

Act 4 Field

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```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.5
```

```
## -- Attaching packages ----- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3      v purrr 0.3.4
## v tibble 3.1.0       v dplyr 1.0.5
## v tidyr 1.1.3        v stringr 1.4.0
## v readr 1.4.0        v forcats 0.5.1
```

```
## Warning: package 'ggplot2' was built under R version 4.0.5
```

```
## Warning: package 'tidyr' was built under R version 4.0.5
```

```
## Warning: package 'readr' was built under R version 4.0.5
```

```
## Warning: package 'forcats' was built under R version 4.0.5
```

```
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
```

```
event <- read_csv("D:/kaya/Documents/2 SY 2021-2022/1st Semester 2021-2022/Bio 115 - Field Biology/Labo
```

```
##
## -- Column specification -----
## cols(
##   .default = col_character(),
##   year = col_double(),
##   month = col_double(),
##   day = col_logical(),
##   decimalLongitude = col_double(),
##   decimalLatitude = col_double(),
##   coordinateUncertaintyInMeters = col_double()
## )
## i Use 'spec()' for the full column specifications.
```

```
##  
## -- Column specification -----  
## cols(  
##   eventID = col_character(),  
##   measurementID = col_character(),  
##   measurementType = col_character(),  
##   measurementValue = col_character(),  
##   measurementUnit = col_character(),  
##   measurementDeterminedDate = col_character(),  
##   measurementDeterminedBy = col_character(),  
##   measurementMethod = col_character(),  
##   measurementRemarks = col_character()  
## )
```

```
##  
## -- Column specification -----  
## cols(  
##   .default = col_character(),  
##   decimalLatitude = col_double(),  
##   decimalLongitude = col_double(),  
##   coordinateUncertaintyInMeters = col_double(),  
##   individualCount = col_double(),  
##   organismQuantity = col_double()  
## )  
## i Use 'spec()' for the full column specifications.
```

2

```

coverttotal<-data.frame(transect, Totalcover)

fish <- newoccurrence %>%
  filter(str_detect(occurrenceID, "fish"))

fishfinal <- fish %>%
  select(occurrenceID, organismQuantityType, scientificName, individualCount) %>%
  separate(col = occurrenceID, into = c("Location", "Transect", "Date", "Benthic", "Species"), sep = ":")
  select(Transect, Species, organismQuantityType, individualCount)

```

```

## Warning: Expected 5 pieces. Additional pieces discarded in 331 rows [1, 2, 3, 4,
## 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].

```

```

fishcount <- fishfinal %>%
  spread(key = Transect, value = individualCount) %>%
  mutate_if(is.integer, as.numeric)

fishtotal <- data.frame(colSums(Filter(is.numeric,fishcount), na.rm = TRUE))
transects <- c("T01", "T02", "T03", "T04", "T05", "T06", "T07", "T08")
fishabundance <- c(286, 280, 488, 445, 248, 72, 36, 241)
totalfish <- data.frame(transects, fishabundance)

coralfish <- data.frame(totalfish, coverttotal)

