically significant impact on the shannon diversity index with an estimate of -0.04.

simpson Index

| Term | Estimate | Std.Error | Statistic | P.Value |
|-------------|-----------|-----------|-----------|-----------|
| (Intercept) | 0.951 | 0.001899 | 500.8 | 1.293e-40 |
| time1 | -0.00155 | 0.001485 | -1.044 | 0.3084 |
| sex1 | 0.00244 | 0.001858 | 1.313 | 0.2047 |
| group1 | -0.003201 | 0.001799 | -1.779 | 0.09122 |

simpson Index Analysis

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

The variable time1 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is 0.

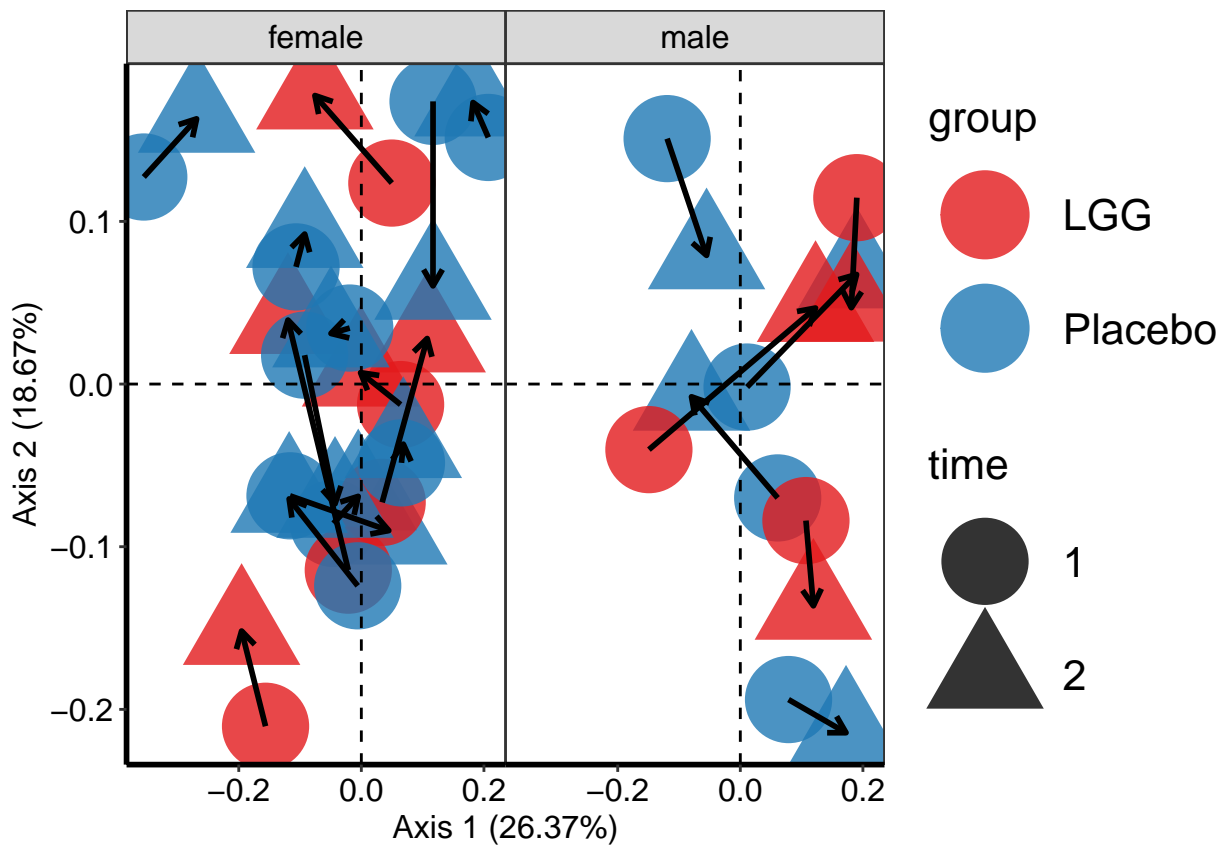
The variable sex1 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is 0.

The variable group1 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is 0.

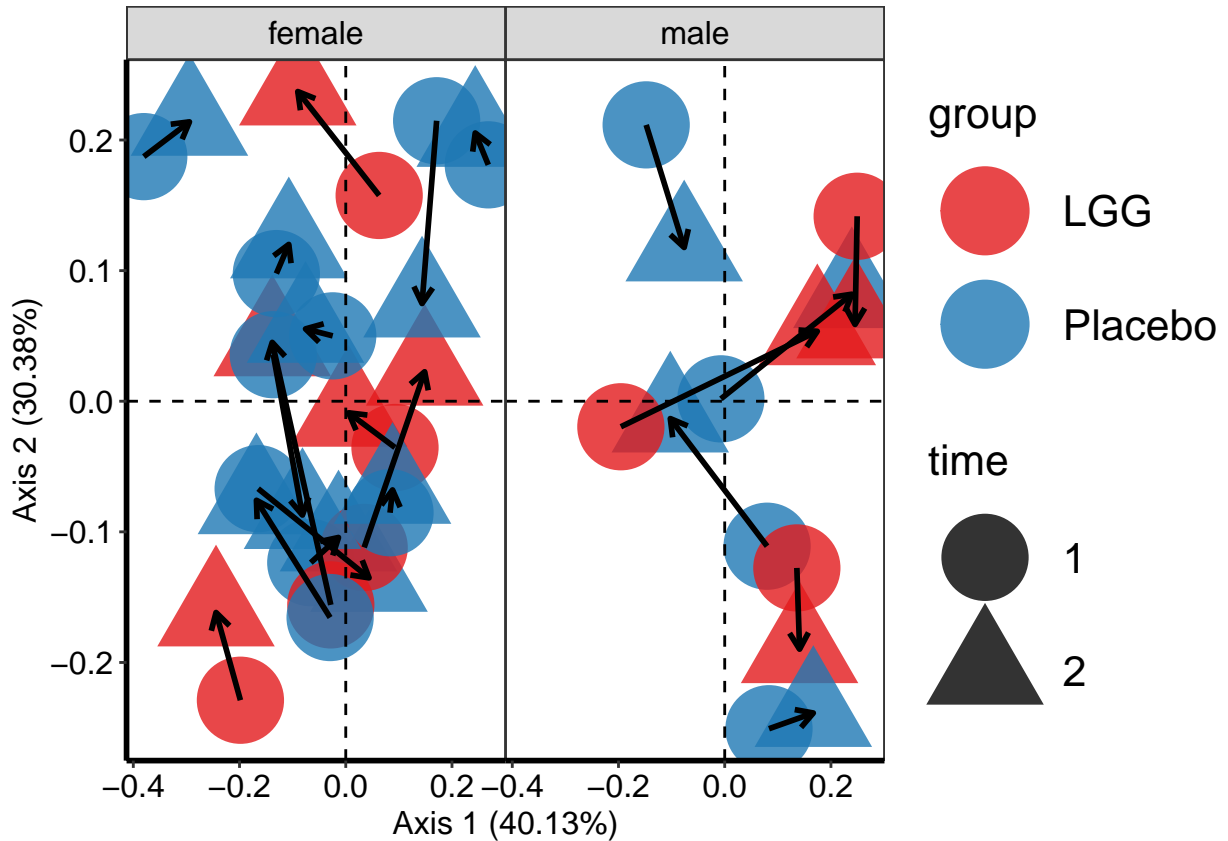
2. Beta Diversity Change Analysis

2.1 Beta Diversity Ordination

```
beta_ordination_results <- generate_beta_ordination_pair(data.obj = data.obj,  
                                                         dist.obj = dist.obj,  
                                                         pc.obj = NULL,  
                                                         subject.var = subject.var,  
                                                         time.var = time.var,  
                                                         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 Pair

```
beta_test_pair_results <- generate_beta_test_pair(data.obj = data.obj,
  dist.obj = dist.obj,
  time.var = time.var,
  subject.var = subject.var,
  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 | 0.445 | 0.48 | 0.469 |
| group | 0.445 | 0.48 | 0.469 |
| time | 0.445 | 0.48 | 0.469 |

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.

Beta Diversity PERMANOVA Analysis for Variable: time

The variable time 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 time 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 time 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 | 0.123 | 0.123 | 1.991 | 0.046 | 0.445 | BC |
| group | 1 | 0.068 | 0.068 | 1.091 | 0.025 | 0.445 | BC |
| time | 1 | 0.019 | 0.019 | 0.311 | 0.007 | 0.445 | BC |
| Residuals | 40 | 2.479 | 0.062 | NA | 0.922 | NA | BC |
| Total | 43 | 2.689 | NA | NA | 1 | NA | BC |
| sex | 1 | 0.228 | 0.228 | 1.737 | 0.04 | 0.48 | Jaccard |
| group | 1 | 0.151 | 0.151 | 1.151 | 0.027 | 0.48 | Jaccard |
| time | 1 | 0.05 | 0.05 | 0.38 | 0.009 | 0.48 | Jaccard |
| Residuals | 40 | 5.258 | 0.131 | NA | 0.924 | NA | Jaccard |
| Total | 43 | 5.687 | 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.

time Variable Analysis

The variable time 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 time 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
```

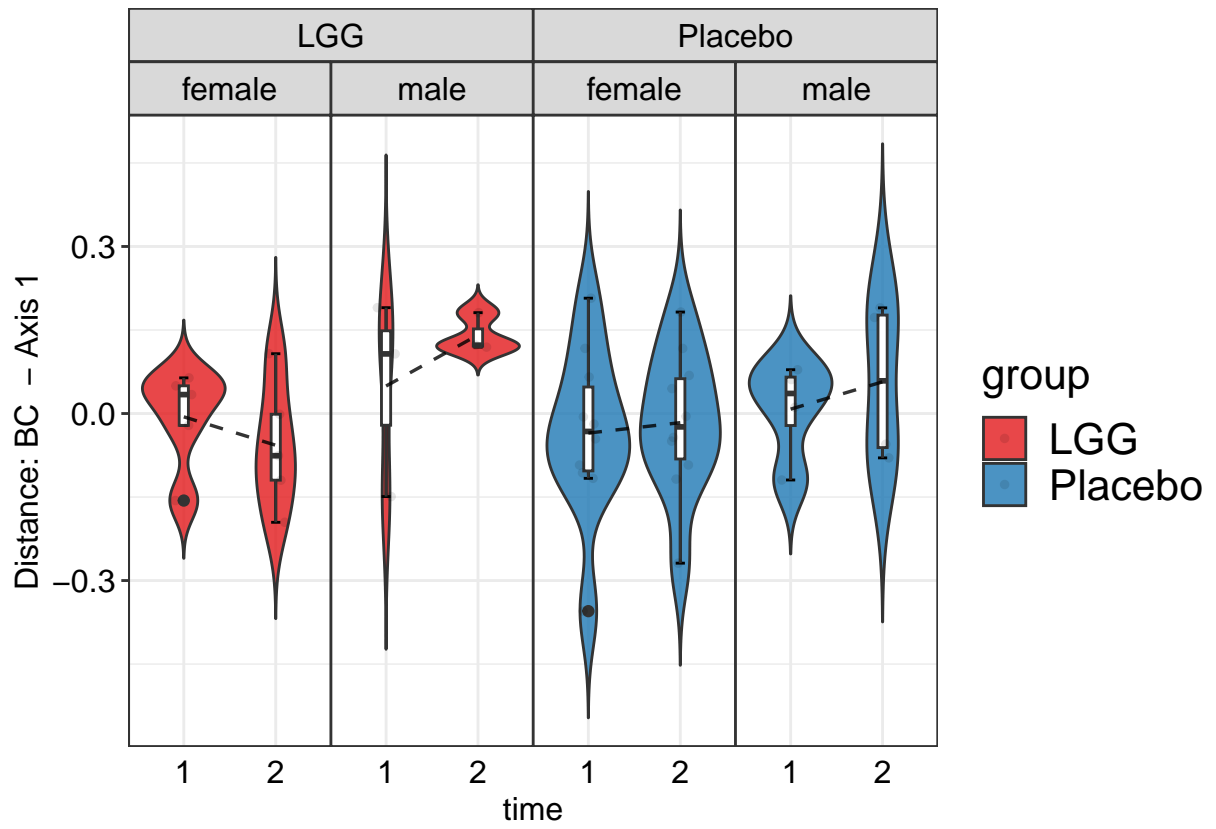
2.3 Beta Diversity PC Boxplot

