# Bee Diversity Analysis using MeanRarity

## Analyzing Bee Diversity in a BACI Study Design

This analysis uses the methods described in Roswell et al. (2021) to analyze bee diversity across multiple sites in a Before-After-Control-Impact (BACI) design.

### Setup

First, we'll load the necessary packages and read in our data.

```r
# Load required packages

library(MeanRarity)  # For calculating Hill diversity metrics
library(iNEXT)       # For coverage-based rarefaction
library(dplyr)       # For data manipulation
library(tidyr)       # For reshaping data
library(ggplot2)     # For visualization
library(lubridate)   # For date handling
library(lme4)        # For mixed-effects models
library(lmerTest)    # For p-values in mixed models
library(emmeans)     # For estimated marginal means

# Read in the data
bee_data <- read.csv("../data/processed/bee_02-18_data.csv")
bee_traits <- read.csv("../data/processed/bee_traits.csv", header = TRUE)
site_data <- read.csv("../data/processed/sites.csv", header = TRUE)
dates_to_drop <- read.csv("../data/processed/02_03_18_datestodrop.csv", header = TRUE)
```

### Data Cleaning

Clean up the data, standardizing site names and formatting dates.

```
'data.frame':	3020 obs. of  11 variables:
 $ barcode      : int  20020087 20020088 20020089 20020090 20020091 20020092 20020094 2002009
 $ genus_name   : chr  "Andrena" "Nomada" "Nomada" "Eucera" ...
 $ species      : chr  "sp. 6" "sp. 3" "sp. 10" "frater" ...
 $ site         : chr  "Goode" "Goode" "Goode" "Goode" ...
 $ start_date   : Date, format: "2002-03-26" "2002-03-26" ...
 $ type         : chr  "Male" "Female" "Female" "Male" ...
 $ det          : chr  "R. W. Brooks" "R. W. Brooks" "R. W. Brooks" "R. W. Brooks" ...
 $ year         : int  2002 2002 2002 2002 2002 2002 2002 2002 2002 2002 ...
 $ number       : int  1 1 1 1 1 1 1 1 1 1 ...
 $ technique    : chr  "netting" "netting" "netting" "netting" ...
 $ combined_name: chr  "Andrena sp. 6" "Nomada sp. 3" "Nomada sp. 10" "Eucera frater" ...
```

### Preparing Data for Diversity Analysis

To calculate Hill diversity metrics, we create a matrix of species abundances per site and year.

```r
#l warning = FALSE
#l echo = FALSE
# Create a wide-format abundance matrix for diversity analysis
# Each row is a site-year combination, columns are species
abundance_matrix <- bee_data_clean %>%
  group_by(site, year, combined_name) %>%
  # Sum abundance of each species at each site-year
  summarize(abundance = sum(number), .groups = "drop") %>%
  # Convert to wide format: species as columns
  pivot_wider(
    id_cols = c(site, year),
    names_from = combined_name,
    values_from = abundance,
    values_fill = 0  # Fill missing species with 0
  )

# Safely extract site_year_ids with base R
site_year_ids <- data.frame(
  site = abundance_matrix$site,
  year = abundance_matrix$year
)

# Safely create abundance_values matrix
# This avoids issues with special characters in species names
abundance_values <- as.matrix(abundance_matrix[, 3:ncol(abundance_matrix)])

# Check dimensions
cat("Number of site-year combinations:", nrow(site_year_ids), "\n")
```

```
Number of site-year combinations: 24
```

```
cat("Number of species columns:", ncol(abundance_values), "\n")
```

```
Number of species columns: 157
```

```
# Add metadata about sampling effort
sampling_effort <- bee_data_clean %>%
  group_by(site, year) %>%
  summarise(sampling_events = n_distinct(start_date))
```

```
`summarise()` has grouped output by 'site'. You can override using the
`.groups` argument.
```

```
# Add treatment information from site_data
site_metadata <- site_year_ids %>%
  left_join(sampling_effort, by = c("site", "year")) %>%
  left_join(site_data %>% dplyr::select(site, treatment), by = "site")

head(site_metadata)
```

```
               site year sampling_events treatment
1 Bouverie Preserve 2002               8    Impact
2 Bouverie Preserve 2003               7    Impact
3 Bouverie Preserve 2018               8    Impact
4             Goode 2002              11   Control
5             Goode 2003               8   Control
6             Goode 2018               9   Control
```

### Coverage-based Standardization

Calculates coverage. Coverage estimates what proportion of the total community (including undetected species) is represented in our sample. Our results are pretty good.

```r
# Calculate coverage for each site-year combination
site_coverage <- data.frame(site_year_ids,
                            coverage = apply(abundance_values, 1, function(x) {
                              # Count singletons (species with only 1 individual)
                              f1 <- sum(x == 1)
                              # Get total number of individuals
                              n <- sum(x)
                              # Calculate coverage using the formula from Chao and Jost (2012)
                              if (f1 == 0) {
                                return(1) # Perfect coverage if no singletons
                              } else {
                                return(1 - (f1/n) * ((n-1)/n))
                              }
                            }))

# Find the minimum coverage across all site-years (to use as standardization point)
min_coverage <- min(site_coverage$coverage)
cat("Minimum coverage across all site-years:", min_coverage, "\n")
```

```
Minimum coverage across all site-years: 0.7696
```

```r
# Display coverage by site and year
site_coverage %>%
  arrange(coverage) %>%
  knitr::kable(caption = "Sample coverage by site and year")
```

Table 1: Sample coverage by site and year

| site | year | coverage |
|:---|---:|---:|
| Quintessa | 2018 | 0.7696000 |
| Hudson | 2018 | 0.8310204 |
| Quintessa | 2002 | 0.8630401 |
| Bouverie Preserve | 2003 | 0.8750139 |
| Veterans | 2003 | 0.8889178 |
| Veterans | 2018 | 0.8955464 |
| Saintsbury | 2003 | 0.9043552 |

| site | year | coverage |
|---|---|---|
| Stags | 2003 | 0.9109000 |
| Bouverie Preserve | 2002 | 0.9121662 |
| Goode | 2018 | 0.9130481 |
| Saintsbury | 2018 | 0.9222320 |
| Goode | 2003 | 0.9222819 |
| Wappo | 2018 | 0.9240537 |
| Stags | 2018 | 0.9289966 |
| Hudson | 2003 | 0.9337374 |
| Goode | 2002 | 0.9381114 |
| Stags | 2002 | 0.9433975 |
| Quintessa | 2003 | 0.9554158 |
| Bouverie Preserve | 2018 | 0.9555612 |
| Hudson | 2002 | 0.9577470 |
| Veterans | 2002 | 0.9584780 |
| Wappo | 2003 | 0.9735688 |
| Saintsbury | 2002 | 0.9857483 |
| Wappo | 2002 | 0.9897810 |

## Calculating Hill Diversity Metrics

Just some notes on Hill Diversity

Hill diversity unifies different diversity metrics (richness, Shannon, Simpson) into a common framework. The parameter  (or q) determines how much weight is given to rare versus common species.

