Biodiversity_Assignment

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10/31/2021

Setting up our packages

Question

How does percent-cover of upright and crust seaweeds affect intertidal invertebrate diversity?

Hypothesis

If an area has a higher percent cover of upright seaweeds, then intertidal diversity will be higher because they provide microhabitats and are recruiters.

Data Collection and Data Type

At Scott's Bay, we placed two transects parallel to the shoreline with one wave exposed and the other wave-sheltered. On each transect, we surveyed three locations using 3-4 quadrats per location to record the following: percent cover of upright algae, percent cover of crustose algae, and the species abundance of invertebrates (down to the lowest taxa possible).

Analysis Summary

We calculated the species richness and diversity (using the Shannon-Wiener index) of quadrates compared to percent cover of upright algae and crustose algae. We then performed a simple linear regression to see if percent cover of crustose or upright algae has a significant effect on diversity and richness.

Results

Calculations

Seaweed percentages

```
seaweeds = perc %>%
    group_by(vertical_transect, quadrat) %>%
  mutate(unique_ID = as.numeric( paste0(vertical_transect, ".", quadrat))) %>%
  dplyr::select(c(unique_ID, quadrat, per_upright, per_crust)) %>%
  arrange(unique_ID)
```

```
## Adding missing grouping variables: `vertical_transect`
```

```r
seaweeds_clean = data.frame(seaweeds[,-c(1,3)])


# setting up our dataframe so that we can use matrify to arrange
#our data in long form and  then calculate diversity with vegan
cleaned_biodiversity = biodiversity %>% # cleaning data to use matrify
    drop_na(n) %>%
    group_by(vertical_transect, quadrat) %>%
  mutate(unique_ID = as.numeric( paste0(vertical_transect, ".", quadrat))) %>%
  dplyr::select(unique_ID, species, n)
```

```
## Adding missing grouping variables: 'vertical_transect', 'quadrat'
```

```r
cleaned_biodiversity = data.frame(cleaned_biodiversity[,-c(1:2)]) # removing extra columns

# putting it into a matrix format
biodiversity_matrix <- matrify(cleaned_biodiversity) # using matrify
```

Calculating diversity indices and linking it to seaweed cover

```r
ShannonIndex <- data.frame(
  diversity(biodiversity_matrix, index = "shannon"))
head(ShannonIndex)
```

```
##     diversity.biodiversity_matrix..index....shannon..
## 1.1                                         0.7595474
## 1.2                                         0.6869616
## 1.3                                         0.7529116
## 1.4                                         0.0000000
## 2.1                                         1.0690737
## 2.2                                         0.8184438
```

```r
ShannonIndex = ShannonIndex %>%
  rename("ShannonIndex" = diversity.biodiversity_matrix..index....shannon..)

richness <- biodiversity %>% # calculating richness per quadrat
  drop_na(n) %>%
  group_by(vertical_transect,quadrat) %>%
  summarize(rich = length(unique(species)))   %>%
  mutate(unique_ID = as.numeric( paste0(vertical_transect, ".", quadrat)))
```

```
## 'summarise()' has grouped output by 'vertical_transect'. You can override using the '.groups' argumen
```

```r
Data = cbind(ShannonIndex, seaweeds_clean, richness[,3]) # comining all our data
```

