

First approach to models

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1. Load the diversity metrics that have been calculated from a table that:

- Had corrected abundance measures using sampling effort
- Had merged sites
- Does not have NaN

```
diversity4 <- readRDS("./output/cleaned_data/02_Statistical_Analysis_Site_metrics.rds")
```

2. I will first explore the number of sites that have a known land use category

```
second_model_data <- diversity4 %>%
  # make a level of Primary minimal
  mutate(
    # collapse primary forest and non-forest together into primary vegetation
    # as these aren't well distinguished
    Predominant_land_use = recode_factor(Predominant_land_use,
                                           "Primary forest" = "Primary",
                                           "Primary non-forest" = "Primary"),
    # indeterminate secondary veg and cannot decide are transformed into NA.
    # Urban too because it has only 40 sites.
    Predominant_land_use = na_if(Predominant_land_use, "Secondary vegetation (indeterminate age)"),
    Predominant_land_use = na_if(Predominant_land_use, "Cannot decide"),
    Predominant_land_use = na_if(Predominant_land_use, "Urban"),
    # Give a shorter name to some land use categories
    Predominant_land_use = str_replace_all(Predominant_land_use,
                                           pattern = c("Young secondary vegetation" =
                                                       "YSV",
                                                       "Intermediate secondary vegetation" =
                                                       "YSV",
                                                       "Mature secondary vegetation" = "MSV")),
    Predominant_land_use = factor(Predominant_land_use),
    Predominant_land_use = relevel(Predominant_land_use, ref = "Primary"),
  )
  # Drop sites that don't have abundance measures or land-use data
```

```

second_model_data1 <- drop_na(second_model_data,
                               Total_abundance, Predominant_land_use) %>% droplevels()

# Check the number of sites for animals and plants
addmargins(table(second_model_data1$Predominant_land_use,
                 second_model_data1$Use_intensity, second_model_data1$Kingdom), 2)

## , , = Animalia
##
##
##                                     Minimal use Light use Intense use
## Primary                           423      214      50
## Cropland                          78       20      66
## MSV                                17      137      0
## Pasture                            0       8      9
## Plantation forest                  28      338     19
## Young secondary vegetation        49       10      0
## YSV                                87      70      2
##
##                                     Cannot decide Sum
## Primary                           10      697
## Cropland                          84      248
## MSV                                24      178
## Pasture                            160     177
## Plantation forest                  0      385
## Young secondary vegetation        74      133
## YSV                                31      190
##
## , , = Plantae
##
##
##                                     Minimal use Light use Intense use
## Primary                           314      89      93
## Cropland                          19       0      60
## MSV                                52       9      6
## Pasture                            21      32      4
## Plantation forest                  81      216     43
## Young secondary vegetation        74      25      0
## YSV                                51      78      2
##
##                                     Cannot decide Sum
## Primary                           68      564
## Cropland                          9       88
## MSV                                0      67
## Pasture                            0      57
## Plantation forest                  6      346
## Young secondary vegetation        3      102
## YSV                                26     157

```

3. Merge use intensities for those land use categories that don't have enough sites to separate them into different intensities

- I will separate Primary into minimal, light and intense uses

- I will separate ISv into minimal and light-intense uses
- I will separate Plantation forest into minimal and light/intense uses
- Everything else I will merge all intensities

```

LandUse_divide <- c("Primary", "ISV", "Plantation forest")

second_model_data2 <- second_model_data1 %>%
  mutate(
    # Drop the Cannot decide intensity levels for the land-use categories that have
    # enough sites for the minimal, and light/intense
    Use_intensity = ifelse(Predominant_land_use %in% LandUse_divide &
      Use_intensity == "Cannot decide",
      NA,
      paste(Use_intensity)),

    # Join the intensity levels of light and intense for Plantation forest and ISV
    Use_intensity = ifelse((Predominant_land_use == "Plantation forest" |
      Predominant_land_use == "ISV") &
      (Use_intensity == "Intense use" |
      Use_intensity == "Light use"),
      str_replace_all(Use_intensity, pattern = c("Intense use" = "Light-intense use",
        "Light use" = "Light-intense use")),
      paste(Use_intensity)),

    # Merge all the intensity levels for those land-use categories that don't have
    # enough sites in each land-use type/intensity combination
    Use_intensity = ifelse(Predominant_land_use %nin% LandUse_divide,
      str_replace_all(Use_intensity, pattern = c("Intense use" =
        "All", "Light
use" = "All",
"Minimal use"
= "All", "Cannot
decide" =
"All")),
      paste(Use_intensity)),

    # Paste the land-use classes and intensity levels
    LandUse = ifelse(Predominant_land_use != "NA" & Use_intensity != "NA",
      paste(Predominant_land_use, Use_intensity),
      NA),

    # set reference level
    LandUse = factor(LandUse),
    LandUse = relevel(LandUse, ref = "Primary Minimal use")
  )
)

```

4. Test for collinearity

Since I'm going to explore the collinearity between categorical variables, I'm going to use the Generalized variance Inflation Factors function provided by Zuur et al., (2009)

```

source("https://highstat.com/Books/Book2/HighstatLibV10.R")

corvif(second_model_data2[ , c("LandUse", "Kingdom")])

##
## Variance inflation factors
##
##          GVIF Df GVIF^(1/2Df)
## LandUse 1.06122 10    1.002975
## Kingdom 1.06122   1    1.030155

```

4. Get complete cases, that means dropping the rows that have NA in the columns of total abundance and LandUse

```

# Create a table with complete cases
second_model_data2 <- drop_na(second_model_data2,
                                Total_abundance, LandUse) %>% droplevels()

# Check number of sites
table(second_model_data2$LandUse, second_model_data2$Kingdom)