```
pc_boxplot_longitudinal_results <- generate_beta_pc_boxplot_long(  
  data.obj = data.obj,  
  dist.obj = dist.obj,  
  pc.obj = NULL,  
  pc.ind = c(1, 2),  
  subject.var = subject.var,  
  time.var = time.var,  
  t0.level = change.base,  
  ts.levels = NULL,  
  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  
)
```

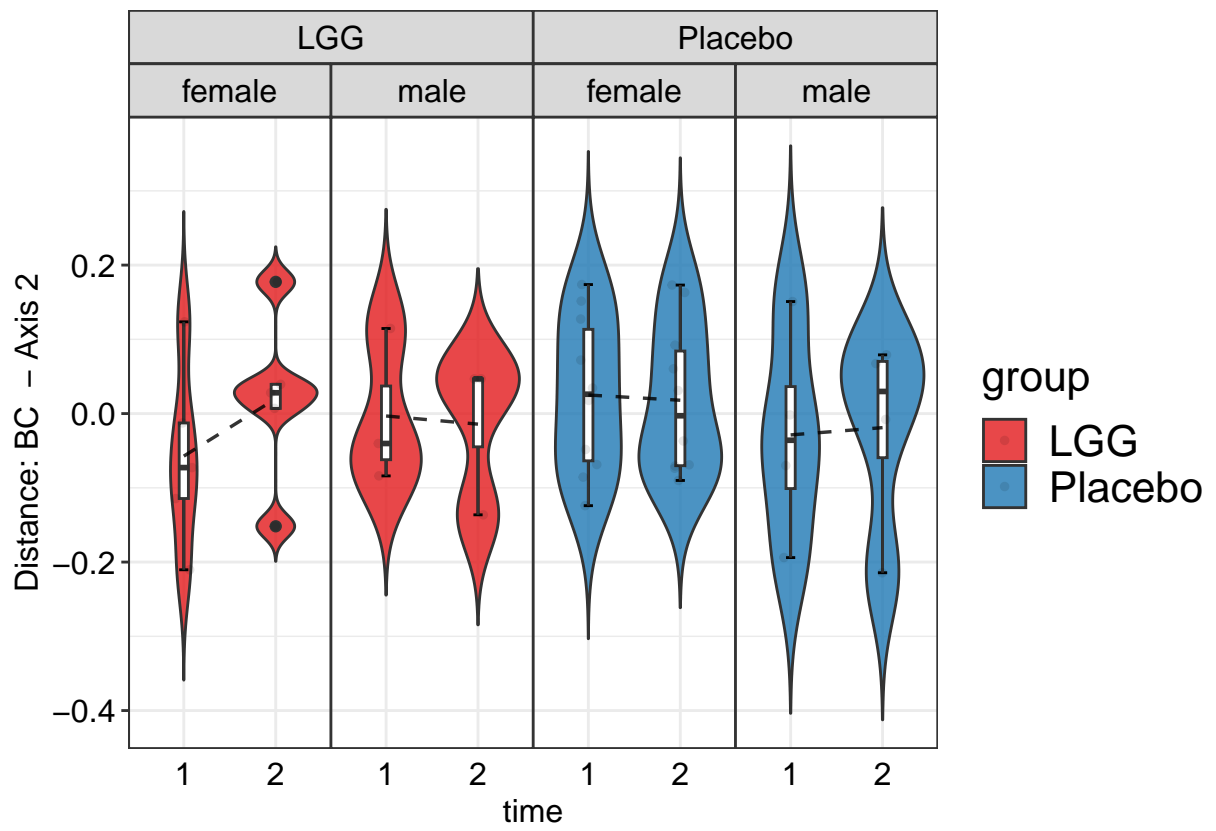
```
## [1] "Initializing distance objects..."  
## [1] "Calculating Bray-Curtis dissimilarity..."  
## [1] "Calculating Jaccard dissimilarity..."  
## [1] "All calculations complete."  
## [1] "Calculating PC..."  
## [1] "Processing BC distance..."  
## [1] "Calculating MDS..."  
## [1] "Calculation complete."  
  
## [1] "Calculating PC..."  
## [1] "Processing Jaccard distance..."  
## [1] "Calculating MDS..."  
## [1] "Calculation complete."
```

