

Practise_FII_Modelling

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Functional Intactness Index Model

To model FII I am using a two stage modeling framework. The first model will take site functional diversity, measured as Rao's Q, as function of land-use type and intensity. While the second model will be focusing on functional similarity differs between sites of primary minimal habitat and all other land use types. Together This is will get a measure of overall functional diversity and the proportion of that function that is retained from primary minimal sites, which once projected on to current maps of the modeled pressures and multiplied together will (hopefully) give a measure of functional intactness.

1.1 Modelling: Functional Diversity (PGLMM)

As sites are not independent of each other as assemblages with similar species may respond similarly to pressure. I am using community phylogenetic generalized linear mixed effects models (PGLMM) using the package `phyr`. `Phyr` allows for bayesian methods of model fitting using INLA, which is advised with larger datasets. Phylogenetic similarity of sites was calculated using 1-UniFrac, UniFrac measures the distance between communities as the percentage of branch length that leads to descendants from only community i.e the fraction of evolution that is unique to that community. By taking the pairwise similarity scores as measured by 1-UniFrac I can generate a variance-covariance matrix that is analogous to that created when looking at species level phylogenetic signal. I am able to incorporate the vcv and have a site level phylogenetic random effect that will identify any phylogenetic signal in sites responses. In modeling I also considered the UN-subregion, human population density ($\ln + 1$ transformed) and density of roads at both a 1km and 50km radius surrounding the site. I included study and study block as additional random effects and tested for the inclusion of random slopes of the other pressures within study by comparing the DIC of the maximal models. The fixed effect structure was then determined through backwards stepwise model simplification by looking at whether the removal of fixed effects significantly reduced the DIC of the model.

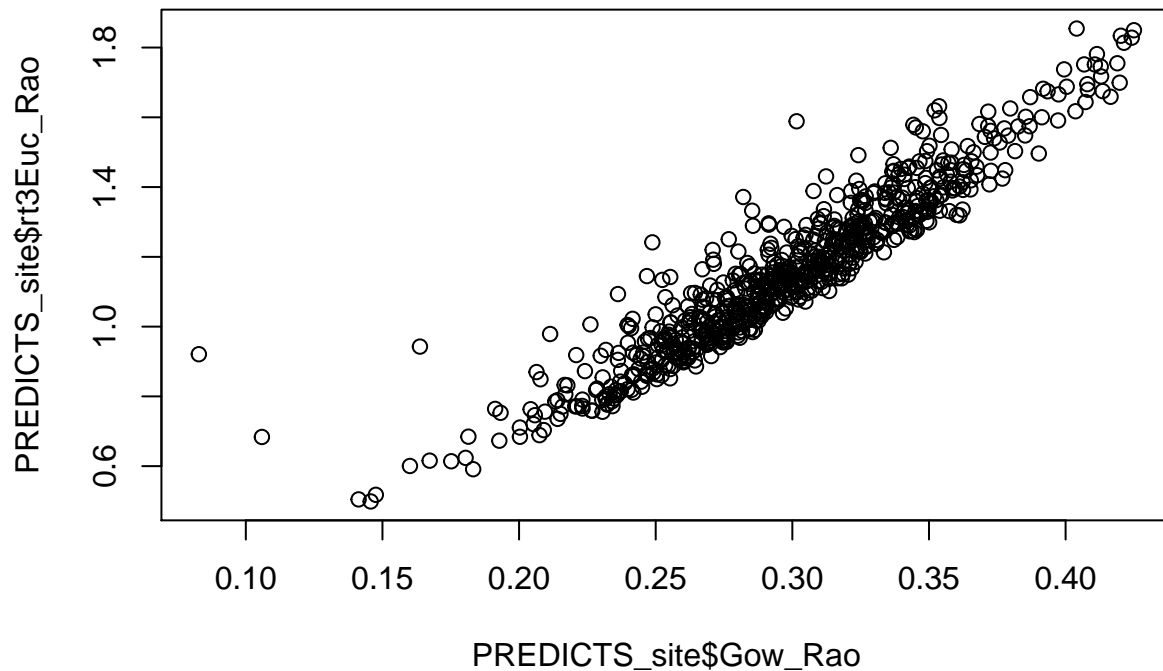
```
rm(list = ls())
require(phytools)
require(picante)
require(phyr)
require(tidyverse)
require(raster)
require(plyr)
require(ggirdges)
require(car)
require(lme4)
require(ggResidpanel)
```

Load in the datasets from the previously calculated metrics.

I calculated Rao's Q based on both eculedean and gower functional distances are reasonably well correlated, so either metric can be carried forward onto the modeling. I chose to use Euclidean based Rao's as my metric as the traits being used are all quantitative and Euclidean distances make more intuitive sense to me in this form. Although slightly positively skewed a cube root transformation normalises.

```
PREDICTS_site$rt3Euc_Rao <- PREDICTS_site$Euc_Rao^(1/3)

plot(PREDICTS_site$Gow_Rao, PREDICTS_site$rt3Euc_Rao)
```



Next we'd like to have a look at how the distribution of land use types and intensities we have across our modeled sites.

```
table(PREDICTS_site$LandUse, PREDICTS_site$Use_intensity)
```

```
##
##           Minimal use Light use Intense use
## Cropland           33      20         0
## Pasture            16      11        25
## Plantation forest   21       0         0
## Primary            250     73         9
## Secondary Vegetation 111     35         2
## Urban              70     56         0
```

Although Plantation forest exists as a land use class within PREDICTS it is rarely incorporated in global land-use layers therefore I included Plantation minimally used habitat in secondary vegetation light use

following De Palma et al, in Review . Additionally, it doesn't look like we have enough combinations of both landuse and use intensity to treat them as separate factors within the model therefore I am going to use the combined factor of 'LandUse_Intensity'.

```
PREDICTS_site$LandUse_Intensity <- ifelse(grepl(PREDICTS_site$LandUse_Intensity, pattern = "Plantation :
                                     "Secondary Vegetation_Light use",
                                     paste(PREDICTS_site$LandUse_Intensity))

### Primary minimal use as reference level

PREDICTS_site$LandUse_Intensity <- relevel(factor(PREDICTS_site$LandUse_Intensity), ref = "Primary_Minimal use")

PREDICTS_site$SSBS <- factor(PREDICTS_site$SSBS)

table(PREDICTS_site$LandUse_Intensity)
```

```
##
##           Primary_Minimal use           Cropland_Light use
##                   250                   20
##           Cropland_Minimal use           Pasture_Intense use
##                   33                   25
##           Pasture_Light use           Pasture_Minimal use
##                   11                   16
##           Primary_Intense use           Primary_Light use
##                   9                   73
## Secondary Vegetation_Intense use Secondary Vegetation_Light use
##                   2                   56
## Secondary Vegetation_Minimal use           Urban_Light use
##                   111                   56
##           Urban_Minimal use
##                   70
```