The MeanRarity package uses parameter q in its code implementation, while their conceptual framework in the paper uses . The relationship between them is  = 1-q, so:

Species richness:  =1 corresponds to q=0 Hill-Shannon:  =0 corresponds to q=1 Hill-Simpson:  =-1 corresponds to q=2

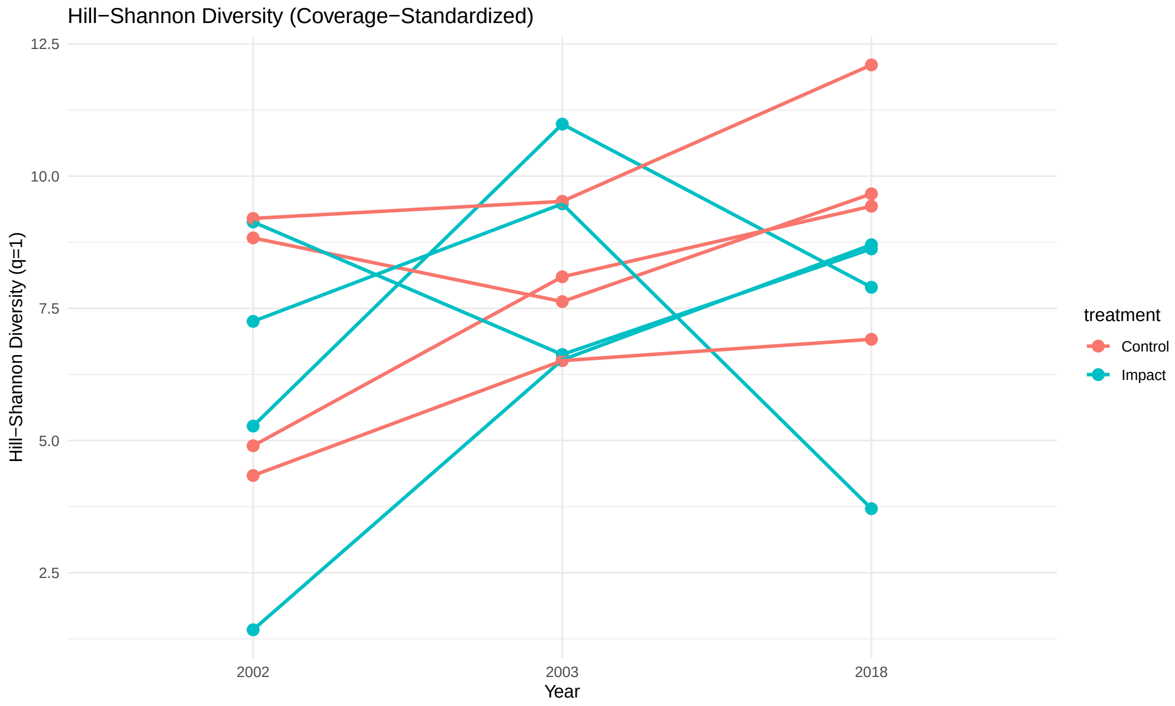
```
# Function to calculate Hill diversity metrics for each site-year
calculate_diversity_metrics <- function() {
  diversity_results <- data.frame()

  for (i in 1:nrow(site_year_ids)) {
    site_id <- site_year_ids$site[i]
    yr <- site_year_ids$year[i]

    # Extract abundance data for this site-year
    site_data_vec <- abundance_values[i, ]
    site_data_vec <- site_data_vec[site_data_vec > 0]  # Remove zeros

    # Calculate raw Hill diversity using the rarity function from MeanRarity
    richness_raw <- rarity(site_data_vec, q = 0)
    hill_shannon_raw <- rarity(site_data_vec, q = 1)
    hill_simpson_raw <- rarity(site_data_vec, q = 2)

    # Use iNEXT to estimate diversity at standardized coverage
    inext_result <- estimateD(site_data_vec, datatype = "abundance",
                             base = "coverage", level = min_coverage)

    # The issue is in extracting values from inext_result
    # Print the structure to understand how to access the values
    # print(str(inext_result))

    # Get the values in the correct way
    # iNEXT results are sorted by order (0, 1, 2)
    richness_std <- inext_result$qD[1]     # First row is q=0 (richness)
    hill_shannon_std <- inext_result$qD[2] # Second row is q=1 (Shannon)
    hill_simpson_std <- inext_result$qD[3] # Third row is q=2 (Simpson)

    # Combine with existing metadata
    result_row <- data.frame(
      site = site_id,
      year = yr,
      raw_richness = richness_raw,
      raw_hill_shannon = hill_shannon_raw,
      raw_hill_simpson = hill_simpson_raw,
      std_richness = richness_std,
      std_hill_shannon = hill_shannon_std,
      std_hill_simpson = hill_simpson_std,
      coverage = site_coverage$coverage[i]
    )

    # Append to the result data frame
    diversity_results <- rbind(diversity_results, result_row)
  }

  # Add metadata about treatment and sampling effort
  diversity_results <- diversity_results %>%
    left_join(site_metadata, by = c("site", "year"))
```

```r
  return(diversity_results)
}

# Calculate diversity metrics
diversity_results <- calculate_diversity_metrics()

# Create factors for time period and ensure proper ordering
diversity_results$period <- ifelse(diversity_results$year == "2018", "After", "Before")
diversity_results$period <- factor(diversity_results$period, levels = c("Before", "After"))
diversity_results$treatment <- factor(diversity_results$treatment, levels = c("Control", "Imp
diversity_results$year <- factor(diversity_results$year, levels = c("2002", "2003", "2018"))
```

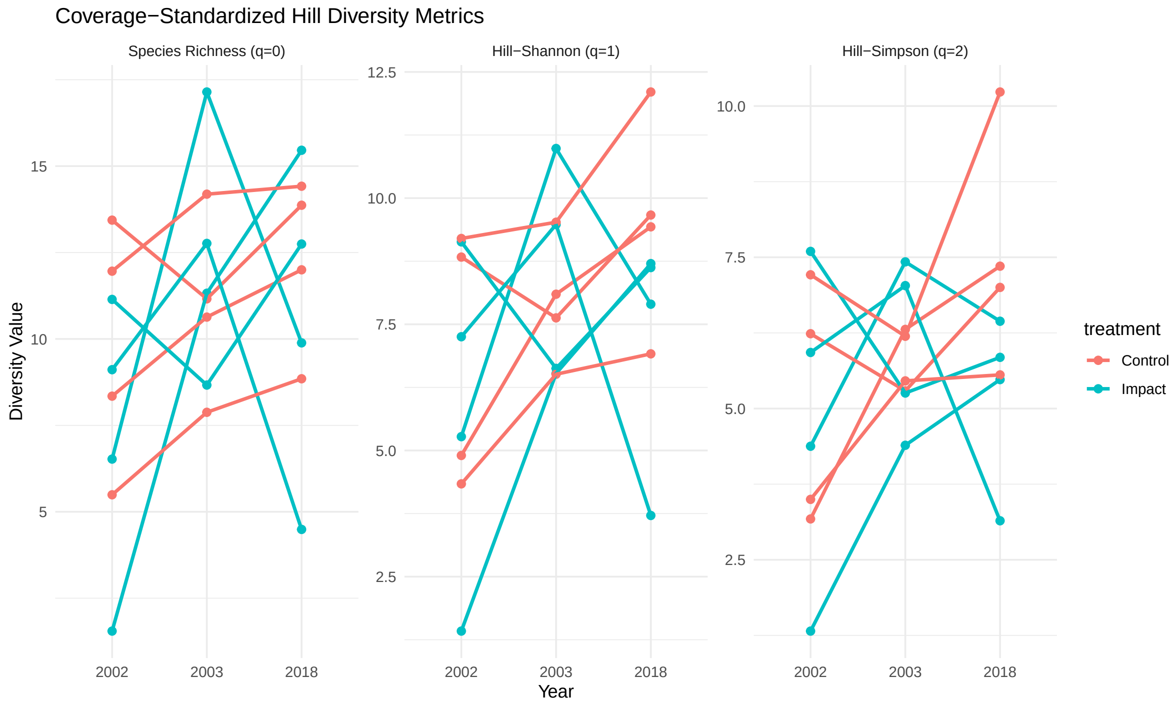
### Visualizing Diversity Metrics

Visualization of the diversity results to understand the patterns across sites, years, and treatments.

```r
# Visualize Hill-Shannon diversity (standardized by coverage)
ggplot(diversity_results, aes(x = year, y = std_hill_shannon, color = treatment, group = sit
  geom_point(size = 3) +
  geom_line(linewidth = 1) +
  labs(title = "Hill-Shannon Diversity (Coverage-Standardized)",
       x = "Year",
       y = "Hill-Shannon Diversity (q=1)") +
  theme_minimal()
```



```
# Compare all three diversity metrics
diversity_long <- diversity_results %>%
  pivot_longer(cols = c(std_richness, std_hill_shannon, std_hill_simpson),
               names_to = "metric",
               values_to = "value") %>%
  mutate(metric = factor(metric,
                       levels = c("std_richness", "std_hill_shannon", "std_hill_simpson"),
                       labels = c("Species Richness (q=0)",
                                 "Hill-Shannon (q=1)",
                                 "Hill-Simpson (q=2)")))

ggplot(diversity_long, aes(x = year, y = value, color = treatment, group = site)) +
  facet_wrap(~ metric, scales = "free_y") +
  geom_point(size = 2) +
  geom_line(linewidth = 1) +
  labs(title = "Coverage-Standardized Hill Diversity Metrics",
       x = "Year",
       y = "Diversity Value") +
  theme_minimal()
```