```
pc_boxplot_longitudinal_results
```

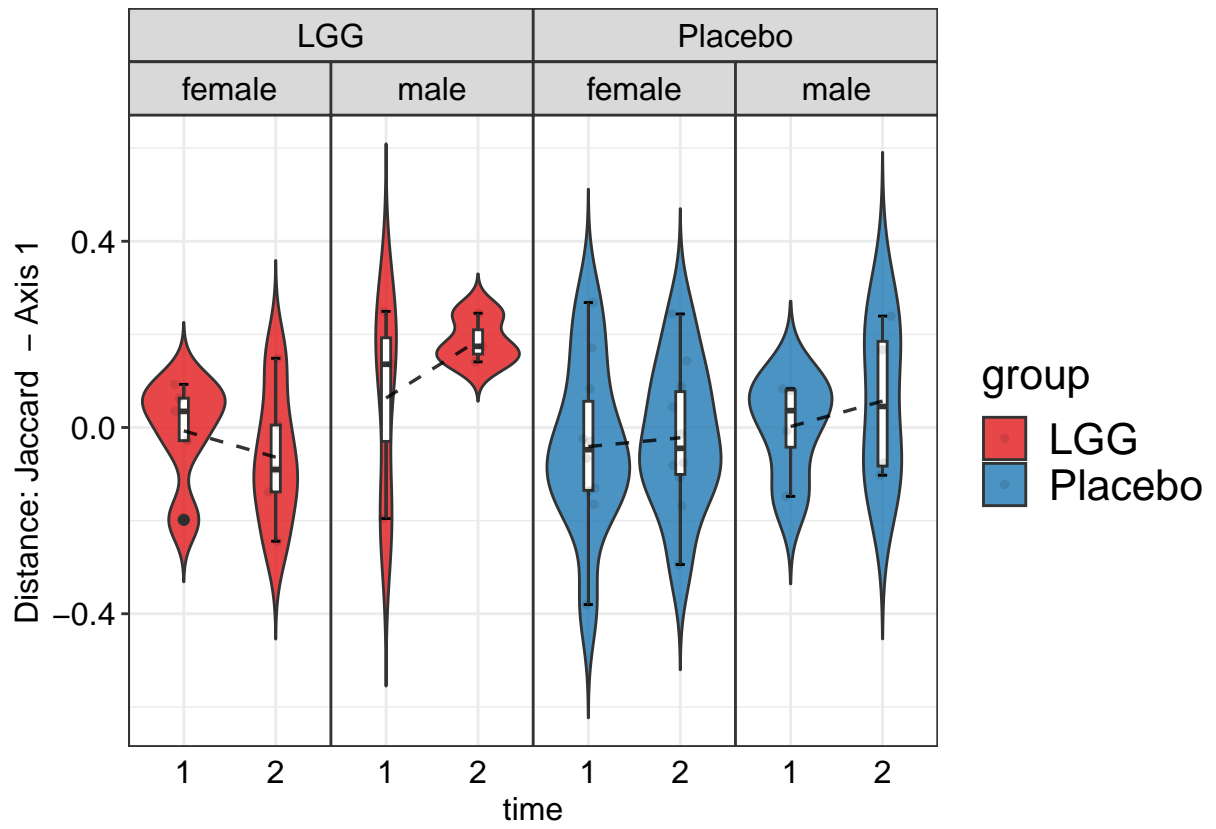
```
## [[1]]  
## [[1]][[1]]
```

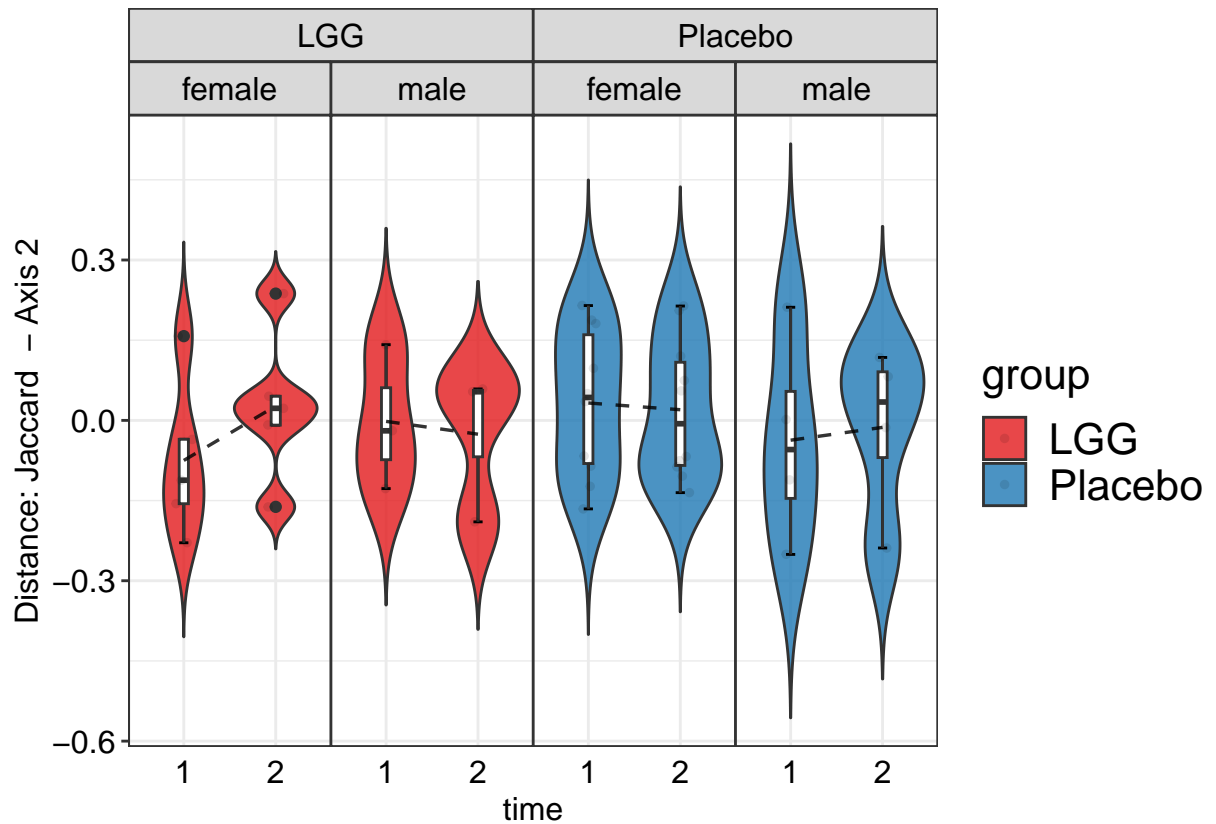
```
##
## [[1]][[2]]
```



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



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



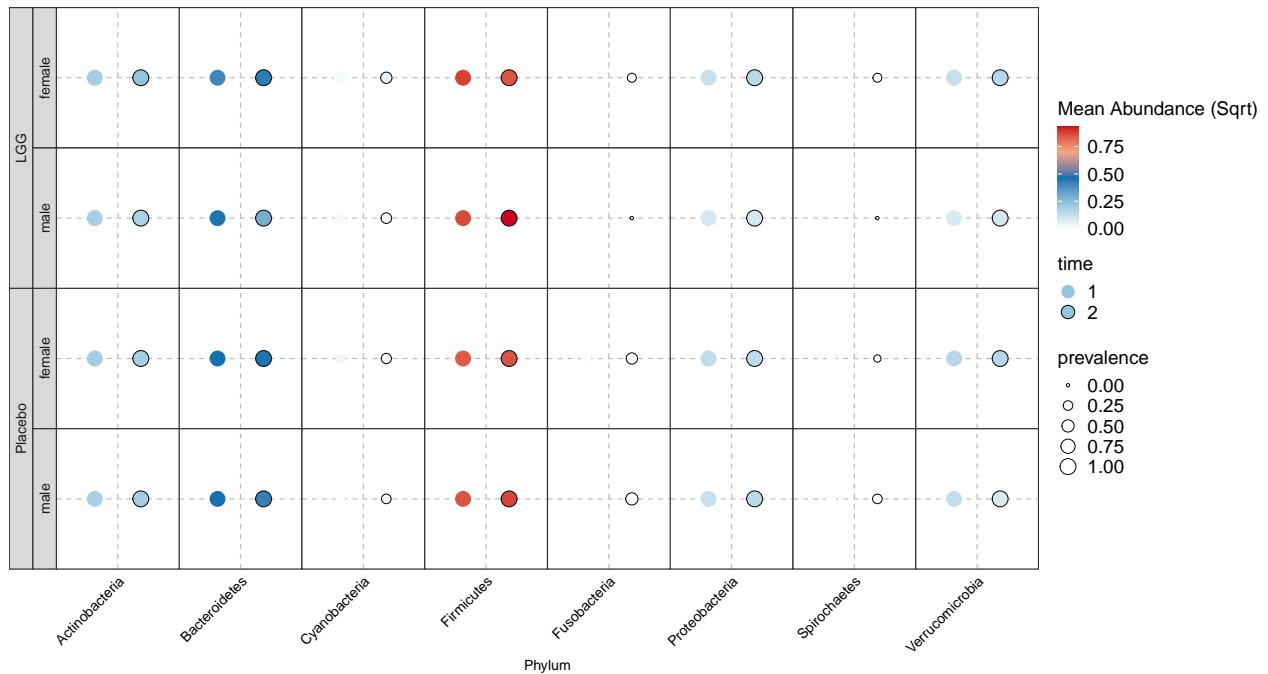
3. Taxonomic Feature Analysis

3.1 Taxa Change Dotplot

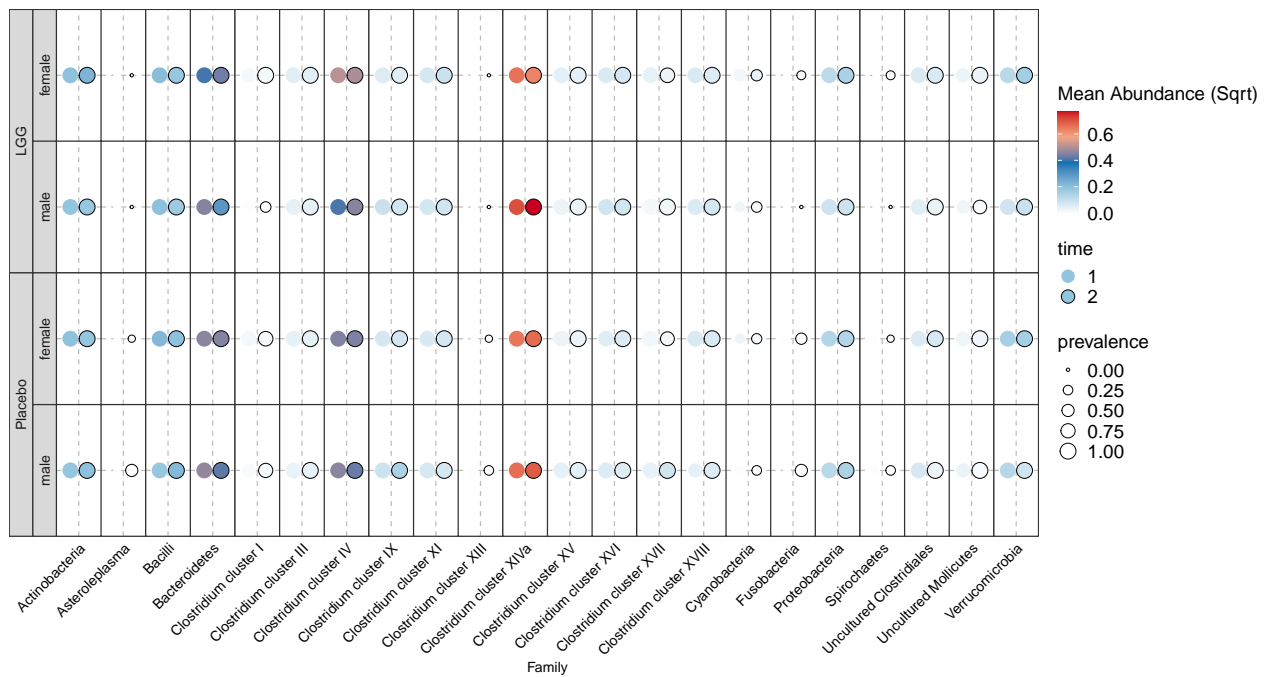
```
taxa_dotplot_results <- generate_taxa_dotplot_pair(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  features.plot = features.plot,
  top.k.plot = top.k.plot,
  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]]
```



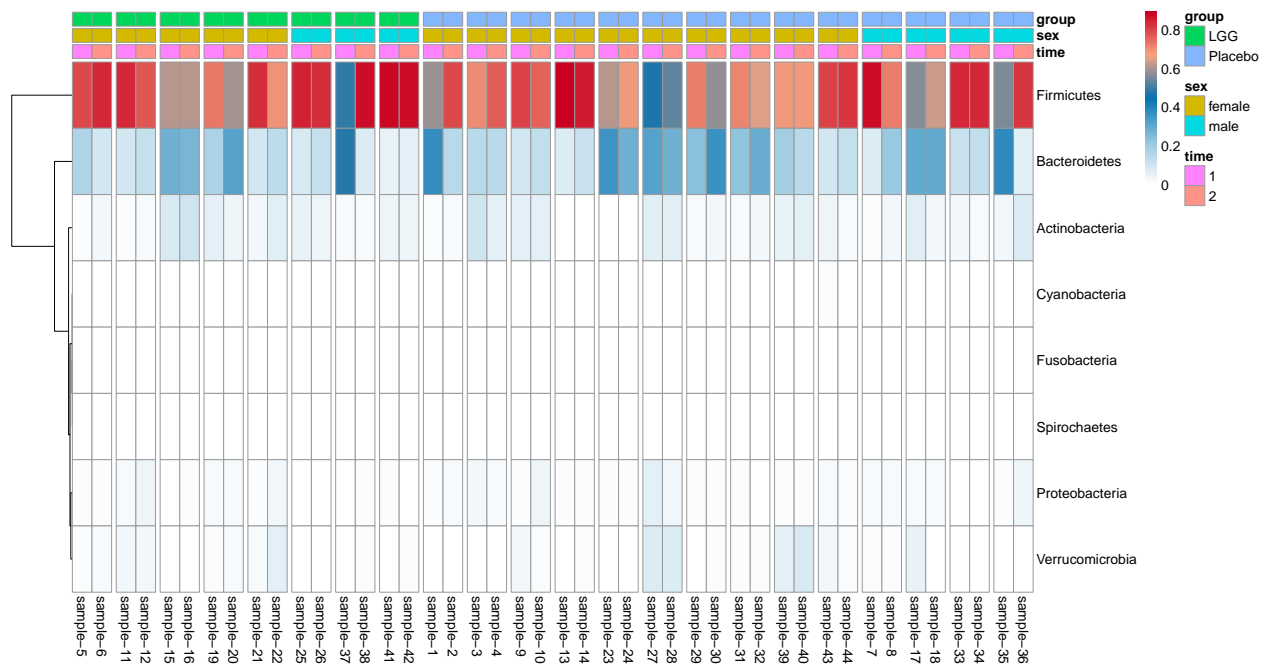
3.2 Taxa Heatmap Pair

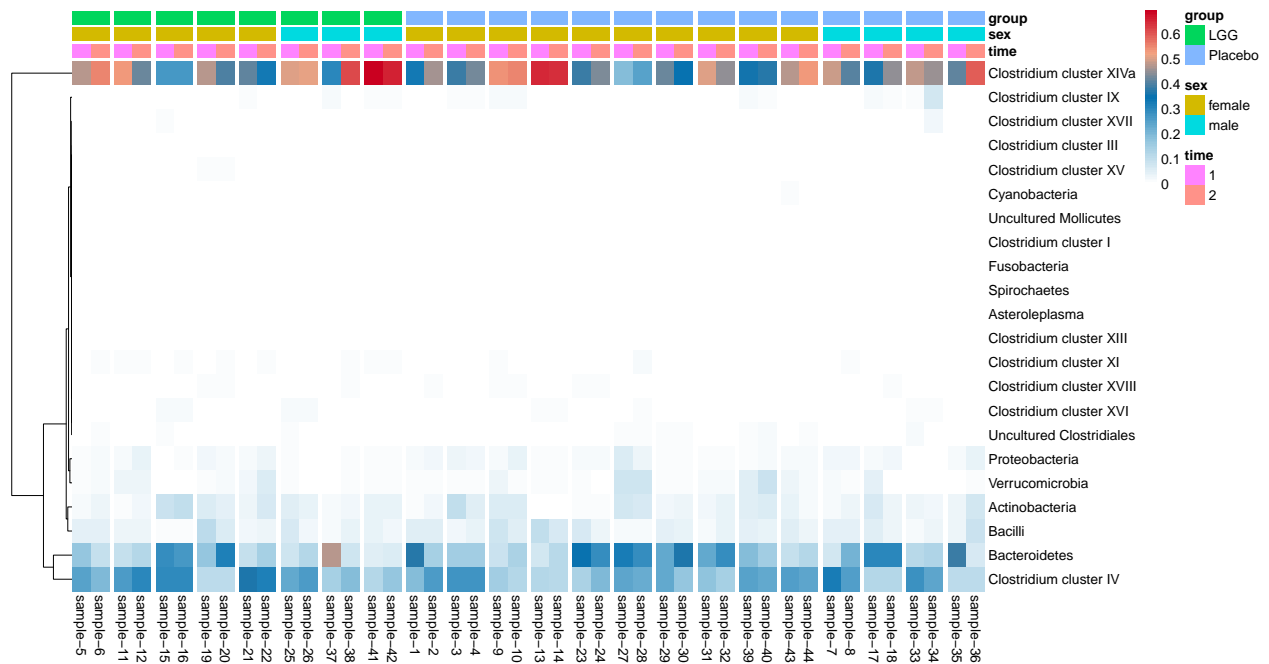
```
taxa_heatmap_pair_results <- generate_taxa_heatmap_pair(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
```

