

Plasmid Alpha and Beta Diversity Using de novo Binary Data

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Load and prepare data for phyloseq

Create counts matrix

```
# Load counts
plasmid_binary <- read.csv("all_results_cluster_simp_pivot.tsv", header = TRUE,
                          skipNul = TRUE, sep = "\t", as.is = TRUE)

#plasmid_binary
#str(plasmid_binary)
#row.names(plasmid_binary)
#class(plasmid_binary)
colnames(plasmid_binary)

##      [1] "Plasmid" "C1"      "C102"    "C103"    "C104"    "C105"    "C107"
##      [8] "C111"    "C114"    "C116"    "C118"    "C119"    "C123"    "C124"
##     [15] "C134"    "C135"    "C136"    "C137"    "C140"    "C142"    "C146"
##     [22] "C147"    "C148"    "C15"     "C152IIP" "C18"     "C19"     "C20"
##     [29] "C21"     "C23"     "C24"     "C26"     "C28"     "C30"     "C32"
##     [36] "C33"     "C34old"  "C35"     "C40"     "C44"     "C46"     "C47"
##     [43] "C48"     "C49"     "C5"      "C51"     "C54"     "C59"     "C65"
##     [50] "C68"     "C69"     "C7"      "C70"     "C72"     "C74"     "C75"
##     [57] "C76II"   "C80"     "C82"     "C85"     "C86"     "C87"     "C88"
##     [64] "C89"     "C9"      "C90"     "C95"     "C96"     "C98"     "P100"
##     [71] "P103"    "P104IIP" "P105"    "P107"    "P10old"  "P114"    "P115"
##     [78] "P116"    "P118"    "P119"    "P11old"  "P12"     "P120"    "P14"
##     [85] "P15"     "P16"     "P17"     "P18"     "P19"     "P20"     "P24"
##     [92] "P26"     "P28"     "P31"     "P34"     "P37"     "P38"     "P4"
##     [99] "P42"     "P43"     "P45"     "P46"     "P47"     "P48"     "P5"
##    [106] "P50"     "P51"     "P52"     "P53"     "P56"     "P57"     "P58"
##    [113] "P59"     "P60"     "P61"     "P62P"    "P63"     "P66"     "P67"
##    [120] "P68"     "P69"     "P70"     "P71"     "P72"     "P73"     "P74"
##    [127] "P77"     "P79"     "P8"      "P83"     "P85"     "P87"     "P88"
##    [134] "P9"      "P94"     "P95II"   "P99"

#head(colnames(plasmid_binary))
#dim(plasmid_binary)
#plasmid_binary$phage

## Put this in `matrix` class for `phyloseq`'s `otu table`, and create it:
counts <- as.matrix(sapply(plasmid_binary, as.numeric))
#head(counts)
#head(colnames(counts))
rownames(counts) <- plasmid_binary$Plasmid
```

```

#head(counts)
#head(colnames(counts))

# delete/remove the newly created "phage" column:
counts <- counts[, -grep("Plasmid", colnames(counts))]
#head(counts)
#head(colnames(counts))
#dim(counts)

otu.table <- otu_table(counts, taxa_are_rows = TRUE)
head(otu.table)

```

```

## OTU Table:          [6 taxa and 136 samples]
##                    taxa are rows
##
##                    C1 C102 C103 C104 C105 C107 C111 C114
## C1-NODE_10182_length_6088_cov_3.171059  1  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  1  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  1  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  1  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528  1  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306  1  0  0  0  0  0  0  0
##
##                    C116 C118 C119 C123 C124 C134 C135 C136
## C1-NODE_10182_length_6088_cov_3.171059  0  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  0  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  0  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528  0  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306  0  0  0  0  0  0  0  0
##
##                    C137 C140 C142 C146 C147 C148 C15
## C1-NODE_10182_length_6088_cov_3.171059  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306  0  0  0  0  0  0  0
##
##                    C152IIP C18 C19 C20 C21 C23 C24 C26 C28
## C1-NODE_10182_length_6088_cov_3.171059  0  0  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  0  0  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  0  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  0  0  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528  0  0  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306  0  0  0  0  0  0  0  0  0
##
##                    C30 C32 C33 C34old C35 C40 C44 C46 C47
## C1-NODE_10182_length_6088_cov_3.171059  0  0  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  0  0  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  0  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  0  0  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528  0  0  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306  0  0  0  0  0  0  0  0  0
##
##                    C48 C49 C5 C51 C54 C59 C65 C68 C69 C7
## C1-NODE_10182_length_6088_cov_3.171059  0  0  0  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722  0  0  0  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700  0  0  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370  0  0  0  0  0  0  0  0  0  0

```

## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	C70	C72	C74	C75	C76II	C80	C82	C85	C86	
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	C87	C88	C89	C9	C90	C95	C96	C98	P100	
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P103	P104IIP	P105	P107	P10old	P114	P115			
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P116	P118	P119	P11old	P12	P120	P14	P15		
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P16	P17	P18	P19	P20	P24	P26	P28	P31	P34
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P37	P38	P4	P42	P43	P45	P46	P47	P48	P5
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P50	P51	P52	P53	P56	P57	P58	P59	P60	P61
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10214_length_6069_cov_3.628700	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10275_length_6034_cov_20.391370	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10759_length_5749_cov_4.134528	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10936_length_5650_cov_3.782306	0	0	0	0	0	0	0	0	0	0
##	P62P	P63	P66	P67	P68	P69	P70	P71	P72	
## C1-NODE_10182_length_6088_cov_3.171059	0	0	0	0	0	0	0	0	0	0
## C1-NODE_10195_length_6078_cov_3.637722	0	0	0	0	0	0	0	0	0	0

```
## C1-NODE_10214_length_6069_cov_3.628700    0  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370    0  0  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528     0  0  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306     0  0  0  0  0  0  0  0  0
##
##          P73 P74 P77 P79 P8  P83 P85 P87 P88 P9
## C1-NODE_10182_length_6088_cov_3.171059    0  0  0  0  0  0  0  0  0  0
## C1-NODE_10195_length_6078_cov_3.637722    0  0  0  0  0  0  0  0  0  0
## C1-NODE_10214_length_6069_cov_3.628700    0  0  0  0  0  0  0  0  0  0
## C1-NODE_10275_length_6034_cov_20.391370    0  0  0  0  0  0  0  0  0  0
## C1-NODE_10759_length_5749_cov_4.134528     0  0  0  0  0  0  0  0  0  0
## C1-NODE_10936_length_5650_cov_3.782306     0  0  0  0  0  0  0  0  0  0
##
##          P94 P95II P99
## C1-NODE_10182_length_6088_cov_3.171059    0    0  0
## C1-NODE_10195_length_6078_cov_3.637722    0    0  0
## C1-NODE_10214_length_6069_cov_3.628700    0    0  0
## C1-NODE_10275_length_6034_cov_20.391370    0    0  0
## C1-NODE_10759_length_5749_cov_4.134528     0    0  0
## C1-NODE_10936_length_5650_cov_3.782306     0    0  0
```

```
head(colnames(otu.table))
```

```
## [1] "C1"    "C102"  "C103"  "C104"  "C105"  "C107"
```

```
dim(otu.table)
```

```
## [1] 29096   136
```

```
#otu.table
```

Create dummy tax table for TAX

```
taxmat = matrix(sample(letters, 29096, replace = TRUE),
                 nrow = nrow(otu.table), ncol = 7)
rownames(taxmat) <- rownames(otu.table)
colnames(taxmat) <- c("Domain", "Phylum", "Class", "Order",
                     "Family", "Genus", "Species")
#taxmat
TAX = tax_table(taxmat)
```

Import the metadata:

```
sampladata <- as.data.frame(read.csv
                           (file = "pd_meta_with_ffq_and_scfa_only_oursamples_3variables_ordered.csv",
                             header = TRUE, sep = ",", row.names = 1))
#rownames(sampladata)
#colnames(otu.table)
identical(rownames(sampladata), colnames(otu.table))

## [1] TRUE
sampladata = sample_data(sampladata)
```

