

# 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

```

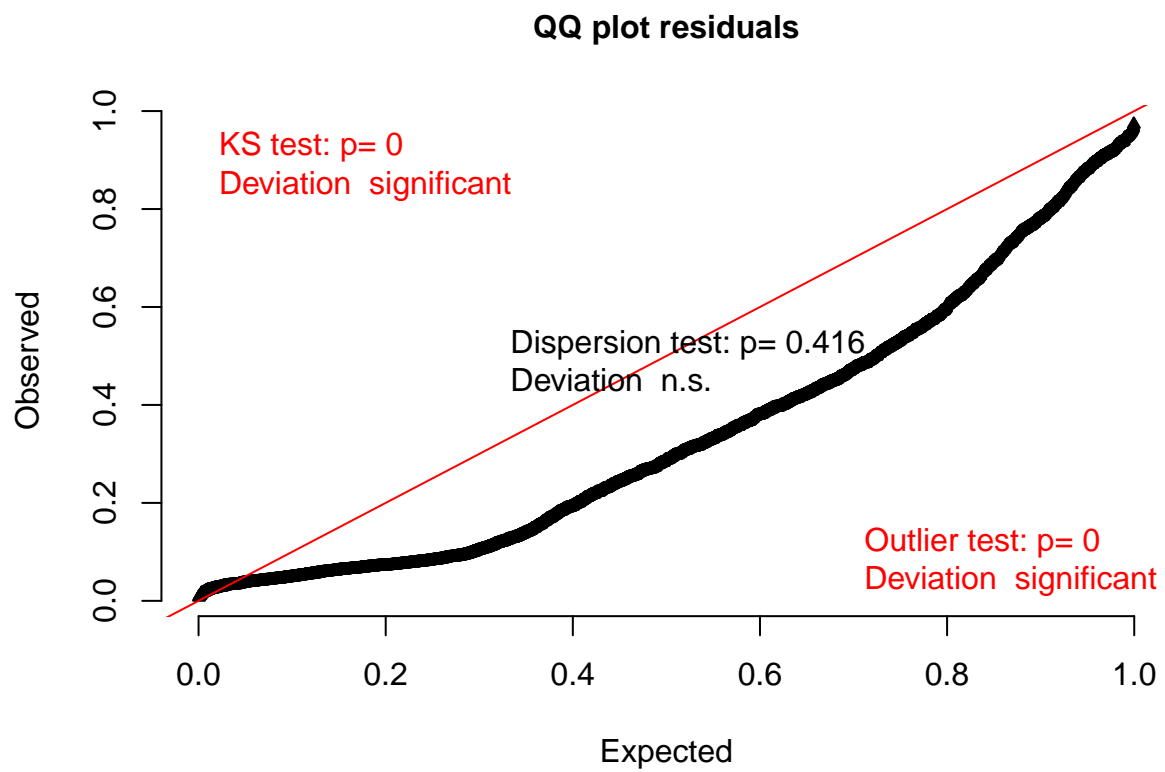
Since the interaction is significant, I am going to leave the two explanatory variables.