```

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

```



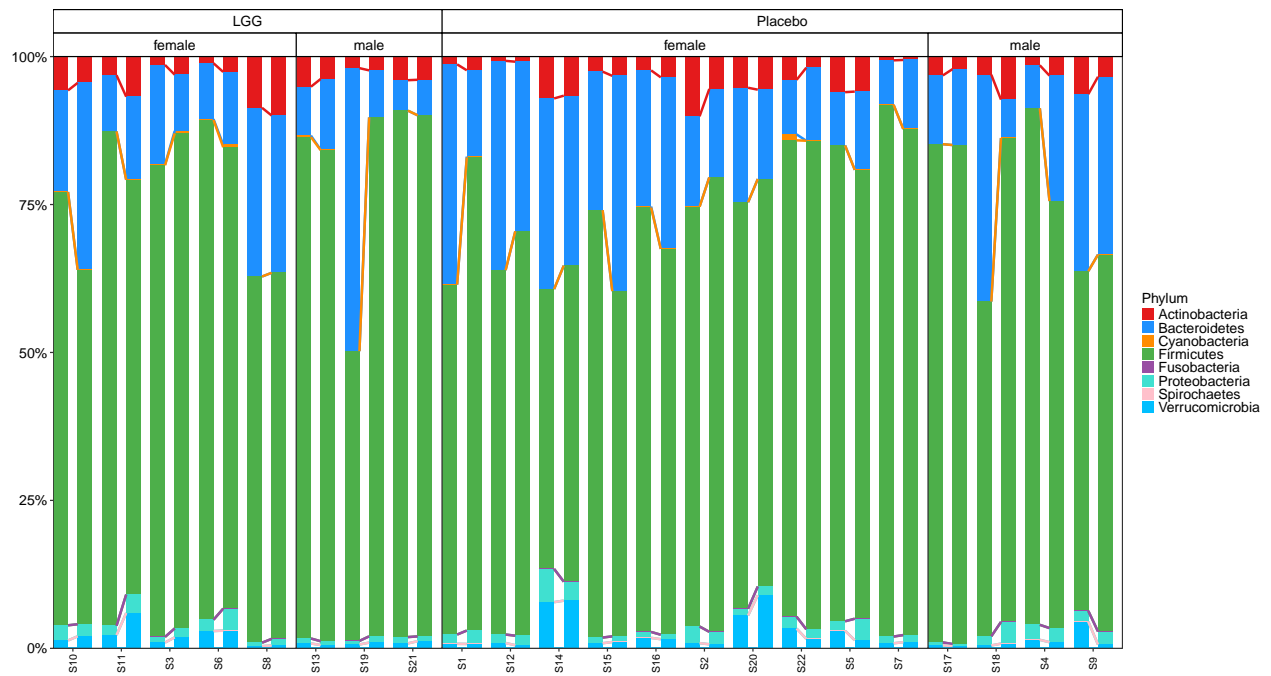


3.3 Taxa Barplot Pair

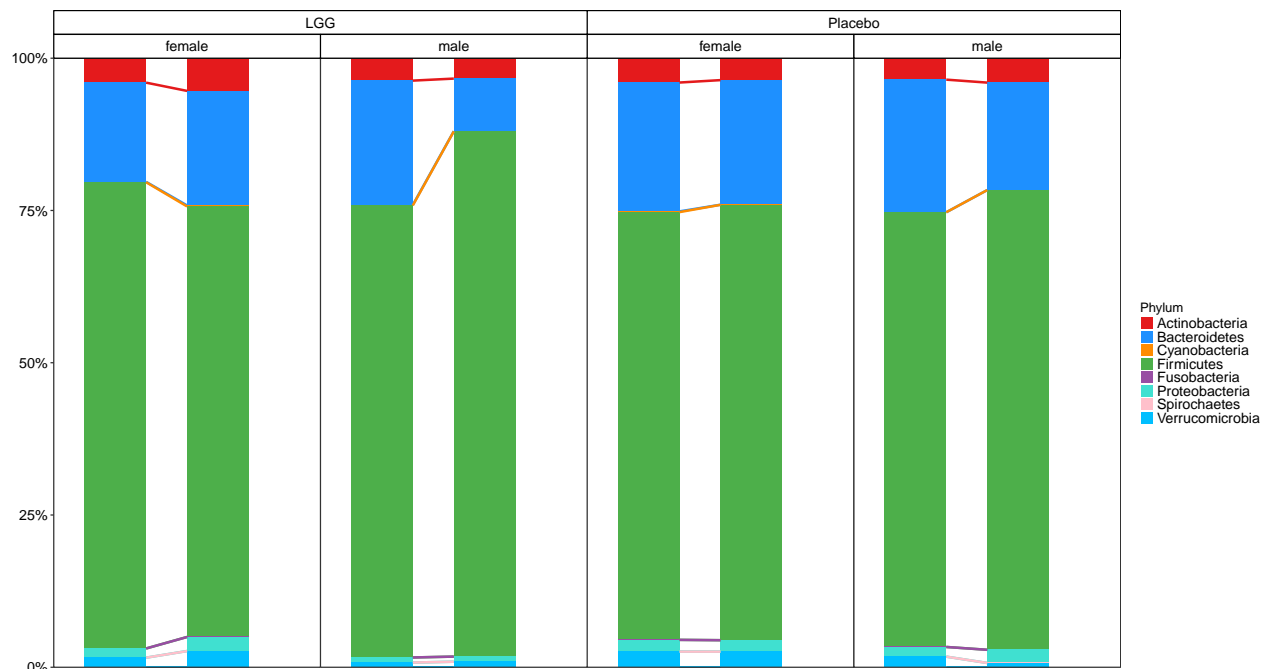
```
taxa_barplot_pair_results <- generate_taxa_barplot_pair(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  feature.number = 20,
  base.size = base.size,
  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_barplot_pair_results
```

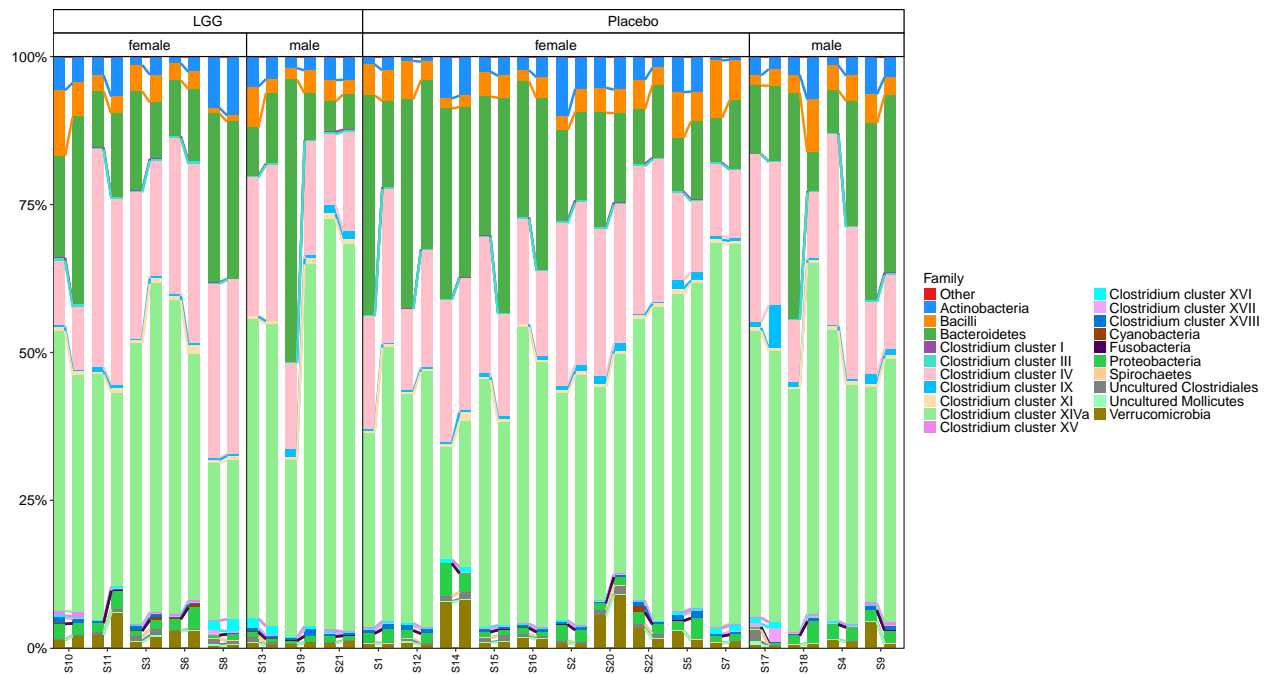
```
## [[1]]
## [[1]][[1]]
```



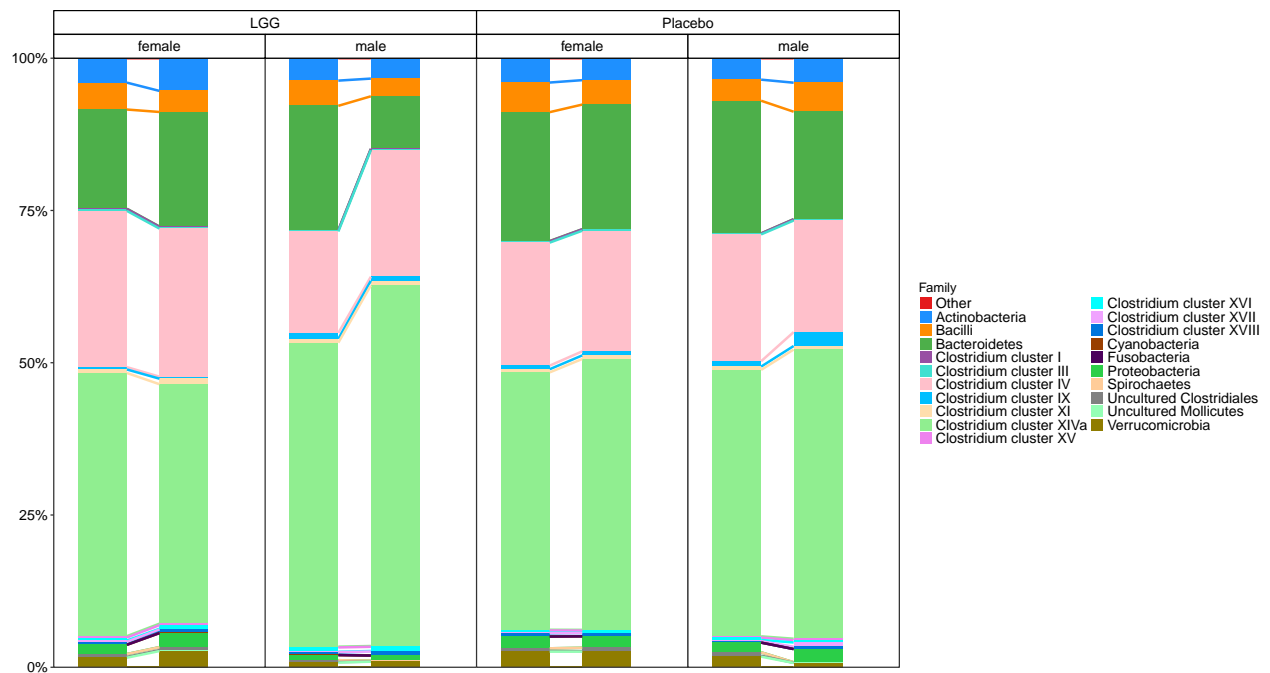
[[1]] [[2]]



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



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



3.4 Taxa Change Test

