

Microbial Ecology Analysis Report

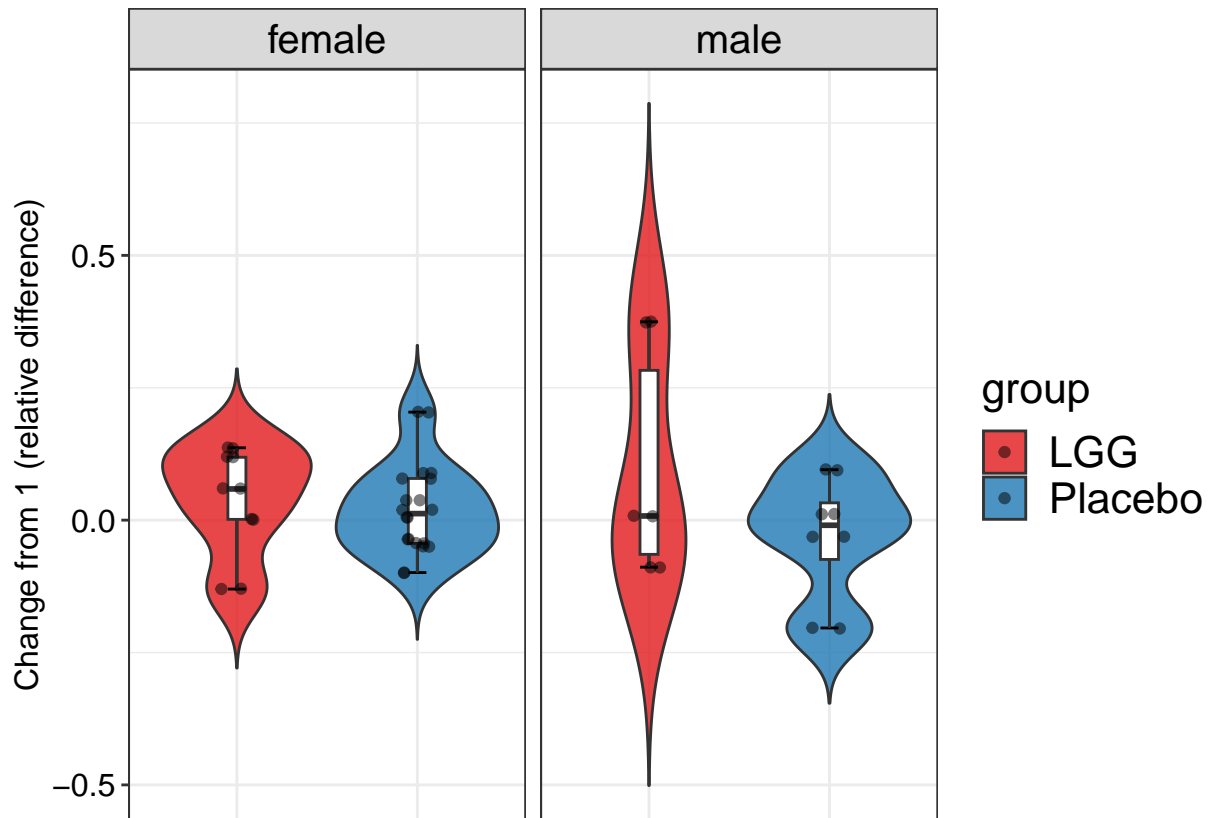
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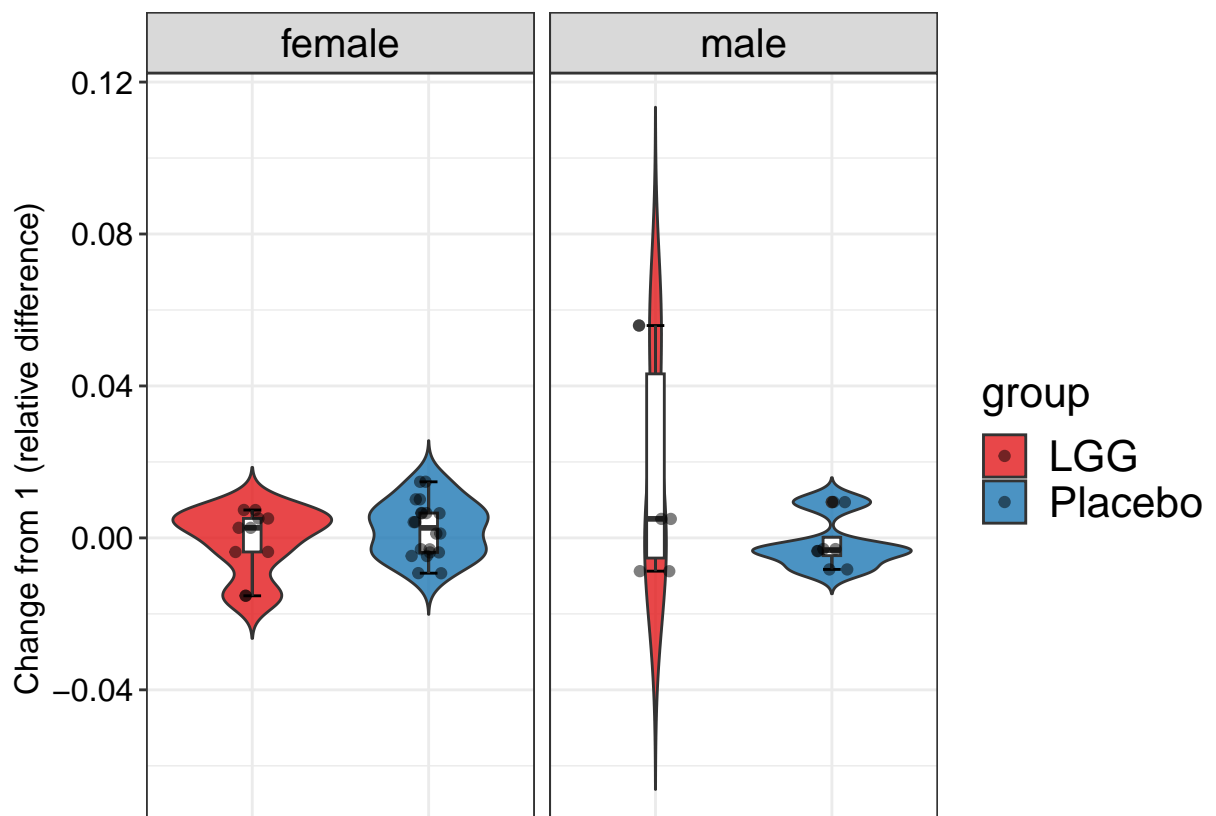
1. Alpha Diversity Change Analysis

