Supporting documentation: Decreasing trends of chinstrap penguin breeding colonies in a region of major and ongoing environmental change suggest population level vulnerability: a reanalysis of Krüger (2023)

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Contents

1 Krüger (2023) reanalysis

This script provides a reanalysis of Krüger (2023) (Citation: Krüger, L. (2023). Decreasing Trends of Chinstrap Penguin Breeding Colonies in a Region of Major and Ongoing Rapid Environmental Changes Suggest Population Level Vulnerability. Diversity, 15(3), 327.). The Krüger (2023) supplementary material provided reproducible R code for that study's analyses. We use that code here to replicate the original results. In addition, we provide additional analysis that cautions that the analysis performed by Krüger (2023) cannot support robust inference.

1.1 Load packages and set plotting theme

```r
# Load packages
# data summary
library(reshape2)
library(plyr)
library(dplyr)
library(tidyverse)
#plots
library(ggplot2)
library(patchwork)
library(sjPlot)
#models
library(energy)
library(optimx)
library(minqa)
library(dfoptim)
library(MCMCglmm)

library(ggforce) # not part of original script, but needed to plot site trends below

# plot theme
th <- theme(axis.text=element_text(size=12, face="bold",colour="grey30"),
           axis.title=element_text(size=14,face="bold"),
           panel.grid.major = element_blank(),
           panel.grid.minor = element_blank(),
           title =element_text(size=12, face="bold",colour="black"))
```

1.2 Load and process MAPPPD data for area 48.1:

```r
# Humphries et al. (2017) Mapping Application for Penguin Populations
# and Projected Dynamics (MAPPPD): data and tools for dynamic management
# and decision support. Polar Record 53 (269): 160-166 doi:10.1017/S0032247417000055

df <- read.csv(here::here("./data/mapppd AllCounts_V_4_0.csv"))

# subset chinstrap penguin
chins<-subset(df,common_name=="chinstrap penguin")

summary(as.factor(chins$common_name))
```

```
## chinstrap penguin
##              1342
```

```r
summary(as.factor(chins$count_type))
```

```
## adults chicks  nests
##     91    147   1104
```

```r
# use only nest counts
nests<-subset(chins,count_type=="nests")

# some populations had multiple counts over the same season:
# this summarises the count with the maximum nests
nestM<-ddply(na.omit(data.frame(nests)), c("season_starting","site_id"),
             summarise,
             nests=max(penguin_count),
             Lat=mean(latitude_epsg_4326),
             Lon=mean(longitude_epsg_4326))
```

Here, the na.omit function removes all rows where there are NA values (missing data). Some rows have missing information for: - the day of the count - the day and month of the count - the accuracy of the count - the vantage point (ground, boat, uav, vhr) - on 4 occasions there are no count data (NA). One can argue that counts with unknown accuracy, vantage point, or count dates should be excluded from analysis, as was done here. Alternatively, one can argue that it makes little sense to exclude counts (e.g., those with high accuracy) where the only data missing is the day on the month where the count was conducted. This is because we did not subset / select counts in any other way (e.g., data was not limited to 'accurate' counts, or those happening within a certain date limit). Thus, this paper could arguably have use more of the available count data (given what was used). It is also worth discussing whether counts with poor accuracy should have been included in analysis, and if included, what the impact of counts with poor accuracy can have on the results.

```r
# summarizing number of populations and number of counts
countsN <-ddply(nestM, c("site_id","Lat","Lon"), summarise,
                ncounts=length(nests),
                interval=(max(season_starting)-min(season_starting)))
head(countsN)
```

```
##   site_id     Lat     Lon ncounts interval
## 1    ACUN -60.761 -44.637       1        0
## 2    AILS -60.780 -44.631       2       36
## 3    AITC -62.407 -59.752       4       21
## 4    AITK -60.738 -44.525       2       35
## 5    ALCO -64.240 -61.127       2       13
## 6    AMPH -60.684 -45.339       2       36
```

```
# summarizing number of populations and number of counts with more than 0 nests
countsN2<-ddply(subset(nestM,nests>0), c("site_id","Lat","Lon"), summarise,
                ncounts=length(nests),
                interval=(max(season_starting)-min(season_starting)))
head(countsN2)
```

```
##   site_id     Lat     Lon ncounts interval
## 1    ACUN -60.761 -44.637       1        0
## 2    AILS -60.780 -44.631       2       36
## 3    AITC -62.407 -59.752       4       21
## 4    AITK -60.738 -44.525       2       35
## 5    ALCO -64.240 -61.127       2       13
## 6    AMPH -60.684 -45.339       2       36
```

```
summary(as.factor(countsN2$ncounts))
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  14  15  21
## 148  89  14   8   4   2   2   3   1   3   2   1   1   1   2
```

```
npops=length(countsN2$ncounts[countsN2$ncounts>1])
npops # number of populations
```

```
## [1] 133
```

```
nestM2<-merge(nestM,countsN) # number of counts for each population by merging

# test for Poisson distribution (Poisson M-test)
poisson.mtest(nestM2$nests[nestM2$ncounts>1 & nestM2$nests>0],R=199)
```

```
##
##  Poisson M-test
##
## data:  nestM2$nests[nestM2$ncounts > 1 & nestM2$nests > 0] replicates:  199
## M-CvM = 158.43, p-value = 0.1709
## sample estimates:
## [1] 3006.691
```

Here, the poisson.mtest is conducted on all the data (nestM2$nests[nestM2$ncounts>1 & nestM2$nests>0]. Yet, a glm is run per site. Should this test not be conducted at the site level, if we are conducting site-specific analysis? Tests for a Poisson distribution at the site level is not really possible as most sites only have two counts. Regardless, we can probably just assume a Poisson distribution because counts are often Poisson distributed.

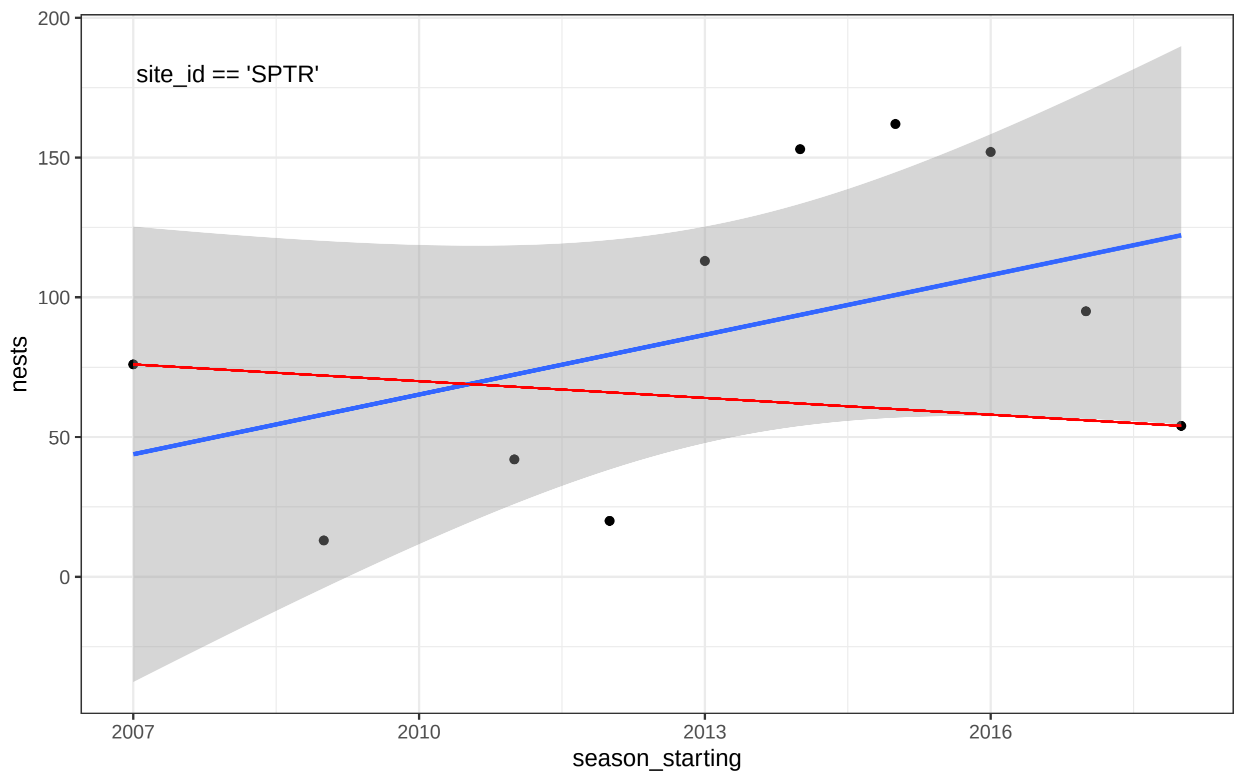
1.3 Calculate the mean slope of the decrease per site (glm)

```r
# subset only populations with at least 2 counts and with any nest recorded
nestm3<-subset(nestM2,ncounts>1 & nests>0)

# calculating population level slope
slopeN <-na.omit(data.frame((nestm3 %>%
                              group_by(site_id,Lat,Lon) %>%
                              do({
                                mod=glm(nests~season_starting,family="poisson",
                                data=.)
                                data.frame(Intercept=coef(mod)[1],
                                           Slope=coef(mod)[2])}))))
```

1.3.1 Sanity check:

We use ‘sanity check’ exploratory plots as part of additional data exploration

```r
# WCO: aside some sites have positive glm slopes (growth) but
# negative proportion change (calculated below) e.g. site_id == "SPTR"
# Reminds me of recommendation by Hill et al. (2019) J of Crustacean Biology 39:316-322.
# "Avoid diagnosing or rejecting a multi-year trend based on a comparison of two years."

chck = subset(nestm3, nestm3$site_id == "SPTR")
chck = chck[order(chck$season_starting),]
ggplot(data = chck, aes(season_starting, nests)) +
         geom_point()+
         geom_smooth(method='lm', formula= y~x) +
         geom_segment(aes(x = min(chck$season_starting),
                          y = chck$nests[1],
                          xend = max(chck$season_starting),
                          yend = chck$nests[10]), colour = "red") +
         theme_bw()+
  annotate("text", x=2008, y=180, label= "site_id == 'SPTR'")
```



```r
# The model slopes are the same if the decrease is the same.
# E.g. these two sites halved in size and have the same slope (0.01925409)
# (but different intercepts)

subset(nestm3, nestm3$site_id == 'ANDE')
```

```
##    site_id     Lat     Lon season_starting nests ncounts interval
## 14    ANDE -60.757 -44.601            2019   200       2       36
## 15    ANDE -60.757 -44.601            1983   100       2       36
```

```r
subset(slopeN, slopeN$site_id == 'ANDE')
```

```
##   site_id     Lat     Lon Intercept      Slope
## 6    ANDE -60.757 -44.601 -33.57569 0.01925409
```

```r
subset(nestm3, nestm3$site_id == 'AILS')
```

```
##   site_id    Lat     Lon season_starting nests ncounts interval
## 2    AILS -60.78 -44.631            2019  3000       2       36
## 3    AILS -60.78 -44.631            1983  6000       2       36
```

```r
subset(slopeN, slopeN$site_id == 'AILS')
```

```
##   site_id    Lat     Lon Intercept       Slope
## 1    AILS -60.78 -44.631  46.88037 -0.01925409
```

Here it is clear that there is rounding of numbers (100, 200, 3000, 6000). Rounding can contribute to uncertainty in true trends.

1.4 Some summary stats (Krüger 2023)

```
sloN <-merge(slopeN,countsN2) # number of counts for each population by merging

summary(as.factor(sloN$ncounts))
```

```
##  2  3  4  5  6  7  8  9 10 11 12 14 15 21
## 89 14  8  4  2  2  3  1  3  2  1  1  1  2
```

```
sloN$stdSlope<-sloN$Slope/sloN$interval
mean(sloN$Slope)
```

```
## [1] -0.02045084
```

```
sd(sloN$Slope)/sqrt(length(sloN$Slope)-1)
```

```
## [1] 0.007251265
```

```
# Note: original code was < but need to include <= to get the same results as older R versions (differe
mean(sloN$Slope[sloN$Slope<=0])
```

```
## [1] -0.04960635
```

```
# Note: original code was < but need to include <= to get the same results as older R versions (differe
sd(sloN$Slope[sloN$Slope<=0])/sqrt(length(sloN$Slope[sloN$Slope<=0])-1)
```

```
## [1] 0.009966612
```

```
# number of populations
length(sloN$Slope)
```

```
## [1] 133
```

```
# Note: number of decreasing populations: # original code was < but need to include <= to get the same
length(sloN$Slope[sloN$Slope<=0])
```

```
## [1] 83
```

```
# proportion of decreasing populations
length(sloN$Slope[sloN$Slope<=0])/length(sloN$Slope)
```

```
## [1] 0.6240602
```

1.5 Identify first and last counts

```
# identify year of first count
firstN<-ddply(nestM, c("site_id"), summarise,
              Ncounts=length(nests),
              season_starting=min(season_starting))

# counts on the first year
firstCount<-merge(nestM,firstN)

# identify year of last count
lastN<-ddply(nestM, c("site_id"), summarise,
             season_starting=max(season_starting))

# counts of the last year
lastCount<-merge(nestM,lastN)

summary(firstCount$Ncounts)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   2.000   2.278   2.000  21.000
```

```
# change names to join data frames
names(firstCount)[names(firstCount) == 'season_starting'] <- 'First'
names(firstCount)[names(firstCount) == 'nests'] <- 'FirstCount'
names(lastCount)[names(lastCount) == 'season_starting'] <- 'Last'
names(lastCount)[names(lastCount) == 'nests'] <- 'LastCount'
firlas<-merge(firstCount,lastCount,by=c("site_id","Lat","Lon")) # first and last counts
firlas<-subset(firlas,Ncounts>1) # subset only pops with more than one count
firlas$PercChange<-((firlas$LastCount/firlas$FirstCount)-1)*100 #percentual change
firlas$PercChange[is.na(as.numeric(firlas$PercChange))]<-0  # make NA = 0
Slope.Counts<-merge(firlas,sloN,by=c("site_id","Lat","Lon")) # merge slope and counts
summary(Slope.Counts$PercChange) #### percent change at the population level
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -100.00  -61.62  -23.08   11.31   28.33  900.00
```

```
sd(Slope.Counts$PercChange) /sqrt(length(Slope.Counts$PercChange)-1) # standard error
```

```
## [1] 11.2554
```

1.6 Krüger 2023 Figure 2 proportion decrease

```
#subset only decreasing populations (WCO: THIS ALSO SELECTS (ONE) STABLE POPULATION)
# original code was < but need to include <= to get the same results as older R versions (different tre

decr<-subset(Slope.Counts,Slope<=0)
decr$YearDecr<-(-1*decr$Slope) # decrease per year
decr$PercDecr<-(-1*decr$PercChange) # absolute percent decrease

### classify range of decrease in categories ($decrCat)
```

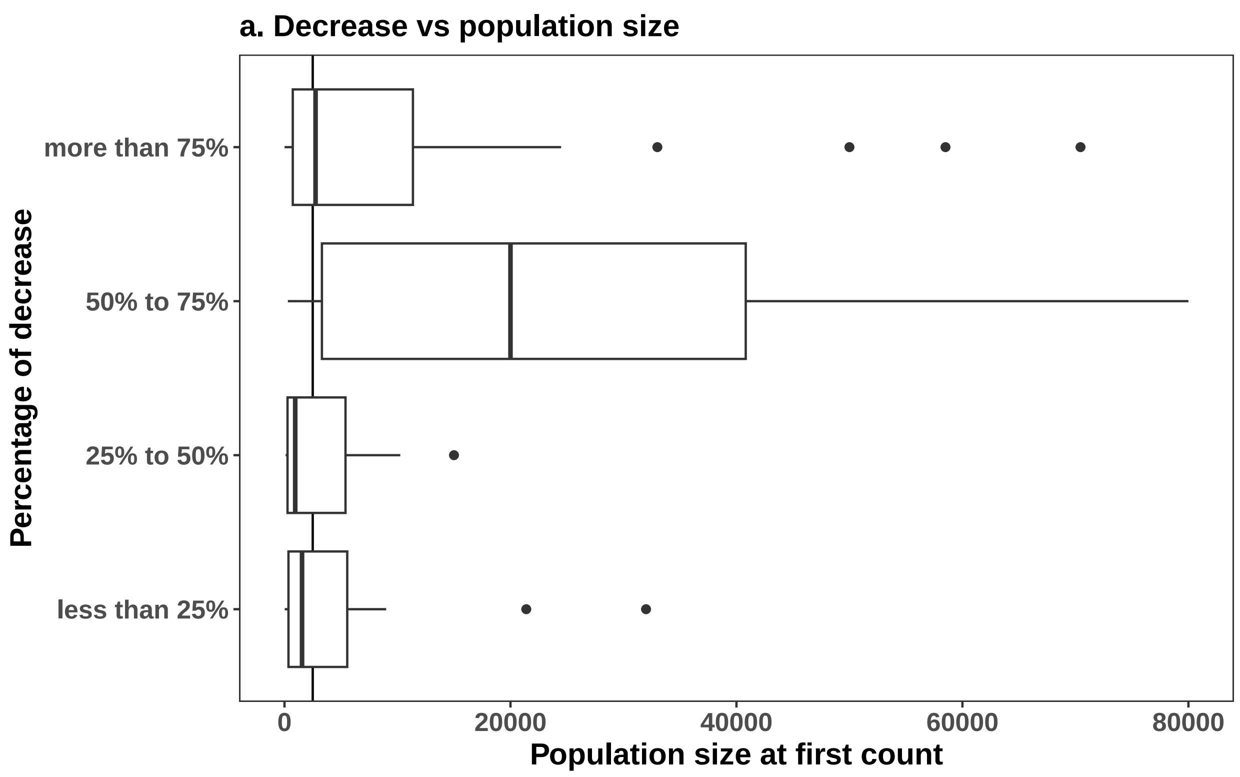
```
decr$decrCat[decr$PercDecr<=25]<-"less than 25%"
decr$decrCat[decr$PercDecr>25 & decr$PercDecr<=50]<-"25% to 50%"
decr$decrCat[decr$PercDecr>50 & decr$PercDecr<=75]<-"50% to 75%"
# WCO: CODING ERROR / BUG. SELECTS >55 %, NOT 75%
decr$decrCat[decr$PercDecr>55]<-"more than 75%"
decr$decrCat<-factor(decr$decrCat,levels=c("less than 25%",
                                           "25% to 50%",
                                           "50% to 75%",
                                           "more than 75%")) # order of levels
n<-ddply(decr, c("decrCat"), summarise,
         N=length(FirstCount))
n
```

```
##         decrCat  N
## 1 less than 25% 19
## 2    25% to 50% 21
## 3    50% to 75%  5
## 4 more than 75% 38
```

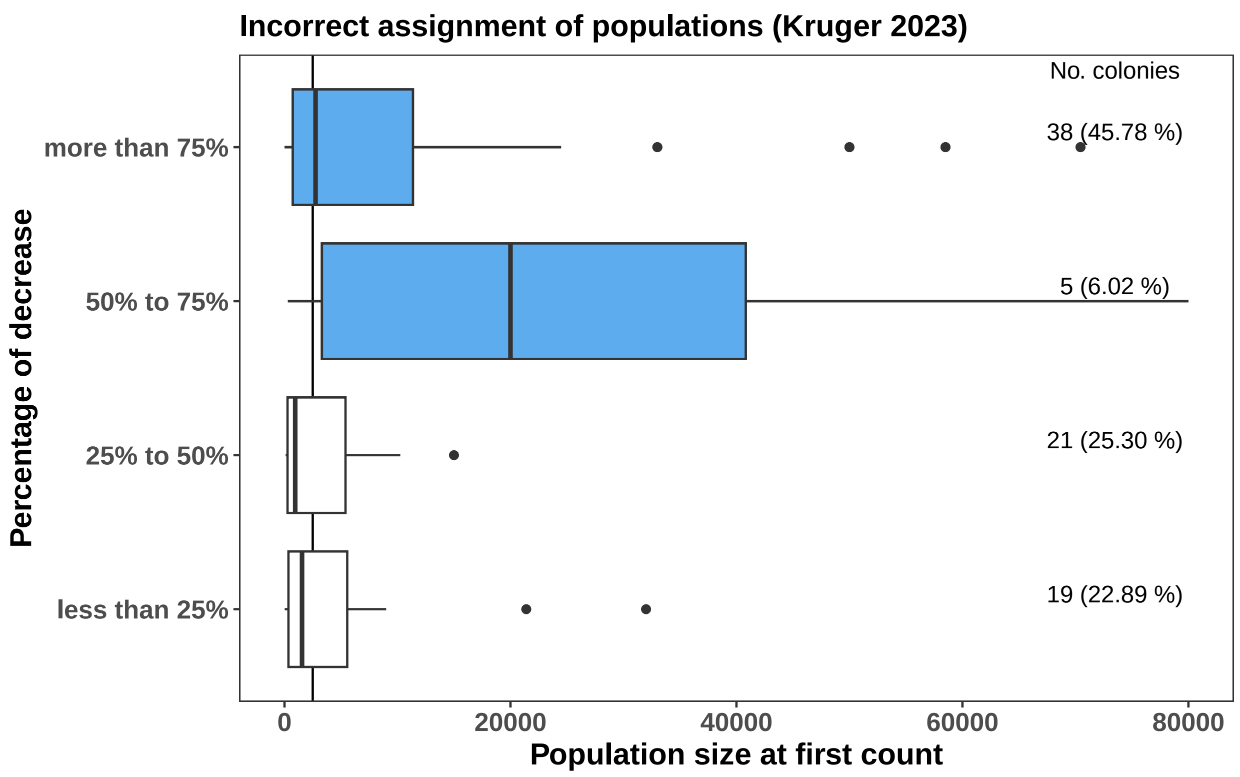
```
sum(n$N) # check number of pops
```

```
## [1] 83
```

```
n$perc<-n$N/83 # percentage of populations in each categories

perc_original = n$perc

#figure 2
ggplot(decr,aes(decrCat,FirstCount))+
  geom_hline(yintercept=2500)+
  geom_boxplot()+
  coord_flip()+theme_bw()+th+
  xlab("Percentage of decrease")+
  ylab("Population size at first count")+
  ggtitle(label="a. Decrease vs population size")
```



```
fig2a = ggplot(decr,aes(decrCat,FirstCount))+
  geom_hline(yintercept=2500)+
  geom_boxplot()+
  geom_boxplot(data=decr[decr$decrCat=="more than 75%",],
                      aes(x = decrCat, y = FirstCount),fill="steelblue2")+
  geom_boxplot(data=decr[decr$decrCat=="50% to 75%",],
                      aes(x = decrCat, y = FirstCount),fill="steelblue2")+
  coord_flip()+theme_bw()+th+
  xlab("Percentage of decrease")+
  ylab("Population size at first count")+
  ggtitle(label="Incorrect assignment of populations (Kruger 2023)") +
  annotate("text", x = c(1.1, 2.1, 3.1, 4.1, 4.5),
           y = c(73500, 73500, 73500,73500,73500),
           label = c("19 (22.89 %)", "21 (25.30 %)",
                     "5 (6.02 %)", "38 (45.78 %)",
                     "No. colonies"), size=4)

fig2a
```



The above figure is incorrect as it includes population declines >55 % in the >75 % category (coding error). In other words, there are too many populations included in the >75 % category.