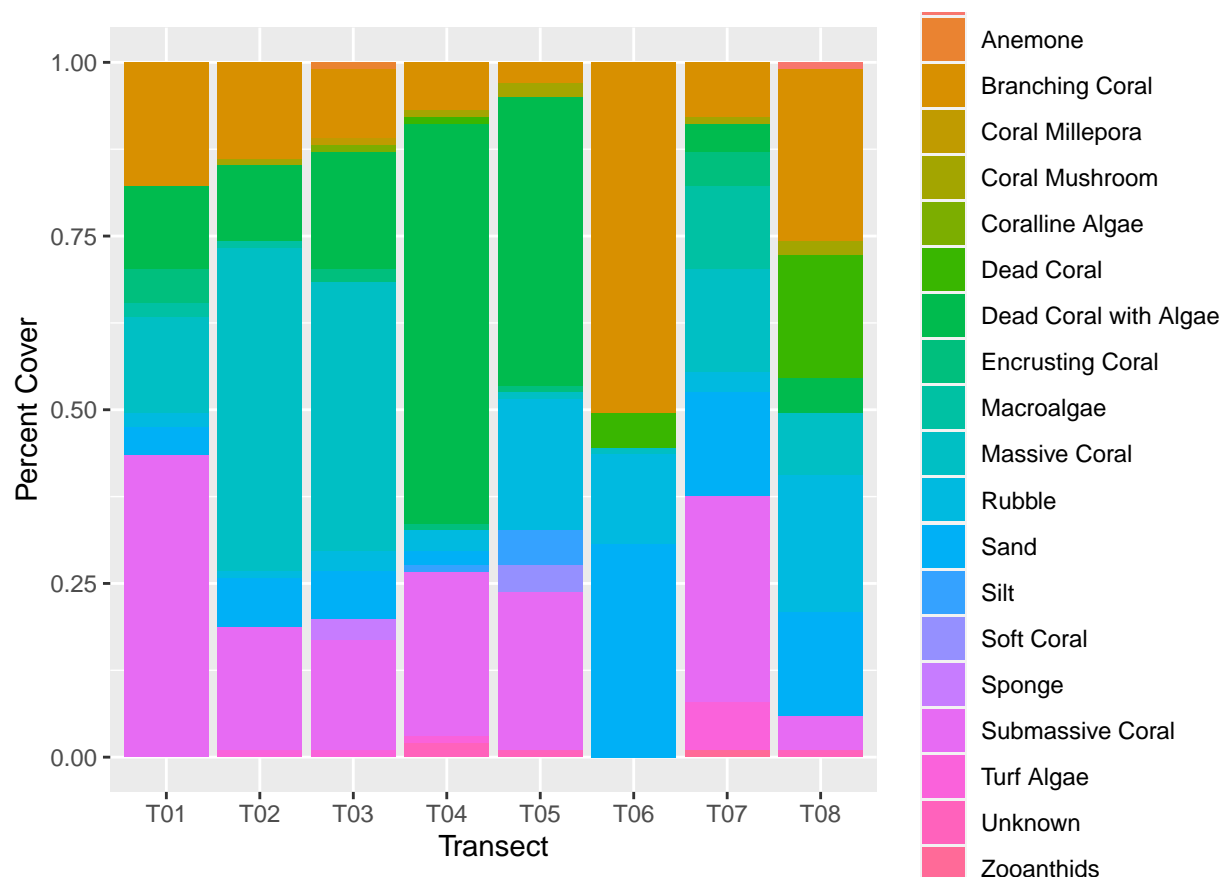
```

% cover per