1.1 Alpha Diversity Change Boxplots

```
alpha_change_boxplot_results <- generate_alpha_change_boxplot_pair(data.obj = data.obj,  
                                                                    alpha.obj = alpha.obj,  
                                                                    alpha.name = alpha.name,  
                                                                    subject.var = subject.var,  
                                                                    time.var = time.var,  
                                                                    change.base = change.base,  
                                                                    change.func = change.func,  
                                                                    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_change_boxplot_results  
  
## [[1]]
```



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



1.2 Alpha Diversity Change Test Results

```
alpha_change_test_results <- generate_alpha_change_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,  
  change.base = change.base,  
  change.func = change.func)
```

shannon Index Change

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	0.0312	0.02975	1.049	0.3074
sex1	0.001823	0.02911	0.06262	0.9507
group1	0.02863	0.02818	1.016	0.3225

shannon Index Change Analysis

The variable (Intercept) does not appear to have a statistically significant effect on the shannon diversity index change. The estimate of its effect is 0.03.

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

The variable group1 does not appear to have a statistically significant effect on the shannon diversity index change. The estimate of its effect is 0.03.

simpson Index Change

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	0.004376	0.003324	1.316	0.2037
sex1	-0.00256	0.003252	-0.787	0.441
group1	0.002152	0.003149	0.6833	0.5027

simpson Index Change Analysis

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

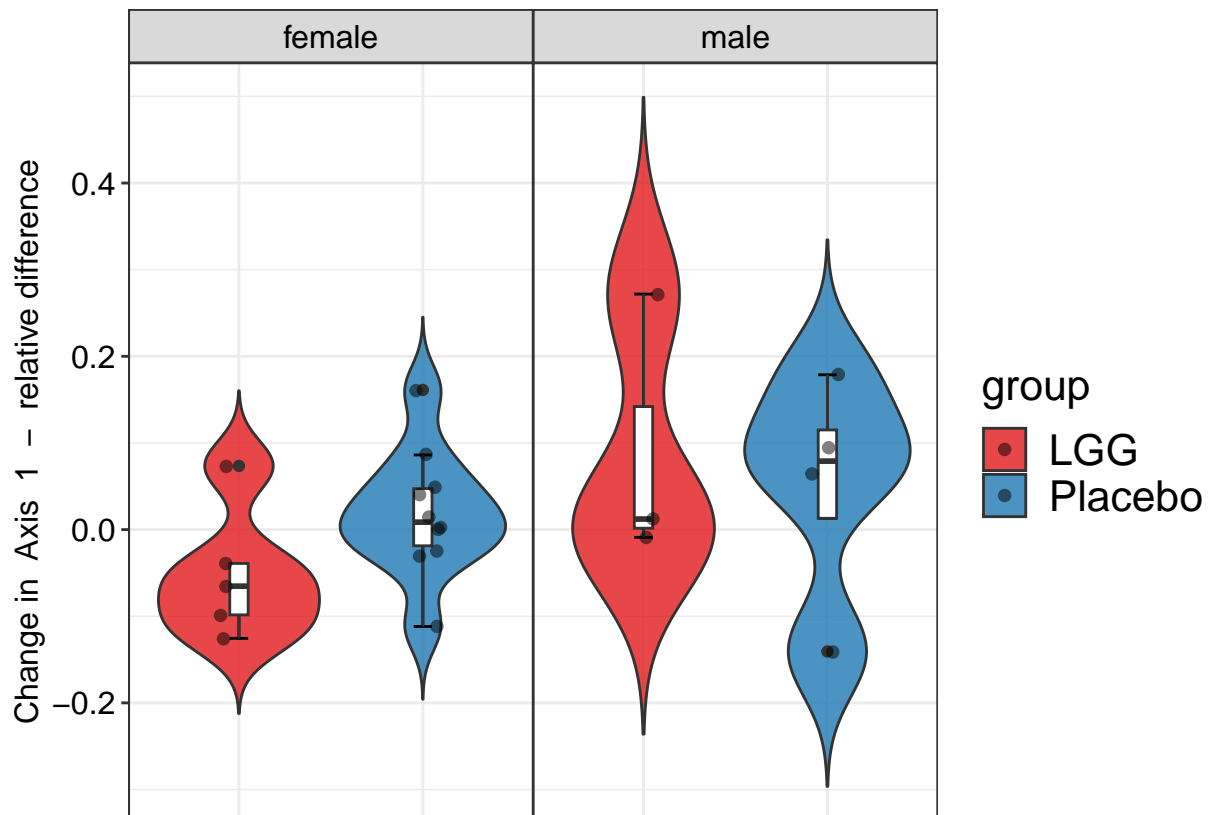
The variable sex1 does not appear to have a statistically significant effect on the simpson diversity index change. The estimate of its effect is 0.