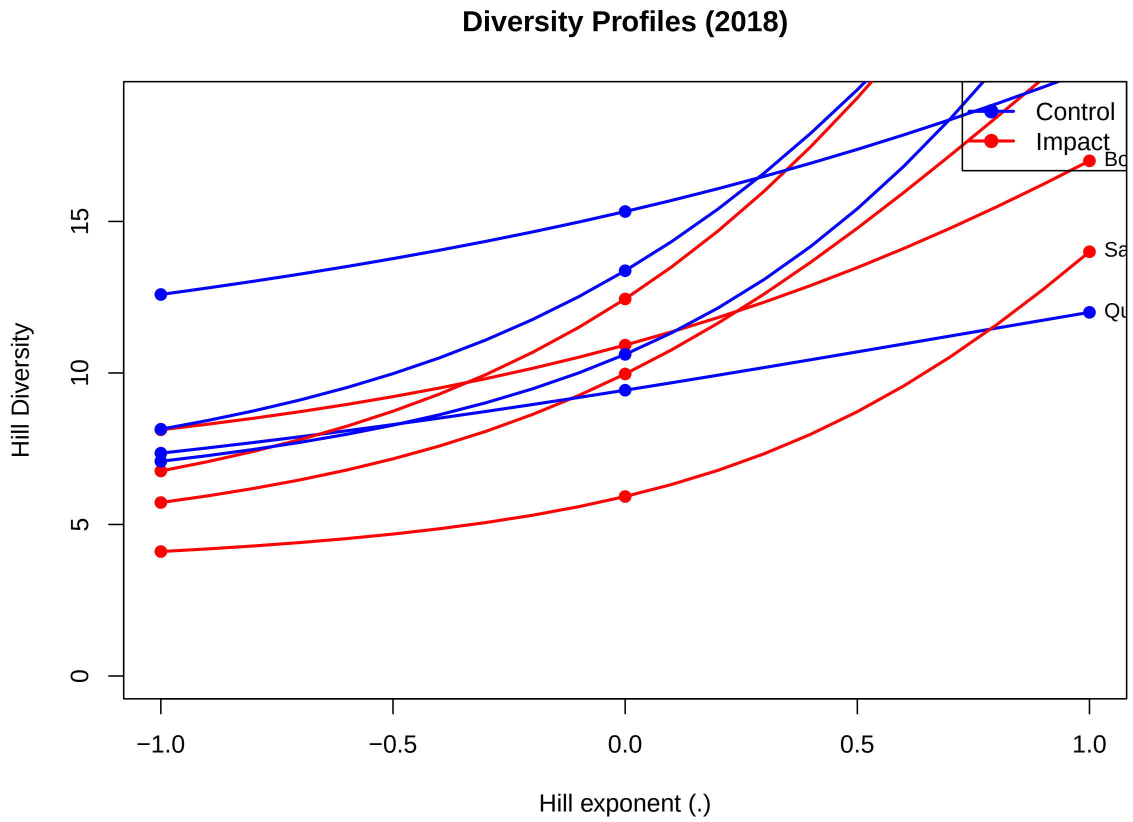


## Diversity Profiles

Diversity profiles show how diversity changes with the Hill exponent , giving a more complete picture of community structure. This is just done for 2018. Could do for all years.

```
# Create diversity profiles for each site in the final year (2018)
# Filter to just 2018 data
data_2018 <- abundance_matrix %>%
  filter(year == "2018")
site_ids_2018 <- data_2018$site

# Safely extract abundance data for 2018 sites
# Using the same approach we used above
abundance_2018 <- as.matrix(data_2018[, 3:ncol(data_2018)])

# Get treatment information
treatments_2018 <- site_metadata %>%
  filter(year == "2018") %>%
  dplyr::select(site, treatment)

# Set up the plot
```

```r
par(mfrow = c(1, 1))
plot(NULL, xlim = c(-1, 1), ylim = c(0, max(diversity_results$std_richness) * 1.1),
     xlab = "Hill exponent ( )", ylab = "Hill Diversity",
     main = "Diversity Profiles (2018)")

# Define colors for treatments
colors <- c("Control" = "blue", "Impact" = "red")

# Calculate and plot diversity profiles
for (i in 1:nrow(abundance_2018)) {
  site_id <- site_ids_2018[i]
  site_abund <- abundance_2018[i, ]
  site_abund <- site_abund[site_abund > 0]  # Remove zeros

  # Get treatment for this site
  site_treatment <- treatments_2018$treatment[treatments_2018$site == site_id]

  # Calculate diversity for a range of exponents
  exponents <- seq(-1, 1, by = 0.1)
  profile_values <- sapply(exponents, function(ell) rarity(site_abund, q = 1 - ell))

  # Plot the profile
  lines(exponents, profile_values, col = colors[site_treatment], lwd = 2)
  points(c(-1, 0, 1), profile_values[c(1, 11, 21)],
         col = colors[site_treatment], pch = 19)
  text(1, profile_values[21], site_id, pos = 4, cex = 0.8)
}

# Add a legend
legend("topright", legend = names(colors), col = colors, lwd = 2, pch = 19)
```