Create physeq

```

physeqfinal <- phyloseq(otu.table,TAX, sampledata)
#physeqfinal
#sample_data(physeqfinal)
#summary(sample_data(physeqfinal))

physeqfinal.2 <- subset_taxa(physeqfinal, taxa_sums(physeqfinal) >0)
#head(sort(taxa_sums(physeqfinal.2), decreasing = FALSE))

physeqfinal.2

## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 29096 taxa and 136 samples ]
## sample_data() Sample Data: [ 136 samples by 4 sample variables ]
## tax_table() Taxonomy Table: [ 29096 taxa by 7 taxonomic ranks ]

physeqfinal

```

```

## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 29096 taxa and 136 samples ]
## sample_data() Sample Data: [ 136 samples by 4 sample variables ]
## tax_table() Taxonomy Table: [ 29096 taxa by 7 taxonomic ranks ]

summary(sample_data(physeqfinal.2))

##      Group      gender      age_at_stool_collection      BMI
## Length:136      Length:136      Min. :51.00      Min. :17.51
## Class :character Class :character 1st Qu.:61.00      1st Qu.:24.13
## Mode :character Mode :character Median :65.00      Median :26.31
##                                     Mean :64.98      Mean :26.69
##                                     3rd Qu.:69.00      3rd Qu.:28.62
##                                     Max. :78.00      Max. :37.87
##                                     NA's :13

```

Alpha Diversity for Group (C vs P)

```

richness.table <- estimate_richness(physeqfinal.2, split = TRUE,
                                   measures = c("Observed", "Chao1",
                                                "ACE", "Shannon", "InvSimpson"))

head(richness.table)

##      Observed   Chao1 se.chao1      ACE se.ACE Shannon InvSimpson
## C1          410 28086.0 13332.893 42230.00 1.413345 6.014294 408.0385
## C102         192 18528.0 2653.502      NaN      NaN 5.257495 192.0000
## C103         204 20910.0 2906.561      NaN      NaN 5.318120 204.0000
## C104         536 35847.5 15595.515 42563.42 2.630661 6.279640 529.2604
## C105         257 5528.0 2075.259 6733.40 2.233336 5.541889 252.3676
## C107         335 56280.0 6122.355      NaN      NaN 5.814131 335.0000

richness.table$Group <- sample_data(physeqfinal.2)$Group

```

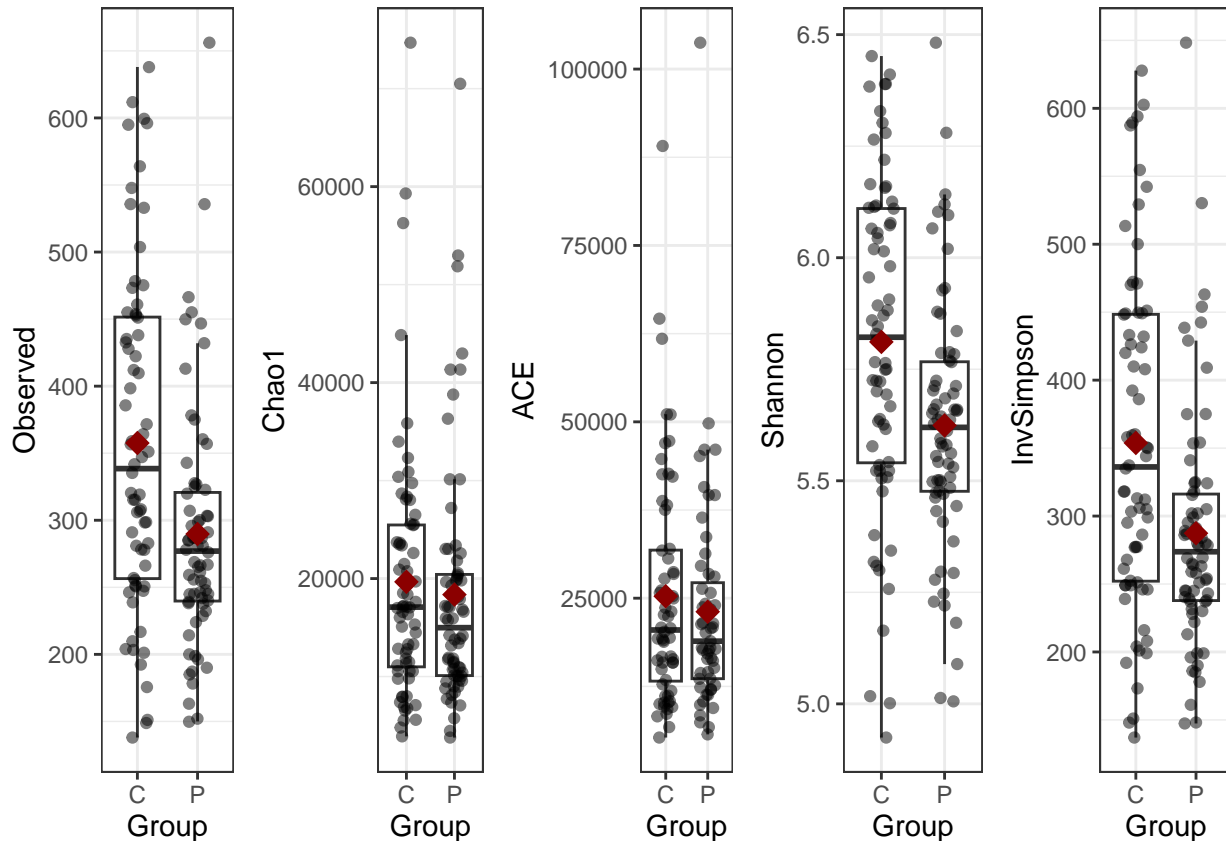
Plot Alpha Diversity

```

theme_set(theme_bw())

grid.arrange(
  ggplot(richness.table, aes(x = Group, y = Observed)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = Group, y = Chao1)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = Group, y = ACE)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = Group, y = Shannon)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = Group, y = InvSimpson)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  nrow = 1)

```



Calculate mean and standard deviation for each alpha diversity metric

```

# Function to calculate mean and SD, ignoring NaN values
calc_mean_sd <- function(x) {
  x_clean <- x[!is.nan(x)]
  if (length(x_clean) > 0) {

```

```

    c(mean = mean(x_clean, na.rm = TRUE),
      sd = sd(x_clean, na.rm = TRUE))
  } else {
    c(mean = NA, sd = NA)
  }
}

# Calculate mean and standard deviation for each index by group, ignoring NaN values
richness_stats <- richness.table %>%
  group_by(Group) %>%
  summarise(
    across(c(Observed, Chao1, ACE, Shannon, InvSimpson),
      list(Mean = ~calc_mean_sd(.)[1],
           SD = ~calc_mean_sd(.)[2]))
  )

## group_by: one grouping variable (Group)
## summarise: now 2 rows and 11 columns, ungrouped

# Print the results
print(richness_stats)

## # A tibble: 2 x 11
##   Group Observed_Mean Observed_SD Chao1_Mean Chao1_SD ACE_Mean ACE_SD
##   <chr>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl> <dbl>
## 1 C          358.        126.       19669.    12951.    25276. 16440.
## 2 P          290.         90.2       18364.    12513.    23086. 15599.
## # i 4 more variables: Shannon_Mean <dbl>, Shannon_SD <dbl>,
## #   InvSimpson_Mean <dbl>, InvSimpson_SD <dbl>

# write the results to a CSV file
write.csv(richness_stats, "group_richness_statistics.csv", row.names = FALSE)

