

2213615_MA334

2213615_NDIDI MERCY

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INTRODUCTION

The Bio_measure dataset involves the collection and compilation of different aspects of biodiversity like the diversity and abundance of plants and providing information on how environmental factors can influence biodiversity. It is key to note that biodiversity is the variety and viability of life on earth. The data contains information on different taxonomical groups which ecologist and environmental scientists has more interest on this dataset because of the quest to understand the relationship between diversity, human activities and enviromental factors. This is due to the fact that there is a significant decline of biodiversity generally so this urgent need can contribute to biodiversity loss and help us on best strategies for conserving and restoring biodiversity.

The earth's ecosystem main component is biodiversity which provides an ecosystem service which is essential to the well being of humans such as pest control, pollination, etc. We aim to investigate how the abundance and distribution of different taxonomic groups are affected by environmental variables. This analysis is based on previous study which investigated the relationship between biodiversity and environmental variables which have shown that a change in climate can change or alter the abundance and distribution of species with potentially significant implications for ecosystem functioning (IPCC, 2014).

By building on the study, we can contribute to a better understanding of the complex relationship between, human activities and environmental variables by our analysis.

SIGNIFICANCE

The significance of this study is to improve our understanding on biodiversity patterns which could be of great information on how we can implement conservation and management strategies and contribute to development of biodiversity monitoring programs and provide training on data exploration, hypothesis testing and statistical modelling for conservation and ecological research which are critical for assessing the effectiveness of conservatiion measures(UNEP, 2021)

DATA EXPLORATION

To explore the data, BD7, BD4 and BD11 were created from the Bio measure dataset.

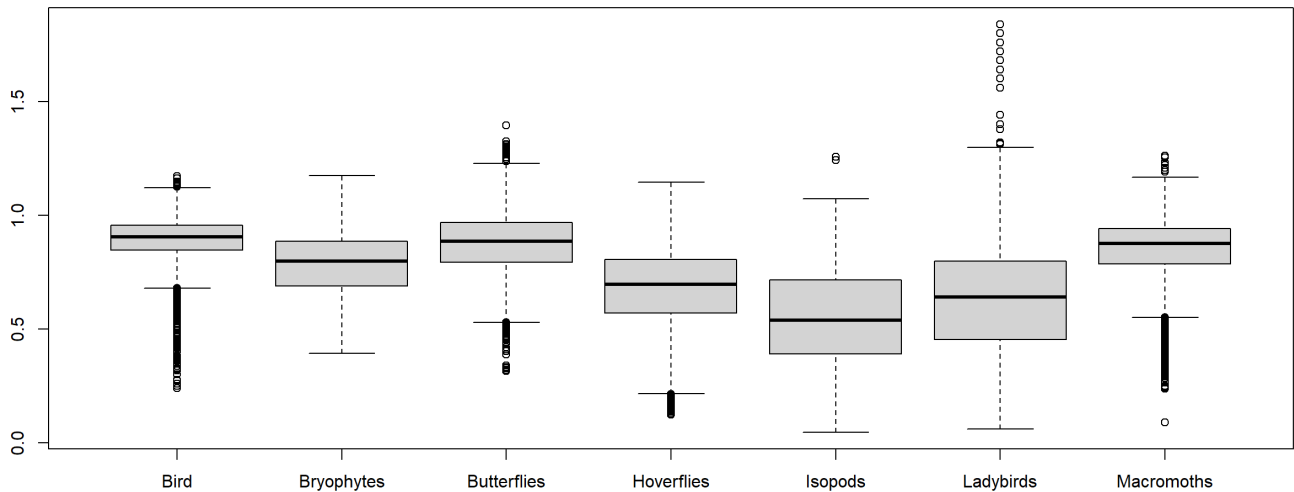
```
#Create BD7, BD4, and BD11 subsets from Bio_measure
BD7 <- Bio_measure %>%
  select(Bird, Bryophytes, Butterflies, Hoverflies, Isopods, Ladybirds, Macromoths)

BD4 <- Bio_measure %>%
  select(Bees, Carabids, Grasshoppers_._Crickets, Vascular_plants)

BD11 <- Bio_measure %>%
  select(Bird, Bryophytes, Carabids, Hoverflies, Isopods, Grasshoppers_._Crickets, Vascular_p
lants, Bees, Macromoths, Butterflies, Ladybirds)
```