Now, we plot the relationship between diversity and seaweed cover using ggplot and geom_point

```r
# visualizing upright percent cover and diversity
figure1<-ggplot(data = Data, aes(x=per_upright, y =ShannonIndex))+
  geom_point()+
```

```
  geom_smooth(method=lm, se=FALSE)+
  labs(x="Percent cover of upright algae (%)", y="Shannon-Wiener index")

# visualizing crust percent cover and diversity
figure2<-ggplot(data = Data, aes(x=per_crust, y =ShannonIndex))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(x="Percent cover of crustose algae (%)", y="Shannon-Wiener index")

# visualizing upright percent cover and richness
figure3<-ggplot(data = Data, aes(x=per_upright, y =rich))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(x="Percent cover of upright algae", y="Richness")

# visualizing crust percent cover and richness
figure4 <- ggplot(data = Data, aes(x=per_crust, y =rich))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  labs(x="Percent cover of crustose algae", y="Richness")


figure1
```
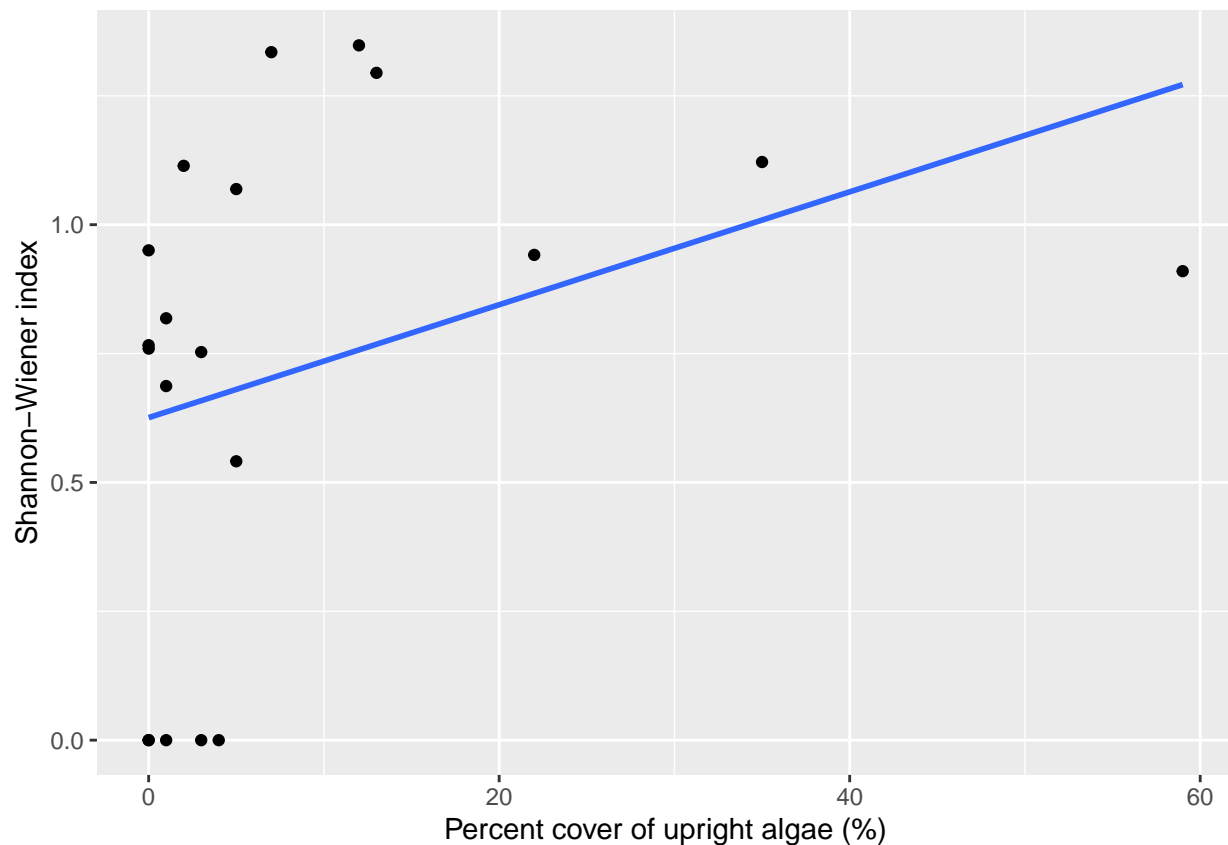
`geom_smooth()` using formula 'y ~ x'

Figure 1. The impact of percent cover of upright algae on the diversity of marine invertebrates (as calculated by the Shannon-Wiener Index)

