

02_Statistical_Analysis_Combination_Landuses

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

In order to know which levels to use in all of the models: I will run the abundance, species richness and Simpson's diversity models with the same land-use/intensities levels, add their AICs and compare which option is better.

```
# Call the function that merges lan-uses and intensities
source("./R/02_Statistical_Analysis_merge_LandUses_Intensities.R")

# Load richness data
diversity_all_richness <- readRDS("./output/cleaned_data/02_Statistical_Analysis_Richness_Site_metrics_all.rds")

# Load abundance data
diversity_all_abundance <- readRDS(file = "./output/cleaned_data/02_Statistical_Analysis_Abundance_Site_metrics_all.rds")

# Transform rescaled abundance
diversity_all_abundance <- dplyr::mutate(diversity_all_abundance,
                                           logAbundance = log(RescaledAbundance + 1))
)

# Load Simpsons data
diversity_all_simpson <- readRDS("./output/cleaned_data/02_Statistical_Analysis_Simpson_Site_metrics_all.rds")

# Transform Simpson's diversity index
diversity_all_simpson <- diversity_all_simpson %>%
  # Create a new column to transform the response variable with log
  dplyr::mutate(log_one_over_D = log(Simpson_diversity))
```

1. First option

- Primary: three level intensities
- Cropland: minimal use and light/intense use
- ISV: minimal use and light/intense use
- MSV: merged
- Pasture: merged
- Plantation forest: minimal use and light/intense
- YSV: merged

```

# Create the vectors that hold the land-uses that we want to keep with
# different use intensities
land_uses_separate <- c("Primary", "Cropland", "ISV", "Plantation forest")
# Create a vector with the land-uses where we want to merge the light and intense use intensities
land_uses_light_intense <- c("Cropland", "ISV", "Plantation forest")

diversity_all_richness <- Merge_landUses_and_intensities(
  dataset = diversity_all_richness,
  index = 1,
  land_uses_separate_intensities = land_uses_separate,
  land_uses_merge_light_intense = land_uses_light_intense,
  "Primary Minimal use")

diversity_all_abundance <- Merge_landUses_and_intensities(
  dataset = diversity_all_abundance,
  index = 1,
  land_uses_separate_intensities = land_uses_separate,
  land_uses_merge_light_intense = land_uses_light_intense,
  "Primary Minimal use")

diversity_all_simpson <- Merge_landUses_and_intensities(
  dataset = diversity_all_simpson,
  index = 1,
  land_uses_separate_intensities = land_uses_separate,
  land_uses_merge_light_intense = land_uses_light_intense,
  "Primary Minimal use")

```

Species richness

```

# Get complete cases, in order to compare models that use the same rows
diversity_richness <- drop_na(diversity_all_richness,
                                Species_richness, LandUse.1) %>%
  droplevels()

# Model richness with those land-use classes
m1_richness <- glmer(Species_richness ~ LandUse.1 + Kingdom + LandUse.1:Kingdom +
  (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
  data = diversity_richness,
  family = poisson,
  control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# AIC
AIC(m1_richness)

```

```
## [1] 16347.91
```

Abundance

```
# Get complete cases, in order to compare models that use the same rows
diversity_abundance <- drop_na(diversity_all_abundance,
                                RescaledAbundance_LandUse_1) %>% droplevels()
```

```

# Model abundance with those land-use classes
m1_abundance <- lmer(logAbundance ~ LandUse.1 + Kingdom + LandUse.1:Kingdom +
                      (1|Source_ID) + (1|SS) + (1|SSB),
                      data = diversity_abundance)

# AIC
AIC(m1_abundance)

```

[1] -3443.747

Simpson's diversity index

```

diversity_simpson <- drop_na(diversity_all_simpson, Simpson_diversity, LandUse.1)

# Model simpson's index with those land-use classes
m1_simpson <- lmer(log_one_over_D ~ LandUse.1 + Kingdom + LandUse.1:Kingdom +
                      (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_simpson)

# AIC
AIC(m1_simpson)

```

[1] 3452.077

2. Second option

- Primary: three level intensities
- Cropland: merged
- ISV: minimal use and light/intense use
- MSV: merged
- Pasture: merged
- Plantation forest: minimal use and light/intense
- YSV: merged

```

# Create the vectors that hold the land-uses that we want to keep with
# different use intensities
land_uses_separate_2 <- c("Primary", "ISV", "Plantation forest")
# Create a vector with the land-uses where we want to merge the light
# and intense use intensities
land_uses_light_intense_2 <- c("ISV", "Plantation forest")

diversity_richness <- Merge_landUses_and_intensities(dataset = diversity_richness,
                                                       index = 2,
                                                       land_uses_separate_intensities = land_uses_separate_2,
                                                       land_uses_merge_light_intense = land_uses_light_intense_2,
                                                       "Primary Minimal use")

diversity_abundance <- Merge_landUses_and_intensities(dataset = diversity_abundance,
                                                       index = 2,
                                                       land_uses_separate_intensities = land_uses_separate_2,
                                                      