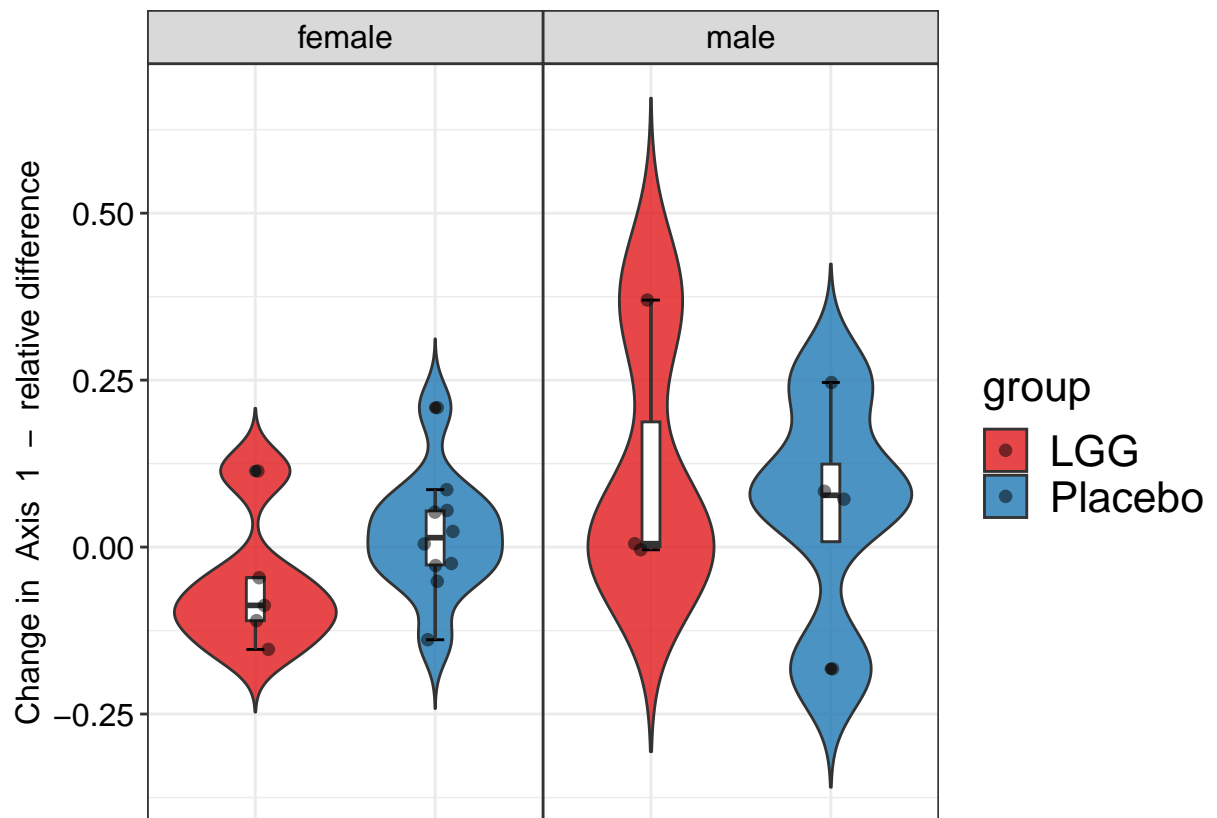
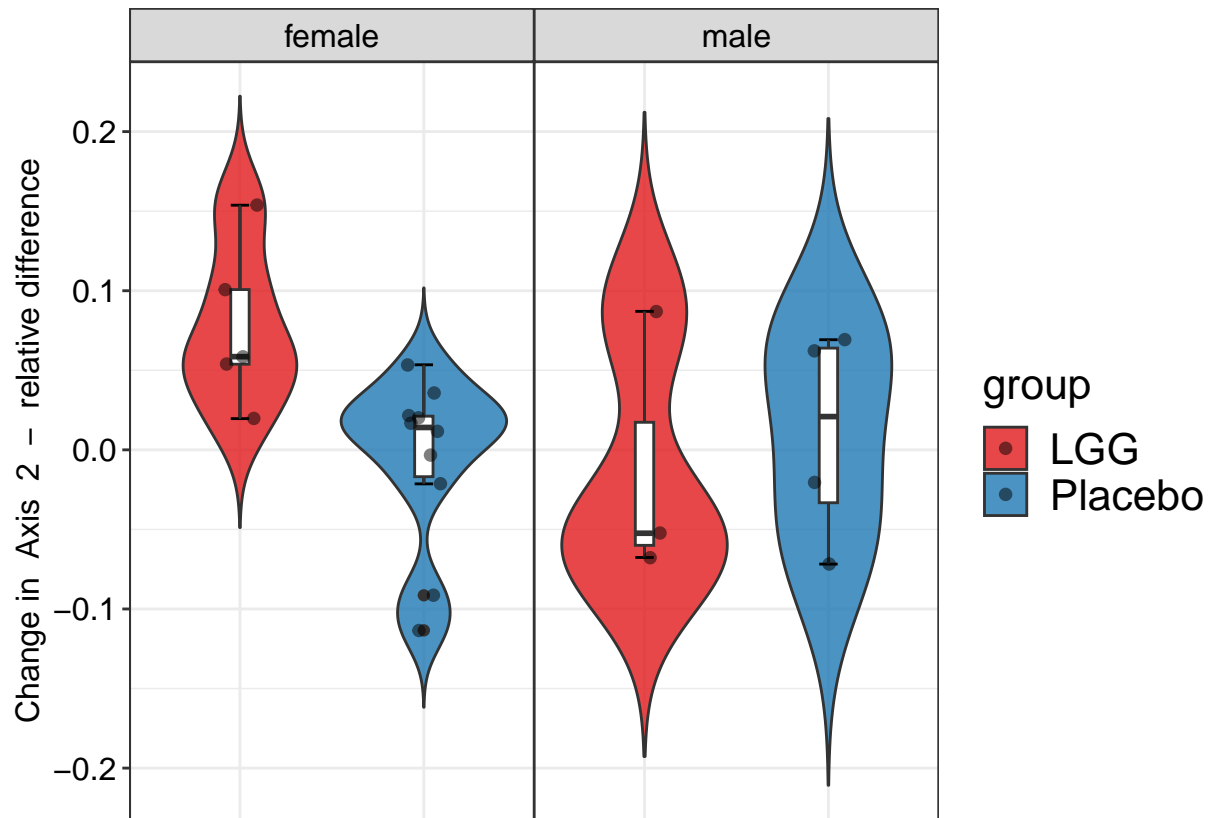
The variable group1 does not appear to have a statistically significant effect on the simpson diversity index change. The estimate of its effect is 0.