```
taxa_test_results <- generate_taxa_test_pair(data.obj = data.obj,
                                             subject.var = subject.var,
                                             time.var = time.var,
                                             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,
...)
```

0 features are filtered! The filtered data has 44 samples and 8 features will be tested! Fit linear mixed effects models ... Completed. 0 features are filtered! The filtered data has 44 samples and 22 features will be tested! Fit linear mixed effects models ... Completed.

Taxa Test Results

• Phylum:

Table 5: Table continues below

| Variable | Group | Base.Mean | Log2.Fold.Change | LFC.SE | Stat |
|-----------------|---------|-----------|------------------|---------|---------|
| Actinobacteria | Placebo | 33971 | -0.3054 | 0.1846 | -1.655 |
| Actinobacteria | LGG | 33971 | -0.3054 | 0.1846 | -1.655 |
| Bacteroidetes | Placebo | 162079 | 0.05483 | 0.152 | 0.3608 |
| Bacteroidetes | LGG | 162079 | 0.05483 | 0.152 | 0.3608 |
| Cyanobacteria | Placebo | 176.1 | -0.4582 | 0.3193 | -1.435 |
| Cyanobacteria | LGG | 176.1 | -0.4582 | 0.3193 | -1.435 |
| Firmicutes | Placebo | 774024 | -0.1266 | 0.1051 | -1.205 |
| Firmicutes | LGG | 774024 | -0.1266 | 0.1051 | -1.205 |
| Fusobacteria | Placebo | 27.42 | 0.06221 | 0.1538 | 0.4045 |
| Fusobacteria | LGG | 27.42 | 0.06221 | 0.1538 | 0.4045 |
| Proteobacteria | Placebo | 14987 | 0.1163 | 0.1059 | 1.098 |
| Proteobacteria | LGG | 14987 | 0.1163 | 0.1059 | 1.098 |
| Spirochaetes | Placebo | 49.27 | -0.04386 | 0.08825 | -0.497 |
| Spirochaetes | LGG | 49.27 | -0.04386 | 0.08825 | -0.497 |
| Verrucomicrobia | Placebo | 14686 | -0.07808 | 0.1682 | -0.4641 |
| Verrucomicrobia | LGG | 14686 | -0.07808 | 0.1682 | -0.4641 |
| Actinobacteria | Placebo | 33971 | -0.2258 | 0.1787 | -1.263 |
| Actinobacteria | LGG | 33971 | -0.2258 | 0.1787 | -1.263 |
| Bacteroidetes | Placebo | 162079 | -0.06315 | 0.1472 | -0.4291 |
| Bacteroidetes | LGG | 162079 | -0.06315 | 0.1472 | -0.4291 |
| Cyanobacteria | Placebo | 176.1 | 0.4332 | 0.3092 | 1.401 |
| Cyanobacteria | LGG | 176.1 | 0.4332 | 0.3092 | 1.401 |
| Firmicutes | Placebo | 774024 | 0.008547 | 0.1017 | 0.084 |
| Firmicutes | LGG | 774024 | 0.008547 | 0.1017 | 0.084 |
| Fusobacteria | Placebo | 27.42 | -0.2345 | 0.1489 | -1.575 |
| Fusobacteria | LGG | 27.42 | -0.2345 | 0.1489 | -1.575 |
| Proteobacteria | Placebo | 14987 | 0.08107 | 0.1025 | 0.7908 |
| Proteobacteria | LGG | 14987 | 0.08107 | 0.1025 | 0.7908 |
| Spirochaetes | Placebo | 49.27 | 0.01399 | 0.08545 | 0.1637 |
| Spirochaetes | LGG | 49.27 | 0.01399 | 0.08545 | 0.1637 |
| Verrucomicrobia | Placebo | 14686 | 0.2714 | 0.1629 | 1.666 |
| Verrucomicrobia | LGG | 14686 | 0.2714 | 0.1629 | 1.666 |
| Actinobacteria | Placebo | 33971 | 0.1065 | 0.1123 | 0.9488 |
| Actinobacteria | LGG | 33971 | 0.1065 | 0.1123 | 0.9488 |
| Bacteroidetes | Placebo | 162079 | 0.2407 | 0.141 | 1.707 |
| Bacteroidetes | LGG | 162079 | 0.2407 | 0.141 | 1.707 |
| Cyanobacteria | Placebo | 176.1 | -0.0213 | 0.2575 | -0.0827 |
| Cyanobacteria | LGG | 176.1 | -0.0213 | 0.2575 | -0.0827 |
| Firmicutes | Placebo | 774024 | 0.02152 | 0.08183 | 0.2629 |

| Variable | Group | Base.Mean | Log2.Fold.Change | LFC.SE | Stat |
|-----------------|---------|-----------|------------------|---------|--------|
| Firmicutes | LGG | 774024 | 0.02152 | 0.08183 | 0.2629 |
| Fusobacteria | Placebo | 27.42 | -0.1807 | 0.1426 | -1.267 |
| Fusobacteria | LGG | 27.42 | -0.1807 | 0.1426 | -1.267 |
| Proteobacteria | Placebo | 14987 | 0.01307 | 0.0941 | 0.1389 |
| Proteobacteria | LGG | 14987 | 0.01307 | 0.0941 | 0.1389 |
| Spirochaetes | Placebo | 49.27 | -0.0712 | 0.06589 | -1.081 |
| Spirochaetes | LGG | 49.27 | -0.0712 | 0.06589 | -1.081 |
| Verrucomicrobia | Placebo | 14686 | 0.2349 | 0.156 | 1.505 |
| Verrucomicrobia | LGG | 14686 | 0.2349 | 0.156 | 1.505 |

| P.Value | Adjusted.P.Value | Mean.Abundance | Mean.Prevalence | Output.Element |
|---------|------------------|----------------|-----------------|----------------|
| 0.1144 | 0.5718 | 0.04218 | 1 | sex1 |
| 0.1144 | 0.5718 | 0.03437 | 1 | sex1 |
| 0.7202 | 0.7202 | 0.1949 | 1 | sex1 |
| 0.7202 | 0.7202 | 0.1753 | 1 | sex1 |
| 0.1676 | 0.5718 | 0.0004066 | 1 | sex1 |
| 0.1676 | 0.5718 | 0.0008344 | 1 | sex1 |
| 0.2431 | 0.5718 | 0.7248 | 1 | sex1 |
| 0.2431 | 0.5718 | 0.7446 | 1 | sex1 |
| 0.688 | 0.7202 | 5.22e-05 | 1 | sex1 |
| 0.688 | 0.7202 | 2.914e-05 | 1 | sex1 |
| 0.2859 | 0.5718 | 0.01655 | 1 | sex1 |
| 0.2859 | 0.5718 | 0.018 | 1 | sex1 |
| 0.6249 | 0.7202 | 5.056e-05 | 1 | sex1 |
| 0.6249 | 0.7202 | 5.371e-05 | 1 | sex1 |
| 0.6451 | 0.7202 | 0.0168 | 1 | sex1 |
| 0.6451 | 0.7202 | 0.02451 | 1 | sex1 |
| 0.2217 | 0.4434 | 0.04218 | 1 | group1 |
| 0.2217 | 0.4434 | 0.03437 | 1 | group1 |
| 0.6702 | 0.8935 | 0.1949 | 1 | group1 |
| 0.6702 | 0.8935 | 0.1753 | 1 | group1 |
| 0.1773 | 0.4434 | 0.0004066 | 1 | group1 |
| 0.1773 | 0.4434 | 0.0008344 | 1 | group1 |
| 0.9339 | 0.9339 | 0.7248 | 1 | group1 |
| 0.9339 | 0.9339 | 0.7446 | 1 | group1 |
| 0.1232 | 0.4434 | 5.22e-05 | 1 | group1 |
| 0.1232 | 0.4434 | 2.914e-05 | 1 | group1 |
| 0.4388 | 0.7021 | 0.01655 | 1 | group1 |
| 0.4388 | 0.7021 | 0.018 | 1 | group1 |
| 0.8717 | 0.9339 | 5.056e-05 | 1 | group1 |
| 0.8717 | 0.9339 | 5.371e-05 | 1 | group1 |
| 0.1035 | 0.4434 | 0.0168 | 1 | group1 |
| 0.1035 | 0.4434 | 0.02451 | 1 | group1 |
| 0.3535 | 0.5656 | 0.04218 | 1 | time1 |
| 0.3535 | 0.5656 | 0.03437 | 1 | time1 |
| 0.09557 | 0.5603 | 0.1949 | 1 | time1 |
| 0.09557 | 0.5603 | 0.1753 | 1 | time1 |
| 0.9349 | 0.9349 | 0.0004066 | 1 | time1 |
| 0.9349 | 0.9349 | 0.0008344 | 1 | time1 |
| 0.7952 | 0.9349 | 0.7248 | 1 | time1 |
| 0.7952 | 0.9349 | 0.7446 | 1 | time1 |

| P.Value | Adjusted.P.Value | Mean.Abandance | Mean.Prevalence | Output.Element |
|---------|------------------|----------------|-----------------|----------------|
| 0.2125 | 0.5656 | 5.22e-05 | 1 | time1 |
| 0.2125 | 0.5656 | 2.914e-05 | 1 | time1 |
| 0.8908 | 0.9349 | 0.01655 | 1 | time1 |
| 0.8908 | 0.9349 | 0.018 | 1 | time1 |
| 0.2921 | 0.5656 | 5.056e-05 | 1 | time1 |
| 0.2921 | 0.5656 | 5.371e-05 | 1 | time1 |
| 0.1401 | 0.5603 | 0.0168 | 1 | time1 |
| 0.1401 | 0.5603 | 0.02451 | 1 | time1 |

- **Family:**

Table 7: Table continues below

| Variable | Group | Base.Mean | Log2.Fold.Change | LFC.SE |
|---------------------------|---------|-----------|------------------|---------|
| Actinobacteria | Placebo | 35289 | -0.3022 | 0.1662 |
| Actinobacteria | LGG | 35289 | -0.3022 | 0.1662 |