```

```

    land_uses_merge_light_intense = land_uses_light_intense_2,
                                    "Primary Minimal use")

diversity_simpson <- Merge_landUses_and_intensities(dataset = diversity_simpson,
                                                       index = 2,
                                                       land_uses_separate_intensities = land_uses_separate_2,
                                                       land_uses_merge_light_intense = land_uses_light_intense_2,
                                                       "Primary Minimal use")

```

Species richness

```

# Model richness with those land-use classes
m2_richness <- glmer(Species_richness ~ LandUse.2 + Kingdom + LandUse.2:Kingdom +
                      (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
                      data = diversity_richness,
                      family = poisson,
                      control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# AIC
AIC(m2_richness)

```

```
## [1] 16397.1
```

Abundance

```

# Model abundance with those land-use classes
m2_abundance <- lmer(logAbundance ~ LandUse.2 + Kingdom + LandUse.2:Kingdom +
                      (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_abundance)

# AIC
AIC(m2_abundance)

```

```
## [1] -3454.782
```

Simpson's diversity index

```

# Model simpson's index with those land-use classes
m2_simpson <- lmer(log_one_over_D ~ LandUse.2 + Kingdom + LandUse.2:Kingdom +
                      (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_simpson)

# AIC
AIC(m2_simpson)

```

```
## [1] 3452.644
```

3. Third option

- Primary: minimal use and light/intense use
- Cropland: merged
- ISV: minimal use and light/intense use

- MSV: merged
- Pasture: merged
- Plantation forest: minimal use and light/intense
- YSV: merged

```
# Create the vectors that hold the land-uses that we want to keep with different
# use intensities
land_uses_separate_3 <- c("Primary", "ISV", "Plantation forest")
# Create a vector with the land-uses where we want to merge the light and
# intense use intensities
land_uses_light_intense_3 <- c("Primary", "ISV", "Plantation forest")

diversity_richness <- Merge_landUses_and_intensities(dataset = diversity_richness,
                                                       index = 3,
                                                       land_uses_separate_intensities = land_uses_separate_3,
                                                       land_uses_merge_light_intense = land_uses_light_intense_3,
                                                       "Primary Minimal use")

diversity_abundance <- Merge_landUses_and_intensities(dataset = diversity_abundance,
                                                       index = 3,
                                                       land_uses_separate_intensities = land_uses_separate_3,
                                                       land_uses_merge_light_intense = land_uses_light_intense_3,
                                                       "Primary Minimal use")

diversity_simpson <- Merge_landUses_and_intensities(dataset = diversity_simpson,
                                                       index = 3,
                                                       land_uses_separate_intensities = land_uses_separate_3,
                                                       land_uses_merge_light_intense = land_uses_light_intense_3,
                                                       "Primary Minimal use")
```

Species richness

```
# Model richness with those land-use classes
m3_richness <- glmer(Species_richness ~ LandUse.3 + Kingdom + LandUse.3:Kingdom +
                      (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
                      data = diversity_richness,
                      family = poisson,
                      control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# AIC
AIC(m3_richness)
```

[1] 16403.98

Abundance

```
# Model abundance with those land-use classes
m3_abundance <- lmer(logAbundance ~ LandUse.3 + Kingdom + LandUse.3:Kingdom +
                       (1|SS) + (1|SSB) + (1|Source_ID),
                       data = diversity_abundance)
```

```

# AIC
AIC(m3_abundance)

## [1] -3466.366

Simpson's diversity

# Model richness with those land-use classes
m3_simpson <- lmer(log_one_over_D ~ LandUse.3 + Kingdom + LandUse.3:Kingdom +
  (1|SS) + (1|SSB) + (1|Source_ID),
  data = diversity_simpson)

# AIC
AIC(m3_simpson)

## [1] 3450.742

```

4. Fourth option

- Primary: minimal use and light/intense use
- Cropland: minimal use and light/intense use
- ISV: minimal use and light/intense use
- MSV: merged
- Pasture: merged
- Plantation forest: minimal use and light/intense
- YSV: merged

```

# Create the vectors that hold the land-uses that we want to keep with
# different use intensities
land_uses_separate_4 <- c("Primary", "Cropland", "ISV", "Plantation forest")
# Create a vector with the land-uses where we want to merge the light
# and intense use intensities
land_uses_light_intense_4 <- c("Primary", "Cropland", "ISV", "Plantation forest")

diversity_richness <- Merge_landUses_and_intensities(dataset = diversity_richness,
  index = 4,
  land_uses_separate_intensities = land_uses_separate_4,
  land_uses_merge_light_intense = land_uses_light_intense_4,
  "Primary Minimal use")

diversity_abundance <- Merge_landUses_and_intensities(dataset = diversity_abundance,
  index = 4,
  land_uses_separate_intensities = land_uses_separate_4,
  land_uses_merge_light_intense = land_uses_light_intense_4,
  "Primary Minimal use")

diversity_simpson <- Merge_landUses_and_intensities(dataset = diversity_simpson,
  index = 4,
  land_uses_separate_intensities = land_uses_separate_4,
  land_uses_merge_light_intense = land_uses_light_intense_4,
  "Primary Minimal use")