transect

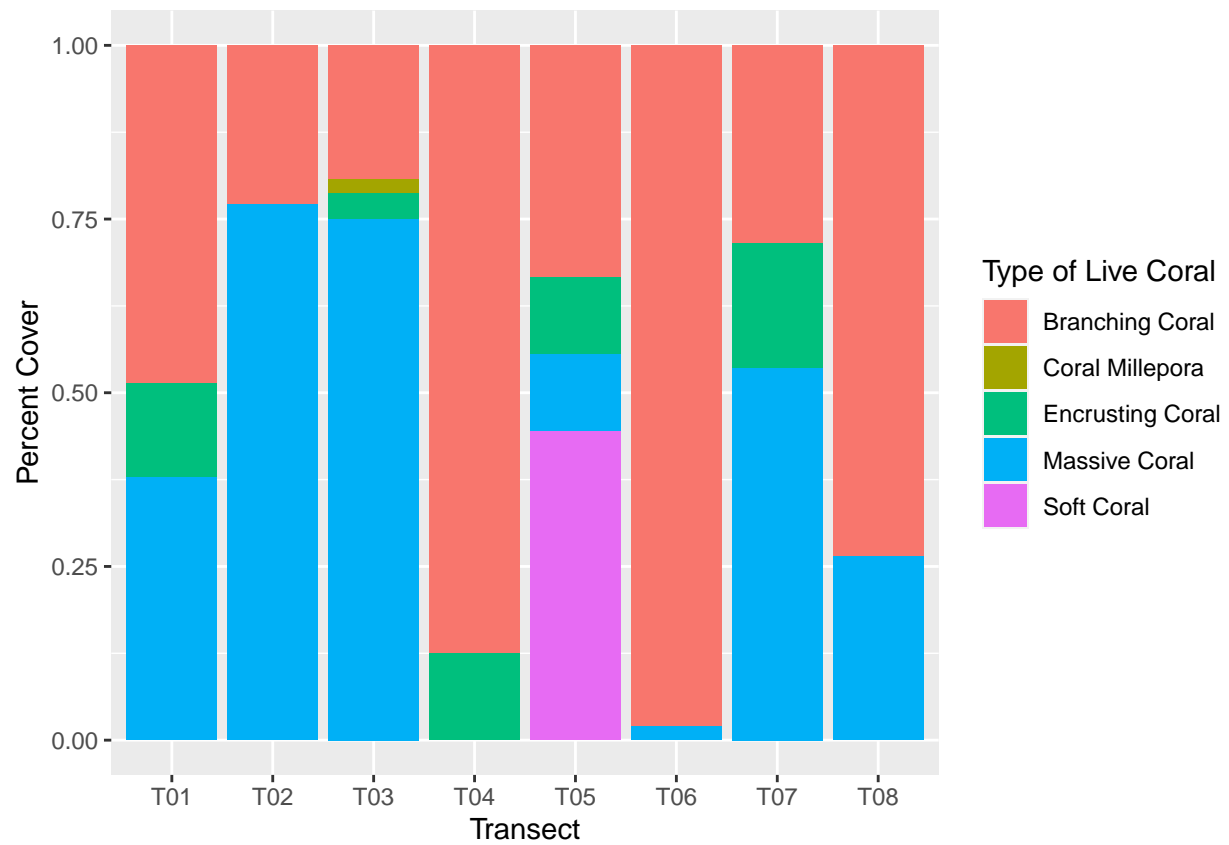
```