UNIVARIATE ANALYSIS OF BD7 VARIABLES

```
boxplot(BD7)
```

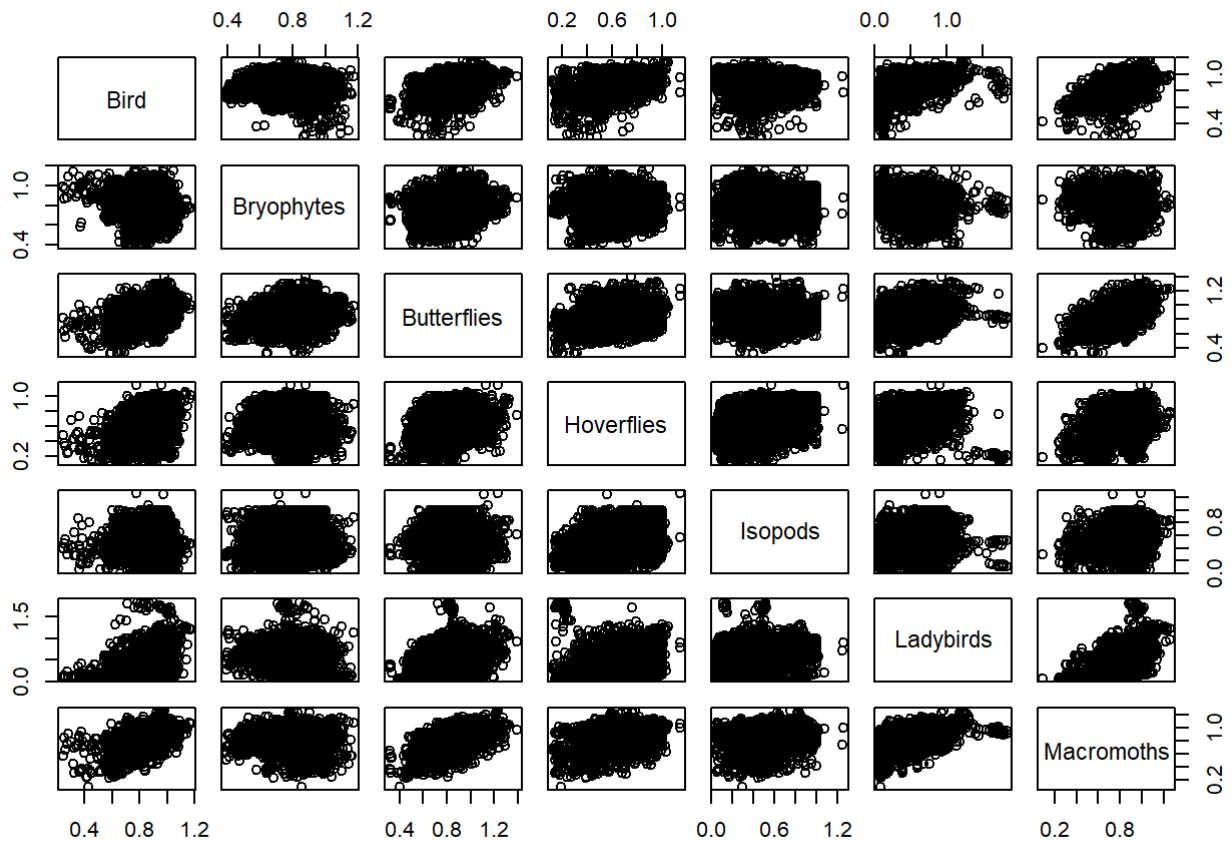


The mean values for all the species present here are high, relatively ranging from 0.614 to 0.887, this indicates the species have a strong presence the ecosystem given. Birds have the highest mean value, followed pretty closely by Butterflies with the lowest mean value observed for Isopods. There is a relatively high median values for all species as well, indicating that the data is not skewed and is fairly distributed. The first and third quartile is between this range and it is relatively small, which indicates that the data is tightly clustered around the median.

From the analysis given, the range of values was observed to vary significantly among the other different species. For instance Bryophytes has a relatively narrow range of values, while Macromoths range is much wider. The maximum value for Isopods is also relatively high, indicating the presence of a few outliers in the data.

MULTIVARIATE ANALYSIS

```
# Multivariate analysis for BD7 correlation
plot(BD7)
```



To determine which variable is positively and negatively correlated, we take a look at the Bio_measure dataset correlation coefficients. From the BD7 Bio_measure, we can see Bird and Macromoths have the highest positive correlation with a coefficient of 0.59411179 and a negative northing correlation of -0.36466208 and positive easting of 0.31531324, followed by Macromoth and Butterfly of 0.56087528, and between Birds and Ladybirds of 0.5496637.

The highest negative correlation is Ladybird and Bryophyte of -0.202599732 with a negative northing correlation of -0.4196844 and positive easting of 0.41606182 and the next is Bird and Bryophyte with -0.085146093. It is important to note that easting and northing has negative correlation with most of the variables and this denotes that as easting and northing value increases, there may be decrease on the values of other variables.

Overall we can make a conclusion that Bird and Macromoths are the most positively correlated variables while Ladybird and Macromoths appeared to be most negatively correlated in the BD7 Bio_measure dataset.

