Mols analysis example

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1 Methods

1.1 Data manipulation

For this test we will only use the larger ring data

To be able to use Cover as a numeric variable, the base level "+" will be transformed into, 1, then transform the variable into numeric and finally scale from 0 to 1. Also there are several taxa that do not appear in all sites, it is assumed that these taxa have a coverage of zero in all of those sites, we add this to the dataset. Then we used the specnumber and diversity from de vegan package [@Oksanen2020] to calculate species richness and Shannon diversity Index. This result in the pattens shown in figures 1, 2.

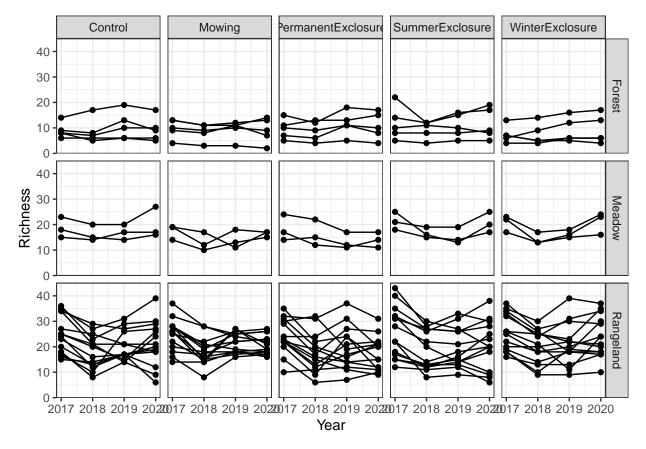


Figure 1: Time series of species richness for each Block, each tile represents a combination of treatment and initial habitat

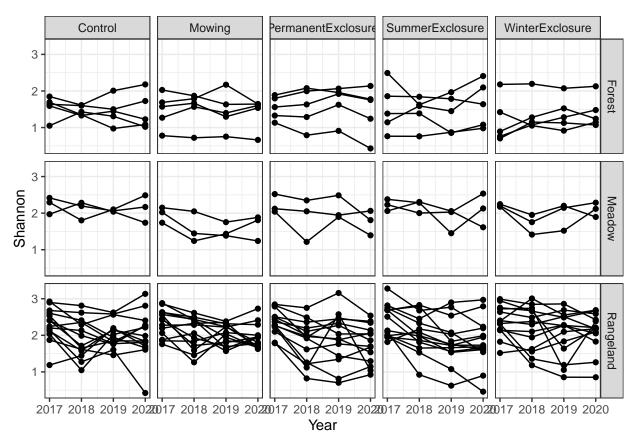


Figure 2: Time series of shannon diversity for each Block, each tile represents a combination of treatment and initial habitat

Table 1: Models that were used for the model average for the same start model

| (Intercept) | I((YEAR - 1)^2) | I(abs(YEAR - 1)) | aspect | Elevation | Initial Habitat | slope | InitialHabitat:YEAR | Treatment:YEAR | R2m | R2c | AICc |
|-------------|-----------------|------------------|--------|-----------|-----------------|-------|---------------------|----------------|------|------|---------|
| 1.94 | NA | 0.16 | NA | 0.01 | + | NA | + | + | 0.51 | 0.79 | 2512.73 |
| 2.07 | NA | 0.16 | NA | NA | + | NA | + | + | 0.49 | 0.79 | 2513.29 |
| 1.97 | NA | 0.16 | NA | 0.01 | + | -0.01 | + | + | 0.51 | 0.79 | 2513.54 |
| 1.91 | -0.03 | 0.22 | NA | 0.01 | + | NA | + | + | 0.51 | 0.79 | 2513.59 |
| 1.90 | NA | 0.16 | 0 | 0.01 | + | NA | + | + | 0.51 | 0.79 | 2513.92 |
| 2.05 | -0.03 | 0.22 | NA | NA | + | NA | + | + | 0.49 | 0.79 | 2514.14 |
| 2.12 | NA | 0.16 | NA | NA | + | -0.01 | + | + | 0.48 | 0.79 | 2514.32 |
| 1.95 | -0.03 | 0.22 | NA | 0.01 | + | -0.01 | + | + | 0.51 | 0.79 | 2514.41 |
| 2.03 | NA | 0.16 | 0 | NA | + | NA | + | + | 0.49 | 0.79 | 2514.46 |