1.7 Corrected Figure 2

```r
# subset only decreasing populations (THIS ALSO SELECTS 1 STABLE POPULATION)
decr<-subset(Slope.Counts,Slope<0)
decr$YearDecr<-(-1*decr$Slope) # decrease per year
decr$PercDecr<-(-1*decr$PercChange) # absolute percent decrease
### classify range of decrease in categories ($decrCat)
decr$decrCat[decr$PercDecr<=25]<-"less than 25%"
decr$decrCat[decr$PercDecr>25 & decr$PercDecr<=50]<-"25% to 50%"
decr$decrCat[decr$PercDecr>50 & decr$PercDecr<=75]<-"50% to 75%"
# This line had a CODING ERROR / BUG. it selected >55 %, NOT 75%
decr$decrCat[decr$PercDecr>75]<-"more than 75%"
decr$decrCat<-factor(decr$decrCat,levels=c("less than 25%",
                                           "25% to 50%",
                                           "50% to 75%",
                                           "more than 75%")) # order of levels
n<-ddply(decr, c("decrCat"), summarise,
         N=length(FirstCount))
n
```

```
##         decrCat  N
## 1 less than 25% 18
## 2    25% to 50% 21
## 3    50% to 75% 26
## 4 more than 75% 17
```

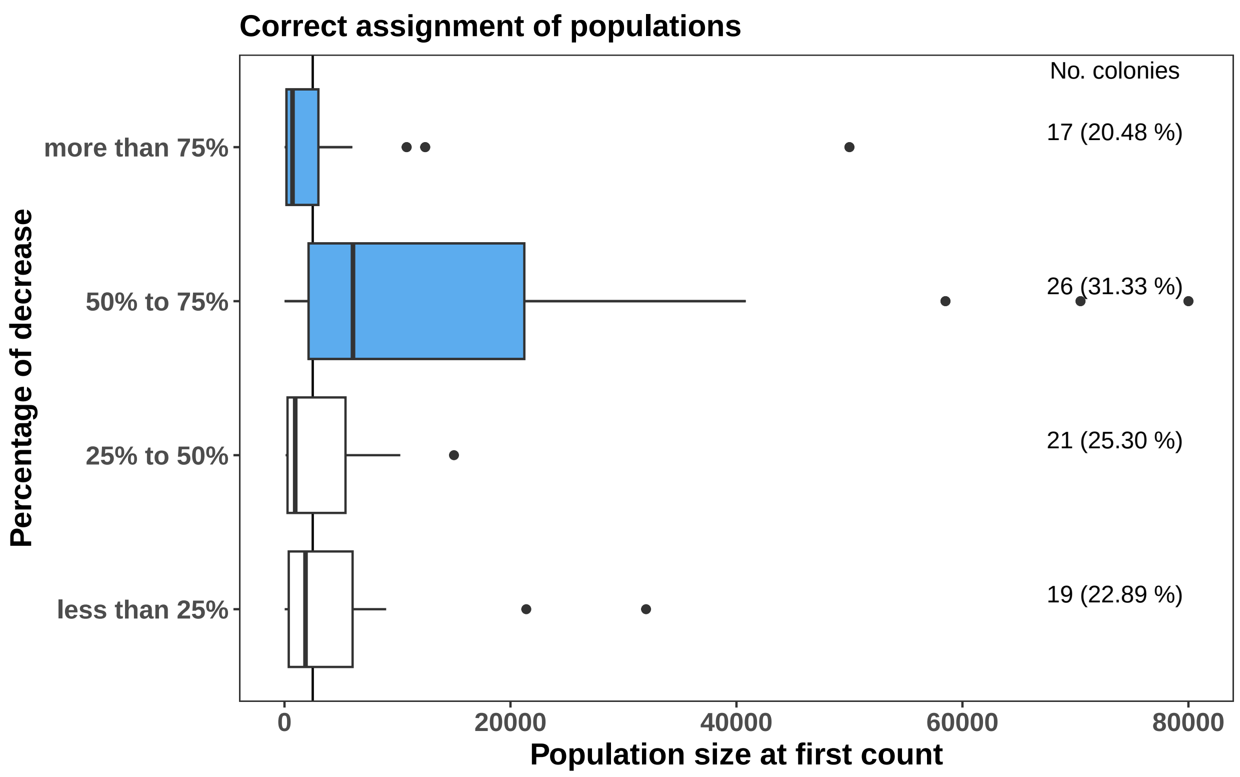
```
#sum(n$N) # check number of pops

n$perc<-n$N/83 # percentage of populations in each categories

perc_corrected =n$perc

## original manuscript percentage of populations in each category
print(perc_original)
```

```
## [1] 0.22891566 0.25301205 0.06024096 0.45783133
```

```
#### corrected percentage of populations in each category
perc_corrected
```

```
## [1] 0.2168675 0.2530120 0.3132530 0.2048193
```

```
#figure 2 corrected

fig2b = ggplot(decr,aes(decrCat,FirstCount))+
  geom_hline(yintercept=2500)+
  geom_boxplot()+
  geom_boxplot(data=decr[decr$decrCat=="more than 75%",],
                      aes(x = decrCat, y = FirstCount),fill="steelblue2")+
  geom_boxplot(data=decr[decr$decrCat=="50% to 75%",],
                      aes(x = decrCat, y = FirstCount),fill="steelblue2")+
  coord_flip()+theme_bw()+th+
  xlab("Percentage of decrease")+
  ylab("Population size at first count")+
  ggtitle(label="Correct assignment of populations") +
   annotate("text", x = c(1.1, 2.1, 3.1, 4.1, 4.5),
           y = c(73500, 73500, 73500,73500,73500),
          label = c("19 (22.89 %)", "21 (25.30 %)",
                    "26 (31.33 %)", "17 (20.48 %)", "No. colonies"),
          size=4)

fig2b
```



```r
# library(cowplot)
# plot_grid(fig2a, fig2b)

## Save Plot
#  pdf("./Figure 2.pdf", useDingbats = FALSE, width = 14, height = 7)
#  plot_grid(fig2a, fig2b,
#            labels = "AUTO", scale = 0.9, vjust = 2, hjust = -4)
# dev.off()
```

1.8 MCMCglmm mixed model data

```r
nestM3<- nestm3   #populations with at least 2 counts and with any nest recorded
length(unique(nestM3$site_id))
```

```
## [1] 146
```

What is the sample size per site? Krüger (2023) reports 133 sites, but the count here is 146 unique sites. But the code gave 133 sites above. Why do we get both 133 and 146? Some sites have 2 counts (e.g., TAYL) but one of the counts are zero. TAYL is included in the nestm3 data frame. It remains in there because the filter (nestm3; paper's code above) is on ncounts>1 & nests>0), and nests is the variable that counts how many nest counts were made. But that variable does not condition on the counts being more than 0. 133 sites had more than one data point in nestM3. 146 sites were included in the GLMM analysis, including some sites with only 1 count.

1.9 Specify MCMCglmm mixed model prior (Krüger 2023)

```
prior<- list(R = list(V = 1, nu = 0.002),
             G = list(G1 = list(V = diag(2), nu = 0.002,
                                alpha.mu = rep(0, 2),
                                alpha.V= diag(133, 2, 2))))
```

1.10 Fit MCMCglmm mixed model (Krüger 2023)

```
mc1<-MCMCglmm(nests~season_starting, random=~us(1 + Lat):site_id, rcov=~units,
              family="poisson", mev=NULL,
              data=nestM3, start=NULL, nodes="ALL", scale=TRUE,
              nitt=13000, thin=10, burnin=3000,
              pr=T, pl=FALSE, verbose=TRUE, DIC=TRUE, singular.ok=FALSE,
              saveX=TRUE,prior=prior, saveZ=TRUE, saveXL=TRUE, slice=FALSE,
              ginverse=NULL, trunc=FALSE)
```

```
##
##                       MCMC iteration = 0
##
##  Acceptance ratio for liability set 1 = 0.000422
##
##                       MCMC iteration = 1000
##
##  Acceptance ratio for liability set 1 = 0.224411
##
##                       MCMC iteration = 2000
##
##  Acceptance ratio for liability set 1 = 0.290159
##
##                       MCMC iteration = 3000
##
##  Acceptance ratio for liability set 1 = 0.309791
##
##                       MCMC iteration = 4000
##
##  Acceptance ratio for liability set 1 = 0.338670
##
##                       MCMC iteration = 5000
##
##  Acceptance ratio for liability set 1 = 0.338858
##
##                       MCMC iteration = 6000
##
##  Acceptance ratio for liability set 1 = 0.337497
##
##                       MCMC iteration = 7000
##
##  Acceptance ratio for liability set 1 = 0.338522
##
```

```
##                         MCMC iteration = 8000
##
##  Acceptance ratio for liability set 1 = 0.339169
##
##                         MCMC iteration = 9000
##
##  Acceptance ratio for liability set 1 = 0.338754
##
##                         MCMC iteration = 10000
##
##  Acceptance ratio for liability set 1 = 0.338612
##
##                         MCMC iteration = 11000
##
##  Acceptance ratio for liability set 1 = 0.337766
##
##                         MCMC iteration = 12000
##
##  Acceptance ratio for liability set 1 = 0.339939
##
##                         MCMC iteration = 13000
##
##  Acceptance ratio for liability set 1 = 0.338380
```

```
# Note: low ESS for random effects. Random effect ESS was 25-27 in Kruger (2023),
# (see supplement), so this is not only a problem that we are encountering.

summary(mc1)
```

```
##
##  Iterations = 3001:12991
##  Thinning interval  = 10
##  Sample size  = 1000
##
##  DIC: 4788.205
##
##  G-structure:  ~us(1 + Lat):site_id
##
##                                post.mean l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id  1534.400 61.63845 4425.278    43.03
## Lat:(Intercept).site_id            25.236  1.23877   71.607    43.47
## (Intercept):Lat.site_id            25.236  1.23877   71.607    43.47
## Lat:Lat.site_id                     0.416  0.02483    1.158    43.98
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.2936   0.2475   0.3397     1000
##
##  Location effects: nests ~ season_starting
##
##                 post.mean  l-95% CI  u-95% CI eff.samp  pMCMC
## (Intercept)     27.688379 21.247594 36.204395     1000 <0.001 ***
## season_starting -0.010401 -0.014436 -0.007007     1000 <0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Random effect syntax: ~us fit different variances across each component in formula, plus the covariances. The linear model inside the variance function has two parameters, an intercept(1) and a regression slope associated with latitude. Each site now has an intercept and a slope specified. But slope (latitude) does not vary within site, and there is only one count per year, per site. This is not a good random effect model structure.

1.10.1 Sanity check:

```r
# Each site only has one latitude value (should be 1)
uniqueLat = nestM3  %>%
  group_by(site_id) %>%
  dplyr::summarise(count = n_distinct(Lat))

max(uniqueLat$count)
```

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

```r
length(unique(nestM3$Lat))
```

```
## [1] 140
```

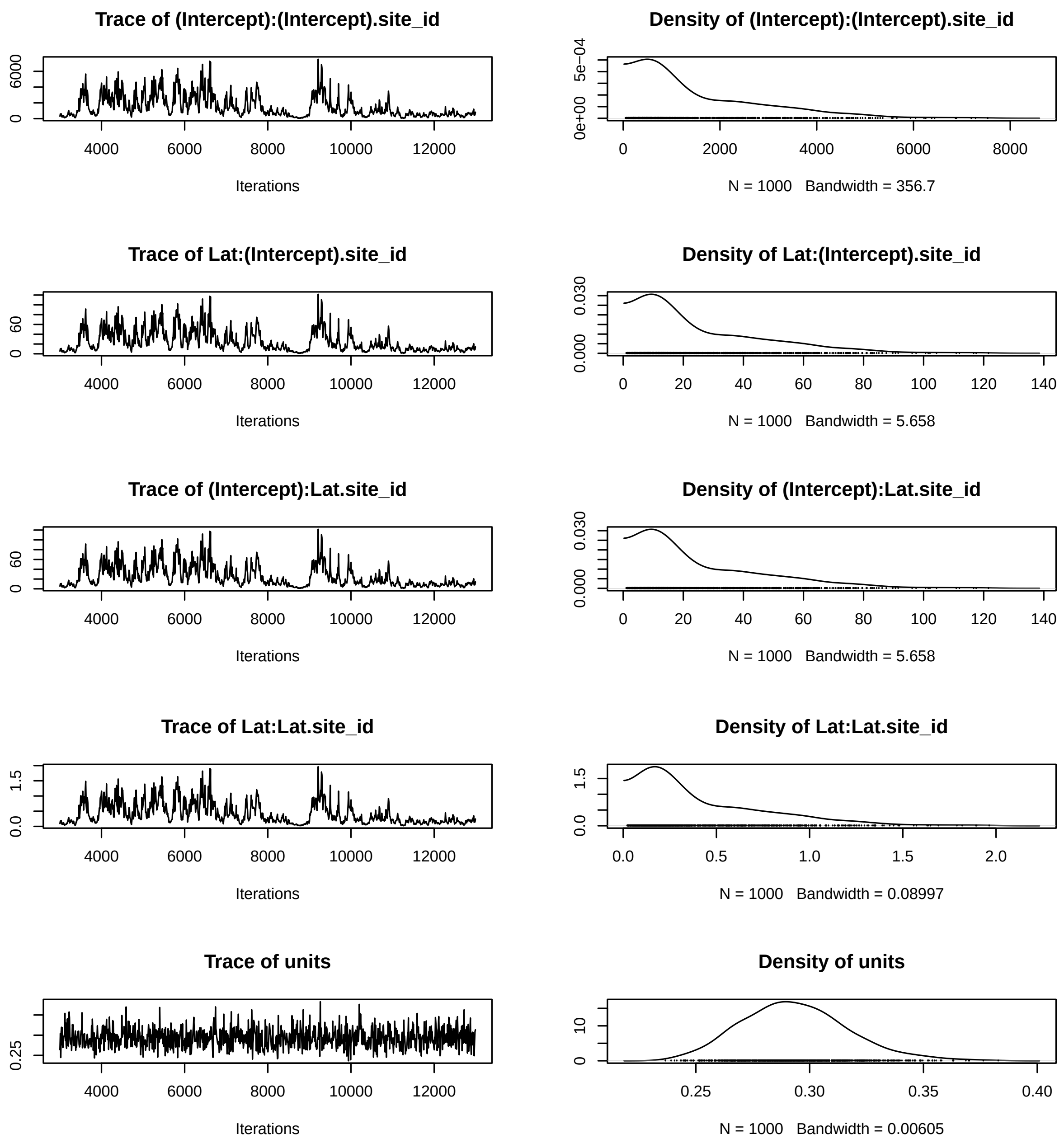
```r
length(unique(nestM3$site_id))
```

```
## [1] 146
```

1.11 MCMCglmm model checking

It is important to evaluate the fit of the model. We saw very low effective sample sizes in the model summary, above. We do further model checking below which shows poor mixing of MCMC chains.

```r
# The samples from the posterior distribution are stored as mcmc objects,
# which can be summarized and visualized using the coda package

# from MCMC Course notes (page 60):
# Aim to store 1,000-2,000 iterations and have the autocorrelation between
# successive stored iterations less than 0.1 (page 22).

# Assessing model convergence. We do this separately for both fixed
# and random effects. The trace plot should look like a fuzzy caterpillar
# plot(mc1$Sol)

# variances of the random effects (trace plots)
plot(mc1$VCV)
```



```
# It looks like some of the variances of the random effects haven't
# mixed very well.

# what are the effective sample size for the random effects?
```

```
coda::effectiveSize(mc1$VCV)
```

```
## (Intercept):(Intercept).site_id         Lat:(Intercept).site_id
##                         43.02760                        43.47420
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                         43.47420                        43.97709
##                            units
##                       1000.00000
```

```
# The effective sample size is very small.

k = 1 # number of fixed effects
autocorr(mc1$Sol[, 1:k])  # fine - low correlation
```

```
## , , 1
##
##                  [,1]
## Lag 0    1.000000000
## Lag 10   0.018828703
## Lag 50   0.001318585
## Lag 100 -0.019896953
## Lag 500  0.034225794
```

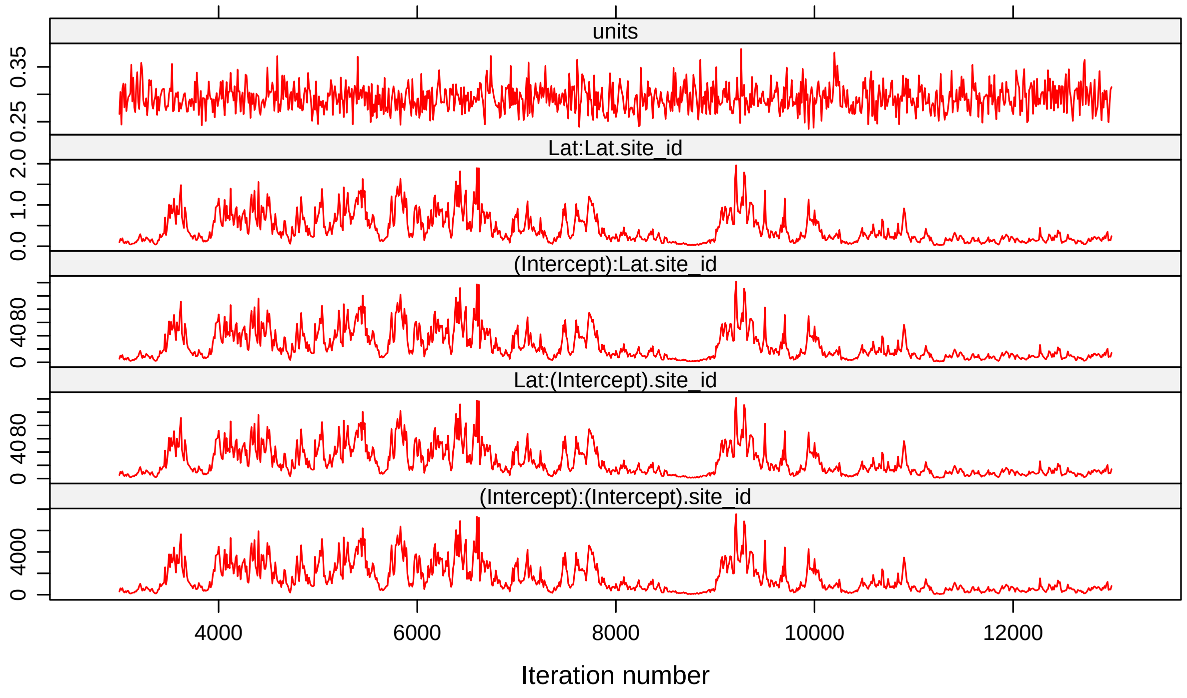
```
# from MCMC Course notes (page 60):
diag(autocorr(mc1$VCV)[2, , ])   # very high autocorrelation
```

```
## (Intercept):(Intercept).site_id         Lat:(Intercept).site_id
##                       0.81252443                      0.80948355
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                       0.80948355                      0.80615891
##                            units
##                       0.02970227
```

```
# Compare the effective sample sizes between mc2 and mc_Kr
# The rvariance components of the Kruger model has MCMC sampling problems
coda::effectiveSize(mc1$VCV)
```

```
## (Intercept):(Intercept).site_id         Lat:(Intercept).site_id
##                         43.02760                        43.47420
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                         43.47420                        43.97709
##                            units
##                       1000.00000
```

```
# check that the mcmc chain is mixing well - should be "white noise"
#lattice::xyplot(as.mcmc(mc1$Sol), layout=c(6,5), par.strip.text=list(cex=0.5))

# the variance components
traceK = lattice::xyplot(as.mcmc(mc1$VCV), par.strip.text=list(cex=0.8), col = "red")
traceK
```



1.12 MCMCglmm Random effects (Krüger 2023)

```r
sol<-data.frame(mc1$Sol) # random effects
# names(sol)
solm<-reshape2::melt(sol,id.vars=c("X.Intercept.","season_starting"))
# head(solm)
solm$site_id<-substring(solm$variable,first=22,last=26)
```

The code above drops all the ‘Lat.site_id’ (these were the slopes) because ‘site_id’ is blank for them in solm. It keeps only the X.Intercept..site_id. The idea was to plot the slope (decrease in population size), not the intercepts. sigma X.Intercept is the amount of variation in intercepts between sites and sigma Lat would be the amount of variation in the regression slopes between sites. One pointer that helps identify that we are not plotting slopes is that the y-axis is from 0 to 40, rather than from 0 to 1. Yet, Figure 3B in Krüger 2023 looks similar to the one produced from our own analysis (for the same data). However, later analysis shows that they are not nearly equivalent (the position of the sites are entirely different - see below)

```r
ranef = plyr::ddply(solm, c("site_id"), summarise,
        int=mean(value),
        intsd=sd(value),
        intse=intsd/sqrt(length(value)-1))

rlat<-merge(ranef,slopeN,by="site_id")
```

1.13 Predicting counts from mixed model (1960 to 2020) (Krüger 2023)

```r
# construct an hypothetical dataframe to generate the populations estimaters
years<-data.frame(season_starting=c(1960:2020))
pops<-data.frame(site_id=countsN$site_id[countsN$ncounts>1],
                 Lat=countsN$Lat[countsN$ncounts>1])
popy<-merge(pops,years)
popy$nests<-c(0) ### MCMCglmm needs a column with the response variable
popypred<-data.frame(predict(mc1,newdata=popy,type="response",
                             marginal=mc1$Random$formula,
                             interval="prediction", posterior="mean"))
popy$fit<-popypred$fit
# Add lower and upper prediction intervals to the data used for inference
popy$lwr<-popypred$lwr
popy$upr<-popypred$upr
```

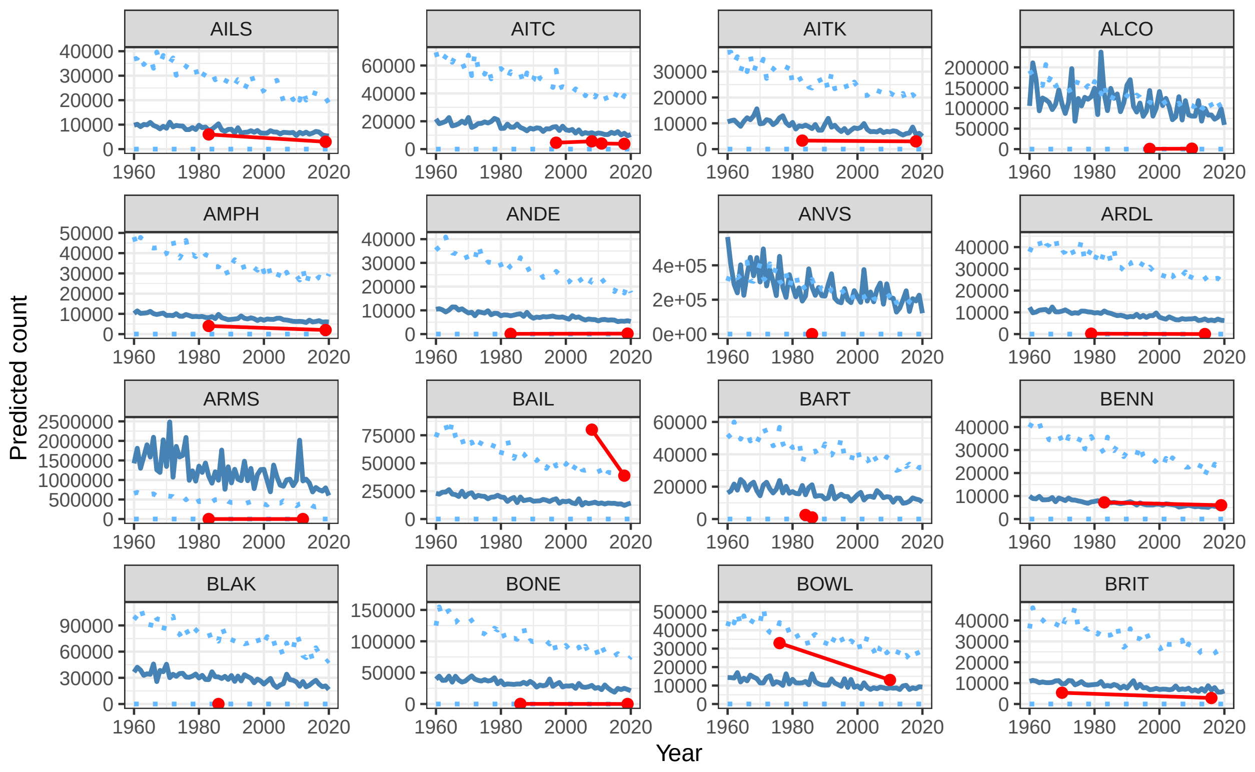
The prediction above contains a high degree of uncertainty, which was ignored. The uncertainty is the lwr and upr columns, which is the Highest Posterior Density intervals, I believe, from coda::HPDinterval. https://rdrr.io/cran/MCMCglmm/src/R/predict.MCMCglmm.R*

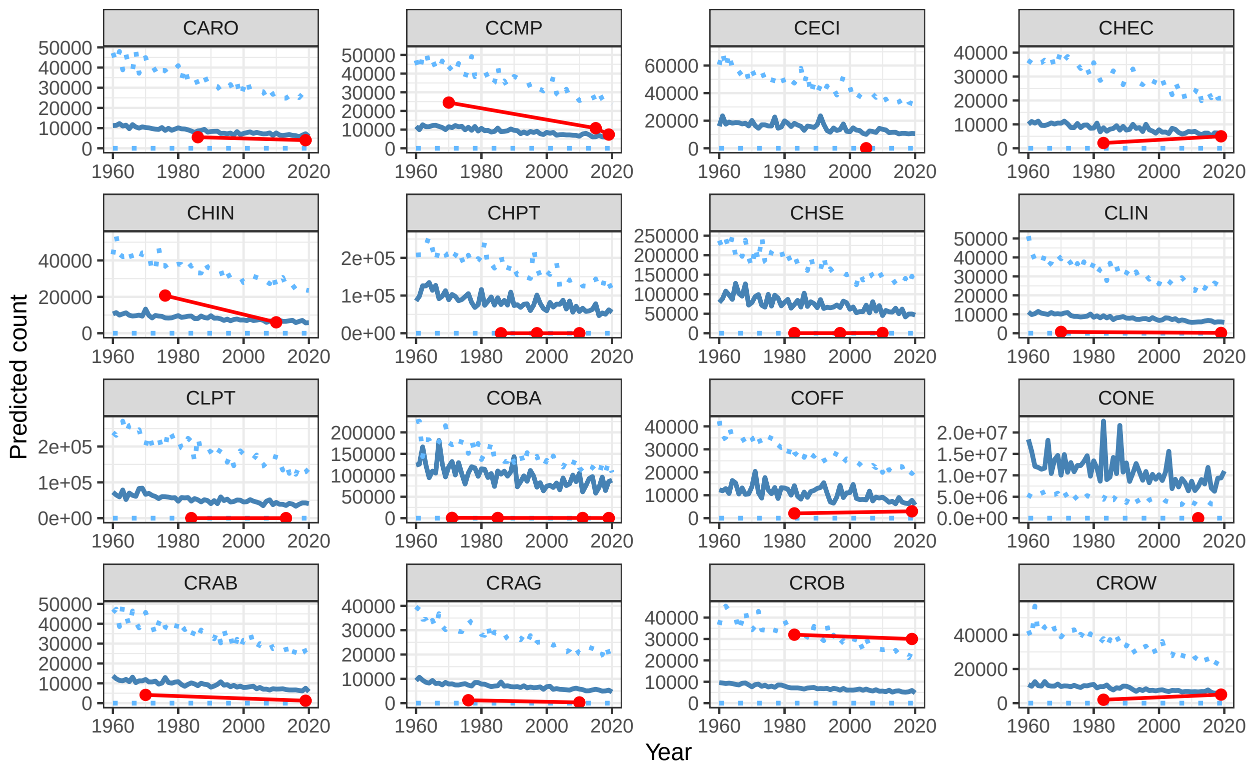
Here, the syntax marginal=mc1*Random*formula was used. This means random effects were marginalized (see simulation study).

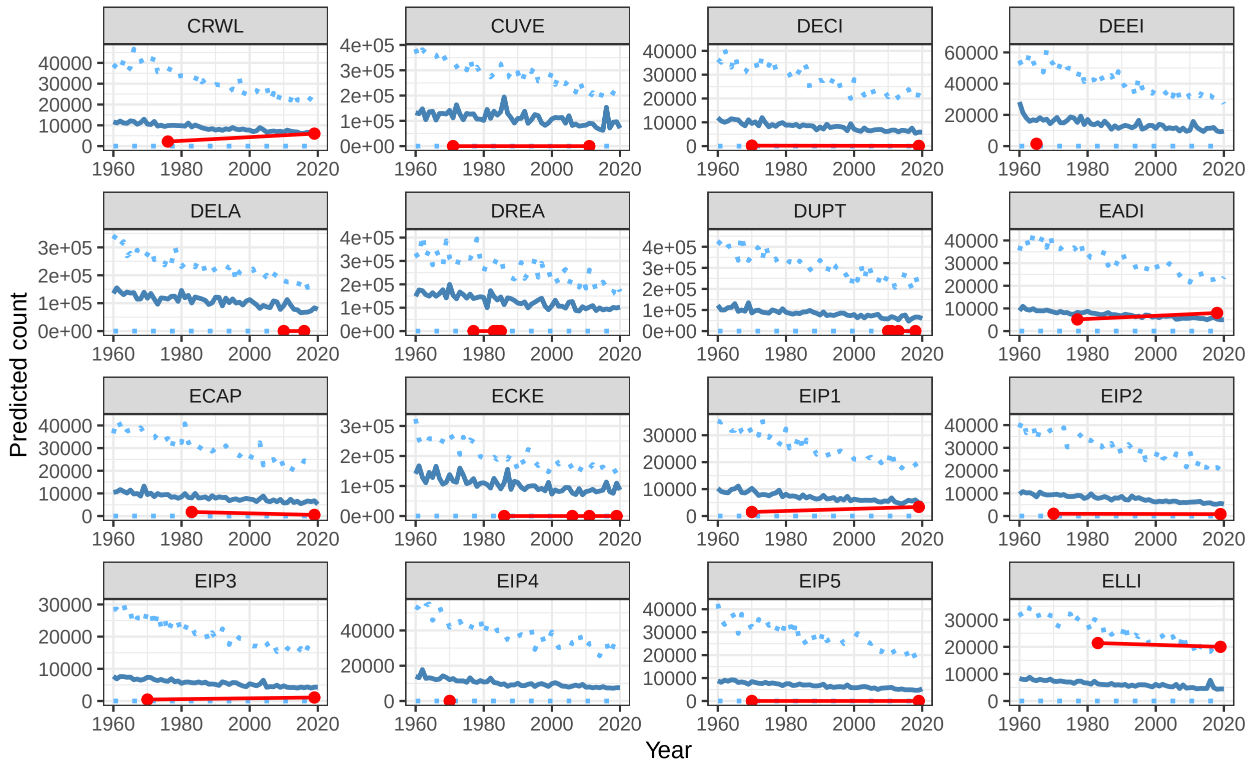
1.14 How accurate are the predictions relative to observed data?

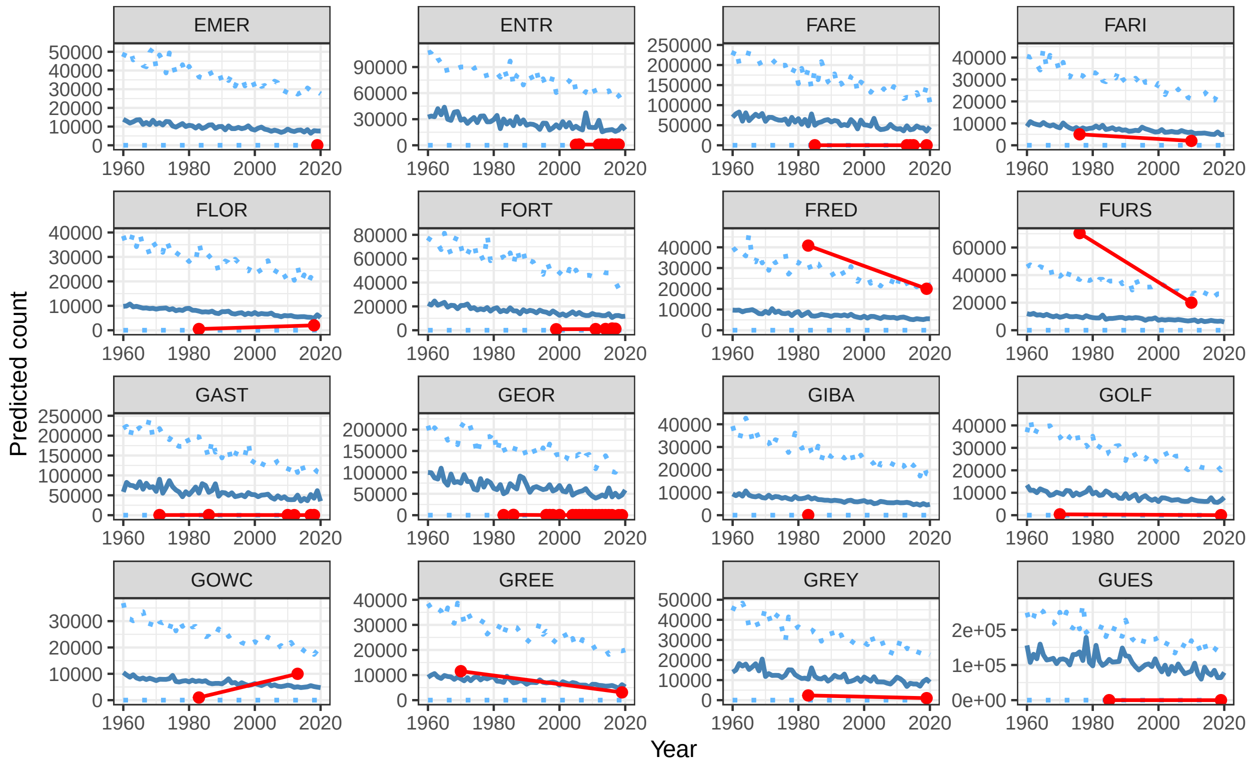
Let us plot the observed data against predicted data, per site, to see whether observed data and predicted data agree.

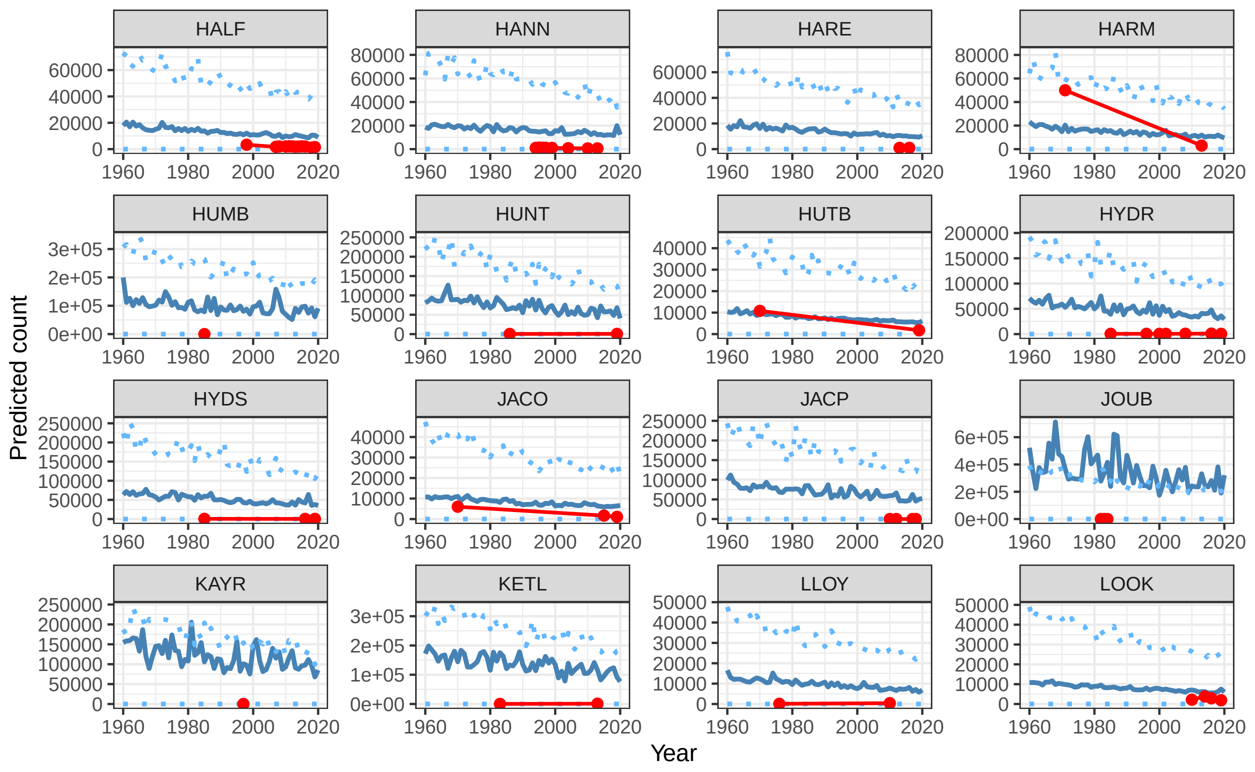
```r
required_n_pages = round(133/16)+1