## 9. Plot residuals of the model

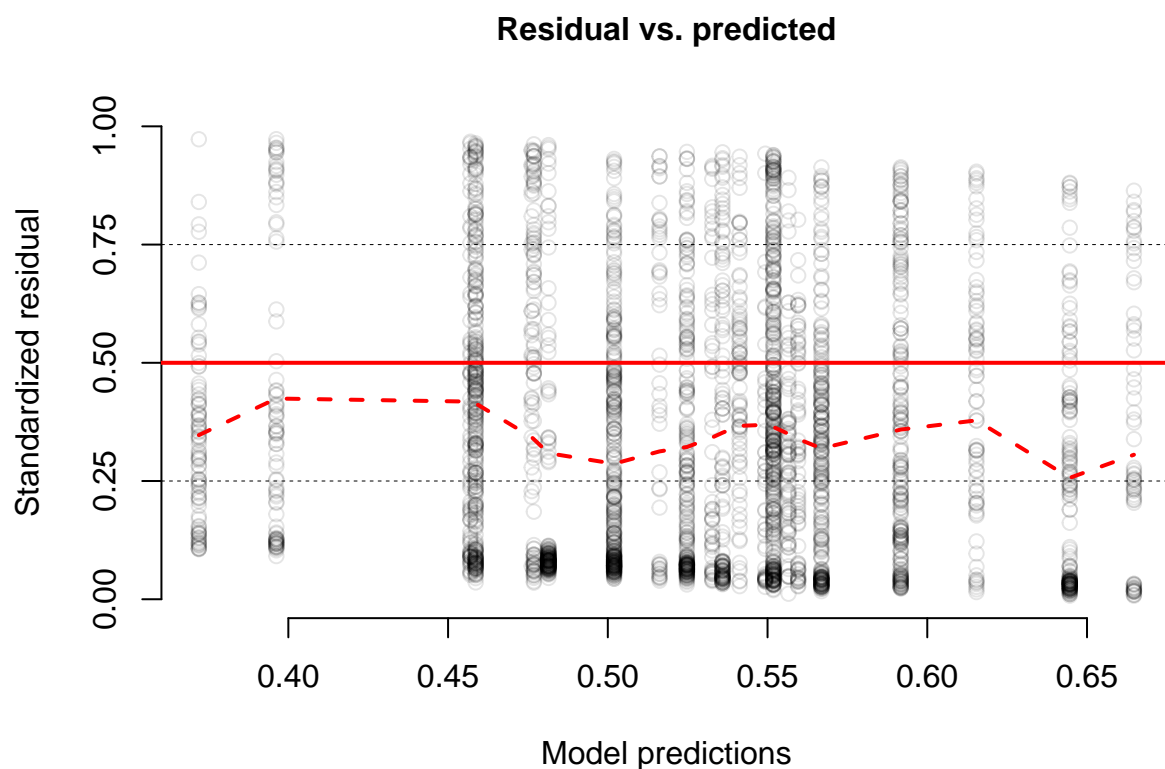
```

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:
##
##                                     Estimate
## (Intercept)                        0.551840
```

## LandUseCropland All	-0.027071
## LandUseISV Light-intensive use	0.007754
## LandUseISV Minimal use	-0.010576
## LandUseMSV All	0.092765
## LandUsePasture All	-0.070403
## LandUsePlantation forest Light-intensive 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-intensive use:KingdomPlantae	