```

```

##
##                               Animalia Plantae
## Primary Minimal use           423     314
## Cropland All                  248      88
## ISV Light-intense use        72       80
## ISV Minimal use              87       51
## MSV All                       178      67
## Pasture All                   177      57
## Plantation forest Light-intense use 357     259
## Plantation forest Minimal use  28       81
## Primary Intense use          50       93
## Primary Light use             214      89
## YSV All                        133     102

```

5. Transform abundance measures

Abundance data usually display a nonnormal error distribution because they have a positive mean-variance relationship and are zero-inflated (Purvis et al., 2018). Given that some abundance measures are not integers (some are relative abundance or densities), I am not going to model the abundance with a Poisson distribution, but I'm going to transform it in order to meet the assumptions of linear mixed models.

```

second_model_data2 <- mutate(second_model_data2,
                             logAbundance = log(RescaledAbundance + 1),
                             sqrtAbundance = sqrt(RescaledAbundance)
)

```

6. Select random effects structure

To select the random-effects structure, we use the method recommended by (Zuur et al., 2009) of taking the most complex fixed-effects structure, including all interactions, that will be tested in the second stage of modelling, and use it to compare different random-effects structures.

```

m2_1 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1|SS) + (1|SSB), data = second_model_data2)

m2_2 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1|SS) + (1|SSB) + (1|Source_ID), data = second_model_data2)

m2_3 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1+LandUse|SS) + (1|SSB), data = second_model_data2)

## boundary (singular) fit: see ?isSingular

m2_5 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1+Predominant_land_use|SS) + (1|SSB), data = second_model_data2)

## boundary (singular) fit: see ?isSingular

```

Compare the models that converge using the Akaike's Information Criterion

```
AIC(m2_1, m2_2)
```

```

##      df      AIC
## m2_1 25 90.96718
## m2_2 26 88.13796

```

8. Select fixed effects structure

```
Anova(m2_2)
```

```

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrtAbundance
##              Chisq Df Pr(>Chisq)
## LandUse       62.8550 10   1.04e-09 ***
## Kingdom        0.6132  1    0.4336
## LandUse:Kingdom 55.4609 10   2.59e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

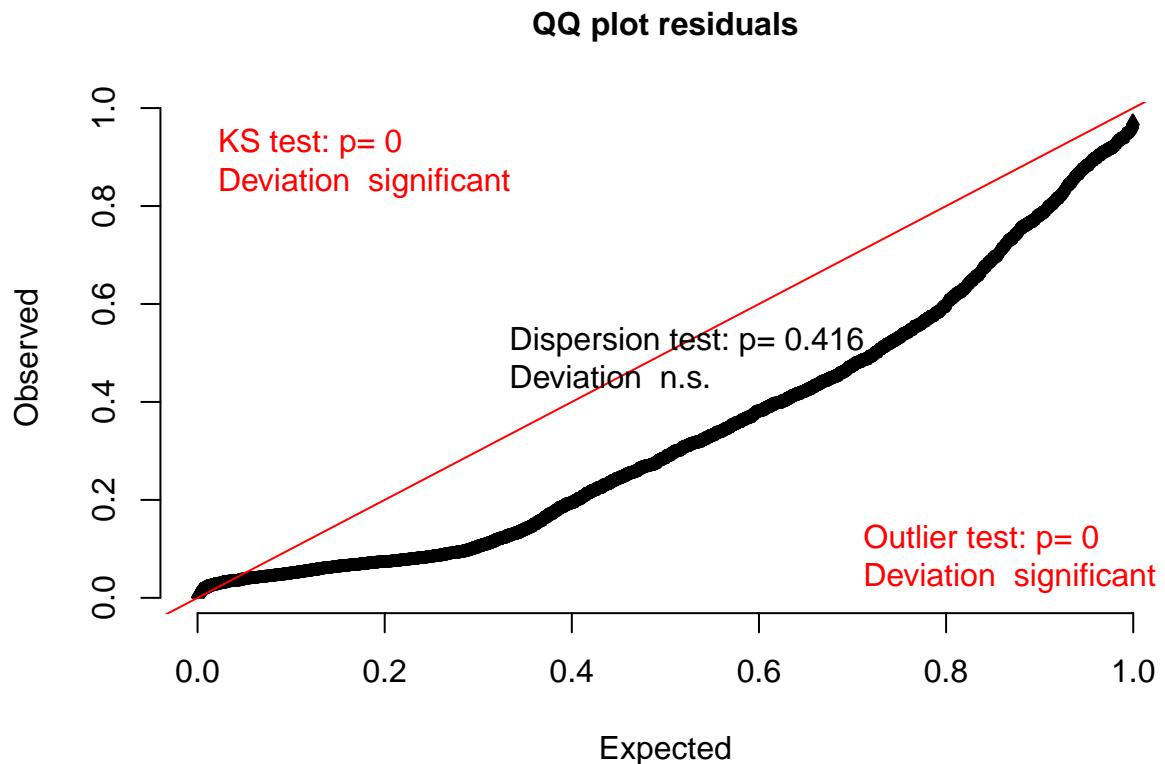
Since the interaction is significant, I am going to leave the two explanatory variables.

9. Plot residuals of the model

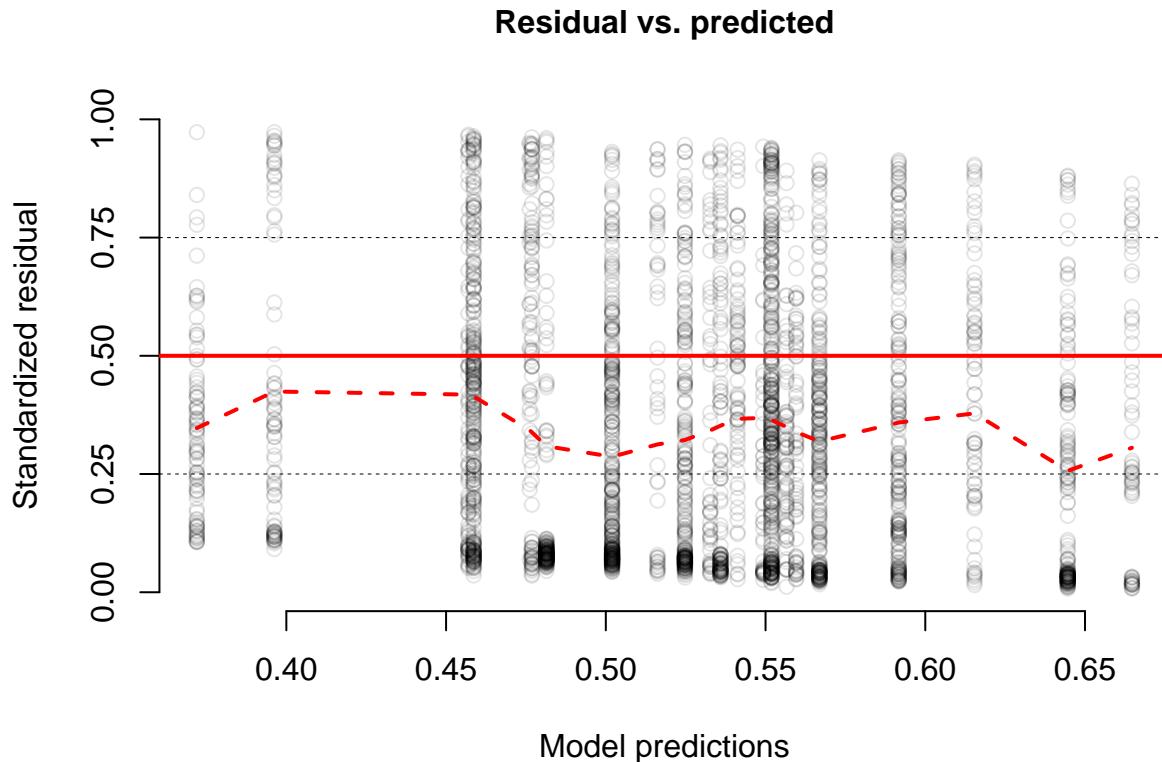
```

