

Supplementary FS2

16 December 2024

This file documents our reanalysis of the dataset used to examine biodiversity and conflict relationships in the Southern Philippines presented in this paper <https://doi.org/10.1038/s44185-024-00044-8>. It should be noted that the analysis below does not take spatial autocorrelation into account; we address this in Supplementary FS3.

Files needed

```
##1. "landcover" folder containing the raster files of 1988 and 2020 land cover types  
##2. "mobios_tab.csv" or the biodiversity data  
##3. "conflict_tab_89-21.csv" or the conflict data  
##4. "1988_lc_classmap.csv" 1988 land cover types code  
##5. "2020_lc_classmap.csv" 2020 land cover types code
```

Load required packages

```
## make sure to install all packages including required dependencies prior to use  
re.lib <- c("tidyverse", "dplyr", "ggplot2", "patchwork",  
          "sf", "terra", "raster", "lme4", "MASS", "piecewiseSEM")  
  
## check if libraries are installed, install them if not  
for (lib in re.lib) {  
  if (!requireNamespace(lib, quietly = TRUE)) {  
    install.packages(lib)  
  }  
  library(lib, character.only = TRUE)  
}
```

Prepare datasets

```
## biodiversity data obtained from https://doi.org/10.15468/rtedgk  
## conflict data obtained from https://data.humdata.org/dataset/ucdp-data-for-philippines?  
## note that only a subset of this dataset (i.e., those from Mindanao and adjacent islands) was used  
  
## biodiversity data  
bio <- read.csv("data/mobios_tab.csv", header = TRUE, sep = ",")  
  
## subset data  
bio.sub <- subset(bio, select = c(12, 23, 20, 15, 16))  
bio.sub <- bio.sub %>% filter(county!="") # remove rows with no county information  
bio.sub <- bio.sub %>% filter(class!="Malacostraca") # exclude this taxon  
bio.sub <- bio.sub %>% filter(class!="Bivalvia") # exclude this taxon  
bio.sub <- bio.sub %>% filter(class!="Gastropoda")# exclude this taxon  
  
## check province name  
## there are rows where the name of the province is uncertain as indicated by "/"  
## "Zamboanga-†del Norte" was changed to "Zamboanga del Norte" prior to import of data  
unique(bio.sub$county)
```

```

## [1] "Lanao del Norte"
## [2] "South Cotabato"
## [3] "North Cotabato"
## [4] "Camiguin Island"
## [5] "Maguindanao"
## [6] "Agusan del Sur"
## [7] "Bukidnon"
## [8] "Davao Oriental"
## [9] "Davao"
## [10] "Misamis Occidental"
## [11] "Surigao del Sur"
## [12] "Davao del sur"
## [13] "Lanao del Sur"
## [14] "Sarangani"
## [15] "Misamis Oriental"
## [16] "Surigao del Norte"
## [17] "Davao de Oro"
## [18] "Davao del Norte"
## [19] "Zamboanga del Sur"
## [20] "Surigao del Norte/Agusan del Sur"
## [21] "Dinagat Island"
## [22] "Basilan"
## [23] "Tawi-Tawi"
## [24] "Sulu"
## [25] "Sultan Kudarat"
## [26] "Agusan del Norte"
## [27] "Cagayan de Oro"
## [28] "Bukidnon/Camiguin"
## [29] "Bukidnon/Misamis Oriental/Iligan"
## [30] "Zamboanga del Norte"
## [31] "Zamboanga Sibugay"
## [32] "Zamboanga del Norte"
## [33] "Misamis Occidental/Misamis Oriental/Camiguin/Bukidnon"
## [34] "Zamboanga City"
## [35] "General Santos"
## [36] "North Cotabato/Davao City"

## remove uncertain province names
bio.sub <- bio.sub %>% filter(!grepl('/', county))

head(bio.sub)

##          county      class      scientificName decimalLatitude
## 1 Lanao del Norte     Aves      Buceros hydrocorax      8.2122
## 2 Lanao del Norte  Mammalia    Eonycteris spelaea      8.3218
## 3 Lanao del Norte  Mammalia    Hipposideros diadema      8.3218
## 4 Lanao del Norte  Mammalia    Pipistrellus javanicus      8.3218
## 5 Lanao del Norte  Mammalia    Rhinolophus inops      8.3218
## 6 Lanao del Norte Mammalia Rousettus amplexicaudatus      8.3218
##      decimalLongitude
## 1            124.3835
## 2            124.2940
## 3            124.2940
## 4            124.2940
## 5            124.2940

```

```

## 6          124.2940

## write to a csv
write.csv(bio.sub, "bio.sub.csv")

## conflict data
con <- read.csv("data/conflict_tab_89-21.csv", header = TRUE, sep = ",")
con.sub <- subset(con, select = c(1,3,15,18,30,32,33))

head(con.sub)

##      id year           side_a side_b      PROVINCE latitude
## 1 124029 1989 Government of Philippines    CPP   Cotabato 6.951400
## 2 125199 1989 Government of Philippines    CPP   Maguindanao 7.270000
## 3 123871 1989 Government of Philippines    CPP Surigao del Sur 8.666670
## 4 122819 1989 Government of Philippines    CPP Agusan del Sur 8.500000
## 5 123283 1989 Government of Philippines    CPP Lanao del Norte 8.000000
## 6 123344 1989 Government of Philippines    CPP Davao Oriental 7.081413
##   longitude
## 1 125.0992
## 2 124.3106
## 3 126.0000
## 4 125.8333
## 5 124.0000
## 6 126.1299

## write to a csv
write.csv(con.sub, "con.sub.csv")

```

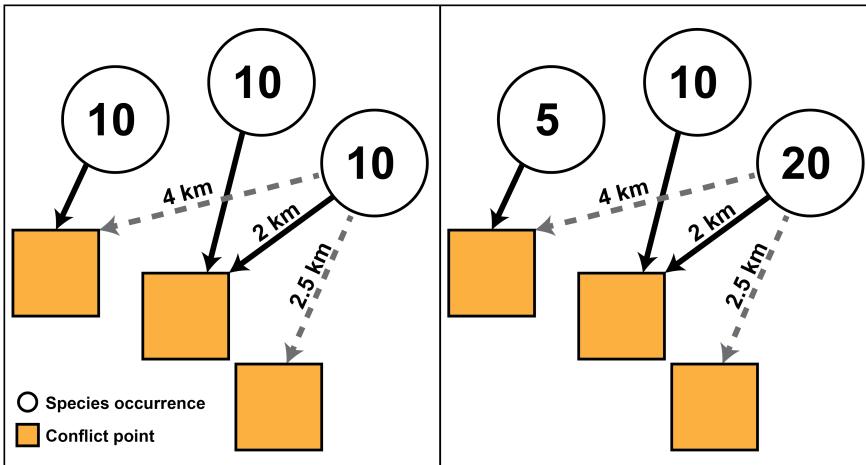
Count recorded species per taxon in each point and within province

```

## the procedures for conducting species counts in each site were not mentioned in the paper
## according to the paper, analysis was done at the provincial level
## there could be two ways that species counts were done (see image below)
## this part is extremely important, which the authors failed to discuss
## the left panel of the figure shows that species counts were aggregated at the provincial level
## each point (within the province) receives the same value of species count (or species richness)
## the right panel shows that each point has a unique number of species count
## note that these values are crucial for other downstream analyses
## particularly when relationships of species counts
## and distance to the nearest conflict sites are considered
## we generated the values for these two scenarios below
## and test whether any of them would match the results presented in the paper

```

```
knitr:::include_graphics("images/bioconflict.png")
```



```

## count unique records (i.e., species richness) per point
bio.data.sum <- bio.sub %>%
  group_by(county, class, decimalLatitude, decimalLongitude) %>%
  mutate(NumbSp = n_distinct(scientificName))

head(bio.data.sum)

## # A tibble: 6 x 6
## # Groups:   county, class, decimalLatitude, decimalLongitude [2]
##   county      class scientificName decimalLatitude decimalLongitude NumbSp
##   <chr>       <chr>   <chr>           <dbl>            <dbl>    <int>
## 1 Lanao del Norte Aves   Buceros hydro~     8.21             124.     1
## 2 Lanao del Norte Mamma~ Eonycteris sp~     8.32             124.     5
## 3 Lanao del Norte Mamma~ Hipposideros ~     8.32             124.     5
## 4 Lanao del Norte Mamma~ Pipistrellus ~     8.32             124.     5
## 5 Lanao del Norte Mamma~ Rhinolophus i~     8.32             124.     5
## 6 Lanao del Norte Mamma~ Rousettus amp~     8.32             124.     5

## write to a csv
write.csv(bio.data.sum, "bio.data.sum.csv")

## count species records per province (this lumps all the data,
## thus each point will have a single species richness value)
prov.bio.data.sum <- bio.sub %>%
  group_by(county, class) %>%
  mutate(NumbSp = n_distinct(scientificName))

head(prov.bio.data.sum)

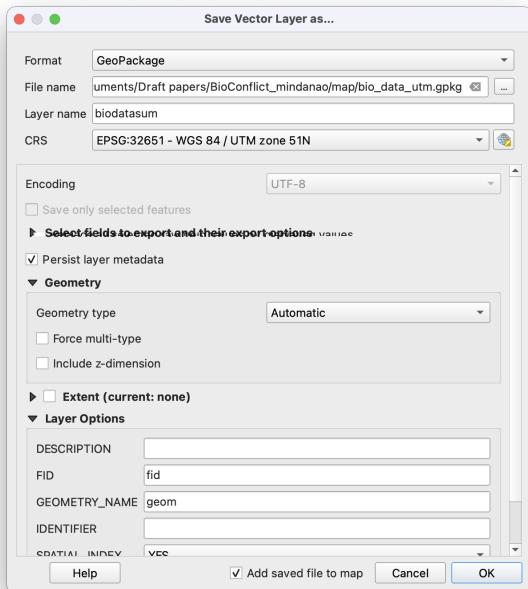
## # A tibble: 6 x 6
## # Groups:   county, class [2]
##   county      class scientificName decimalLatitude decimalLongitude NumbSp
##   <chr>       <chr>   <chr>           <dbl>            <dbl>    <int>
## 1 Lanao del Norte Aves   Buceros hydro~     8.21             124.     1
## 2 Lanao del Norte Mamma~ Eonycteris sp~     8.32             124.     5
## 3 Lanao del Norte Mamma~ Hipposideros ~     8.32             124.     5
## 4 Lanao del Norte Mamma~ Pipistrellus ~     8.32             124.     5
## 5 Lanao del Norte Mamma~ Rhinolophus i~     8.32             124.     5
## 6 Lanao del Norte Mamma~ Rousettus amp~     8.32             124.     5

