**Browsing Modelling Ideas**

**1. Terms**

**Relative abundance of species**: 2 possibilities

* ‘species evenness’ might be calculated by Shannon’s equitability index <https://studylib.net/doc/7336283/diversity-indices--shannon-s-h-and-e>

<https://microbeatic.wordpress.com/2012/01/26/diversity-index-shannon-indexshannon-weaver-index-h/>

<https://www.statology.org/shannon-diversity-index/>

* Find abundance for T1, abundance for T2, and abundance for Control. Then compare these to get some measure of relative abundance across all treatments. (use the Braun-Blanquet Cover Abundance Scale as an indicator of abundance)

**Richness**: *S*, is the number of species for which at least one individual exists at a location and/or a time point

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6182778/#:~:text=Definition%201,and%2For%20a%20time%20point>.

**Diversity**: calculated with abundance and richness as input, might use Shanon’s diversity index

<https://studylib.net/doc/7336283/diversity-indices--shannon-s-h-and-e>

**2. Modelling ideas**

\*note: there’s no data for fenced control plots. So, we are only able to test the effect of browsing exclusion between 2 treatments, but not the control.

**Hypothesis 1: Removal of browsing will cause a greater increase in understorey species richness in T1 compared to T2**

**Response**: the change in species richness (+ - count number)

**Explanatory variable**: type of treatment (dummy variable)

**Models to try**:

1). Poisson (GLM)

- because it’s a count data

- but the data can’t be negative 🡪 “a poisson family can still often be invoked so long as the sample mean is positive” (<https://stats.stackexchange.com/questions/303660/manipulating-negative-count-response-variable-in-glm>)

- assume mean=variance, if not 🡪 use Quasi Poisson instead

2). Negative Binomial (GLM)

- also for non-negative count data

- check for Pearson Chi2 dispersion statistic

if close to 1 🡪 Poisson

if >1 🡪 Negative Binomial

- Plot standardized residual

if between -2 and 2 🡪 Poisson

else 🡪 Negative Binomial

3). Linear model

- if y ~ Normal

**Test:**

Whether a model with intercept only is better than the model with treatment as a predictor (using Likelihood Ratio Test)

if better 🡪 The effect of browsing exclusion is not different between different treatments

if not better 🡪 see the sign of to agree with or reject the hypothesis

**Hypothesis 2: Removal of browsing will cause a greater increase in understorey species diversity in T1 as compared to T2**

**Response**: the change in species diversity (+ - continuous)

**Explanatory variable**: type of treatment (dummy variable)

**Models to try**:

1). Linear model

- if y ~ Normal

2). Gamma (GLM)

- if y is non-negative and positively skewed

3). Inverse Gaussian (GLM)

- if the response is non-negative

**Test:**

Whether a model with intercept only is better than the model with treatment as a predictor (using Likelihood Ratio Test)

if better 🡪 The effect of browsing exclusion is not different between different treatments

if not better 🡪 see the sign of to agree with or reject the hypothesis

**Hypothesis 3: Removal of browsing will cause a greater increase in relative abundances of species in the understorey community in T1 as compared to T2**

**Response**: the change in relative abundances of species (+ - continuous)

**Explanatory variable**: type of treatment (dummy variable)

**Models to try**:

1). Linear model

- if y ~ Normal

2). Gamma (GLM)

- if y is non-negative and positively skewed

3). Inverse Gaussian (GLM)

- if the response is non-negative

**Test:**

Whether a model with intercept only is better than the model with treatment as a predictor (using Likelihood Ratio Test)

if better 🡪 The effect of browsing exclusion is not different between different treatments

if not better 🡪 see the sign of to agree with or reject the hypothesis

**3. How to deal with negative responses?**

**idea 1**

Add constant ‘a’ to all responses to make them non-negative. Do this only to compare the effects, it might not change the interpretation?

Reference : <https://www.sciencedirect.com/science/article/pii/S0378112721004023/pdfft?isDTMRedir=true&download=true>

**idea 2**

Run a Box-Cox Transformation to make the dependent variable Normal. Then apply Linear Model instead of GLM

**idea 3**

Use Wilcoxon Rank Sum test to test the hypothesis (<https://data.library.virginia.edu/the-wilcoxon-rank-sum-test/>)

Wilcoxon Rank Sum test is a nonparametric version of t-test. It tests whether two samples are likely to derive from the same population (i.e., that the two populations have the same shape). Some investigators interpret this test as comparing the medians between the two populations.

**4. Additional modelling idea**

Use Linear/GL **mixed** model, including plot and quadrat numbers as a nested random effect (I haven’t learnt this, but can explore more if it’s worth it)

**5. Hypothesis testing result so far**

|  |  |  |  |
| --- | --- | --- | --- |
| **Hypothesis** | **Y0 to 3** | **Y3 to 6** | **Y0 to 6** |
| 1). Removal of browsing will cause a greater increase in understorey species richness in T1 compared to T2 | No evidence | No evidence | No evidence |
| 2). Removal of Browsing will cause Species richness to be higher across all treatments (T1 & T2) | No evidence | **There is evidence** Removal of Browsing have a more positive effect on Species richness across all treatments (T1 & T2) | No evidence |
| 3). Removal of browsing will cause a greater increase in understorey species diversity in T1 as compared to T2 | No evidence | No evidence | No evidence |
| 4). Removal of Browsing will cause Species diversity to be higher across all treatments (T1 & T2) | No evidence | There is evidence  Removal of Browsing have a more positive effect on Species diversity across all treatments (T1 & T2) | No evidence |