```

Observed Richness Wilcoxon rank sum test (Group)

```

wilcox.test(richness.table$Observed ~ sample_data(physeqfinal.2)$Group,
  conf.level = 0.95, conf.int = TRUE)

##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$Observed by sample_data(physeqfinal.2)$Group
## W = 3090.5, p-value = 0.0007085
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  23.00004 101.00003
## sample estimates:
## difference in location
## 60.99996

```

CHAO1 Wilcoxon rank sum test (Group)

```

wilcox.test(richness.table$Chao1 ~ sample_data(physeqfinal.2)$Group,
  conf.level = 0.95, conf.int = TRUE)

```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$Chao1 by sample_data(physeqfinal.2)$Group
## W = 2524.5, p-value = 0.3562
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## -1693 4664
## sample estimates:
## difference in location
## 1357.992
```

ACE Wilcoxon rank sum test (Group)

```
wilcox.test(richness.table$ACE ~ sample_data(physeqfinal.2)$Group,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$ACE by sample_data(physeqfinal.2)$Group
## W = 1749.5, p-value = 0.5794
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## -2648.000 5501.083
## sample estimates:
## difference in location
## 1349.771
```

InvSimpson Wilcoxon rank sum test (Group)

```
wilcox.test(richness.table$InvSimpson ~ sample_data(physeqfinal.2)$Group,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$InvSimpson by sample_data(physeqfinal.2)$Group
## W = 3082.5, p-value = 0.0008043
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## 22.93046 99.45676
## sample estimates:
## difference in location
## 59.97253
```

Shannon Wilcoxon rank sum test (Group)

```
wilcox.test(richness.table$Shannon ~ sample_data(physeqfinal.2)$Group,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
```



```
## data: richness.table$Shannon by sample_data(physeqfinal.2)$Group
## W = 3086.5, p-value = 0.0007551
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## 0.08128253 0.32375666
## sample estimates:
## difference in location
## 0.2047963
```

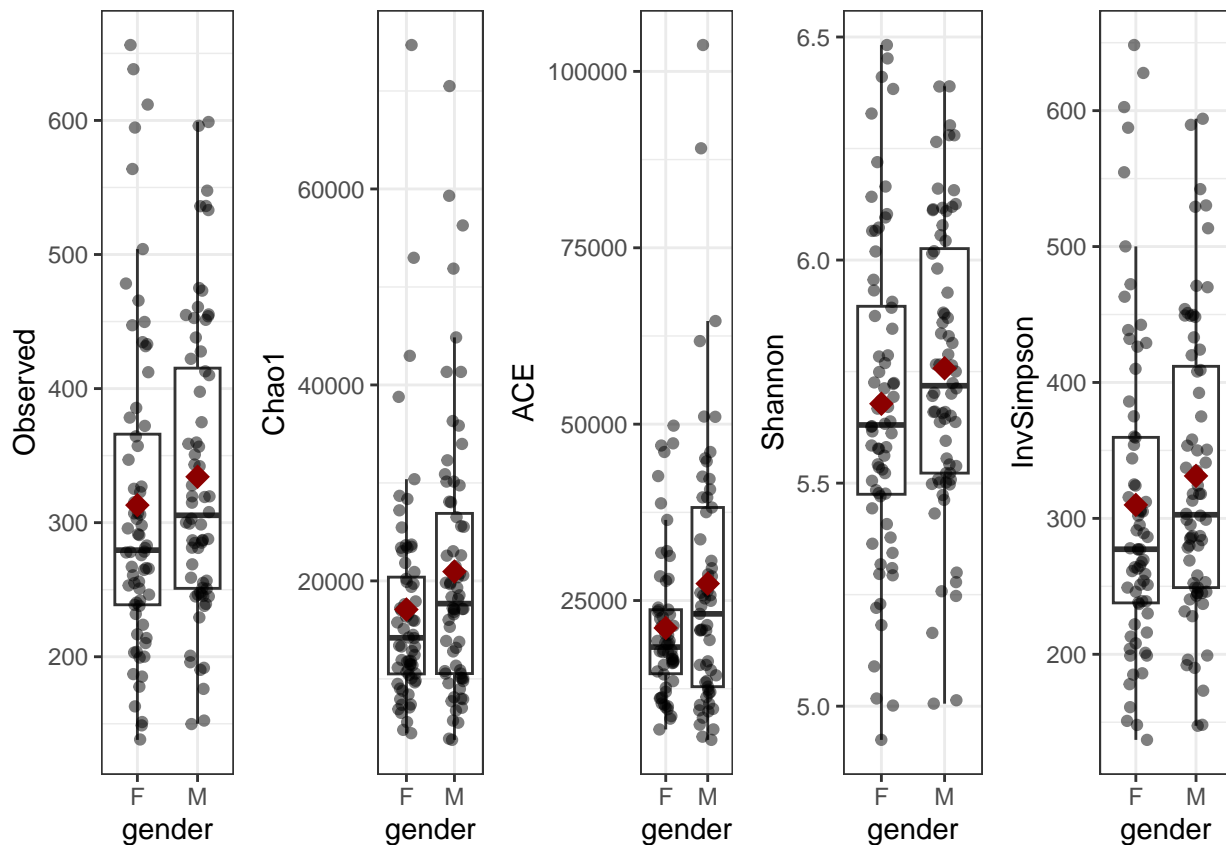
Alpha Diversity for Gender (F vs M)

```
richness.table$gender <- sample_data(physeqfinal.2)$gender
```

Plot Alpha Diversity for Gender (F vs M)

```
theme_set(theme_bw())

grid.arrange(
  ggplot(richness.table, aes(x = gender, y = Observed)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = gender, y = Chao1)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = gender, y = ACE)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = gender, y = Shannon)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  ggplot(richness.table, aes(x = gender, y = InvSimpson)) +
    geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2, alpha = .5) +
    stat_summary(fun = mean, color = "darkred", geom = "point", shape = 18, size = 4),
  nrow = 1)
```



Calculate mean and standard deviation for each alpha diversity metric

```
# Function to calculate mean and SD, ignoring NaN values
calc_mean_sd <- function(x) {
  x_clean <- x[!is.nan(x)]
  if (length(x_clean) > 0) {
    c(mean = mean(x_clean, na.rm = TRUE),
      sd = sd(x_clean, na.rm = TRUE))
  } else {
    c(mean = NA, sd = NA)
  }
}

# Calculate mean and standard deviation for each index by group, ignoring NaN values
richness_stats <- richness.table %>%
  group_by(gender) %>%
  summarise(
    across(c(Observed, Chao1, ACE, Shannon, InvSimpson),
      list(Mean = ~calc_mean_sd(.)[1],
           SD = ~calc_mean_sd(.)[2]))
  )
```

```
## group_by: one grouping variable (gender)
## summarise: now 2 rows and 11 columns, ungrouped
```

```
# Print the results
print(richness_stats)
```

```
## # A tibble: 2 x 11
##   gender Observed_Mean Observed_SD Chao1_Mean Chao1_SD ACE_Mean ACE_SD
##   <chr>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl> <dbl>
## 1 F          313.        120.       17080.     11359.     21109. 10520.
## 2 M          334.        108.       20953.     13731.     27403. 19720.
## # i 4 more variables: Shannon_Mean <dbl>, Shannon_SD <dbl>,
## #   InvSimpson_Mean <dbl>, InvSimpson_SD <dbl>
# write the results to a CSV file
write.csv(richness_stats, "gender_richness_statistics.csv", row.names = FALSE)
```

Observed Richness Wilcoxon rank sum test (gender)

```
wilcox.test(richness.table$Observed ~ sample_data(physeqfinal.2)$gender,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$Observed by sample_data(physeqfinal.2)$gender
## W = 1960.5, p-value = 0.1266
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## -58.999938 7.999976
## sample estimates:
## difference in location
## -25.00002
```

CHAO1 Wilcoxon rank sum test (gender)