Colinearity

Next I am going to check for colinearity in the predictor variables, but beforehand I apply the square and cube root transformation to the density of roads at 1km and 50km respectively and scale all variables to reduce possible colinearity issues.

```
PREDICTS_site$logHPD <- scale(PREDICTS_site$logHPD)
PREDICTS_site$density_1km <- scale(PREDICTS_site$density_1km^(1/3))
PREDICTS_site$density_50km <- scale(PREDICTS_site$density_50km^(1/2))

source("https://highstat.com/Books/Book2/HighstatLibV10.R")
corvif(PREDICTS_site[,c( "LandUse_Intensity", "logHPD", "density_1km", "density_50km" , "UN_subregion")])

##
##
## Variance inflation factors
##
##           GVIF Df GVIF^(1/2Df)
## LandUse_Intensity 45.559072 12      1.172485
```

```
## logHPD          11.279866  1    3.358551
## density_1km     1.779668  1    1.334042
## density_50km    11.176927  1    3.343191
## UN_subregion    37.531642  3    1.829783
```

a lot of colinearity try removing UN-subregion

```
corvif(PREDICTS_site[,c( "LandUse_Intensity", "logHPD", "density_1km","density_50km")])
```

```
##
##
## Variance inflation factors
##
##              GVIF Df GVIF^(1/2Df)
## LandUse_Intensity  5.958072 12    1.077199
## logHPD             10.225058  1    3.197664
## density_1km        1.496609  1    1.223360
## density_50km       7.464187  1    2.732066
```

better but a VIF > 5 is still a bit too high lets try to remove log HPD or density 50km

```
corvif(PREDICTS_site[,c( "LandUse_Intensity", "density_50km", "density_1km")])
```

```
##
##
## Variance inflation factors
##
##              GVIF Df GVIF^(1/2Df)
## LandUse_Intensity  2.055130 12    1.030469
## density_50km       2.131787  1    1.460064
## density_1km        1.492131  1    1.221528
```

```
corvif(PREDICTS_site[,c( "LandUse_Intensity", "logHPD", "density_1km")])
```

```
##
##
## Variance inflation factors
##
##              GVIF Df GVIF^(1/2Df)
## LandUse_Intensity  3.232907 12    1.050106
## logHPD             2.920297  1    1.708888
## density_1km        1.465995  1    1.210783
```

removing either density of roads at 50km or logHPD improves the colinearity to a good level - remov

Phylogenetic Similarity

Finally I calculate the pairwise phylogenetic similarity between sites, as mentioned before I will be using 1-unifrac.

```
#### Load in Phylogeny - just take the first one when running the initial models
```

```
all_bird_tree <- read.tree("Datasets/AllBirdsHackett1.tre")  
all_bird_tree <- all_bird_tree[[1]]
```

```
#####  
#### Unifrac for all sites among studies ####  
#####
```

```
among_site_unifrac <- function(data) {
```

```
  data <- droplevels(data)  
  species <- sub(unique(data$Jetz_Name), pattern = " ", replacement = "_")  
  drop.species <- all_bird_tree$tip.label[which(!(all_bird_tree$tip.label %in% species))]
```

```
  study_tree <- drop.tip(all_bird_tree, drop.species)
```

```
  sites <- as.character(unique(PREDICTS_site[, "SSBS"]))
```

```
  comm_data <- t(species)  
  colnames(comm_data) <- species  
  comm_data <- data.frame(comm_data[-1,])
```

```
  for(i in 1:length(sites)){
```

```
    site_data <- data.frame(data[data$SSBS == sites[i], c("Jetz_Name", "Effort_Corrected_Measurement")])
```

```
    for(spp in species){  
      comm_data[i, paste(spp)] <- ifelse(any(site_data[site_data$Jetz_Name == sub(spp, pattern = "_", replacement = " ")]$Effort_Corrected_Measurement == 0), NA, mean(site_data[site_data$Jetz_Name == sub(spp, pattern = "_", replacement = " ")]$Effort_Corrected_Measurement))  
    }
```

```
    rownames(comm_data)[i] <- sites[i]  
  }
```

```
  for(i in 1:ncol(comm_data)){  
    comm_data[, i] <- as.numeric(comm_data[, i])  
  }
```

```
  comm_data <- as.matrix(comm_data)
```

```

among_site_vcv <- 1 - as.matrix(unifrac(comm = comm_data, tree = study_tree))
}

among_site_vcv <- among_site_unifrac(PREDICTS_abundance)

write_rds(file = "Functional_Intactness_Index/Site_Among_Study_Vcv.rds", among_site_vcv)

```

PGLMMs

With that we now have everything ready to begin modeling. Random effects that I will be including in the models will be study, to account for between study differences in location, method and sampling effort; study block, to account for spatial configuration of sites; and phylogenetic and non-phylogenetic effect of individual site, to account for non-independence of sites. Additionally, I will be testing for random slopes for each of the predictor variables within study by identifying which random effect structure has the lowest DIC in the maximal model.

```

PREDICTS_site <- PREDICTS_site %>% droplevels()

among_site_vcv <- readRDS("Functional_Intactness_Index/Site_Among_Study_Vcv.rds")

Rao_Model1 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_50km + LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

#### adding random slopes

Rao_Model2 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_50km + LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) + (density_50km|SS) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

Rao_Model3 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_50km + LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) + (LandUse_Intensity|SS) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

```

```

Rao_Model4 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_50km + LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) + (density_1km|SS) , data = PREDICTS,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

#####

Random_DIC <- data.frame(Rao_Model11 = Rao_Model11$DIC, Rao_Model12 = Rao_Model12$DIC,
  Rao_Model13 = Rao_Model13$DIC, Rao_Model14 = Rao_Model14$DIC)

Random_DIC

```

Here we can see that Model1 has the lowest DIC and therefore there is the most support for the random effect structure that include the density of Roads @ 1km radius to be included as a random slope within study.

Next to identify the optimal fixed effect structure I removed both interactions in turn to see whether that reduced the DIC of the model. Typically a reduction >2 will provide support for the simplified model.

```

#### Remove each interaction to see if this improves the model at all.

## LandUSE Intensity:RoadD1

Rao_Model5 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_50km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE )

## log HPd so lets see what happens if I remove the density_50km interaction

Rao_Model6 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

#####

ModelDiffs <- data.frame(density_1km = Rao_Model5$DIC - Rao_Model1$DIC,
  density_50km = Rao_Model6$DIC - Rao_Model1$DIC)

ModelDiffs

```

THE DIC in the model removing the interaction between LandUse_intensity and density_50km was great.

```
Rao_Model7 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_1km +
  LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)

Rao_Model8 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)
```

```
ModelDiffs2 <- data.frame(density_50km = Rao_Model7$DIC - Rao_Model6$DIC,
  density_1km = Rao_Model8$DIC - Rao_Model6$DIC)
```

ModelDiffs2

Removing the either term did not improve the model therefore Model 6 is retained

Final Model

I also fitted models that included logHPD instead of density of roads at 50km radius to test whether there was more support for that model. However, the DIC of the best model was not lower than that for density_50km. Therefore, I chose the best model to be Rao_Model_6.

```
among_site_vcv <- read_rds("Functional_Intactness_Index/Site_Among_Study_Vcv.rds")

Rao_Model6 <- phyr::communityPGLMM(rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
  LandUse_Intensity:density_1km +
  (1|SS) + (1|SSB) + (1|SSBS__) , data = PREDICTS_site,
  cov_ranef = list(SSBS = among_site_vcv), bayes = TRUE)
```