```

Species richness

```
# Model richness with those land-use classes
m4_richness <- glmer(Species_richness ~ LandUse.4 + Kingdom + LandUse.4:Kingdom +
                      (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
                      data = diversity_richness, family = poisson,
                      control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# AIC
AIC(m4_richness)
```

```
## [1] 16354.62
```

Abundance

```
# Model abundance with those land-use classes
m4_abundance <- lmer(logAbundance ~ LandUse.4 + Kingdom + LandUse.4:Kingdom +
                       (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_abundance)

# AIC
AIC(m4_abundance)
```

```
## [1] -3455.283
```

Simpson's diversity index

```
# Model simpsons index with those land-use classes
m4_simpson <- lmer(log_one_over_D ~ LandUse.4 + Kingdom + LandUse.4:Kingdom +
                      (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_simpson)

# AIC
AIC(m4_simpson)
```

```
## [1] 3450.226
```

4. Choose the best combination

```
# First option
sum(AIC(m1_richness) + AIC(m1_abundance), AIC(m1_simpson))
```

```
## [1] 16356.24
```

```
# Second option
sum(AIC(m2_richness) + AIC(m2_abundance), AIC(m2_simpson))
```

```
## [1] 16394.97
```

```

# Third option
sum(AIC(m3_richness) + AIC(m3_abundance), AIC(m3_simpson))

## [1] 16388.36

# Fourth option
sum(AIC(m4_richness) + AIC(m4_abundance), AIC(m4_simpson))

## [1] 16349.56

```

According to the results, the best option is option 4:
 * Primary: minimal use and light/intense use
 * Cropland: minimal use and light/intense use
 * ISV: minimal use and light/intense use
 * MSV: merged
 * Pasture: merged
 * Plantation forest: minimal use and light/intense use
 * YSV: merged

The results therefore will be

Species richness

The best model is: m4_richness <- glmer(Species_richness ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS), data = diversity_richness, family = poisson, control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

Compare with a model that has all the land-use intensities merged

```

# Create the vectors that hold the land-uses that we want to keep with
# different use intensities
land_uses_separate_null_5 <- "NA"
# Create a vector with the land-uses that we want to merge
land_uses_light_intense_null_5 <- "NA"

# This function creates new columns with the land-uses and use intensities that we want,
# then it then merges both columns into a LanUse column
diversity_richness <- Merge_landUses_and_intensities(diversity_richness,
                                                       5,
                                                       land_uses_separate_null_5,
                                                       land_uses_light_intense_null_5,
                                                       "Primary All")

# Model richness with those land-use classes
m4_null_1_richness <- glmer(Species_richness ~ LandUse.5 + Kingdom + LandUse.5:Kingdom +
                             (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
                             data = diversity_richness,
                             family = poisson,
                             control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# Next we will check if we've lost a significant amount of explanatory power
# by removing this interaction. If we have, we want to keep the more complex
# model. If we haven't lost a significant amount of explanatory power, then we
# can keep the simpler model.

anova(m4_richness, m4_null_1_richness)

```

```

## Data: diversity_richness
## Models:
## m4_null_1_richness: Species_richness ~ LandUse.5 + Kingdom + LandUse.5:Kingdom +
## m4_null_1_richness: (1 | Source_ID) + (1 | SS) + (1 | SSB) + (1 | SSBS)
## m4_richness: Species_richness ~ LandUse.4 + Kingdom + LandUse.4:Kingdom +
## m4_richness: (1 | Source_ID) + (1 | SS) + (1 | SSB) + (1 | SSBS)
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)
## m4_null_1_richness 25 16615 16778 -8282.6 16565
## m4_richness 37 16355 16596 -8140.3 16281 284.63 12 < 2.2e-16
##
## m4_null_1_richness
## m4_richness ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Plant contrast

```

# For the null model I am going to replace the nePlantae for Plantae
diversity_richness <- diversity_richness %>%
  mutate(
    # Create a new kingdom column as the copy of the kingdom column we used
    # in the first model
    Kingdom.1 = paste(Kingdom),
    # Replace nePlantae for Plantae
    Kingdom.1 = recode_factor(Kingdom.1, "nePlantae" = "Plantae"),
    # set reference level
    Kingdom.1 = factor(Kingdom.1),
    Kingdom.1 = relevel(Kingdom.1, ref = "Animalia"))

m4_null_2_richness <- glmer(Species_richness ~ LandUse.4 + Kingdom.1 + LandUse.4:Kingdom.1 +
  (1|Source_ID) + (1|SS) + (1|SSB) + (1|SSBS),
  data = diversity_richness,
  family = poisson,
  control = glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 20000)))