0.090167
## LandUseISV Minimal use:KingdomPlantae	0.068129
## LandUseMSV All:KingdomPlantae	0.113290
## LandUsePasture All:KingdomPlantae	0.144463
## LandUsePlantation forest Light-intensive 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-intensive use	0.034321
## LandUseISV Minimal use	0.033079
## LandUseMSV All	0.032570
## LandUsePasture All	0.031716
## LandUsePlantation forest Light-intensive 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-intensive use:KingdomPlantae	0.048707
## LandUseISV Minimal use:KingdomPlantae	0.052457
## LandUseMSV All:KingdomPlantae	0.051776
## LandUsePasture All:KingdomPlantae	0.055527
## LandUsePlantation forest Light-intensive 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-intensive use	0.226
## LandUseISV Minimal use	-0.320
## LandUseMSV All	2.848
## LandUsePasture All	-2.220
## LandUsePlantation forest Light-intensive 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

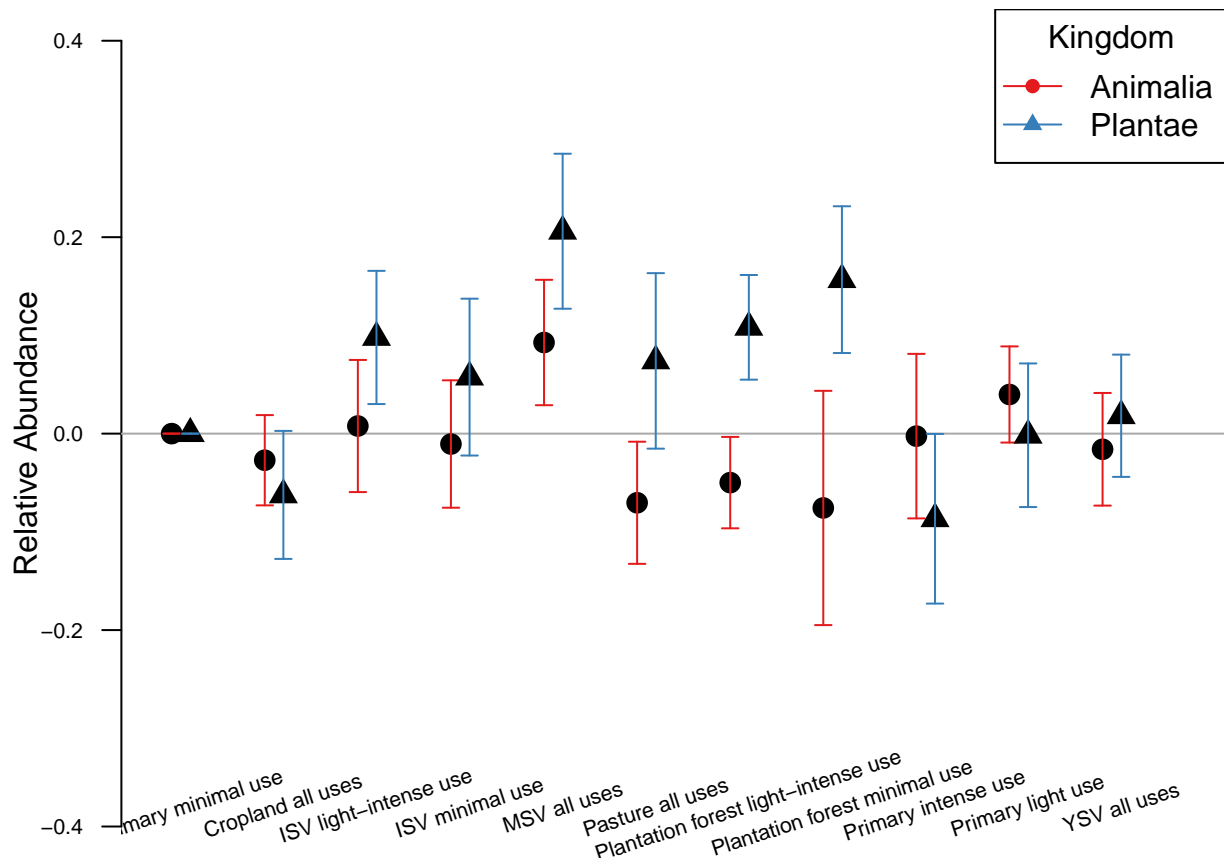
```

#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)