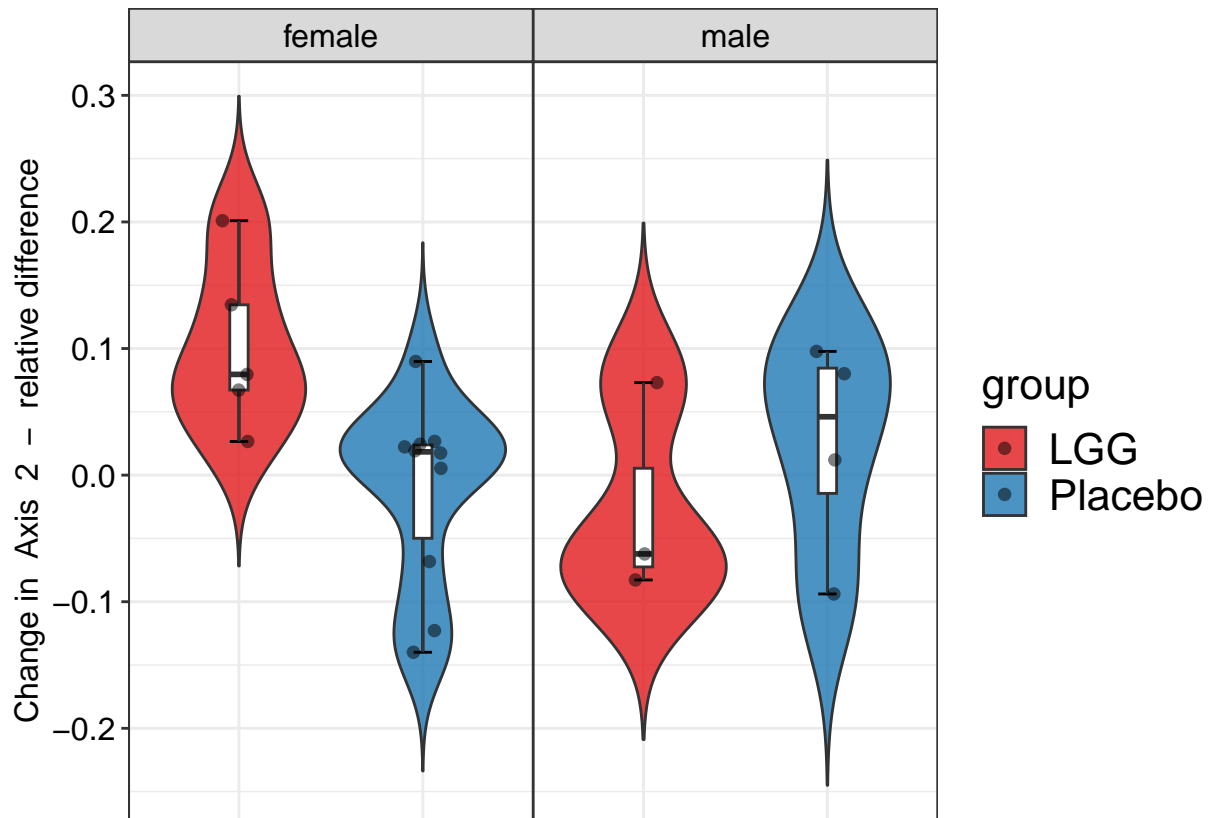
2. Beta Diversity Change Analysis

2.1 Beta Diversity PC Change Boxplot Pairs

```
pc_change_boxplot_pairs <- generate_beta_pc_change_boxplot_pair(  
  data.obj = data.obj,  
  dist.obj = dist.obj,  
  pc.obj = NULL,  
  pc.ind = c(1, 2),  
  subject.var = subject.var,  
  time.var = time.var,  
  group.var = group.var,  
  strata.var = strata.var,  
  change.base = change.base,  
  change.func = change.func,  
  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  
)  
  
pc_change_boxplot_pairs
```



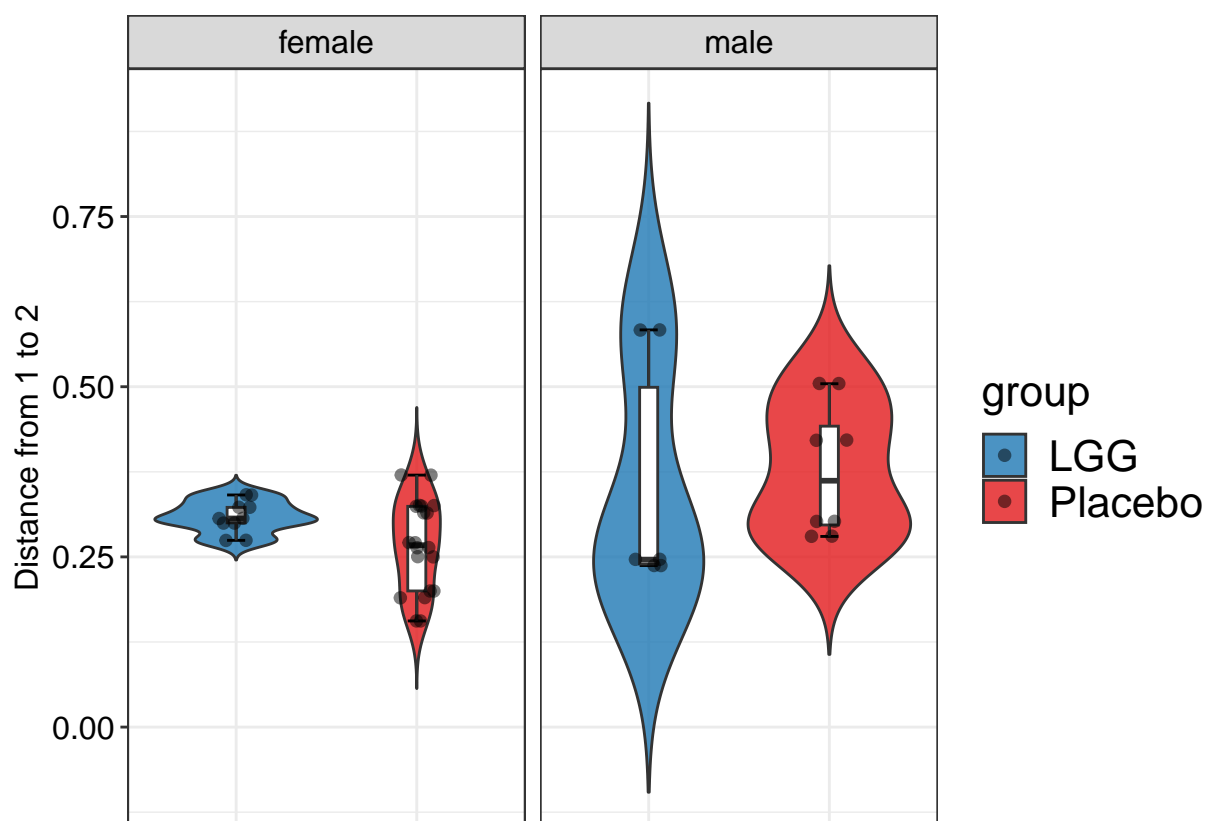
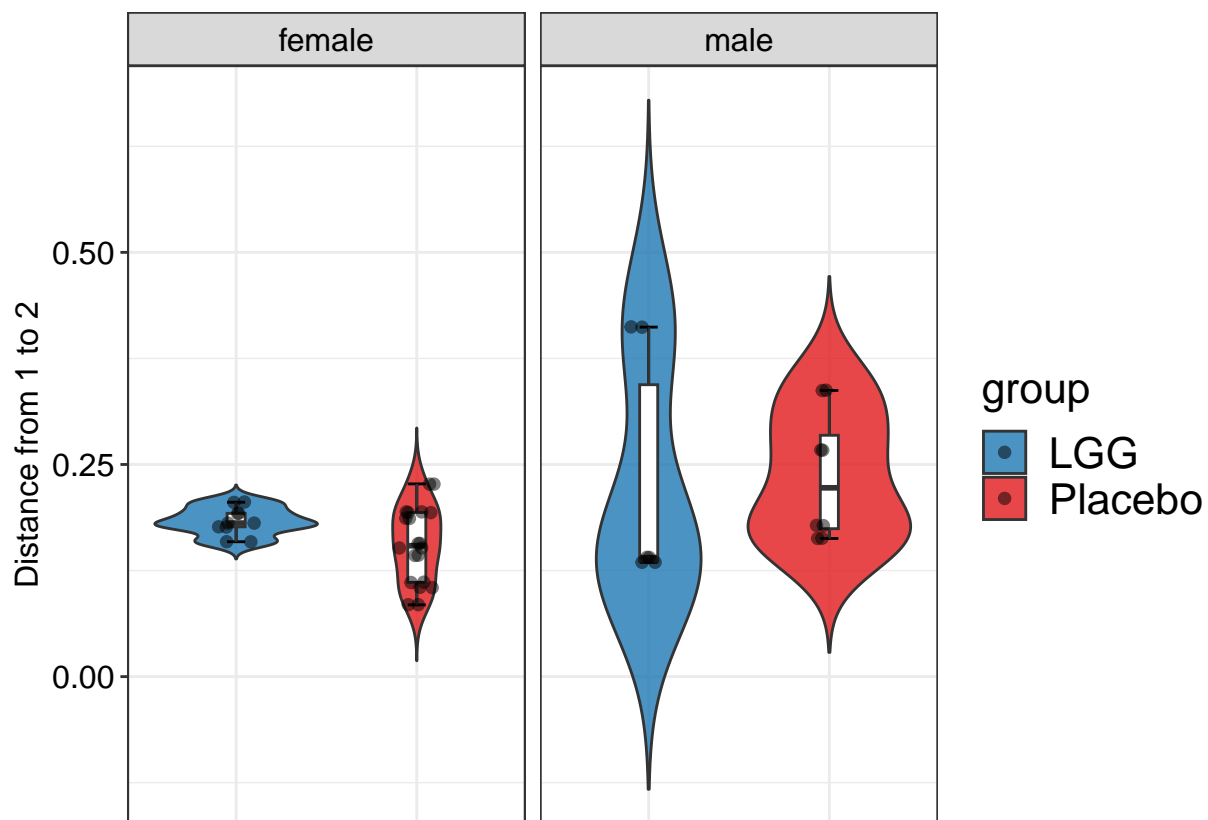