for(i in 1:required_n_pages){

print(ggplot(data = popy) +
    geom_line(aes(x = season_starting, y = fit), col = "steelblue",linewidth=1.04) +
    geom_line(aes(x = season_starting, y = lwr), col = "steelblue1",
              linetype="dotted", linewidth = 1.02) +
    geom_line(aes(x = season_starting, y = upr), col = "steelblue1",
              linetype="dotted",linewidth = 1.02) +
    geom_point(data = nestm3, aes(season_starting, y = nests),
               color = "red", cex = 2) +
    geom_line(data = nestm3, aes(season_starting, y = nests),
              color = "red",linewidth=0.8) +
    theme_bw() +
    xlab("Year") +
    ylab("Predicted count") +
  #  theme(strip.text = element_text(size = 1.5)) +
    facet_wrap_paginate(~ site_id, ncol = 4, nrow = 4,
                        page = i,
                        scales = 'free'))}
```

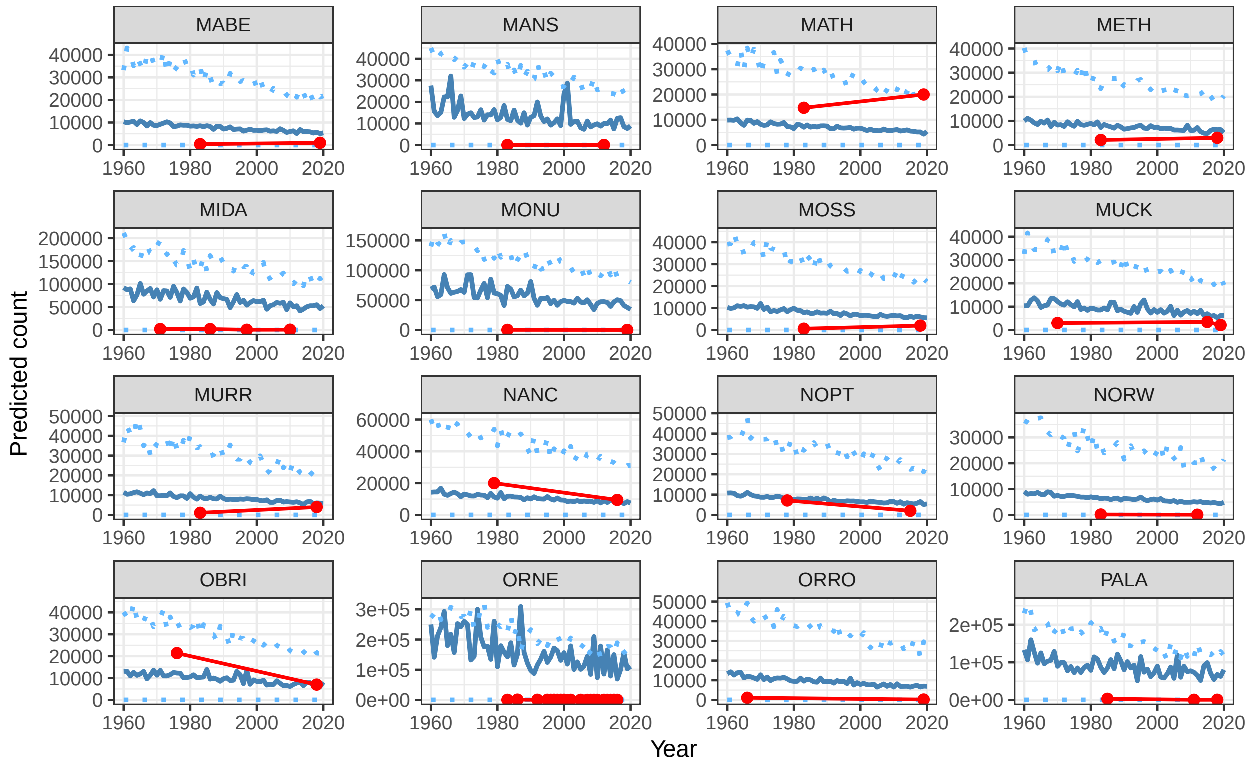

AILS
AITC
AITK
ALCO
AMPH
ANDE
ANVS
ARDL
ARMS
BAIL
BART
BENN
BLAK
BONE
BOWL
BRIT
Predicted count
Year

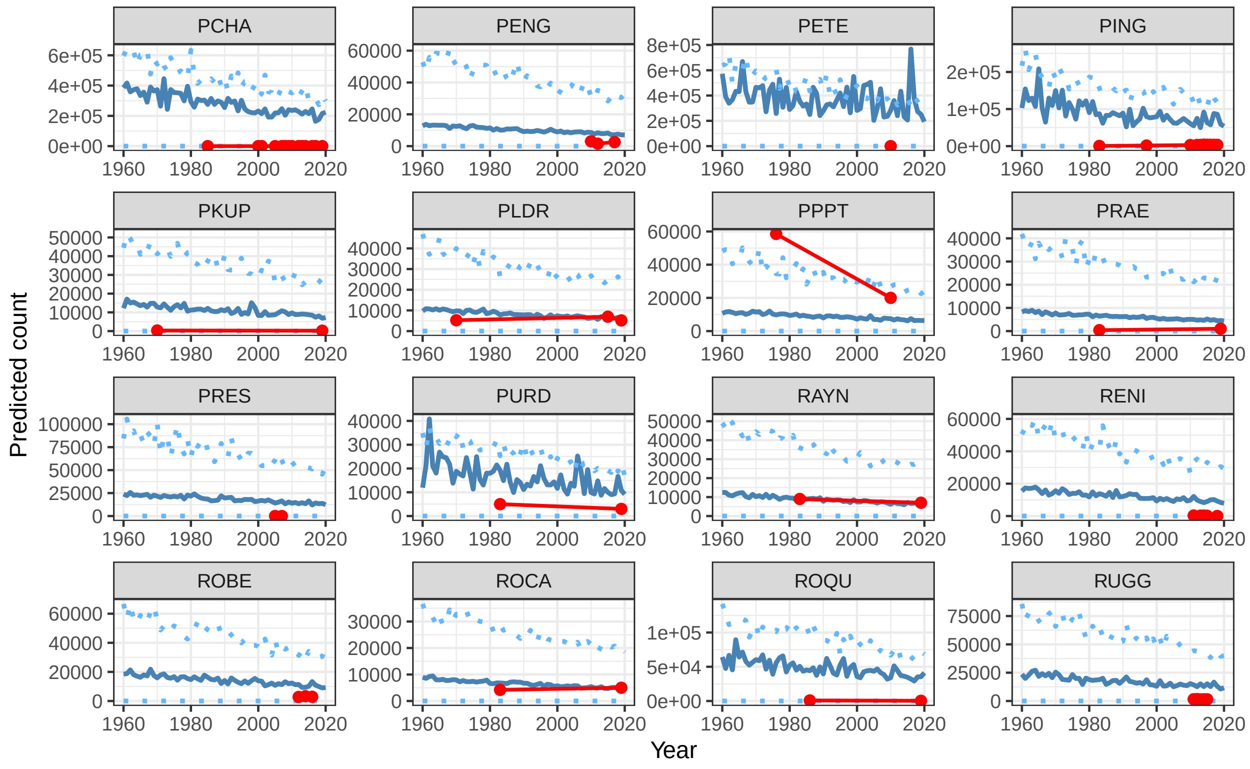

CARO
CCMP
CECI
CHEC
CHIN
CHPT
CHSE
CLIN
CLPT
COBA
COFF
CONE
CRAB
CRAG
CROB
CROW
Predicted count
Year

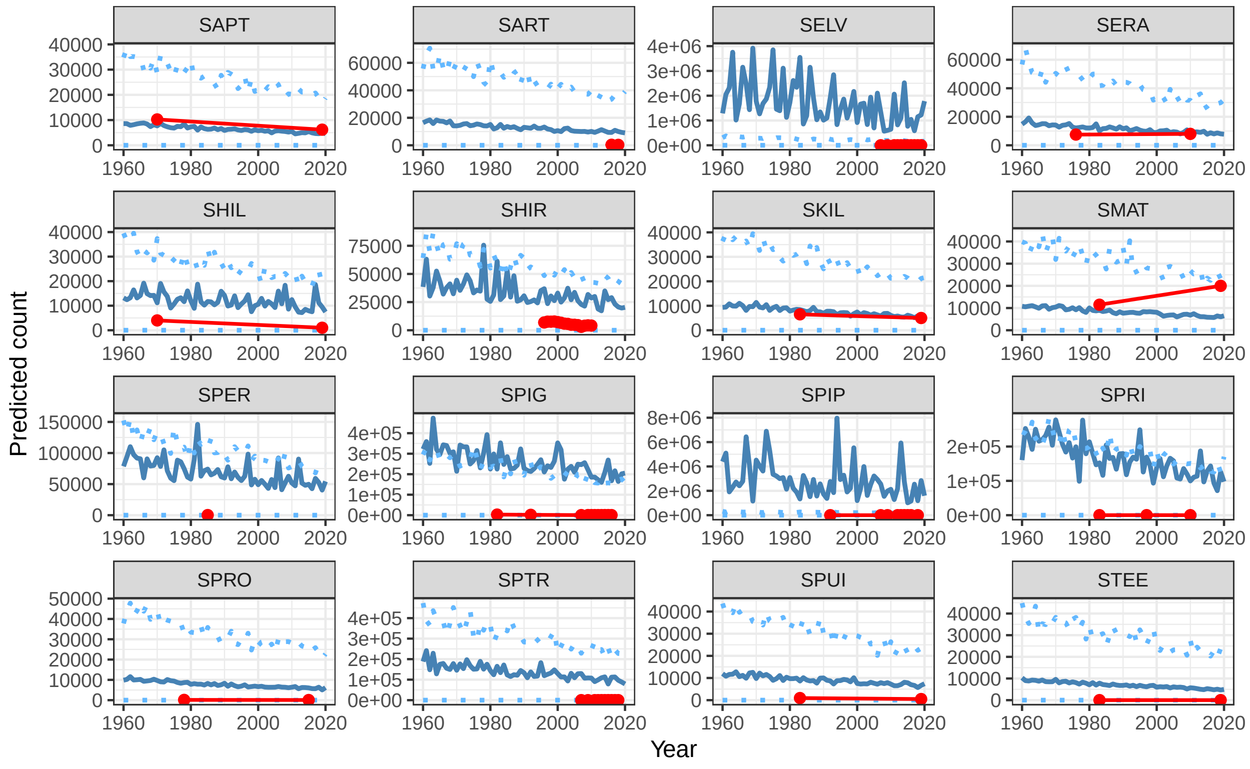

CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

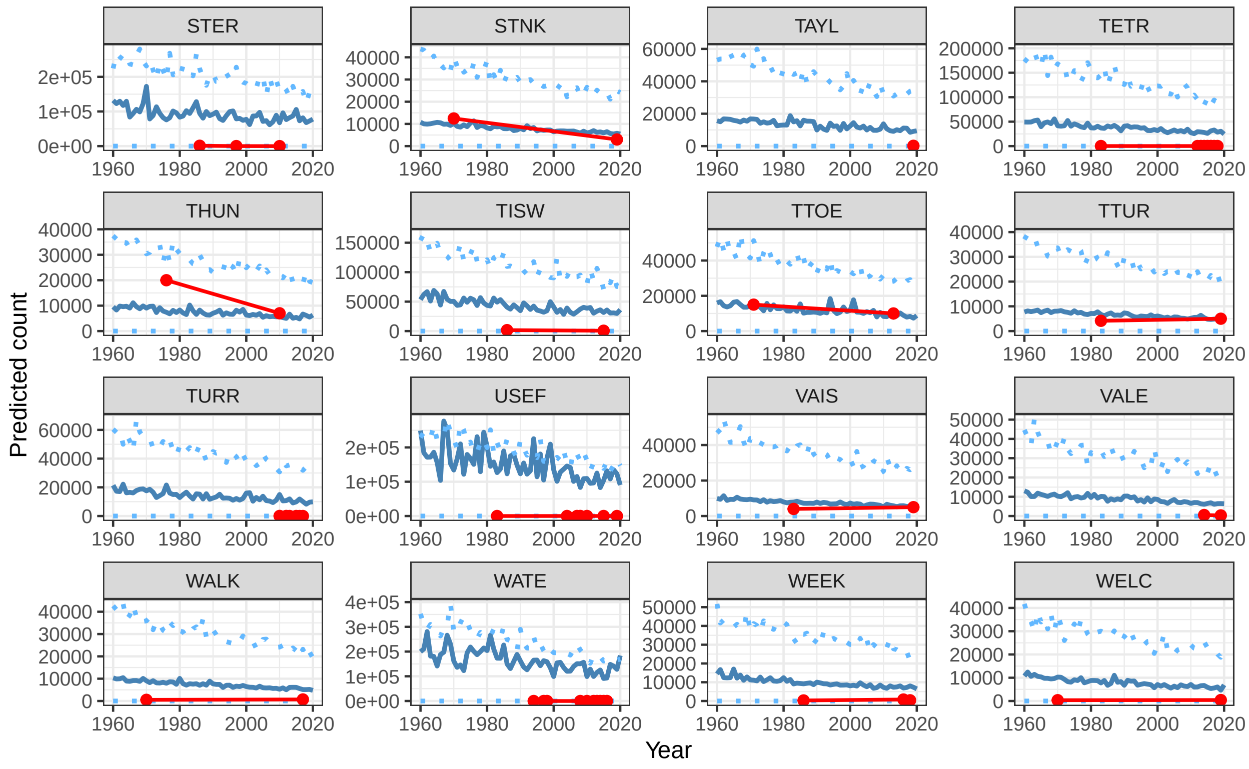

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year


HALF
HANN
HARE
HARM
HUMB
HUNT
HUTB
HYDR
HYDS
JACO
JACP
JOUB
KAYR
KETL
LLOY
LOOK
Predicted count
Year


MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year


PCHA
PENG
PETE
PING
PKUP
PLDR
PPPT
PRAE
PRES
PURD
RAYN
RENI
ROBE
ROCA
ROQU
RUGG
Predicted count
Year


SAPT
SART
SELV
SERA
SHIL
SHIR
SKIL
SMAT
SPER
SPIG
SPIP
SPRI
SPRO
SPTR
SPUI
STEE
Predicted count
Year

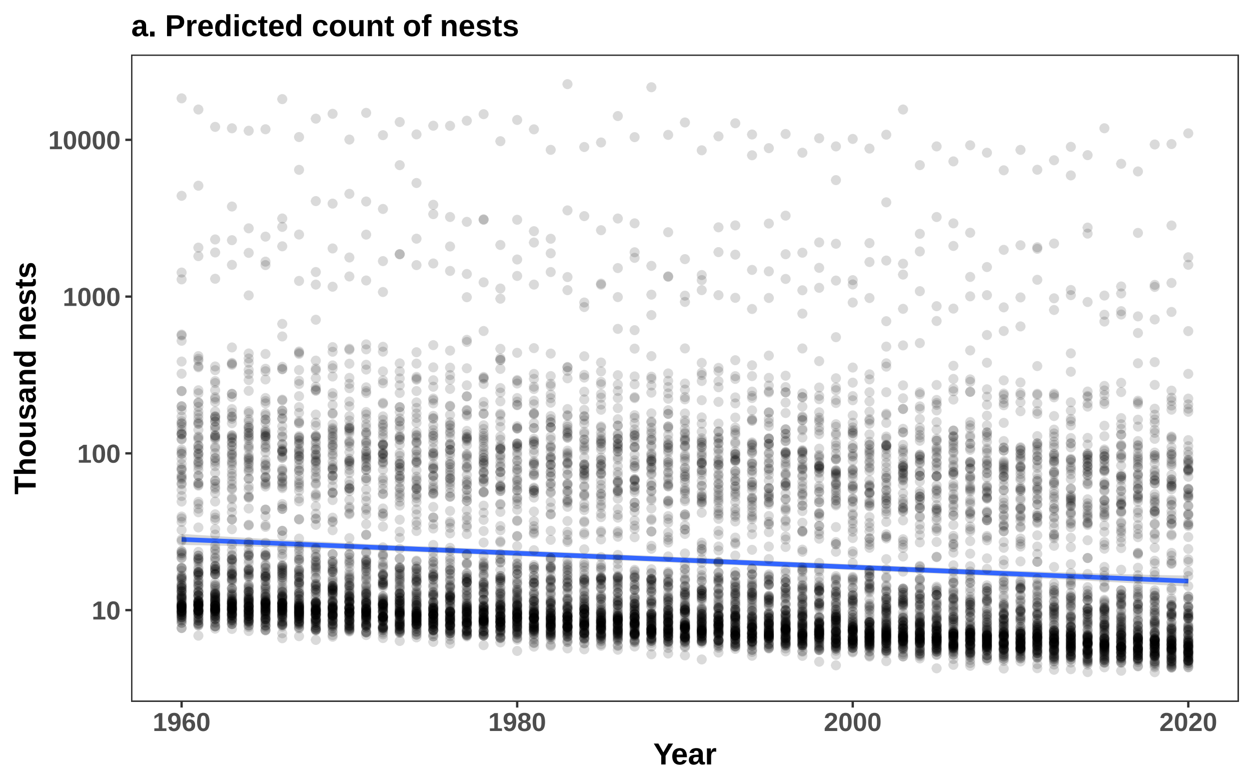


```
# Blue solid lines are the predicted abundance (posterior mean) used by Krüger (2023)
# to predict regional declines. Light blue dots are the 95 % Highest Posterior Density
# interval for this prediction. Red points are the observed counts
# (connected with a red line).
```

1.15 Figure 3A (Krüger 2023)

```
p1v2<-ggplot(popy,aes(season_starting,fit/1000))+
  geom_smooth()+
  geom_point(alpha=0.15)+xlab("Year")+
  theme_bw()+th+ylab("Thousand nests")+
  ggtitle(label="a. Predicted count of nests")+
  scale_y_log10() # plot from the predicted fit

p1v2
```

```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```



This figure plots all the individual site level predictions. It cannot be sensible given the poor model fit and predictions shown above. On some model runs the output look similar to that of Kruger (2023). In other model runs the y-axis scale is much larger (e.g. to 1e+05).

