

TransferPAT-16S OTU

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Contents

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.

1a. Install and load the necessary libraries

```
source("scripts/estimate_pd.R")
library(phyloseq)
library(RColorBrewer)
library(tidyverse)
library(vegan)
library(ape)
library(picante)
library(forcats)
```

1b. Import the OTU table, map and OTU-representative tree

```
data <- import_biom(BIOMfilename = 'data/transfer_m0001.biom',
                   treefilename = 'data/rep_set.tre',
                   parseFunction = parse_taxonomy_greenengenes)
mapping = import_qiime_sample_data(mapfilename = 'data/transpat_mapping.txt')
phylo <- merge_phyloseq(data, mapping)

# Convert time to factor
sample_data(phylo)$Days_post_transfer <- factor(x = sample_data(phylo)$Days_post_transfer,
                                                levels = c("In", "1", "6", "12", "20", "43", "64", "76"))
```

Calculate Faith's Phylogenetic Diversity values for all samples

```
# use Picante to generate Faith PD values
sample_data(phylo)$PD_tree = estimate_pd(phylo)$PD
```

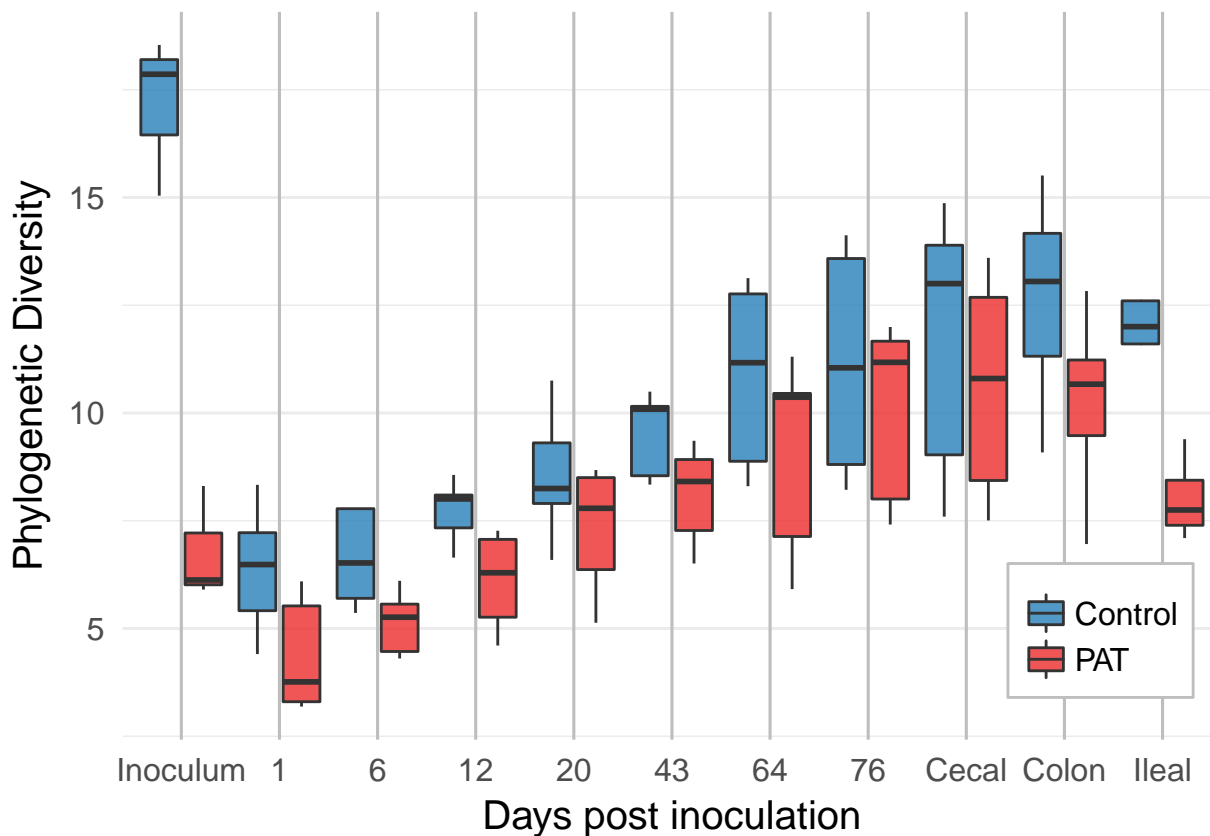
```
## Calculating Faiths PD-index...
```

```
sample_data(phylo)$PD_sr = estimate_pd(phylo)$SR
```

```
## Calculating Faiths PD-index...
```