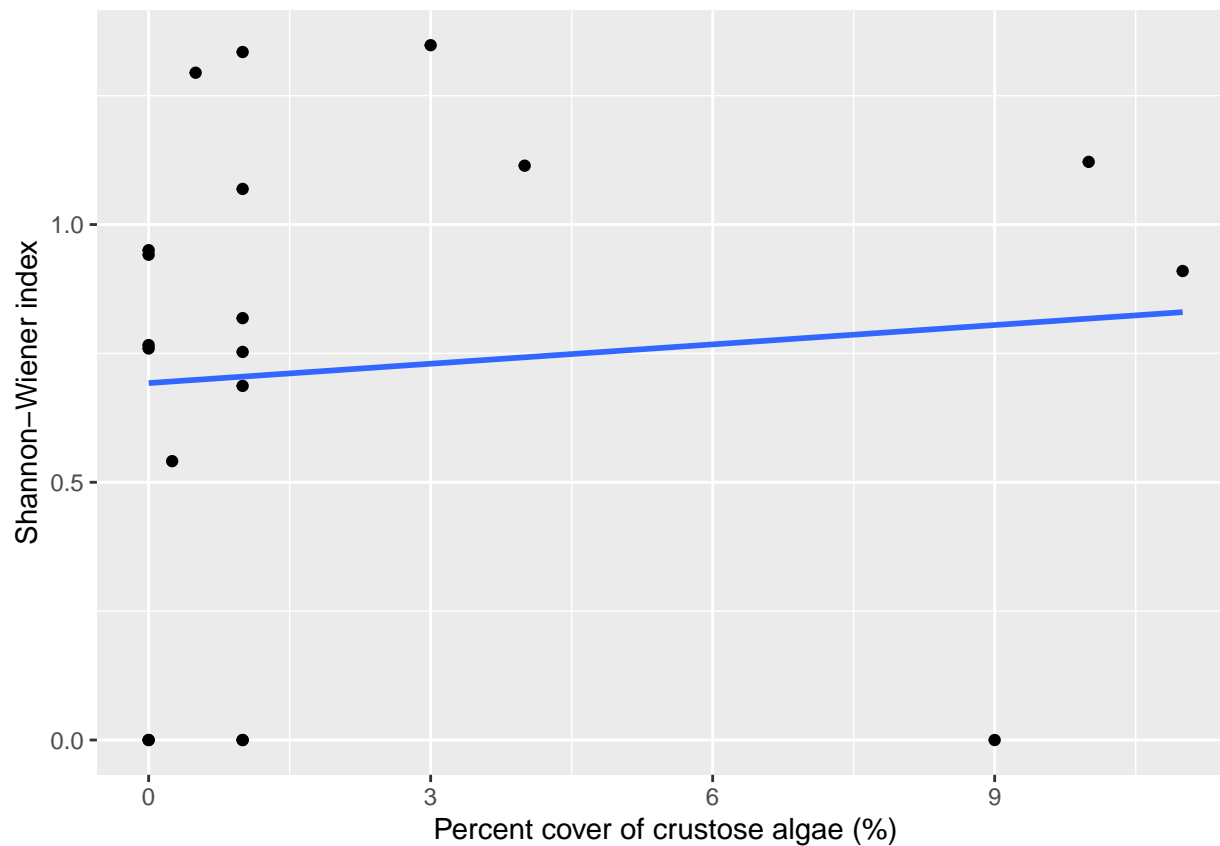figure2

`geom_smooth()` using formula 'y ~ x'

Figure 2. The impact of percent cover of crustose algae on the diversity of marine invertebrates (as calculated by the Shannon-Wiener Index)

figure3

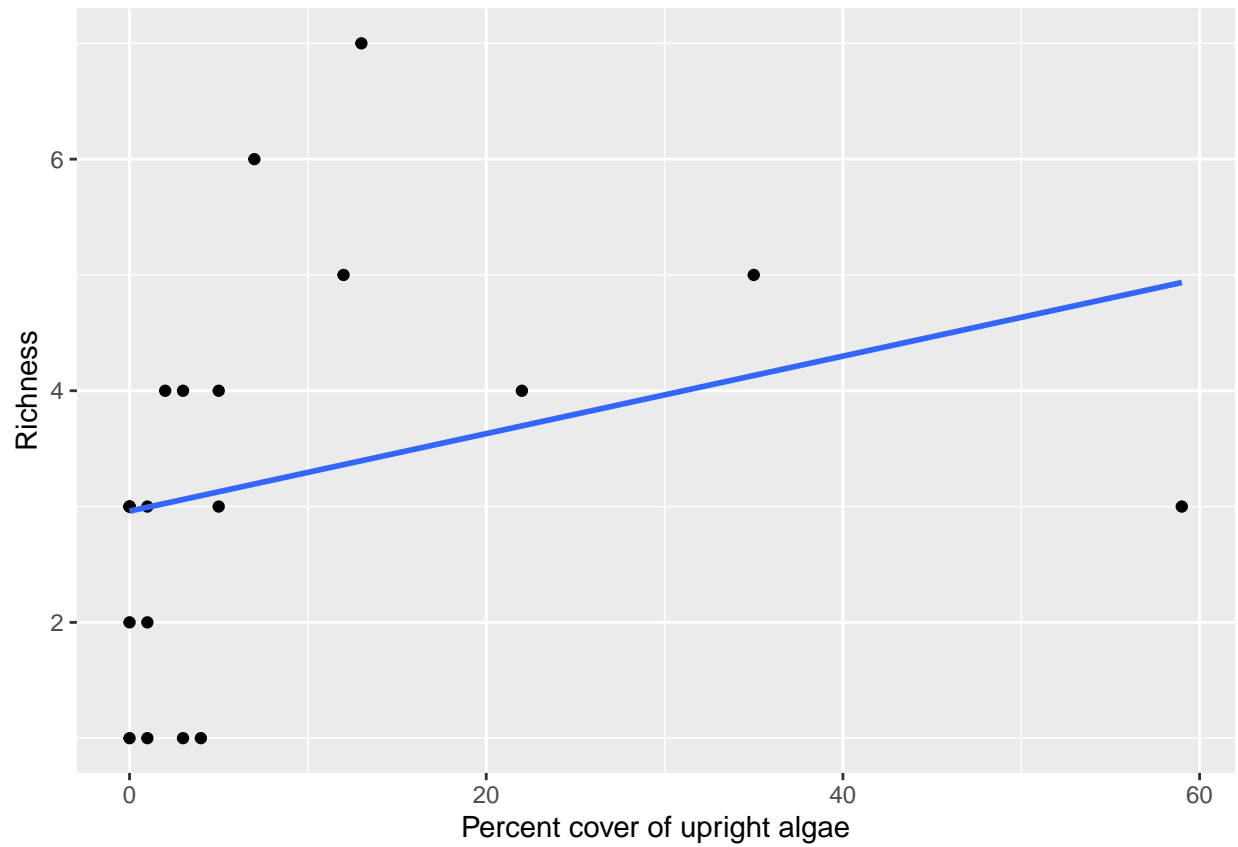## `geom_smooth()` using formula 'y ~ x'