HYPOTHESIS TESTING

```
model <- lm(Bio_measure$Bird ~ Bio_measure$Easting, data = Bio_measure)
summary(model)
```

```
##
## Call:
## lm(formula = Bio_measure$Bird ~ Bio_measure$Easting, data = Bio_measure)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.58099 -0.04791  0.01337  0.06834  0.25106
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.932e-01  4.133e-03  191.92  <2e-16 ***
## Bio_measure$Easting 2.662e-07  1.103e-08   24.14  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1011 on 5278 degrees of freedom
## Multiple R-squared:  0.09942,    Adjusted R-squared:  0.09925
## F-statistic: 582.7 on 1 and 5278 DF,  p-value: < 2.2e-16
```

```
##
## Call:
## lm(formula = Bio_measure$Macromoths ~ Bio_measure$Easting, data = Bio_measure)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.70823 -0.07303  0.02358  0.09333  0.42496
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.826e-01  5.667e-03  138.1  <2e-16 ***
## Bio_measure$Easting 1.890e-07  1.512e-08   12.5  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1386 on 5278 degrees of freedom
## Multiple R-squared:  0.02875,    Adjusted R-squared:  0.02856
## F-statistic: 156.2 on 1 and 5278 DF,  p-value: < 2.2e-16
```

The model above suggests that there is a relationship between Birds and Macromoths. However, we did a test on Macromoth but the model coefficient of determination was low which suggested that predicting a response variable by the model may not be useful. We would proceed to do an hypothesis test for the extent to which Birds and Eastings have a strong correlation.

The hypothesis would be:

H0: There is no relationship between Birds and Eastings.

H1: There is a relationship between Birds and Eastings.

Starting with the coefficients, the estimated coefficient for the Intercept is 7.932e-01 indicating the predicted value of 0.7932 is Bird population when Easting. 2.662e-07 is the estimated coefficient for Easting and this indicates that for each unit increase in Easting, 2.662e-07 increase appears to be the predicted Bird population. There is a statistically significant at a p-value less than 0.05 for both coefficient and this suggests a strong linear relationship between Bird population and Easting thereby rejecting the null hypothesis.

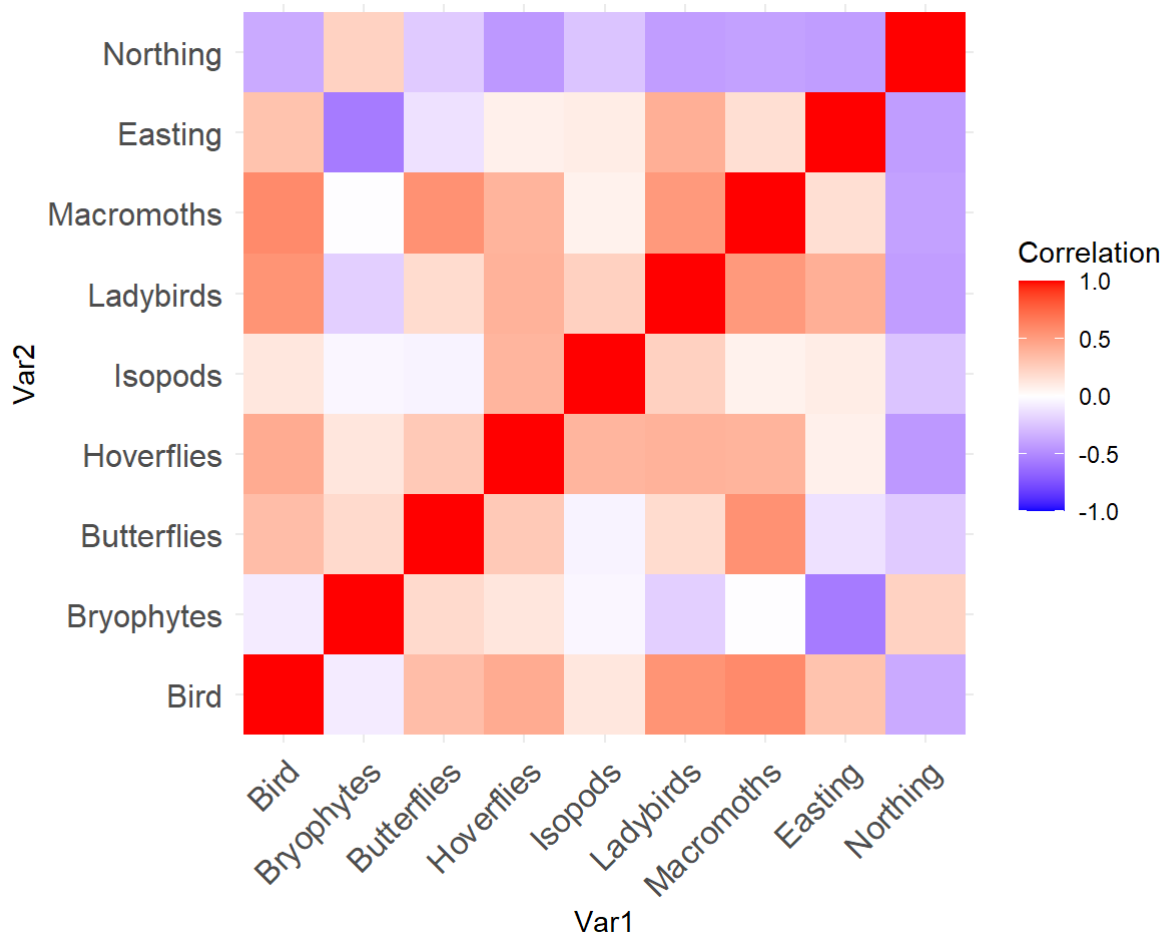
In residuals, the minimum value is -0.58099 and the maximum value is 0.25106. The median residual value is positive (0.01337) which indicates that, on average, the model Bird population is underestimated. The residual standard error is 0.1011, and this represents the average distance between the actual values and predicted values of the Bird population.