2.2 Beta Diversity Change Boxplot

```
beta_change_boxplot_results <- generate_beta_change_boxplot_pair(data.obj = data.obj,
  dist.obj = dist.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
  change.base = change.base,
  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_change_boxplot_results
```



2.3 Beta Diversity Change Test Results

```
beta_change_test_results <- generate_beta_change_test_pair(data.obj = data.obj,  
  dist.obj = dist.obj,  
  subject.var = subject.var,  
  time.var = time.var,  
  group.var = group.var,  
  adj.vars = adj.vars,  
  dist.name = dist.name,  
  change.base = change.base)
```

BC Results

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	0.2007	0.0111	18.09	3.755e-21
sex1	-0.03356	0.01086	-3.091	0.003576
group1	0.007842	0.01051	0.746	0.4599

BC Distance Analysis

The variable (Intercept) has a statistically significant impact on the BC beta diversity change with an estimate of 0.2.

The variable sex1 has a statistically significant impact on the BC beta diversity change with an estimate of -0.03.

The variable group1 does not appear to have a statistically significant effect on the BC beta diversity change. The estimate of its effect is 0.01.

Jaccard Results

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	0.3267	0.01471	22.21	1.782e-24
sex1	-0.04263	0.01439	-2.962	0.005061
group1	0.01037	0.01393	0.7441	0.4611

Jaccard Distance Analysis

The variable (Intercept) has a statistically significant impact on the Jaccard beta diversity change with an estimate of 0.33.

The variable sex1 has a statistically significant impact on the Jaccard beta diversity change with an estimate of -0.04.

The variable group1 does not appear to have a statistically significant effect on the Jaccard beta diversity change. The estimate of its effect is 0.01.

3. Taxonomic Feature Analysis

3.1 Taxa Change Dotplot

```
taxa_change_dotplot_results <- generate_taxa_change_dotplot_pair(data.obj = data.obj,  
  subject.var = subject.var,
```