```

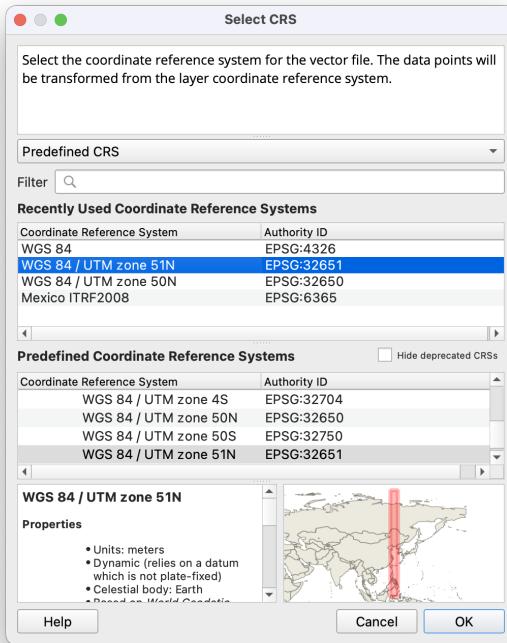
```
## write to a csv  
write.csv(prov.bio.data.sum, "prov.data.sum.csv")
```

Calculate distance of species record to the nearest conflict sites using QGIS

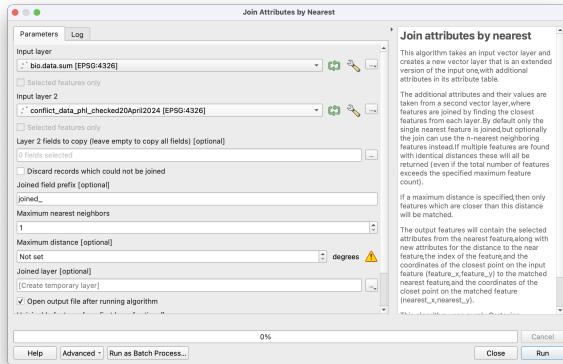
```
## in QGIS, import the "bio.data.sum.csv" and "con.sub.csv" from R as delimited text files.  
## export these files as GeoPackage or Shapefile to convert the data to meters prior to calculation  
## use the CRS UTM Zone 51N  
knitr:::include_graphics("images/qgis_geo.png")
```



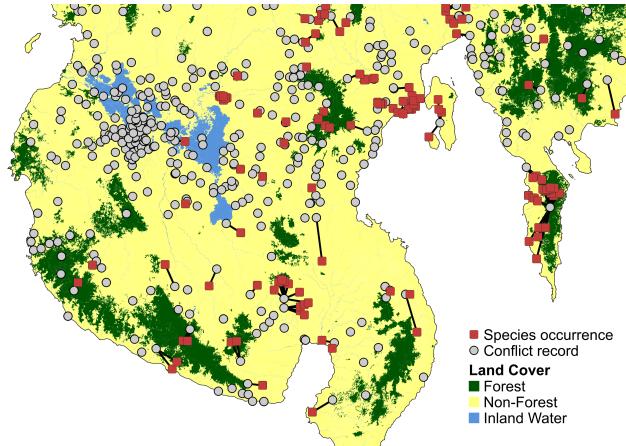
```
knitr:::include_graphics("images/qgis_utm.png")
```



```
## import back the newly saved data to QGIS
## get the distance of nearest conflict areas using the "Joint attributes by nearest" plugin
## QGIS > Processing Toolbox > Join attributes by nearest
knitr:::include_graphics("images/qgis_join.png")
```



```
## after calculating the distance, a new layer will be created.
## the new layer contains the calculated distance in the attribute table
## this also includes the x and y coordinates of the nearest conflict site
## then export this new layer as a csv file so we can use the data in R for other analysis
## repeat the entire process for provincial data (i.e., prov.bio.data.sum.csv) if necessary
## figure below shows the nearest conflict point to species record (black line)
## notice the remainder of conflict points are not included
knitr:::include_graphics("images/hub.png")
```



Calculate average distance

```

## species richness per point in each province
## read file with calculated distance from QGIS
bio.con.dist <- read.csv("data/bio.con.dist.csv", header = TRUE, sep = ",")

## get average distance by province for each taxon
mean.dist <- bio.con.dist %>%
  group_by(county, class, NumbSp, decimalLatitude, decimalLongitude) %>%
  summarize(meanDistance = mean(distance, na.rm = TRUE))

## `summarise()` has grouped output by 'county', 'class', 'NumbSp',
## 'decimalLatitude'. You can override using the `.`groups` argument.

head(mean.dist)

## # A tibble: 6 x 6
## # Groups:   county, class, NumbSp, decimalLatitude [6]
##   county       class   NumbSp decimalLatitude decimalLongitude meanDistance
##   <chr>        <chr>    <int>        <dbl>           <dbl>          <dbl>
## 1 Agusan del Norte Amphib~     5        9.00         126.          5108.
## 2 Agusan del Norte Amphib~    20        8.97         126.          1594.
## 3 Agusan del Norte Amphib~    20        9.05         126.          8659.
## 4 Agusan del Norte Amphib~    20        9.05         126.          8052.
## 5 Agusan del Norte Amphib~    20        9.10         126.          2949.
## 6 Agusan del Norte Amphib~    20        9.15         126.          5850.

write.csv(mean.dist, "mean.distance.csv")

## species richness lumped per province
## read file with calculated distance in QGIS
prov.bio.con.dist <- read.csv("data/prov.bio.con.dist.csv", header = TRUE, sep = ",")

## get average distance by province for each taxon
prov.mean.dist <- prov.bio.con.dist %>%
  group_by(county, class, NumbSp, decimalLatitude, decimalLongitude) %>%
  summarize(meanDistance = mean(distance, na.rm = TRUE))

## `summarise()` has grouped output by 'county', 'class', 'NumbSp',
## 'decimalLatitude'. You can override using the `.`groups` argument.

```

```

write.csv(prov.mean.dist, "prov.mean.distance.csv")

#> #get average distance by province without considering the long/lat data (i.e., lumped average)
#> prov.lmp.dist <- prov.bio.con.dist %>%
#>   group_by(county, class, NumbSp) %>%
#>   summarize(lmpMeanDistance = mean(distance, na.rm = TRUE))

## `summarise()` has grouped output by 'county', 'class'. You can override using
## the ` `.groups` argument.
write.csv(prov.lmp.dist, "prov.lmp.distance.csv")

Plot species record vs average distance

## get taxa names
key.lab <- unique(mean.dist$class)

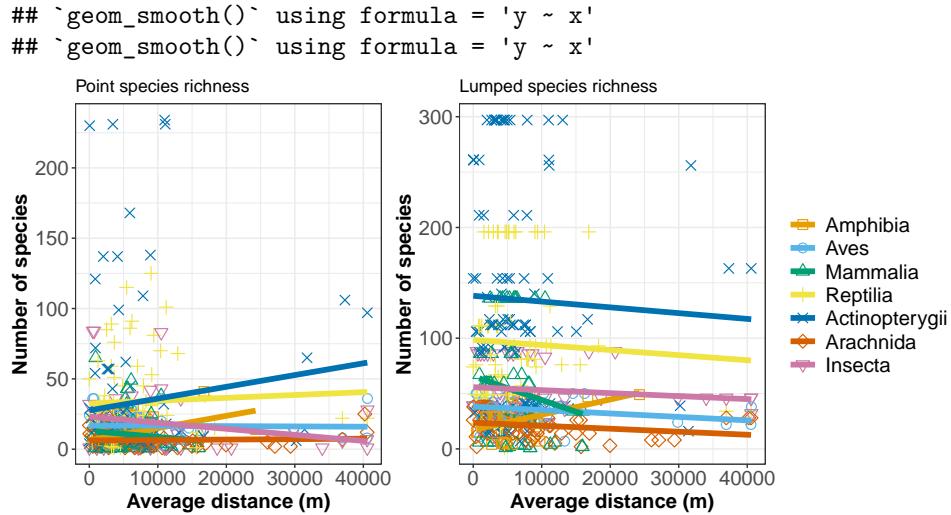
## assign point shapes and colors
plot.color <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
point.shape <- c(0,1,2,3,4,5,6,7,8,9,10)

## plot per point species richness vs. mean distance
p1 <- ggplot(mean.dist, (aes(x=meanDistance, y=NumbSp, color=class, shape=class))) + theme_bw() +
  theme(axis.text=element_text(size=15), axis.title=element_text(size=15, face="bold"),
        legend.key.width = unit(0.8, units = "cm"), legend.text = element_text(size=15),
        legend.key=element_blank()) +
  ylab("Number of species") +
  xlab("Average distance (m)") +
  labs(title = "Point species richness") +
  geom_point(size = 3, stroke = 0.6) +
  geom_smooth(method=lm, se=FALSE, fullrange=FALSE, size = 2) +
  scale_color_manual(name = "", labels = key.lab, values = plot.color) +
  scale_shape_manual(name = "", labels = key.lab, values = point.shape)

## plot lumped species richness vs. mean distance
p2 <- ggplot(prov.mean.dist, (aes(x=meanDistance, y=NumbSp, color=class, shape=class))) + theme_bw() +
  theme(axis.text=element_text(size=15), axis.title=element_text(size=15, face="bold"),
        legend.key.width = unit(0.8, units = "cm"), legend.text = element_text(size=15),
        legend.key=element_blank()) +
  ylab("Number of species") +
  xlab("Average distance (m)") +
  labs(title = "Lumped species richness") +
  geom_point(size = 3, stroke = 0.6) +
  geom_smooth(method=lm, se=FALSE, fullrange=FALSE, size = 2) +
  scale_color_manual(name = "", labels = key.lab, values = plot.color) +
  scale_shape_manual(name = "", labels = key.lab, values = point.shape)

## combine plots
comb.plot <- (p1 + p2 +
  plot_annotation(title = ""))
comb.plot <- comb.plot +
  plot_layout(guides = "collect") &
  theme(legend.position = "right")
comb.plot