The multiple R-squared value is 0.09942 and this indicates that the Easting coordinate explains variance in the Bird population up to an approximate of 9.94%. The adjusted R-squared value appears a little bit lower (0.09925) bearing the predictor in mind. The F-statistic is 582.7 with a p-value less than $2.2e-16$, which indicates the significant and fit of the model in the data.

In conclusion, the linear regression analysis suggests there is a positive significant linear relationship between Bird population and Easting coordinates in the given ecosystem, although the Easting coordinate only explains a small proportion of the variance in the Bird population. To identify other factors that may contribute to the Bird population in the ecosystem, more investigation and analysis is required.

CORRELATION BETWEEN BD7 AND OTHER VARIABLES

```
#Visualize the correlation matrix using ggplot2
melted_cor_matrix <- melt(cor_matrix)
ggplot(data = melted_cor_matrix, aes(x = Var1, y = Var2, fill = value)) +
  geom_tile() +
  scale_fill_gradient2(low = "blue", high = "red", mid = "white", midpoint = 0, limit = c(-1,
1), name = "Correlation") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, size = 12, hjust = 1),
        axis.text.y = element_text(size = 12)) +
  coord_fixed()
```



The above plot shows the relationship between BD7 and other variables, including period, Easting, Northing, and dominantLandClass. The visualization helps us highlights the correlations that exist between the variables which can help in understanding the relationships between the different factors.

LINEAR REGRESSION FOR BD7 VARIABLES

```
##
## Call:
## lm(formula = ecologicalStatus ~ Bird)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.34006 -0.05836 -0.00550  0.05899  0.30906
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.16110    0.00983   16.39  <2e-16 ***
## Bird         0.62475    0.01100   56.79  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08514 on 5278 degrees of freedom
## Multiple R-squared:  0.3793, Adjusted R-squared:  0.3792
## F-statistic: 3225 on 1 and 5278 DF, p-value: < 2.2e-16
```

```
##
## Call:
## lm(formula = ecologicalStatus ~ Bryophytes)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.36705 -0.06225  0.00486  0.07432  0.39160
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.650726   0.008956  72.659  < 2e-16 ***
## Bryophytes   0.082166   0.011229   7.317 2.91e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1075 on 5278 degrees of freedom
## Multiple R-squared:  0.01004, Adjusted R-squared:  0.009855
## F-statistic: 53.54 on 1 and 5278 DF, p-value: 2.91e-13
```

```
##
## Call:
## lm(formula = ecologicalStatus ~ Butterflies)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.27904 -0.06664  0.00450  0.07230  0.33443
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.408883   0.008406  48.64  <2e-16 ***
## Butterflies  0.350429   0.009491  36.92  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09634 on 5278 degrees of freedom
## Multiple R-squared:  0.2053, Adjusted R-squared:  0.2051
## F-statistic: 1363 on 1 and 5278 DF, p-value: < 2.2e-16
```

```
##
## Call:
## lm(formula = ecologicalStatus ~ Hoverflies)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.30638 -0.04688 -0.00182  0.04796  0.33934
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.413379   0.004039  102.35  <2e-16 ***
## Hoverflies   0.444403   0.005752   77.27  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07403 on 5278 degrees of freedom
## Multiple R-squared:  0.5308, Adjusted R-squared:  0.5307
## F-statistic: 5970 on 1 and 5278 DF, p-value: < 2.2e-16
```