| Asteroleplasma | Placebo | 23.94 | 0.0136 | 0.1099 |
| Asteroleplasma | LGG | 23.94 | 0.0136 | 0.1099 |
| Bacilli | Placebo | 38826 | 0.07496 | 0.166 |
| Bacilli | LGG | 38826 | 0.07496 | 0.166 |
| Bacteroidetes | Placebo | 168364 | 0.05804 | 0.1402 |
| Bacteroidetes | LGG | 168364 | 0.05804 | 0.1402 |
| Clostridium cluster I | Placebo | 157.6 | 0.1807 | 0.4096 |
| Clostridium cluster I | LGG | 157.6 | 0.1807 | 0.4096 |
| Clostridium cluster III | Placebo | 2182 | -0.2539 | 0.1601 |
| Clostridium cluster III | LGG | 2182 | -0.2539 | 0.1601 |
| Clostridium cluster IV | Placebo | 220427 | -0.1993 | 0.103 |
| Clostridium cluster IV | LGG | 220427 | -0.1993 | 0.103 |
| Clostridium cluster IX | Placebo | 4775 | -0.07251 | 0.2203 |
| Clostridium cluster IX | LGG | 4775 | -0.07251 | 0.2203 |
| Clostridium cluster XI | Placebo | 6362 | -0.08547 | 0.09576 |
| Clostridium cluster XI | LGG | 6362 | -0.08547 | 0.09576 |
| Clostridium cluster XIII | Placebo | 26.74 | -0.01264 | 0.09212 |
| Clostridium cluster XIII | LGG | 26.74 | -0.01264 | 0.09212 |
| Clostridium cluster XIVa | Placebo | 480369 | -0.1085 | 0.1095 |
| Clostridium cluster XIVa | LGG | 480369 | -0.1085 | 0.1095 |
| Clostridium cluster XV | Placebo | 1320 | 0.1052 | 0.1949 |
| Clostridium cluster XV | LGG | 1320 | 0.1052 | 0.1949 |
| Clostridium cluster XVI | Placebo | 3559 | -0.1469 | 0.2689 |
| Clostridium cluster XVI | LGG | 3559 | -0.1469 | 0.2689 |
| Clostridium cluster XVII | Placebo | 491 | -0.524 | 0.3771 |
| Clostridium cluster XVII | LGG | 491 | -0.524 | 0.3771 |
| Clostridium cluster XVIII | Placebo | 3328 | 0.08725 | 0.2782 |
| Clostridium cluster XVIII | LGG | 3328 | 0.08725 | 0.2782 |
| Cyanobacteria | Placebo | 182.9 | -0.455 | 0.3583 |
| Cyanobacteria | LGG | 182.9 | -0.455 | 0.3583 |
| Fusobacteria | Placebo | 28.48 | 0.06542 | 0.1678 |
| Fusobacteria | LGG | 28.48 | 0.06542 | 0.1678 |
| Proteobacteria | Placebo | 15568 | 0.1195 | 0.1241 |
| Proteobacteria | LGG | 15568 | 0.1195 | 0.1241 |
| Spirochaetes | Placebo | 51.18 | -0.04065 | 0.08924 |

| Variable | Group | Base.Mean | Log2.Fold.Change | LFC.SE |
|---------------------------|---------|-----------|------------------|---------|
| Spirochaetes | LGG | 51.18 | -0.04065 | 0.08924 |
| Uncultured Clostridiales | Placebo | 2929 | -0.5293 | 0.3006 |
| Uncultured Clostridiales | LGG | 2929 | -0.5293 | 0.3006 |
| Uncultured Mollicutes | Placebo | 486.4 | -1.06 | 0.3895 |
| Uncultured Mollicutes | LGG | 486.4 | -1.06 | 0.3895 |
| Verrucomicrobia | Placebo | 15256 | -0.07487 | 0.185 |
| Verrucomicrobia | LGG | 15256 | -0.07487 | 0.185 |
| Actinobacteria | Placebo | 35289 | -0.2184 | 0.161 |
| Actinobacteria | LGG | 35289 | -0.2184 | 0.161 |
| Asteroleplasma | Placebo | 23.94 | -0.1085 | 0.1065 |
| Asteroleplasma | LGG | 23.94 | -0.1085 | 0.1065 |
| Bacilli | Placebo | 38826 | 0.1157 | 0.1607 |
| Bacilli | LGG | 38826 | 0.1157 | 0.1607 |
| Bacteroidetes | Placebo | 168364 | -0.05571 | 0.1357 |
| Bacteroidetes | LGG | 168364 | -0.05571 | 0.1357 |
| Clostridium cluster I | Placebo | 157.6 | 0.2279 | 0.3966 |
| Clostridium cluster I | LGG | 157.6 | 0.2279 | 0.3966 |
| Clostridium cluster III | Placebo | 2182 | -0.09452 | 0.155 |
| Clostridium cluster III | LGG | 2182 | -0.09452 | 0.155 |
| Clostridium cluster IV | Placebo | 220427 | -0.02172 | 0.09968 |
| Clostridium cluster IV | LGG | 220427 | -0.02172 | 0.09968 |
| Clostridium cluster IX | Placebo | 4775 | -0.3542 | 0.2133 |
| Clostridium cluster IX | LGG | 4775 | -0.3542 | 0.2133 |
| Clostridium cluster XI | Placebo | 6362 | 0.01901 | 0.09272 |
| Clostridium cluster XI | LGG | 6362 | 0.01901 | 0.09272 |
| Clostridium cluster XIII | Placebo | 26.74 | -0.07978 | 0.0892 |
| Clostridium cluster XIII | LGG | 26.74 | -0.07978 | 0.0892 |
| Clostridium cluster XIVa | Placebo | 480369 | 0.02607 | 0.106 |
| Clostridium cluster XIVa | LGG | 480369 | 0.02607 | 0.106 |
| Clostridium cluster XV | Placebo | 1320 | 0.002068 | 0.1887 |
| Clostridium cluster XV | LGG | 1320 | 0.002068 | 0.1887 |
| Clostridium cluster XVI | Placebo | 3559 | 0.1685 | 0.2603 |
| Clostridium cluster XVI | LGG | 3559 | 0.1685 | 0.2603 |
| Clostridium cluster XVII | Placebo | 491 | -0.6377 | 0.3651 |
| Clostridium cluster XVII | LGG | 491 | -0.6377 | 0.3651 |
| Clostridium cluster XVIII | Placebo | 3328 | 0.004551 | 0.2694 |
| Clostridium cluster XVIII | LGG | 3328 | 0.004551 | 0.2694 |
| Cyanobacteria | Placebo | 182.9 | 0.4407 | 0.3469 |
| Cyanobacteria | LGG | 182.9 | 0.4407 | 0.3469 |
| Fusobacteria | Placebo | 28.48 | -0.227 | 0.1625 |
| Fusobacteria | LGG | 28.48 | -0.227 | 0.1625 |
| Proteobacteria | Placebo | 15568 | 0.08851 | 0.1202 |
| Proteobacteria | LGG | 15568 | 0.08851 | 0.1202 |
| Spirochaetes | Placebo | 51.18 | 0.02142 | 0.0864 |
| Spirochaetes | LGG | 51.18 | 0.02142 | 0.0864 |
| Uncultured Clostridiales | Placebo | 2929 | 0.1455 | 0.2911 |
| Uncultured Clostridiales | LGG | 2929 | 0.1455 | 0.2911 |
| Uncultured Mollicutes | Placebo | 486.4 | 0.3234 | 0.3771 |
| Uncultured Mollicutes | LGG | 486.4 | 0.3234 | 0.3771 |
| Verrucomicrobia | Placebo | 15256 | 0.2789 | 0.1791 |
| Verrucomicrobia | LGG | 15256 | 0.2789 | 0.1791 |
| Actinobacteria | Placebo | 35289 | 0.08206 | 0.1211 |

| Variable | Group | Base.Mean | Log2.Fold.Change | LFC.SE |
|---------------------------|---------|-----------|------------------|---------|
| Actinobacteria | LGG | 35289 | 0.08206 | 0.1211 |
| Asteroleplasma | Placebo | 23.94 | 0.02459 | 0.09874 |
| Asteroleplasma | LGG | 23.94 | 0.02459 | 0.09874 |
| Bacilli | Placebo | 38826 | -0.1114 | 0.07465 |
| Bacilli | LGG | 38826 | -0.1114 | 0.07465 |
| Bacteroidetes | Placebo | 168364 | 0.2162 | 0.13 |
| Bacteroidetes | LGG | 168364 | 0.2162 | 0.13 |
| Clostridium cluster I | Placebo | 157.6 | -0.04603 | 0.2159 |
| Clostridium cluster I | LGG | 157.6 | -0.04603 | 0.2159 |
| Clostridium cluster III | Placebo | 2182 | 0.152 | 0.07007 |
| Clostridium cluster III | LGG | 2182 | 0.152 | 0.07007 |
| Clostridium cluster IV | Placebo | 220427 | 0.04121 | 0.09359 |
| Clostridium cluster IV | LGG | 220427 | 0.04121 | 0.09359 |
| Clostridium cluster IX | Placebo | 4775 | -0.03185 | 0.1832 |
| Clostridium cluster IX | LGG | 4775 | -0.03185 | 0.1832 |
| Clostridium cluster XI | Placebo | 6362 | 0.0268 | 0.07295 |
| Clostridium cluster XI | LGG | 6362 | 0.0268 | 0.07295 |
| Clostridium cluster XIII | Placebo | 26.74 | 0.07004 | 0.05675 |
| Clostridium cluster XIII | LGG | 26.74 | 0.07004 | 0.05675 |
| Clostridium cluster XIVa | Placebo | 480369 | -0.005182 | 0.07042 |
| Clostridium cluster XIVa | LGG | 480369 | -0.005182 | 0.07042 |