```



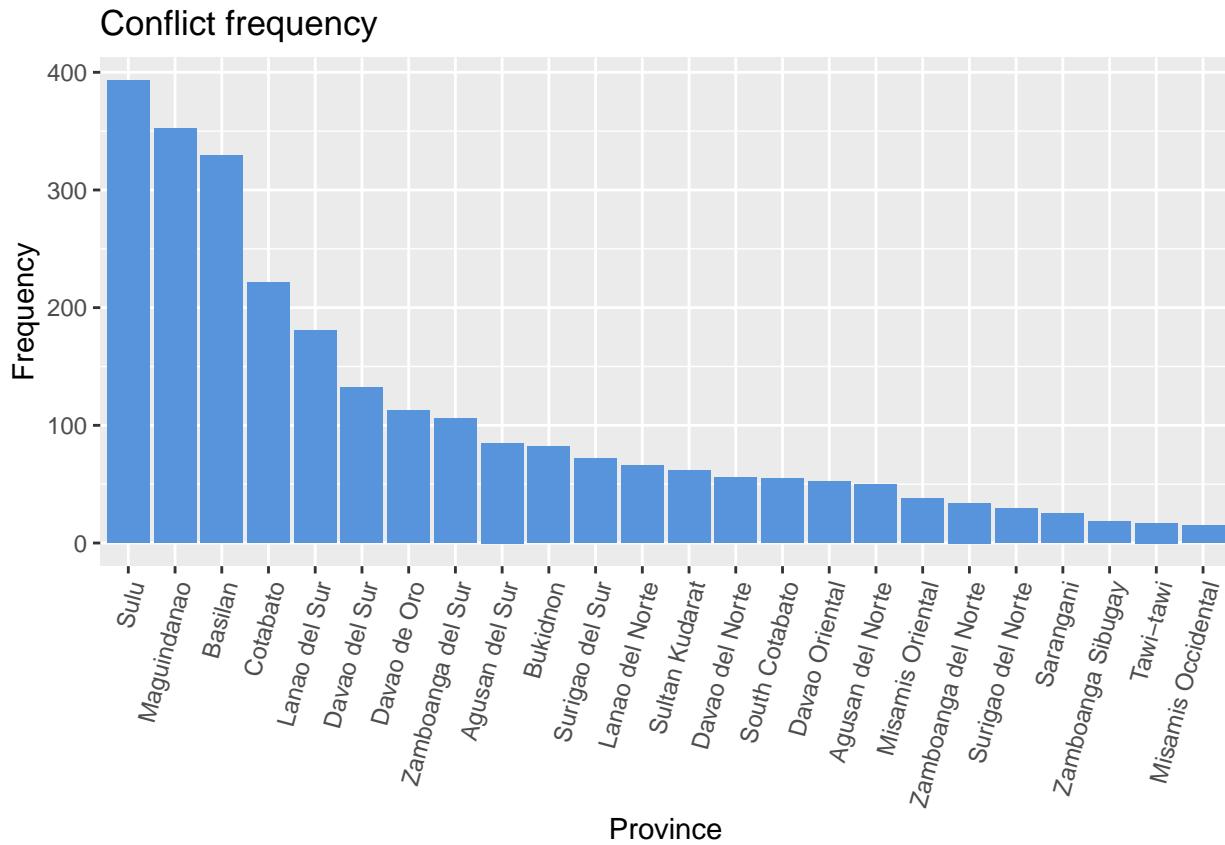
Get number of conflict sites per province

```
## we are not sure how the frequency of conflicts were scored in the paper as it was not mentioned
## we can get frequency based on the number of unique conflict points within each province
con.sub.2 <- con.sub
con.sub.2 <- con.sub.2 %>% filter(PROVINCE!="") #filter empty rows

con.freq <- con.sub.2 %>%
  group_by(PROVINCE) %>%
  mutate(ConflictFreq = n_distinct(latitude, longitude)) #use only the unique latitude
con.freq1 <- con.freq %>% distinct(PROVINCE, .keep_all = TRUE)
write.csv(con.freq1, "conflict.frequency.unique.csv")

## or we count each row as a unique report of conflict regardless of coordinates
con.freq2 <- con.sub.2 %>%
  group_by(PROVINCE) %>%
  count()
write.csv(con.freq2, "conflict.frequency.rows.csv")

ggplot(data=con.freq2, aes(x=reorder(PROVINCE, -n), y=n)) +
  geom_bar(stat="identity", fill="#5794db") +
  ylab("Frequency") +
  xlab("Province") +
  labs(title = "Conflict frequency") +
  guides(x = guide_axis(angle = 75))
```



```
## combine biodiversity and conflict data (lumped)
prov.comb <- prov.lmp.dist %>% mutate(conflictFreq = if_else(county == "Agusan del Norte", 50,
  if_else(county == "Agusan del Sur", 85,
  if_else(county == "Basilan", 329,
  if_else(county == "Bukidnon", 82,
  if_else(county == "Cagayan de Oro", 0,
  if_else(county == "Camiguin Island", 0,
  if_else(county == "Cotabato", 221,
  if_else(county == "Davao", 0,
  if_else(county == "Davao Oriental", 52,
  if_else(county == "Davao de Oro", 113,
  if_else(county == "Davao del Norte", 56,
  if_else(county == "Davao del sur", 181,
  if_else(county == "Dinagat Island", 0,
  if_else(county == "General Santos", 0,
  if_else(county == "Lanao del Norte", 66,
  if_else(county == "Lanao del Sur", 181,
  if_else(county == "Maguindanao", 352,
  if_else(county == "Misamis Occidental", 15,
  if_else(county == "Misamis Oriental", 38,
  if_else(county == "North Cotabato", 0,
  if_else(county == "Sarangani", 25,
  if_else(county == "South Cotabato", 55,
  if_else(county == "Sultan Kudarat", 62,
  if_else(county == "Sulu", 393,
  if_else(county == "Surigao del Norte", 29,
  if_else(county == "Surigao del Sur", 72,
```

```

if_else(county == "Tawi-Tawi", 17,
if_else(county == "Zamboanga City", 0,
if_else(county == "Zamboanga Sibugay", 18,
if_else(county == "Zamboanga del Norte", 34,
if_else(county == "Zamboanga del Sur", 106, 0)))))))))))))))))))))))))))))))
```

`write.csv(prov.comb, "prov.lmp.comb.csv")`

combine biodiversity and conflict data (per point)

```

perpoint.comb <- mean.dist %>% mutate(conflictFreq = if_else(county == "Agusan del Norte", 50,
  if_else(county == "Agusan del Sur", 85,
  if_else(county == "Basilan", 329,
  if_else(county == "Bukidnon", 82,
  if_else(county == "Cagayan de Oro", 0,
  if_else(county == "Camiguin Island", 0,
  if_else(county == "Cotabato", 221,
  if_else(county == "Davao", 0,
  if_else(county == "Davao Oriental", 52,
  if_else(county == "Davao de Oro", 113,
  if_else(county == "Davao del Norte", 56,
  if_else(county == "Davao del sur", 181,
  if_else(county == "Dinagat Island", 0,
  if_else(county == "General Santos", 0,
  if_else(county == "Lanao del Norte", 66,
  if_else(county == "Lanao del Sur", 181,
  if_else(county == "Maguindanao", 352,
  if_else(county == "Misamis Occidental", 15,
  if_else(county == "Misamis Oriental", 38,
  if_else(county == "North Cotabato", 0,
  if_else(county == "Sarangani", 25,
  if_else(county == "South Cotabato", 55,
  if_else(county == "Sultan Kudarat", 62,
  if_else(county == "Sulu", 393,
  if_else(county == "Surigao del Norte", 29,
  if_else(county == "Surigao del Sur", 72,
  if_else(county == "Tawi-Tawi", 17,
  if_else(county == "Zamboanga City", 0,
  if_else(county == "Zamboanga Sibugay", 18,
  if_else(county == "Zamboanga del Norte", 34,
  if_else(county == "Zamboanga del Sur", 106, 0)))))))))))))))))))))))))))
```

`write.csv(perpoint.comb, "perpoint.comb.csv")`

Perform GLM

```

# set seed
set.seed(12345)

## plot data
p1 <- ggplot(prov.comb, aes(x = lmpMeanDistance, y = NumbSp)) +
  geom_point(pch = 1) + geom_smooth(method = lm) +
  ylab("Number of species") +
  xlab("Average distance (m)") +
  labs(title = "Richness vs. average distance")
```

```

p2 <- ggplot(prov.comb, aes(x = conflictFreq, y = NumbSp)) +
  geom_point(pch = 1) + geom_smooth(method = lm) +
  ylab("Number of species") +
  xlab("Number of conflict") +
  labs(title = "Richness vs. conflict frequency")