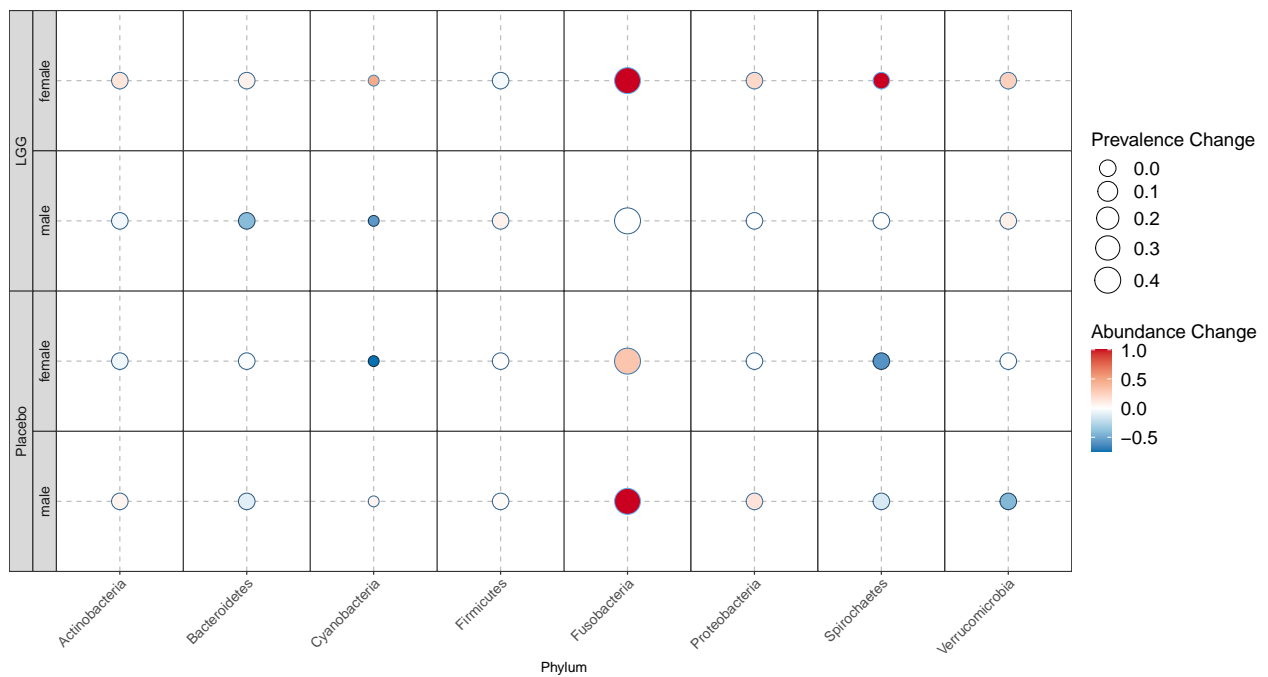
```

time.var = time.var,
change.base = change.base,
change.func = change.func,
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)

```

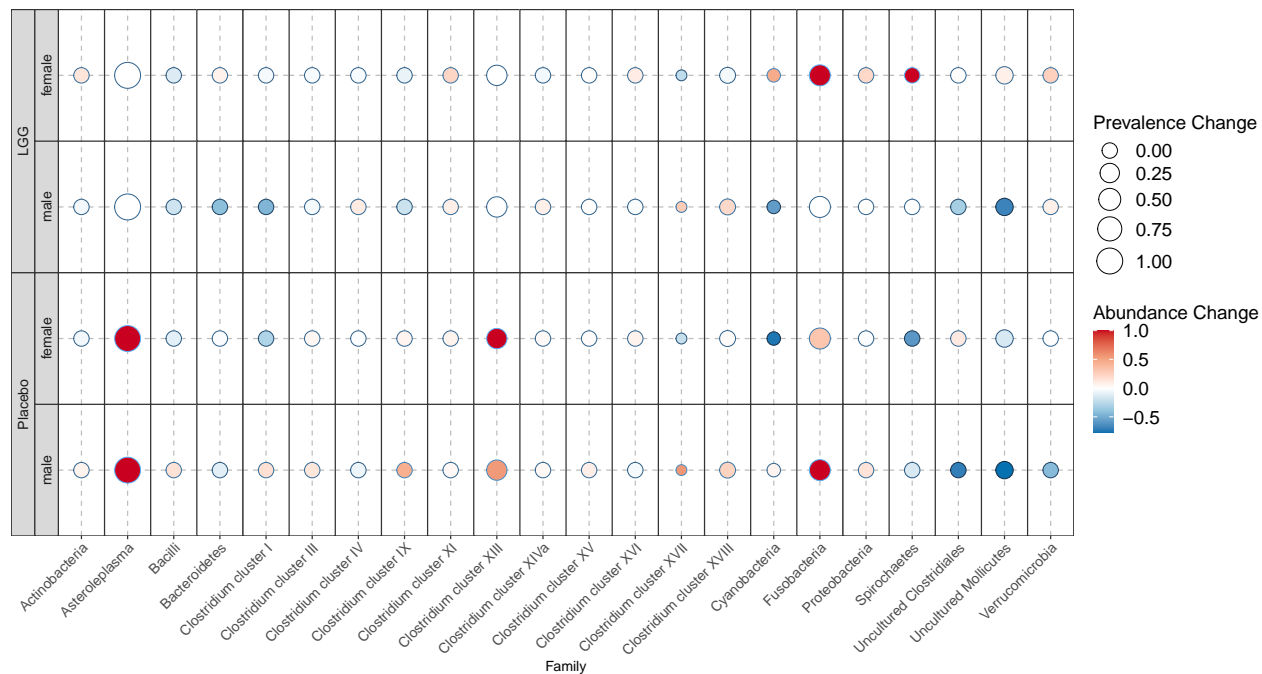
taxa_change_dotplot_results

[[1]]