Figure 3. The impact of percent cover of crustose algae on the richness of marine invertebrates (as calculated by the Shannon-Wiener Index)

```
figure4
```

```
## `geom_smooth()` using formula 'y ~ x'
```
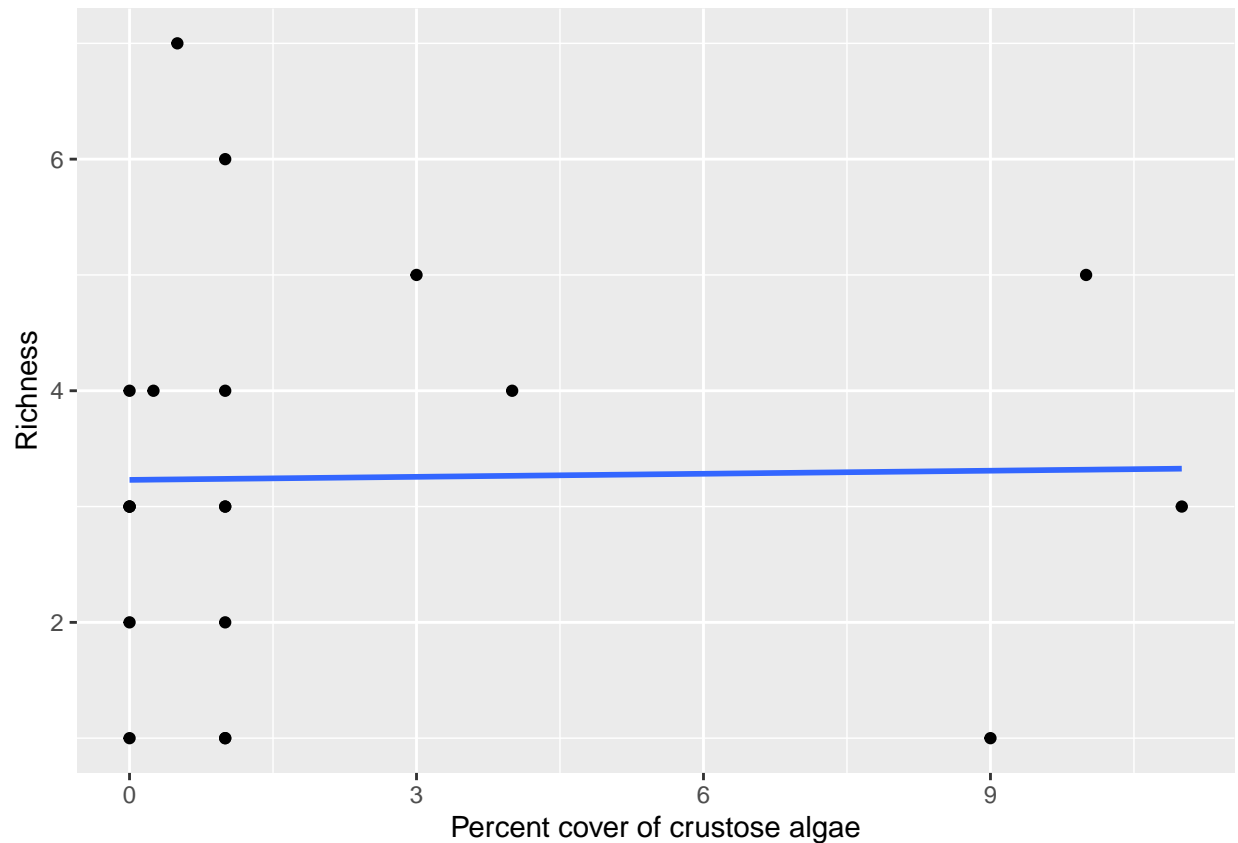
Figure 4. The impact of percent cover of crustose algae on the richness of marine invertebrates (as calculated by the Shannon-Wiener Index)