```

```

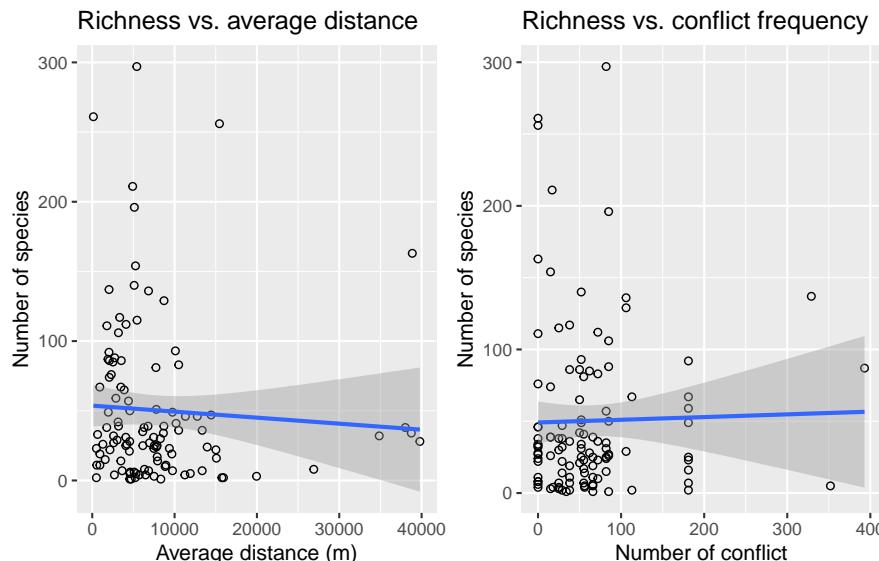
## combine plots
comb.plot <- (p1 + p2 +
  plot_annotation(title = ""))
comb.plot <- comb.plot +
  plot_layout(guides = "collect") &
  theme(legend.position = "right")
comb.plot

```

```

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'

```



```

## perform glm using lumped species richness
## assign taxa as a factor
prov.comb$class <- factor(prov.comb$class)

## transform data
prov.comb$distlog <- log(prov.comb$ImpMeanDistance + 1)
prov.comb$freqlog <- log(prov.comb$conflictFreq + 1)

## perform glm
glm.res.1 <- glm(NumbSp ~ freqlog + distlog + class,
  family = "poisson"(link = "log"), data = prov.comb)
glm.res.2 <- glm(NumbSp ~ freqlog + class,
  family = "poisson"(link = "log"), data = prov.comb)
glm.res.3 <- glm(NumbSp ~ distlog + class,
  family = "poisson"(link = "log"), data = prov.comb)
glm.res.4 <- glm(NumbSp ~ freqlog + distlog,
  family = "poisson"(link = "log"), data = prov.comb)

## compare glm results

```

```

aic.values <- AIC(glm.res.1, glm.res.2, glm.res.3, glm.res.4)
aic.values

##          df      AIC
## glm.res.1 9 3611.665
## glm.res.2 8 3621.243
## glm.res.3 8 3651.504
## glm.res.4 3 6078.562
## identify the model with the lowest AIC
best.model <- rownames(aic.values)[which.min(aic.values$AIC)]
best.model

## [1] "glm.res.1"
stepAIC(glm.res.1, direction='both') #use stepAIC function

## Start:  AIC=3611.67
## NumbSp ~ freqlog + distlog + class
##
##          Df Deviance   AIC
## <none>     3019.9 3611.7
## - distlog  1    3031.5 3621.2
## - freqlog  1    3061.7 3651.5
## - class    6    5498.8 6078.6
##
## Call: glm(formula = NumbSp ~ freqlog + distlog + class, family = poisson(link = "log"),
##           data = prov.comb)
##
## Coefficients:
## (Intercept)      freqlog      distlog  classAmphibia
##            3.53068     -0.04845     -0.04300      0.38063
## classArachnida classAves    classInsecta  classMammalia
##            0.45877      1.30923      1.73036     -0.23588
## classReptilia
##            0.79056
##
## Degrees of Freedom: 111 Total (i.e. Null); 103 Residual
## Null Deviance: 5683
## Residual Deviance: 3020  AIC: 3612
## get summary for best model
summary(get(best.model))

##
## Call:
## glm(formula = NumbSp ~ freqlog + distlog + class, family = poisson(link = "log"),
##       data = prov.comb)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.530676  0.126575 27.894 < 2e-16 ***
## freqlog     -0.048453  0.007399 -6.548 5.82e-11 ***
## distlog     -0.043000  0.012579 -3.418 0.00063 ***
## classAmphibia 0.380634  0.078973  4.820 1.44e-06 ***
## classArachnida 0.458767  0.076184  6.022 1.72e-09 ***

```

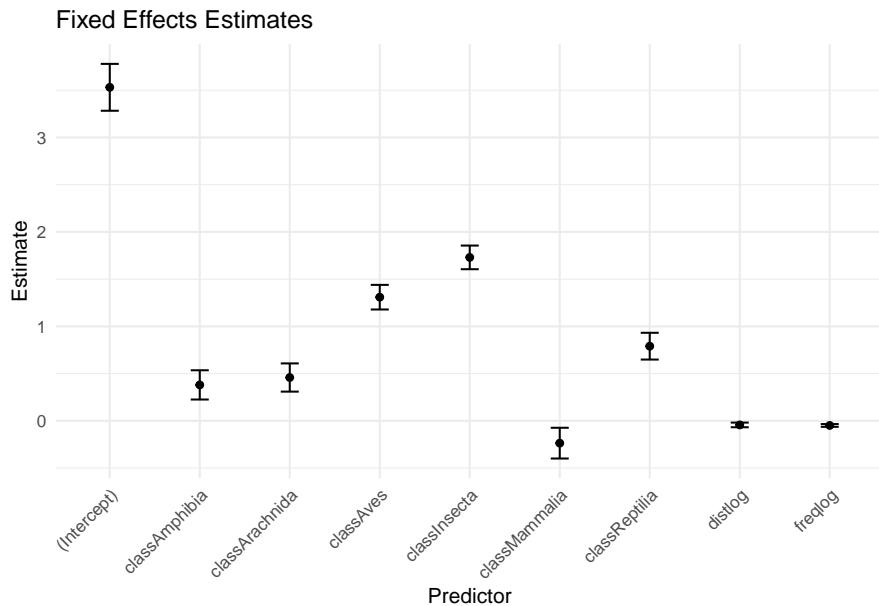
```

## classAves      1.309235  0.066414 19.713 < 2e-16 ***
## classInsecta   1.730364  0.063853 27.099 < 2e-16 ***
## classMammalia -0.235879  0.083000 -2.842  0.00448 **
## classReptilia  0.790565  0.072266 10.940 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 5683.2 on 111 degrees of freedom
## Residual deviance: 3019.9 on 103 degrees of freedom
## AIC: 3611.7
##
## Number of Fisher Scoring iterations: 5
## plot results
## get fixed effects coefficients and their confidence intervals
fix.eff <- summary(best.model)$coefficients

# create a data frame
fix.eff_df <- as.data.frame(fix.eff)
fix.eff_df$term <- rownames(fix.eff_df)

## plot coefficients
ggplot(fix.eff_df, aes(x = term, y = Estimate)) +
  geom_point() +
  geom_errorbar(aes(ymax = Estimate - 1.96 * `Std. Error`,
                    ymin = Estimate + 1.96 * `Std. Error`), width = 0.2) +
  theme_minimal() +
  labs(title = "Fixed Effects Estimates", x = "Predictor", y = "Estimate") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

```



```

## glm with taxa as a random variable
glm.res.5 <- glmer(NumbSp ~ freqlog + distlog + (1|class),
                     family = "poisson"(link = "log"), data = prov.comb)

```

```

summary(glm.res.5)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: NumbSp ~ freqlog + distlog + (1 | class)
## Data: prov.comb
##
##      AIC      BIC  logLik deviance df.resid
##  3647.4  3658.2 -1819.7   3639.4     108
##
## Scaled residuals:
##      Min      1Q  Median      3Q     Max
## -9.9419 -3.1795 -0.6166  2.4163 19.6111
##
## Random effects:
## Groups Name        Variance Std.Dev.
## class  (Intercept) 0.4187   0.6471
## Number of obs: 112, groups: class, 7
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 4.166851  0.268727 15.506 < 2e-16 ***
## freqlog     -0.048435  0.007397 -6.548 5.84e-11 ***
## distlog     -0.043257  0.012577 -3.439 0.000583 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) freqlg
## freqlog -0.087
## distlog -0.400 -0.006
## get R^2
## marginal accounts for proportion of variance explained only by the fixed effects
## conditional accounts for proportion of variance explained by the entire mode
rsquared(glm.res.5, method="trigamma")

