

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$Plot_number)
  res <- data.frame(PlotNum=plots, Year=rep(c(0,3,6), each=length(plots)), SDI=rep(c(0,0,0), each=length(plots)))
  for (p in plots) {
    for (i in c(0, 3, 6)) {
      total_count <- nrow(subset(df, Year_monitoring==i & Plot_number==p))
      yr_subset <- df[df$Year_monitoring==i & df$Plot_number==p,]
      yr_unique_species <- yr_subset[!duplicated(yr_subset[,c("T002_Flora_Species_name")]),]
    }
  }
  res$SDI <- total_count * log2(total_count) - sum(yr_unique_species * log2(yr_unique_species))
  return(res)
}

```

```

sdi <- 0
for (j in 1:nrow(yr_unique_species)) {
  species_count <- nrow(subset(yr_subset, T002_Flora_Species_name==yr_unique_species[j,]$T002_Flor
  species_prop <- species_count / total_count
  sdi <- sdi + (species_prop * log(species_prop))
}
res$SDI[res$Year==i & res$PlotNum==p] <- -1 * sdi
}
}
print(res)
}

```

```
t1_sdi <- calc_sdi(t1)
```

```
##      PlotNum Year      SDI
## 1         1    0 3.396190
## 2         8    0 3.570599
## 3        10    0 3.248776
## 4        12    0 3.480528
## 5         1    3 3.565659
## 6         8    3 3.622884
## 7        10    3 3.637501
## 8        12    3 3.841378
## 9         1    6 3.716489
## 10        8    6 3.592581
## 11       10    6 3.496979
## 12       12    6 3.636152

```

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

```
##      PlotNum Year      SDI
## 1         3    0 3.484266
## 2         5    0 3.604049
## 3         7    0 3.416730
## 4         9    0 3.513846
## 5         3    3      NaN
## 6         5    3 3.430041
## 7         7    3 3.540569
## 8         9    3 3.669570
## 9         3    6 3.522283
## 10        5    6 3.612561
## 11        7    6 3.469017
## 12        9    6 3.474665

```

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

```
##      PlotNum Year      SDI
## 1         2    0 3.519377
## 2         4    0 3.451738
## 3         6    0 3.561226
## 4        11    0 3.649595
## 5         2    3 3.647595
## 6         4    3 3.576774
## 7         6    3 3.561440
## 8        11    3 3.563004

```

## 9	2	6	3.688135
## 10	4	6	3.524383
## 11	6	6	3.758788
## 12	11	6	3.799040

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)