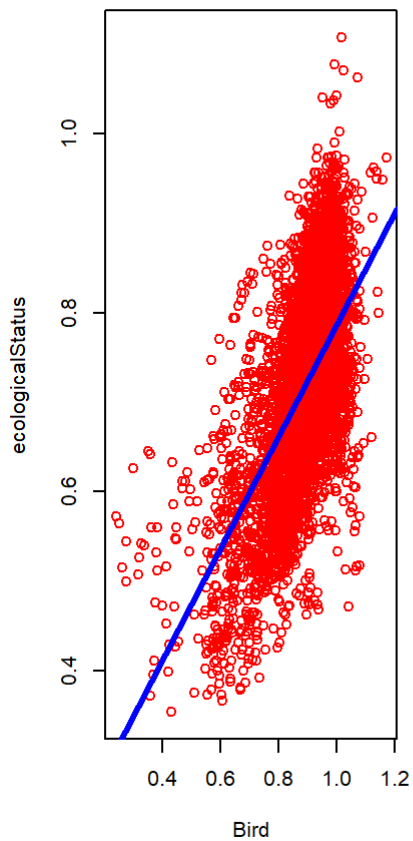
```
##
## Call:
## lm(formula = ecologicalStatus ~ Isopods)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.30209 -0.06081  0.00268  0.06475  0.43868
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.588178   0.003618  162.57  <2e-16 ***
## Isopods      0.231257   0.006125   37.75  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09589 on 5278 degrees of freedom
## Multiple R-squared:  0.2126, Adjusted R-squared:  0.2125
## F-statistic: 1425 on 1 and 5278 DF, p-value: < 2.2e-16
```



```
##
## Call:
## lm(formula = ecologicalStatus ~ Ladybirds)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.39241 -0.04269 -0.00008  0.04664  0.25841
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.536386   0.002606  205.86  <2e-16 ***
## Ladybirds    0.291470   0.003894   74.86  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07526 on 5278 degrees of freedom
## Multiple R-squared:  0.515, Adjusted R-squared:  0.5149
## F-statistic: 5603 on 1 and 5278 DF, p-value: < 2.2e-16
```

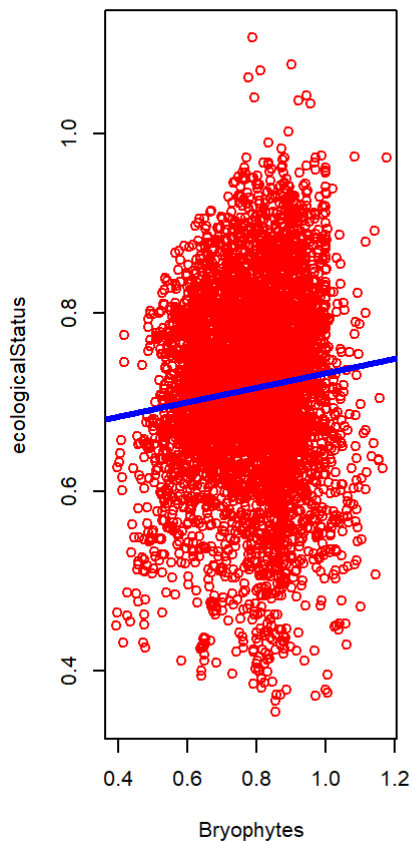
```
##
## Call:
## lm(formula = ecologicalStatus ~ Macromoths)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.28495 -0.05800 -0.00077  0.05953  0.38172
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.293749   0.006949   42.27  <2e-16 ***
## Macromoths   0.496439   0.008073   61.50  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08248 on 5278 degrees of freedom
## Multiple R-squared:  0.4174, Adjusted R-squared:  0.4173
## F-statistic: 3782 on 1 and 5278 DF, p-value: < 2.2e-16
```

```
par(mfrow = c(1,3))
plot(Bird, ecologicalStatus, col= "red")
abline(model.Bird, lwd = 3, col = "blue")
```



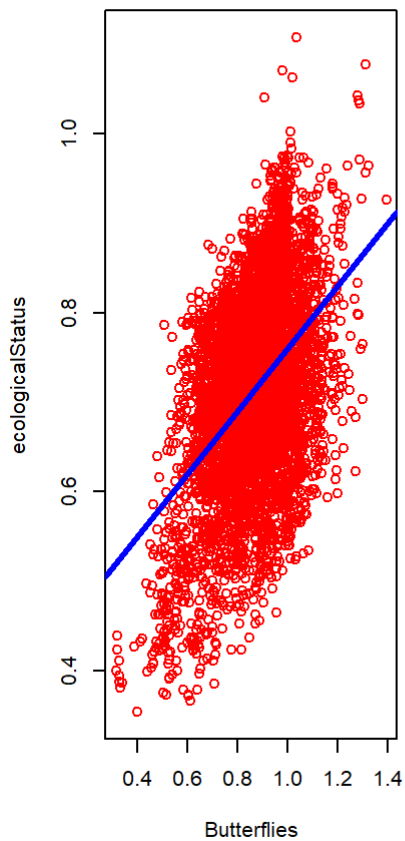
Here we investigate the relationship between `Bird` and its ecological status. The model the `Bird` has a significant positive effect on its ecological status ($\beta = 0.625$, $p < 2.2e-16$). This has a good fit with 0.3793 as the R-squared value which indicates Birds index explanation for 37.93% of the variance in ecological status. Therefore this `Bird` index can be used as a predictor of birds ecological status.

```
par(mfrow = c(1,3))
plot(Bryophytes, ecologicalStatus, col= "red")
abline(model.Bryophytes, lwd = 3, col = "blue")
```