simulationOutput2 <- simulateResiduals(fittedModel = m2_2)
# Acces the qq plot
plotQQunif(simulationOutput2)

```



```
# Plot the residuals against the predicted value
plotResiduals(simulationOutput2)
```



10. Model estimates

```
summary(m2_2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom + (1 | SS) +
##           (1 | SSB) + (1 | Source_ID)
## Data: second_model_data2
##
## REML criterion at convergence: 36.1
##
## Scaled residuals:
##      Min     1Q   Median     3Q    Max 
## -3.1804 -0.6436 -0.1916  0.5944  3.7547 
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## SSB      (Intercept) 0.005197 0.07209
## SS       (Intercept) 0.021094 0.14524
## Source_ID (Intercept) 0.028766 0.16960
## Residual            0.051983 0.22800
## Number of obs: 3248, groups: SSB, 286; SS, 102; Source_ID, 85
##
## Fixed effects:
## (Intercept)                         Estimate
##                                         0.551840
```

## LandUseCropland All	-0.027071
## LandUseISV Light-intense use	0.007754
## LandUseISV Minimal use	-0.010576
## LandUseMSV All	0.092765
## LandUsePasture All	-0.070403
## LandUsePlantation forest Light-intense use	-0.049876
## LandUsePlantation forest Minimal use	-0.075674
## LandUsePrimary Intense use	-0.002556
## LandUsePrimary Light use	0.039855
## LandUseYSV All	-0.015930
## KingdomPlantae	-0.093202
## LandUseCropland All:KingdomPlantae	-0.035319
## LandUseISV Light-intense use:KingdomPlantae	0.090167
## LandUseISV Minimal use:KingdomPlantae	0.068129
## LandUseMSV All:KingdomPlantae	0.113290
## LandUsePasture All:KingdomPlantae	0.144463
## LandUsePlantation forest Light-intense use:KingdomPlantae	0.158109
## LandUsePlantation forest Minimal use:KingdomPlantae	0.232444
## LandUsePrimary Intense use:KingdomPlantae	-0.084098
## LandUsePrimary Light use:KingdomPlantae	-0.041494
## LandUseYSV All:KingdomPlantae	0.034141
##	Std. Error
## (Intercept)	0.034853
## LandUseCropland All	0.023443
## LandUseISV Light-intense use	0.034321
## LandUseISV Minimal use	0.033079
## LandUseMSV All	0.032570
## LandUsePasture All	0.031716
## LandUsePlantation forest Light-intense use	0.023739
## LandUsePlantation forest Minimal use	0.060847
## LandUsePrimary Intense use	0.042731
## LandUsePrimary Light use	0.024981
## LandUseYSV All	0.029256
## KingdomPlantae	0.054347
## LandUseCropland All:KingdomPlantae	0.040668
## LandUseISV Light-intense use:KingdomPlantae	0.048707
## LandUseISV Minimal use:KingdomPlantae	0.052457
## LandUseMSV All:KingdomPlantae	0.051776
## LandUsePasture All:KingdomPlantae	0.055527
## LandUsePlantation forest Light-intense use:KingdomPlantae	0.036059
## LandUsePlantation forest Minimal use:KingdomPlantae	0.071809
## LandUsePrimary Intense use:KingdomPlantae	0.061375
## LandUsePrimary Light use:KingdomPlantae	0.044860
## LandUseYSV All:KingdomPlantae	0.043179
##	t value
## (Intercept)	15.833
## LandUseCropland All	-1.155
## LandUseISV Light-intense use	0.226
## LandUseISV Minimal use	-0.320
## LandUseMSV All	2.848
## LandUsePasture All	-2.220
## LandUsePlantation forest Light-intense use	-2.101
## LandUsePlantation forest Minimal use	-1.244
## LandUsePrimary Intense use	-0.060

