Diversity Analyses

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Comparing diversity between Pollard walks and Malaise traps.

```r
library("vegan")
library("dplyr")
source(file = "bioscan-functions.R")
bioscan <- CompleteBioscan()
```

Perform calculation for Shannon's diversity index, *H*.

```r
# 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

```r
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 Maliase traps and Pollard walks [-0.745, -0.161]). On average, *H~Pollard walks~* was 0.453 than *H~Malaise traps~*.

We can compare the two types visually with a boxplot:

```r
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(richness.boxplot)
```
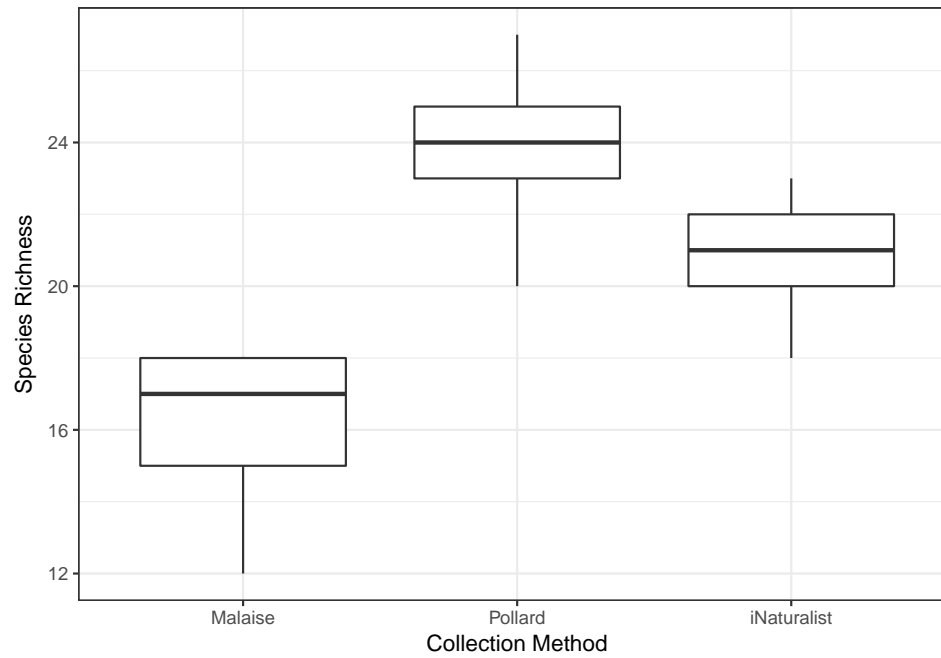


```
ggsave(filename = "output/figure-diversity-pairwise.png", plot = diversity.boxplot)
```

```
## Saving 6.5 x 4.5 in image
```