```

```

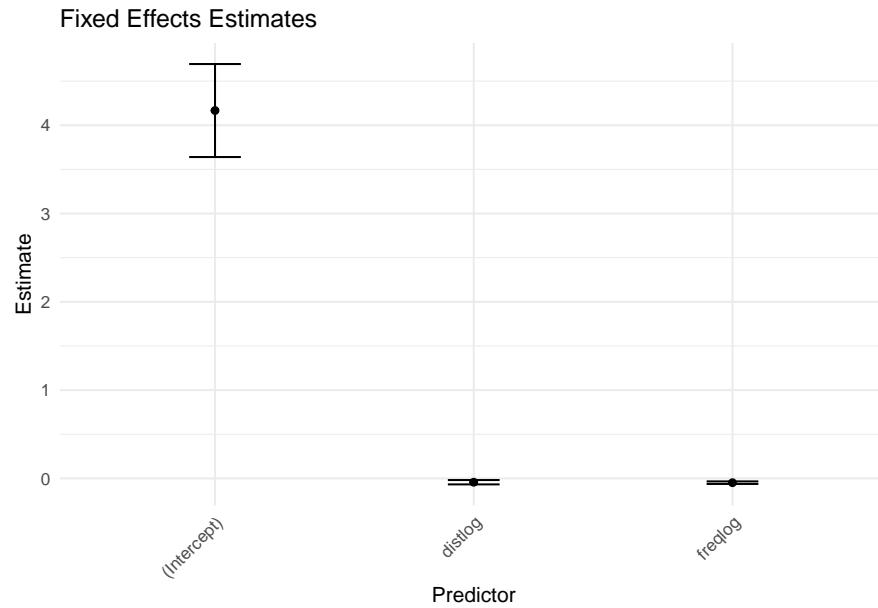
## Response family link method Marginal Conditional
## 1  NumbSp poisson  log trigamma 0.01744259  0.9517855
## plot results
## get fixed effects coefficients and their confidence intervals
fix.eff <- summary(glm.res.5)$coefficients

# create a data frame
fix.eff_df <- as.data.frame(fix.eff)
fix.eff_df$term <- rownames(fix.eff_df)

## plot coefficients
ggplot(fix.eff_df, aes(x = term, y = Estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = Estimate - 1.96 * `Std. Error`,
                    ymax = Estimate + 1.96 * `Std. Error`), width = 0.2) +
  theme_minimal() +

```

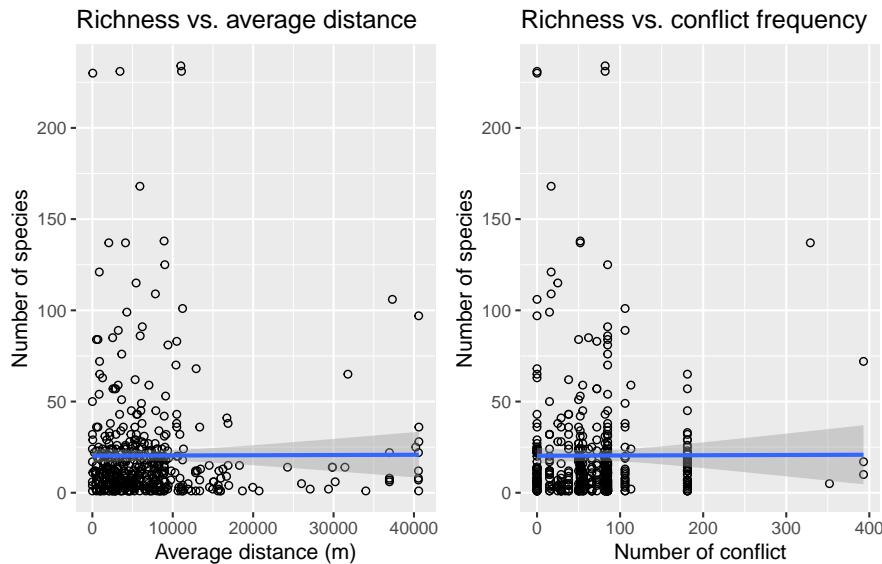
```
labs(title = "Fixed Effects Estimates", x = "Predictor", y = "Estimate") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
## use species richness per point
#plot data
p1 <- ggplot(perpoint.comb, aes(x = meanDistance, y = NumbSp)) +
  geom_point(pch = 1) + geom_smooth(method = lm) +
  ylab("Number of species") +
  xlab("Average distance (m)") +
  labs(title = "Richness vs. average distance")
p2 <- ggplot(perpoint.comb, aes(x = conflictFreq, y = NumbSp)) +
  geom_point(pch = 1) + geom_smooth(method = lm) +
  ylab("Number of species") +
  xlab("Number of conflict") +
  labs(title = "Richness vs. conflict frequency")

## combine plots
comb.plot <- (p1 + p2 +
  plot_annotation(title = ""))
comb.plot <- comb.plot +
  plot_layout(guides = "collect") &
  theme(legend.position = "right")
comb.plot

## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



```

## assign taxa as a factor
perpoint.comb$class <- factor(perpoint.comb$class)

## transform data
perpoint.comb$distlog <- log(perpoint.comb$meanDistance + 1)
perpoint.comb$freqlog <- log(perpoint.comb$conflictFreq + 1)

## perform glm
glm.res.1 <- glm(NumbSp ~ freqlog + distlog + class,
                   family = "poisson"(link = "log"), data = perpoint.comb)
glm.res.2 <- glm(NumbSp ~ freqlog + class,
                   family = "poisson"(link = "log"), data = perpoint.comb)
glm.res.3 <- glm(NumbSp ~ distlog + class,
                   family = "poisson"(link = "log"), data = perpoint.comb)
glm.res.4 <- glm(NumbSp ~ freqlog + distlog,
                   family = "poisson"(link = "log"), data = perpoint.comb)

## compare glm results
aic.values <- AIC(glm.res.1, glm.res.2, glm.res.3, glm.res.4)
aic.values

##          df      AIC
## glm.res.1 9 11573.48
## glm.res.2 8 11571.98
## glm.res.3 8 11656.29
## glm.res.4 3 14335.01

## identify the model with the lowest AIC
best.model <- rownames(aic.values)[which.min(aic.values$AIC)]
best.model

## [1] "glm.res.2"
stepAIC(glm.res.1, direction = 'both') #use stepAIC function

## Start:  AIC=11573.48
## NumbSp ~ freqlog + distlog + class
## 
```

```

##          Df Deviance AIC
## - distlog  1  9650.3 11572
## <none>      9649.8 11574
## - freqlog  1  9734.6 11656
## - class    6 12423.3 14335
##
## Step:  AIC=11571.98
## NumbSp ~ freqlog + class
##
##          Df Deviance AIC
## <none>      9650.3 11572
## + distlog  1  9649.8 11574
## - freqlog  1  9735.8 11656
## - class    6 12459.8 14370
##
## Call: glm(formula = NumbSp ~ freqlog + class, family = poisson(link = "log"),
##           data = perpoint.comb)
##
## Coefficients:
## (Intercept)      freqlog  classAmphibia  classArachnida
## 2.67229         -0.05869     0.33428      -0.05851
## classAves       classInsecta  classMammalia  classReptilia
## 1.05117         1.04212      -0.63838      0.42480
##
## Degrees of Freedom: 457 Total (i.e. Null); 450 Residual
## Null Deviance: 12510
## Residual Deviance: 9650 AIC: 11570
# get summary for best model
summary(get(best.model))

```

```

##
## Call:
## glm(formula = NumbSp ~ freqlog + class, family = poisson(link = "log"),
##       data = perpoint.comb)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 2.672293  0.054198 49.306 < 2e-16 ***
## freqlog     -0.058693  0.006224 -9.430 < 2e-16 ***
## classAmphibia 0.334275  0.059180  5.648 1.62e-08 ***
## classArachnida -0.058513  0.061455 -0.952  0.341
## classAves    1.051174  0.052513 20.017 < 2e-16 ***
## classInsecta  1.042122  0.051502 20.235 < 2e-16 ***
## classMammalia -0.638384  0.067229 -9.496 < 2e-16 ***
## classReptilia  0.424802  0.058706  7.236 4.62e-13 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 12508.2 on 457 degrees of freedom
## Residual deviance: 9650.3 on 450 degrees of freedom
## AIC: 11572

```

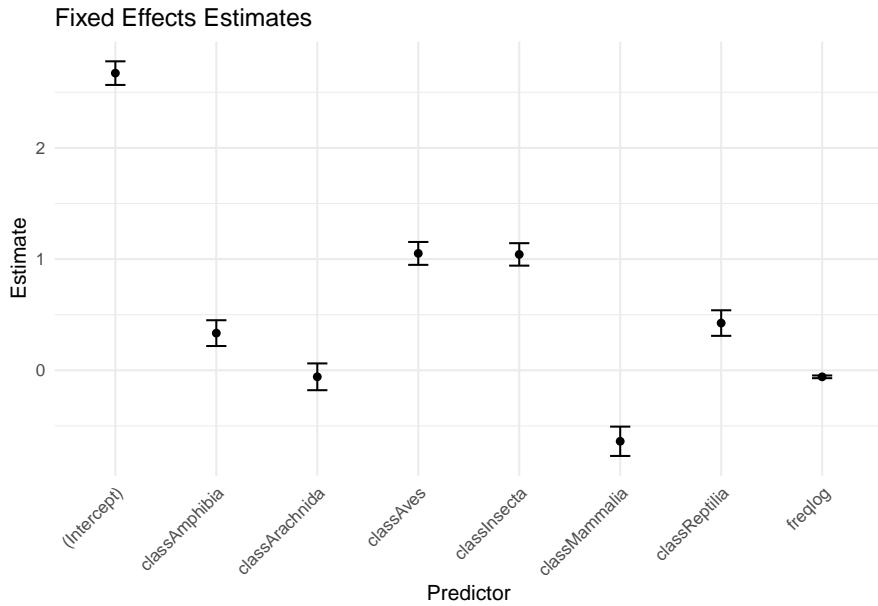
```

## Number of Fisher Scoring iterations: 6
## plot results
## get fixed effects coefficients and their confidence intervals
fix.eff <- summary(best.model)$coefficients