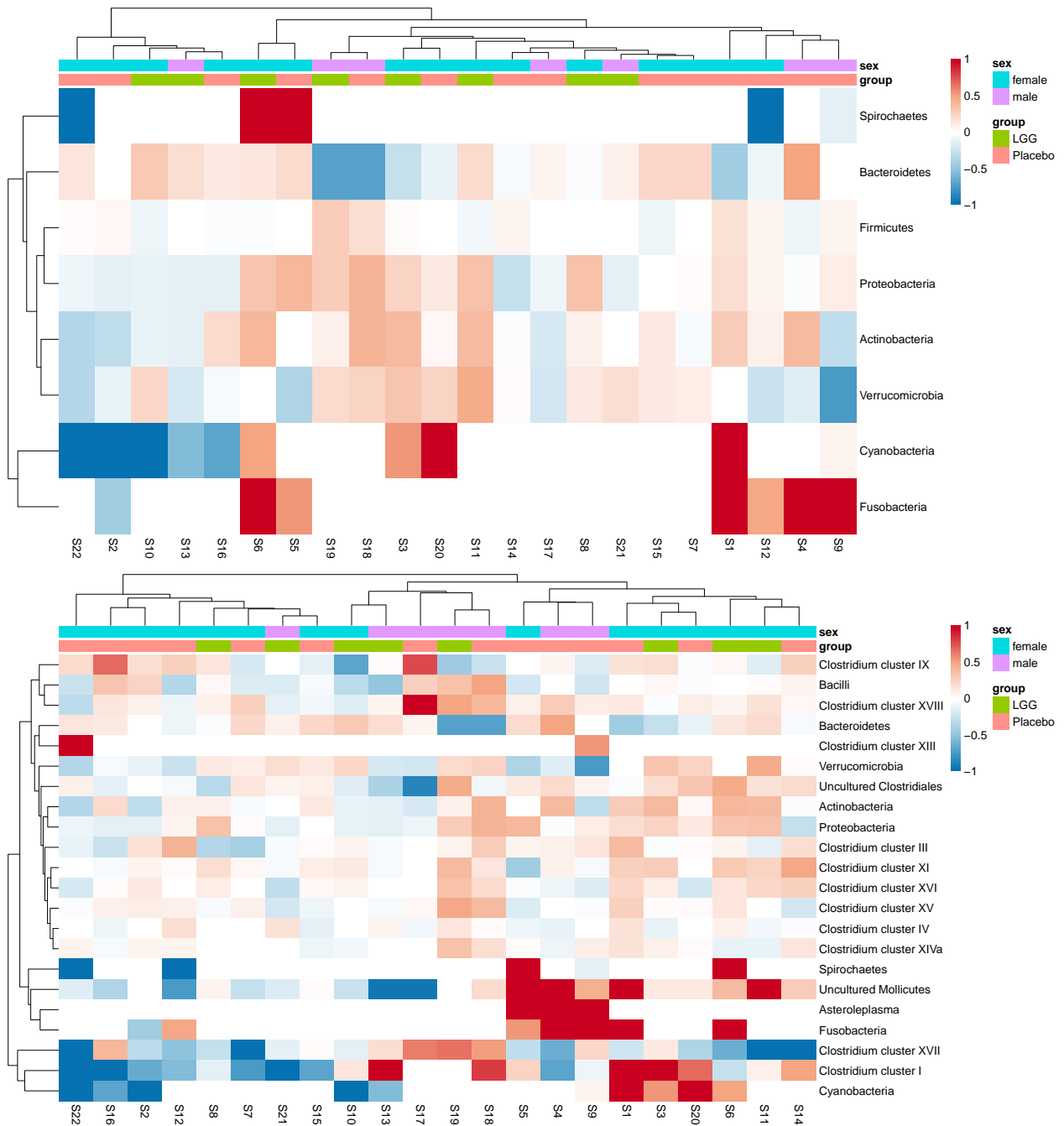
##

[[2]]



3.2 Taxa Change Heatmap

```
taxa_heatmap_results <- generate_taxa_change_heatmap_pair(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  change.base = change.base,
  change.func = change.func,
  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)
```



3.3 Taxa Change Scatterplot

```
if (is_continuous_numeric(data.obj[[group.var]])) {
  taxa_change_scatterplot_results <- generate_taxa_indiv_change_scatterplot_pair(data.obj = data.obj,
    subject.var = subject.var,
    time.var = time.var,
    change.base = change.base,
    change.func = change.func,
    group.var = group.var,
    strata.var = strata.var,
    feature.level = feature.level,
```

```

features.plot = features.plot,
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 = 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_change_scatterplot_results
} else {
  message(paste0('The variable ', group.var, ' is not a continuous numeric. The function generate_taxa_
})

```

3.4 Taxa Change Test

```

taxa_change_test_results <- generate_taxa_change_test_pair(data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  change.base = change.base,
  change.func = change.func,
  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,
  ...)

```

Taxa Change Test Results

- Phylum:

Table 5: Table continues below

	Variable	Group	R.Squared	F.Statistic
Verrucomicrobia	Verrucomicrobia	Placebo	0.273	7.475
Verrucomicrobia1	Verrucomicrobia	LGG	0.273	7.475

Table 6: Table continues below

	Estimate	P.Value	Adjusted.P.Value
Verrucomicrobia	0.248530840321361	0.04	0.09091
Verrucomicrobia1	0.248530840321361	0.04	0.09091

Table 7: Table continues below

	Mean.Abandance_Change	Mean.Prevalence_Change
Verrucomicrobia	-0.1144	0.3571
Verrucomicrobia1	0.1581	0.875

	SD.Abandance_Change	SD.Prevalence_Change
Verrucomicrobia	0.2633	0.488
Verrucomicrobia1	0.1878	0.3416

- **Family:**

Table 9: Table continues below

	Variable	Group	R.Squared	F.Statistic
Verrucomicrobia	Verrucomicrobia	Placebo	0.273	7.475
Verrucomicrobia1	Verrucomicrobia	LGG	0.273	7.475

Table 10: Table continues below

	Estimate	P.Value	Adjusted.P.Value
Verrucomicrobia	0.248530840321361	0.02	0.2424
Verrucomicrobia1	0.248530840321361	0.02	0.2424

Table 11: Table continues below

	Mean.Abandance_Change	Mean.Prevalence_Change
Verrucomicrobia	-0.1144	0.3571
Verrucomicrobia1	0.1581	0.875