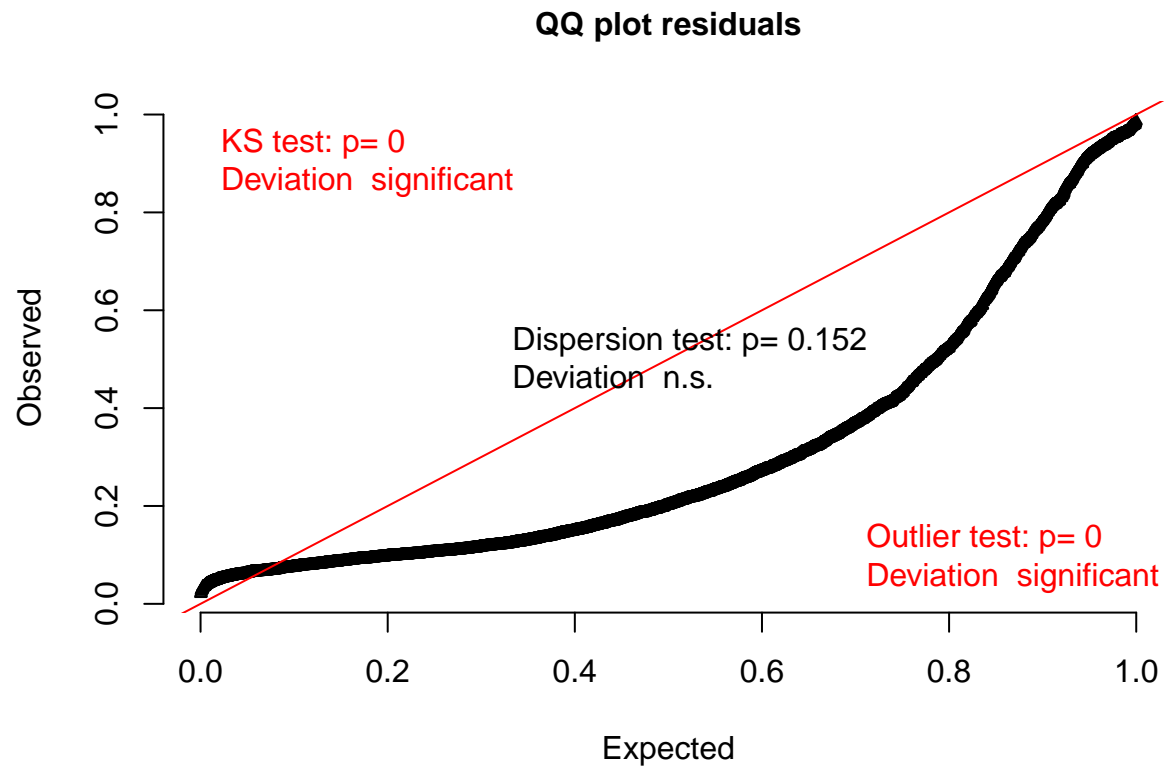
```



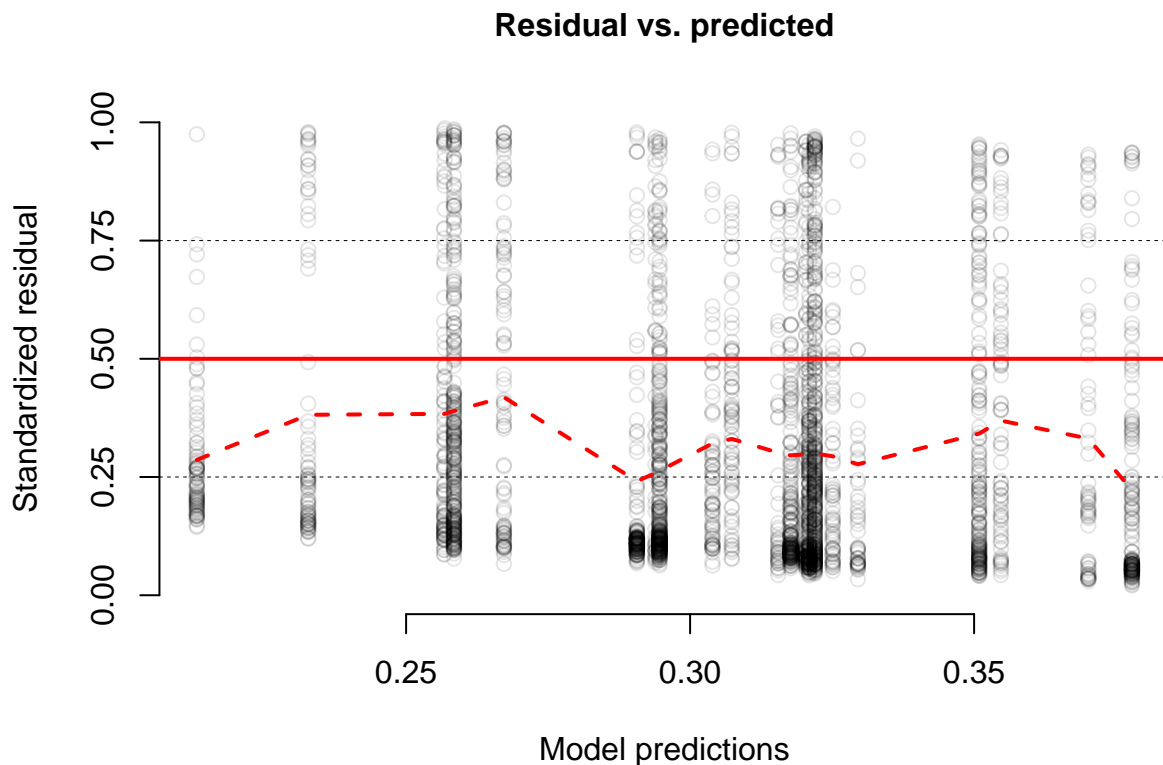
12. Run the models with the log of Abundance

```
m2l_2 <- lmer(logAbundance ~ LandUse + Kingdom + LandUse:Kingdom +
              (1|SS) + (1|SSB) + (1|Source_ID), data = second_model_data2)
```

```
simulationOutput2l <- simulateResiduals(fittedModel = m2l_2)
# Acces the qq plot
plotQQunif(simulationOutput2l)
```



```
# Plot the residuals against the predicted value
plotResiduals(simulationOutput2l)
```



### 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
```