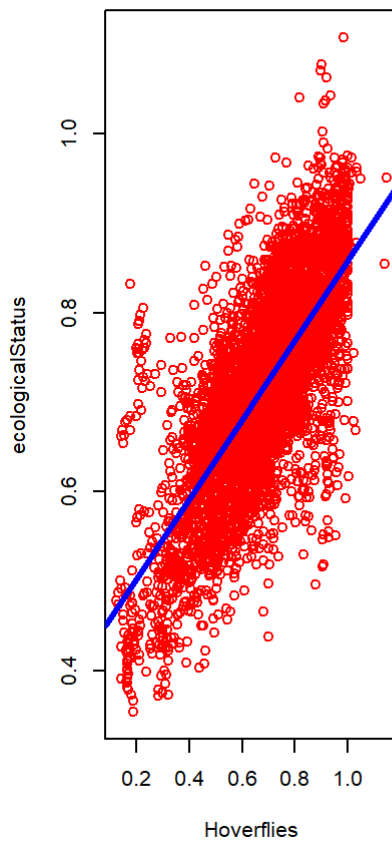
This represents a linear regression where ecological status is the response variable and is regressed against Bryophytes the predictor variable. There is statistical significance of the estimated coefficient for the intercept and Bryophyte with p-values less than 0.001 which indicates they both have association with the ecological status. However, with the multiple R-squared being only 0.01004, this only explains a small proportion of the variation in ecological status. There is a significant F-statistics with a p-value of 0.001 which indicated the model is significant generally. The residual standard error gives an indication that there is a good fit to the data in the model with a small error variance.

```
par(mfrow = c(1,3))  
plot(Butterflies, ecologicalStatus, col= "red")  
abline(model.Butterflies, lwd = 3, col = "blue")
```



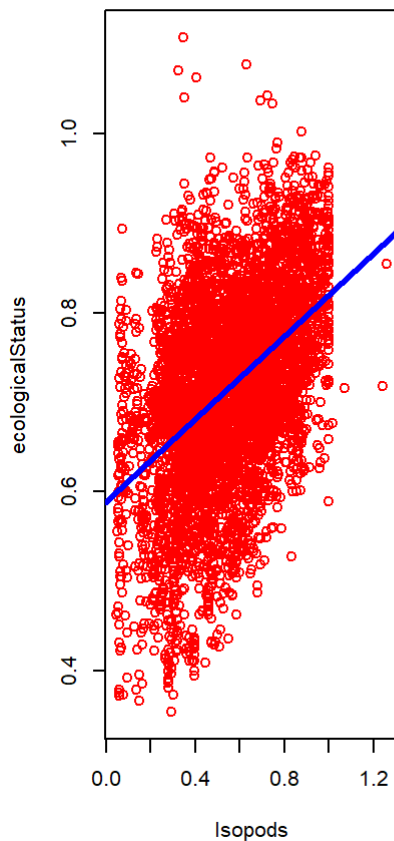
There is a statistically significant relationship between the two variables with a positive coefficient estimate of 0.350429 and an intercept estimate of 0.408883 meaning that as butterflies increase, the ecological status also tends to have an increase. There is a high R-squared value of 0.2053 indicating 20.5% of the bird variation explains the ecological status. The F-statistics is 1363 with a really low p-value of less than $2.2e-16$ which indicates a good fit in the model and that the relationship between ecological status and butterfly is statistically significant.

```
par(mfrow = c(1,3))  
plot(Hoverflies, ecologicalStatus, col= "red")  
abline(model.Hoverflies, lwd = 3, col = "blue")
```