```

## LandUsePrimary Light use           1.595
## LandUseYSV All                  -0.544
## KingdomPlantae                 -1.715
## LandUseCropland All:KingdomPlantae -0.868
## LandUseISV Light-intense use:KingdomPlantae 1.851
## LandUseISV Minimal use:KingdomPlantae 1.299
## LandUseMSV All:KingdomPlantae 2.188
## LandUsePasture All:KingdomPlantae 2.602
## LandUsePlantation forest Light-intense use:KingdomPlantae 4.385
## LandUsePlantation forest Minimal use:KingdomPlantae 3.237
## LandUsePrimary Intense use:KingdomPlantae -1.370
## LandUsePrimary Light use:KingdomPlantae -0.925
## LandUseYSV All:KingdomPlantae 0.791

##
## Correlation matrix not shown by default, as p = 22 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

```

Table with confidence intervals

```

CI_m2_2 <- read.csv("./output/summary_m2_2.csv", header = TRUE, sep = ";")
kable(CI_m2_2, format="latex", booktabs=TRUE) %>%
  kable_styling(latex_options="scale_down")

```

X	Estimate	Std..Error	t.value	Actual.estimate	CI.lower	CI.upper
(Intercept)	0.552	0.035	15.83	0.552	0.484	0.620
Cropland All	-0.027	0.023	-1.15	0.525	0.479	0.571
ISV Light-in	0.008	0.034	0.23	0.560	0.492	0.627
ISV Minimal	-0.011	0.033	-0.32	0.541	0.476	0.606
MSV All	0.093	0.033	2.85	0.645	0.581	0.708
Pasture All	-0.070	0.032	-2.22	0.481	0.419	0.544
Plantation forest Light-in	-0.050	0.024	-2.10	0.502	0.455	0.548
Plantation forest Minimal	-0.076	0.061	-1.24	0.476	0.357	0.595
Primary Intense	-0.003	0.043	-0.06	0.549	0.466	0.633
Primary Light	0.040	0.025	1.60	0.592	0.543	0.641
YSV All	-0.016	0.029	-0.54	0.536	0.479	0.593
Plantae	-0.093	0.054	-1.71	0.459	0.352	0.565
Cropland All:Plantae	-0.035	0.041	-0.87	0.396	0.317	0.476
ISV Light-in :Plantae	0.090	0.049	1.85	0.557	0.461	0.652
ISV Minimal :Plantae	0.068	0.052	1.30	0.516	0.413	0.619
MSV All:Plantae	0.113	0.052	2.19	0.665	0.563	0.766
Pasture All:Plantae	0.144	0.056	2.60	0.533	0.424	0.642
Plantation forest Light-in :Plantae	0.158	0.036	4.38	0.567	0.496	0.638
Plantation forest Minimal :Plantae	0.232	0.072	3.24	0.615	0.475	0.756
Primary Intense :Plantae	-0.084	0.061	-1.37	0.372	0.252	0.492
Primary Light :Plantae	-0.041	0.045	-0.92	0.457	0.369	0.545
YSV All:Plantae	0.034	0.043	0.79	0.477	0.392	0.561

11. Plot the results

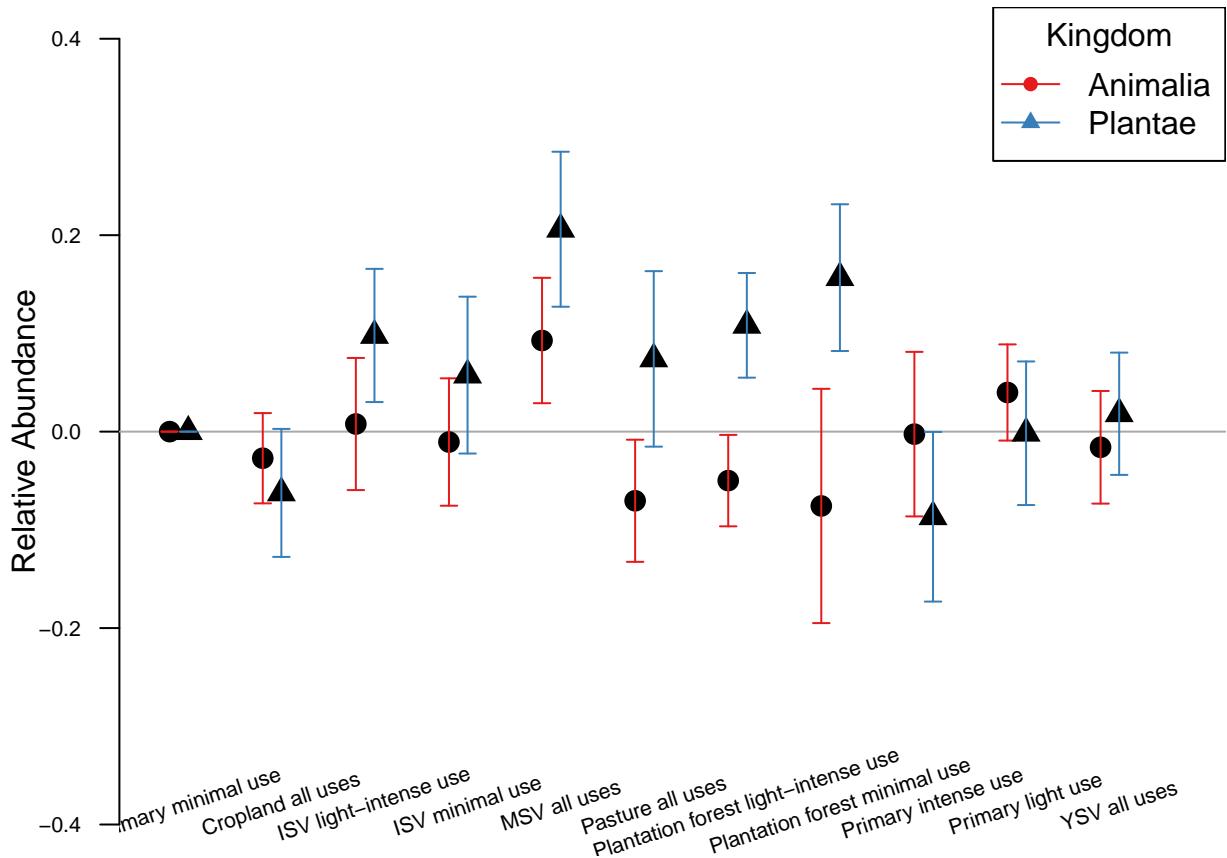
```