# check if we've lost a significant amount of explanatory power
anova(m4_richness, m4_null_2_richness, test = "F")

## Data: diversity_richness
## Models:
## m4_null_2_richness: Species_richness ~ LandUse.4 + Kingdom.1 + LandUse.4:Kingdom.1 +
## m4_null_2_richness: (1 | Source_ID) + (1 | SS) + (1 | SSB) + (1 | SSBS)
## m4_richness: Species_richness ~ LandUse.4 + Kingdom + LandUse.4:Kingdom +
## m4_richness: (1 | Source_ID) + (1 | SS) + (1 | SSB) + (1 | SSBS)
## npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)
## m4_null_2_richness 26 17754 17924 -8851.2 17702
## m4_richness 37 16355 16596 -8140.3 16281 1421.8 11 < 2.2e-16

```

```

## 
## m4_null_2_richness
## m4_richness      ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Estimates of the selected model

```

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

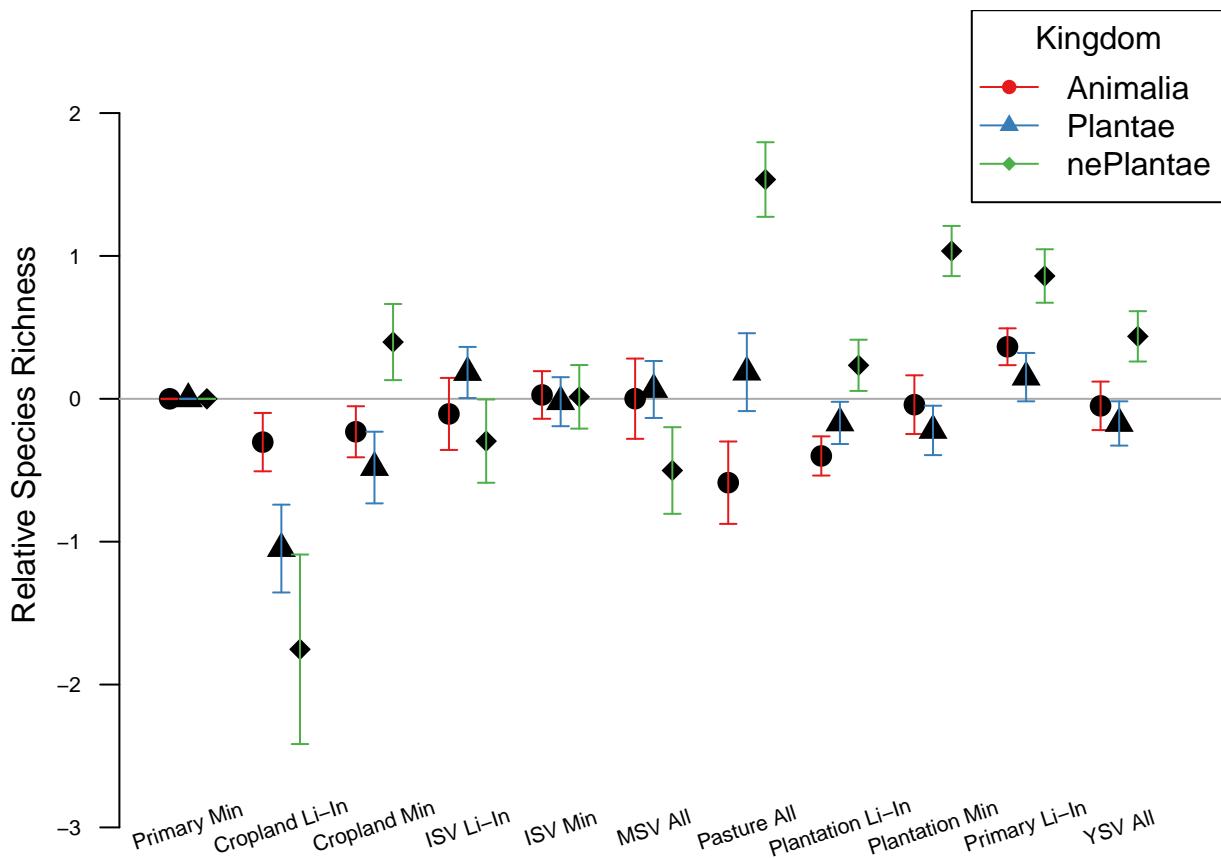
```