```
wilcox.test(richness.table$Chao1 ~ sample_data(physeqfinal.2)$gender,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$Chao1 by sample_data(physeqfinal.2)$gender
## W = 1918.5, p-value = 0.08718
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
## -6133.867 369.500
## sample estimates:
## difference in location
## -2753.91
```

ACE Wilcoxon rank sum test (gender)

```
wilcox.test(richness.table$ACE ~ sample_data(physeqfinal.2)$gender,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$ACE by sample_data(physeqfinal.2)$gender
```

```
## W = 1417.5, p-value = 0.1887
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -8120.625  1617.865
## sample estimates:
## difference in location
##                -3048.683
```

InvSimpson Wilcoxon rank sum test (gender)

```
wilcox.test(richness.table$InvSimpson ~ sample_data(physeqfinal.2)$gender,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$InvSimpson by sample_data(physeqfinal.2)$gender
## W = 1962.5, p-value = 0.1288
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -58.397175  6.950941
## sample estimates:
## difference in location
##                -25.75633
```

Shannon Wilcoxon rank sum test (gender)

```
wilcox.test(richness.table$Shannon ~ sample_data(physeqfinal.2)$gender,
             conf.level = 0.95, conf.int = TRUE)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: richness.table$Shannon by sample_data(physeqfinal.2)$gender
## W = 1964.5, p-value = 0.131
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -0.20358297  0.02492071
## sample estimates:
## difference in location
##                -0.08627405
```

Alpha Diversity for BMI (Continuous variable)

```
richness.table$BMI <- sample_data(physeqfinal.2)$BMI
```

Plot Alpha Diversity for BMI (Continuous variable)

```
common_theme <- theme(
  axis.text.x = element_text(angle = 45, hjust = 1),
)
```

```

grid.arrange(
  ggplot(richness.table, aes(x = BMI, y = Observed)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "BMI", y = "Observed") +
    scale_x_continuous(breaks = seq(20, 35, by = 5)) + # Adjust range as needed
    common_theme,

  ggplot(richness.table, aes(x = BMI, y = Chao1)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "BMI", y = "Chao1") +
    scale_x_continuous(breaks = seq(20, 35, by = 5)) +
    common_theme,

  ggplot(richness.table, aes(x = BMI, y = ACE)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "BMI", y = "ACE") +
    scale_x_continuous(breaks = seq(20, 35, by = 5)) +
    common_theme,

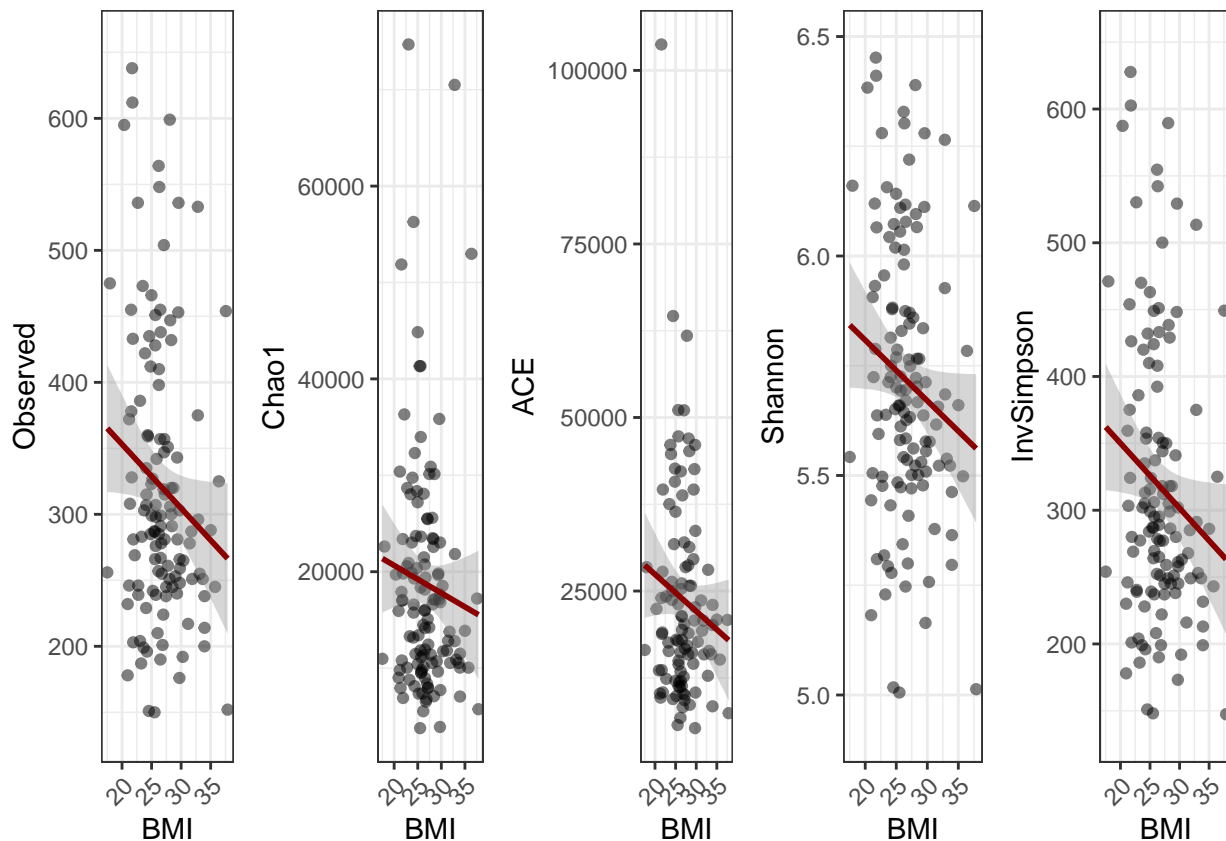
  ggplot(richness.table, aes(x = BMI, y = Shannon)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "BMI", y = "Shannon") +
    scale_x_continuous(breaks = seq(20, 35, by = 5)) +
    common_theme,

  ggplot(richness.table, aes(x = BMI, y = InvSimpson)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "BMI", y = "InvSimpson") +
    scale_x_continuous(breaks = seq(20, 35, by = 5)) +
    common_theme,

  nrow = 1
)

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'

```



Observed Richness Spearman rank sum test (BMI)

```
cor.test(richness.table$Observed, sample_data(physeqfinal.2)$BMI, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: richness.table$Observed and sample_data(physeqfinal.2)$BMI
## S = 357951, p-value = 0.08855
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.1542187
```

CHAO1 Richness Spearman rank sum test (BMI)

```
cor.test(richness.table$Chao1, sample_data(physeqfinal.2)$BMI, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: richness.table$Chao1 and sample_data(physeqfinal.2)$BMI
## S = 357269, p-value = 0.09324
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
```

```
## -0.1520187
```

ACE Richness Spearman rank sum test (BMI)

```
cor.test(richness.table$ACE, sample_data(physeqfinal.2)$BMI, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: richness.table$ACE and sample_data(physeqfinal.2)$BMI  
## S = 197939, p-value = 0.573  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## -0.0558989
```

InvSimpson Richness Spearman rank sum test (BMI)

```
cor.test(richness.table$InvSimpson, sample_data(physeqfinal.2)$BMI, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: richness.table$InvSimpson and sample_data(physeqfinal.2)$BMI  
## S = 358359, p-value = 0.08583  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## -0.1555335
```

Shannon Richness Spearman rank sum test (BMI)

```
cor.test(richness.table$Shannon, sample_data(physeqfinal.2)$BMI, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: richness.table$Shannon and sample_data(physeqfinal.2)$BMI  
## S = 358100, p-value = 0.08755  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## -0.1546983
```

Alpha Diversity for Age (Continuous variable)

```
richness.table$Age <- sample_data(physeqfinal.2)$age_at_stool_collection
```

Plot Alpha Diversity for Age (Continuous variable)

```
common_theme <- theme(  
  axis.text.x = element_text(angle = 45, hjust = 1),
```