## Statistical Analysis

Linear mixed-effects models with a BACI design. Dependent variable is Hill-Shannon diversity but also anlyze richness and Simpson diversity. Repeated the model with and without taking into account sampling effort. AICs for models with and without taking sampling effort into account are virtually identical

```
# Model for Hill-Shannon diversity
model_hill_shannon <- lmer(std_hill_shannon ~ year * treatment + (1 | site),
                           data = diversity_results)
summary(model_hill_shannon)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_hill_shannon ~ year * treatment + (1 | site)
   Data: diversity_results
```

```
REML criterion at convergence: 90.2

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-1.7334 -0.6492  0.1059  0.7308  1.3771 

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 0.8421   0.9176  
 Residual             4.8132   2.1939  
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error     df t value Pr(>|t|)    
(Intercept)                 6.818      1.189 17.236   5.734 2.31e-05 ***
year2003                    1.121      1.551 12.000   0.723    0.484    
year2018                    2.710      1.551 12.000   1.747    0.106    
treatmentImpact            -1.047      1.682 17.236  -0.623    0.542    
year2003:treatmentImpact    1.511      2.194 12.000   0.689    0.504    
year2018:treatmentImpact   -1.247      2.194 12.000  -0.568    0.580    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI y2003:
year2003    -0.652                            
year2018    -0.652  0.500                     
trtmntImpct -0.707  0.461  0.461              
yr2003:trtI  0.461 -0.707 -0.354 -0.652       
yr2018:trtI  0.461 -0.354 -0.707 -0.652  0.500
```

```r
# Model for Hill-Shannon diversity including sampling events
model_hill_shannon_with_sampling <- lmer(std_hill_shannon ~ year * treatment + sampling_even
                                       data = diversity_results)
summary(model_hill_shannon_with_sampling)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_hill_shannon ~ year * treatment + sampling_events + (1 |  
    site)
   Data: diversity_results
```

```
REML criterion at convergence: 90.1

Scaled residuals:
    Min      1Q  Median      3Q     Max 
-1.5857 -0.5336  0.1877  0.5641  1.3678 

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 1.435    1.198   
 Residual             4.666    2.160   
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error      df t value Pr(>|t|)  
(Intercept)                4.8545     3.8724 14.6372   1.254   0.2296  
year2003                   1.4312     1.6337 12.2661   0.876   0.3978  
year2018                   3.1237     1.7118 13.2722   1.825   0.0906 .
treatmentImpact           -0.9957     1.7493 14.7115  -0.569   0.5778  
sampling_events            0.2067     0.3863 14.6287   0.535   0.6007  
year2003:treatmentImpact   1.6144     2.1688 10.7831   0.744   0.4726  
year2018:treatmentImpact  -1.8150     2.4073 13.1567  -0.754   0.4641  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI smpln_ y2003:
year2003    -0.521                                   
year2018    -0.604  0.577                            
trtmntImpct -0.278  0.428  0.415                     
smplng_vnts -0.948  0.355  0.451  0.055              
yr2003:trtI  0.054 -0.627 -0.274 -0.610  0.089       
yr2018:trtI  0.543 -0.453 -0.765 -0.578 -0.441  0.408
```

```r
# Compare models
anova(model_hill_shannon, model_hill_shannon_with_sampling)
```

```
refitting model(s) with ML (instead of REML)

Data: diversity_results
Models:
model_hill_shannon: std_hill_shannon ~ year * treatment + (1 | site)
```

```
model_hill_shannon_with_sampling: std_hill_shannon ~ year * treatment + sampling_events + (1
                                 npar    AIC    BIC  logLik deviance Chisq Df
model_hill_shannon                  8 118.29 127.72 -51.146   102.29
model_hill_shannon_with_sampling    9 120.02 130.63 -51.012   102.02 0.268  1
                                 Pr(>Chisq)
model_hill_shannon
model_hill_shannon_with_sampling     0.6047
```

```
# Extract p-values
p_values <- summary(model_hill_shannon)$coefficients[, "Pr(>|t|)"]
print(p_values)
```

```
             (Intercept)                year2003                year2018
            2.307004e-05            4.837059e-01            1.061402e-01
         treatmentImpact year2003:treatmentImpact year2018:treatmentImpact
            5.415425e-01            5.040872e-01            5.803520e-01
```

```
# Calculate estimated marginal means
emm_hill_shannon <- emmeans(model_hill_shannon, ~ year * treatment)
pairs(emm_hill_shannon)
```

```
 contrast                            estimate   SE   df t.ratio p.value
 year2002 Control - year2003 Control   -1.121 1.55 12.0  -0.723  0.9752
 year2002 Control - year2018 Control   -2.710 1.55 12.0  -1.747  0.5295
 year2002 Control - year2002 Impact     1.047 1.68 17.2   0.623  0.9877
 year2002 Control - year2003 Impact    -1.585 1.68 17.2  -0.942  0.9296
 year2002 Control - year2018 Impact    -0.416 1.68 17.2  -0.248  0.9998
 year2003 Control - year2018 Control   -1.589 1.55 12.0  -1.024  0.9009
 year2003 Control - year2002 Impact     2.168 1.68 17.2   1.290  0.7866
 year2003 Control - year2003 Impact    -0.464 1.68 17.2  -0.276  0.9997
 year2003 Control - year2018 Impact     0.705 1.68 17.2   0.419  0.9980
 year2018 Control - year2002 Impact     3.758 1.68 17.2   2.235  0.2722
 year2018 Control - year2003 Impact     1.125 1.68 17.2   0.669  0.9831
 year2018 Control - year2018 Impact     2.294 1.68 17.2   1.364  0.7466
 year2002 Impact - year2003 Impact     -2.632 1.55 12.0  -1.697  0.5580
 year2002 Impact - year2018 Impact     -1.464 1.55 12.0  -0.943  0.9271
 year2003 Impact - year2018 Impact      1.169 1.55 12.0   0.753  0.9705

Degrees-of-freedom method: kenward-roger
P value adjustment: tukey method for comparing a family of 6 estimates
```

```
# Calculate estimated marginal means accounting for sampling events
# Using emmeans for a specific level of sampling_events (mean value)
mean_sampling <- mean(diversity_results$sampling_events)
emm_hill_shannon_sampling <- emmeans(model_hill_shannon_with_sampling,
                                   ~ year * treatment,
                                   at = list(sampling_events = mean_sampling))
pairs(emm_hill_shannon_sampling)
```

```
 contrast                            estimate   SE   df t.ratio p.value
 year2002 Control - year2003 Control   -1.431 1.66 12.7  -0.861  0.9494
 year2002 Control - year2018 Control   -3.124 1.76 13.7  -1.774  0.5114
 year2002 Control - year2002 Impact     0.996 1.75 15.0   0.569  0.9917
 year2002 Control - year2003 Impact    -2.050 2.01 15.0  -1.022  0.9034
 year2002 Control - year2018 Impact    -0.313 1.76 15.0  -0.178  1.0000
 year2003 Control - year2018 Control   -1.692 1.54 11.4  -1.097  0.8732
 year2003 Control - year2002 Impact     2.427 1.83 15.0   1.326  0.7672
 year2003 Control - year2003 Impact    -0.619 1.78 15.0  -0.348  0.9992
 year2003 Control - year2018 Impact     1.118 1.95 15.0   0.572  0.9915
 year2018 Control - year2002 Impact     4.119 1.91 15.0   2.159  0.3109
 year2018 Control - year2003 Impact     1.074 1.75 15.0   0.614  0.9883
 year2018 Control - year2018 Impact     2.811 2.06 15.0   1.363  0.7470
 year2002 Impact - year2003 Impact     -3.046 1.76 13.7  -1.729  0.5367
 year2002 Impact - year2018 Impact     -1.309 1.56 11.6  -0.838  0.9541
 year2003 Impact - year2018 Impact      1.737 1.95 15.0   0.893  0.9425

Degrees-of-freedom method: kenward-roger
P value adjustment: tukey method for comparing a family of 6 estimates
```

```
# Also analyze richness and Simpson diversity for comparison
model_richness <- lmer(std_richness ~ year * treatment + (1 | site),
                      data = diversity_results)
summary(model_richness)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_richness ~ year * treatment + (1 | site)
   Data: diversity_results

REML criterion at convergence: 105.5

Scaled residuals:
     Min       1Q   Median       3Q      Max 
-1.70784 -0.50146 -0.02167  0.58058  1.36244 

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept)  0.2659  0.5156  
 Residual             12.6736  3.5600  
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error     df t value Pr(>|t|)    
(Intercept)                 9.809      1.799 17.985   5.454 3.53e-05 ***
year2003                    1.156      2.517 12.000   0.459    0.654    
year2018                    2.475      2.517 12.000   0.983    0.345    
treatmentImpact            -2.727      2.544 17.985  -1.072    0.298    
year2003:treatmentImpact    4.236      3.560 12.000   1.190    0.257    
year2018:treatmentImpact    1.088      3.560 12.000   0.306    0.765    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI y2003:
year2003    -0.700                            
year2018    -0.700  0.500                     
trtmntImpct -0.707  0.495  0.495              
yr2003:trtI  0.495 -0.707 -0.354 -0.700       
yr2018:trtI  0.495 -0.354 -0.707 -0.700  0.500
```

```
# Update richness model to include sampling events
model_richness_with_sampling <- lmer(std_richness ~ year * treatment + sampling_events + (1
                                   data = diversity_results)
summary(model_richness_with_sampling)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_richness ~ year * treatment + sampling_events + (1 | site)
   Data: diversity_results

REML criterion at convergence: 104.8

Scaled residuals: 
     Min       1Q   Median       3Q      Max 
```

```
-1.69154 -0.37122  0.01469  0.51107  1.40249

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept)  1.374   1.172
 Residual             12.426   3.525
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error      df t value Pr(>|t|)
(Intercept)                7.9015     5.7339 11.9698   1.378    0.193
year2003                   1.4571     2.6356 11.6763   0.553    0.591
year2018                   2.8767     2.7417 12.8212   1.049    0.313
treatmentImpact           -2.6766     2.6307 16.2499  -1.017    0.324
sampling_events            0.2008     0.5710 11.4175   0.352    0.732
year2003:treatmentImpact   4.3367     3.5365 10.0903   1.226    0.248
year2018:treatmentImpact   0.5362     3.8590 12.6869   0.139    0.892

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI smpln_ y2003:
year2003    -0.513
year2018    -0.592  0.565
trtmntImpct -0.280  0.466  0.453
smplng_vnts -0.946  0.325  0.417  0.054
yr2003:trtI  0.077 -0.640 -0.287 -0.663  0.081
yr2018:trtI  0.525 -0.438 -0.757 -0.634 -0.407  0.422
```

```
# Compare richness models
anova(model_richness, model_richness_with_sampling)
```

```
refitting model(s) with ML (instead of REML)
```

```
Data: diversity_results
Models:
model_richness: std_richness ~ year * treatment + (1 | site)
model_richness_with_sampling: std_richness ~ year * treatment + sampling_events + (1 | site)
                             npar    AIC    BIC  logLik deviance  Chisq Df
model_richness                  8 138.64 148.07 -61.321   122.64
model_richness_with_sampling    9 140.58 151.18 -61.290   122.58 0.0616  1
                             Pr(>Chisq)
model_richness
model_richness_with_sampling      0.804
```

```
model_simpson <- lmer(std_hill_simpson ~ year * treatment + (1 | site),
                     data = diversity_results)
summary(model_simpson)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_hill_simpson ~ year * treatment + (1 | site)
   Data: diversity_results

REML criterion at convergence: 79.9

Scaled residuals: 
     Min       1Q   Median       3Q      Max 
-1.73870 -0.59927  0.06513  0.63334  1.50122 

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 0.619    0.7867  
 Residual             2.612    1.6162  
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error      df t value Pr(>|t|)    
(Intercept)                5.0304     0.8987 16.7691   5.597 3.37e-05 ***
year2003                   0.7827     1.1428 12.0000   0.685   0.5064    
year2018                   2.5056     1.1428 12.0000   2.193   0.0488 *  
treatmentImpact           -0.2248     1.2710 16.7691  -0.177   0.8618    
year2003:treatmentImpact   0.4380     1.6162 12.0000   0.271   0.7910    
year2018:treatmentImpact  -2.0831     1.6162 12.0000  -1.289   0.2217    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI y2003:
year2003    -0.636                            
year2018    -0.636  0.500                     
trtmntImpct -0.707  0.450  0.450              
yr2003:trtI  0.450 -0.707 -0.354 -0.636       
yr2018:trtI  0.450 -0.354 -0.707 -0.636  0.500
```

```r
# Update Simpson model to include sampling events
model_simpson_with_sampling <- lmer(std_hill_simpson ~ year * treatment + sampling_events +
                                  data = diversity_results)
summary(model_simpson_with_sampling)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: std_hill_simpson ~ year * treatment + sampling_events + (1 |
    site)
   Data: diversity_results

REML criterion at convergence: 80.4

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.5794 -0.5174  0.0958  0.6229  1.4835

Random effects:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 0.8641   0.9296
 Residual             2.6060   1.6143
Number of obs: 24, groups:  site, 8

Fixed effects:
                         Estimate Std. Error      df t value Pr(>|t|)
(Intercept)                3.8388     2.9201 15.0585   1.315    0.208
year2003                   0.9708     1.2223 12.6771   0.794    0.442
year2018                   2.7565     1.2816 13.6110   2.151    0.050 *
treatmentImpact           -0.1934     1.3192 14.7667  -0.147    0.885
sampling_events            0.1254     0.2913 15.0909   0.431    0.673
year2003:treatmentImpact   0.5007     1.6209 11.2709   0.309    0.763
year2018:treatmentImpact  -2.4281     1.8022 13.5045  -1.347    0.200
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) yr2003 yr2018 trtmnI smpln_ y2003:
year2003    -0.521
year2018    -0.605  0.578
trtmntImpct -0.278  0.424  0.410
smplng_vnts -0.948  0.358  0.455  0.055
yr2003:trtI  0.052 -0.626 -0.273 -0.604  0.090
```