1.16 Figure 3B (Krüger 2023)

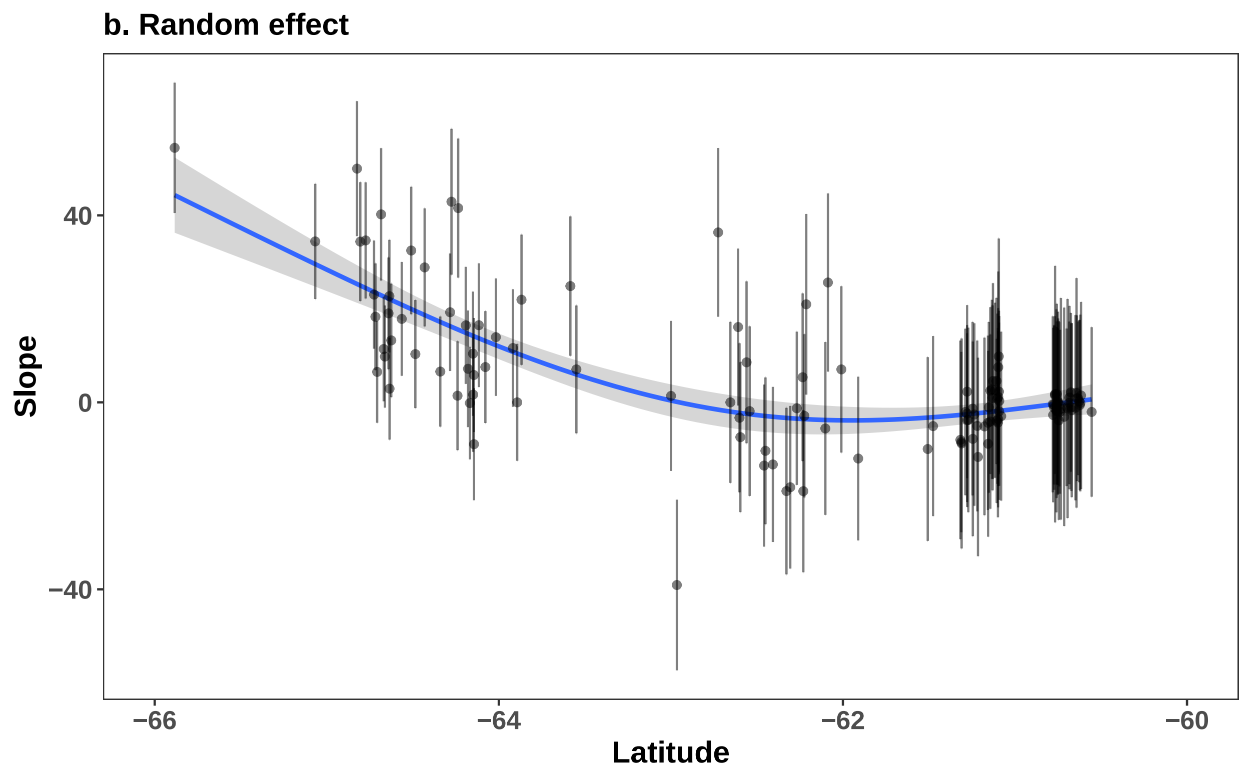
This plots the MCMCglmm intercept - it is (even) labelled "int" here. But the paper legend says slope (which is what we are interested in). This figure makes use of a very poor fitting model (mc1), but initally the output looks similar to that from our own analysis. That is because both plots latitude on the x-axis - so the distibution of points on the x-axis are the same. The sites vary a lot on the y-axis. This plot does not represent changes in population rate of change.

The error bar is calculated as sd/2. The paper caption refers to 'standard deviation' But why divide the standard deviation by 2?

```
p2<- ggplot(subset(rlat,Lat>(-67)),aes(Lat,int))+
  stat_smooth(method="gam",formula=y~s(x,k=2))+
  geom_errorbar(aes(ymin=int-(intsd/2),ymax=int+(intsd/2)),alpha=0.5)+
  geom_point(alpha=0.5)+
  theme_bw()+th+
  ggtitle(label="b. Random effect")+
  ylab("Slope")+xlim(-66,-60)+
  xlab("Latitude")
```

```
p2
```

```
## Warning in smooth.construct.tp.smooth.spec(object, dk$data, dk$knots): basis dimension, k, increased
```



```
# ps: as results are based on randomization
# expect slight differences every time you run the model
# but the trends are consistent everytime
# lagged analysis to determine how much pops have decreased
```

1.17 Population change in 3 generations

> We did not consider this part of the Krüger (2023) analysis, as it is dependent on the above predictions to be reasonable approximations of (observed) abundance.

```
library(lubridate)
library(tidyr)
#library(tidyquant)
library(dplyr)
library(broom)
library(purrr)
library(stringr)
library(knitr)
#library(timetk)
```

```
# Use library(xts) instead, below:

head(popy)
```

```
##   site_id     Lat season_starting nests        fit lwr    upr
## 1    AILS -60.780            1960     0   9781.345   5  36836
## 2    AITC -62.407            1960     0  21646.243   1  69484
## 3    AITK -60.738            1960     0  10599.392   1  37417
## 4    ALCO -64.240            1960     0 105823.245   0 192118
## 5    AMPH -60.684            1960     0  10177.982   2  47998
## 6    ANDE -60.757            1960     0  10440.108   4  36775
```

```
popT<-ddply(popy, c("season_starting"), summarise,
            tot=sum(fit), ### total population
            mean=mean(fit)) ### mean population

# create a time stamp for year
popT$TS<-(as.POSIXct(strptime(paste(popT$season_starting,c("01-01"),sep="-"),
                              format="%Y-%m-%d" ,tz="GMT")) )
# create a time stamp for year
popy$TS<-(as.POSIXct(strptime(paste(popy$season_starting,c("01-01"),sep="-"),
                              format="%Y-%m-%d" ,tz="GMT")) )

mts<-xts::xts(popT$tot,order.by=popT$TS) # create a temporal data frame

# create a lag data frame
mlag<-((data.frame(year=popT$season_starting,mts %>%
                     xts::lag.xts(k = c(0,27,28,29,30)))))
mlag
```

```
##            year     lag0    lag27    lag28    lag29    lag30
## 1960-01-01 1960 33449693       NA       NA       NA       NA
## 1961-01-01 1961 32211540       NA       NA       NA       NA
## 1962-01-01 1962 24848532       NA       NA       NA       NA
## 1963-01-01 1963 26674367       NA       NA       NA       NA
## 1964-01-01 1964 24497740       NA       NA       NA       NA
## 1965-01-01 1965 24365405       NA       NA       NA       NA
## 1966-01-01 1966 33700437       NA       NA       NA       NA
## 1967-01-01 1967 27745307       NA       NA       NA       NA
## 1968-01-01 1968 27776727       NA       NA       NA       NA
## 1969-01-01 1969 28934595       NA       NA       NA       NA
## 1970-01-01 1970 24706699       NA       NA       NA       NA
## 1971-01-01 1971 29688964       NA       NA       NA       NA
## 1972-01-01 1972 23916108       NA       NA       NA       NA
## 1973-01-01 1973 30013459       NA       NA       NA       NA
## 1974-01-01 1974 26623250       NA       NA       NA       NA
## 1975-01-01 1975 27549716       NA       NA       NA       NA
## 1976-01-01 1976 25534959       NA       NA       NA       NA
## 1977-01-01 1977 25251237       NA       NA       NA       NA
## 1978-01-01 1978 28581839       NA       NA       NA       NA
## 1979-01-01 1979 20868327       NA       NA       NA       NA
## 1980-01-01 1980 25646738       NA       NA       NA       NA
## 1981-01-01 1981 24023804       NA       NA       NA       NA
## 1982-01-01 1982 20605031       NA       NA       NA       NA
## 1983-01-01 1983 34573389       NA       NA       NA       NA
## 1984-01-01 1984 19929738       NA       NA       NA       NA
## 1985-01-01 1985 20730844       NA       NA       NA       NA
## 1986-01-01 1986 25918973       NA       NA       NA       NA
## 1987-01-01 1987 23330287 33449693       NA       NA       NA
## 1988-01-01 1988 30840750 32211540 33449693       NA       NA
## 1989-01-01 1989 21680335 24848532 32211540 33449693       NA
## 1990-01-01 1990 22241567 26674367 24848532 32211540 33449693
## 1991-01-01 1991 17921907 24497740 26674367 24848532 32211540
## 1992-01-01 1992 21611126 24365405 24497740 26674367 24848532
## 1993-01-01 1993 23802455 33700437 24365405 24497740 26674367
## 1994-01-01 1994 26419812 27745307 33700437 24365405 24497740
## 1995-01-01 1995 19877947 27776727 27745307 33700437 24365405
## 1996-01-01 1996 22615150 28934595 27776727 27745307 33700437
## 1997-01-01 1997 17437237 24706699 28934595 27776727 27745307
## 1998-01-01 1998 20247246 29688964 24706699 28934595 27776727
## 1999-01-01 1999 23504325 23916108 29688964 24706699 28934595
## 2000-01-01 2000 18596382 30013459 23916108 29688964 24706699
## 2001-01-01 2001 18659326 26623250 30013459 23916108 29688964
## 2002-01-01 2002 22534737 27549716 26623250 30013459 23916108
## 2003-01-01 2003 24349941 25534959 27549716 26623250 30013459
## 2004-01-01 2004 17415924 25251237 25534959 27549716 26623250
## 2005-01-01 2005 18471289 28581839 25251237 25534959 27549716
## 2006-01-01 2006 18192937 20868327 28581839 25251237 25534959
## 2007-01-01 2007 19259856 25646738 20868327 28581839 25251237
## 2008-01-01 2008 16197521 24023804 25646738 20868327 28581839
## 2009-01-01 2009 14491515 20605031 24023804 25646738 20868327
## 2010-01-01 2010 16746017 34573389 20605031 24023804 25646738
## 2011-01-01 2011 16444221 19929738 34573389 20605031 24023804
## 2012-01-01 2012 15742085 20730844 19929738 34573389 20605031
## 2013-01-01 2013 21634281 25918973 20730844 19929738 34573389
## 2014-01-01 2014 18530093 23330287 25918973 20730844 19929738
## 2015-01-01 2015 18753517 30840750 23330287 25918973 20730844
## 2016-01-01 2016 14915868 21680335 30840750 23330287 25918973
## 2017-01-01 2017 14608933 22241567 21680335 30840750 23330287
## 2018-01-01 2018 16785519 17921907 22241567 21680335 30840750
## 2019-01-01 2019 18507668 21611126 17921907 22241567 21680335
## 2020-01-01 2020 19115562 23802455 21611126 17921907 22241567
```

```r
# proportional change for all lags
mlag$ch3<-(mlag$lag0/mlag$lag27)-1
mlag$ch4<-(mlag$lag0/mlag$lag28)-1
mlag$ch5<-(mlag$lag0/mlag$lag29)-1
mlag$ch6<-(mlag$lag0/mlag$lag30)-1

mlags<-data.frame(year=mlag$year,mlag[7:10])

chm<-na.omit(melt(mlags,id.vars="year"))
summary(chm$value)
```

```
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -0.54468 -0.32938 -0.24911 -0.24089 -0.14815  0.08553
```

```r
quantile(chm$value,probs=0.95)
```

```
##        95%
## -0.0198668
```

```r
quantile(chm$value,probs=0.05)
```

```
##         5%
## -0.4397207
```

```r
mean(chm$value)
```

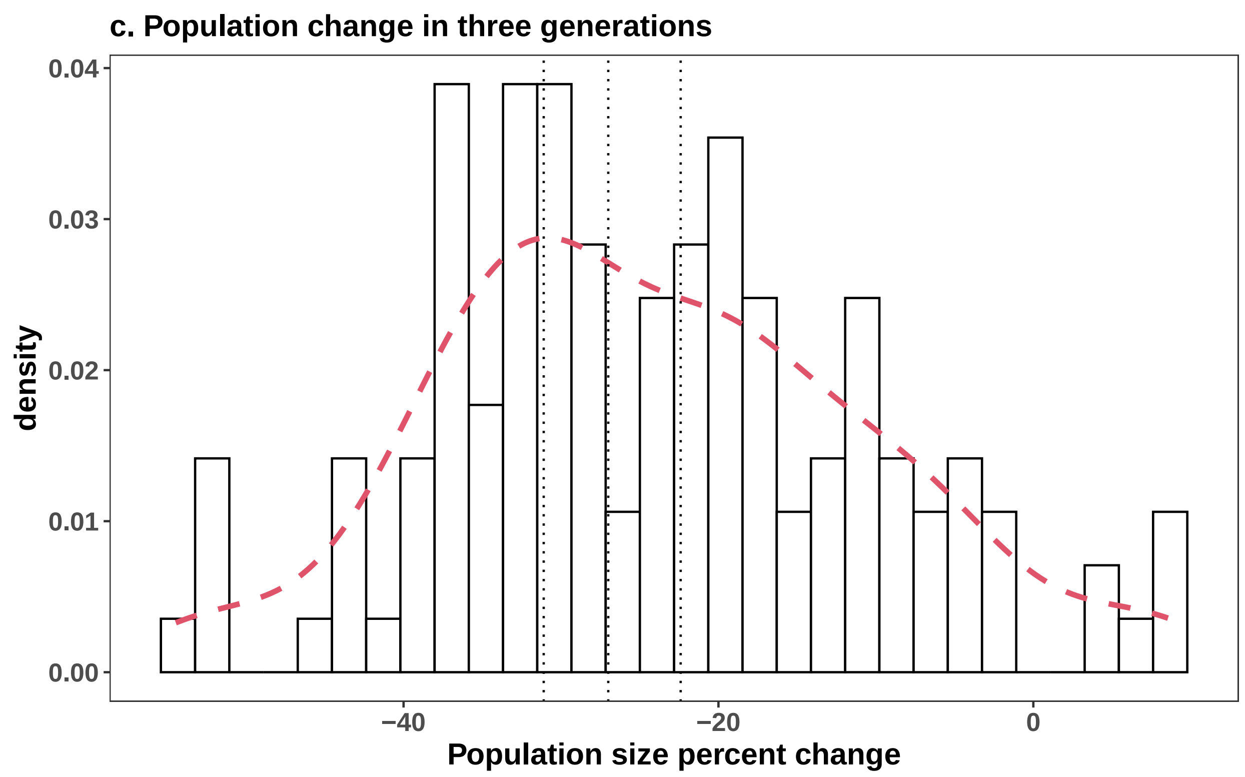
```
## [1] -0.2408862
```

```r
sd(chm$value)
```

```
## [1] 0.1364754
```

```r
p3<-ggplot(chm,aes(value*100))+
  geom_histogram(aes(y = ..density..), colour = 1, fill = "white") +
  geom_density(lwd = 1.2, linetype = 2,colour = 2)+
  theme_bw()+th+
  geom_vline(xintercept = c(-22.4,-27.0,-31.1),linetype="dotted")+
  xlab("Population size percent change")+
  ggtitle(label="c. Population change in three generations")

p3
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
# p1v2/p2/p3
```

2 Reanalysis for Oosthuizen et al.

2.1 Fit a better GLMM

How is this model different to Kruger (2023)? Here, we used the same data, but we: 1) used a different model specification for fixed and random effects 2) z-standardized the covariates before running the model 3) used longer mcmc chains 4) when predicting from the fitted model, we did not marginalise the random effects

```
# head(nestM3)

# Covariates should be standardized.
nestM3$Zseason_starting = scale(nestM3$season_starting)
nestM3$ZLat = scale(nestM3$Lat)
```

```
mc2 <- MCMCglmm(nests ~ Zseason_starting * ZLat,
                random=~us(1 + Zseason_starting):site_id,
                rcov=~units,
              family="poisson", mev=NULL,
              data=nestM3,start=NULL, nodes="ALL", scale=TRUE,
              nitt=23000, thin=10, burnin=13000, pr=T,
              pl=FALSE, verbose=TRUE, DIC=TRUE, singular.ok=FALSE, saveX=TRUE,
              prior=prior, saveZ=TRUE, saveXL=TRUE, slice=FALSE,
              ginverse=NULL, trunc=FALSE)
```

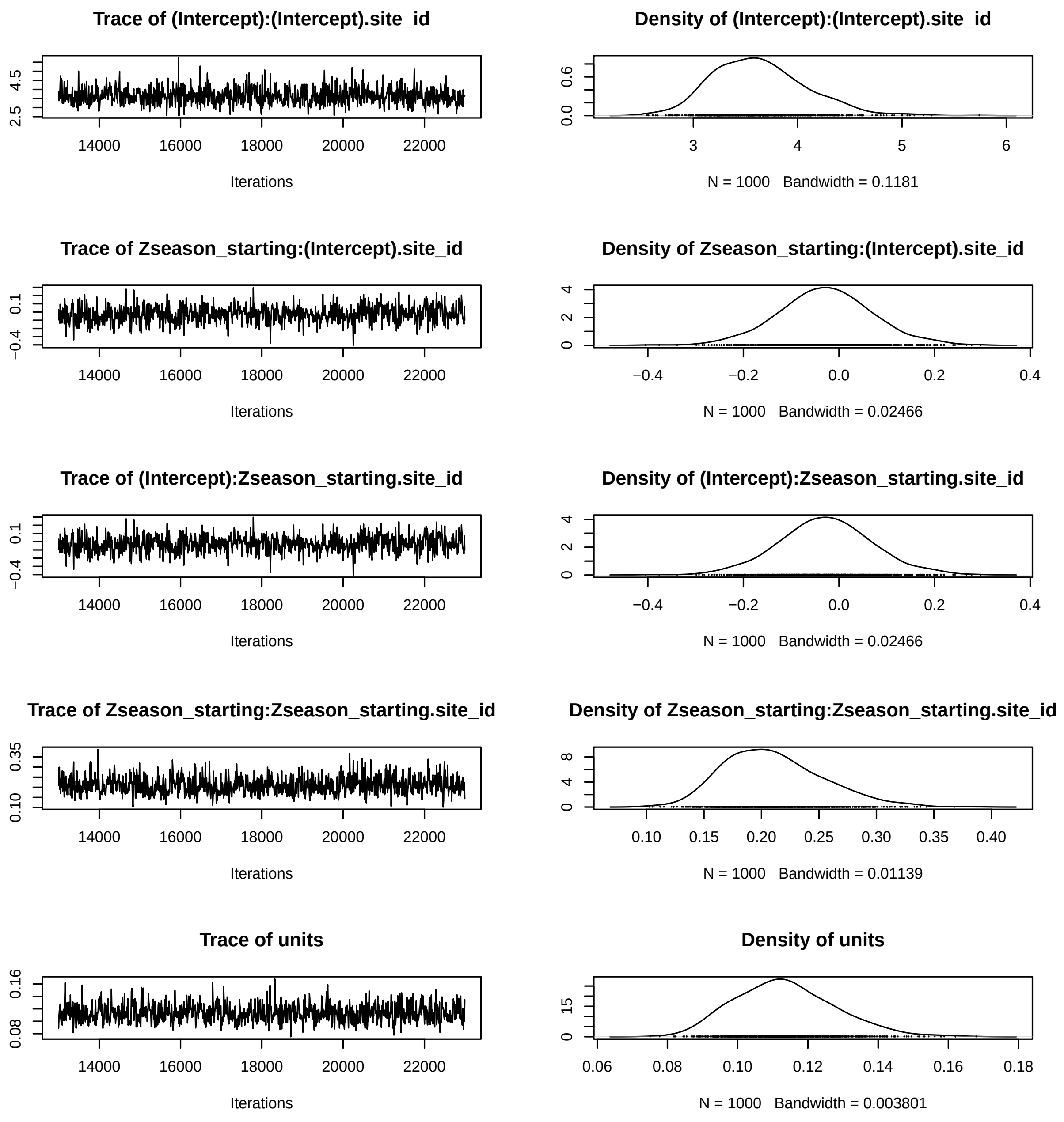
```
summary(mc2)
```

```
##
##  Iterations = 13001:22991
##  Thinning interval  = 10
##  Sample size  = 1000
##
##  DIC: 4793.07
##
##  G-structure:  ~us(1 + Zseason_starting):site_id
##
##                                           post.mean l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id             3.63436   2.8317   4.5233    707.0
## Zseason_starting:(Intercept).site_id       -0.02806  -0.2195   0.1776    581.7
## (Intercept):Zseason_starting.site_id       -0.02806  -0.2195   0.1776    581.7
## Zseason_starting:Zseason_starting.site_id   0.21049   0.1395   0.2989    789.2
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.1136  0.08888   0.1426    729.3
##
##  Location effects: nests ~ Zseason_starting * ZLat
##
##                       post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)             5.81341  5.48014  6.14692   1000.0 <0.001 ***
## Zseason_starting       -0.17735 -0.27767 -0.07628   1000.0  0.002 **
## ZLat                    1.42540  1.08721  1.72268   1000.0 <0.001 ***
## Zseason_starting:ZLat   0.04721 -0.04902  0.14181    728.2  0.328
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.2 MCMCglmm diagnostics for mc2

Assessing model convergence. We do this separately for both fixed and random effects. The trace plot should look like a fuzzy caterpillar

```
# plot(mc2$Sol)

# variances of the random effects - shows good mixing
plot(mc2$VCV)
```



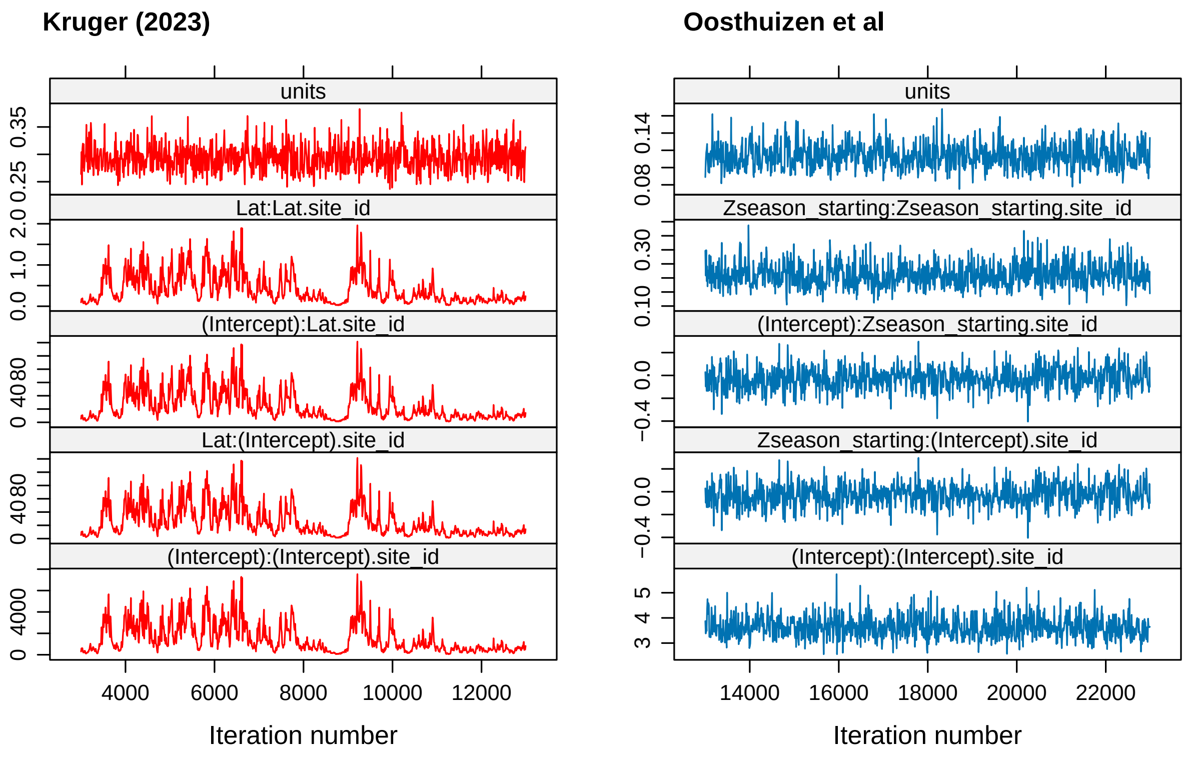
```r
# what are the effective sample size for the random effects?
coda::effectiveSize(mc2$VCV)
```

```
##            (Intercept):(Intercept).site_id
##                                    706.9680
##      Zseason_starting:(Intercept).site_id
##                                    581.6882
##      (Intercept):Zseason_starting.site_id
##                                    581.6882
## Zseason_starting:Zseason_starting.site_id
##                                    789.2229
##                                       units
##                                    729.3490
```

```
# The effective sample size is large

# from MCMC Course notes (page 60):
diag(autocorr(mc2$VCV)[2, , ])   # low autocorrelation
```

```
##           (Intercept):(Intercept).site_id
##                                  0.03956651
##      Zseason_starting:(Intercept).site_id
##                                  0.09865474
##      (Intercept):Zseason_starting.site_id
##                                  0.09865474
## Zseason_starting:Zseason_starting.site_id
##                                  0.04962261
##                                       units
##                                  0.15601607
```

```
# the variance components
trace2 = lattice::xyplot(as.mcmc(mc2$VCV), par.strip.text=list(cex=0.8))

cowplot::plot_grid(traceK, trace2, labels = c('Kruger (2023)', 'Oosthuizen et al'), ncol = 2, label_siz
```



```
# Save Plot
# pdf("./figures/Supp_Trace plots.pdf",
#       useDingbats = FALSE, width = 8, height = 12)
# cowplot::plot_grid(traceK, trace2, labels = c('A', 'B'),
#                    ncol = 2, label_size = 14,  vjust = 3.5, hjust = -.5)
# dev.off()
```

2.3 Predict using MCMCglmm mc2

```
# construct an hypothetical dataframe to predict to

# need to predict to z-standardized variables
Z1 = dplyr::select(nestM3, season_starting, Lat)
Z2 <- scale(Z1)
attr(Z2,"scaled:center")
```

```
## season_starting             Lat
##      2003.32985       -62.96523
```

```
attr(Z2,"scaled:scale")
```

```
## season_starting             Lat
##       15.685180        1.600454
```

```r
ave_ss = attr(Z2,"scaled:center")[[1]]
ave_lat = attr(Z2,"scaled:center")[[2]]

sd_ss = attr(Z2,"scaled:scale")[[1]]
sd_lat = attr(Z2,"scaled:scale")[[2]]

years<-data.frame(season_starting=c(1960:2020)) # extrapolate to 1960
#years<-data.frame(season_starting=c(1980:2020)) # extrapolate to 1980

pops<-data.frame(site_id=countsN$site_id[countsN$ncounts>1],
                 Lat=countsN$Lat[countsN$ncounts>1])
popy<-merge(pops,years)
popy$nests<-c(0) ### MCMCglmm needs a column with the response variable

popy$Zseason_starting = (popy$season_starting - ave_ss)/sd_ss
popy$ZLat = (popy$Lat - ave_lat)/sd_lat

head(popy)
```

```
##   site_id     Lat season_starting nests Zseason_starting       ZLat
## 1    AILS -60.780            1960     0        -2.762471  1.3653784
## 2    AITC -62.407            1960     0        -2.762471  0.3487919
## 3    AITK -60.738            1960     0        -2.762471  1.3916209
## 4    ALCO -64.240            1960     0        -2.762471 -0.7965080
## 5    AMPH -60.684            1960     0        -2.762471  1.4253614
## 6    ANDE -60.757            1960     0        -2.762471  1.3797493
```