```

)

grid.arrange(
  ggplot(richness.table, aes(x = age, y = Observed)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "age", y = "Observed") +
    scale_x_continuous(breaks = seq(50, 80, by = 10)) + # Adjust range as needed
    common_theme,

  ggplot(richness.table, aes(x = age, y = Chao1)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "age", y = "Chao1") +
    scale_x_continuous(breaks = seq(50, 80, by = 10)) +
    common_theme,

  ggplot(richness.table, aes(x = age, y = ACE)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "age", y = "ACE") +
    scale_x_continuous(breaks = seq(50, 80, by = 10)) +
    common_theme,

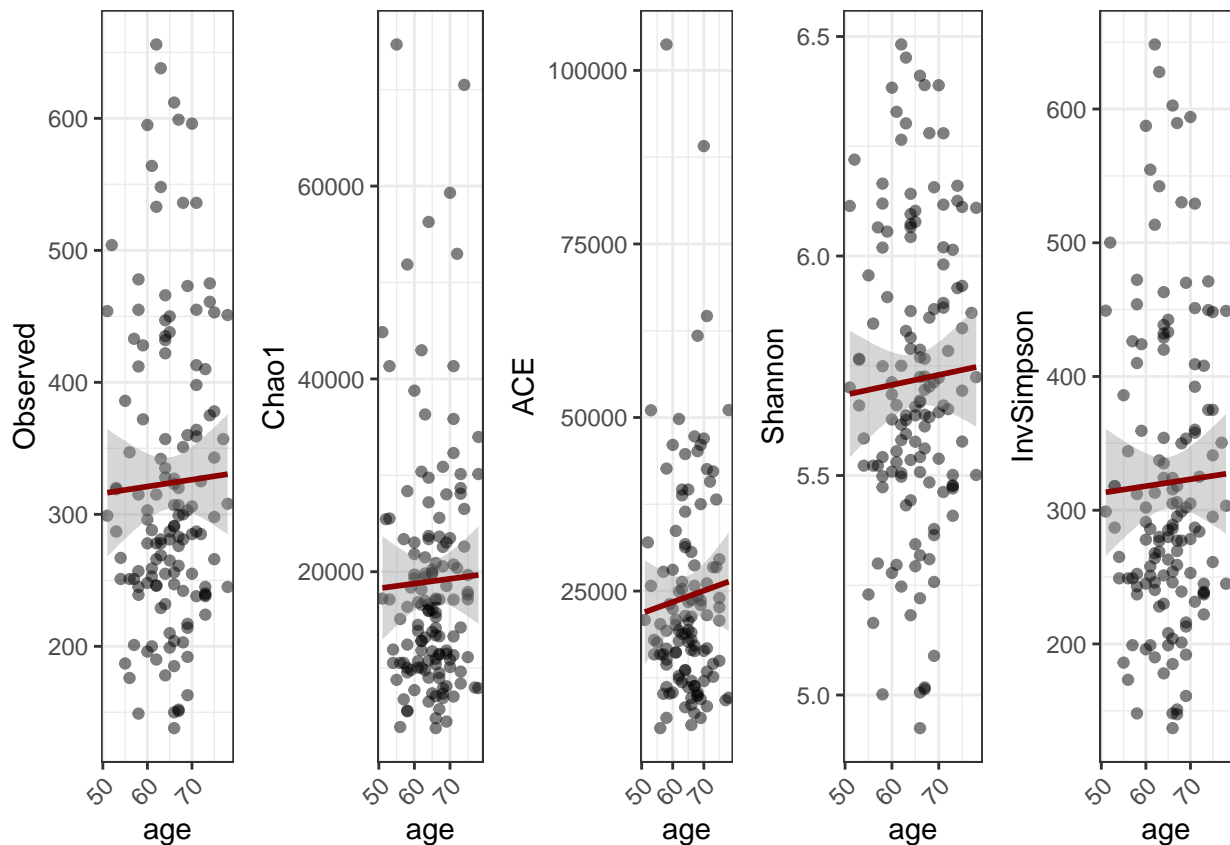
  ggplot(richness.table, aes(x = age, y = Shannon)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "age", y = "Shannon") +
    scale_x_continuous(breaks = seq(50, 80, by = 10)) +
    common_theme,

  ggplot(richness.table, aes(x = age, y = InvSimpson)) +
    geom_point(alpha = 0.5) +
    geom_smooth(method = "lm", color = "darkred") +
    labs(x = "age", y = "InvSimpson") +
    scale_x_continuous(breaks = seq(50, 80, by = 10)) +
    common_theme,

  nrow = 1
)

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'

```

Observed Richness Spearman rank sum test (age)

```
cor.test(richness.table$Observed,
         sample_data(physeqfinal.2)$age_at_stool_collection, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: richness.table$Observed and sample_data(physeqfinal.2)$age_at_stool_collection
## S = 399673, p-value = 0.5899
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.04662687
```

CHAO1 Richness Spearman rank sum test (age)

```
cor.test(richness.table$Chao1,
         sample_data(physeqfinal.2)$age_at_stool_collection, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: richness.table$Chao1 and sample_data(physeqfinal.2)$age_at_stool_collection
## S = 391793, p-value = 0.4492
## alternative hypothesis: true rho is not equal to 0
```

```
## sample estimates:
##      rho
## 0.06542371
```

ACE Richness Spearman rank sum test (age)

```
cor.test(richness.table$ACE,
         sample_data(physeqfinal.2)$age_at_stool_collection, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: richness.table$ACE and sample_data(physeqfinal.2)$age_at_stool_collection
## S = 237101, p-value = 0.4932
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.06454271
```

InvSimpson Richness Spearman rank sum test (age)

```
cor.test(richness.table$InvSimpson,
         sample_data(physeqfinal.2)$age_at_stool_collection, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: richness.table$InvSimpson and sample_data(physeqfinal.2)$age_at_stool_collection
## S = 400239, p-value = 0.6007
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.04527809
```

Shannon Richness Spearman rank sum test (age)