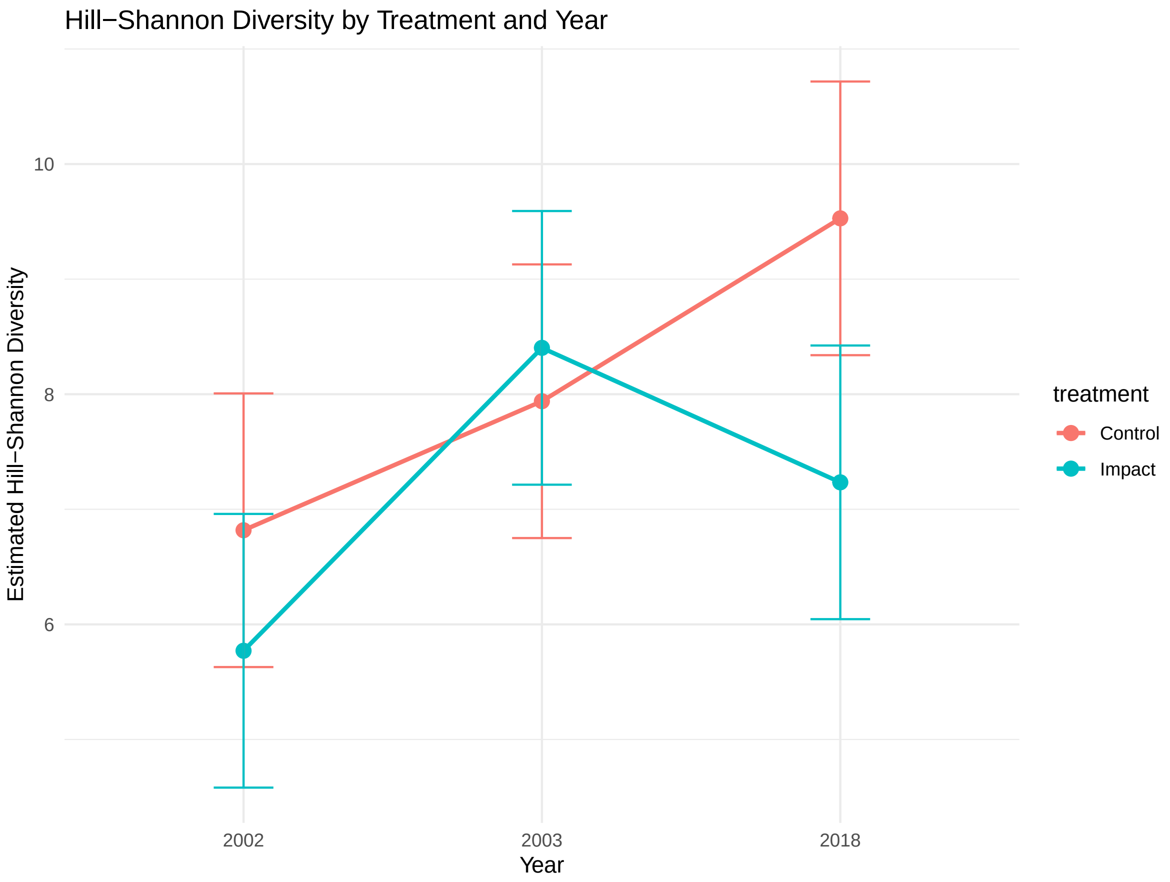
```
yr2018:trtI  0.545 -0.455 -0.766 -0.573 -0.445  0.406
```

```
# Compare Simpson models
anova(model_simpson, model_simpson_with_sampling)
```