```r
# Don't extrapolate more than X years
first_last_season = nestM3 %>%
        dplyr::group_by(site_id) %>%
        dplyr::summarise(minyear = min(season_starting),
                         maxyear = max(season_starting)) %>%
        dplyr::arrange(minyear)
first_last_season
```

```
## # A tibble: 146 x 3
##    site_id minyear maxyear
##    <chr>     <int>   <int>
##  1 DEEI       1965    1965
##  2 ORRO       1966    2019
##  3 BRIT       1970    2016
##  4 CCMP       1970    2019
##  5 CLIN       1970    2019
##  6 CRAB       1970    2019
##  7 DECI       1970    2019
##  8 EIP1       1970    2019
##  9 EIP2       1970    2019
## 10 EIP3       1970    2019
## # i 136 more rows
```

```r
popy = merge(popy, first_last_season)
```

```
# subset so that you only predict for sites with counts at least 20 years from begin and end

#popy = subset(popy, popy$minyear < 1990)
#popy = subset(popy, popy$maxyear > 2010)

length(unique(popy$site_id))
```

```
## [1] 146
```

```
popypred <- data.frame(predict(mc2,
                              newdata=popy,
                              type="response",
                              marginal=NULL,      # crucial, and not default code.
                              interval="prediction",
                              posterior="all"))

head(popypred)
```

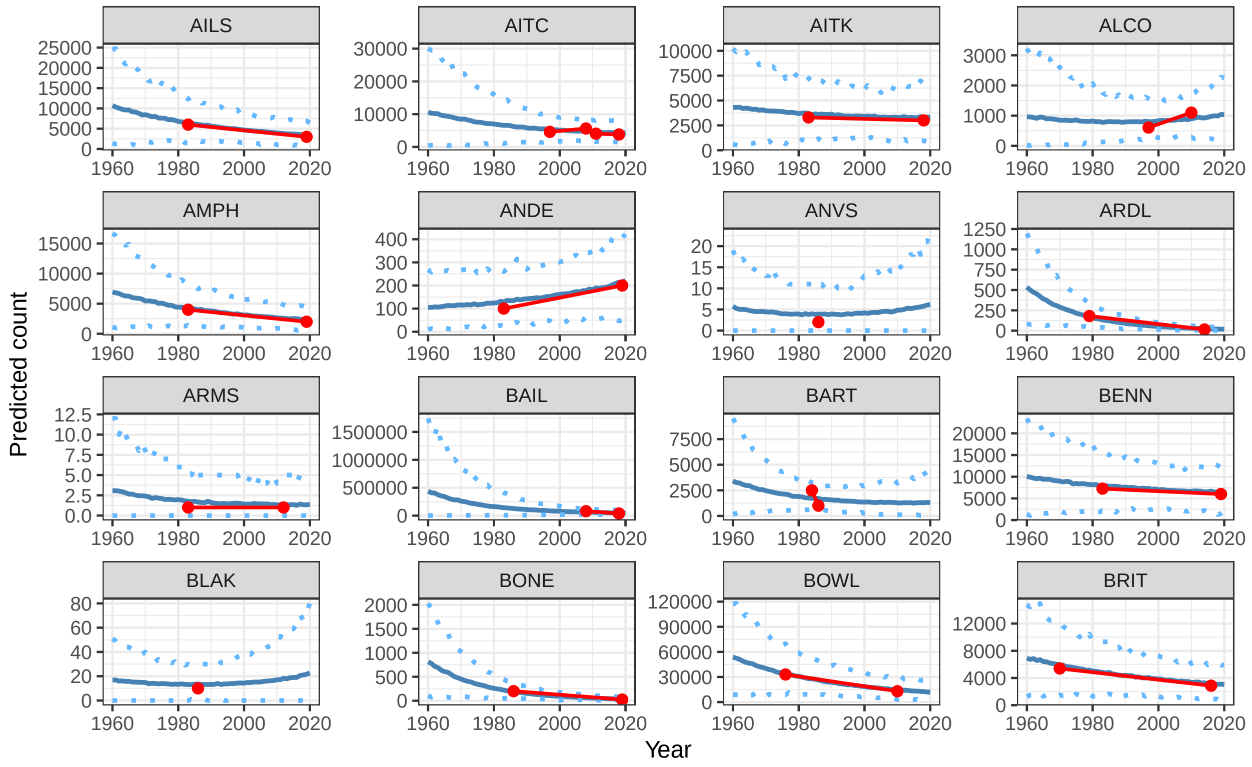
```
##          fit  lwr   upr
## 1 10686.768 1436 24457
## 2  5802.043 1866 11310
## 3  9639.242  962 21828
## 4  8450.036 1378 18253
## 5  7611.752 1968 16277
## 6  4461.350 1694  8276
```

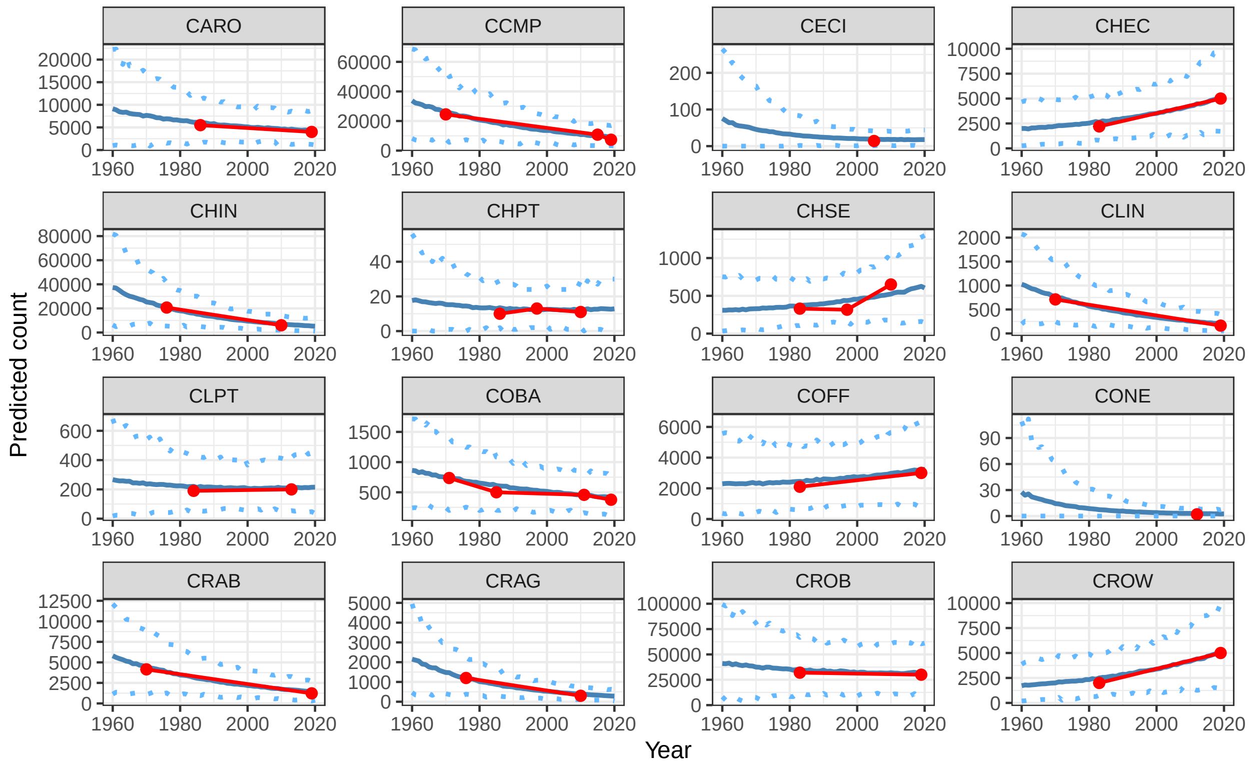
```
popy$Zfit = popypred$fit
popy$Zlwr = popypred$lwr
popy$Zupr = popypred$upr

## How accurate are the predictions relative to observed data?
```

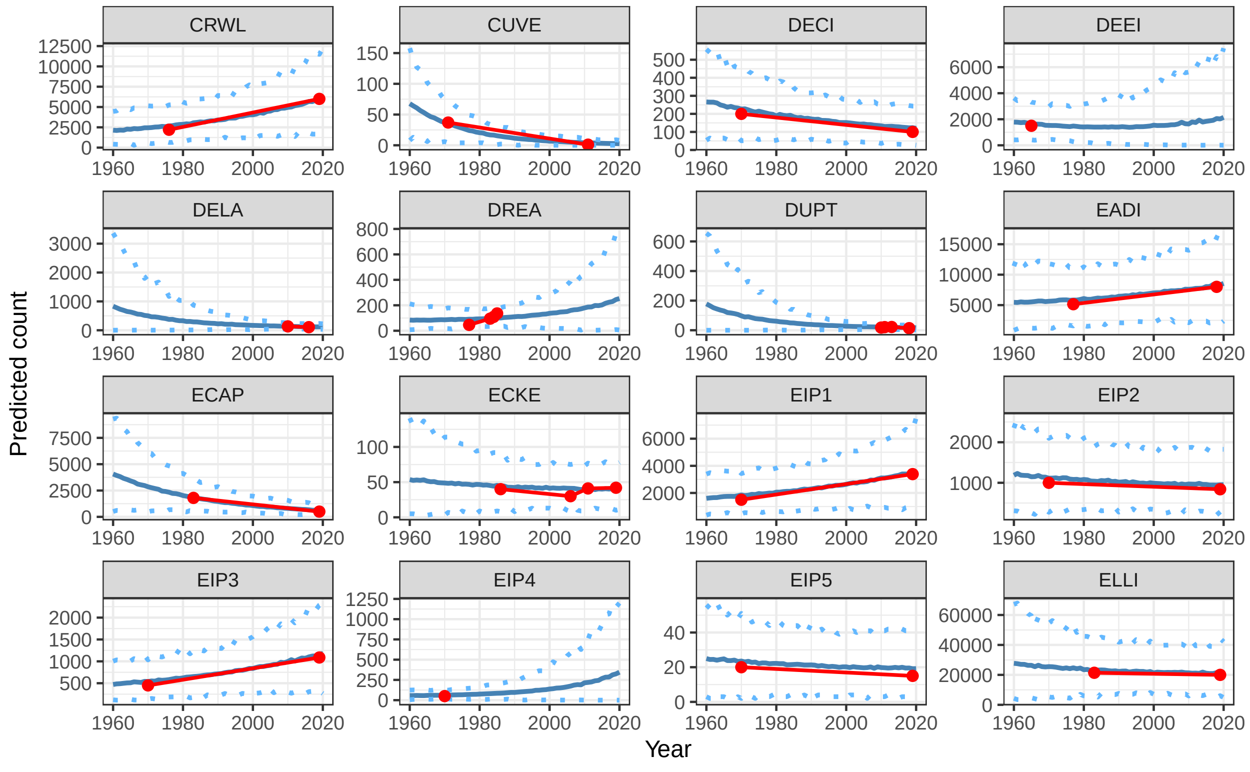
2.4 Conditional model predictions

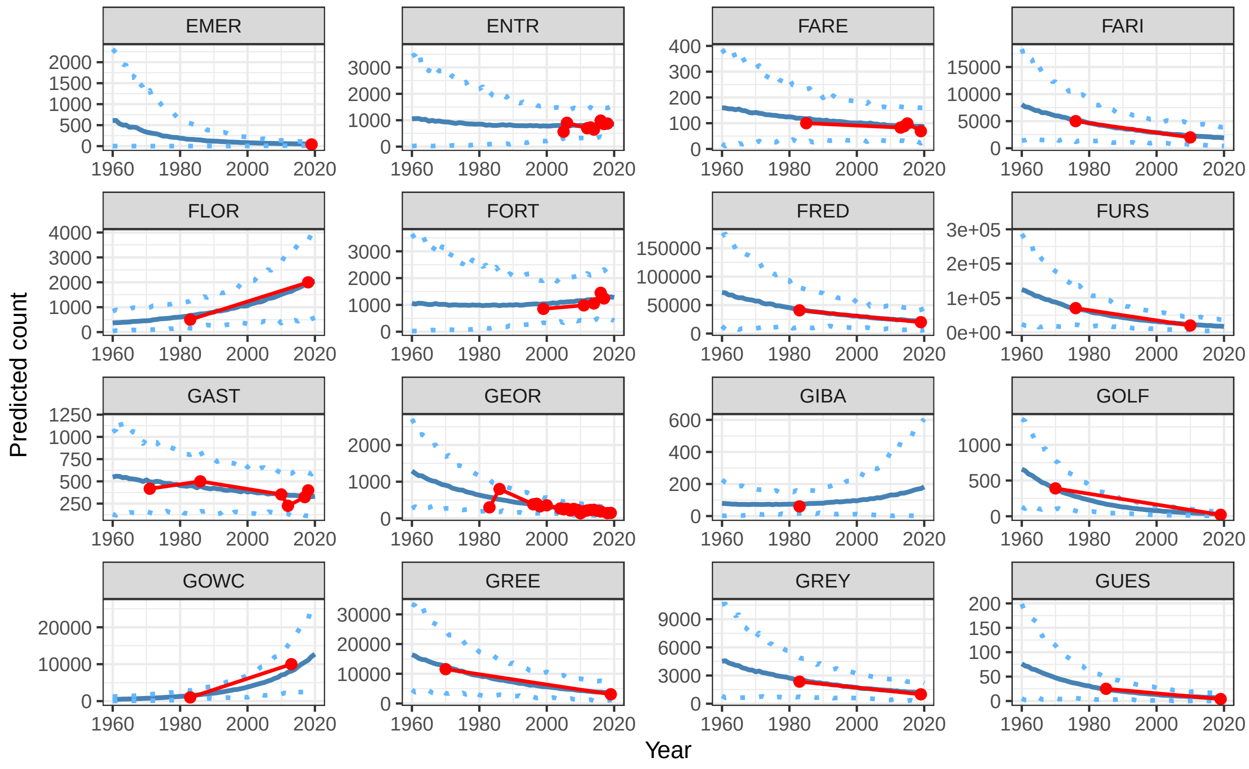
Plot the observed data against predicted data, per site, to see whether observed data and predicted data agree for the revised analysis

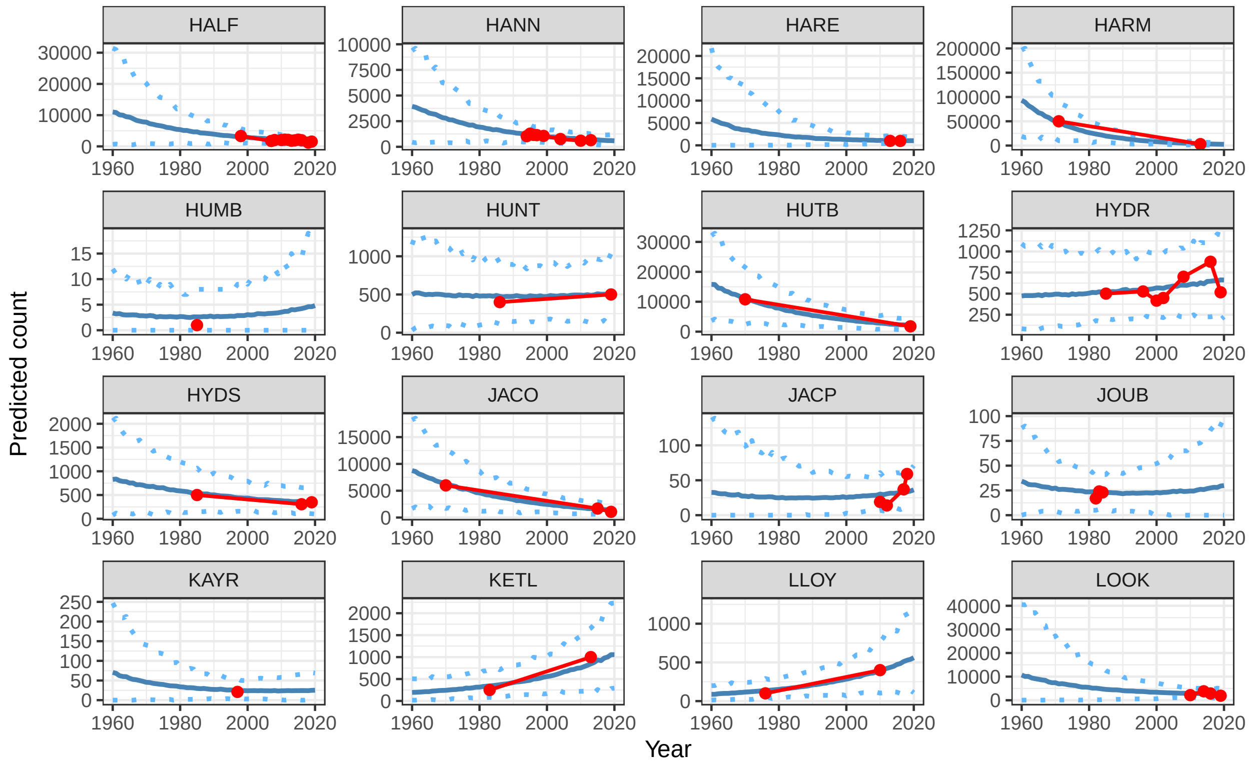
```
required_n_pages = round(133/16)+1

for(i in 1:required_n_pages){

print(ggplot(data = popy) +
    geom_line(aes(x = season_starting, y = Zfit),
              col = "steelblue", linewidth=1.04) +
    geom_line(aes(x = season_starting, y = Zlwr),
              col = "steelblue1", linetype="dotted", linewidth = 1.02) +
    geom_line(aes(x = season_starting, y = Zupr),
              col = "steelblue1", linetype="dotted", linewidth=1.02) +
    geom_point(data = nestm3, aes(season_starting, y = nests),
               color = "red", cex = 2) +
    geom_line(data = nestm3, aes(season_starting, y = nests),
              color = "red",linewidth=0.8) +
    theme_bw() +
    xlab("Year") +
    ylab("Predicted count") +
  # theme(strip.text = element_text(size = 1.5)) +
    facet_wrap_paginate(~ site_id, ncol = 4, nrow = 4,
                        page = i,
                        scales = 'free'))}
```

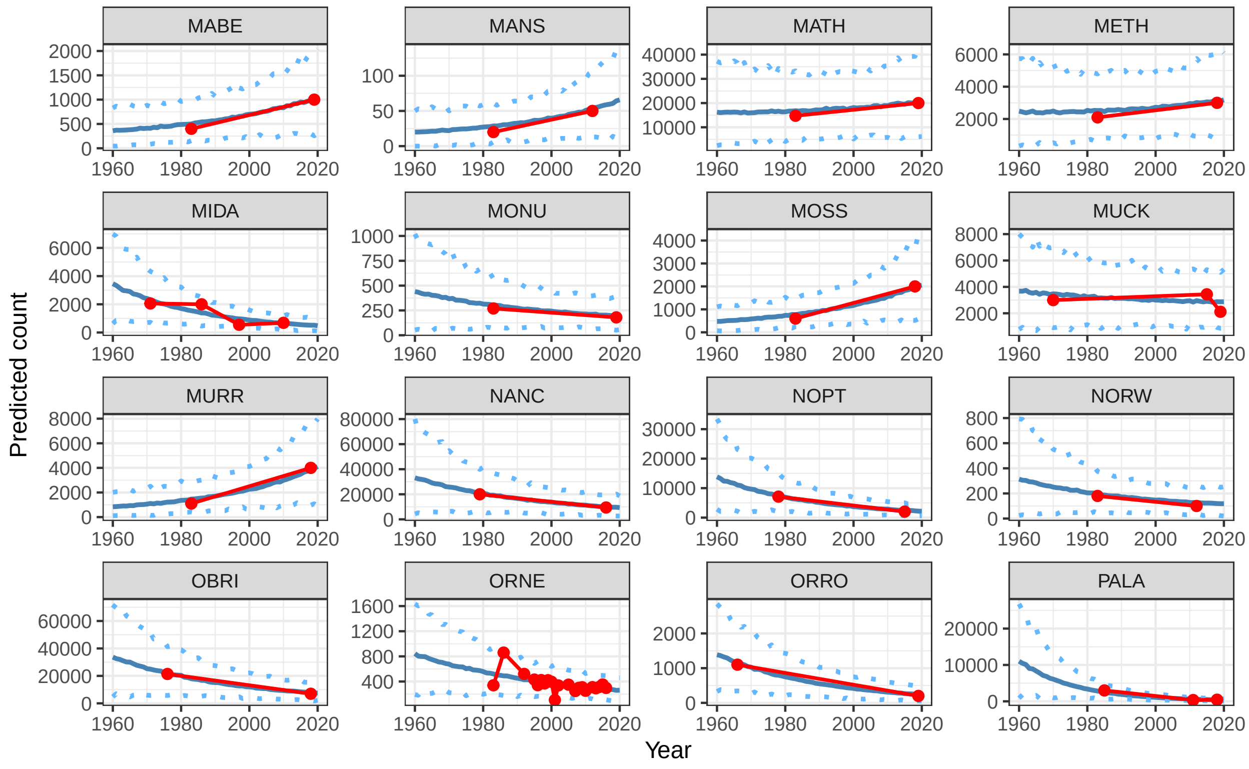


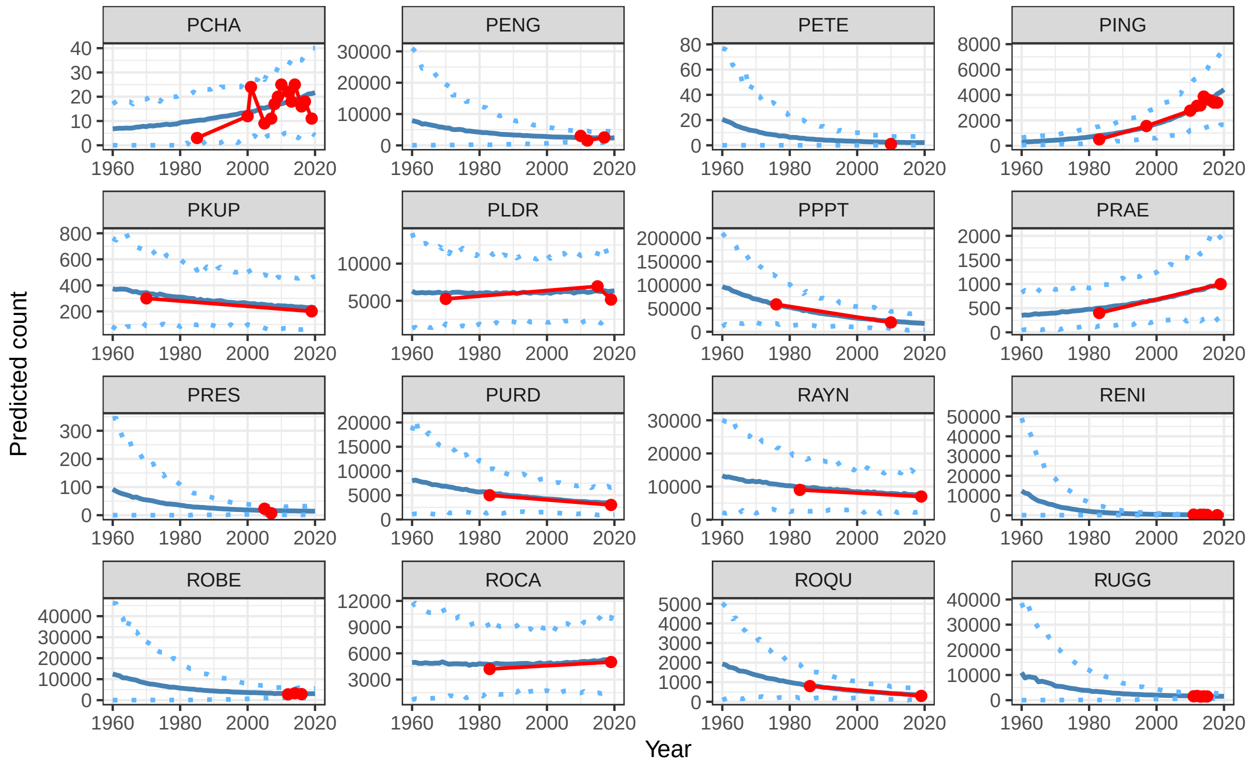

CARO
CCMP
CECI
CHEC
CHIN
CHPT
CHSE
CLIN
CLPT
COBA
COFF
CONE
CRAB
CRAG
CROB
CROW
Predicted count
Year

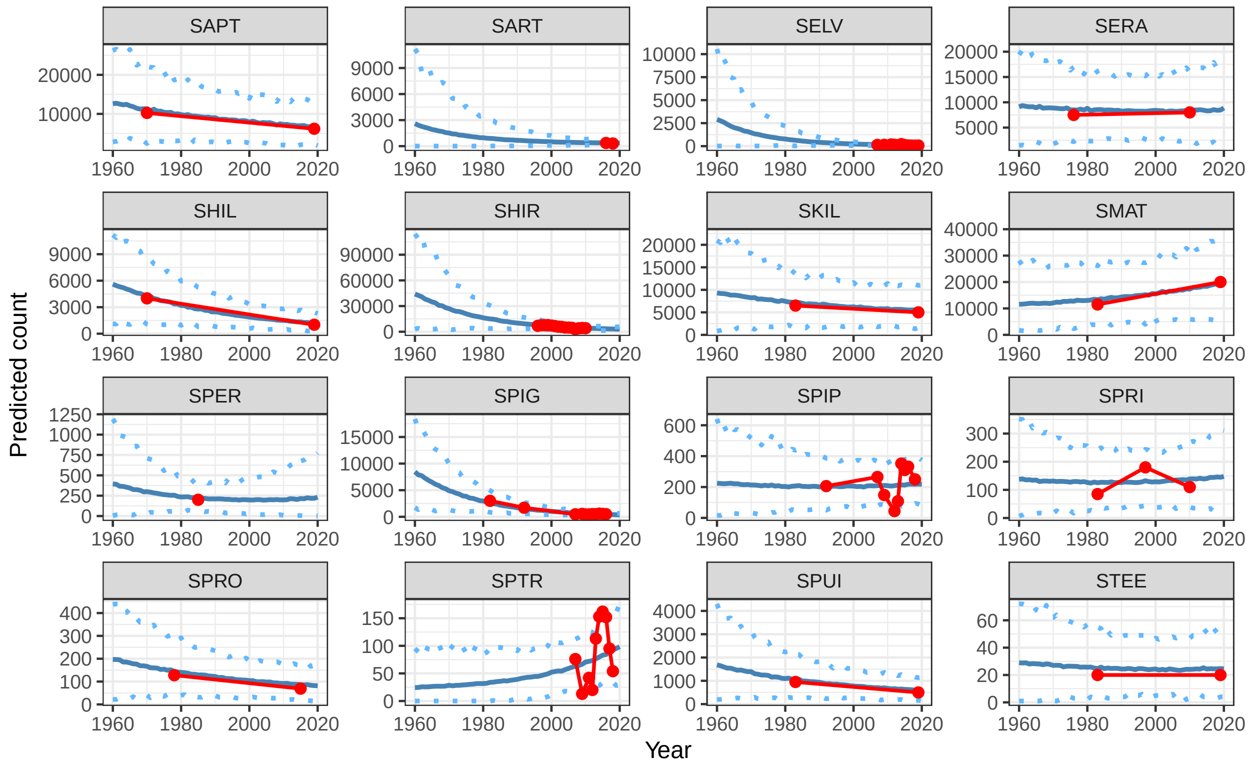

CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

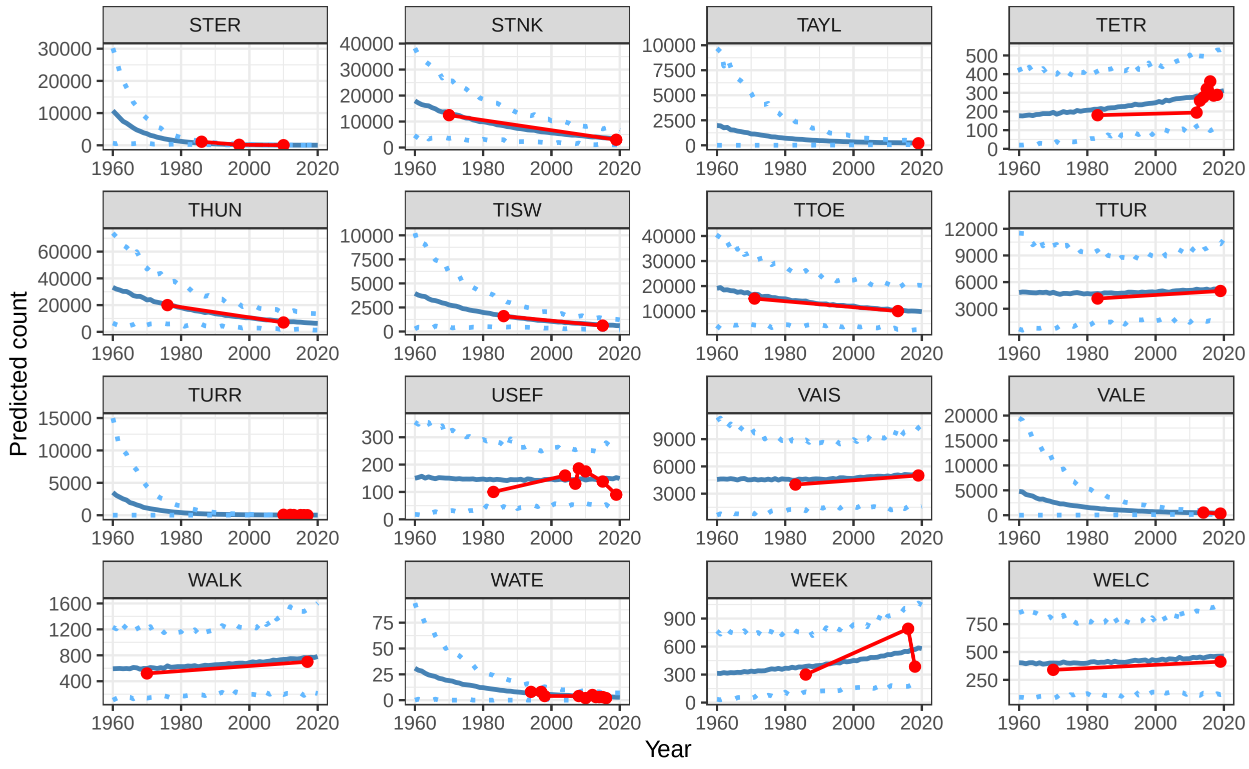

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year
1960
1980
2000
2020


HALF
HANN
HARE
HARM
HUMB
HUNT
HUTB
HYDR
HYDS
JACO
JACP
JOUB
KAYR
KETL
LLOY
LOOK
Predicted count
Year
1960
1980
2000
2020


MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year


PCHA
PENG
PETE
PING
PKUP
PLDR
PPPT
PRAE
PRES
PURD
RAYN
RENI
ROBE
ROCA
ROQU
RUGG
Predicted count
Year



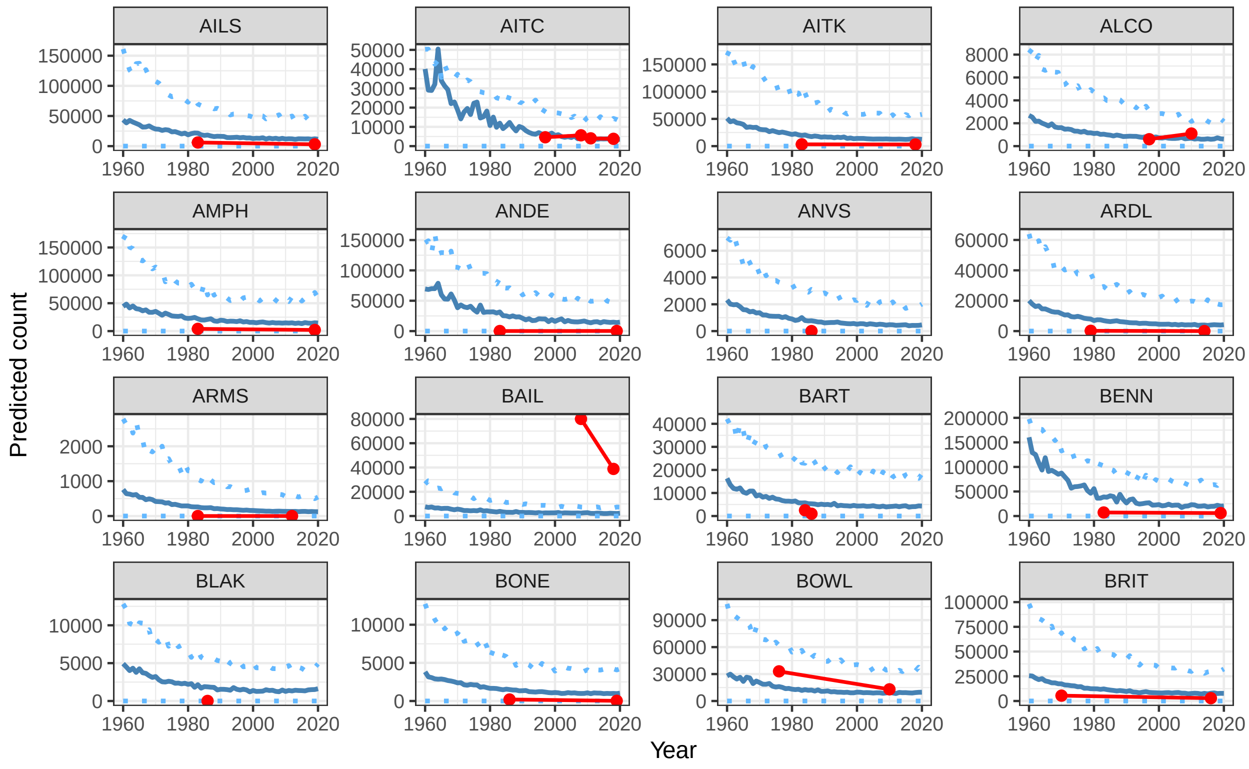