```
cor.test(richness.table$Shannon,
         sample_data(physeqfinal.2)$age_at_stool_collection, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: richness.table$Shannon and sample_data(physeqfinal.2)$age_at_stool_collection
## S = 399416, p-value = 0.585
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.04723938
```

Distance-based multivariate analysis / beta diversity

Jaccard distance calculation (Binary Data)

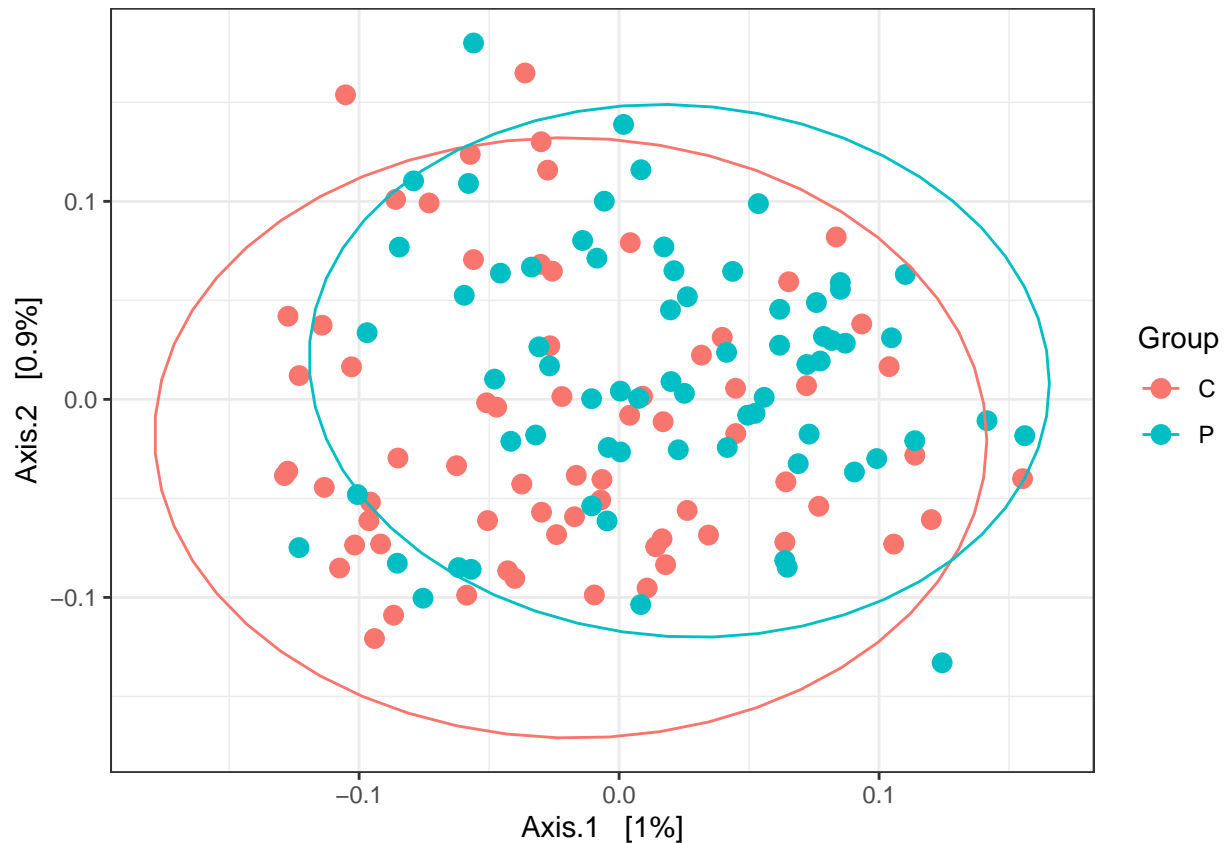
```
#physeqfinal.2.clr <- microbiome::transform(physeqfinal.2, transform = "clr", target = "OTU",  
#                                         shift = 0, scale = 1)  
  
#do not apply clr transformation to binary data  
physeqfinal.2.clr <- physeqfinal.2  
physeqfinal.2.clr.jaccard_dist <- vegdist(t(as.data.frame(as.matrix(otu_table(physeqfinal.2.clr)))),  
                                         method = "jaccard", binary = TRUE)  
  
sample_data(physeqfinal.2.clr)$Group <- factor(sample_data(physeqfinal.2.clr)$Group,  
                                              levels=c("C" , "P"),  
                                              ordered = FALSE)  
sample_data(physeqfinal.2.clr)$gender <- factor(sample_data(physeqfinal.2.clr)$gender,  
                                              levels=c("F" , "M"),  
                                              ordered = FALSE)
```

Run the statistics for group variable

```
adonis.Res.clr <- adonis2(physeqfinal.2.clr.jaccard_dist ~  
                        sample_data(physeqfinal.2.clr)$Group,  
                        perm = 10000,  
                        na.action = na.exclude,  
                        parallel = 10)  
  
adonis.Res.clr  
  
## Permutation test for adonis under reduced model  
## Terms added sequentially (first to last)  
## Permutation: free  
## Number of permutations: 10000  
##  
## adonis2(formula = physeqfinal.2.clr.jaccard_dist ~ sample_data(physeqfinal.2.clr)$Group, permutations = 10000)  
##              Df SumOfSqs      R2      F Pr(>F)  
## sample_data(physeqfinal.2.clr)$Group    1    0.514 0.00778 1.0507 2e-04 ***  
## Residual                               134   65.490 0.99222  
## Total                                   135   66.004 1.00000  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Principal Coordinates Analysis (PCoA) for Group

```
ord_clr <- ordinate(physeqfinal.2.clr, method = "PCoA",  
                   distance = "jaccard", binary = TRUE, autotransform = FALSE,  
                   trymax = 1000, maxit = 10000, sratmax = 0.999999,  
                   previous.best, parallel = 10)  
  
plot_ordination(physeqfinal.2.clr, ord_clr,  
                type = "Samples", color = "Group") + geom_point(size = 3) +  
  stat_ellipse(level = 0.95)
```



Run the statistics for gender variable

```
adonis.Res.clr <- adonis2(physeqfinal.2.clr.jaccard_dist ~
  sample_data(physeqfinal.2.clr)$gender,
  perm = 10000,
  na.action = na.exclude,
  parallel = 10)

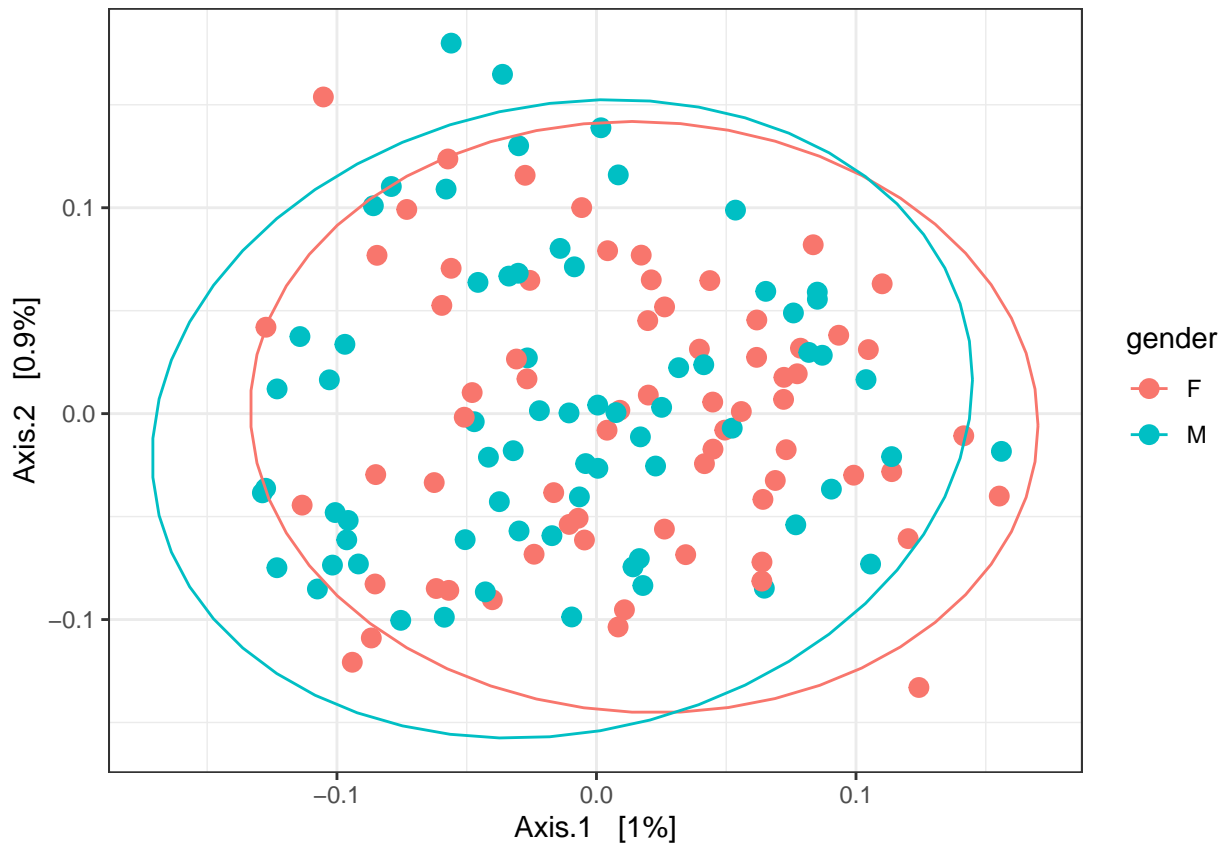
adonis.Res.clr
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## adonis2(formula = physeqfinal.2.clr.jaccard_dist ~ sample_data(physeqfinal.2.clr)$gender, permutation
##
##               Df SumOfSqs    R2    F Pr(>F)
## sample_data(physeqfinal.2.clr)$gender  1    0.494 0.00748 1.0101 0.184
## Residual                        134   65.510 0.99252
## Total                          135   66.004 1.00000
```