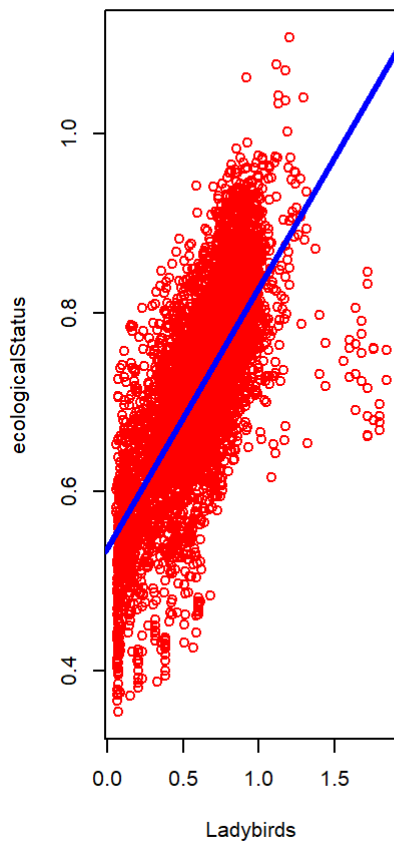
The intercept and hoverflies coefficients were found to have a very high level of significance ($<2e-16$) with the model explaining 53.08% of the variation in the ecological status. The F-statistic is significant at a very high level of significance ($<2.2e-16$). There is normally distributed residual with a residual standard error of 0.07403. The results suggest a strong positive linear relationship between the number of hoverflies and the ecological status.

```
par(mfrow = c(1,3))
plot(Isopods, ecologicalStatus, col= "red")
abline(model.Isopods, lwd = 3, col = "blue")
```



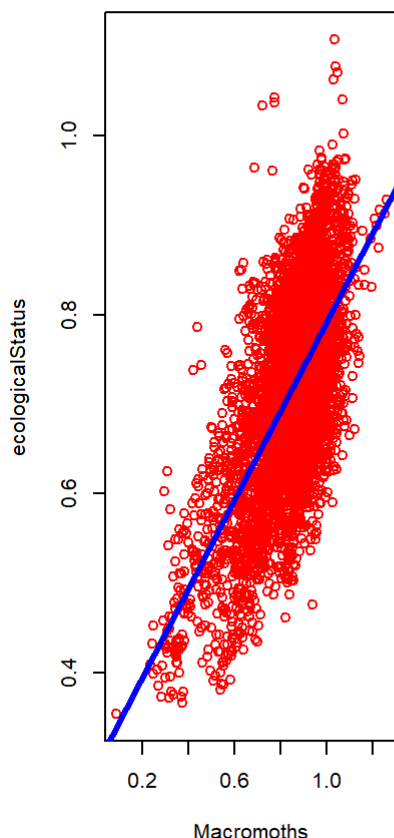
The dependent variable is ecological status and Isopods the independent variable. The analysis shows a p-value of $< 2.2e-16$ indicating that there is a positive relationship between ecological status and isopods since the coefficient estimate for isopods is 0.231257, which has a statistical significant at the 0.001. The R-squared value of 0.2126 indicates isopods explain 21.26% of the variation in ecological status. The standard error of the residuals is 0.09589, indicating that the model has a good fit.

```
par(mfrow = c(1,3))
plot(Ladybirds, ecologicalStatus, col= "red")
abline(model.Ladybirds, lwd = 3, col = "blue")
```



This shows ecological status as the response variable and Ladybirds as the predictor variable. The intercept value is 0.5364 with a standard error of 0.0026 and the estimated coefficient for Ladybirds is 0.2915 with a standard error of 0.0039. Both coefficient of intercept and Ladybirds are significant with a p-value of $<2.2e-16$. The multiple R-squared value is 0.515, which indicates the predictor variable are approximately 51.5% of the variability in the response variable. The F-statistic value is 5603 with a p-value of $<2.2e-16$, which indicated the model is significant. The residual standard error value is 0.07526, indicating that the model has a good fit.

```
par(mfrow = c(1,3))  
plot(Macromoths, ecologicalStatus, col= "red")  
abline(model.Macromoths, lwd = 3, col = "blue")
```



This is the results of a linear regression analysis between ecological status and the number of Macromoths in a dataset. The intercept has a value of 0.293749 with a standard error of 0.006949, and the coefficient for Macromoths is 0.496439 with a standard error of 0.008073. Both the intercept and Macromoths are statistically significant with p-values $< 2.2e-16$. The multiple R-squared is 0.4174, which indicates that the Macromoths variable explains 41.74% of the variation in ecological status. The adjusted R-squared is 0.4173, suggesting that adding the Macromoths variable did not improve the models fit significantly. The F-statistic has a value of 3782 and the residual standard error is 0.08248, which indicates the models predictions have a mean deviation of 0.08248 from the observed values.

SIMPLE LINEAR REGRESSION BETWEEN BD7 AND BD11

The response variable is the abundance of bees, carabids, grasshoppers and crickets, and vascular plants, while we have Birds, bryophytes, hoverflies, isopods, macromoths, butterflies and ladybirds as the explanatory variables. 0.4746 being the adjusted R-squared value suggests 47.46% of the response variable variation indicates a moderate fit for the model. p-value of less than $2.2e-16$ and F-statistics of 682.1 there is a statistical significance of the overall model which denotes that at least there is significant effect on the response variable of one of the explanatory variable.