#Read r code from a file which contains the function to make the plot
source("./R/PlotErrBar_interactions.R")
source("./R/PlotErrBar_interactions_modified.R")

# Plot the differences between estimates
PlotErrBar_interactions_modi(model = m2_2, resp = "Abundance", Effect1 = "LandUse",
                               Effect2 = "Kingdom",
                               ylims = c(-0.4,0.4), pointtype = c(16,17),blackwhite = FALSE)

# Plot the x label
text(x = c(0.8:10.8), y = -0.38, labels = c("Primary minimal use",
                                                "Cropland all uses",
                                                "ISV light-intense use",
                                                "ISV minimal use",
                                                "MSV all uses",
                                                "Pasture all uses",
                                                "Plantation forest light-intense use",
                                                "Plantation forest minimal use",
                                                "Primary intense use",
                                                "Primary light use",
                                                "YSV all uses"), srt = 18, cex= 0.7)

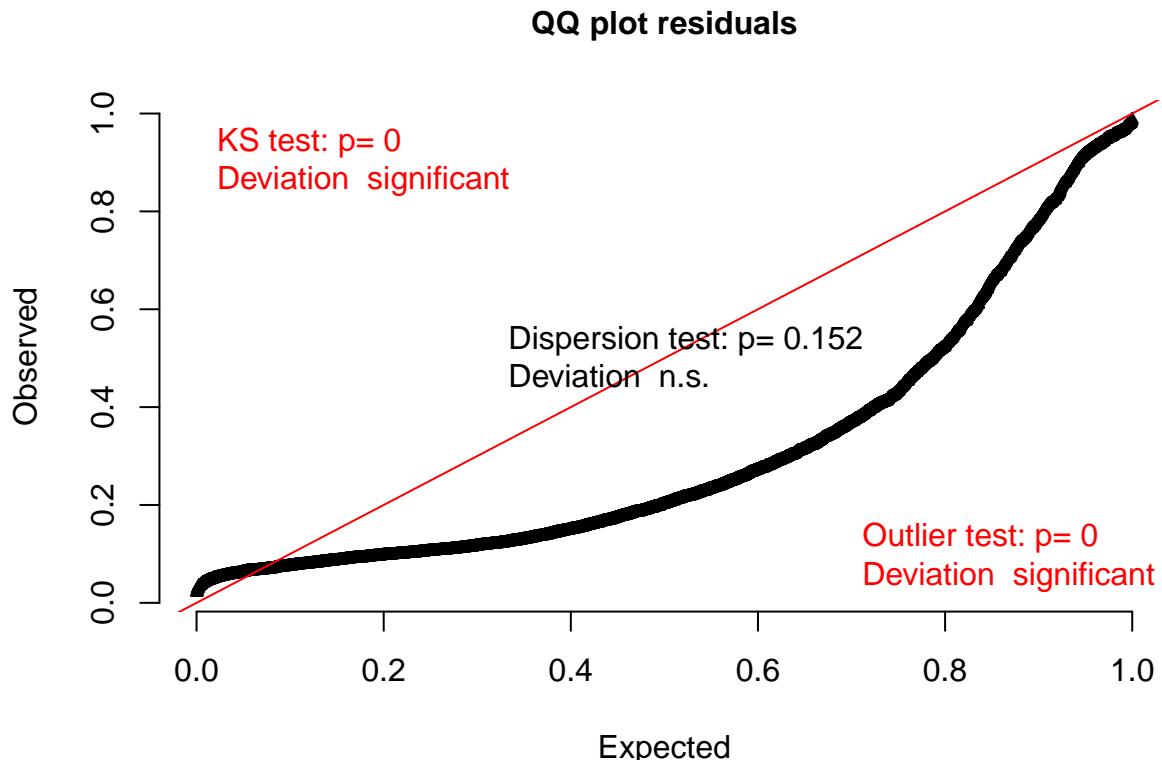
```



12. Run the models with the log of Abundance

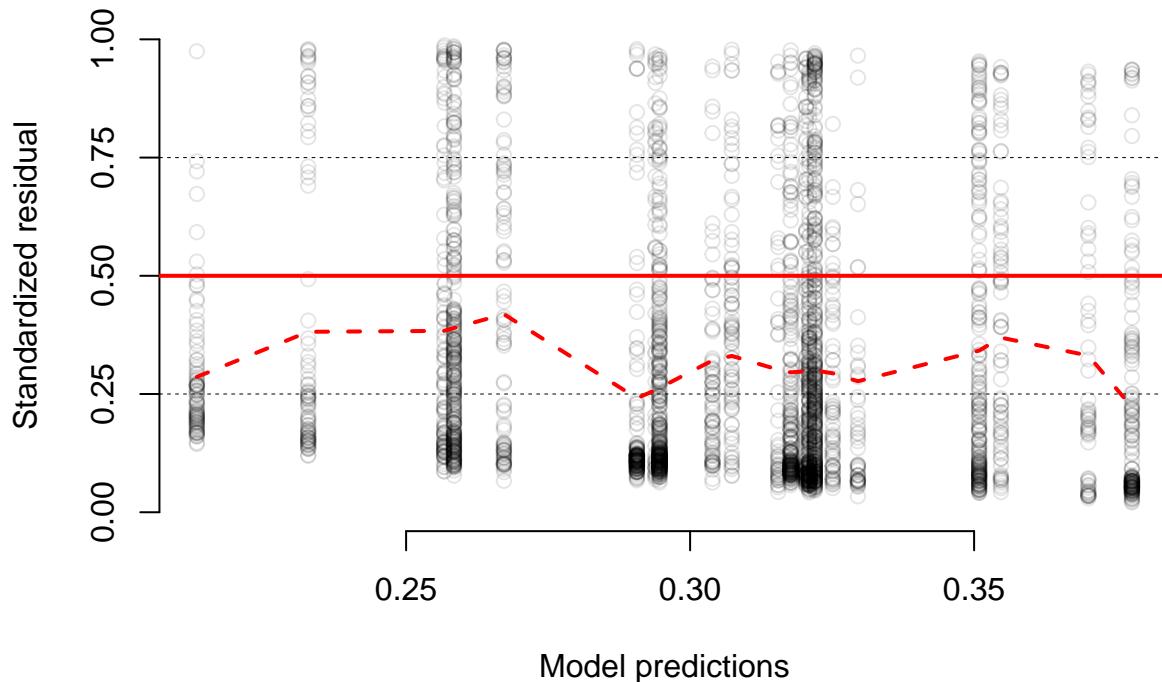
```
m21_2 <- lmer(logAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
  (1|SS) + (1|SSB) + (1|Source_ID), data = second_model_data2)
```