Principal Coordinates Analysis (PCoA) for Gender

```
ord_clr <- ordinate(physeqfinal.2.clr, method = "PCoA",
  distance = "jaccard", binary = TRUE, autotransform = FALSE,
  trymax = 1000, maxit = 10000, sratmax = 0.999999,
  previous.best, parallel = 10)
```

```
plot_ordination(physeqfinal.2.clr, ord_clr,
  type = "Samples", color = "gender") + geom_point(size = 3) +
  stat_ellipse(level = 0.95)
```



Run the statistics for BMI variable

```
adonis.Res.clr <- adonis2(physeqfinal.2.clr.jaccard_dist ~
  sample_data(physeqfinal.2.clr)$BMI,
  perm = 10000,
  na.action = na.exclude,
  parallel = 10)
```

```
adonis.Res.clr
```

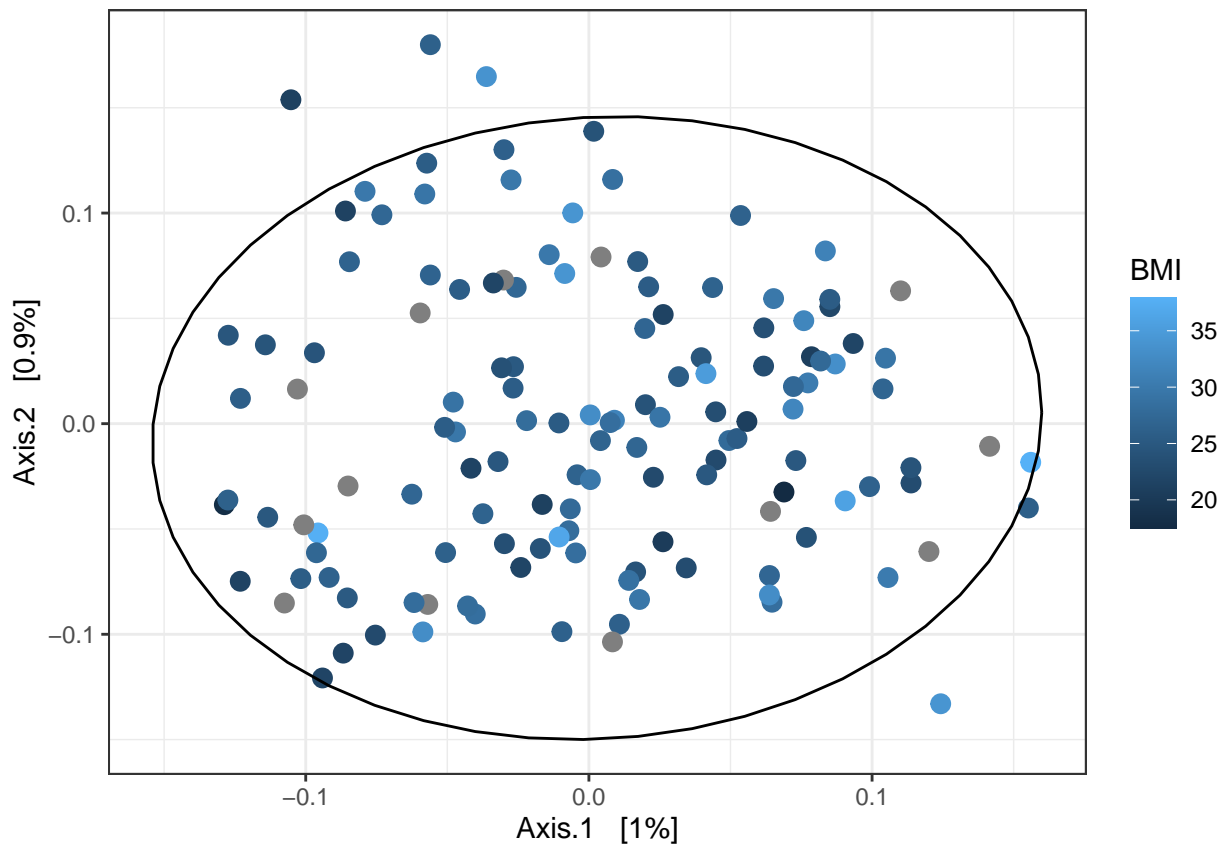
```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
```

```
## adonis2(formula = physeqfinal.2.clr.jaccard_dist ~ sample_data(physeqfinal.2.clr)$BMI, permutations = 10000)
##
```

	Df	SumOfSqs	R2	F	Pr(>F)
sample_data(physeqfinal.2.clr)\$BMI	1	0.488	0.00818	0.9981	0.5457
Residual	121	59.146	0.99182		
Total	122	59.634	1.00000		

Principal Coordinates Analysis (PCoA) for BMI

```
ord_clr <- ordinate(physeqfinal.2.clr, method = "PCoA",
  distance = "jaccard", binary = TRUE, autotransform = FALSE,
  trymax = 1000, maxit = 10000, sratmax = 0.999999,
  previous.best, parallel = 10)
plot_ordination(physeqfinal.2.clr, ord_clr,
  type = "Samples", color = "BMI") + geom_point(size = 3) +
  stat_ellipse(level = 0.95)
```



Run the statistics for Age variable

```
adonis.Res.clr <- adonis2(physeqfinal.2.clr.jaccard_dist ~
  sample_data(physeqfinal.2.clr)$age_at_stool_collection,
  perm = 10000,
  na.action = na.exclude,
  parallel = 10)
```

```
adonis.Res.clr
```

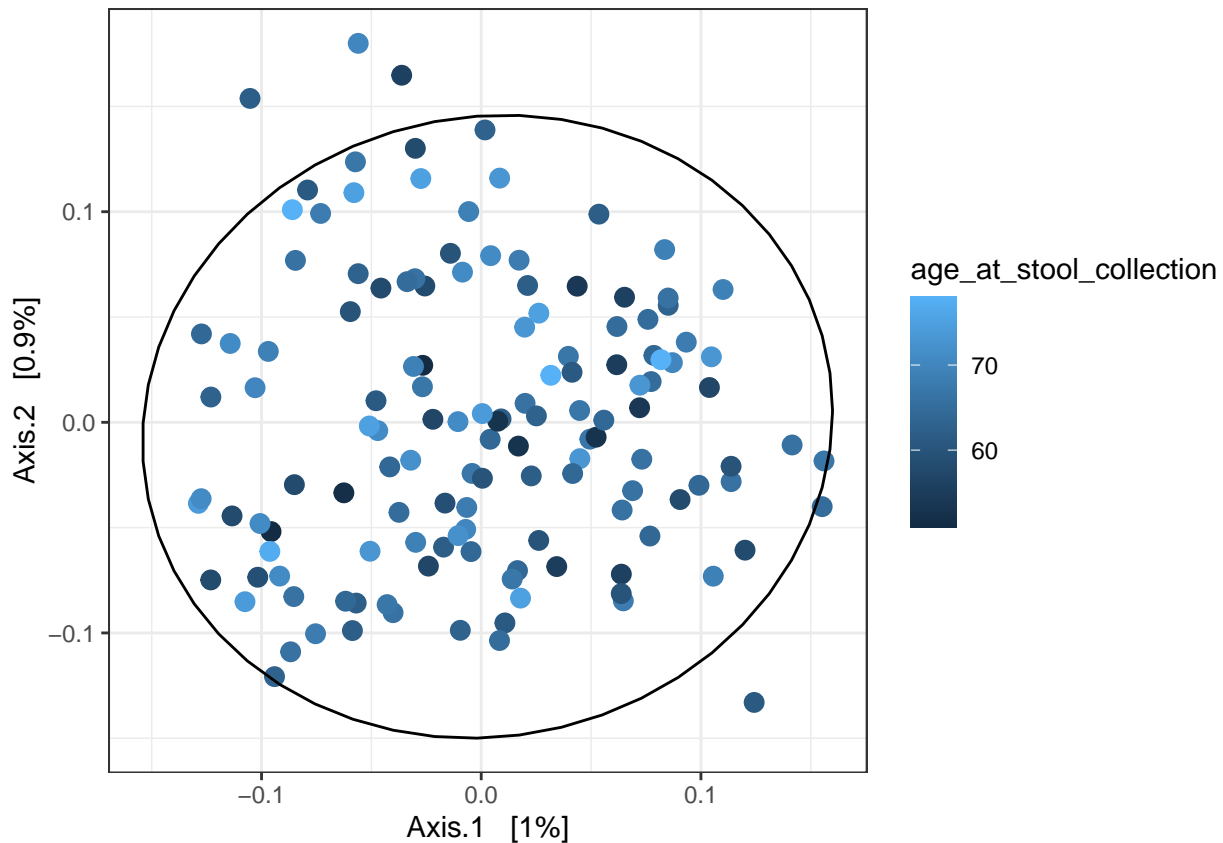
```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 10000
##
## adonis2(formula = physeqfinal.2.clr.jaccard_dist ~ sample_data(physeqfinal.2.clr)$age_at_stool_colle
##
```