# create a data frame
fix.eff_df <- as.data.frame(fix.eff)
fix.eff_df$term <- rownames(fix.eff_df)

## plot coefficients
ggplot(fix.eff_df, aes(x = term, y = Estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = Estimate - 1.96 * `Std. Error`,
                     ymax = Estimate + 1.96 * `Std. Error`), width = 0.2) +
  theme_minimal() +
  labs(title = "Fixed Effects Estimates", x = "Predictor", y = "Estimate") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

```



```

## glm with taxa as a random variable
glm.res.5 <- glmer(NumbSp ~ freqlog + distlog + (1|class),
                     family = "poisson"(link = "log"), data = perpoint.comb)
summary(glm.res.5)

```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: NumbSp ~ freqlog + distlog + (1 | class)
## Data: perpoint.comb
##
##      AIC      BIC  logLik deviance df.resid
##  11610.8  11627.3 -5801.4   11602.8      454
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max

```

```

## -6.247 -2.944 -1.306  0.986 36.119
##
## Random effects:
##   Groups Name      Variance Std.Dev.
##   class  (Intercept) 0.3172   0.5632
## Number of obs: 458, groups: class, 7
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.025796  0.223254 13.553 <2e-16 ***
## freqlog     -0.058451  0.006229 -9.384 <2e-16 ***
## distlog     -0.005461  0.007561 -0.722    0.47
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) freqlg
## freqlog -0.082
## distlog -0.280 -0.049
## get R^2
rsquared(glm.res.5, method = "trigamma")

## Response family link method Marginal Conditional
## 1 NumbSp poisson log trigamma 0.02317399  0.8564394

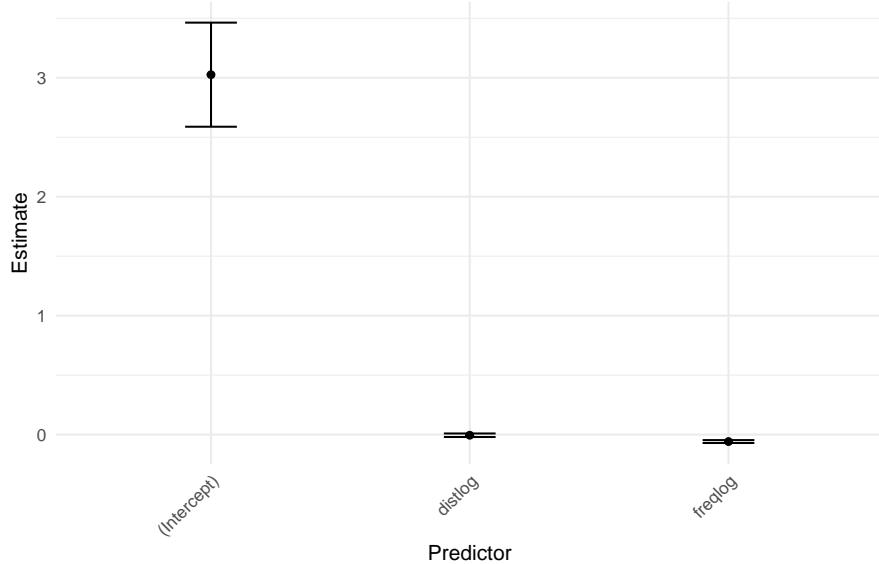
## plot results
## get fixed effects coefficients and their confidence intervals
fix.eff <- summary(glm.res.5)$coefficients

# create a data frame
fix.eff_df <- as.data.frame(fix.eff)
fix.eff_df$term <- rownames(fix.eff_df)

## plot coefficients
ggplot(fix.eff_df, aes(x = term, y = Estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = Estimate - 1.96 * `Std. Error`,
                    ymax = Estimate + 1.96 * `Std. Error`), width = 0.2) +
  theme_minimal() +
  labs(title = "Fixed Effects Estimates", x = "Predictor", y = "Estimate") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

```

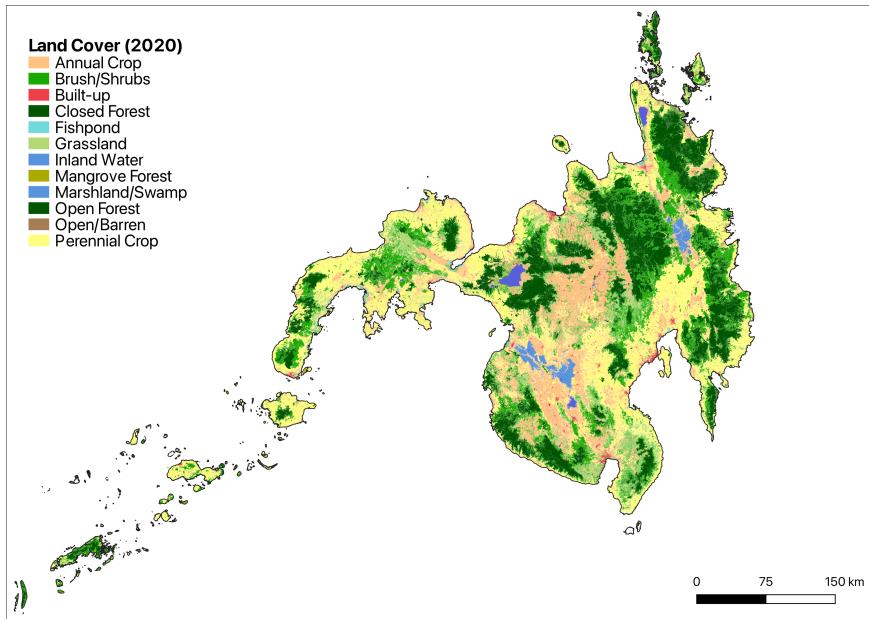
Fixed Effects Estimates



Calculate proportion of species occurrence records and conflict sites positioned in different land cover types

```
## here we calculate the number of sites found in different land cover types
## this demonstrates the artifact of sampling, which was not considered in the paper
## land cover data of 1988 was from Swedish Space Corporation (SSC 1988)
## land cover of 2020 was from the Philippine National Mapping and Resource Information Authority
## data was retrieved from geoportal PH (https://www.geoportal.gov.ph/)
## we used land cover as a proxy for tree density and forest canopy data
## the national land cover data is ground-truthed
## this is only for simplistic illustration of sampling artifact
## the original land cover format is shapefile
## we converted it to raster file for fast data processing
## data conversion was done in QGIS using the plugin "rasterize"
## raster pixel size is 0.008 or approximately 1000 meters
## all raster files have the uniform coordinate reference system, resolution and extent

## here is the 2020 land cover of Mindanao
knitr:::include_graphics("images/lc_2020.png")
```



```

## read data
files <- list.files("data/landcover/", pattern = "tif", full.names=TRUE)
raster.files <- lapply(files, raster)

raster.files

## [[1]]
## class      : RasterLayer
## dimensions : 736, 903, 664608  (nrow, ncol, ncell)
## resolution : 0.008000454, 0.007996592  (x, y)
## extent     : 119.3807, 126.6051, 4.58649, 10.47198  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs
## source     : 1988_lc_rast1km.tif
## names      : X1988_lc_rast1km
##
##
## [[2]]
## class      : RasterLayer
## dimensions : 736, 903, 664608  (nrow, ncol, ncell)
## resolution : 0.008000454, 0.007996592  (x, y)
## extent     : 119.3807, 126.6051, 4.58649, 10.47198  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs
## source     : 2020_lc_rast1km.tif
## names      : X2020_lc_rast1km

## make rasters to have common extent
common_extent <- do.call(union, lapply(raster.files, extent))

raster.files <- lapply(raster.files, function(r) {
  extend(r, common_extent)
  extent(r) <- common_extent
  r
})

## check extent

```

```

lapply(raster.files, extent)

## [[1]]
## class       : Extent
## xmin        : 119.3807
## xmax        : 126.6051
## ymin        : 4.58649
## ymax        : 10.47198
##
## [[2]]
## class       : Extent
## xmin        : 119.3807
## xmax        : 126.6051
## ymin        : 4.58649
## ymax        : 10.47198

## resample raster files to have a uniform dimension/resolution
standard <- raster.files[[1]]
raster.files <- lapply(raster.files, function(r) {
  resample(r, standard, method = "bilinear")
})

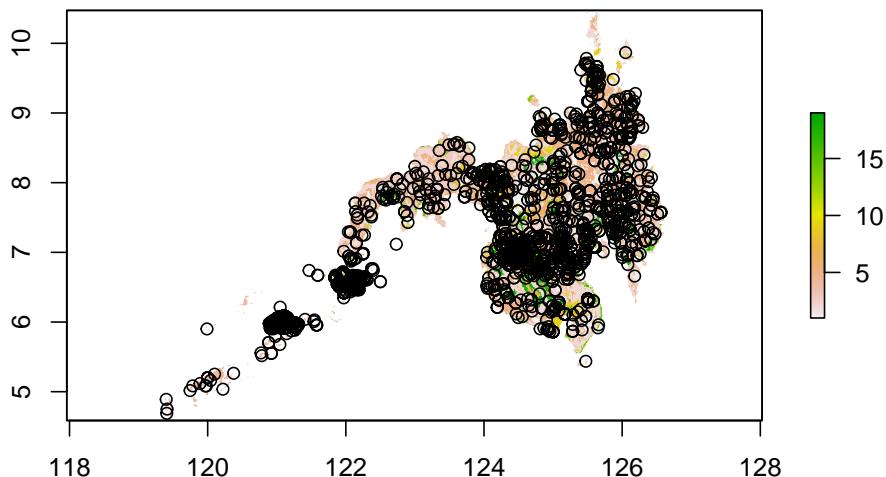
## check resolution
lapply(raster.files, res)

## [[1]]
## [1] 0.008000454 0.007996592
##
## [[2]]
## [1] 0.008000454 0.007996592

## stack raster files
lc <- stack(raster.files)

## plot data
plot(lc$X1988_lc_rast1km)
points(con.sub$longitude, con.sub$latitude)