X	Estimate	Std.Error	t.value	Actual.estimate
Intercept	1.19	0.15	8.00	1.19
Cropland Light-intense use	-0.30	0.10	-2.91	0.89
Cropland Minimal use	-0.23	0.09	-2.53	0.96
ISV Light-intense use	-0.11	0.13	-0.82	1.08
ISV Minimal use	0.03	0.09	0.32	1.22
MSV All	0.00	0.14	0.01	1.19
Pasture All	-0.59	0.15	-3.99	0.60
Plantation forest Light-intense use	-0.40	0.07	-5.72	0.79
Plantation forest Minimal use	-0.04	0.10	-0.39	1.15
Primary Light-intense use	0.36	0.07	5.54	1.55
YSV All	-0.05	0.09	-0.57	1.14
KingdomPlantae	-0.03	0.20	-0.15	1.16
KingdomnePlantae	-1.08	0.20	-5.35	0.11
Cropland Light-intense use:KingdomPlantae	-0.74	0.19	-3.96	0.11
Cropland Minimal use:KingdomPlantae	-0.25	0.16	-1.59	0.68
ISV Light-intense use:KingdomPlantae	0.29	0.16	1.84	1.34
ISV Minimal use:KingdomPlantae	-0.05	0.12	-0.39	1.14
MSV All:KingdomPlantae	0.06	0.18	0.37	1.22
Pasture All:KingdomPlantae	0.77	0.20	3.83	1.34
Plantation forest Light-intense use:KingdomPlantae	0.23	0.10	2.25	0.99
Plantation forest Minimal use:KingdomPlantae	-0.18	0.14	-1.32	0.94
Primary Light-intense use:KingdomPlantae	-0.21	0.11	-1.97	1.31
YSV All:KingdomPlantae	-0.12	0.12	-1.05	0.99
Cropland Light-intense use:KingdomnePlantae	-1.45	0.35	-4.10	-1.64
Cropland Minimal use:KingdomnePlantae	0.63	0.16	3.84	0.51
ISV Light-intense use:KingdomnePlantae	-0.19	0.20	-0.97	-0.19
ISV Minimal use:KingdomnePlantae	-0.01	0.14	-0.09	0.12
MSV All:KingdomnePlantae	-0.50	0.21	-2.38	-0.39
Pasture All:KingdomnePlantae	2.12	0.20	10.70	1.64
Plantation forest Light-intense use:KingdomnePlantae	0.63	0.11	5.52	0.34
Plantation forest Minimal use:KingdomnePlantae	1.08	0.14	7.81	1.14
Primary Light-intense use:KingdomnePlantae	0.50	0.12	4.30	0.97
YSV All:KingdomnePlantae	0.49	0.12	3.90	0.55
sd_(Intercept).SSBS	0.26	NA	NA	NA
sd_(Intercept).SSB	0.25	NA	NA	NA
sd_(Intercept).SS	0.31	NA	NA	NA
sd_(Intercept).Source_ID	1.03	NA	NA	NA

Plot of the results

```
# Plot the differences between estimates
PlotErrBar_interactions_modi(model = m4_richness,
                               resp = "Species Richness",
                               Effect1 = "LandUse.4",
                               Effect2 = "Kingdom",
                               ylims = c(-3,2.5),
                               pointtype = c(16,17, 18),
                               blackwhite = FALSE)

# Plot the x label
text(x = c(0.8:10.8),
     y = -3, labels = c("Primary Min",
                         "Cropland Li-In",
                         "Cropland Min",
                         "ISV Li-In",
                         "ISV Min",
                         "MSV All",
                         "Pasture All",
                         "Plantation Li-In",
                         "Plantation Min",
                         "Primary Li-In",
                         "YSV All"),
     srt = 18, cex= 0.7)
```



Abundance

```
m4_abundance <- lmer(logAbundance ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_abundance)
```

Compare with a model that has all the land-use intensities merged

```
# This function creates new columns with the land-uses and use intensities that we want, # then it then merges both columns into a LanUse column
diversity_abundance <- Merge_landUses_and_intensities(diversity_abundance,
  5,
  land_uses_separate_null_5,
  land_uses_light_intense_null_5,
  "Primary All")

# Model abundance with those land-use classes
m4_null_1_abundance <- lmer(logAbundance ~ LandUse.5 + Kingdom +
  LandUse.5:Kingdom +
  (1|Source_ID) + (1|SS) + (1|SSB),
  data = diversity_abundance)

# Next we will check if we've lost a significant amount of explanatory power
anova(m4_abundance, m4_null_1_abundance)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: diversity_abundance
## Models:
## m4_null_1_abundance: logAbundance ~ LandUse.5 + Kingdom + LandUse.5:Kingdom + (1 |
## m4_null_1_abundance:     Source_ID) + (1 | SS) + (1 | SSB)
## m4_abundance: logAbundance ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1 |
## m4_abundance:     SS) + (1 | SSB) + (1 | Source_ID)
##           npar      AIC      BIC logLik deviance Chisq Df
## m4_null_1_abundance  25 -3652.1 -3493.1 1851.1 -3702.1
## m4_abundance        37 -3650.5 -3415.1 1862.3 -3724.5 22.401 12
##           Pr(>Chisq)
## m4_null_1_abundance
## m4_abundance          0.03327 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plant constraint

```
# For the null model I am going to replace the nePlantae for Plantae
diversity_abundance <- diversity_abundance %>%
  mutate(
    # Create a new kingdom column as the copy of the kingdom column we used
    # in the first model
    Kingdom.1 = paste(Kingdom),
    # Replace nePlantae for Plantae
```

```

Kingdom.1 = recode_factor(Kingdom.1, "nePlantae" = "Plantae"),

# set reference level
Kingdom.1 = factor(Kingdom.1),
Kingdom.1 = relevel(Kingdom.1, ref = "Animalia"))

m4_null_2_abundance <- lmer(logAbundance ~ LandUse.4 + Kingdom.1 +
                           LandUse.4:Kingdom.1 +
                           (1|Source_ID) + (1|SS) + (1|SSB),
                           data = diversity_abundance)