```
# Predictions are good, although back-predicting to 1960 is extrapolation
# (there are only 2 counts prior to 1970) so uncertainty (prediction intervals)
# is high.
```

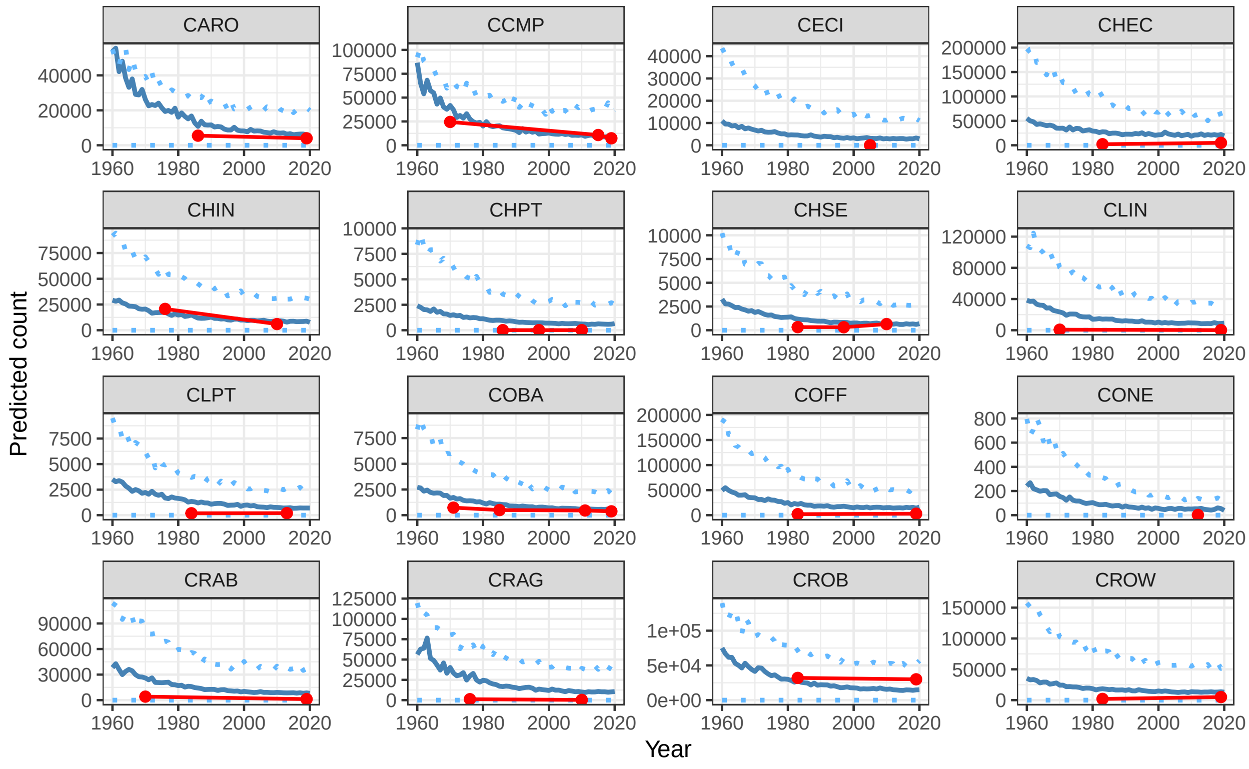
2.5 Marginal model predictions

```r
# This predicts the population average response - i.e., a similar prediction at all sites.
# If you are adding up the individual sites, as Kruger 2023 did to calculate popT,
# then you are adding predictions of the average response every time.
popypred_marg <- data.frame(predict(mc2,
                             newdata=popy,
                             type="response",
                             #marginal=NULL,      # crucial, and not default code.
                             marginal=~us(1 + Zseason_starting):site_id,
                             interval="prediction",
                             posterior="all"))

popy$Zfit_marg = popypred_marg$fit
popy$Zlwr_marg = popypred_marg$lwr
popy$Zupr_marg = popypred_marg$upr

## How accurate are the predictions relative to observed data?

required_n_pages = round(133/16)+1

for(i in 1:required_n_pages){

print(ggplot(data = popy) +
    geom_line(aes(x = season_starting, y = Zfit_marg),
              col = "steelblue", linewidth=1.04) +
    geom_line(aes(x = season_starting, y = Zlwr_marg),
              col = "steelblue1", linetype="dotted", linewidth = 1.02) +
    geom_line(aes(x = season_starting, y = Zupr_marg),
              col = "steelblue1", linetype="dotted", linewidth=1.02) +
    geom_point(data = nestm3, aes(season_starting, y = nests),
               color = "red", cex = 2) +
    geom_line(data = nestm3, aes(season_starting, y = nests),
              color = "red",size=0.8) +
    theme_bw() +
    xlab("Year") +
    ylab("Predicted count") +
  #  theme(strip.text = element_text(size = 1.5)) +
    facet_wrap_paginate(~ site_id, ncol = 4, nrow = 4,
                        page = i,
                        scales = 'free'))}
```

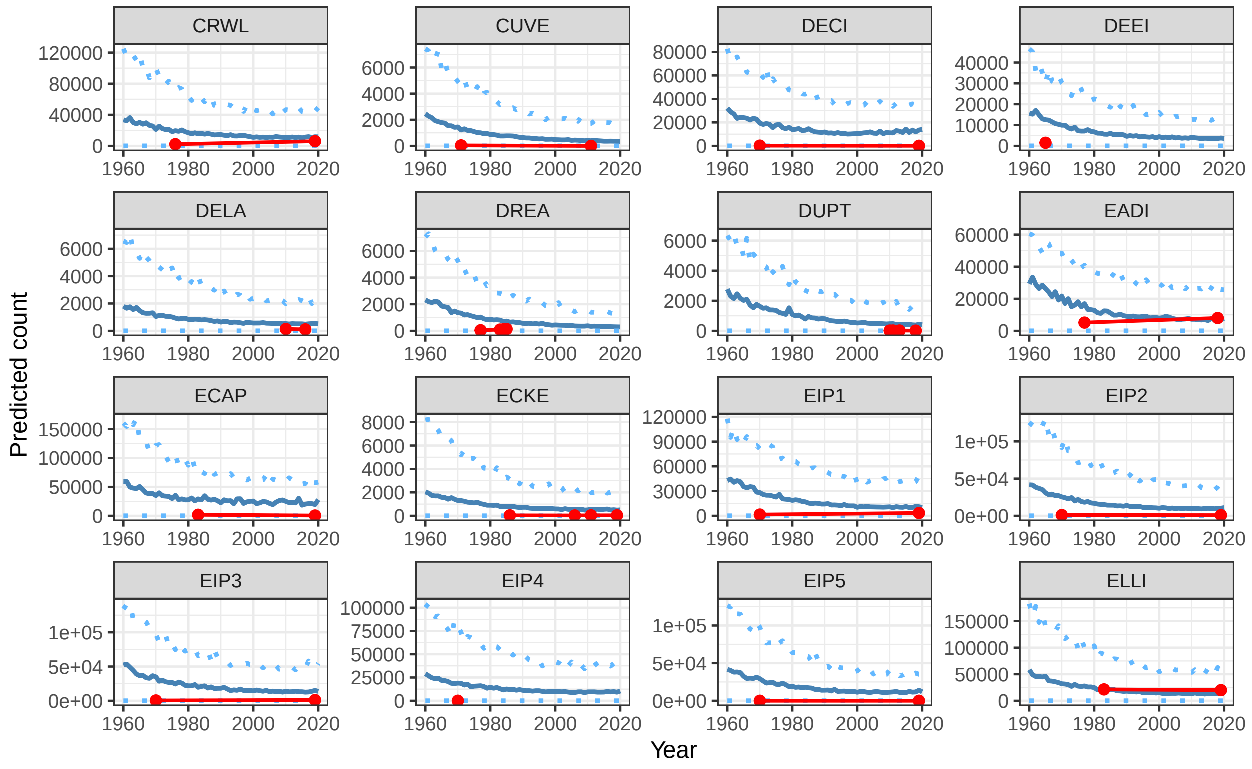
```
## Warning: Using ‘size‘ aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use ‘linewidth‘ instead.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.
```

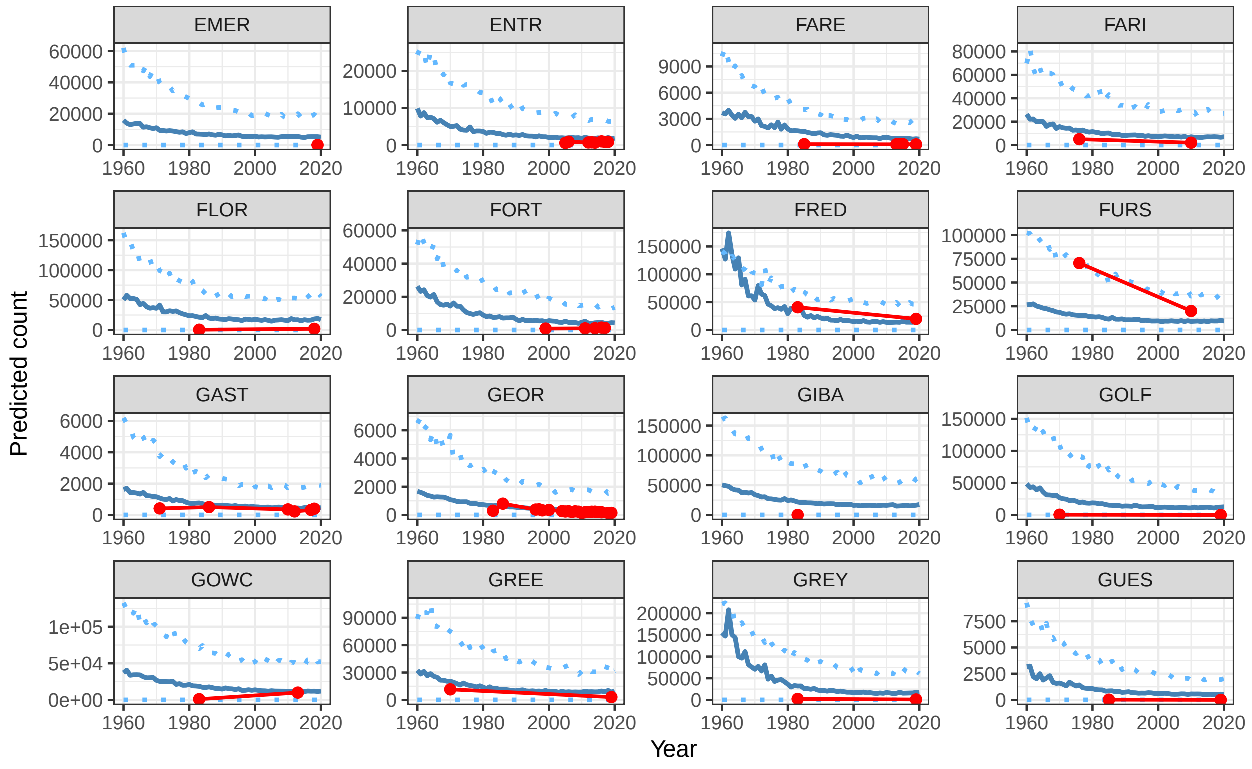


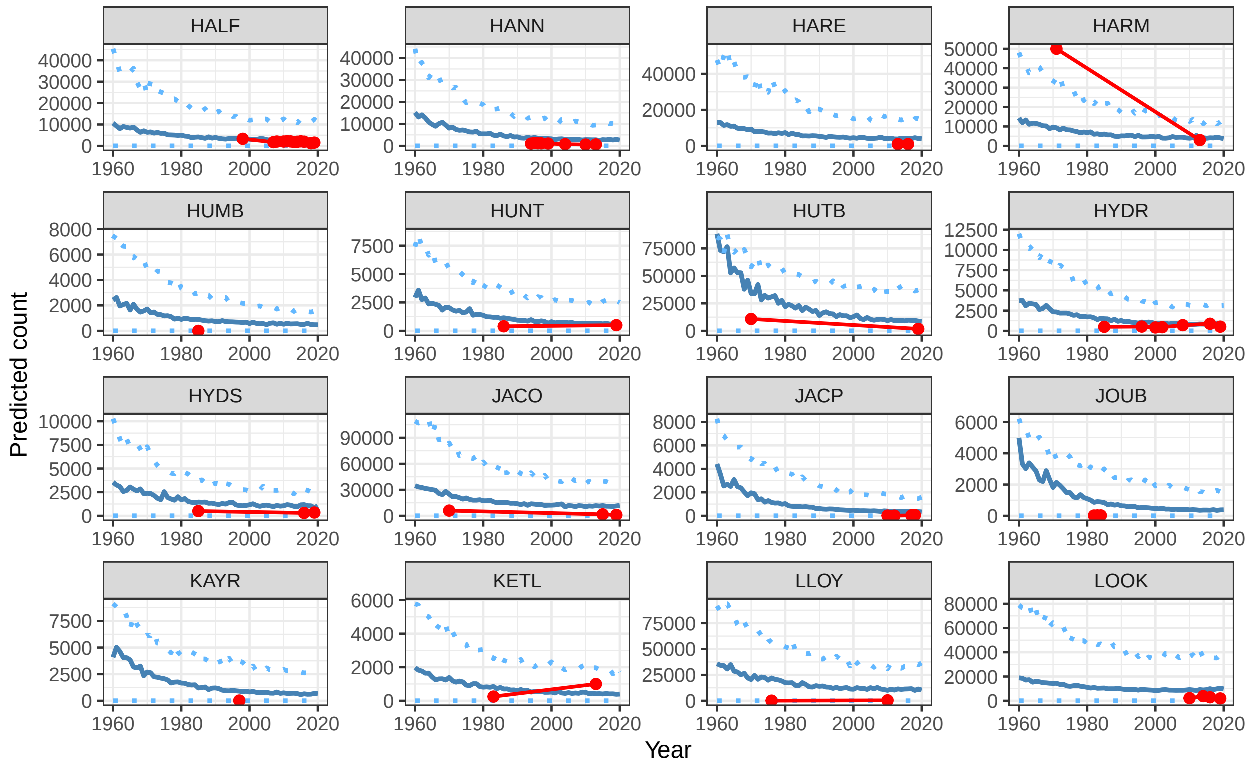
AILS
AITC
AITK
ALCO
AMPH
ANDE
ANVS
ARDL
ARMS
BAIL
BART
BENN
BLAK
BONE
BOWL
BRIT
Predicted count
Year

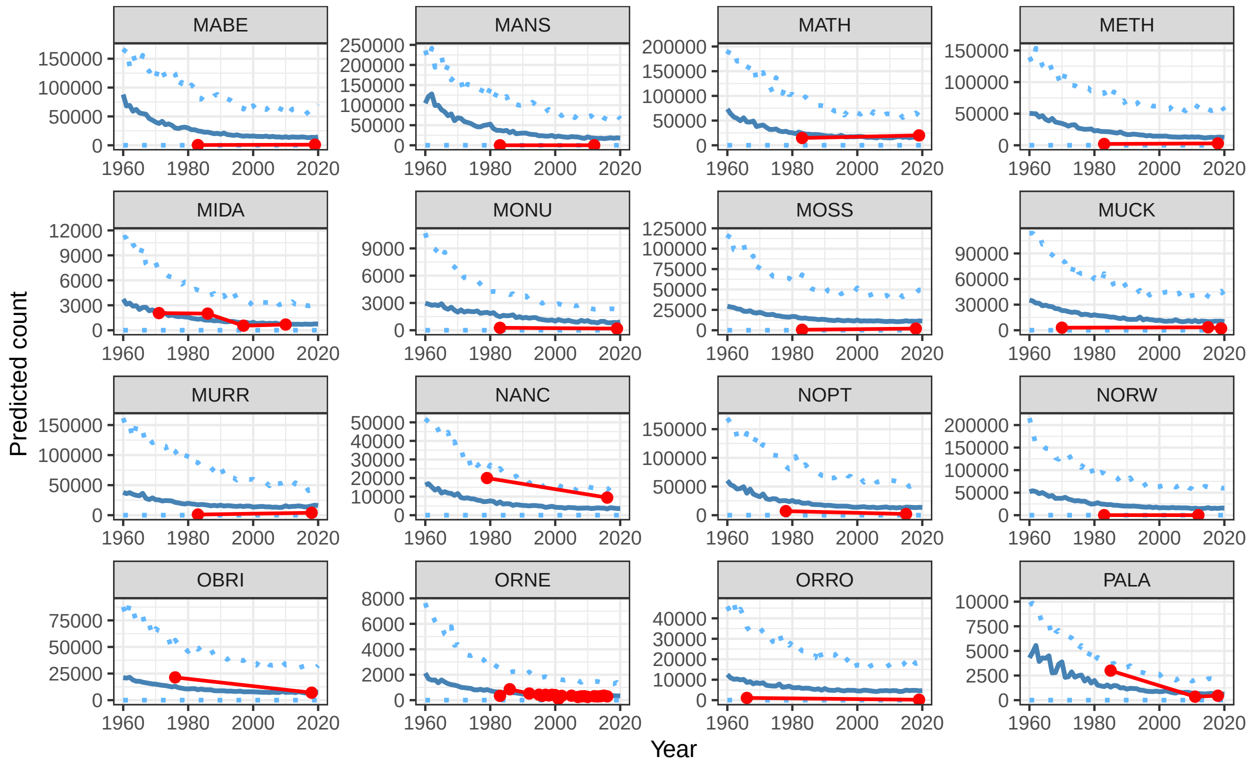


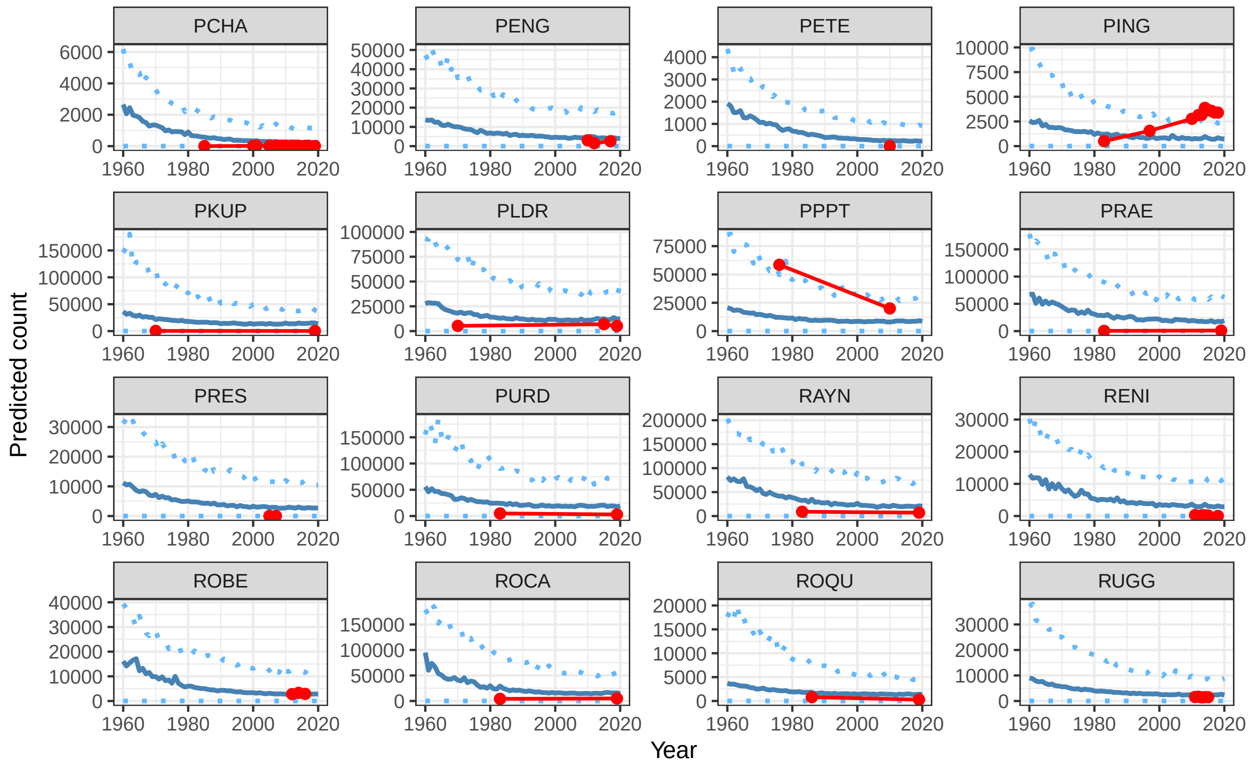
CARO
CCMP
CECI
CHEC
CHIN
CHPT
CHSE
CLIN
CLPT
COBA
COFF
CONE
CRAB
CRAG
CROB
CROW
Predicted count
Year

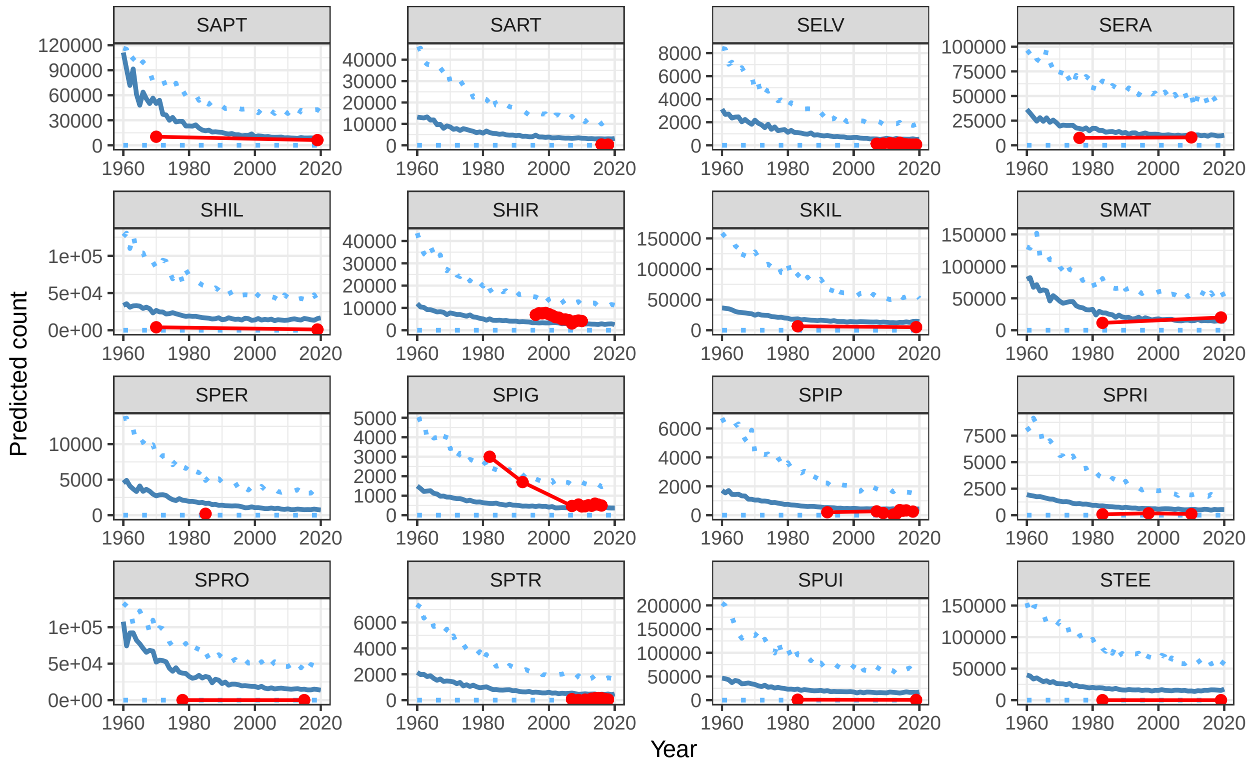

CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

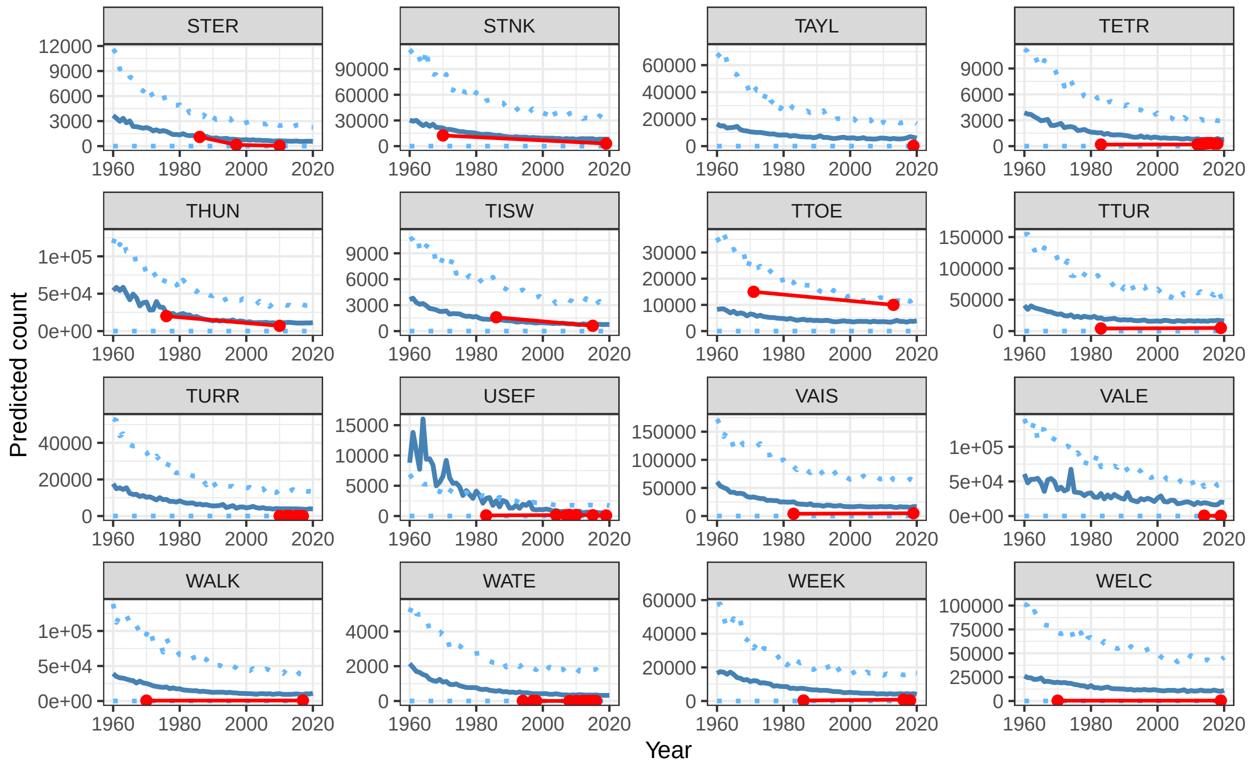

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year


HALF
HANN
HARE
HARM
HUMB
HUNT
HUTB
HYDR
HYDS
JACO
JACP
JOUB
KAYR
KETL
LLOY
LOOK
Predicted count
Year


MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year


PCHA
PENG
PETE
PING
PKUP
PLDR
PPPT
PRAE
PRES
PURD
RAYN
RENI
ROBE
ROCA
ROQU
RUGG
Predicted count
Year
1960
1980
2000
2020


SAPT
SART
SELV
SERA
SHIL
SHIR
SKIL
SMAT
SPER
SPIG
SPIP
SPRI
SPRO
SPTR
SPUI
STEE
Predicted count
Year
1960
1980
2000
2020



2.6 Revised plots of latitude and slope (population change)

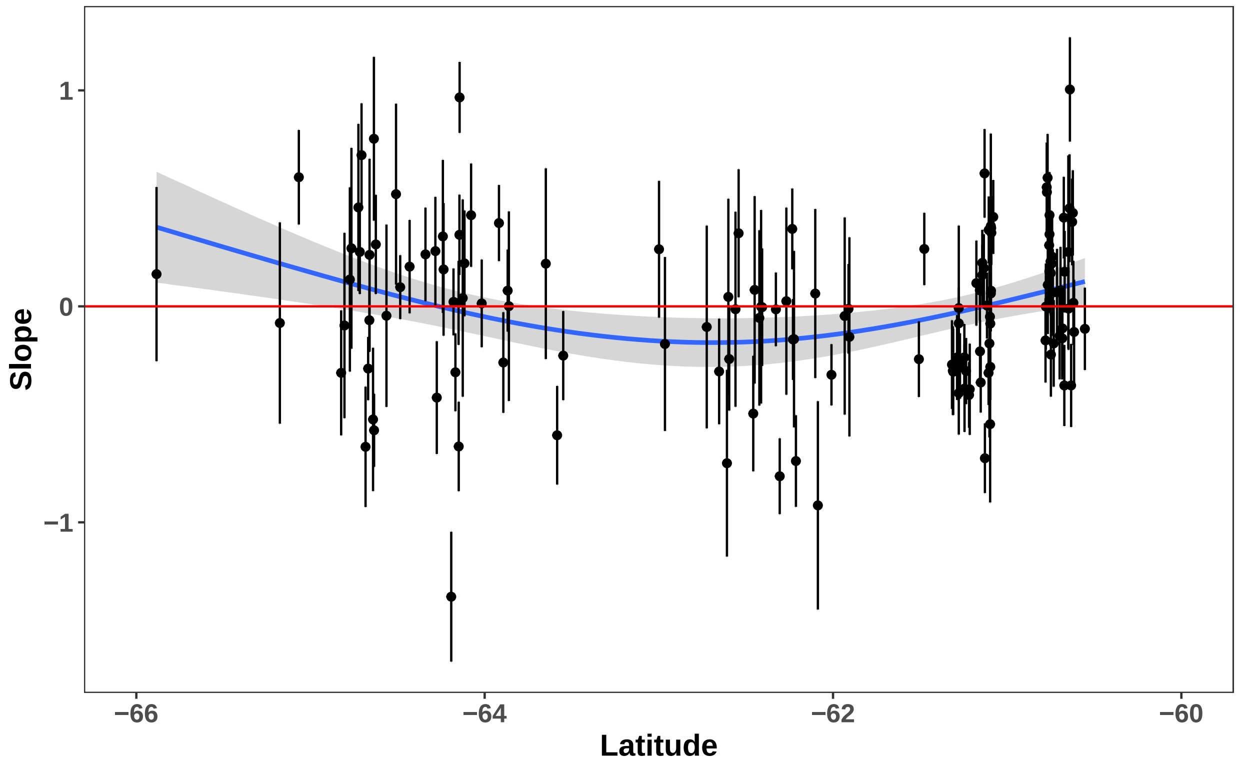
```r
# extract random effects from MCMCglmm
# https://stackoverflow.com/questions/64562052/extract-random-effects-from-mcmcglmm
library(broom.mixed)
re = tidy(mc2, effects="ran_vals")
unique(re$group)
```