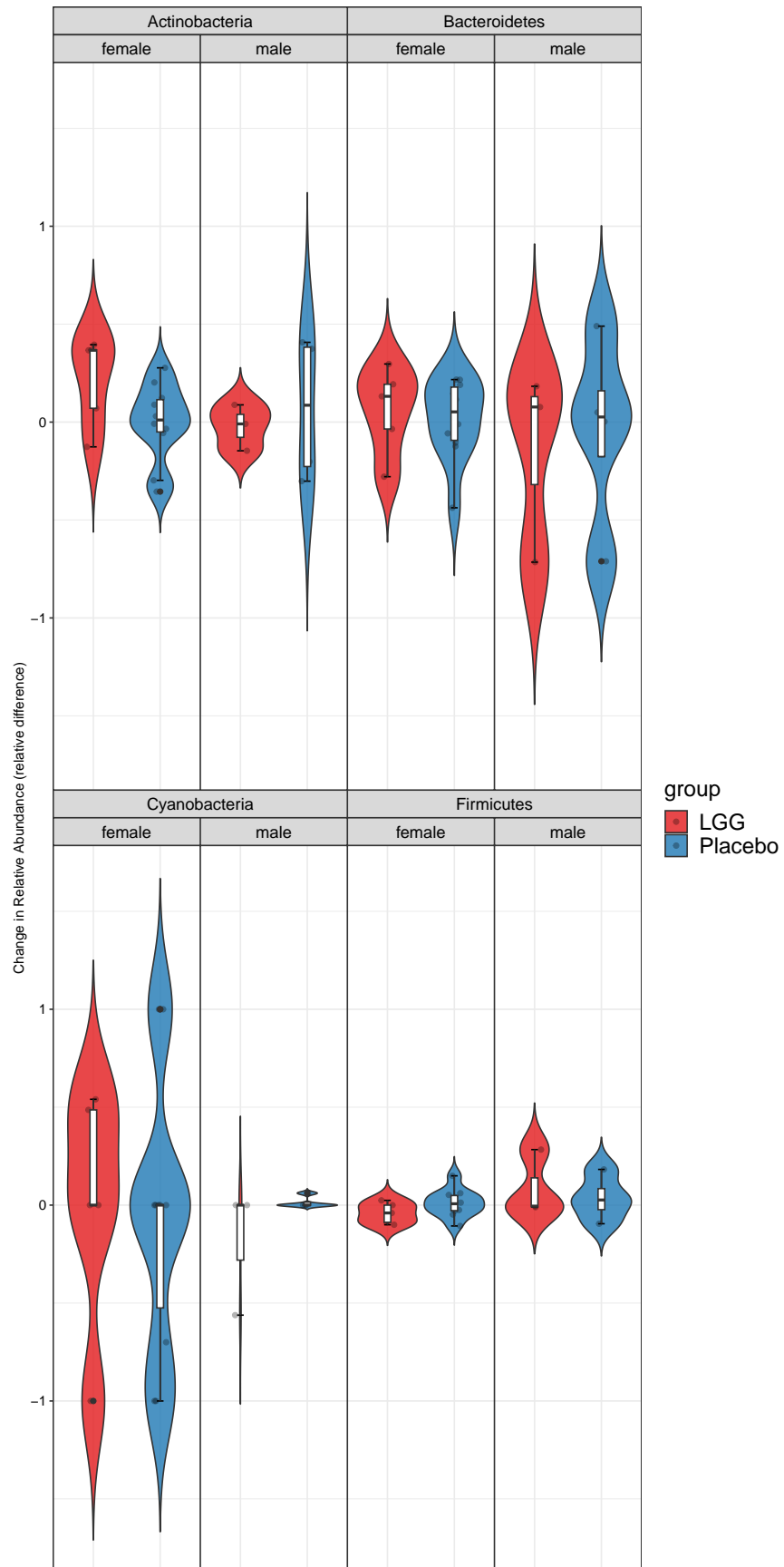
	SD.Abandance_Change	SD.Prevalence_Change
Verrucomicrobia	0.2633	0.488
Verrucomicrobia1	0.1878	0.3416

3.5 Taxa Boxplot for Significant Taxa

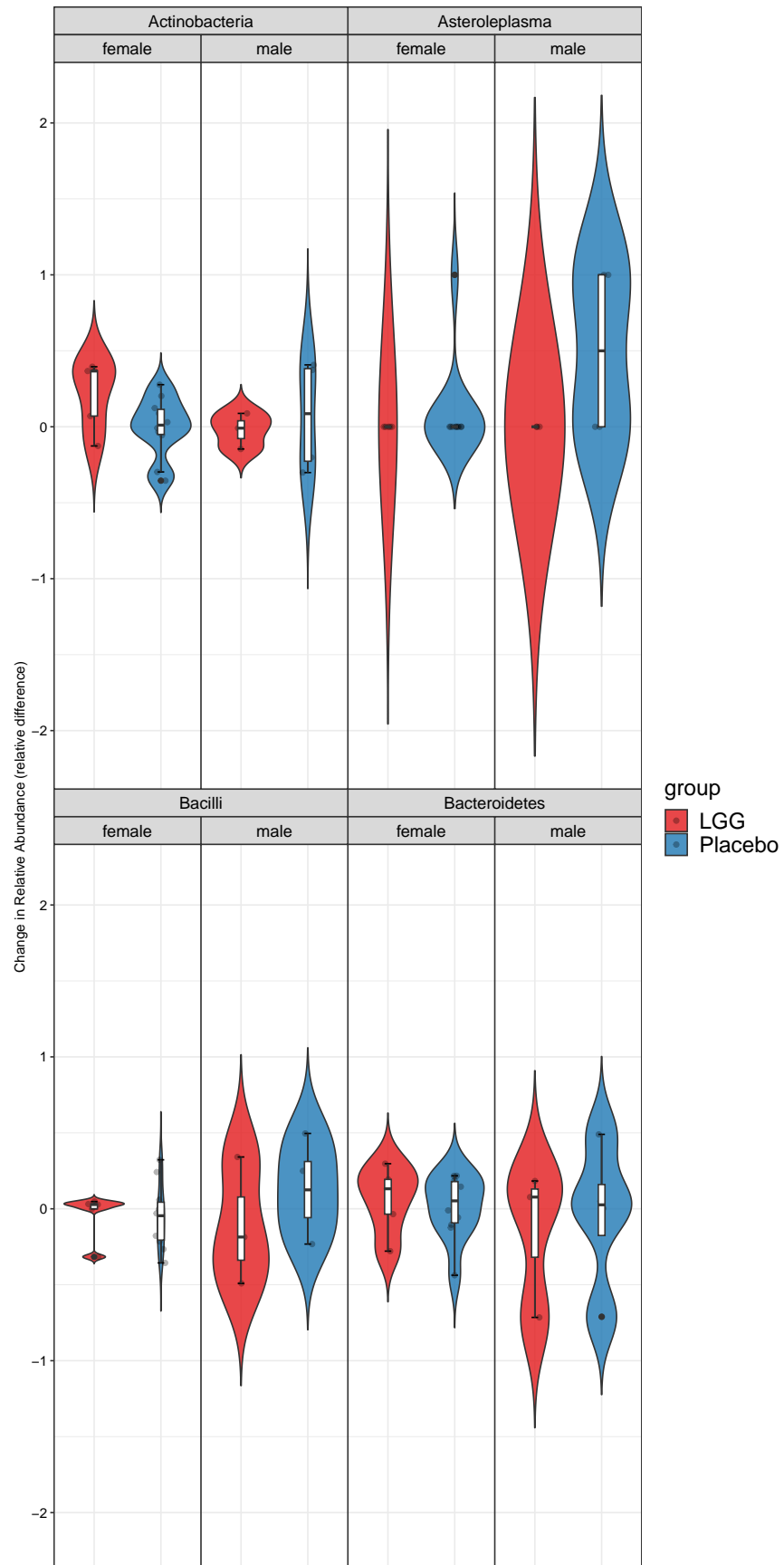
```
significant_taxa <- taxa_change_test_results$Taxa[taxa_change_test_results$Adjusted.P.Value < 1]

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.