Warning: The cov matrix is not standarized, we will do this now...

```
summary(Rao_Model6)
```

```
## Linear mixed model fit by Bayesian INLA
##
## Call:rt3Euc_Rao ~ LandUse_Intensity + density_50km + density_1km +
##      LandUse_Intensity:density_1km
##
## marginal logLik          DIC          WAIC
##           431          -2505          -2583
##
## Random effects:
##      Variance Std.Dev lower.CI upper.CI
## 1|SS    6.518e-03 0.080737 2.638e-03 0.0205032
```



```

## 1|SSB      5.002e-05 0.007072 1.439e-05 0.0005105
## 1|SSBS     5.867e-05 0.007659 1.617e-05 0.0007218
## 1|SSBS__   9.237e-03 0.096110 8.009e-03 0.0107736
## residual  7.496e-04 0.027378 3.681e-04 0.0016073
##
## Fixed effects:
##
##                                     Value
## (Intercept)                        1.1655e+00
## LandUse_IntensityCropland_Light use -7.7171e-02
## LandUse_IntensityCropland_Minimal use -4.0604e-02
## LandUse_IntensityPasture_Intense use  7.6052e-02
## LandUse_IntensityPasture_Light use   1.8570e-01
## LandUse_IntensityPasture_Minimal use  9.2644e-02
## LandUse_IntensityPrimary_Intense use  8.6389e-02
## LandUse_IntensityPrimary_Light use   2.5677e-04
## LandUse_IntensitySecondary_Vegetation_Intense use 1.5900e-02
## LandUse_IntensitySecondary_Vegetation_Light use  1.7528e-02
## LandUse_IntensitySecondary_Vegetation_Minimal use -8.9596e-03
## LandUse_IntensityUrban_Light use     -7.7168e-03
## LandUse_IntensityUrban_Minimal use    -1.4758e-02
## density_50km                        5.9376e-03
## density_1km                         1.8944e-02
## LandUse_IntensityCropland_Light use:density_1km 3.6853e-02
## LandUse_IntensityCropland_Minimal use:density_1km -9.3844e-04
## LandUse_IntensityPasture_Intense use:density_1km -2.5412e-02
## LandUse_IntensityPasture_Light use:density_1km  -3.6815e-02
## LandUse_IntensityPasture_Minimal use:density_1km 1.8287e-02
## LandUse_IntensityPrimary_Intense use:density_1km -4.1256e-02
## LandUse_IntensityPrimary_Light use:density_1km  -1.6312e-02
## LandUse_IntensitySecondary_Vegetation_Intense use:density_1km -7.5929e-03
## LandUse_IntensitySecondary_Vegetation_Light use:density_1km 4.8614e-03
## LandUse_IntensitySecondary_Vegetation_Minimal use:density_1km 1.3400e-02
## LandUse_IntensityUrban_Light use:density_1km    -9.4901e-03
## LandUse_IntensityUrban_Minimal use:density_1km   -1.4280e-02
##                                     lower.CI
## (Intercept)                        1.1152e+00
## LandUse_IntensityCropland_Light use -2.6832e+01
## LandUse_IntensityCropland_Minimal use -1.0744e-01
## LandUse_IntensityPasture_Intense use  -9.0731e-02
## LandUse_IntensityPasture_Light use    1.7120e-02
## LandUse_IntensityPasture_Minimal use  -3.1337e-02
## LandUse_IntensityPrimary_Intense use  -2.6669e+01
## LandUse_IntensityPrimary_Light use    -3.7617e-02
## LandUse_IntensitySecondary_Vegetation_Intense use -2.6740e+01
## LandUse_IntensitySecondary_Vegetation_Light use  -5.1881e-02
## LandUse_IntensitySecondary_Vegetation_Minimal use -5.5912e-02
## LandUse_IntensityUrban_Light use       -7.5416e-02
## LandUse_IntensityUrban_Minimal use     -7.2565e-02
## density_50km                        -2.9944e-02
## density_1km                        -2.6489e-02
## LandUse_IntensityCropland_Light use:density_1km -5.5989e+01
## LandUse_IntensityCropland_Minimal use:density_1km -7.3175e-02
## LandUse_IntensityPasture_Intense use:density_1km  -8.4017e-02
## LandUse_IntensityPasture_Light use:density_1km   -1.2691e-01