Linear Regression

Using regression to examine the relationships between seaweed % cover and shannon weiner diversity We used poission distribution because it's more appropriate for data that's never negative

```
# simple linear regression for upright and diversity
upright_diversity = lm(ShannonIndex ~ per_upright, data = Data)
summary(upright_diversity) # not significant
```

```
##
## Call:
## lm(formula = ShannonIndex ~ per_upright, data = Data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.6695 -0.4279  0.1035  0.3406  0.6323
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.625711   0.120190   5.206 5.96e-05 ***
## per_upright 0.010950   0.007155   1.530    0.143
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4608 on 18 degrees of freedom
## Multiple R-squared:  0.1151, Adjusted R-squared:  0.06596
## F-statistic: 2.342 on 1 and 18 DF,  p-value: 0.1433
```

```
# simple linear regression for crust and diversity
crust_diversity = lm(ShannonIndex ~ per_crust, data = Data)
summary(crust_diversity) # not significant
```

```
##
## Call:
## lm(formula = ShannonIndex ~ per_crust, data = Data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.80504 -0.28904  0.07679  0.31905  0.62975
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.69243    0.13030   5.314 4.73e-05 ***
## per_crust    0.01251    0.03187   0.393    0.699
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4877 on 18 degrees of freedom
## Multiple R-squared:  0.008489,  Adjusted R-squared:  -0.0466
## F-statistic: 0.1541 on 1 and 18 DF,  p-value: 0.6993
```

```
# simple linear regression for upright and richness
upright_rich = lm(rich ~ per_upright, data = Data)
summary(upright_rich) # not significant
```

```
##
## Call:
## lm(formula = rich ~ per_upright, data = Data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.0944 -1.2292  0.0394  0.8889  3.6044
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.96055    0.43086   6.871 1.99e-06 ***
## per_upright  0.03346    0.02565   1.305    0.208
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.652 on 18 degrees of freedom
## Multiple R-squared:  0.08638,  Adjusted R-squared:  0.03562
## F-statistic: 1.702 on 1 and 18 DF,  p-value: 0.2085
```

```
# simple linear regression for crust and richness
crust_rich = lm(rich ~ per_crust, data = Data)
summary(crust_rich) # not significant
```

```
##
## Call:
## lm(formula = rich ~ per_crust, data = Data)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -2.3096 -1.2325 -0.2303  0.7681  3.7653
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.230294   0.461596   6.998 1.56e-06 ***
## per_crust   0.008807   0.112902   0.078    0.939
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.728 on 18 degrees of freedom
## Multiple R-squared:  0.0003379,  Adjusted R-squared:  -0.0552
## F-statistic: 0.006085 on 1 and 18 DF,  p-value: 0.9387
```

```
# we have no significant results (teehee) but that's ok! science
```

Table 1: Table 1. Linear regression results of the relationship between algae morphology and both Shannon-Wiener Index and Richness

Analysis	Algae.Type	P.Value	Adjusted.R.squared
Shannon-Wiener Index	upright	0.1433	0.06596
Shannon-Wiener Index	crustose	0.6993	-0.0466
Richness	upright	0.2085	0.03562
Richness	crustose	0.9387	-0.0552

Conclusions

As none of the p-values are less than 0.05, there is no significant relationship between algae type and both diversity and richness.