Figure 3e. Faiths PD tree across time

```
# Take the values from PD and plot over time
sample_data(phylo) %>%
  as("data.frame") %>%
  ggplot(aes(x = Days_post_transfer, y = PD_tree, fill = Treatment)) +
  geom_boxplot(outlier.colour = NA,
              alpha = 0.80,
              position = position_dodge(width = .9)) +
  theme_minimal(base_size = 15) +
  theme(panel.grid.major.x = element_line(colour = "grey", size = 0.55),
        legend.title = element_blank(), legend.position = c(0.89, 0.15),
        legend.background = element_rect(size = 0.5, linetype = "solid", colour = "gray")) +
  xlab("Days post inoculation") + ylab("Phylogenetic Diversity") +
  guides(fill = guide_legend(title = "Treatment")) +
  scale_fill_manual(values = c("Control" = "#2980b9", "PAT" = "firebrick2"))
```



```
sessionInfo()
```

```
## R version 3.3.1 (2016-06-21)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.5 (Yosemite)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
```

```

##
## other attached packages:
## [1] scales_0.4.1      forcats_0.2.0      picante_1.6-2
## [4] nlme_3.1-131      ape_4.1            vegan_2.4-3
## [7] lattice_0.20-35   permute_0.9-4      dplyr_0.5.0
## [10] purrr_0.2.2       readr_1.1.0        tidyr_0.6.1
## [13] tibble_1.3.0      ggplot2_2.2.1      tidyverse_1.1.1
## [16] RColorBrewer_1.1-2 phyloseq_1.19.1
##
## loaded via a namespace (and not attached):
## [1] reshape2_1.4.2     splines_3.3.1      haven_1.0.0
## [4] rhdf5_2.18.0       colorspace_1.3-2   htmltools_0.3.5
## [7] stats4_3.3.1       yaml_2.1.14        mgcv_1.8-17
## [10] survival_2.41-3    foreign_0.8-68     DBI_0.6-1
## [13] BiocGenerics_0.20.0 readxl_1.0.0        modelr_0.1.0
## [16] foreach_1.4.3      plyr_1.8.4         stringr_1.2.0
## [19] zlibbioc_1.20.0    Biostrings_2.42.1  cellranger_1.1.0
## [22] munsell_0.4.3      gtable_0.2.0       rvest_0.3.2
## [25] codetools_0.2-15   psych_1.7.3.21     evaluate_0.10
## [28] Biobase_2.34.0     knitr_1.15.1       IRanges_2.8.1
## [31] biomformat_1.2.0   parallel_3.3.1     broom_0.4.2
## [34] Rcpp_0.12.10       backports_1.0.5    S4Vectors_0.12.1
## [37] jsonlite_1.4       XVector_0.14.0     mnormt_1.5-5
## [40] hms_0.3            digest_0.6.12      stringi_1.1.5
## [43] grid_3.3.1         ade4_1.7-6         rprojroot_1.2
## [46] tools_3.3.1        magrittr_1.5       lazyeval_0.2.0
## [49] cluster_2.0.6      MASS_7.3-47        Matrix_1.2-8
## [52] xml2_1.1.1         data.table_1.10.4  lubridate_1.6.0
## [55] httr_1.2.1         assertthat_0.2.0   rmarkdown_1.5
## [58] iterators_1.0.8    R6_2.2.0           multtest_2.30.0
## [61] igraph_1.0.1

```