# check if we've lost a significant amount of explanatory power
anova(m4_abundance, m4_null_2_abundance, test = "F")

## refitting model(s) with ML (instead of REML)

## Data: diversity_abundance
## Models:
## m4_null_2_abundance: logAbundance ~ LandUse.4 + Kingdom.1 + LandUse.4:Kingdom.1 +
## m4_null_2_abundance:      (1 | Source_ID) + (1 | SS) + (1 | SSB)
## m4_abundance: logAbundance ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1 |
## m4_abundance:      SS) + (1 | SSB) + (1 | Source_ID)
##                  npar   AIC     BIC logLik deviance Chisq Df
## m4_null_2_abundance  26 -3583.9 -3418.4 1817.9  -3635.9
## m4_abundance         37 -3650.5 -3415.1 1862.3  -3724.5 88.679 11
##                  Pr(>Chisq)
## m4_null_2_abundance
## m4_abundance        3.024e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Estimates of the selected model

```

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

```

X	Estimate	Std.error	t.value	Actual.estimate
Intercept	0.32	0.02	13.35	0.32
Cropland Light-intense use	-0.01	0.02	-0.64	0.31
Cropland Minimal use	0.01	0.02	0.67	0.34
ISV Light-intense use	0.00	0.02	0.02	0.32
ISV Minimal use	-0.01	0.02	-0.62	0.31
MSV All	0.06	0.02	2.61	0.38
Pasture All	-0.04	0.03	-1.57	0.28
Plantation forest Light-intense use	-0.03	0.02	-1.83	0.29
Plantation forest Minimal use	-0.07	0.04	-1.67	0.26
Primary Light-intense use	0.03	0.02	1.77	0.35
YSV All	-0.01	0.02	-0.42	0.31
KingdomPlantae	-0.08	0.04	-2.09	0.25
KingdomnePlantae	-0.12	0.04	-3.27	0.20
Cropland Light-intense use:KingdomPlantae	-0.01	0.03	-0.29	0.22
Cropland Minimal use:KingdomPlantae	0.08	0.05	1.75	0.34
ISV Light-intense use:KingdomPlantae	0.07	0.03	2.36	0.32
ISV Minimal use:KingdomPlantae	0.08	0.03	2.24	0.31
MSV All:KingdomPlantae	0.09	0.03	2.56	0.39
Pasture All:KingdomPlantae	0.12	0.04	3.28	0.33
Plantation forest Light-intense use:KingdomPlantae	0.13	0.02	5.64	0.35
Plantation forest Minimal use:KingdomPlantae	0.14	0.05	3.12	0.32
Primary Light-intense use:KingdomPlantae	-0.02	0.02	-0.70	0.26
YSV All:KingdomPlantae	0.04	0.03	1.38	0.28
Cropland Light-intense use:KingdomnePlantae	0.01	0.03	0.25	0.20
Cropland Minimal use:KingdomnePlantae	0.05	0.05	1.11	0.27
ISV Light-intense use:KingdomnePlantae	0.05	0.03	1.51	0.25
ISV Minimal use:KingdomnePlantae	0.08	0.03	2.44	0.27
MSV All:KingdomnePlantae	-0.05	0.04	-1.07	0.21
Pasture All:KingdomnePlantae	0.20	0.04	5.30	0.36
Plantation forest Light-intense use:KingdomnePlantae	0.09	0.02	3.75	0.26
Plantation forest Minimal use:KingdomnePlantae	0.09	0.05	2.01	0.23
Primary Light-intense use:KingdomnePlantae	0.02	0.02	0.62	0.25
YSV All:KingdomnePlantae	0.07	0.03	2.35	0.26
sd_(Intercept).SSB	0.04	NA	NA	NA
sd_(Intercept).SS	0.09	NA	NA	NA
sd_(Intercept).Source_ID	0.13	NA	NA	NA
sd_Observation.Residual	0.15	NA	NA	NA
	NA	NA	NA	NA