	Df	SumOfSqs	R2

```
## sample_data(physeqfinal.2.clr)$age_at_stool_collection 1 0.489 0.0074
## Residual 134 65.515 0.9926
## Total 135 66.004 1.0000
## F Pr(>F)
## sample_data(physeqfinal.2.clr)$age_at_stool_collection 0.9992 0.5255
## Residual
## Total
```

Principal Coordinates Analysis (PCoA) for Age

```
ord_clr <- ordinate(physeqfinal.2.clr, method = "PCoA",
                    distance = "jaccard", binary = TRUE, autotransform = FALSE,
                    trymax = 1000, maxit = 10000, sratmax = 0.999999,
                    previous.best, parallel = 10)
plot_ordination(physeqfinal.2.clr, ord_clr,
                type = "Samples", color = "age_at_stool_collection") + geom_point(size = 3) +
  stat_ellipse(level = 0.95)
```



Session Info for Reproducibility

```
sessionInfo()
```

```
## R version 4.4.1 (2024-06-14)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 22.04.4 LTS
##
```

```

## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p0.3.20.so; LAPACK version 3.10.0
##
## locale:
## [1] LC_CTYPE=en_GB.UTF-8 LC_NUMERIC=C
## [3] LC_TIME=en_GB.UTF-8 LC_COLLATE=en_GB.UTF-8
## [5] LC_MONETARY=en_GB.UTF-8 LC_MESSAGES=en_GB.UTF-8
## [7] LC_PAPER=en_GB.UTF-8 LC_NAME=C
## [9] LC_ADDRESS=C LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Europe/Helsinki
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats4 stats graphics grDevices utils datasets methods
## [8] base
##
## other attached packages:
## [1] microbiome_1.26.0 fido_1.1.1
## [3] DESeq2_1.44.0 SummarizedExperiment_1.34.0
## [5] Biobase_2.64.0 MatrixGenerics_1.16.0
## [7] matrixStats_1.3.0 GenomicRanges_1.56.1
## [9] GenomeInfoDb_1.40.1 IRanges_2.38.1
## [11] S4Vectors_0.42.1 BiocGenerics_0.50.0
## [13] vegan_2.6-6.1 lattice_0.22-5
## [15] permute_0.9-7 phyloseq_1.48.0
## [17] dabestr_2023.9.12 coin_1.4-3
## [19] survival_3.7-0 ggridges_0.5.6
## [21] qqplotr_0.0.6 MatrixCorrelation_0.10.0
## [23] energy_1.7-11 corrr_0.4.4
## [25] GGally_2.2.1 patchwork_1.2.0
## [27] cowplot_1.1.3 gridExtra_2.3
## [29] kableExtra_1.4.0 magrittr_2.0.3
## [31] purrr_1.0.2 reshape2_1.4.4
## [33] tidylog_1.1.0 tidyr_1.3.1
## [35] dplyr_1.1.4 RColorBrewer_1.1-3
## [37] ggplot2_3.5.1 BiocParallel_1.38.0
## [39] knitr_1.48
##
## loaded via a namespace (and not attached):
## [1] libcoin_1.0-10 tensorA_0.36.2.1 rstudioapi_0.16.0
## [4] jsonlite_1.8.8 TH.data_1.1-2 modeltools_0.2-23
## [7] farver_2.1.2 rmarkdown_2.27 zlibbioc_1.50.0
## [10] vctrs_0.6.5 multtest_2.60.0 tinytex_0.52
## [13] htmltools_0.5.8.1 S4Arrays_1.4.1 progress_1.2.3
## [16] distributional_0.4.0 plotrix_3.8-4 tidybayes_3.0.6
## [19] Rhdf5lib_1.26.0 SparseArray_1.4.8 rhdf5_2.48.0
## [22] pracma_2.4.4 plyr_1.8.9 sandwich_3.1-0
## [25] zoo_1.8-12 igraph_2.0.3 lifecycle_1.0.4
## [28] iterators_1.0.14 pkgconfig_2.0.3 Matrix_1.6-5
## [31] R6_2.5.1 fastmap_1.2.0 GenomeInfoDbData_1.2.12
## [34] digest_0.6.36 colorspace_2.1-1 RSpectra_0.16-2

```


## [37] labeling_0.4.3	fansi_1.0.6	httr_1.4.7
## [40] abind_1.4-5	mgcv_1.9-1	compiler_4.4.1
## [43] withr_3.0.1	doParallel_1.0.17	gsl_2.1-8
## [46] backports_1.5.0	ggstats_0.6.0	highr_0.11
## [49] MASS_7.3-61	DelayedArray_0.30.1	biomformat_1.32.0
## [52] caTools_1.18.2	tools_4.4.1	ape_5.8
## [55] qqconf_1.3.2	glue_1.7.0	nlme_3.1-165
## [58] rhdf5filters_1.16.0	grid_4.4.1	Rtsne_0.17
## [61] checkmate_2.3.2	cluster_2.1.6	ade4_1.7-22
## [64] generics_0.1.3	gtable_0.3.5	data.table_1.15.4
## [67] hms_1.1.3	xml2_1.3.6	utf8_1.2.4
## [70] XVector_0.44.0	ggdist_3.3.2	foreach_1.5.2
## [73] pillar_1.9.0	stringr_1.5.1	posterior_1.6.0
## [76] robustbase_0.99-3	splines_4.4.1	tidyselect_1.2.1
## [79] locfit_1.5-9.10	Biostrings_2.72.1	arrayhelpers_1.1-0
## [82] svglite_2.1.3	xfun_0.46	DEoptimR_1.1-3
## [85] stringi_1.8.4	UCSC.utils_1.0.0	yaml_2.3.10
## [88] boot_1.3-30	evaluate_0.24.0	codetools_0.2-19
## [91] twosamples_2.0.1	tibble_3.2.1	cli_3.6.3
## [94] pbmcapply_1.5.1	systemfonts_1.1.0	munsell_0.5.1
## [97] Rcpp_1.0.13	coda_0.19-4.1	svUnit_1.0.6
## [100] parallel_4.4.1	prettyunits_1.2.0	opdisDownsampling_1.0.1
## [103] bitops_1.0-8	viridisLite_0.4.2	mvtnorm_1.2-5
## [106] scales_1.3.0	crayon_1.5.3	clisymbols_1.2.0
## [109] rlang_1.1.4	multcomp_1.4-26	