```
## [1] "site_id"
```

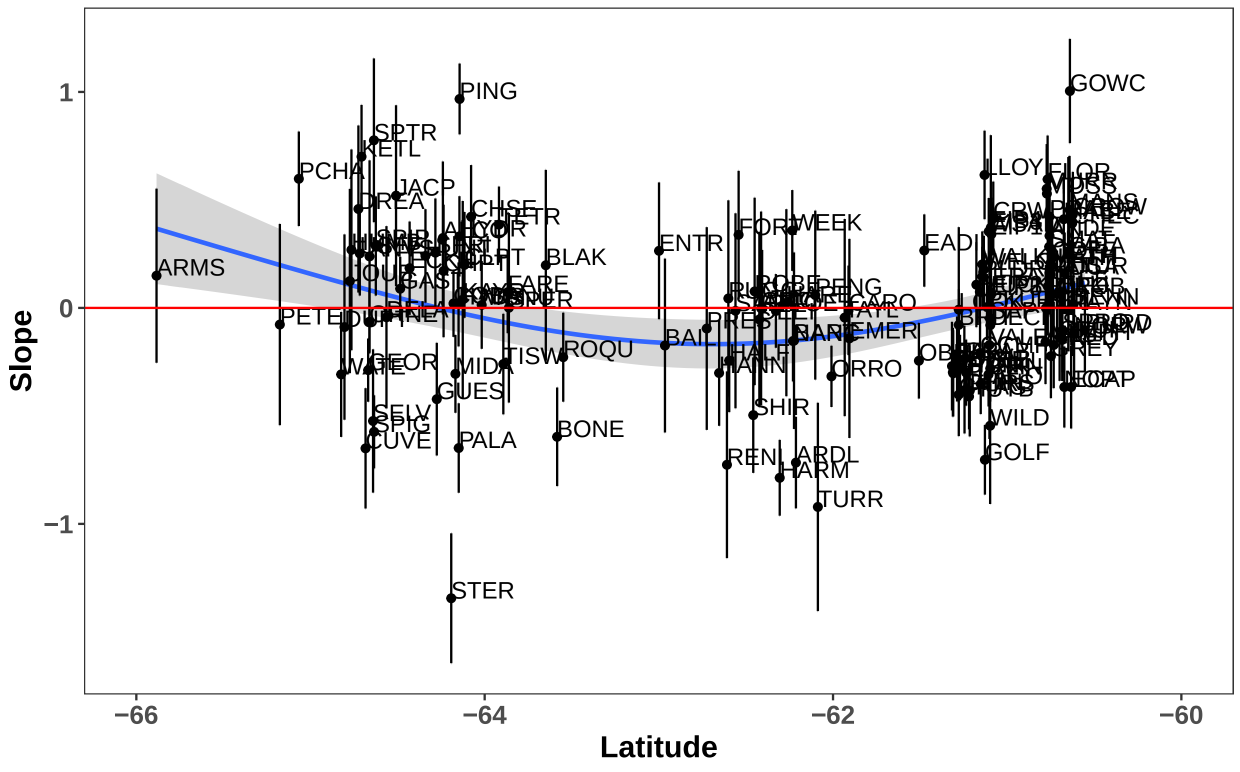
```r
re = re %>%
    dplyr::select(-group, -effect) %>%
    pivot_wider(names_from = term, values_from = c(estimate, std.error))

head(re)
```

```
## # A tibble: 6 x 5
##   level `estimate_(Intercept)` estimate_Zseason_starting `std.error_(Intercept)`
##   <chr>                  <dbl>                     <dbl>                   <dbl>
## 1 AILS                  0.554                   -0.158                     0.337
## 2 AITC                  2.12                    -0.00379                   0.243
## 3 AITK                  0.236                    0.0640                    0.324
## 4 ALCO                  1.97                     0.324                     0.335
## 5 AMPH                  0.0614                  -0.148                     0.339
## 6 ANDE                 -2.74                     0.334                     0.318
## # i 1 more variable: std.error_Zseason_starting <dbl>
```

```r
# estimate_(Intercept) is related to the initial population size
# estimate_Zseason_starting is the slope of population increase (+)
# or decrease (-)

names(re) = c("site_id", "est_int", "estZss",
              "se_int", "seZss")
# add latitude
nestM3_lat = dplyr::select(nestM3, Lat, site_id) %>%
             dplyr::distinct(site_id, Lat)

re = left_join(re, nestM3_lat, by = "site_id")

# plot relationship between slope and latitude

ggplot(data = re, aes(x = Lat, y = estZss))+
  stat_smooth(method="gam",formula=y~s(x,k=2))+
  # geom_smooth(method='lm', formula= y~x)+
  geom_point()+
  geom_errorbar(aes(ymin=estZss-seZss,
                    ymax=estZss+seZss))+
  theme_bw()+th+
  ylab("Slope")+xlim(-66,-60)+
  xlab("Latitude")+
  geom_hline(yintercept=0,
             color = "red")
```



```
ggplot(data = re, aes(x = Lat, y = estZss, label = site_id))+
  stat_smooth(method="gam",formula=y~s(x,k=2))+
  # geom_smooth(method='lm', formula= y~x)+
  geom_point()+
  geom_text(hjust=0, vjust=0) +
  geom_errorbar(aes(ymin=estZss-seZss,
                    ymax=estZss+seZss))+
  theme_bw()+th+
  ylab("Slope")+xlim(-66,-60)+
  xlab("Latitude")+
  geom_hline(yintercept=0,
             color = "red")
```



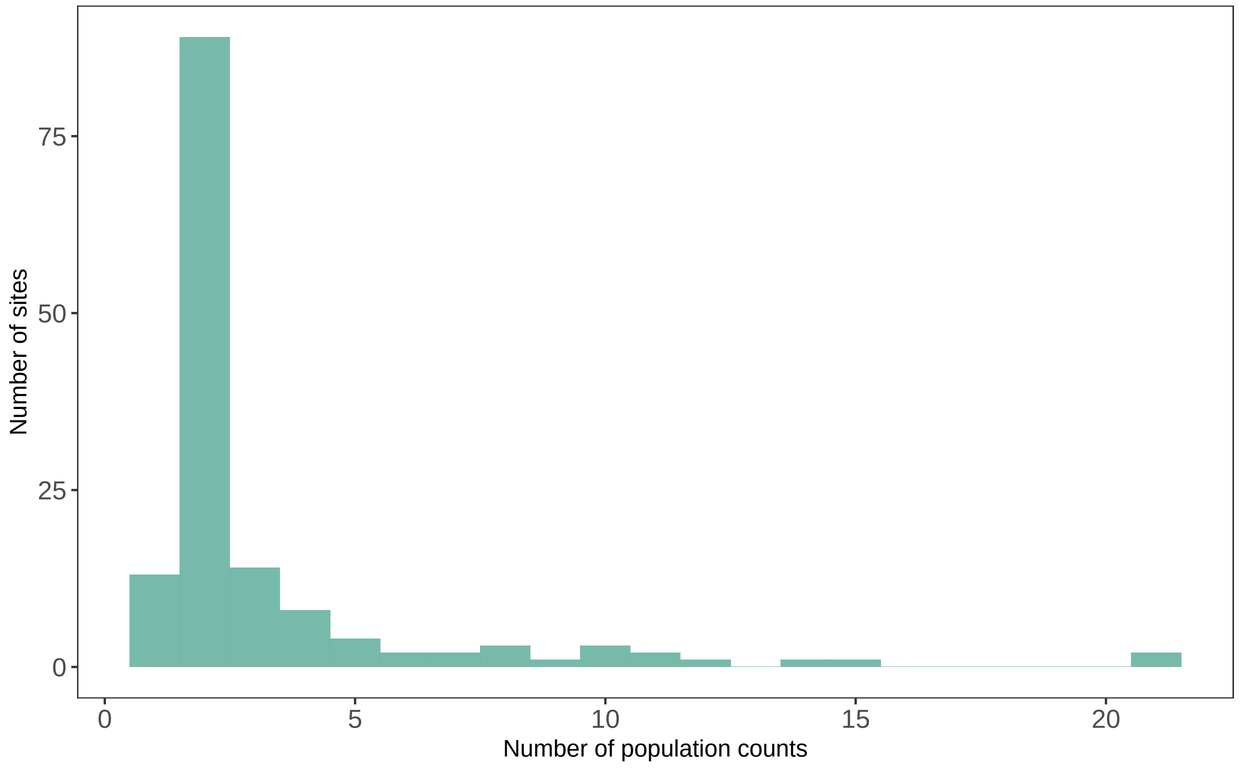
The following figures plot the data from the original study

3 Oosthuizen et al data distribution figures

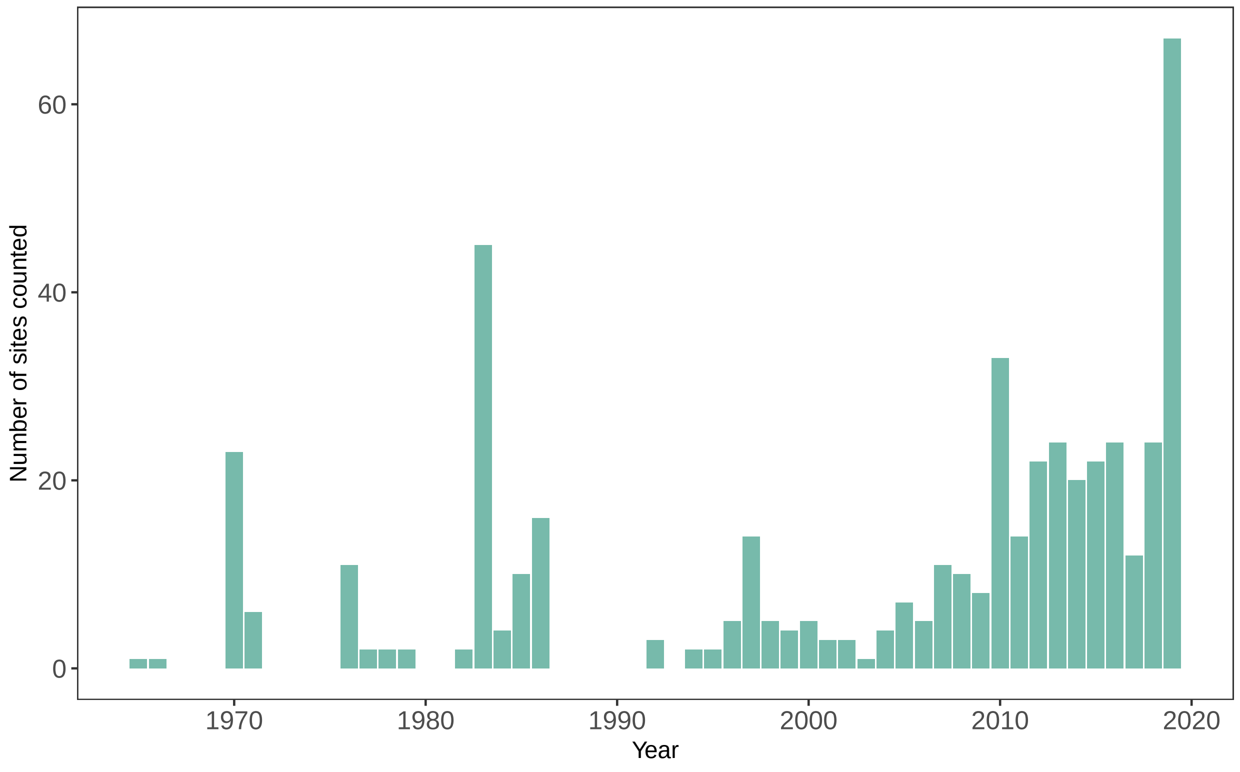
```
# This shows that there are some 1-count sites in the data being analysed
# (n = 146, not n = 133)
samplesize = nestM3 %>% group_by(site_id, ncounts) %>% tally()
length(unique(nestM3$site_id))
```