```

```

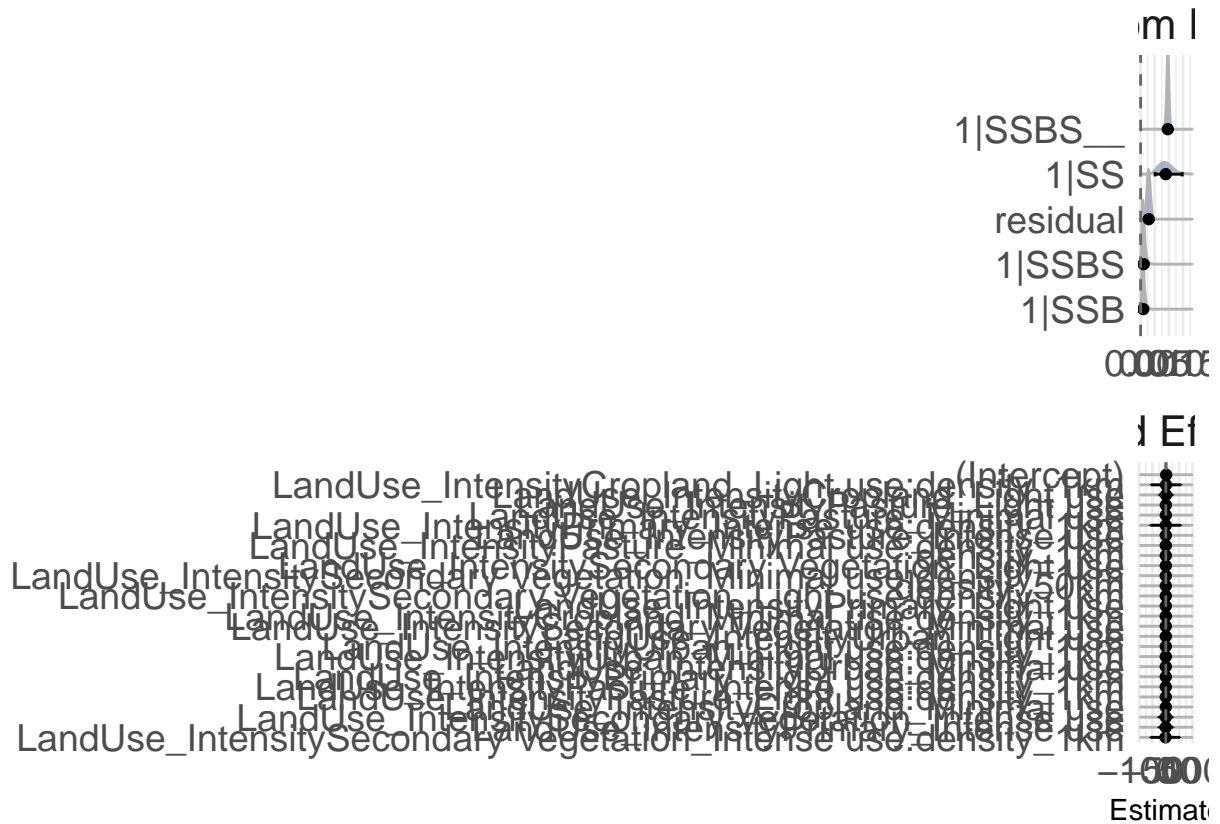
## LandUse_IntensityPasture_Minimal use:density_1km -5.3997e-02
## LandUse_IntensityPrimary_Intense use:density_1km -5.6067e+01
## LandUse_IntensityPrimary_Light use:density_1km -6.9429e-02
## LandUse_IntensitySecondary_Vegetation_Intense use:density_1km -5.6033e+01
## LandUse_IntensitySecondary_Vegetation_Light use:density_1km -4.6206e-02
## LandUse_IntensitySecondary_Vegetation_Minimal use:density_1km -3.7273e-02
## LandUse_IntensityUrban_Light use:density_1km -5.8800e-02
## LandUse_IntensityUrban_Minimal use:density_1km -6.2783e-02
## upper.CI
## (Intercept) 1.2189
## LandUse_IntensityCropland_Light use 26.6558
## LandUse_IntensityCropland_Minimal use 0.0262
## LandUse_IntensityPasture_Intense use 0.2366
## LandUse_IntensityPasture_Light use 0.3541
## LandUse_IntensityPasture_Minimal use 0.2135
## LandUse_IntensityPrimary_Intense use 26.8194
## LandUse_IntensityPrimary_Light use 0.0381
## LandUse_IntensitySecondary_Vegetation_Intense use 26.7492
## LandUse_IntensitySecondary_Vegetation_Light use 0.0868
## LandUse_IntensitySecondary_Vegetation_Minimal use 0.0379
## LandUse_IntensityUrban_Light use 0.0600
## LandUse_IntensityUrban_Minimal use 0.0431
## density_50km 0.0430
## density_1km 0.0643
## LandUse_IntensityCropland_Light use:density_1km 56.0155
## LandUse_IntensityCropland_Minimal use:density_1km 0.0712
## LandUse_IntensityPasture_Intense use:density_1km 0.0331
## LandUse_IntensityPasture_Light use:density_1km 0.0532
## LandUse_IntensityPasture_Minimal use:density_1km 0.0910
## LandUse_IntensityPrimary_Intense use:density_1km 55.9374
## LandUse_IntensityPrimary_Light use:density_1km 0.0368
## LandUse_IntensitySecondary_Vegetation_Intense use:density_1km 55.9711
## LandUse_IntensitySecondary_Vegetation_Light use:density_1km 0.0559
## LandUse_IntensitySecondary_Vegetation_Minimal use:density_1km 0.0640
## LandUse_IntensityUrban_Light use:density_1km 0.0398
## LandUse_IntensityUrban_Minimal use:density_1km 0.0342

```

```

phyr::plot_bayes(Rao_Model6)

```



funtion to visualise the residuals from the PGLMM and check whether they are normally distributed

```
residuals.communityPGLMM <- function(
  object,
  type = if(object$family %in% c("binomial","poisson")) "deviance" else "response",
  scaled = FALSE, ...){
  if(object$family == "gaussian"){
    y <- object$Y
    mu <- pglmm_predicted_values(object)$Y_hat
    res <- switch(type,
      deviance = stop("no deviance residuals for gaussian model", call. = FALSE),
      response = y - mu
    )
    if(scaled) res/sqrt(object$s2resid)
  }

  if(object$family %in% c("binomial","poisson")){
    y <- as.numeric(object$Y)
    mu <- unname(object$mu[, 1])
    if(object$family == "binomial") dres <- sqrt(binomial()$dev.resids(y, mu, 1))
    if(object$family == "poisson") dres <- sqrt(poisson()$dev.resids(y, mu, 1))
    res <- switch(type,
      deviance = {
        dres
        ifelse(y > mu, dres, - dres)
      },

```

```

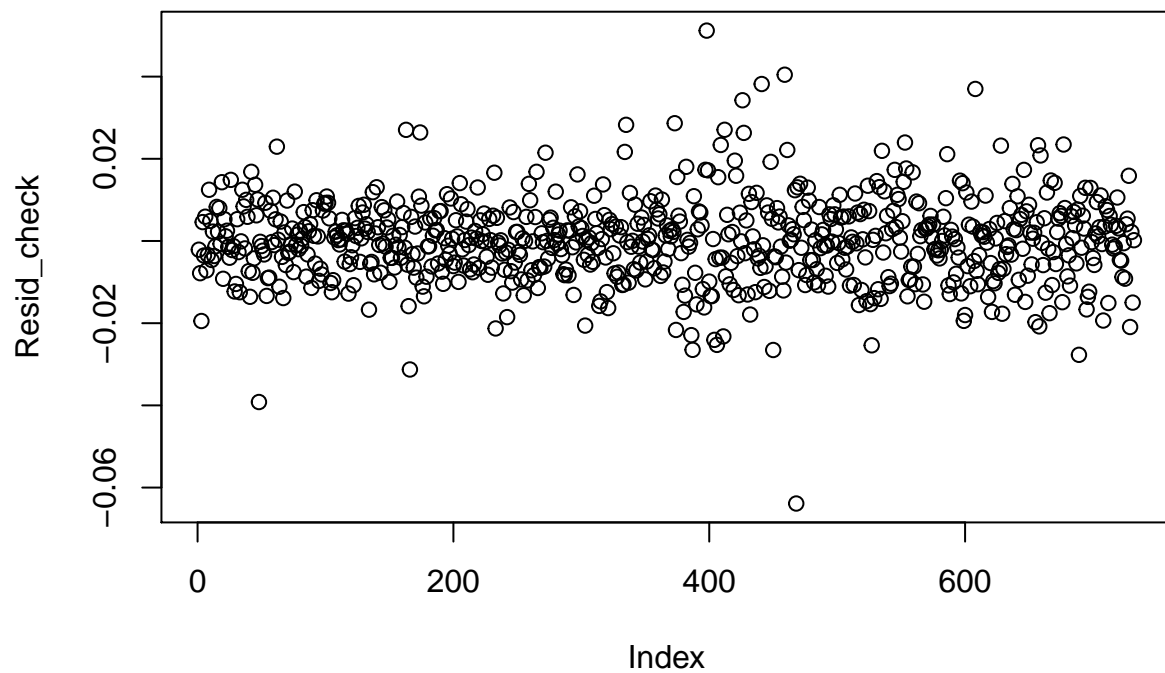
        response = y - mu
    )
}
if(object$family %nin% c("gaussian", "binomial", "poisson"))
  stop("no residual methods for family other than gaussian, binomial and poisson, yet", call. = FALSE)

  unname(res)
}

Resid_check <- residuals.communityPGLMM(Rao_Model6)

plot(Resid_check)

