DSproj

```
df <- read.csv("../preprocessed data/understoreydata2020.csv", header = TRUE)
#df <- read_excel("../datasets/Ecothining_understoreydata2020.xlsx", col_names = TRUE)
head(df)
```

```
##   Year_monitoring Date_monitoring Observer1 Observer2 Plot_number
## 1               6      2019-10-22        PH                    1
## 2               6      2019-10-22        PH                    1
## 3               6      2019-10-22        PH                    1
## 4               6      2019-10-22        PH                    1
## 5               6      2019-10-22        PH                    1
## 6               6      2019-10-22        PH                    1
##   Plot_treatment Plot_percent_burgan Quadrat_number Quadrat_fenced
## 1            Gap                  NA              1          False
## 2            Gap                  NA              1          False
## 3            Gap                  NA              1          False
## 4            Gap                  NA              1          False
## 5            Gap                  NA              1          False
## 6            Gap                  NA              1          False
##   Quadrat_Can_Cov Quadrat_gap_or_no Record_ID T002_Flora_Species_name Score
## 1                                      10733          Stellaria spp.   0.5
## 2                                      10730       Rytidosperma spp.   1.0
## 3                                      10731       Rytidosperma spp.   0.5
## 4                                      10732            Senecio spp   0.5
## 5                                      10734        Wahlenbergia spp   0.5
## 6                                      10735            Senecio spp   0.5
##   Percentage_range
## 1        Trace <1%
## 2             1-5%
## 3        Trace <1%
## 4        Trace <1%
## 5        Trace <1%
## 6        Trace <1%
```

```
unique(df$Plot_number)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12
```

```
df$Group <- 0

for (i in 1:nrow(df)) {
  if (df[i,5] %in% c(1, 8, 10, 12)) {
    df[i,]$Group <- "t1"
  } else if (df[i,5] %in% c(3,5,7,9)) {
    df[i,]$Group <- "t2"
  } else if (df[i,5] %in% c(2,4,6,11)){
    df[i,]$Group <- "control"
  }
}
```

```
#df$Group
```

```
t1 <- df[df$Plot_number %in% c(1,8,10,12),]
t2 <- df[df$Plot_number %in% c(3,5,7,9),]
control <- df[df$Plot_number %in% c(2,4,6,11),]

grp_col <- rep(c("t1", "t2", "control"), each=length(unique(t1$Quadrat_number)))
quadrat_col <- rep(c(1:32), 3)
summary_df <- data.frame(Grp = grp_col, Quadrat_num = quadrat_col)
summary_df$Fenced <- FALSE
summary_df$Species_num <- 0

# T1
t1_summary <- t1[!duplicated(t1[,c("Year_monitoring","Plot_number","Quadrat_number")]),]
t1_summary <- t1_summary[c("Year_monitoring","Plot_number","Quadrat_number", "Quadrat_fenced")]
t1_summary$Species_num <- 0
for (i in 1:nrow(t1_summary)) {
  t1_summary[i,]$Species_num <- nrow(subset(t1,Quadrat_number==t1_summary[i,]$Quadrat_number &
                                            Plot_number==t1_summary[i,]$Plot_number &
                                            Year_monitoring==t1_summary[i,]$Year_monitoring))
}

# T2
t2_summary <- t2[!duplicated(t2[,c("Year_monitoring","Plot_number","Quadrat_number")]),]
t2_summary <- t2_summary[c("Year_monitoring","Plot_number","Quadrat_number", "Quadrat_fenced")]
t2_summary$Species_num <- 0
for (i in 1:nrow(t2_summary)) {
  t2_summary[i,]$Species_num <- nrow(subset(t2,Quadrat_number==t2_summary[i,]$Quadrat_number &
                                            Plot_number==t2_summary[i,]$Plot_number &
                                            Year_monitoring==t2_summary[i,]$Year_monitoring))
}

# Control
ctl_summary <- control[!duplicated(control[,c("Year_monitoring","Plot_number","Quadrat_number")]),]
ctl_summary <- ctl_summary[c("Year_monitoring","Plot_number","Quadrat_number", "Quadrat_fenced")]
ctl_summary$Species_num <- 0
for (i in 1:nrow(ctl_summary)) {
  ctl_summary[i,]$Species_num <- nrow(subset(control,Quadrat_number==ctl_summary[i,]$Quadrat_number &
                                            Plot_number==ctl_summary[i,]$Plot_number &
                                            Year_monitoring==ctl_summary[i,]$Year_monitoring))
}
```

Calculate Shannon Diversity Index

Per group per plot

```
calc_sdi <- function(df) {
  plots <- unique(df$Plot_number)
  res <- data.frame(PlotNum=plots, Year=rep(c(0,3,6), each=length(plots)), SDI=rep(c(0,0,0), each=lengt
  for (p in plots) {
    for (i in c(0, 3, 6)) {
      total_count <- nrow(subset(df, Year_monitoring==i, Plot_number==p))
      yr_subset <- df[df$Year_monitoring==i & df$Plot_number==p,]
      yr_unique_species <- yr_subset[!duplicated(yr_subset[,c("T002_Flora_Species_name")]),]
```

```
      sdi <- 0
      for (j in 1:nrow(yr_unique_species)) {
        species_count <- nrow(subset(yr_subset, T002_Flora_Species_name==yr_unique_species[j,]$T002_Flo
        species_prop <- species_count / total_count
        sdi <- sdi + (species_prop * log(species_prop))
      }
      res$SDI[res$Year==i & res$PlotNum==p] <- -1 * sdi
    }
  }
  print(res)
}

t1_sdi <- calc_sdi(t1)
```

```
##    PlotNum Year       SDI
## 1        1    0 0.9222610
## 2        8    0 1.1223121
## 3       10    0 1.2254141
## 4       12    0 1.5145278
## 5        1    3 0.9005132
## 6        8    3 0.9367936
## 7       10    3 1.4155919
## 8       12    3 1.7763121
## 9        1    6 1.1897271
## 10       8    6 0.9565097
## 11      10    6 1.3682500
## 12      12    6 1.4588044
```

```
t2_sdi <- calc_sdi(t2)
```

```
##    PlotNum Year       SDI
## 1        3    0 0.8918756
## 2        5    0 1.0092410
## 3        7    0 1.3319095
## 4        9    0 1.6086427
## 5        3    3       NaN
## 6        5    3 0.9224845
## 7        7    3 1.7211333
## 8        9    3 1.9708567
## 9        3    6 0.9401303
## 10       5    6 1.0981401
## 11       7    6 1.4521953
## 12       9    6 1.3814491
```

```
ctl_sdi <- calc_sdi(control)
```

```
##    PlotNum Year       SDI
## 1        2    0 0.9099518
## 2        4    0 1.3636064
## 3        6    0 0.9440040
## 4       11    0 1.6739795
## 5        2    3 1.0058809
## 6        4    3 1.7288514
## 7        6    3 0.7609158
## 8       11    3 1.4033217
```

```
## 9        2    6 0.9921600
## 10       4    6 1.3317823
## 11       6    6 0.9707314
## 12      11    6 1.7422611
```

Hypothesis

There will be a greater increase in understorey species diversity in T1 as compared to T2, and in T2 compared to Control plots (diversity is a measure of both abundance and richness)