```
simulationOutput21 <- simulateResiduals(fittedModel = m21_2)
# Acces the qq plot
plotQQunif(simulationOutput21)
```



```
# Plot the residuals against the predicted value
plotResiduals(simulationOutput21)
```

Residual vs. predicted



13. Merge all land-use intensities

```

Third_model_data <- diversity4 %>%
  # make a level of Primary minimal
  mutate(
    # collapse primary forest and non-forest together into primary vegetation
    # as these aren't well distinguished
    Predominant_land_use = recode_factor(Predominant_land_use,
                                           "Primary forest" = "Primary",
                                           "Primary non-forest" = "Primary"),
    # indeterminate secondary veg and cannot decide are transformed into NA.
    # Urban too because it has only 40 sites.
    Predominant_land_use = na_if(Predominant_land_use, "Secondary vegetation (indeterminate age)"),
    Predominant_land_use = na_if(Predominant_land_use, "Cannot decide"),
    Predominant_land_use = na_if(Predominant_land_use, "Urban"),
    # Give a shorter name to some land use categories
    Predominant_land_use = str_replace_all(Predominant_land_use, pattern =
      c("Young secondary vegetation" = "YSV",
        "Intermediate secondary vegetation" = "ISV",
        "Mature secondary vegetation" = "MSV"))
  )

```

```

# Merge all the intensity levels for all land-use categories
Use_intensity = ifelse(Use_intensity != "NA", "All", "NA"),

# Paste the land-use classes and intensity levels
LandUse = ifelse(Predominant_land_use != "NA" & Use_intensity != "NA",
                  paste(Predominant_land_use, Use_intensity),
                  NA),

# set reference level
LandUse = factor(LandUse),
LandUse = relevel(LandUse, ref = "Primary All")
)

```

14. Test for collinearity

```

# Calculate the VIF
corvif(Third_model_data[ , c("LandUse", "Kingdom")])

```

```

##
##
## Variance inflation factors
##
##          GVIF Df GVIF^(1/2Df)
## LandUse 1.050652 6    1.004126
## Kingdom 1.050652 1    1.025013

```

15. Complete cases

```

# Create a table with complete cases
Third_model_data2 <- drop_na(Third_model_data,
                           Total_abundance, LandUse) %>% droplevels()

# Check number of sites
table(Third_model_data2$LandUse, Third_model_data2$Kingdom)

```

```

##
##          Animalia Plantae
## Primary All      697     564
## Cropland All    248      88
## ISV All         190     157
## MSV All         178      67
## Pasture All     177      57
## Plantation forest All 385     346
## YSV All         133     102

```

16. Transform abundance measures

```

# Transform RescaledAbundance.
Third_model_data2 <- mutate(Third_model_data2,
                           logAbundance = log(RescaledAbundance + 1),
                           sqrtAbundance = sqrt(RescaledAbundance)
)

```

17. Select random effects structure

```
m3_1 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1|SS) + (1|SSB), data = Third_model_data2)

m3_2 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1|SS) + (1|SSB) + (1|Source_ID), data = Third_model_data2)

m3_3 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1+LandUse|SS) + (1|SSB), data = Third_model_data2)

## boundary (singular) fit: see ?isSingular

m3_5 <- lmer(sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
               (1+Predominant_land_use|SS) + (1|SSB), data = Third_model_data2)

## boundary (singular) fit: see ?isSingular

# Compare the models that converged
AIC(m3_1, m3_2)
```

```
##      df      AIC
## m3_1 17 43.83383
## m3_2 18 40.43808
```

18. Choose fixed effects structure

```
# See the significance of the terms in the model.
Anova(m3_2)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrtAbundance
##              Chisq Df Pr(>Chisq)
## LandUse       48.8740  6  7.902e-09 ***
## Kingdom        0.9595  1    0.3273
## LandUse:Kingdom 53.2995  6  1.021e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# The Land_use:kingdom interaction is significant, so I won't remove this term
# from the model.