```

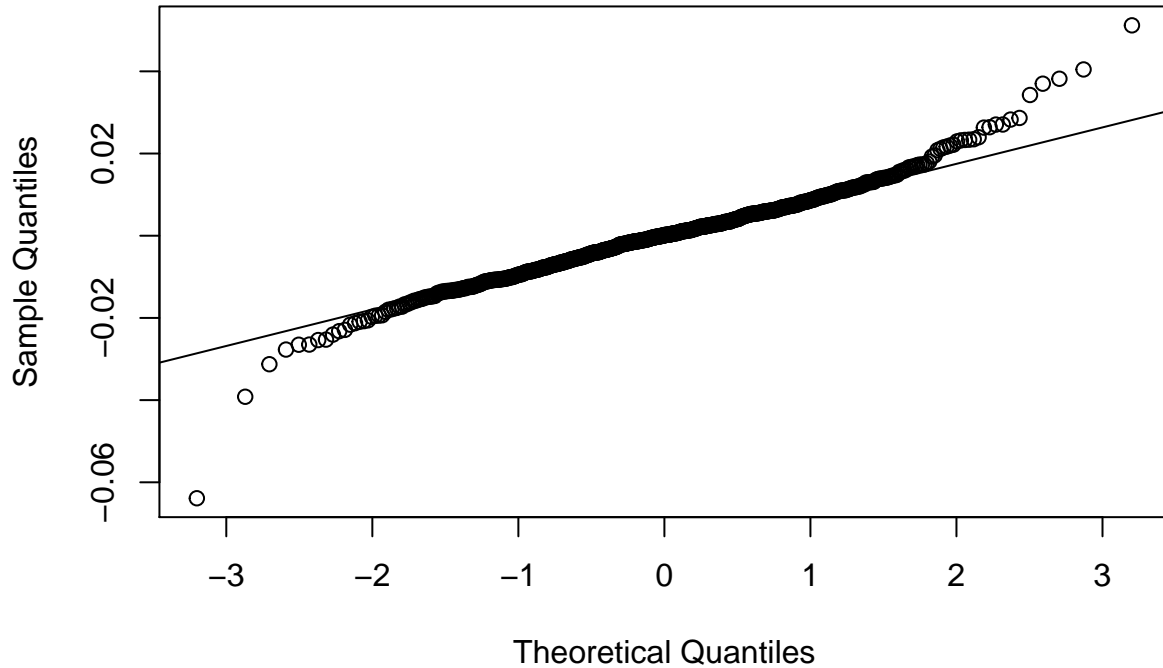


```

qqnorm(Resid_check)
qqline(Resid_check)

```

Normal Q-Q Plot



```
write_rds(file = "Functional_Intactness_Index/Rao_model.rds", Rao_Model6)
```

Briefly, the summary of the final model indicates that Functional diversity, compared to that of Primary minimally used land use, is reduced in cropland, urban and minimally used secondary vegetation, while it increases in intensely used and lightly used secondary vegetation, and pasture and primary land use across intensity gradients. Additionally,

1.2 Modelling: Functional Similarity/Overlap (GLMM)

To assess the impact of landuse change and other pressures on functional similarity I used GLMMS. The other pressures include human population density, density of roads @ 1 and 50km radii, and geographic and environmental distances. Additionally, since the functional similarity of sites may be influenced by the absolute level of pressure experienced at that site but also the difference in pressure experience between the sites, I included the pressure at site 2 (the site being compared to Primary minimal land use) and the difference in pressures between site 1 and 2.

To determine the optimal random effect structure I used the aforementioned selection process picking the structure with the lowest AIC. To determine the best fixed effect structure is more difficult however, as the comparisons are not-independent of each other as a single primary minimal site will be compared to multiple of other sites, therefore traditional likelihood ratio tests will not be suitable. Again following De Palma et al. In review, I permuted the data 1000 times by randomly shuffling the functional similarity scores within studies and refitted the full and simplified model to each permuted dataset to generate a distribution of Likelihood ratio scores. Comparing the likelihood ratio score between models using the observed data to this distribution, a simplified model would be supported if the score is lower than the 95th percentile of the distribution as it has not significantly reduced the explanatory power of the model.

```

Overlap_data <- readRDS("Functional_Intactness_Index/Functional_Overlap_data.rds")
Similarity_data <- readRDS("Functional_Intactness_Index/similarity_data.rds")

### Also want to add in a variable for the minimum number of species in either of the sites used to con

## lets have a look at the other variables and what transformations will be best

hist(car::logit(Overlap_data$hyper_overlap, adjust = 0.001, percents = FALSE))

## because the similarity metric is bound between 0 and 1 and i performed a logit transformation as wel

Overlap_data <- Overlap_data %>% dplyr::mutate(logitOver = car::logit(hyper_overlap, adjust = 0.001, per
  dplyr::mutate(logdist = log(distance + 1),
    rt3env = env_distance^(1/3),
    sqrtS2RD1K = S2RD1K^(1/2),
    sqrtS2RD50K = S2RD50K^(1/2))

table(Overlap_data$Contrast)

Overlap_data$Contrast <- ifelse(grepl(Overlap_data$Contrast, pattern = "Plantation forest"),
  "Primary_Minimal use-Secondary Vegetation_Light use",
  paste(Overlap_data$Contrast))

table(Overlap_data$Contrast)

Overlap_data$Contrast <- relevel(factor(Overlap_data$Contrast), ref = "Primary_Minimal use-Primary_Minim

Overlap_data$rt3env <- scale(Overlap_data$rt3env)
Overlap_data$s2logHPD <- scale(Overlap_data$s2logHPD)
Overlap_data$logHPDdiff <- scale(Overlap_data$logHPDdiff)
Overlap_data$logdist <- scale(Overlap_data$logdist)
Overlap_data$sqrtS2RD1K <- scale(Overlap_data$sqrtS2RD1K)
Overlap_data$sqrtS2RD50K <- scale(Overlap_data$sqrtS2RD50K)
Overlap_data$RD1Kdiff <- scale(Overlap_data$RD1Kdiff)
Overlap_data$RD50Kdiff <- scale(Overlap_data$RD50Kdiff)

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

corvif(Overlap_data[,c("Contrast", "logdist", "rt3env", "s2logHPD", "logHPDdiff", "sqrtS2RD1K", "sqrtS2RD50K", "RD1Kdiff", "RD50Kdiff")])

### some collinearity problems lets drop site2HPD

corvif(Overlap_data[,c("Contrast", "logdist", "rt3env", "logHPDdiff", "sqrtS2RD1K", "sqrtS2RD50K", "RD1Kdiff", "RD50Kdiff")])