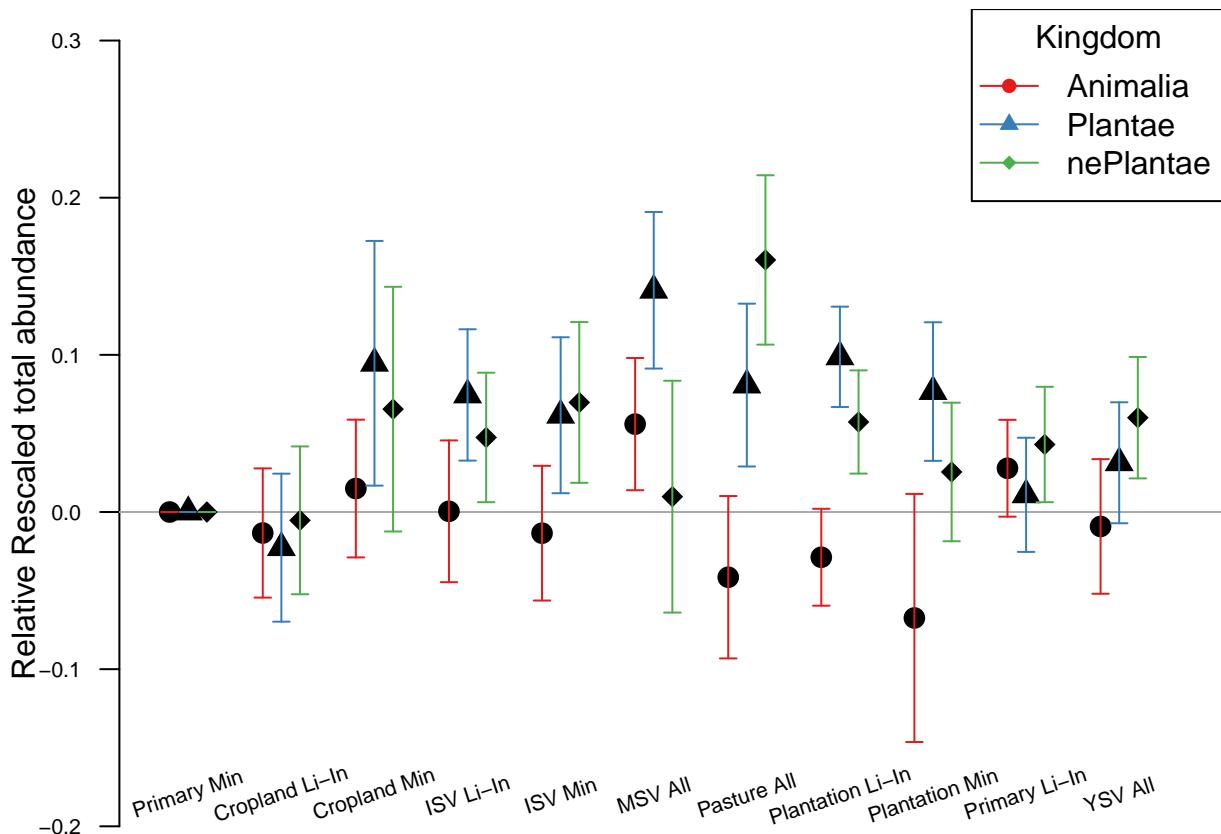
Plot of the results

```
# Plot the differences between estimates
PlotErrBar_interactions_modi(model = m4_abundance,
                               resp = "Rescaled total abundance",
                               Effect1 = "LandUse.4",
                               Effect2 = "Kingdom",
                               ylims = c(-0.2, 0.3),
                               pointtype = c(16,17, 18),
                               blackwhite = FALSE)
```

```

# Plot the x label
text(x = c(0.8:10.8),
y = -0.18, labels = c("Primary Min",
                      "Cropland Li-In",
                      "Cropland Min",
                      "ISV Li-In",
                      "ISV Min",
                      "MSV All",
                      "Pasture All",
                      "Plantation Li-In",
                      "Plantation Min",
                      "Primary Li-In",
                      "YSV All"),
srt = 18, cex= 0.7)

```



Simpson's diversity

```
m4_simpson <- lmer(log_one_over_D ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1|SS) + (1|SSB) + (1|Source_ID), data = diversity_simpson)
```

Compare with a model that has all the land-use intensities merged

```
# This function creates new columns with the land-uses and use intensities that we want,
# then it then merges both columns into a LanUse column
```

```

diversity_simpson <- Merge_landUses_and_intensities(diversity_simpson,
                                                     5,
                                                     land_uses_separate_null_5,
                                                     land_uses_light_intense_null_5,
                                                     "Primary All")

# Model 1/D with those land-use classes
m4_null_1_simpson <- lmer(log_one_over_D ~ LandUse.5 + Kingdom +
                           LandUse.5:Kingdom +
                           (1|Source_ID) + (1|SS) + (1|SSB),
                           data = diversity_simpson)

# Next we will check if we've lost a significant amount of explanatory power

anova(m4_simpson, m4_null_1_simpson)

## refitting model(s) with ML (instead of REML)

## Data: diversity_simpson
## Models:
## m4_null_1_simpson: log_one_over_D ~ LandUse.5 + Kingdom + LandUse.5:Kingdom + (1 | Source_ID) + (1 | SS) + (1 | SSB)
## m4_simpson: log_one_over_D ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1 | SS) + (1 | SSB) + (1 | Source_ID)
##          npqr      AIC      BIC   logLik deviance Chisq Df Pr(>Chisq)
## m4_null_1_simpson  25 3409.8 3557.4 -1679.9    3359.8
## m4_simpson        37 3338.1 3556.5 -1632.1    3264.1 95.68 12  3.89e-15
##
## m4_null_1_simpson
## m4_simpson      ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Plant contrast

```
# For the null model I am going to replace the nePlantae for Plantae
diversity_simpson <- diversity_simpson %>%
  mutate(
    # Create a new kingdom column as the copy of the kingdom column we used
    # in the first model
    Kingdom.1 = paste(Kingdom),
    # Replace nePlantae for Plantae
    Kingdom.1 = recode_factor(Kingdom.1, "nePlantae" = "Plantae"),
    # set reference level
    Kingdom.1 = factor(Kingdom.1),
    Kingdom.1 = relevel(Kingdom.1, ref = "Animalia"))
```