```



```
con.coor <- cbind(con.sub$longitude, con.sub$latitude)
```

```

## extract data from land cover using conflict data coordinates
con.lc.data <- extract(lc, con.coor)

colnames(con.lc.data)[1] <- "LC_1988"
colnames(con.lc.data)[2] <- "LC_2020"

con.lc.data <- as.data.frame(na.omit(con.lc.data))
con.lc.data$LC_1988 <- as.integer(con.lc.data$LC_1988)
con.lc.data$LC_2020 <- as.integer(con.lc.data$LC_2020)
head(con.lc.data)

##    LC_1988 LC_2020
## 1       18      3
## 2        3      1
## 3        1      3
## 4        3      9
## 5        3      1
## 6        4      9

## read land cover types code
lc.88.d <- read.csv("data/1988_lc_classmap.csv")
lc.88.d

##                                     category code
## 1                           Closed Canopy   1
## 2 Cultivated Area mixed with brushland/grassland   2
## 3     Crop land mixed with coconut plantation   3
## 4                               Unclassified   4
## 5                           Open Canopy   5
## 6 Arable land, crops mainly cereals and sugar   6
## 7           Fishponds derived from mangrove   7
## 8                  Coral Reef   8
## 9      Grassland, grass covering > 70 percent   9
## 10                          Lake   10
## 11            Mangrove vegetation   11
## 12             Built-up Area   12
## 13                      Quarry   13
## 14          Coconut plantations   14
## 15      Siltation pattern in lake   15
## 16            Marshy area and swamp   16
## 17                 Riverbeds   17
## 18     Crop land mixed with other plantation   18
## 19                    Other plantations   19

lc.20.d <- read.csv("data/2020_lc_classmap.csv")
lc.20.d

##           category code
## 1     Grassland   1
## 2 Annual Crop   2
## 3 Marshland/Swamp   3
## 4 Perennial Crop   4
## 5      Built-up   5
## 6     Fishpond   6
## 7 Inland Water   7
## 8 Mangrove Forest   8

```

```

## 9      Brush/Shrubs      9
## 10     Closed Forest    10
## 11     Open Forest      11
## 12     Open/Barren      12

## add land cover descriptions
con.lc.data.m1 <- con.lc.data %>% mutate(class_1988 = if_else(LC_1988 == 1, "Closed Canopy",
  if_else(LC_1988 == 2, "Cultivated Area mixed with brushland/grassland",
  if_else(LC_1988 == 3, "Crop land mixed with coconut plantation",
  if_else(LC_1988 == 4, "Unclassified",
  if_else(LC_1988 == 5, "Open Canopy",
  if_else(LC_1988 == 6, "Arable land, crops mainly cereals and sugar",
  if_else(LC_1988 == 7, "Fishponds derived from mangrove",
  if_else(LC_1988 == 8, "Coral Reef",
  if_else(LC_1988 == 9, "Grassland, grass covering > 70 percent",
  if_else(LC_1988 == 10, "Lake",
  if_else(LC_1988 == 11, "Mangrove vegetation",
  if_else(LC_1988 == 12, "Built-up Area",
  if_else(LC_1988 == 13, "Quarry",
  if_else(LC_1988 == 14, "Coconut plantations",
  if_else(LC_1988 == 15, "Siltation pattern in lake",
  if_else(LC_1988 == 16, "Marshy area and swamp",
  if_else(LC_1988 == 17, "Riverbeds",
  if_else(LC_1988 == 18, "Crop land mixed with other plantation",
  if_else(LC_1988 == 19, "Other plantations", "No data"))))))))))))))))))))

con.lc.data.m2 <- con.lc.data %>% mutate(con.lc.data.m1,
  class_2020 = if_else(LC_2020 == 1, "Grassland",
  if_else(LC_2020 == 2, "Annual Crop",
  if_else(LC_2020 == 3, "Marshland/Swamp",
  if_else(LC_2020 == 4, "Perennial Crop",
  if_else(LC_2020 == 5, "Built-up",
  if_else(LC_2020 == 6, "Fishpond",
  if_else(LC_2020 == 7, "Inland Water",
  if_else(LC_2020 == 8, "Mangrove Forest",
  if_else(LC_2020 == 9, "Brush/Shrubs",
  if_else(LC_2020 == 10, "Closed Forest",
  if_else(LC_2020 == 11, "Open Forest",
  if_else(LC_2020 == 12, "Open/Barren", "No data"))))))))))))

## count the number of conflict sites in each land cover type
## 1988 data
con.lc.count.88 <- con.lc.data.m2 %>%
  group_by(class_1988) %>%
  summarise(n())
colnames(con.lc.count.88)[2] <- "count"

con.lc.count.88

## # A tibble: 14 x 2
##   class_1988               count
##   <chr>                  <int>
## 1 Arable land, crops mainly cereals and sugar      344
## 2 Built-up Area                      186
## 3 Closed Canopy                     528

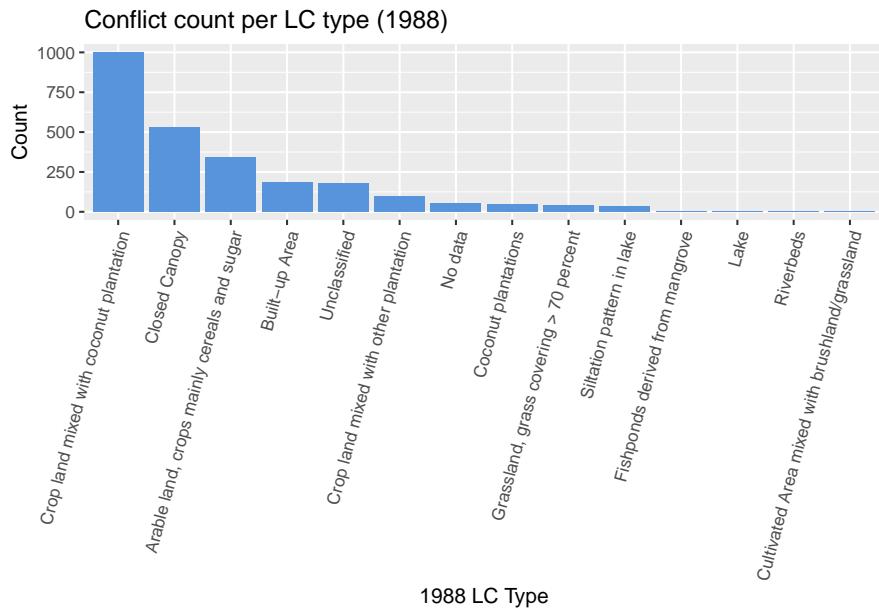
```

```

## 4 Coconut plantations 46
## 5 Crop land mixed with coconut plantation 1001
## 6 Crop land mixed with other plantation 98
## 7 Cultivated Area mixed with brushland/grassland 1
## 8 Fishponds derived from mangrove 5
## 9 Grassland, grass covering > 70 percent 39
## 10 Lake 5
## 11 No data 52
## 12 Riverbeds 3
## 13 Siltation pattern in lake 37
## 14 Unclassified 176

ggplot(data=con.lc.count.88, aes(x=reorder(class_1988, -count), y=count)) +
  geom_bar(stat="identity", fill="#5794db") +
  guides(x = guide_axis(angle = 75)) +
  xlab("1988 LC Type") +
  ylab("Count") +
  labs(title = "Conflict count per LC type (1988)")

```



```

con.lc.count.88 <- as.data.frame(con.lc.count.88)

write.csv(con.lc.count.88, "con.lc.count.88.csv")

## 2020 data
con.lc.count.20 <- con.lc.data.m2 %>%
  group_by(class_2020) %>%
  summarise(n())

colnames(con.lc.count.20)[2] <- "count"

con.lc.count.20

## # A tibble: 11 x 2
##   class_2020      count
##   <chr>          <int>
## 1 Brush/Shrubs    274

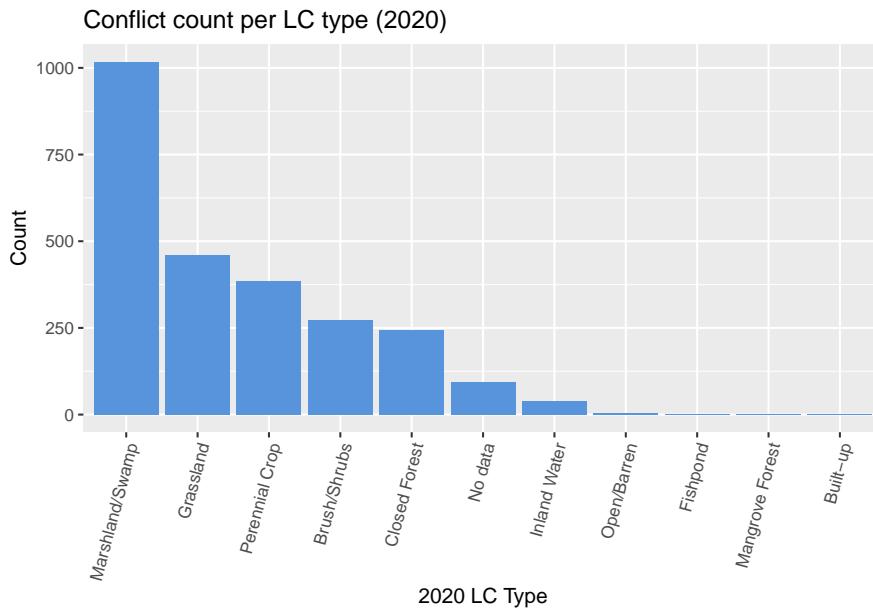
```

```

## 2 Built-up           1
## 3 Closed Forest     245
## 4 Fishpond          2
## 5 Grassland          459
## 6 Inland Water       40
## 7 Mangrove Forest    2
## 8 Marshland/Swamp   1017
## 9 No data            93
## 10 Open/Barren        3
## 11 Perennial Crop    385

ggplot(data=con.lc.count.20, aes(x=reorder(class_2020, -count), y=count)) +
  geom_bar(stat="identity", fill="#5794db") +
  guides(x = guide_axis(angle = 75)) +
  xlab("2020 LC Type") +
  ylab("Count") +
  labs(title = "Conflict count per LC type (2020)")