ggplot()+ geom_col(data = benthicfinal, aes(x = Transect, y = cover, fill = measurementType), position = "stack")

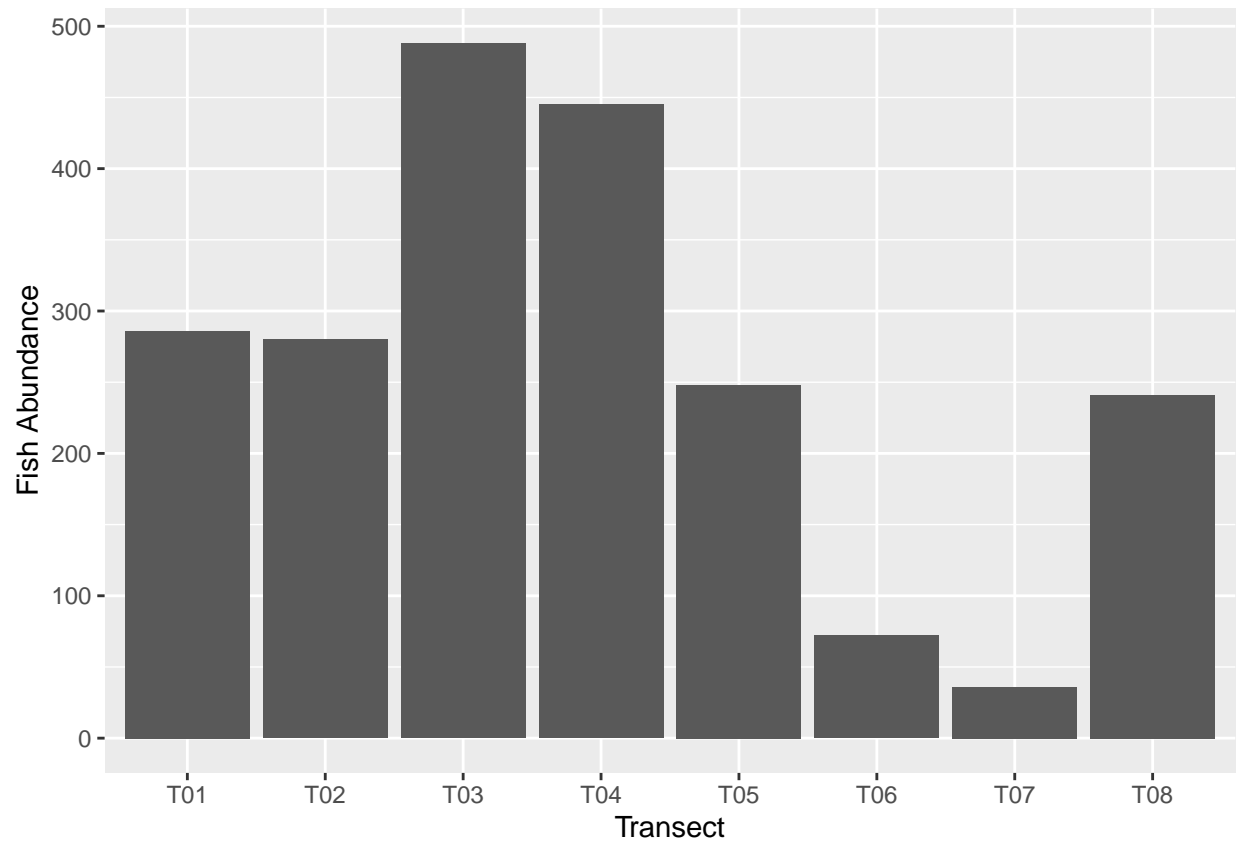
```



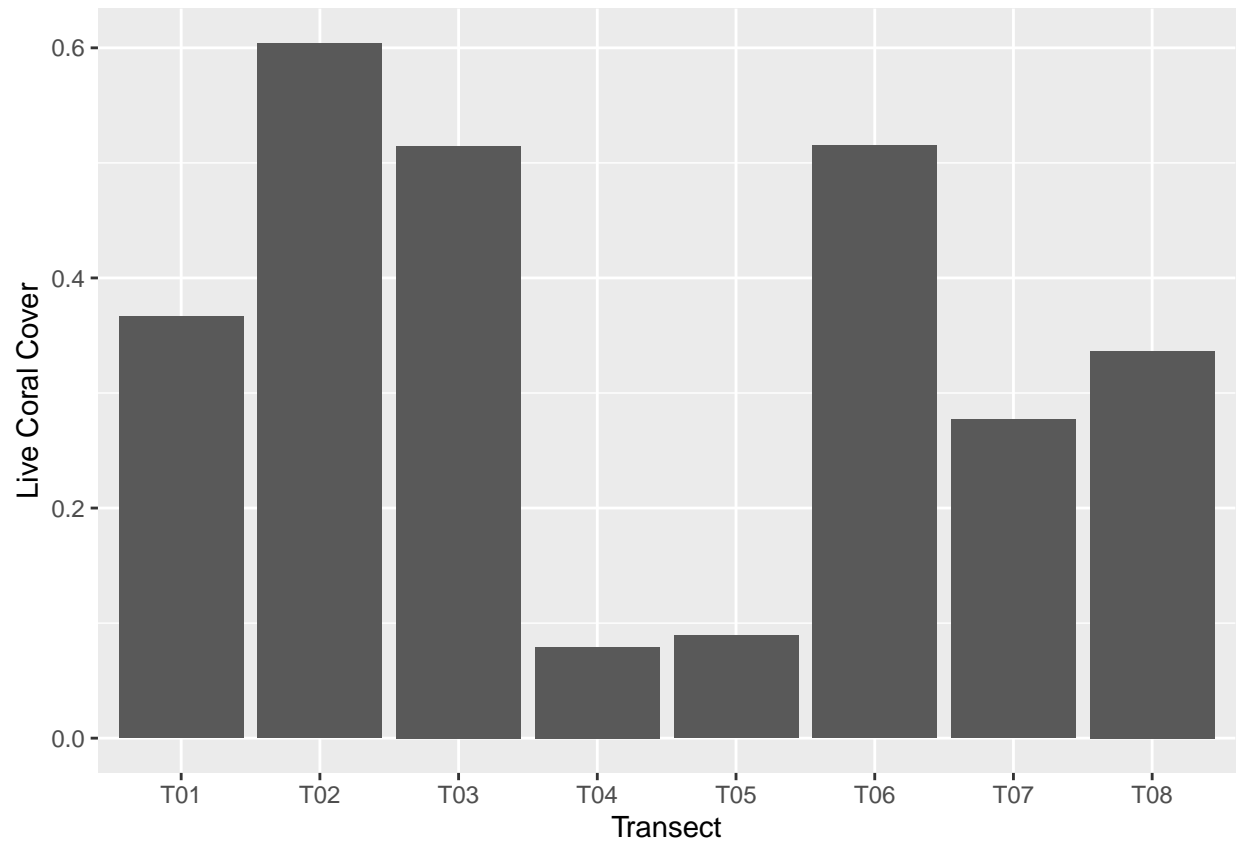
```
ggplot()+ geom_col(data = livecoral, aes(x = Transect, y = cover, fill = measurementType), position = "stack")
```



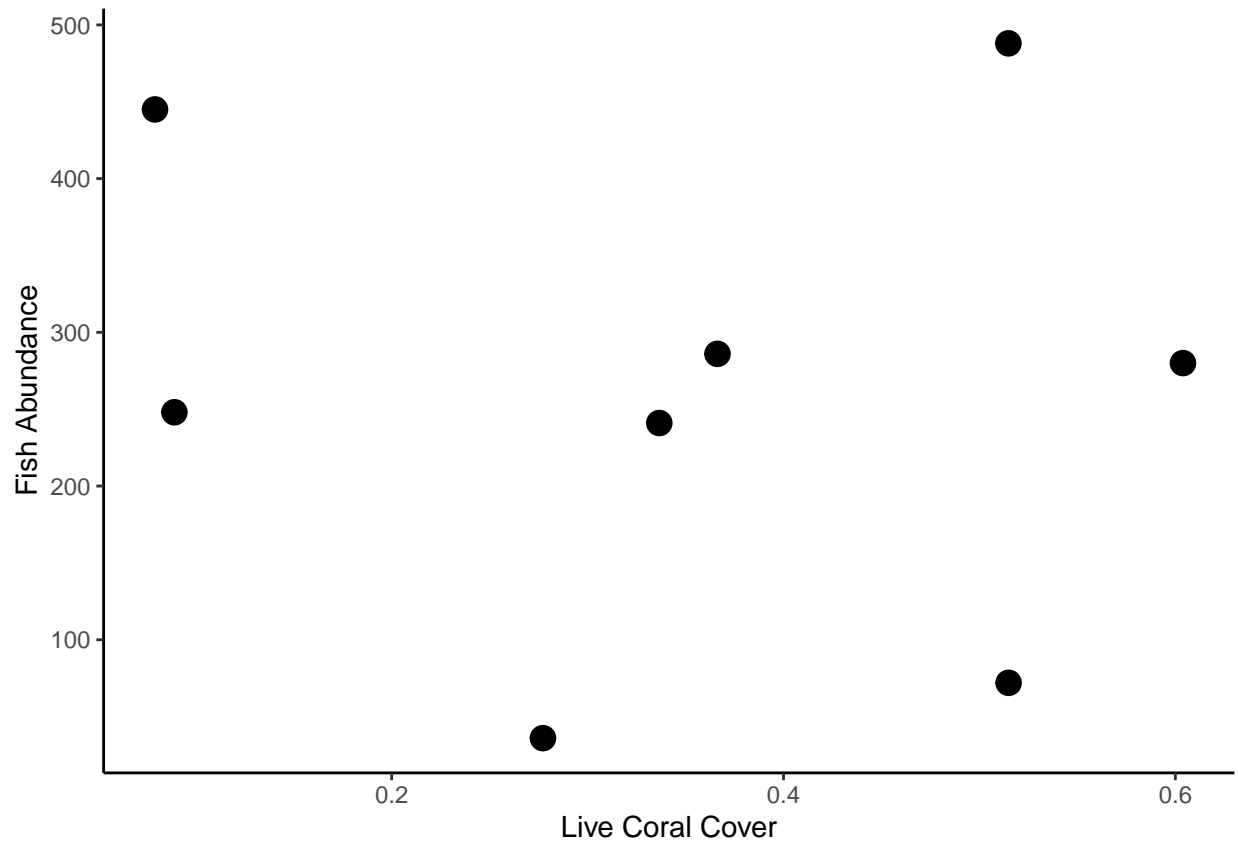
```
ggplot(data = totalfish, aes(x = transects, y = fishabundance)) + geom_col() + labs (x = "Transect", y = "Fish Abundance")
```