Table 2: Parameters for the model average for the same start model

| term | estimate | std.error | statistic | p.value |
|--|----------|-----------|-----------|---------|
| TreatmentControl:YEAR | 0.046 | 0.020 | 2.317 | 0.021 |
| TreatmentMowing:YEAR | 0.035 | 0.020 | 1.767 | 0.077 |
| ${\bf Treatment Summer Exclosure: YEAR}$ | 0.042 | 0.020 | 2.136 | 0.033 |
| ${\bf Treatment Winter Exclosure: YEAR}$ | 0.067 | 0.019 | 3.458 | 0.001 |

1.2 Statistical analysis

The most general mixed model effect was generated using the lme4 package [@bates2010lme4], then all variations of such model were tested using the MuMIn package [@Barton2020] and ranked using the corrected Akaike Information Criterion (AICc). If the best model had at least a difference of two in AICc with the next model the best model was used. If that was not the case, all the models within that range were used to generate a full model average following @anderson2004model.

There where two phenomenons to take into account, the change of diversity, richness or cover for a specific group due to the treatment for each time of initial habitat, and the regional drought from 2018. In order to deal with this we used the following general equation:

```
y ~ aspect + Elevation + InitialHabitat + I(abs(YEAR - 1)) + I((YEAR - 1)^2) + slope +
Treatment:InitialHabitat + YEAR:InitialHabitat + YEAR:Treatment + YEAR:Treatment:InitialHabitat +
(1 | BlockNo)
```

The Year interaction with Initial Habitat, Treatment or both without adding the Year term on its own ensures that if the year 2017 is coded as year 0 that the effect to be tested will be that if a plot was started in the same block, they should start with the same Richness/Diversity/Taxa cover, whereas the |(Year - 1)| and $(Year - 1)^2$ terms will show the spike or dip that might have been caused by the drought year. For each of the different analyses a glmm with the propper family or basic lmm was performed depending on the nature of the response variable:

- Richess: Since richness can only be a discrete positive value, we used a Poisson GLMM
- **Diversity:** For diversity, we did a similar approach but with a regular mixed effects linear model, since the response variable (Shannon's diversity index)

2 Results

2.1 Richness

For the richness model a total of 192 models were tested and we ended up with 9 models to be used to generate an average model. The models with the selected variable parameters and with the marginal and conditional R^2 [@nakagawa2017coefficient] can be seen in table 1 and the parameters of the average model are in table 2, and the response of each treatment for each habitat in average conditions is shown in figure 3.

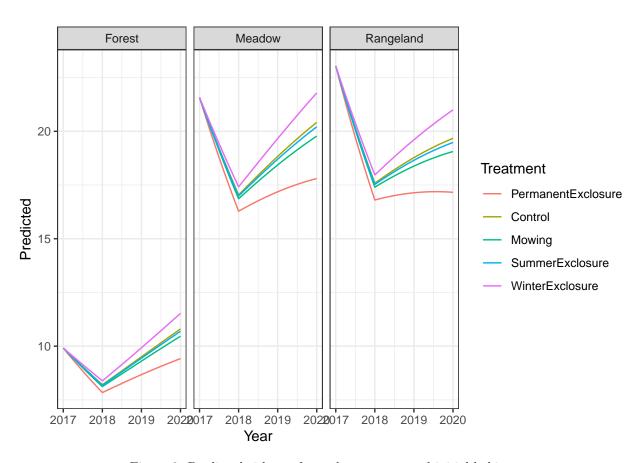


Figure 3: Predicted richness for each treatment and initial habitat

3 References

4 Reproducibility ticket

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##
            Ubuntu 18.04.5 LTS
##
   system
            x86_64, linux-gnu
##
   ui
            X11
##
   language (EN)
   collate en US.UTF-8
##
   ctype
            en_US.UTF-8
##
   tz
            America/Santiago
##
            2021-04-13
   date
##
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                                    lib source
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                  0.2.1
   backports
                  1.2.1
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                          2021-01-26 [1] CRAN (R 4.0.4)
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                 0.8.2
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                 0.21
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   broomExtra
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                 0.19 - 4
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  codetools
                          2020-11-04 [1] CRAN (R 4.0.4)
##
                 0.2-18
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  crayon
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    MASS
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## [2] /usr/local/lib/R/site-library
```

- ## [3] /usr/lib/R/site-library
- ## [4] /usr/lib/R/library