```

```
write_rds(file = "Functional_Intactness_Index/Overlap_modelling_data.rds", Overlap_data)
## that improve colinearity to acceptable levels so we can move onto modeling
```

```
#####
#### Modelling #####
#####
```

```
Model_1 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
               sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
               Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
               Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
               (1|SS),
               data = Overlap_data, weights = min_site_spp )
```

```
summary(Model_1)
```

```
AIC(Model_1)
```

```
#### random slopes
```

```
## logdist
```

```
Model_2 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
               sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
               Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
               Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
               (1|SS) + (1 + logdist|SS),
               data = Overlap_data, weights = min_site_spp )
```

```
summary(Model_2)
```

```
AIC(Model_2)
```

```
## rt3env
```

```
Model_3 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
               sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
               Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
               Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
               (1|SS) + (1 + rt3env|SS),
               data = Overlap_data, weights = min_site_spp )
```

```
summary(Model_3)
```

```
AIC(Model_3)
```

```
## logHPDdiff
```

```
Model_4 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
```

```

      sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
      Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
      Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
      (1|SS) + (1 + logHPDdiff|SS),
      data = Overlap_data, weights = min_site_spp )

summary(Model_4)

AIC(Model_4)

## sqrtS2RD1K

Model_5 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
      sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
      Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
      Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
      (1|SS) + (1 + sqrtS2RD1K|SS),
      data = Overlap_data, weights = min_site_spp )

summary(Model_5)

AIC(Model_5)

## sqrtS2RD50K

Model_6 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
      sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
      Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
      Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
      (1|SS) + (1 + sqrtS2RD50K|SS),
      data = Overlap_data, weights = min_site_spp )

summary(Model_6)

AIC(Model_6)

## RoadDdiff1k

Model_7 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
      sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
      Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
      Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
      (1|SS) + (1 + RD1Kdiff|SS),
      data = Overlap_data, weights = min_site_spp )

summary(Model_7)

AIC(Model_7)

## RoadDdiff50k

Model_8 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
      sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +

```



```

        Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
        Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff + Contrast:RD50Kdiff +
        (1|SS) + (1 + RD50Kdiff|SS),
        data = Overlap_data, weights = min_site_spp )

summary(Model_8)

AIC(Model_8)

MOD_AIC <- data.frame(Mod1 = AIC(Model_1),Mod2 = AIC(Model_2),Mod3 = AIC(Model_3),
                      Mod4 = AIC(Model_4),Mod5 = AIC(Model_5),Mod6 = AIC(Model_6),
                      Mod7 = AIC(Model_7),Mod8 = AIC(Model_8))

```

Model 1 seems to have the most support so we will carry on without any random slopes. Next stage is to perform backwards stepwise model simplification based on the likelihood ratio distribution test on 1000 permuted datasets.

```

Permuted_data <- rep(list(NA),1000)

for(i in 1:1000){

  sample_data <-c()

  for(study in unique(Overlap_data$SS)){
    data <- Overlap_data %>% filter(SS == study)

    data$logitOver <- data[sample(NROW(data)),"logitOver"]

    sample_data <- rbind(sample_data,data)
  }

  Permuted_data[[i]] <- sample_data
}

#### function to generate the LR distribution across the 100 datasets

##### Likelihood ratio function

Permuted_model_simplification <- function(data, model1, model2){

  LRT_dist <- c()

  for(i in 1:length(data)){

    mod1 <- lmer(model1@call, data = data[[i]], weights = min_site_spp, REML = FALSE)
    mod2 <- lmer(model2@call, data = data[[i]], weights = min_site_spp, REML = FALSE)

    LRT <- anova(mod1,mod2)
    LRT <- LRT[which(!is.na(LRT$Chisq)),"Chisq"]
  }
}

```

```

LRT_dist <- rbind(LRT_dist,LRT)

}

return(LRT_dist)

}

### so lets look at our best maximal model

Anova(Model_1, type = "II")

### with the lowest p-value we should remove the interaction between Contrast and RD50Kdiff

Model_9 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
                sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff + RD50Kdiff +
                Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
                Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
                (1|SS),
                data = Overlap_data, weights = min_site_spp )

summary(Model_9)

AIC(Model_9)

Like_ratio <- anova(Model_1, Model_9)

LRT_dist1 <- Permuted_model_simplification(Permuted_data,model1 = Model_1, model2 = Model_9)

ninety_five <- quantile(LRT_dist1,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_9,type = "II")

### lets remove RD50Kdiff fixed effect

Model_10 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
                sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff +
                Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
                Contrast:sqrtS2RD1K + Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
                (1|SS),
                data = Overlap_data, weights = min_site_spp )

summary(Model_10)

AIC(Model_10)

```

```

Like_ratio <- anova(Model_9, Model_10)

LRT_dist2 <- Permuted_model_simplification(Permuted_data,model1 = Model_9, model2 = Model_10)

ninety_five <- quantile(LRT_dist2,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_10,type = "II")

### next if we will remove sqrtS2RD1k interaction

Model_11 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
                sqrtS2RD1K + sqrtS2RD50K + RD1Kdiff +
                Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
                Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
                (1|SS),
                data = Overlap_data, weights = min_site_spp )

summary(Model_11)

AIC(Model_11)

Like_ratio <- anova(Model_10, Model_11)

LRT_dist3 <- Permuted_model_simplification(Permuted_data,model1 = Model_10, model2 = Model_11)

ninety_five <- quantile(LRT_dist3,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_11,type = "II")

### next we will remove sqrtS2RD1k fixed effect

Model_12 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
                sqrtS2RD1K + RD1Kdiff +
                Contrast:logdist + Contrast:rt3env + Contrast:logHPDdiff +
                Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
                (1|SS),
                data = Overlap_data, weights = min_site_spp )

```

```

summary(Model_12)

AIC(Model_12)

Like_ratio <- anova(Model_11, Model_12)

LRT_dist4 <- Permuted_model_simplification(Permuted_data,model11 = Model_11, model12 = Model_12)

  ninety_five <- quantile(LRT_dist4,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_12,type = "II")

### next we will remove the interaction between rt3env and Contrast

Model_13 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
  sqrtS2RD1K + RD1Kdiff +
  Contrast:logdist + Contrast:logHPDdiff +
  Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
  (1|SS),
  data = Overlap_data, weights = min_site_spp )

summary(Model_13)

AIC(Model_13)

Like_ratio <- anova(Model_12, Model_13)

LRT_dist5 <- Permuted_model_simplification(Permuted_data,model11 = Model_12, model12 = Model_13)

  ninety_five <- quantile(LRT_dist5,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_13,type = "II")

### next we will remove the interaction between logdist and Contrast

Model_14 <- lmer(logitOver ~ Contrast + logdist + rt3env + logHPDdiff +
  sqrtS2RD1K + RD1Kdiff +
  Contrast:logHPDdiff +

