

Diversity Analyses

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Comparing diversity between Pollard walks and Malaise traps.

```
library("vegan")
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.5-2
```

```
library("ggplot2")
```

```
library("tidyr")
```

```
source(file = "bioscan-functions.R")
```

```
bioscan <- CompleteBioscan()
```

Perform calculation for Shannon's diversity index, H .

```
# Identify those columns with species data
```

```
species.cols <- c(5:33)
```

```
# Create data frame with only individual counts for each species.
```

```
species.counts <- bioscan[, species.cols]
```

```
# Calculate Shannon's diversity for each site
```

```
shannons.h <- vegan::diversity(x = species.counts, index = "shannon")
```

```
# Create a data frame we'll use for plotting
```

```
diversity.long <- data.frame(Site.Number = bioscan$Site.Number,  
                             Collection.Method = bioscan$Collection.Method,  
                             Diversity = shannons.h)
```

```
# And another for t-tests of diversity
```

```
diversity.wide <- diversity.long %>% spread(key = Collection.Method, value = Diversity)
```

Run a paired t-test to see if the collection methods differ

```
diversity.t <- t.test(x = diversity.wide$Malaise,  
                     y = diversity.wide$`Pollard Walk`,  
                     paired = TRUE)
```

```
# Have to do some formatting if p-value is really low, otherwise it just gets
```

```
# reported as "0"
```

```
p.value <- "< 0.001"
```

```
if (diversity.t$p.value > 0.001) {
```

```
  p.value <- paste0("=", round(diversity.t$p.value, 3))
```

```
}
```

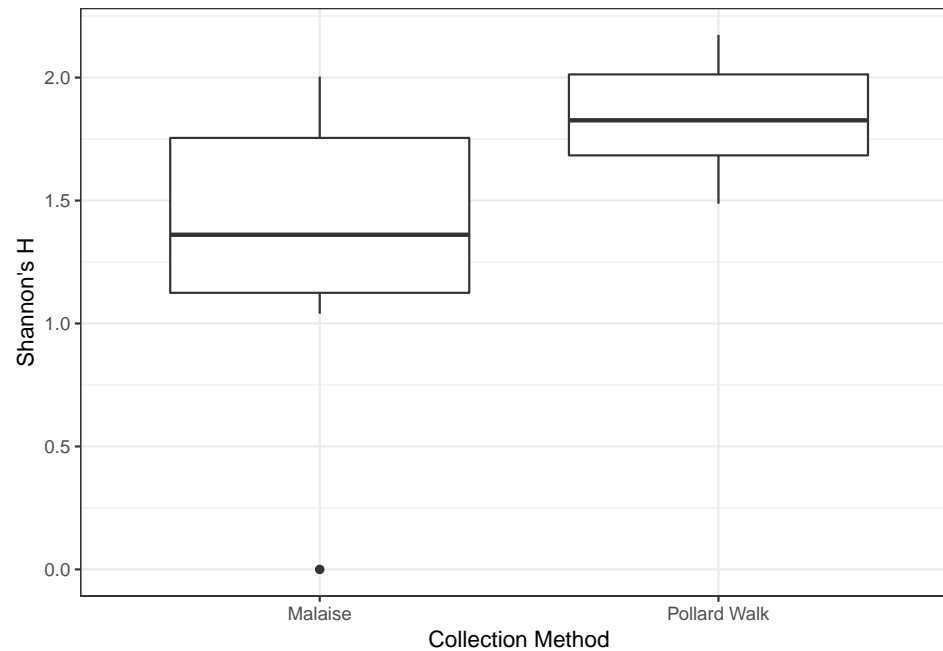
The t-test shows a significant difference between the two collection methods ($t = -3.307$, $p = 0.005$, 95%CI of the mean difference between Malaise traps and Pollard walks [-0.745, -0.161]). On average, $H_{\text{Pollard walks}}$ was 0.453 than $H_{\text{Malaise traps}}$.

We can compare the two types visually with a boxplot:

```

diversity.boxplot <- ggplot(data = diversity.long, mapping = aes(x = Collection.Method, y = Diversity))
  geom_boxplot() +
  xlab(label = "Collection Method") +
  ylab(label = "Shannon's H") +
  theme_bw()
print(diversity.boxplot)

```



```

ggsave(filename = "output/diversity-pairwise-boxplot.png", plot = diversity.boxplot)

```

```

## Saving 6.5 x 4.5 in image

```