| Clostridium cluster XV | Placebo | 1320 | 0.03479 | 0.1082 |
| Clostridium cluster XV | LGG | 1320 | 0.03479 | 0.1082 |
| Clostridium cluster XVI | Placebo | 3559 | -0.02628 | 0.127 |
| Clostridium cluster XVI | LGG | 3559 | -0.02628 | 0.127 |
| Clostridium cluster XVII | Placebo | 491 | -0.3649 | 0.2613 |
| Clostridium cluster XVII | LGG | 491 | -0.3649 | 0.2613 |
| Clostridium cluster XVIII | Placebo | 3328 | -0.1445 | 0.1793 |
| Clostridium cluster XVIII | LGG | 3328 | -0.1445 | 0.1793 |
| Cyanobacteria | Placebo | 182.9 | -0.04578 | 0.2696 |
| Cyanobacteria | LGG | 182.9 | -0.04578 | 0.2696 |
| Fusobacteria | Placebo | 28.48 | -0.2052 | 0.1557 |
| Fusobacteria | LGG | 28.48 | -0.2052 | 0.1557 |
| Proteobacteria | Placebo | 15568 | -0.01141 | 0.1086 |
| Proteobacteria | LGG | 15568 | -0.01141 | 0.1086 |
| Spirochaetes | Placebo | 51.18 | -0.09568 | 0.06559 |
| Spirochaetes | LGG | 51.18 | -0.09568 | 0.06559 |
| Uncultured Clostridiales | Placebo | 2929 | 0.165 | 0.1919 |
| Uncultured Clostridiales | LGG | 2929 | 0.165 | 0.1919 |
| Uncultured Mollicutes | Placebo | 486.4 | 0.1781 | 0.2956 |
| Uncultured Mollicutes | LGG | 486.4 | 0.1781 | 0.2956 |
| Verrucomicrobia | Placebo | 15256 | 0.2104 | 0.1716 |
| Verrucomicrobia | LGG | 15256 | 0.2104 | 0.1716 |

Table 8: Table continues below

| Stat | P.Value | Adjusted.P.Value | Mean.Abundance | Mean.Prevalence |
|--------|---------|------------------|----------------|-----------------|
| -1.818 | 0.08488 | 0.5192 | 0.04218 | 1 |
| -1.818 | 0.08488 | 0.5192 | 0.03437 | 1 |
| 0.1237 | 0.9029 | 0.9029 | 3.022e-05 | 1 |
| 0.1237 | 0.9029 | 0.9029 | 2.051e-05 | 1 |

| Stat | P.Value | Adjusted.P.Value | Mean.Abandance | Mean.Prevalence |
|---------|---------|------------------|----------------|-----------------|
| 0.4516 | 0.6567 | 0.833 | 0.0385 | 1 |
| 0.4516 | 0.6567 | 0.833 | 0.04534 | 1 |
| 0.414 | 0.6811 | 0.833 | 0.1949 | 1 |
| 0.414 | 0.6811 | 0.833 | 0.1753 | 1 |
| 0.4412 | 0.6641 | 0.833 | 0.00033 | 1 |
| 0.4412 | 0.6641 | 0.833 | 0.0003955 | 1 |
| -1.586 | 0.1293 | 0.569 | 0.002347 | 1 |
| -1.586 | 0.1293 | 0.569 | 0.002078 | 1 |
| -1.936 | 0.06788 | 0.5192 | 0.2095 | 1 |
| -1.936 | 0.06788 | 0.5192 | 0.2045 | 1 |
| -0.3291 | 0.7457 | 0.833 | 0.007537 | 1 |
| -0.3291 | 0.7457 | 0.833 | 0.004222 | 1 |
| -0.8925 | 0.3833 | 0.833 | 0.006057 | 1 |
| -0.8925 | 0.3833 | 0.833 | 0.006176 | 1 |
| -0.1372 | 0.8923 | 0.9029 | 2.892e-05 | 1 |
| -0.1372 | 0.8923 | 0.9029 | 2.327e-05 | 1 |
| -0.9904 | 0.3344 | 0.833 | 0.4377 | 1 |
| -0.9904 | 0.3344 | 0.833 | 0.464 | 1 |
| 0.5395 | 0.5958 | 0.833 | 0.001648 | 1 |
| 0.5395 | 0.5958 | 0.833 | 0.001587 | 1 |
| -0.5465 | 0.5911 | 0.833 | 0.004221 | 1 |
| -0.5465 | 0.5911 | 0.833 | 0.004837 | 1 |
| -1.39 | 0.1807 | 0.6627 | 0.001405 | 1 |
| -1.39 | 0.1807 | 0.6627 | 0.0005492 | 1 |
| 0.3136 | 0.7572 | 0.833 | 0.004429 | 1 |
| 0.3136 | 0.7572 | 0.833 | 0.004493 | 1 |
| -1.27 | 0.2195 | 0.6898 | 0.0004066 | 1 |
| -1.27 | 0.2195 | 0.6898 | 0.0008344 | 1 |
| 0.3898 | 0.6988 | 0.833 | 5.22e-05 | 1 |
| 0.3898 | 0.6988 | 0.833 | 2.914e-05 | 1 |
| 0.9625 | 0.3479 | 0.833 | 0.01655 | 1 |
| 0.9625 | 0.3479 | 0.833 | 0.018 | 1 |
| -0.4555 | 0.6539 | 0.833 | 5.056e-05 | 1 |
| -0.4555 | 0.6539 | 0.833 | 5.371e-05 | 1 |
| -1.761 | 0.09439 | 0.5192 | 0.003867 | 1 |
| -1.761 | 0.09439 | 0.5192 | 0.004424 | 1 |
| -2.721 | 0.01355 | 0.2981 | 0.0008387 | 1 |
| -2.721 | 0.01355 | 0.2981 | 0.001109 | 1 |
| -0.4047 | 0.6879 | 0.833 | 0.0168 | 1 |
| -0.4047 | 0.6879 | 0.833 | 0.02451 | 1 |
| -1.357 | 0.1908 | 0.8042 | 0.04218 | 1 |
| -1.357 | 0.1908 | 0.8042 | 0.03437 | 1 |
| -1.019 | 0.321 | 0.8994 | 3.022e-05 | 1 |
| -1.019 | 0.321 | 0.8994 | 2.051e-05 | 1 |
| 0.7201 | 0.4802 | 0.8994 | 0.0385 | 1 |
| 0.7201 | 0.4802 | 0.8994 | 0.04534 | 1 |
| -0.4104 | 0.6837 | 0.9237 | 0.1949 | 1 |
| -0.4104 | 0.6837 | 0.9237 | 0.1753 | 1 |
| 0.5746 | 0.5723 | 0.8994 | 0.00033 | 1 |
| 0.5746 | 0.5723 | 0.8994 | 0.0003955 | 1 |
| -0.6097 | 0.5493 | 0.8994 | 0.002347 | 1 |
| -0.6097 | 0.5493 | 0.8994 | 0.002078 | 1 |

| Stat | P.Value | Adjusted.P.Value | Mean.Abandance | Mean.Prevalence |
|---------|---------|------------------|----------------|-----------------|
| -0.2179 | 0.8299 | 0.9237 | 0.2095 | 1 |
| -0.2179 | 0.8299 | 0.9237 | 0.2045 | 1 |
| -1.66 | 0.1133 | 0.8042 | 0.007537 | 1 |
| -1.66 | 0.1133 | 0.8042 | 0.004222 | 1 |
| 0.205 | 0.8398 | 0.9237 | 0.006057 | 1 |
| 0.205 | 0.8398 | 0.9237 | 0.006176 | 1 |
| -0.8945 | 0.3823 | 0.8994 | 2.892e-05 | 1 |
| -0.8945 | 0.3823 | 0.8994 | 2.327e-05 | 1 |
| 0.2458 | 0.8084 | 0.9237 | 0.4377 | 1 |
| 0.2458 | 0.8084 | 0.9237 | 0.464 | 1 |
| 0.01096 | 0.9914 | 0.9914 | 0.001648 | 1 |
| 0.01096 | 0.9914 | 0.9914 | 0.001587 | 1 |
| 0.6471 | 0.5253 | 0.8994 | 0.004221 | 1 |
| 0.6471 | 0.5253 | 0.8994 | 0.004837 | 1 |
| -1.747 | 0.09686 | 0.8042 | 0.001405 | 1 |
| -1.747 | 0.09686 | 0.8042 | 0.0005492 | 1 |
| 0.0169 | 0.9867 | 0.9914 | 0.004429 | 1 |
| 0.0169 | 0.9867 | 0.9914 | 0.004493 | 1 |
| 1.27 | 0.2193 | 0.8042 | 0.0004066 | 1 |
| 1.27 | 0.2193 | 0.8042 | 0.0008344 | 1 |
| -1.397 | 0.1701 | 0.8042 | 5.22e-05 | 1 |
| -1.397 | 0.1701 | 0.8042 | 2.914e-05 | 1 |
| 0.7365 | 0.4704 | 0.8994 | 0.01655 | 1 |
| 0.7365 | 0.4704 | 0.8994 | 0.018 | 1 |
| 0.2479 | 0.8069 | 0.9237 | 5.056e-05 | 1 |
| 0.2479 | 0.8069 | 0.9237 | 5.371e-05 | 1 |
| 0.4998 | 0.623 | 0.9137 | 0.003867 | 1 |
| 0.4998 | 0.623 | 0.9137 | 0.004424 | 1 |
| 0.8574 | 0.4019 | 0.8994 | 0.0008387 | 1 |
| 0.8574 | 0.4019 | 0.8994 | 0.001109 | 1 |
| 1.557 | 0.1274 | 0.8042 | 0.0168 | 1 |
| 1.557 | 0.1274 | 0.8042 | 0.02451 | 1 |
| 0.6776 | 0.5054 | 0.942 | 0.04218 | 1 |
| 0.6776 | 0.5054 | 0.942 | 0.03437 | 1 |
| 0.249 | 0.8058 | 0.942 | 3.022e-05 | 1 |
| 0.249 | 0.8058 | 0.942 | 2.051e-05 | 1 |
| -1.493 | 0.1503 | 0.6346 | 0.0385 | 1 |
| -1.493 | 0.1503 | 0.6346 | 0.04534 | 1 |
| 1.662 | 0.1043 | 0.6346 | 0.1949 | 1 |
| 1.662 | 0.1043 | 0.6346 | 0.1753 | 1 |
| -0.2132 | 0.8332 | 0.942 | 0.00033 | 1 |
| -0.2132 | 0.8332 | 0.942 | 0.0003955 | 1 |
| 2.17 | 0.04164 | 0.6346 | 0.002347 | 1 |
| 2.17 | 0.04164 | 0.6346 | 0.002078 | 1 |
| 0.4403 | 0.6642 | 0.942 | 0.2095 | 1 |
| 0.4403 | 0.6642 | 0.942 | 0.2045 | 1 |
| -0.1739 | 0.8636 | 0.942 | 0.007537 | 1 |
| -0.1739 | 0.8636 | 0.942 | 0.004222 | 1 |
| 0.3674 | 0.717 | 0.942 | 0.006057 | 1 |
| 0.3674 | 0.717 | 0.942 | 0.006176 | 1 |
| 1.234 | 0.2307 | 0.6346 | 2.892e-05 | 1 |
| 1.234 | 0.2307 | 0.6346 | 2.327e-05 | 1 |

[illegible]

[illegible]

| Output.Element |
|----------------|
| time1 |
| time1 |
| time1 |

3.5 Taxa Boxplot for Significant Taxa