```

```

        Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
        (1|SS),
        data = Overlap_data, weights = min_site_spp )

summary(Model_14)

AIC(Model_14)

Like_ratio <- anova(Model_13, Model_14)

LRT_dist6 <- Permuted_model_simplification(Permuted_data,model1 = Model_13, model2 = Model_14)

ninety_five <- quantile(LRT_dist6,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_14,type = "II")

### next we will remove the rt3env fixed effect

Model_15 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +
        sqrtS2RD1K + RD1Kdiff +
        Contrast:logHPDdiff +
        Contrast:sqrtS2RD50K + Contrast:RD1Kdiff +
        (1|SS),
        data = Overlap_data, weights = min_site_spp )

summary(Model_15)

AIC(Model_15)

Like_ratio <- anova(Model_14, Model_15)

LRT_dist7 <- Permuted_model_simplification(Permuted_data,model1 = Model_14, model2 = Model_15)

ninety_five <- quantile(LRT_dist7,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_15,type = "II")

### next we will remove the interaction between the interaction between sqrtS2RD50k

```

```

Model_16 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +
  sqrtS2RD1K + RD1Kdiff +
  Contrast:logHPDdiff +
  Contrast:RD1Kdiff +
  (1|SS),
  data = Overlap_data, weights = min_site_spp )

summary(Model_16)

AIC(Model_16)

Like_ratio <- anova(Model_15, Model_16)

LRT_dist8 <- Permuted_model_simplification(Permuted_data,model1 = Model_15, model2 = Model_16)

ninety_five <- quantile(LRT_dist8,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is not significantly different from the distribution of LRT
##### interaction can be dropped from the model.

Anova(Model_16,type = "II")

### next we will remove the interaction between the interaction between RD1Kdiff

Model_17 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +
  sqrtS2RD1K + RD1Kdiff +
  Contrast:logHPDdiff +
  (1|SS),
  data = Overlap_data, weights = min_site_spp )

summary(Model_17)

AIC(Model_17)

Like_ratio <- anova(Model_16, Model_17)

LRT_dist9 <- Permuted_model_simplification(Permuted_data,model1 = Model_16, model2 = Model_17)

ninety_five <- quantile(LRT_dist9,0.95)

Like_ratio[2,"Chisq"] > ninety_five

##### LRT of models using the observed data is significantly different from the distribution of LRT usi
Anova(Model_16,type = "II")

```

next we will remove the interaction between the interaction between Contrast and logHPDdiff

```
Model_18 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +  
  sqrtS2RD1K + RD1Kdiff +  
  Contrast:RD1Kdiff +  
  (1|SS),  
  data = Overlap_data, weights = min_site_spp )
```

```
summary(Model_18)
```

```
AIC(Model_18)
```

```
Like_ratio <- anova(Model_16, Model_18)
```

```
LRT_dist10 <- Permuted_model_simplification(Permuted_data,model11 = Model_16, model12 = Model_18)
```

```
ninety_five <- quantile(LRT_dist10,0.95)
```

```
Like_ratio[2,"Chisq"] > ninety_five
```

LRT of models using the observed data is significantly different from the distribution of LRT using

```
Anova(Model_16,type = "II")
```

next we will remove the sqrtS2RD1K fixed effect

```
Model_19 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +  
  RD1Kdiff +  
  Contrast:RD1Kdiff +  
  Contrast:logHPDdiff +  
  (1|SS),  
  data = Overlap_data, weights = min_site_spp )
```

```
summary(Model_19)
```

```
AIC(Model_19)
```

```
Like_ratio <- anova(Model_16, Model_19)
```

```
LRT_dist11 <- Permuted_model_simplification(Permuted_data,model11 = Model_16, model12 = Model_19)
```

```
ninety_five <- quantile(LRT_dist11,0.95)
```

```
Like_ratio[2,"Chisq"] > ninety_five
```

LRT of models using the observed data is significantly different from the distribution of LRT using

```
Anova(Model_16,type = "II")
```

```

### next we will remove the logdist fixed effect

Model_20 <- lmer(logitOver ~ Contrast + logHPDdiff +
                 RD1Kdiff + sqrtS2RD1K +
                 Contrast:RD1Kdiff +
                 Contrast:logHPDdiff +
                 (1|SS),
                 data = Overlap_data, weights = min_site_spp )

summary(Model_20)

AIC(Model_20)

Like_ratio <- anova(Model_16, Model_20)

LRT_dist12 <- Permuted_model_simplification(Permuted_data,model1 = Model_16, model2 = Model_20)

ninety_five <- quantile(LRT_dist12,0.95)

Like_ratio[2,"Chisq"] > ninety_five

```

Finally testing the removal of all other fixed effects and interactions in the model I have found that `Model_16` is the best model where these removals result in a model with significantly less explanatory power based on the permuted datasets.

Looking more closely at the model output we can see that the similarity of communities compared to that of primary minimally used sites

```

Overlap_data <- readRDS("Functional_Intactness_Index/Overlap_modelling_data.rds")

Model_16 <- lmer(logitOver ~ Contrast + logdist + logHPDdiff +
                 sqrtS2RD1K + RD1Kdiff +
                 Contrast:logHPDdiff +
                 Contrast:RD1Kdiff +
                 (1|SS),
                 data = Overlap_data, weights = min_site_spp )

```

```
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

```
Anova(Model_16,type = "III")
```

```

## Analysis of Deviance Table (Type III Wald chisquare tests)
##
## Response: logitOver
##           Chisq Df Pr(>Chisq)
## (Intercept)   1.8013  1  0.1795599
## Contrast     30.7702  6  2.804e-05 ***
## logdist       8.2886  1  0.0039895 **
## logHPDdiff    1.8614  1  0.1724586
## sqrtS2RD1K   11.9396  1  0.0005495 ***

```



```
## RD1Kdiff          0.0100  1  0.9204791
## Contrast:logHPDdiff 23.2714  6  0.0007105 ***
## Contrast:RD1Kdiff  20.4826  5  0.0010141 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
### next we will remove the interaction between the interaction between sqrtS2RD50k
summary(Model_16)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: logitOver ~ Contrast + logdist + logHPDdiff + sqrtS2RD1K + RD1Kdiff +
## Contrast:logHPDdiff + Contrast:RD1Kdiff + (1 | SS)
## Data: Overlap_data
## Weights: min_site_spp
##
## REML criterion at convergence: 407.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6664 -0.6624 -0.0711  0.5601  2.7336
##
## Random effects:
##   Groups      Name                Variance Std.Dev.
##   SS          (Intercept)  0.3757     0.613
##   Residual                3.9700     1.992
## Number of obs: 456, groups:  SS, 12
##
## Fixed effects:
##                                     Estimate
## (Intercept)                        0.254452
## ContrastPrimary_Minimal use-Cropland_Light use -0.566685
## ContrastPrimary_Minimal use-Cropland_Minimal use -0.738923
## ContrastPrimary_Minimal use-Primary_Intense use -0.004459
## ContrastPrimary_Minimal use-Primary_Light use  0.133104
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use 0.428480
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use 0.230904
## logdist                            -0.120402
## logHPDdiff                         -0.093311
## sqrtS2RD1K                        -0.099347
## RD1Kdiff                           -0.004857
## ContrastPrimary_Minimal use-Cropland_Light use:logHPDdiff -0.432748
## ContrastPrimary_Minimal use-Cropland_Minimal use:logHPDdiff -1.095858
## ContrastPrimary_Minimal use-Primary_Intense use:logHPDdiff  0.055166
## ContrastPrimary_Minimal use-Primary_Light use:logHPDdiff    -0.021091
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:logHPDdiff 0.903093
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:logHPDdiff 0.742916
## ContrastPrimary_Minimal use-Cropland_Minimal use:RD1Kdiff  0.275284
## ContrastPrimary_Minimal use-Primary_Intense use:RD1Kdiff    0.073205
## ContrastPrimary_Minimal use-Primary_Light use:RD1Kdiff      0.072402
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:RD1Kdiff 0.216565
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:RD1Kdiff 0.203252
##                                     Std. Error
## (Intercept)                        0.189591
## ContrastPrimary_Minimal use-Cropland_Light use 0.277496
```