```



```

con.lc.count.20 <- as.data.frame(con.lc.count.20)

write.csv(con.lc.count.20, "con.lc.count.20.csv")

## extract data from land cover using biodiversity data coordinates
bio.coor <- cbind(bio.sub$decimalLongitude, bio.sub$decimalLatitude)

bio.lc.data <- extract(lc, bio.coor)

colnames(bio.lc.data )[1] <- "LC_1988"
colnames(bio.lc.data )[2] <- "LC_2020"

bio.lc.data <- as.data.frame(na.omit(bio.lc.data))
bio.lc.data$LC_1988 <- as.integer(bio.lc.data$LC_1988)
bio.lc.data$LC_2020 <- as.integer(bio.lc.data$LC_2020)
head(bio.lc.data)

```

```
##   LC_1988 LC_2020
```

```

## 1      1      0
## 2      1      3
## 3      1      3
## 4      1      3
## 5      1      3
## 6      1      3

## add land cover descriptions
bio.lc.data.m1 <- bio.lc.data %>% mutate(class_1988 = if_else(LC_1988 == 1, "Closed Canopy",
  if_else(LC_1988 == 2, "Cultivated Area mixed with brushland/grassland",
  if_else(LC_1988 == 3, "Crop land mixed with coconut plantation",
  if_else(LC_1988 == 4, "Unclassified",
  if_else(LC_1988 == 5, "Open Canopy",
  if_else(LC_1988 == 6, "Arable land, crops mainly cereals and sugar",
  if_else(LC_1988 == 7, "Fishponds derived from mangrove",
  if_else(LC_1988 == 8, "Coral Reef",
  if_else(LC_1988 == 9, "Grassland, grass covering > 70 percent",
  if_else(LC_1988 == 10, "Lake",
  if_else(LC_1988 == 11, "Mangrove vegetation",
  if_else(LC_1988 == 12, "Built-up Area",
  if_else(LC_1988 == 13, "Quarry",
  if_else(LC_1988 == 14, "Coconut plantations",
  if_else(LC_1988 == 15, "Siltation pattern in lake",
  if_else(LC_1988 == 16, "Marshy area and swamp",
  if_else(LC_1988 == 17, "Riverbeds",
  if_else(LC_1988 == 18, "Crop land mixed with other plantation",
  if_else(LC_1988 == 19, "Other plantations", "No data"))))))))))))))))))))

bio.lc.data.m2<- bio.lc.data %>% mutate(bio.lc.data.m1,
  class_2020 = if_else(LC_2020 == 1, "Grassland",
  if_else(LC_2020 == 2, "Annual Crop",
  if_else(LC_2020 == 3, "Marshland/Swamp",
  if_else(LC_2020 == 4, "Perennial Crop",
  if_else(LC_2020 == 5, "Built-up",
  if_else(LC_2020 == 6, "Fishpond",
  if_else(LC_2020 == 7, "Inland Water",
  if_else(LC_2020 == 8, "Mangrove Forest",
  if_else(LC_2020 == 9, "Brush/Shrubs",
  if_else(LC_2020 == 10, "Closed Forest",
  if_else(LC_2020 == 11, "Open Forest",
  if_else(LC_2020 == 12, "Open/Barren", "No data)))))))))))

## count the number of biodiversity points in each land cover type
## 1988 data
bio.lc.count.88 <- bio.lc.data.m2 %>%
  group_by(class_1988) %>%
  summarise(n())
colnames(bio.lc.count.88)[2] <- "count"

bio.lc.count.88

## # A tibble: 12 x 2
##   class_1988           count
##   <chr>              <int>
## 1 Arable land, crops mainly cereals and sugar    617

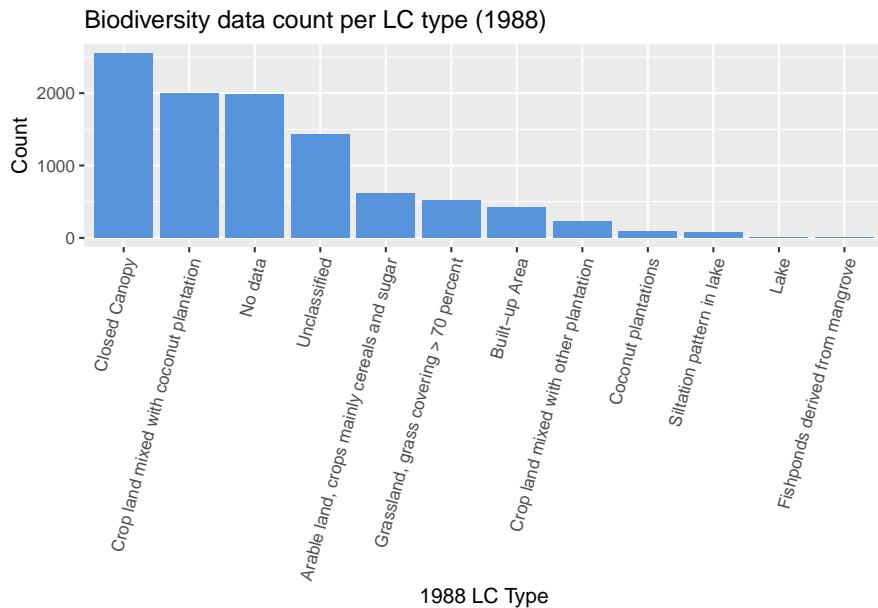
```

```

## 2 Built-up Area 427
## 3 Closed Canopy 2549
## 4 Coconut plantations 95
## 5 Crop land mixed with coconut plantation 1997
## 6 Crop land mixed with other plantation 226
## 7 Fishponds derived from mangrove 10
## 8 Grassland, grass covering > 70 percent 517
## 9 Lake 12
## 10 No data 1979
## 11 Siltation pattern in lake 75
## 12 Unclassified 1429

ggplot(data=bio.lc.count.88, aes(x=reorder(class_1988, -count), y=count)) +
  geom_bar(stat="identity", fill="#5794db") +
  guides(x = guide_axis(angle = 75)) +
  xlab("1988 LC Type") +
  ylab("Count") +
  labs(title = "Biodiversity data count per LC type (1988)")

```



```

bio.lc.count.88 <- as.data.frame(bio.lc.count.88)

write.csv(bio.lc.count.88, "bio.lc.count.88.csv")

## 2020 data
bio.lc.count.20 <- bio.lc.data.m2 %>%
  group_by(class_2020) %>%
  summarise(n())
colnames(bio.lc.count.20)[2] <- "count"

bio.lc.count.20

## # A tibble: 9 x 2
##   class_2020      count
##   <chr>          <int>
## 1 Brush/Shrubs    3393
## 2 Closed Forest   1593

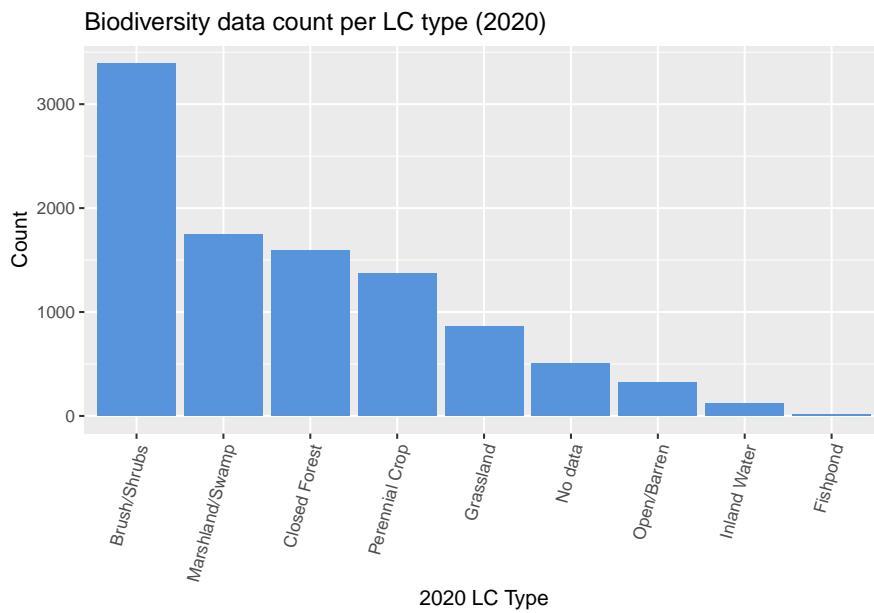
```

```

## 3 Fishpond          17
## 4 Grassland        862
## 5 Inland Water     119
## 6 Marshland/Swamp  1748
## 7 No data          507
## 8 Open/Barren       319
## 9 Perennial Crop   1375

ggplot(data=bio.lc.count.20, aes(x=reorder(class_2020, -count), y=count)) +
  geom_bar(stat="identity", fill="#5794db") +
  guides(x = guide_axis(angle = 75)) +
  xlab("2020 LC Type") +
  ylab("Count") +
  labs(title = "Biodiversity data count per LC type (2020)")

```



```

bio.lc.count.20 <- as.data.frame(bio.lc.count.20)

write.csv(bio.lc.count.20, "bio.lc.count.20.csv")

```