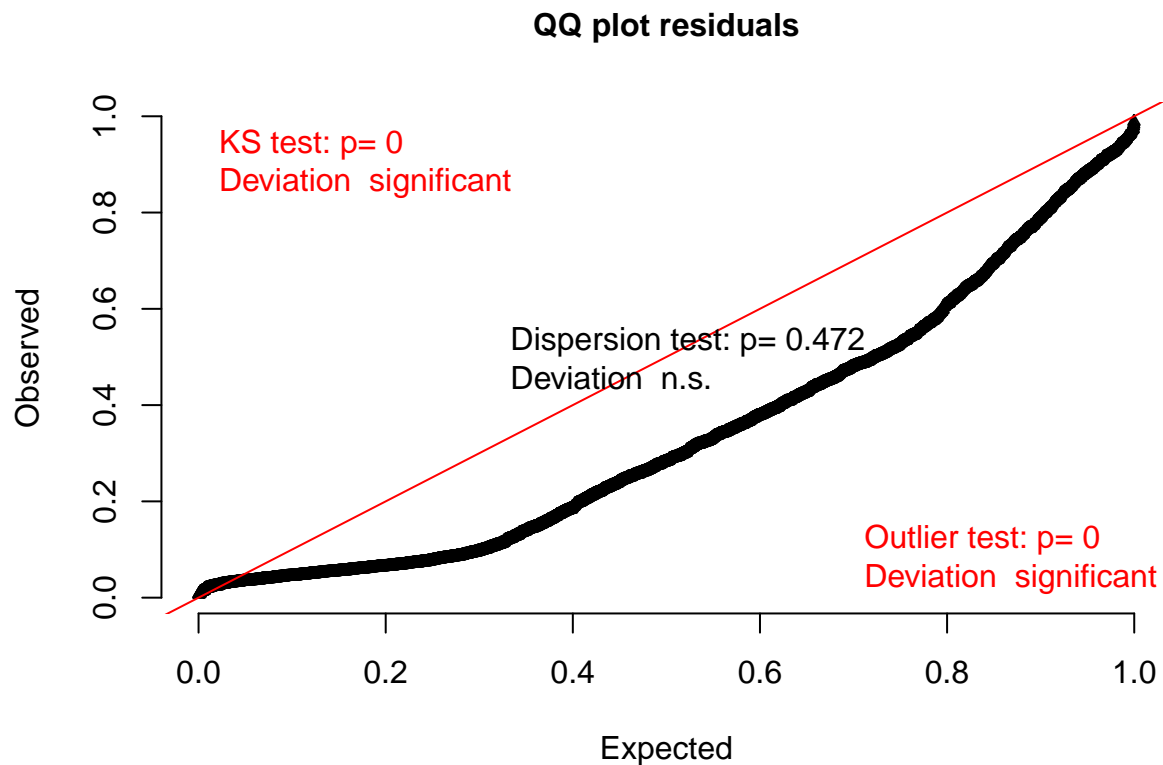
```
##      df      AIC
## m2_1 25 90.96718
## m2_2 26 88.13796
## m3_1 17 43.83383
## m3_2 18 40.43808
```

```
anova(m3_2, m2_1)
```

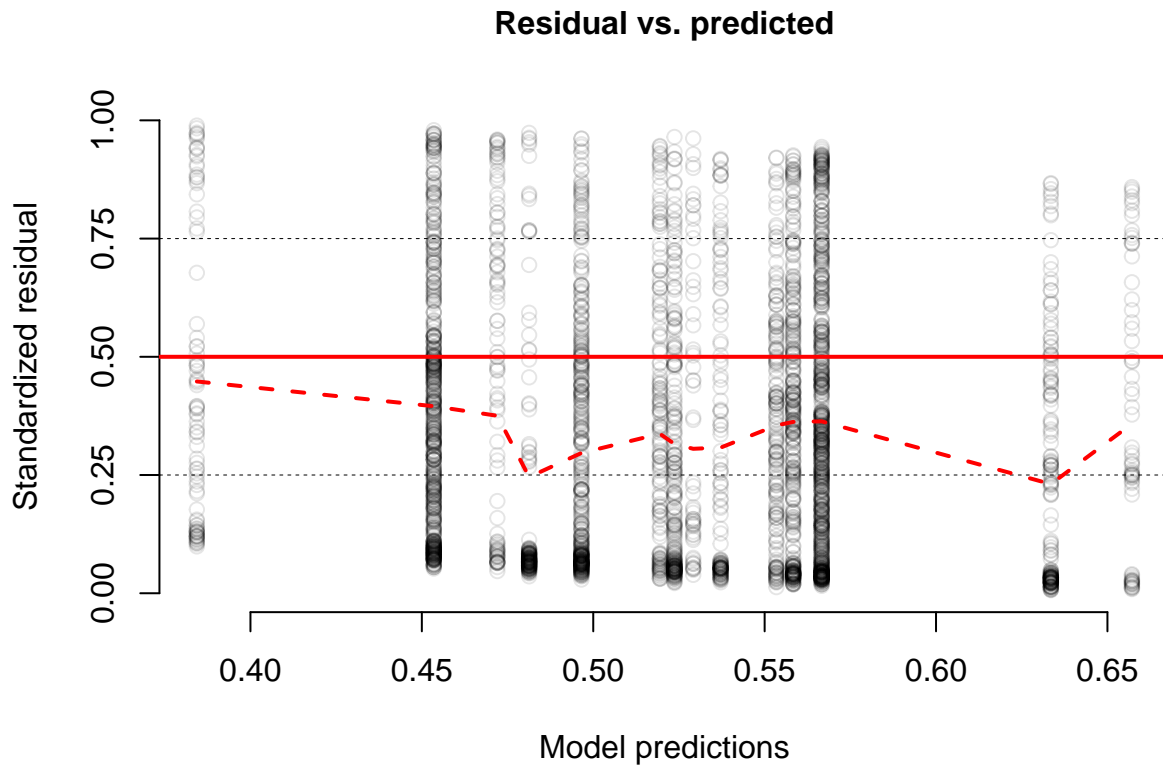
```
## Error in anova.merMod(m3_2, m2_1): models were not all fitted to the same size of dataset
```

## 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:
##
##              Estimate Std. Error t value
## (Intercept)    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)
```