```
ggplot(data = covertotal, aes(x = transect, y = Totalcover)) + geom_col() + labs (x = "Transect", y = "Totalcover")
```



```
ggplot(data = coralfish, aes(x = Totalcover, y = fishabundance), fill = transect) + geom_point(size = 4,
```



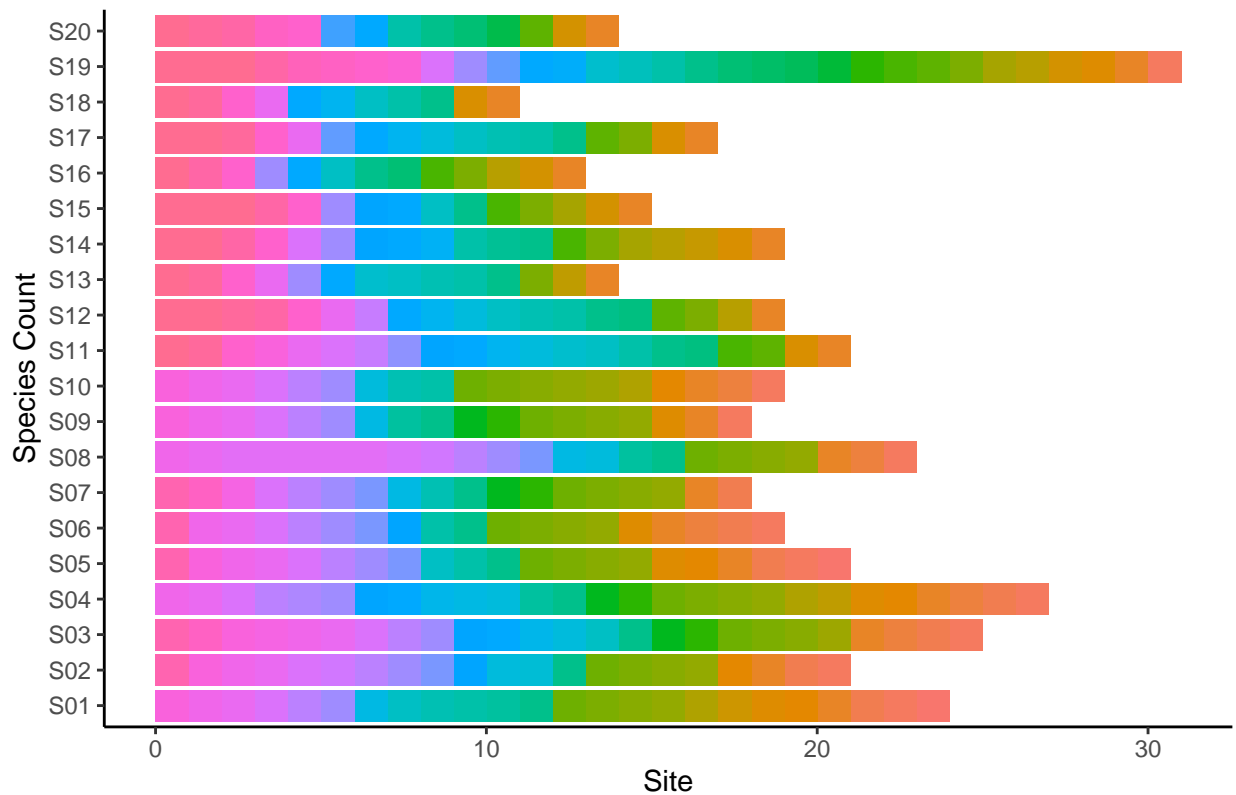
plankton biodiversity

```
plankton <- newoccurrence %>%
  filter(str_detect(occurrenceID, "phytoplankton"))

phytoplankton <- plankton %>%
  select(occurrenceID, organismQuantityType, scientificName, individualCount) %>%
  separate(col = occurrenceID, into = c("Location", "Site", "Date", "Benthic", "Species"), sep = ":") %>%
  select(Site, Species, organismQuantityType, individualCount)

ggplot(phytoplankton, aes(x=as.factor(Site), fill=as.factor(Species))) +
  geom_bar() + theme_classic() +
  theme(legend.position="none") + labs(y = "Site", x = "Species Count", title = "Phytoplankton species")
```


Phytoplankton species count across sites



```
phytoplanktonNew <- phytoplankton %>%
  select(Site,Species,individualCount) %>%
  group_by(Species, Site)
```

```
planktonwide <- phytoplanktonNew %>% pivot_wider(names_from = Species, values_from = individualCount, S
```

```
## Warning: Values are not uniquely identified; output will contain list-cols.
## * Use 'values_fn = list' to suppress this warning.
## * Use 'values_fn = length' to identify where the duplicates arise
## * Use 'values_fn = {summary_fun}' to summarise duplicates
```

```
planktonwide[planktonwide == "NULL"] <- NA
```

```
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.0.5
```

```
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 4.0.5
```

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

```
## Warning: package 'permute' was built under R version 4.0.5
```

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

```
## This is vegan 2.5-7
```

```
Diversity <- read_excel("D:/kaya/Documents/2 SY 2021-2022/1st Semester 2021-2022/Bio 115 - Field Biology",  
  sheet = "Sheet2")
```

```
diversity_results <- diversity(x = Diversity, index = "shannon")  
spa <- specaccum(Diversity)
```

```
## Warning in cor(x > 0): the standard deviation is zero
```

```
plot(spa)
```