# compare the models that converged using all use intensities merged, and the models that converged
# separating the use-intensities for some land uses
AIC(m2_1, m2_2, m3_1, m3_2)

## Warning in AIC.default(m2_1, m2_2, m3_1, m3_2): models are not all fitted
## to the same number of observations
```

```

##      df      AIC
## m2_1 25 90.96718
## m2_2 26 88.13796
## m3_1 17 43.83383
## m3_2 18 40.43808

anova(m3_2, m2_1)

## Error in anova.merMod(m3_2, m2_1): models were not all fitted to the same size of dataset

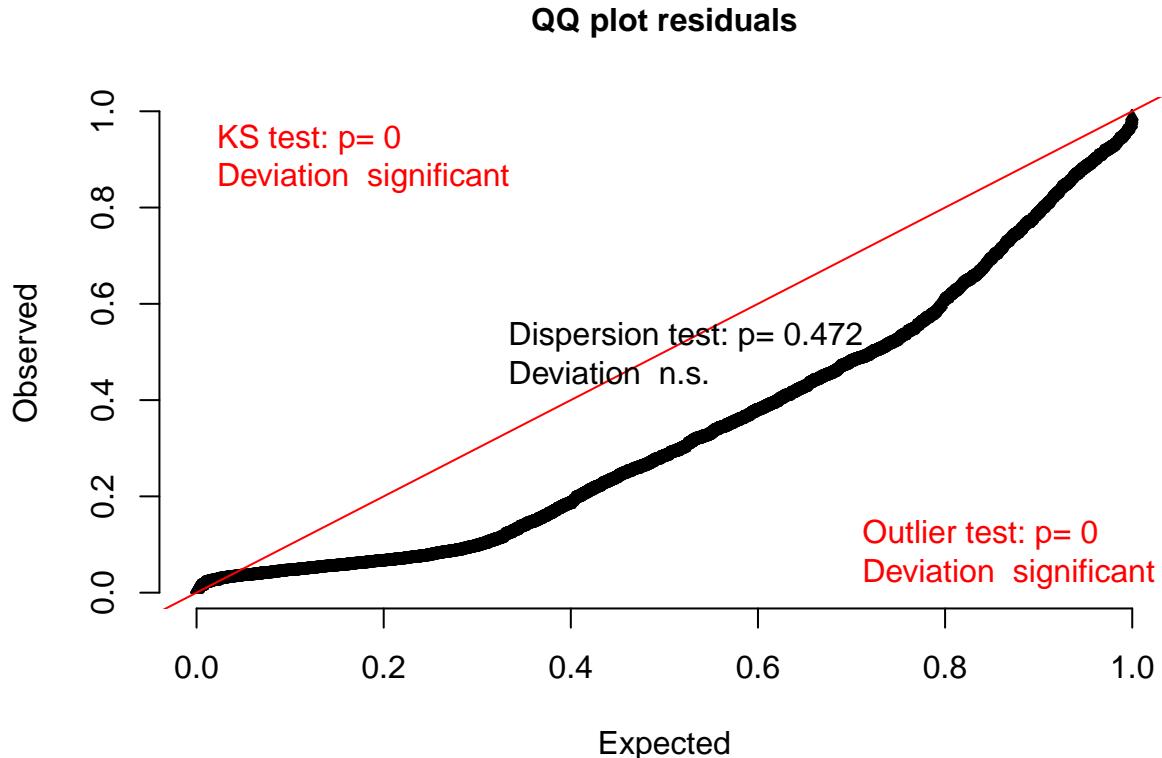
```

19. Plot residuals

```

simulationOutput3 <- simulateResiduals(fittedModel = m3_2)
# Acces the qq plot
plotQQunif(simulationOutput3)