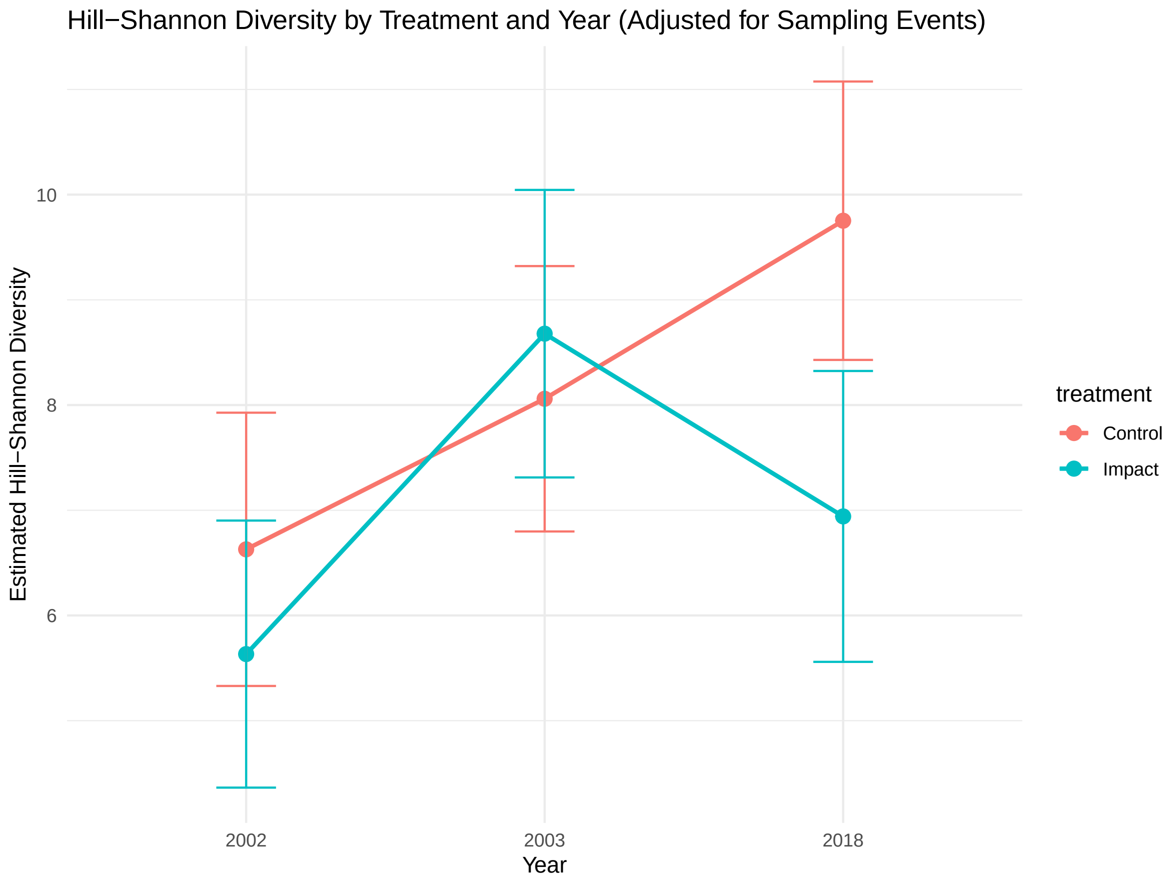
```
refitting model(s) with ML (instead of REML)
```

```
Data: diversity_results
Models:
model_simpson: std_hill_simpson ~ year * treatment + (1 | site)
model_simpson_with_sampling: std_hill_simpson ~ year * treatment + sampling_events + (1 | si
                            npar    AIC    BIC  logLik deviance  Chisq Df
model_simpson                  8 104.54 113.97 -44.272   88.543
model_simpson_with_sampling    9 106.34 116.94 -44.170   88.340 0.2036  1
                            Pr(>Chisq)
model_simpson
model_simpson_with_sampling     0.6518
```

```
# Plot the estimated means with error bars
emm_data <- as.data.frame(emm_hill_shannon)
ggplot(emm_data, aes(x = year, y = emmean, color = treatment, group = treatment)) +
  geom_point(size = 3) +
  geom_line(linewidth = 1) +
  geom_errorbar(aes(ymin = emmean - SE, ymax = emmean + SE), width = 0.2) +
  labs(title = "Hill-Shannon Diversity by Treatment and Year",
       x = "Year",
       y = "Estimated Hill-Shannon Diversity") +
  theme_minimal()
```



```
# Plot the estimated means with error bars, adjusted for sampling events
emm_data_sampling <- as.data.frame(emm_hill_shannon_sampling)
ggplot(emm_data_sampling, aes(x = year, y = emmean, color = treatment, group = treatment)) +
  geom_point(size = 3) +
  geom_line(linewidth = 1) +
  geom_errorbar(aes(ymin = emmean - SE, ymax = emmean + SE), width = 0.2) +
  labs(title = "Hill-Shannon Diversity by Treatment and Year (Adjusted for Sampling Events)"
       x = "Year",
       y = "Estimated Hill-Shannon Diversity") +
  theme_minimal()
```



## Analysis of Raw vs. Coverage-standardized Results

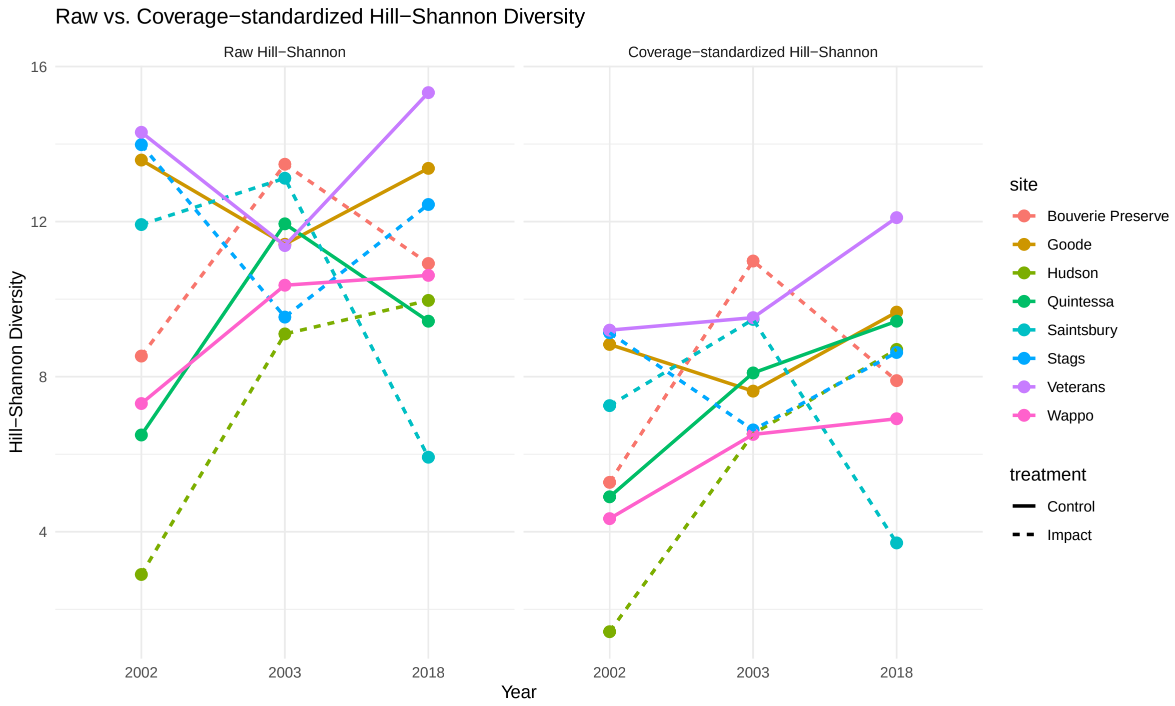
Compares the raw diversity metrics with the coverage-standardized metrics to see how standardization affects our conclusions.

Also does some plotting of effect of sampling_events.