```

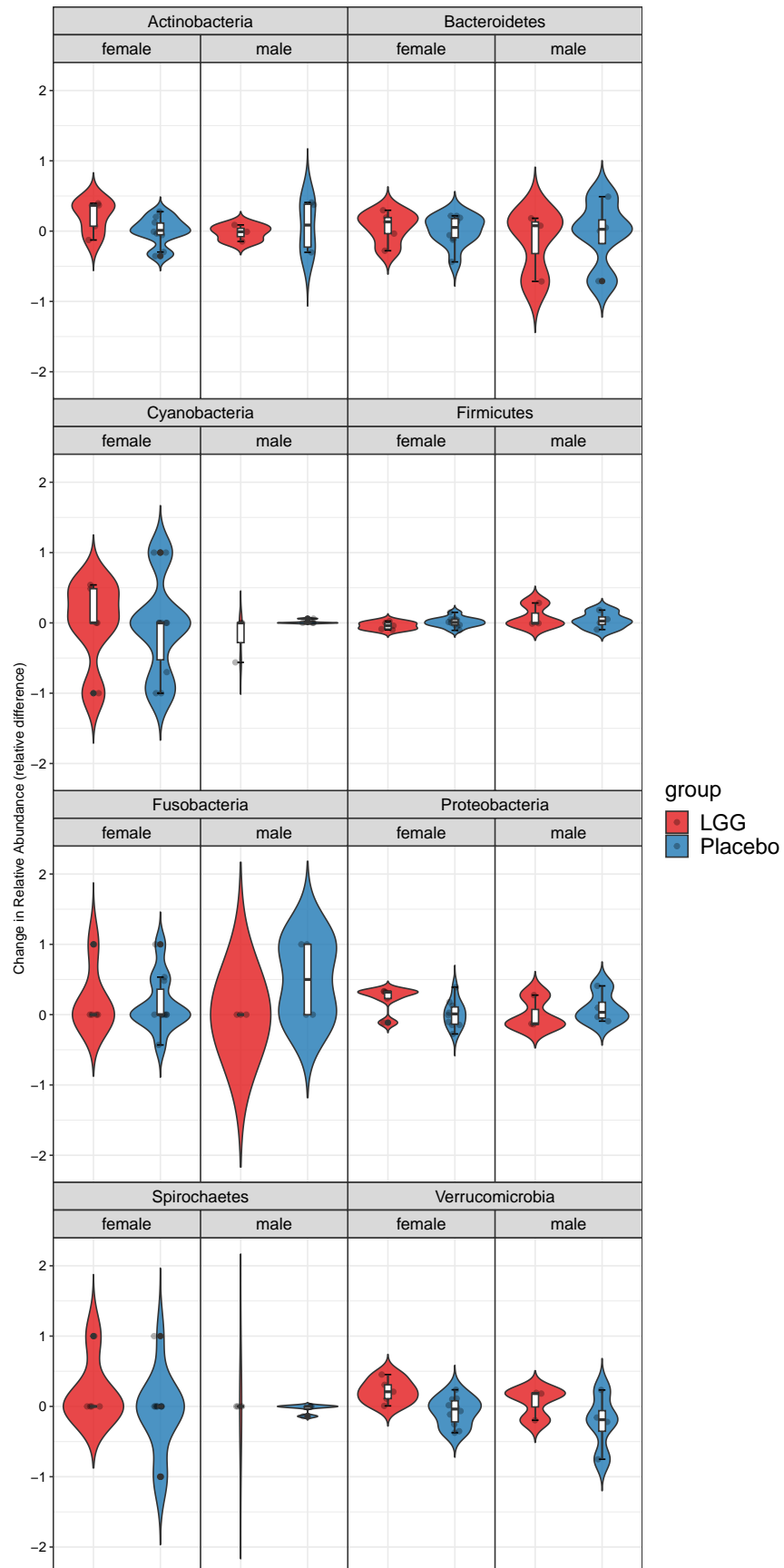
taxa_test_results <- do.call('rbind', taxa_test_results)
significant_taxa <- taxa_test_results$Variable[taxa_test_results$Adjusted.P.Value < 1]

taxa_change_boxplot_results <- generate_taxa_change_boxplot_pair(data.obj = data.obj,
                                                                  subject.var = subject.var,
                                                                  time.var = time.var,
                                                                  group.var = group.var,
                                                                  strata.var = strata.var,
                                                                  change.base = change.base,
                                                                  change.func = change.func,
                                                                  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,
                                                                  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)

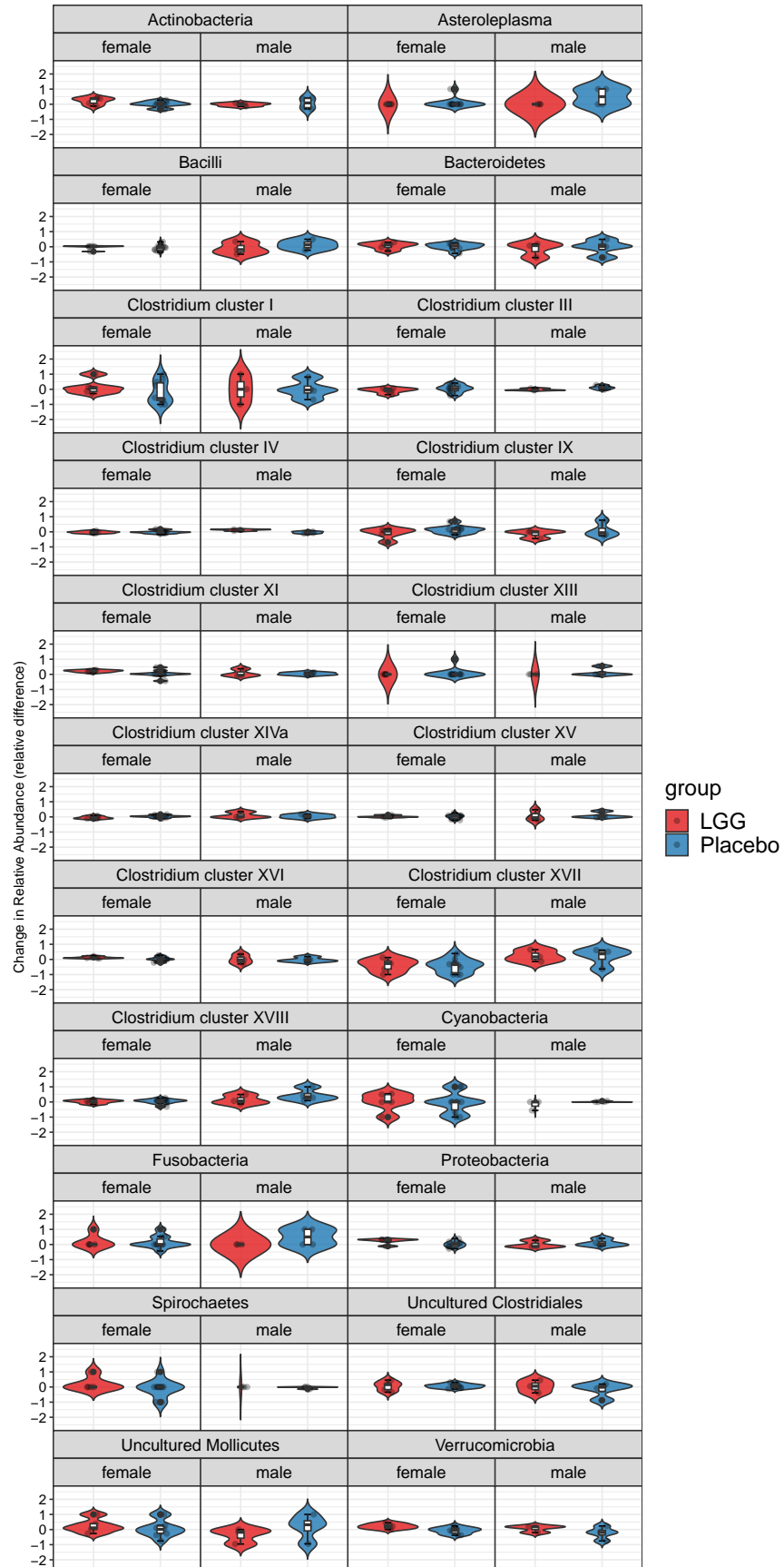
taxa_change_boxplot_results

## [[1]]

```



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



```

taxa_indiv_change_boxplot_results <- generate_taxa_indiv_change_boxplot_pair(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
  change.base = change.base,
  change.func = change.func,
  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,
  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_change_boxplot_pair_subject_subject_time_time_change_base_1_feature_level_Phylum_prev_filter_0_abund_filter_0_group_group_strata_sex.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_change_boxplot_pair_subject_subject_time_time_change_base_1_feature_level_Family_prev_filter_0_abund_filter_0_group_group_strata_sex.pdf. Please refer to this file for more detailed visualizations.