```

## ContrastPrimary_Minimal use-Cropland_Minimal use 0.292105
## ContrastPrimary_Minimal use-Primary_Intense use 0.087027
## ContrastPrimary_Minimal use-Primary_Light use 0.084758
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use 0.133861
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use 0.122025
## logdist 0.041821
## logHPDdiff 0.068392
## sqrtS2RD1K 0.028752
## RD1Kdiff 0.048656
## ContrastPrimary_Minimal use-Cropland_Light use:logHPDdiff 0.778912
## ContrastPrimary_Minimal use-Cropland_Minimal use:logHPDdiff 0.835789
## ContrastPrimary_Minimal use-Primary_Intense use:logHPDdiff 0.074562
## ContrastPrimary_Minimal use-Primary_Light use:logHPDdiff 0.079283
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:logHPDdiff 0.276255
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:logHPDdiff 0.245864
## ContrastPrimary_Minimal use-Cropland_Minimal use:RD1Kdiff 0.264463
## ContrastPrimary_Minimal use-Primary_Intense use:RD1Kdiff 0.052539
## ContrastPrimary_Minimal use-Primary_Light use:RD1Kdiff 0.060886
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:RD1Kdiff 0.068053
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:RD1Kdiff 0.057114
## t value
## (Intercept) 1.342
## ContrastPrimary_Minimal use-Cropland_Light use -2.042
## ContrastPrimary_Minimal use-Cropland_Minimal use -2.530
## ContrastPrimary_Minimal use-Primary_Intense use -0.051
## ContrastPrimary_Minimal use-Primary_Light use 1.570
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use 3.201
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use 1.892
## logdist -2.879
## logHPDdiff -1.364
## sqrtS2RD1K -3.455
## RD1Kdiff -0.100
## ContrastPrimary_Minimal use-Cropland_Light use:logHPDdiff -0.556
## ContrastPrimary_Minimal use-Cropland_Minimal use:logHPDdiff -1.311
## ContrastPrimary_Minimal use-Primary_Intense use:logHPDdiff 0.740
## ContrastPrimary_Minimal use-Primary_Light use:logHPDdiff -0.266
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:logHPDdiff 3.269
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:logHPDdiff 3.022
## ContrastPrimary_Minimal use-Cropland_Minimal use:RD1Kdiff 1.041
## ContrastPrimary_Minimal use-Primary_Intense use:RD1Kdiff 1.393
## ContrastPrimary_Minimal use-Primary_Light use:RD1Kdiff 1.189
## ContrastPrimary_Minimal use-Secondary_Vegetation_Light use:RD1Kdiff 3.182
## ContrastPrimary_Minimal use-Secondary_Vegetation_Minimal use:RD1Kdiff 3.559

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

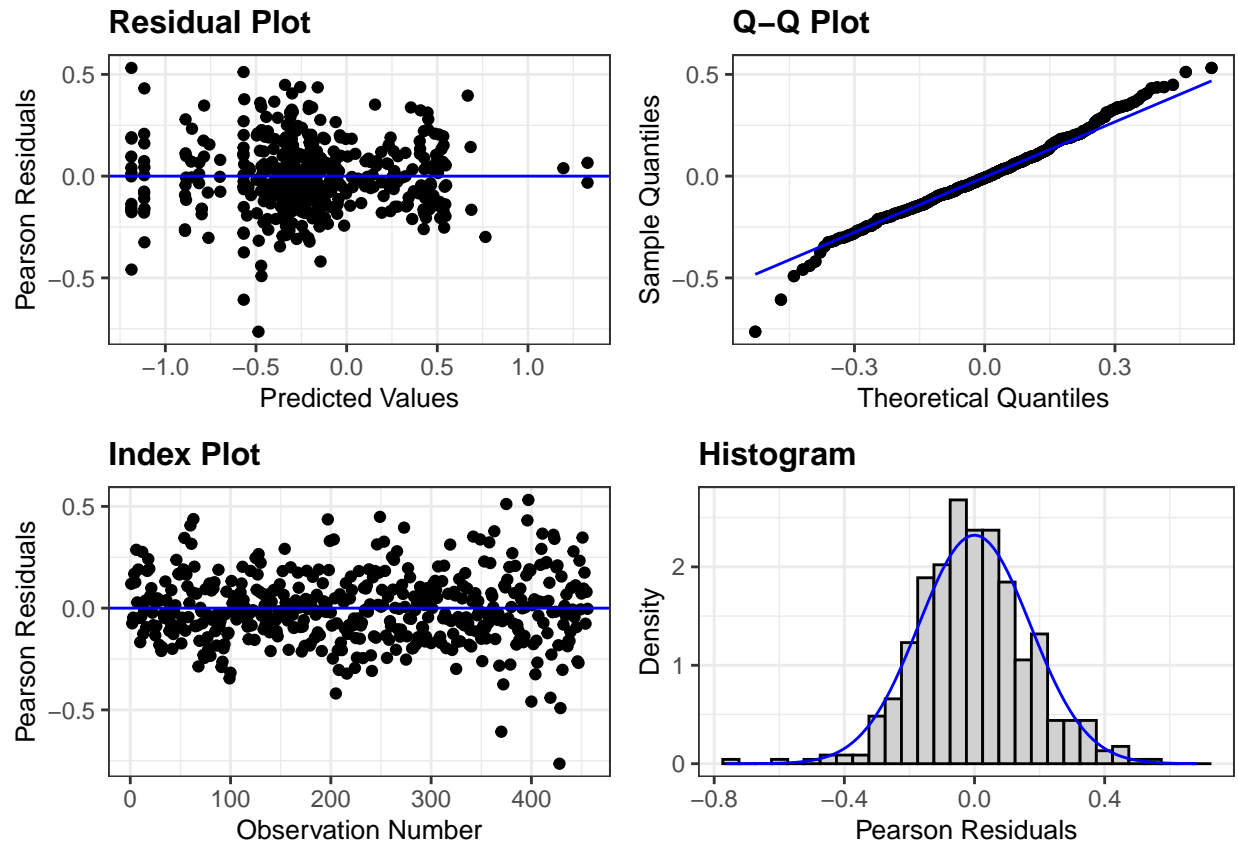
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient

```

```
AIC(Model_16)
```

```
## [1] 455.1823
```

```
resid_panel(Model_16)
```



```
write_rds(file = "Functional_Intactness_Index/Overlap_GLMM.rds", Model_16)
```