```

m4_null_2_simpson <- lmer(log_one_over_D ~ LandUse.4 + Kingdom.1 +
                           LandUse.4:Kingdom.1 +
                           (1|Source_ID) + (1|SS) + (1|SSB),
                           data = diversity_simpson)

# check if we've lost a significant amount of explanatory power
anova(m4_simpson, m4_null_2_simpson, test = "F")

## refitting model(s) with ML (instead of REML)

## Data: diversity_simpson
## Models:
## m4_null_2_simpson: log_one_over_D ~ LandUse.4 + Kingdom.1 + LandUse.4:Kingdom.1 +
## m4_null_2_simpson:      (1 | Source_ID) + (1 | SS) + (1 | SSB)
## m4_simpson: log_one_over_D ~ LandUse.4 + Kingdom + LandUse.4:Kingdom + (1 |
## m4_simpson:      SS) + (1 | SSB) + (1 | Source_ID)
##           npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
## m4_null_2_simpson  26 3592.7 3746.2 -1770.4    3540.7
## m4_simpson         37 3338.1 3556.5 -1632.1    3264.1 276.6 11  < 2.2e-16
##
## m4_null_2_simpson
## m4_simpson      ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Estimates of the selected model

```

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

```

X	Estimate	Std.error	t.value	Actual.estimate
Intercept	0.83	0.09	9.23	0.83
Cropland Light-intense use	-0.22	0.07	-3.32	0.60
Cropland Minimal use	-0.15	0.07	-2.22	0.67
ISV Light-intense use	-0.15	0.08	-1.91	0.68
ISV Minimal use	0.06	0.07	0.93	0.89
MSV All	-0.03	0.11	-0.27	0.80
Pasture All	-0.25	0.12	-2.06	0.58
Plantation forest Light-intense use	-0.27	0.05	-5.29	0.56
Plantation forest Minimal use	0.10	0.12	0.84	0.93
Primary Light-intense use	0.30	0.05	5.77	1.13
YSV All	-0.19	0.07	-2.55	0.64
KingdomPlantae	0.09	0.13	0.71	0.92
KingdomnePlantae	-0.37	0.13	-2.94	0.45
Cropland Light-intense use:KingdomPlantae	-0.33	0.11	-3.07	0.36
Cropland Minimal use:KingdomPlantae	0.08	0.14	0.61	0.85
ISV Light-intense use:KingdomPlantae	0.13	0.10	1.31	0.90
ISV Minimal use:KingdomPlantae	0.05	0.11	0.50	1.03
MSV All:KingdomPlantae	0.08	0.14	0.57	0.97
Pasture All:KingdomPlantae	0.24	0.15	1.61	0.91
Plantation forest Light-intense use:KingdomPlantae	0.01	0.07	0.13	0.66
Plantation forest Minimal use:KingdomPlantae	-0.16	0.14	-1.15	0.86
Primary Light-intense use:KingdomPlantae	-0.26	0.08	-3.13	0.96
YSV All:KingdomPlantae	-0.03	0.10	-0.27	0.70
Cropland Light-intense use:KingdomnePlantae	0.20	0.19	1.06	1.26
Cropland Minimal use:KingdomnePlantae	0.33	0.13	2.44	1.45
ISV Light-intense use:KingdomnePlantae	0.03	0.12	0.23	1.16
ISV Minimal use:KingdomnePlantae	-0.14	0.11	-1.35	1.20
MSV All:KingdomnePlantae	-0.44	0.16	-2.77	0.82
Pasture All:KingdomnePlantae	0.72	0.15	4.79	1.75
Plantation forest Light-intense use:KingdomnePlantae	0.27	0.09	3.20	1.28
Plantation forest Minimal use:KingdomnePlantae	0.16	0.14	1.17	1.54
Primary Light-intense use:KingdomnePlantae	0.02	0.08	0.21	1.60
YSV All:KingdomnePlantae	0.37	0.10	3.75	1.47
sd_(Intercept).SSB	0.10	NA	NA	NA
sd_(Intercept).SS	0.23	NA	NA	NA
sd_(Intercept).Source_ID	0.52	NA	NA	NA
sd_Observation.Residual	0.42	NA	NA	NA
	NA	NA	NA	NA
	NA	NA	NA	NA

Plot the results

```
# Plot the differences between estimates
PlotErrBar_interactions_modi(model = m4_simpson,
                               resp = "Simpson's diversity index",
                               Effect1 = "LandUse.4",
                               Effect2 = "Kingdom",
                               ylims = c(-1, 1),
                               pointtype = c(16,17, 18),
```

```

blackwhite = FALSE)

# Plot the x label
text(x = c(0.8:10.8),
y = -0.9, labels = c("Primary Min",
"Cropland Li-In",
"Cropland Min",
"ISV Li-In",
"ISV Minimal",
"MSV All",
"Pasture All",
"Plantation Li-In",
"Plantation Min",
"Primary Li-In",
"YSV All"),
srt = 18, cex= 0.7)

```