Generally, we are able to suggest from this output that ladybirds and hoverflies have strongest effect on bees, carabids, grasshoppers and crickets, and vascular plants being abundant, while bryophytes, macromoths, isopods, and butterflies have positive effects also. The bird coefficient is not significant and has no significant effect on response variables.

SIMPLE LINEAR REGRESSION FOR EACH PERIOD:

Y70 PERIOD: There is an adjusted R-squared value of 0.485 in the model which indicates the predictor variable can explain 48.5% of the variance in the response variable. Bryophytes, Hoverflies, Isopods, Macromoths, Butterflies, and Ladybirds are predictor variables having significant coefficients ($p < 0.05$) also having a significant intercept coefficient. From the result we can perceive that the abundance of these biological groups has a positive association with the abundance of the four biological measures.

Y00 PERIOD: Here 0.4905 is the adjusted R-squared value of the model which indicates that predictor variables explain 49.05% of the variance in the response variable. Hoverflies, Isopods, Macromoths, Butterflies, and Ladybirds are the predictor variables with significant coefficients ($p < 0.05$) with a significant intercept coefficient and can perceive that the abundance of these biological groups is positively associated with the abundance of the four biological measures.

MULTIPLE LINEAR REGRESSION

1. Mean of the proportional species richness values for BD4: Here we fit in the response variable BD4_mean with seven predictor BD7 and the intercept p-value of $1.53e-13$ is statistically significant which means that we have an estimated value BD4 mean of 0.126814 when all the predictor variables are zero and apart from Bird, all the coefficients for all predictor variables are statistically significant with p-values less than 0.05 which indicates that response variable has a significant relationship. Bryophytes, Butterflies, Hoverflies, Isopods, Ladybirds and Macromoths have positive effect on the BD4-mean which tells us that BD-4 mean tends to increase as the taxa increases.

The R-square value is 0.4753 meaning that 47.53% of the BD4 mean variation is a predictor variable. The Adjusted R-squared value is 0.4746 which suggests that the addition of more predictor variables won't improve the fit. F-statistics value is 682.1 with a small p-value ($< 2.2e-16$) which indicates the model is generally significant. Residual standard error is small which indicates the model fits the data.

2. BD7 mean using all the other variables in BD7 dataset: The independent variable has significant effect on BD7 with a p-value less than 0.05 and from the summary we see that the model fits the data perfectly with all residuals close to zero showing there is a positive correlation indicating that each variable contributes to the BD7 mean prediction as estimated value of $1.429e-01$ is the same thereby suggesting this model may not be useful in predicting BD7 mean.

FEATURE SELECTION: To get the best model fit, we'd use Akaike information criterion (AIC). The stepwise regression was used to select the best subset of predictors variables which provides the best fit for the dependent variable. The summary output shows that only Bryophytes, Butterflies, Hoverflies, Isopods, Ladybirds, and Macromoths are selected as the best subset of predictor variables, and they all have a statistically significant relationship with BD4_mean

TRAINING AND TEST

The adjusted value of 0.4699 indicated the model explains up to 47% of the variance in the data. The model was tested on the test data which suggested the residuals are approximately distributed with mean close to zero.

OPEN ANALYSIS

The species have a strong presence in the ecosystem from the mean and median values for present species the ecosystem. Bryophytes and Macromoths have a wider range variation and same way it is among different species. Isopod has a relatively high maximum value indicating the presence of a few outliers in the data. The correlation coefficients from the BD7 Bio_measure dataset show the highest correlation is between Bird and Macromoths, followed by Macromoth and Butterfly then between Birds and Ladybirds. On the other hand, Ladybird and Bryophyte has the highest negative correlation, followed by Bird and Bryophyte. Easting and northing was seen to have a negative correlation with most of the variables, which indicates that an increase in

these values may lead to a decrease in the values of other variables. The hypothesis testing for the relationship between Birds and Eastings indicated there is a statistically significant relationship between the two variables and we saw from the linear regression model that the Easting coordinate explains up to 9.94% of the variance in the Bird population, with Bird population and Easting having a strong linear relationship and we saw from the R-squared value of 0.3793 for the relationship between Bird and ecological status that we can use Bird as a predictor.

Furthermore, the regression model for ecological status against Bryophytes showed the two variables have a statistically significant association but the multiple R-squared being only 0.01004 indicated that the model explains only a small proportion of the ecological status variation. The regression model for the relationship between Butterflies and ecological status shows a statistically significant positive relationship between the two variables, with the R-squared value of 0.2053 indicating that 20.5% of the bird variation.

Overall, the analysis provides an insights on the relationships between the variables and their impact on the ecosystem although it is required to explore the cause of the observed relationships to provide useful insight on the relationship between variables in the dataset as well as inform decision making processes that relates to biodiversity conservation.

REFERENCE

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