TransPAT - 16S OTU

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Introduction

This Notebook is meant to contain the 16S_OTU data found within the respective manuscript. It contains only the code used to generate the figures found within the main text. This entire dataset is publically available in QIITA under the ID 10527. More details about the procedures used to generate the data can be found within the **Methods** section of the manuscript. The table found within the data folder has been processed to remove any OTU less than 0.01% relative abundance.

Make Taxanomic Abundance Plots (Figure 4d)

These commands will generate the graphs found within the multi-panel **Figure 4d**. The command must be run on each of the 4 permutations. The final PDF is composed of multiple plots across the different Treatment groups and genders.

Note: The barplot abundance coors were changed in post-processing after generating the figure. The colors were changed to highlight the important bacteria.

```
[12]    # Split the table by Treatment and Gender
        split_otu_table.py \
        -i data/transfer_m0001.biom \
        -o data/per_study_otu_tables \
        -m data/transpat_mapping.txt \
        -f Sex,Treatment
```

```
[19]    # Make a directory to store the results
        mkdir -p analysis/taxa_plots/

        # Plot barplot with only Male-Control
        summarize_taxa_through_plots.py \
        -i
        data/per_study_otu_tables/transfer_m0001__Sex_Male_Treatment_Control__.b
        iom \
        -o analysis/taxa_plots/male_control \
```

```
-m
data/per_study_otu_tables/transpat_mapping__Sex_Male_Treatment_Control__
.txt \
-c Days_post_transfer \
--sort

# Plot barplot with only Male-PAT
summarize_taxa_through_plots.py \
-i
data/per_study_otu_tables/transfer_m0001__Sex_Male_Treatment_PAT__.biom
\
-o analysis/taxa_plots/male_pat1 \
-m
data/per_study_otu_tables/transpat_mapping__Sex_Male_Treatment_PAT__.txt
\
-c Days_post_transfer \
--sort

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - #

# Plot barplot with only Female-Control
summarize_taxa_through_plots.py \
-i
data/per_study_otu_tables/transfer_m0001__Sex_Female_Treatment_Control__
.biom \
-o analysis/taxa_plots/female_control \
-m
data/per_study_otu_tables/transpat_mapping__Sex_Female_Treatment_Control
__.txt \
-c Days_post_transfer \
--sort

# Plot barplot with only Female-PAT
summarize_taxa_through_plots.py \
-i
data/per_study_otu_tables/transfer_m0001__Sex_Female_Treatment_PAT__.bio
m \
-o analysis/taxa_plots/female_pat1 \
-m
data/per_study_otu_tables/transpat_mapping__Sex_Female_Treatment_PAT__.t
xt \
-c Days_post_transfer \
--sort
```

Make Taxanomic Abundance Plots (Figure 4f)

These commands will generate the graphs found within the multi-panel **Figure 4f**. A 3D plot is generate using the Emperor tool. The figure was composed of multiple views generated with the

plot. The file plot can be found within
analysis/bdiv_pcoa/unweighted_unifrac_emperor_pcoa_plot/index.html

```
[5]    # Create analysis folder
       mkdir -p analysis

       # Run beta diversity through plots
       beta_diversity_through_plots.py \
       -i data/transfer_m0001.biom \
       -o analysis/bdiv_pcoa \
       -m data/transpat_mapping.txt \
       -t data/rep_set.tre
```