The shape of the curves are similar although estimated species of the Hill Shannon estimate is lower.

```
# Combine raw and standardized metrics for comparison
diversity_compare <- diversity_results %>%
  dplyr::select(site, year, treatment, period,
         raw_hill_shannon, std_hill_shannon,
         sampling_events, coverage) %>%
  pivot_longer(
    cols = c(raw_hill_shannon, std_hill_shannon),
    names_to = "metric_type",
    values_to = "hill_shannon"
  ) %>%
  mutate(metric_type = factor(metric_type,
                            levels = c("raw_hill_shannon", "std_hill_shannon"),
                            labels = c("Raw Hill-Shannon", "Coverage-standardized Hill-Shann

# Plot the comparison
ggplot(diversity_compare, aes(x = year, y = hill_shannon, linetype = treatment, color = site
  facet_wrap(~ metric_type) +
  geom_point(size = 3) +
  geom_line(size = 1) +
    labs(title = "Raw vs. Coverage-standardized Hill-Shannon Diversity",
       x = "Year",
       y = "Hill-Shannon Diversity") +
  theme_minimal()
```

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
i Please use `linewidth` instead.
```



```
# Check correlation between sampling events and raw diversity
cor_sampling_raw <- cor(diversity_results$sampling_events, diversity_results$raw_hill_shannon
cat("Correlation between sampling events and raw Hill-Shannon diversity:", cor_sampling_raw,
```

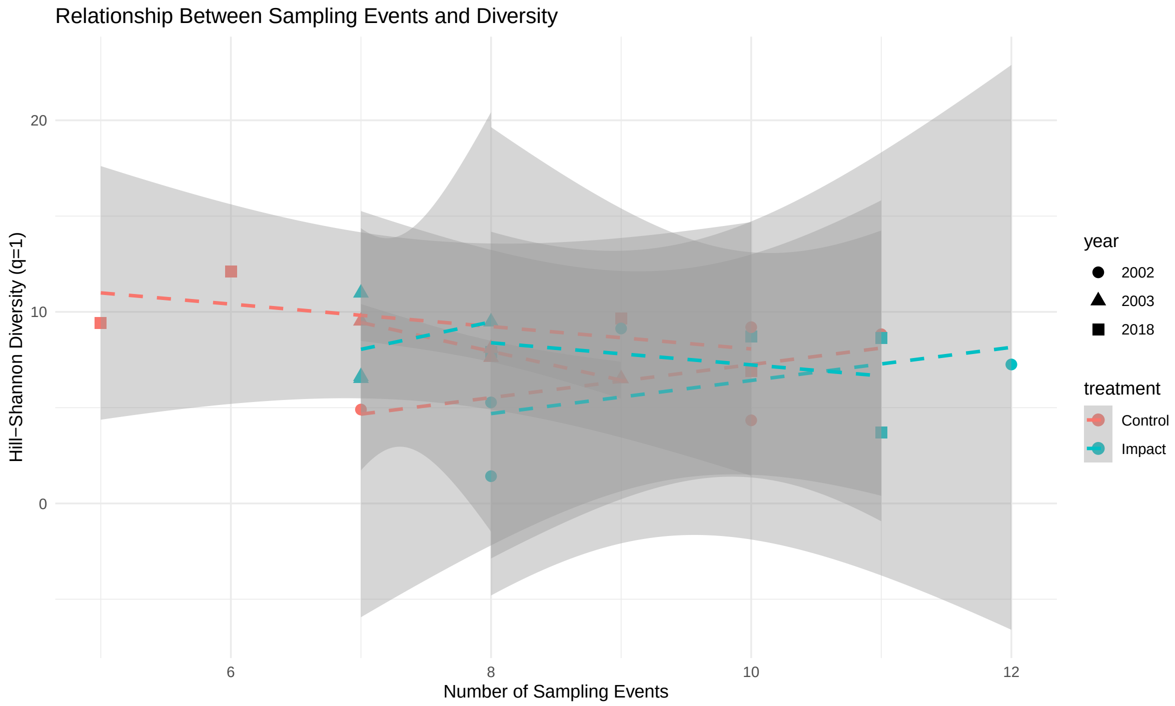
```
Correlation between sampling events and raw Hill-Shannon diversity: 0.05416637
```

```
# Check correlation between sampling events and standardized diversity
cor_sampling_std <- cor(diversity_results$sampling_events, diversity_results$std_hill_shannon
cat("Correlation between sampling events and standardized Hill-Shannon diversity:", cor_sampl
```

```
Correlation between sampling events and standardized Hill-Shannon diversity: -0.2178351
```

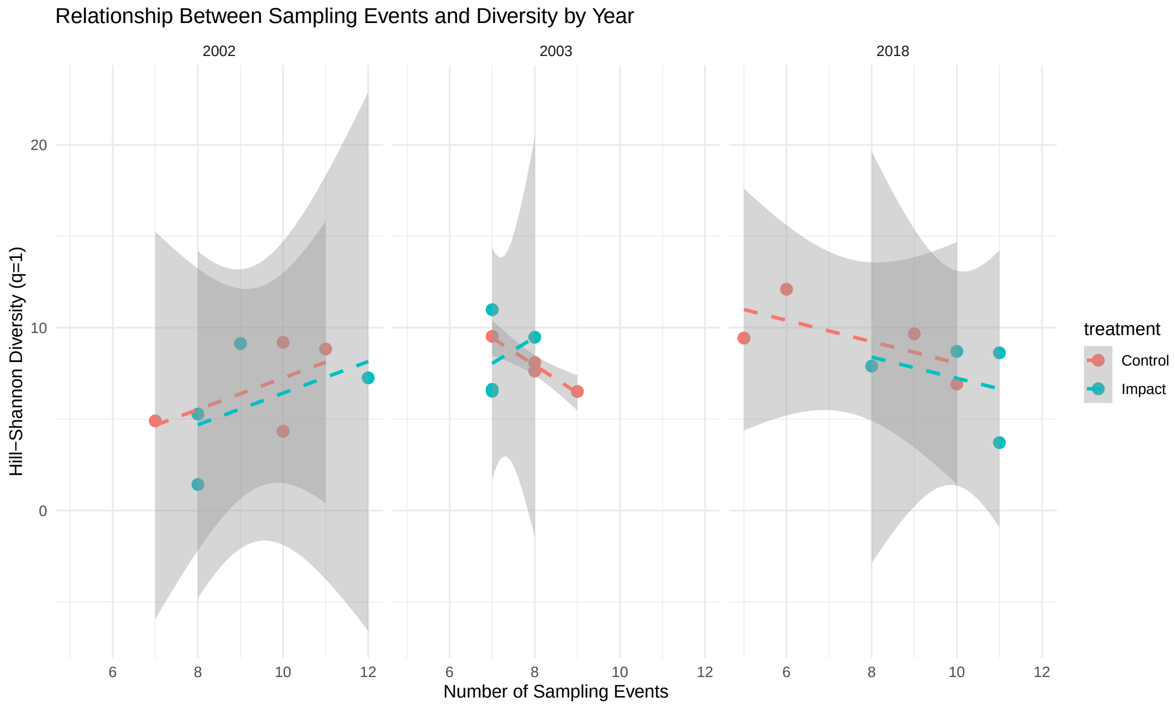
```
# Visualize diversity by sampling events
ggplot(diversity_results, aes(x = sampling_events, y = std_hill_shannon, color = treatment, s
  geom_point(size = 3) +
  geom_smooth(method = "lm", se = TRUE, linetype = "dashed") +
  labs(title = "Relationship Between Sampling Events and Diversity",
       x = "Number of Sampling Events",
       y = "Hill-Shannon Diversity (q=1)") +
  theme_minimal()
```

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

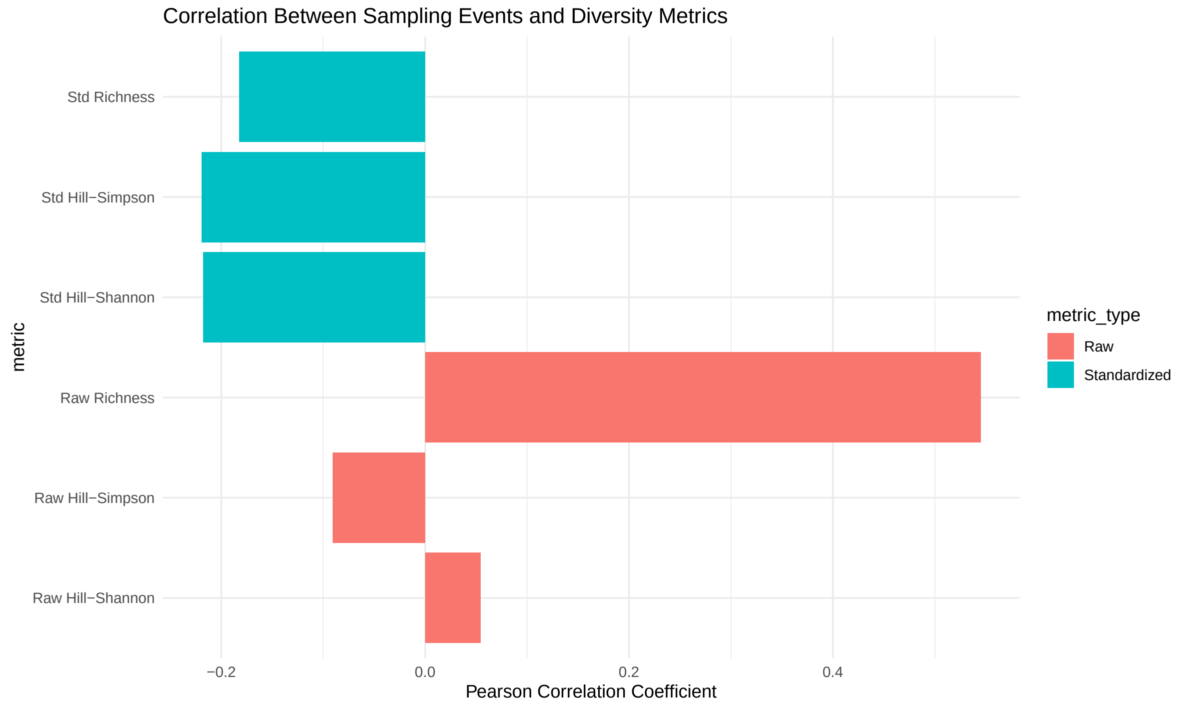