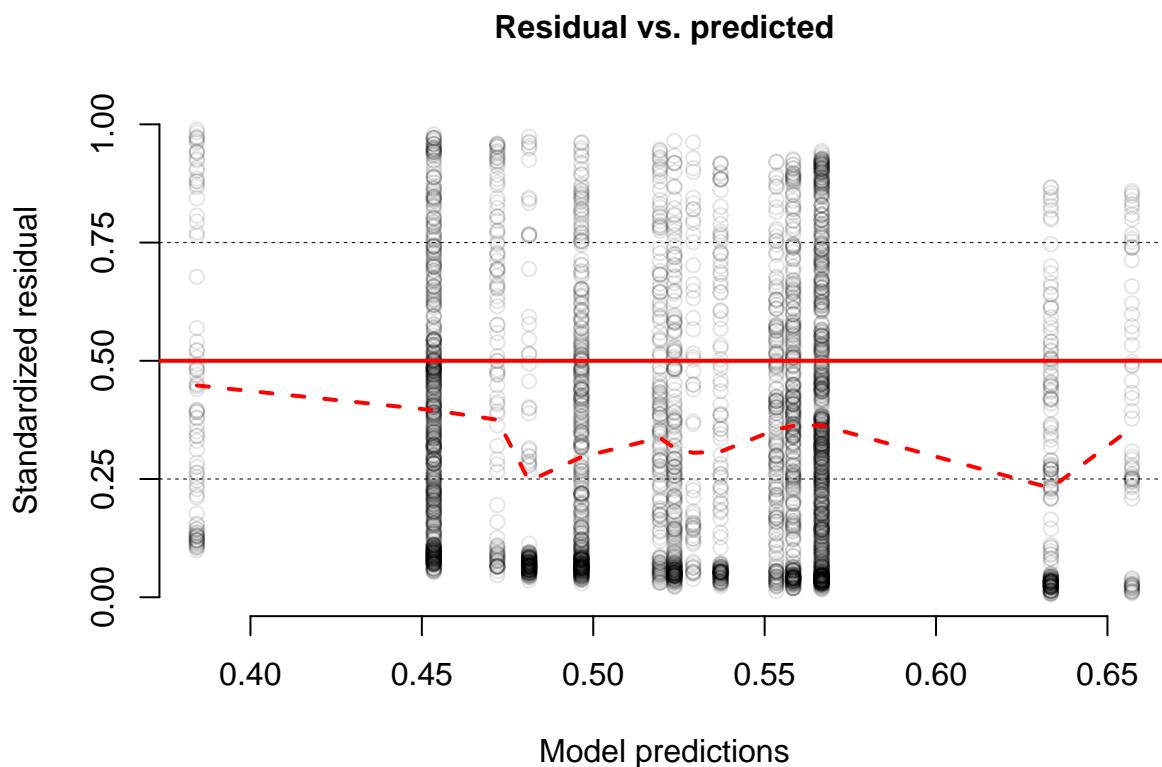
```



```

# Plot the residuals against the predicted value
plotResiduals(simulationOutput3)

```



20. Model estimates

```
summary(m3_2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: sqrtAbundance ~ LandUse + Kingdom + LandUse:Kingdom + (1 | SS) +
##           (1 | SSB) + (1 | Source_ID)
## Data: Third_model_data2
##
## REML criterion at convergence: 4.4
##
## Scaled residuals:
##      Min     1Q   Median     3Q    Max 
## -3.2118 -0.6410 -0.2025  0.5986  4.0009 
## 
## Random effects:
## Groups   Name        Variance Std.Dev.
## SSB      (Intercept) 0.003841 0.06198
## SS       (Intercept) 0.021589 0.14693
## Source_ID (Intercept) 0.028785 0.16966
## Residual            0.052160 0.22839
## Number of obs: 3389, groups: SSB, 305; SS, 104; Source_ID, 86
##
## Fixed effects:
## (Intercept)          Estimate Std. Error t value
##                   0.56664   0.03379  16.770
```

```

## LandUseCropland All           -0.04295  0.02218 -1.936
## LandUseISV All              -0.01321  0.02351 -0.562
## LandUseMSV All               0.06686  0.02969  2.252
## LandUsePasture All            -0.08535  0.03086 -2.766
## LandUsePlantation forest All -0.07009  0.02090 -3.353
## LandUseYSV All                -0.02947  0.02850 -1.034
## KingdomPlantae                 -0.11315  0.05209 -2.172
## LandUseCropland All:KingdomPlantae -0.02618  0.03879 -0.675
## LandUseISV All:KingdomPlantae   0.07916  0.03463  2.286
## LandUseMSV All:KingdomPlantae   0.13680  0.04908  2.787
## LandUsePasture All:KingdomPlantae 0.16102  0.05066  3.178
## LandUsePlantation forest All:KingdomPlantae 0.17493  0.03122  5.603
## LandUseYSV All:KingdomPlantae    0.04801  0.04178  1.149

##
## Correlation matrix not shown by default, as p = 14 > 12.
## Use print(x, correlation=TRUE)  or
##      vcov(x)      if you need it

```

Table with confidence intervals

```

CI_m3_2 <- read.csv("./output/summary_m3_2.csv", header = TRUE, sep = ";")
kable(CI_m3_2, format="latex", booktabs=TRUE) %>%
  kable_styling(latex_options="scale_down")

```

X	Estimate	Std..Error	t.value	Actual.estimate	CI.lower	CI.upper
(Intercept)	0.567	0.034	16.77	0.567	0.500	0.633
Cropland All	-0.043	0.022	-1.94	0.524	0.480	0.567
ISV All	-0.013	0.024	-0.56	0.553	0.507	0.600
MSV All	0.067	0.030	2.25	0.634	0.575	0.692
Pasture All	-0.085	0.031	-2.77	0.481	0.421	0.542
Plantation forest All	-0.070	0.021	-3.35	0.497	0.456	0.538
YSV All	-0.029	0.029	-1.03	0.537	0.481	0.593
Plantae	-0.113	0.052	-2.17	0.453	0.351	0.556
Cropland All:Plantae	-0.026	0.039	-0.67	0.384	0.308	0.460
ISV All:Plantae	0.079	0.035	2.29	0.519	0.452	0.587
MSV All:Plantae	0.137	0.049	2.79	0.657	0.561	0.753
Pasture All:Plantae	0.161	0.051	3.18	0.529	0.430	0.628
Plantation forest All:Plantae	0.175	0.031	5.60	0.558	0.497	0.620
YSV All:Plantae	0.048	0.042	1.15	0.472	0.390	0.554

21. Plot results

```

# Plot the differences between estimates
PlotErrBar_interactions_modi(model = m3_2, resp = "Abundance", Effect1 = "LandUse",
                               Effect2 = "Kingdom",
                               ylims = c(-0.4,0.4), pointtype = c(16,17), blackwhite = FALSE)

# Plot the x label
text(x = c(0.8, 1.8, 2.8, 3.8, 4.7, 5.7, 6.8), y = -0.38, labels = c("Primary",

```

```
"Cropland",
"ISV",
"MSV",
"Pasture",
"Plantation forest",
"YSV all"), srt = 15, cex= 0.9)
```