```r
# Add facets to see the relationship by year
ggplot(diversity_results, aes(x = sampling_events, y = std_hill_shannon, color = treatment))
  geom_point(size = 3) +
  geom_smooth(method = "lm", se = TRUE, linetype = "dashed") +
  facet_wrap(~ year) +
  labs(title = "Relationship Between Sampling Events and Diversity by Year",
       x = "Number of Sampling Events",
       y = "Hill-Shannon Diversity (q=1)") +
  theme_minimal()
```

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

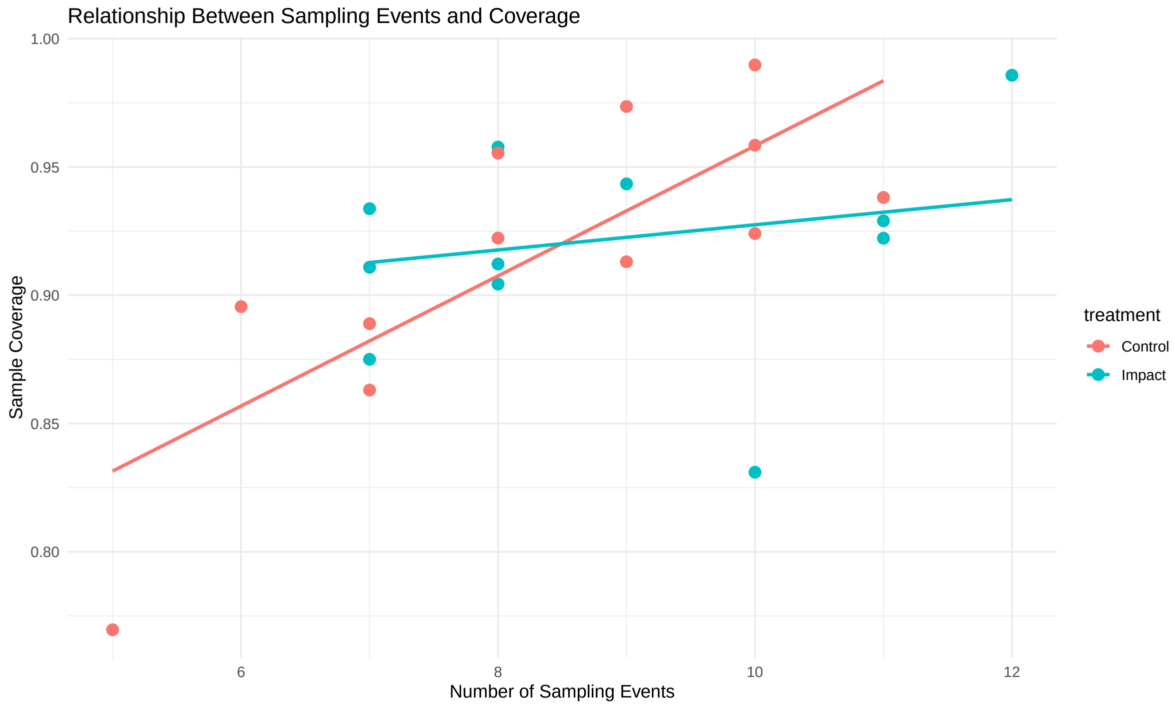


```
# Compare correlations across all diversity metrics
cor_data <- data.frame(
  metric = c("Raw Richness", "Raw Hill-Shannon", "Raw Hill-Simpson",
             "Std Richness", "Std Hill-Shannon", "Std Hill-Simpson"),
  correlation = c(
    cor(diversity_results$sampling_events, diversity_results$raw_richness),
    cor(diversity_results$sampling_events, diversity_results$raw_hill_shannon),
    cor(diversity_results$sampling_events, diversity_results$raw_hill_simpson),
    cor(diversity_results$sampling_events, diversity_results$std_richness),
    cor(diversity_results$sampling_events, diversity_results$std_hill_shannon),
    cor(diversity_results$sampling_events, diversity_results$std_hill_simpson)
  ),
  metric_type = rep(c("Raw", "Standardized"), each = 3)
)

# Plot correlations
ggplot(cor_data, aes(x = metric, y = correlation, fill = metric_type)) +
  geom_col() +
  coord_flip() +
  labs(title = "Correlation Between Sampling Events and Diversity Metrics",
       y = "Pearson Correlation Coefficient") +
  theme_minimal()
```



```
# Visualize relationship between sampling events and coverage
ggplot(diversity_results, aes(x = sampling_events, y = coverage, color = treatment)) +
  geom_point(size = 3) +
  geom_smooth(method = "lm", se = FALSE) +
  labs(title = "Relationship Between Sampling Events and Coverage",
       x = "Number of Sampling Events",
       y = "Sample Coverage") +
  theme_minimal()
```

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



**Notes and resultss.**

**Hill Diversity Metrics**: The three Hill diversity metrics (richness, Shannon, and Simpson) provide different perspectives on community diversity:

```
-   Species richness ( =1, q=0) gives equal weight to all species and is most sensitive to ra
-   Hill-Shannon diversity ( =0, q=1) provides a balanced view of diversity
-   Hill-Simpson diversity ( =-1, q=2) emphasizes common species
```

All Hill diversity metrics are expressed in "effective number of species," making them more intuitive to interpret than traditional indices.

1. **Coverage Standardization**: SThe minimum coverage across our samples was 0.769, which means we're comparing equally complete samples from each community.

2. **BACI Analysis**:

   - None of the models are significant
   - We have no interaction terms that are significant
   - Using the Simpson diversity which emphasizes common diversity, there is a difference between 2002 and 2018

3. **Sampling Effort Analysis**: Our analysis of sampling effort shows:

- The relationship between the number of sampling events and both raw and coverage-standardized diversity metrics
- How well coverage standardization accounts for differences in sampling effort
- Whether accounting for sampling events in our statistical models changes our conclusions about treatment effects
-

## References

Roswell, M., Dushoff, J., & Winfree, R. (2021). A conceptual guide to measuring species diversity. Oikos, 130(3), 321-338.