```
## [1] 146
```

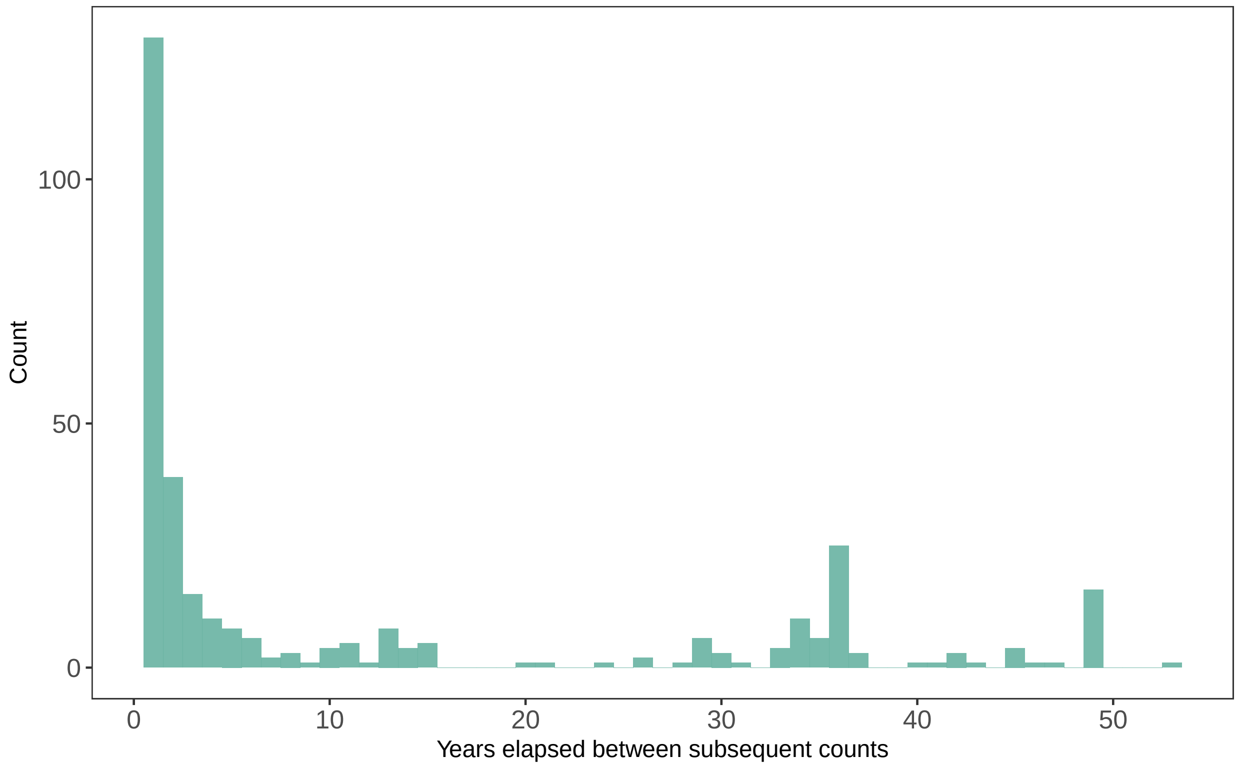
```r
samplesize.plot <- samplesize %>%
  ggplot(aes(x=n)) +
  geom_histogram(binwidth=1, fill="#69b3a2",  alpha=0.9) +
  theme_bw()+
  ylab("Number of sites")+
  xlab("Number of population counts") +
  theme(axis.text=element_text(size=12),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())

samplesize.plot
```



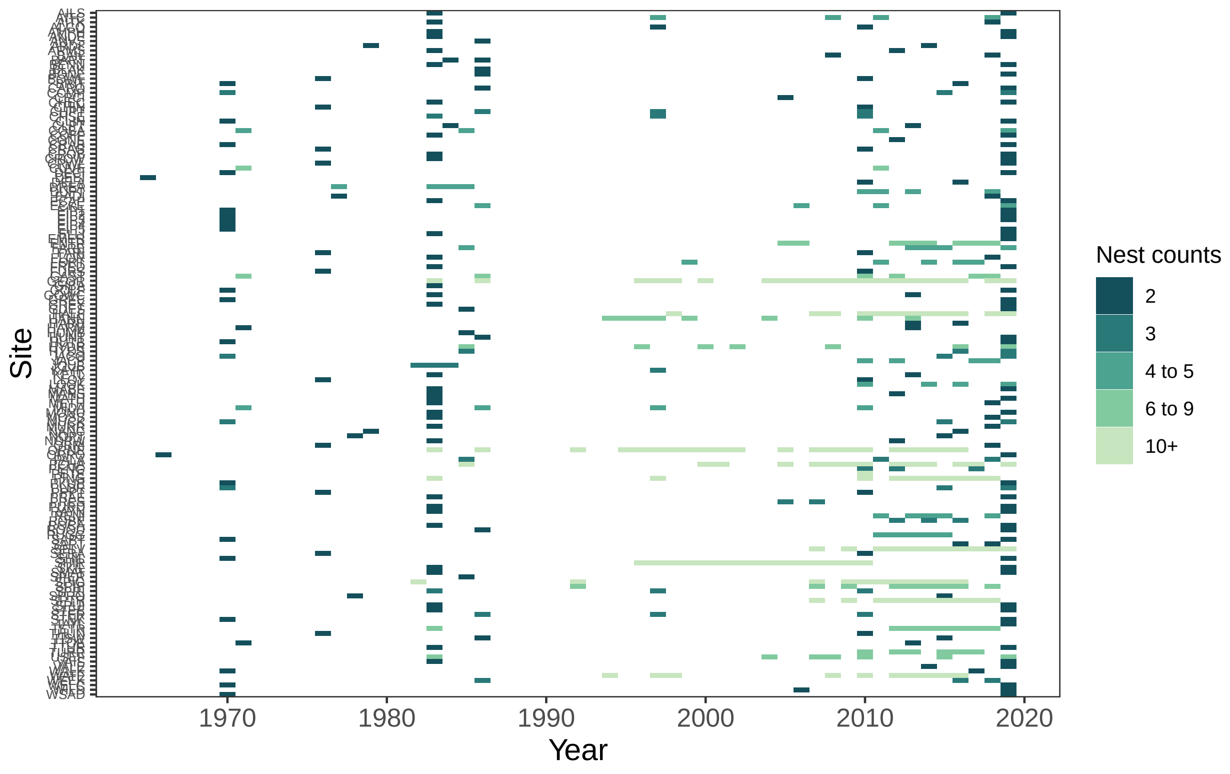
```r
## Save Plot
# pdf("./Figure samplesize.pdf",
#     useDingbats = FALSE, width = 4, height = 4)
# samplesize.plot
# dev.off()

samplesizeYear = nestM3 %>% group_by(season_starting) %>% tally()
#samplesizeYear

samplesizeYear.plot = samplesizeYear %>%
  ggplot(aes(x=season_starting, y = n)) +
  geom_bar(stat = "identity", fill="#69b3a2",  alpha=0.9) +
  theme_bw() +
  ylab("Number of sites counted")+
  xlab("Year") +
  theme(axis.text=element_text(size=12),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())+
  scale_x_continuous(breaks = seq(1960, 2020, by = 10))

samplesizeYear.plot
```



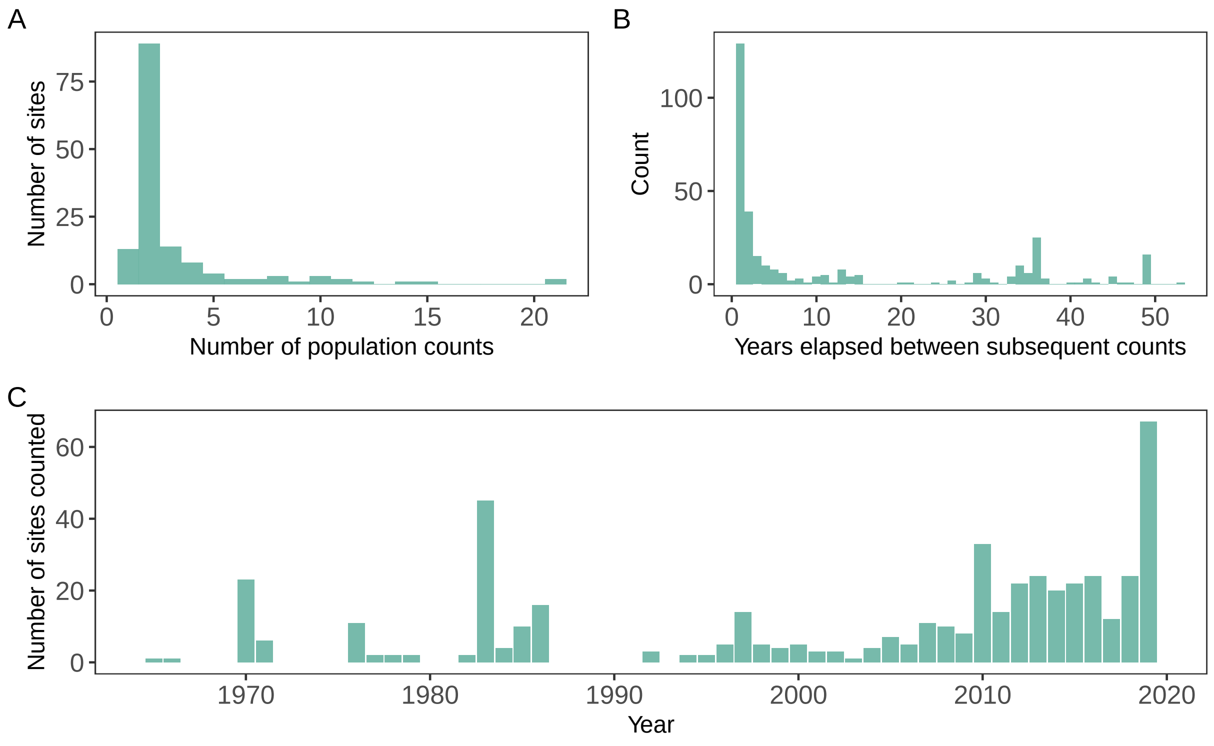
```
## Save Plot
# pdf("./Figure samplesizeYear.pdf",
#     useDingbats = FALSE, width = 6, height = 4)
# samplesizeYear.plot
# dev.off()

# time between counts per site
diff = nestm3 %>%
  dplyr::arrange(site_id, season_starting) %>%
  dplyr::group_by(site_id) %>%
  dplyr::mutate(time.difference = season_starting - lag(season_starting))
#diff

diff.plot = diff %>%
  ggplot(aes(x=time.difference)) +
  geom_histogram(binwidth=1, fill="#69b3a2",  alpha=0.9) +
  theme_bw()+
  ylab("Count")+
  xlab("Years elapsed between subsequent counts") +
  theme(axis.text=element_text(size=12),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())+
  scale_x_continuous(breaks = seq(0, 50, by = 10))

diff.plot
```



```
## Save Plot
# pdf("./Figure timedifferance.pdf",
#     useDingbats = FALSE, width = 6, height = 4)
# diff.plot
# dev.off()

library(colorspace)
library(scales)

nestm3$countbreaks = cut(nestm3$ncounts, c(0, 2, 3, 5, 9, Inf))

heat = ggplot(nestm3, aes(x = as.numeric(season_starting),
                   y = site_id,
                   fill= cut(ncounts, c(0, 2, 3, 5, 9, Inf),
                             labels = c('2','3','4 to 5','6 to 9','10+')))) +
  geom_tile() +
  scale_fill_discrete_sequential(palette = "BluGrn", rev = F)+
  guides(fill=guide_legend(title="Nest counts")) +
  theme_bw()+
  ylab("Site")+
  xlab("Year") +
  theme(axis.text.x=element_text(size=12),
        axis.title.x=element_text(size=14),
        axis.text.y = element_text(size = 6),
        axis.title.y=element_text(size=14),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank())+
  scale_x_continuous(breaks = seq(1960, 2020, by = 10))+
  scale_y_discrete(limits=rev)

heat
```



```
## Save Plot
# pdf("./Figure samplesize_heat.pdf",
#     useDingbats = FALSE, width = 7, height = 8)
# heat
# dev.off()

library(patchwork)
combinedfig = (samplesize.plot | diff.plot) / samplesizeYear.plot +
  plot_layout(nrow = 2, widths = c(1, 3)) +
  plot_annotation(tag_levels = 'A')
combinedfig
```



```
## Save Plot
# pdf("./figures/Figure combined.pdf",
#      useDingbats = FALSE, width = 8, height = 6)
#   combinedfig
#   dev.off()
```

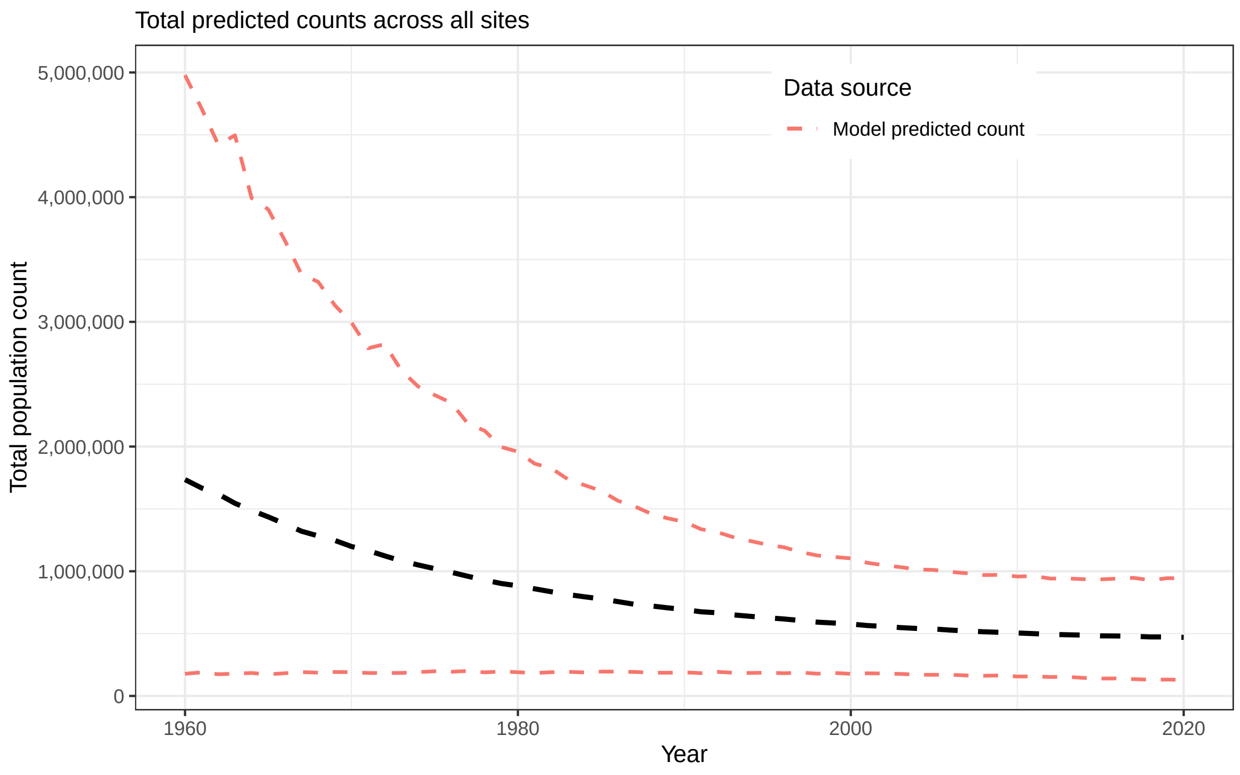
4 Oosthuizen et al - population change:

How many penguins were there, per year, across all sites? We don't know this from counts, as we only have intermittent counts. Estimate and plot the total population size predicted per year (how many penguins were there in all populations?)

```
head(popy)
```

```
##   site_id    Lat season_starting nests Zseason_starting     ZLat minyear
## 1    AILS -60.78            1960     0      -2.76247100 1.365378    1983
## 2    AILS -60.78            1988     0      -0.97734640 1.365378    1983
## 3    AILS -60.78            1965     0      -2.44369875 1.365378    1983
## 4    AILS -60.78            1970     0      -2.12492650 1.365378    1983
## 5    AILS -60.78            1975     0      -1.80615425 1.365378    1983
## 6    AILS -60.78            2003     0      -0.02102965 1.365378    1983
##   maxyear      Zfit Zlwr  Zupr Zfit_marg Zlwr_marg Zupr_marg
## 1    2019 10686.768 1436 24457  43594.28         2    161105
## 2    2019  5802.043 1866 11310  15768.98         3     61786
## 3    2019  9639.242  962 21828  35380.12         2    137438
## 4    2019  8450.036 1378 18253  28326.87         1    107576
## 5    2019  7611.752 1968 16277  23647.49         1     81882
## 6    2019  4461.350 1694  8276  13905.43         3     50014
```

```
pop_predict = popy %>%
              dplyr::group_by(season_starting) %>%
              dplyr::summarise(total_pred = sum(Zfit),
                       min_pred = sum(Zlwr),
                       max_pred = sum(Zupr))

pop_predict.p = ggplot(data = pop_predict) +
 geom_line(aes(x = season_starting, y = total_pred),
          lty = 2, linewidth = 1.1)+
  geom_line(aes(x = season_starting, y = min_pred,
             color = "Model predicted count"), lty = 2, size = 0.8)+
  geom_line(aes(x = season_starting, y = max_pred,
             color = "Model predicted count"), lty = 2, size = 0.8)+
  labs(x = "Year", y = "Total population count") +
  theme_bw()+
  scale_y_continuous(label = comma)+
  labs(subtitle = "Total predicted counts across all sites")+
  guides(color=guide_legend(title="Data source"))+
  theme(legend.position = c(0.7, 0.9))

pop_predict.p
```



```
delta.y = 100 * (pop_predict[61,2] - pop_predict[1,2]) / pop_predict[1,2]
delta.y
```

```
##   total_pred
## 1  -72.91479
```

5 Predicting population change with entire posterior distribution

Calculate population change over a 30 year period (~ 3 generations according to the original study)

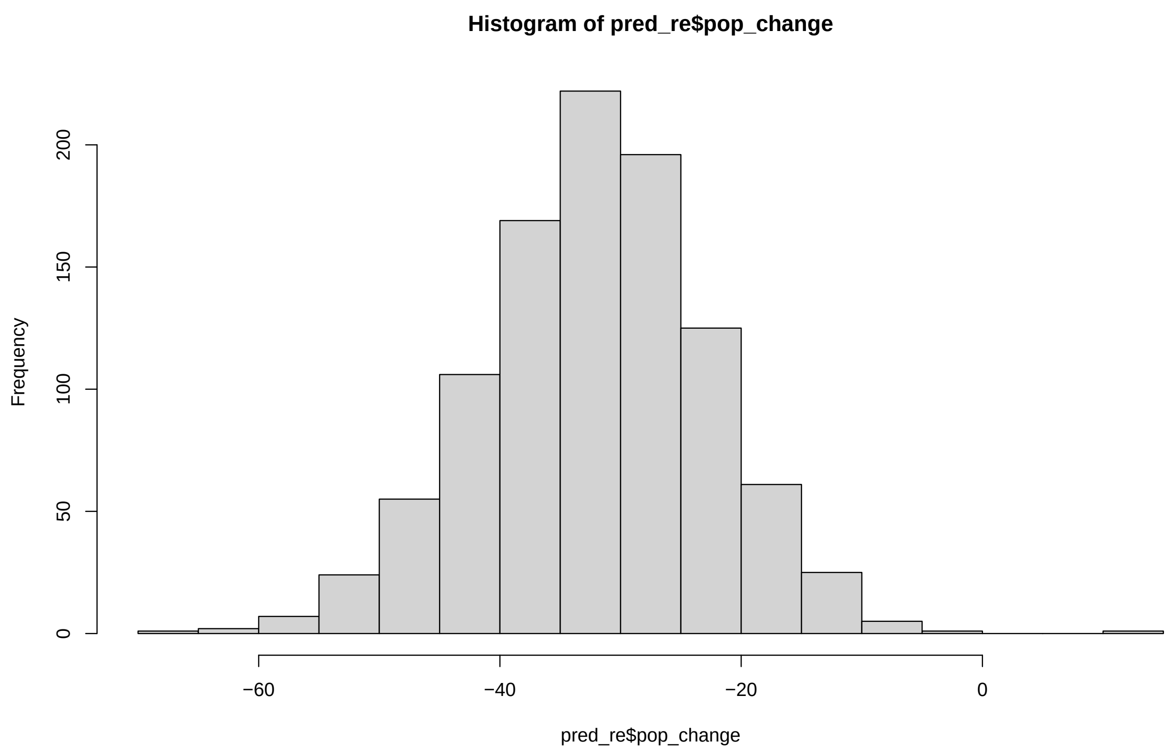
```
# extract posterior draws of fixed effects and random effects
posterior <- as.matrix(mc2$Sol)

# collect site-level information
site_and_lat <- nestM3 %>%
  as_tibble() %>%
  select(site_id, ZLat) %>%
  distinct()

site_and_lat
```

```
## # A tibble: 146 x 2
##    site_id  ZLat[,1]
##    <chr>       <dbl>
##  1 AILS      1.37
##  2 AITC      0.349
##  3 AITK      1.39
##  4 ALCO     -0.797
##  5 AMPH      1.43
##  6 ANDE      1.38
##  7 ANVS     -1.06
##  8 ARDL      0.470
##  9 ARMS     -1.82
## 10 BAIL      0.000141
## # i 136 more rows
```

```
# map years which to predict to (standardised scale)
# Here, the first year is 1990 and the last year is 2020 (30 year change)

year1 = 1990
year2 = 2019

first_year <- (year1 - mean(df$year)) / sd(df$year)
last_year <- (year2 - mean(df$year)) / sd(df$year)

# define function to predict with or without random effects
get_predictions <- function(posterior,
                            site_and_lat,
                            first_year,
```

```r
                            last_year,
                            use_random_effects = FALSE) {
# matrices for predictions at each site in year 1 (1990) and year 2 (2020)
# each row is a prediction from a different posterior sample, each column is a site
pred_pop_per_site.first <- matrix(NA, nrow = nrow(posterior), ncol = nrow(site_and_lat))
pred_pop_per_site.last <- matrix(NA, nrow = nrow(posterior), ncol = nrow(site_and_lat))

for (s in 1:nrow(posterior)) {
  theta <- posterior[s,]
  for (j in 1:nrow(site_and_lat)) {
    site_id <- site_and_lat$site_id[j]
    ZLat <- site_and_lat$ZLat[j]

    # predict pop at site j in first year
    lin_pred <- theta["(Intercept)"] +
      theta["Zseason_starting"] * first_year +
      theta["ZLat"] * ZLat +
      theta["Zseason_starting:ZLat"] * first_year * ZLat
    if (use_random_effects) {
      lin_pred <- lin_pred +
        theta[ str_c("(Intercept).site_id.",site_id) ] +
        theta[ str_c("Zseason_starting.site_id.",site_id) ] * first_year
    }
    pred_pop_per_site.first[s,j] <- exp( lin_pred )

    # predict pop at site j in last year
    lin_pred <- theta["(Intercept)"] +
      theta["Zseason_starting"] * last_year +
      theta["ZLat"] * ZLat +
      theta["Zseason_starting:ZLat"] * last_year * ZLat
    if (use_random_effects) {
      lin_pred <- lin_pred +
        theta[ str_c("(Intercept).site_id.",site_id) ] +
        theta[ str_c("Zseason_starting.site_id.",site_id) ] * last_year
    }
    pred_pop_per_site.last[s,j] <- exp( lin_pred )
  }
}

# sum over sites for population level predictions
pred_pop.first <- rowSums(pred_pop_per_site.first)
pred_pop.last <- rowSums(pred_pop_per_site.last)

# percent change from year1 to year2
pred_pop_change <- 100 * ( pred_pop.last - pred_pop.first ) / pred_pop.first

# outputs
predictions <- list(pop_per_site.first = pred_pop_per_site.first,
                    pop_per_site.last = pred_pop_per_site.last,
                    pop.first = pred_pop.first,
                    pop.last = pred_pop.last,
                    pop_change = pred_pop_change)
predictions
```

```
}


# Make predictions with and without random effects
pred_re <- get_predictions(posterior, site_and_lat, first_year, last_year,
                           use_random_effects = TRUE)

# Plot histogram of population change using random effects in prediction:
hist(pred_re$pop_change, breaks = 20)
```

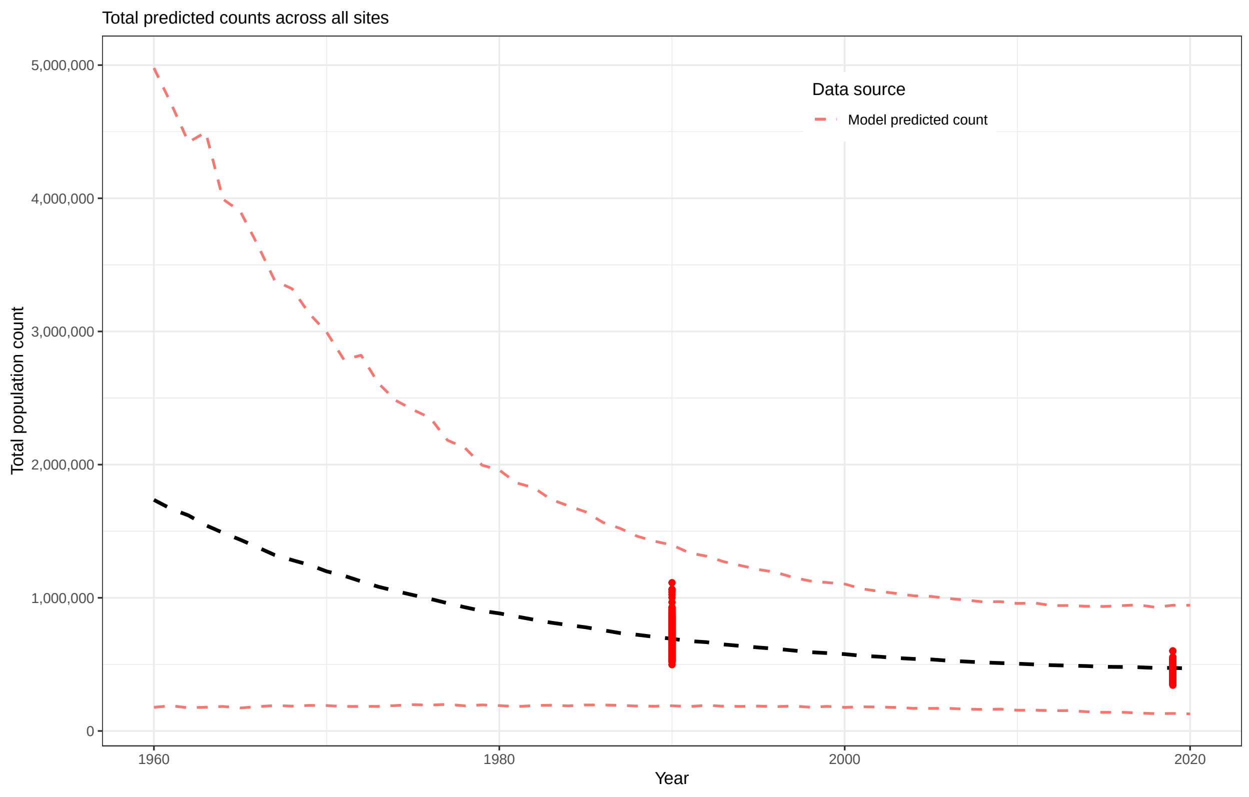


```
# can calculate the probability that the population has decreased by
# at least thirty percent with
mean(pred_re$pop_change < -30)
```

```
## [1] 0.586
```

```
# estimated population size in year1 (with random effects)
pred_first = as.data.frame(pred_re$pop.first)
names(pred_first) = "pred_first"
#hist(pred_first$pred_first, breaks = 20)

# estimated population size in year2 (with random effects)
pred_last = as.data.frame(pred_re$pop.last)
names(pred_last) = "pred_last"
#hist(pred_last$pred_last, breaks = 20)
```

```r
#---------------------------------------------------------------------------
# pred_no_re <- get_predictions(posterior, site_and_lat, first_year, last_year,
#                                use_random_effects = FALSE)
#
# # Plot histogram of population change without random effects in prediction:
# hist(pred_no_re$pop_change, breaks = 20)
#
# # estimated population size in year1 (no random effects)
# pred_first_noRE = as.data.frame(pred_no_re$pop.first)
# names(pred_first_noRE) = "pred_first"
#
# # estimated population size in year2 (no random effects)
# pred_last_noRE = as.data.frame(pred_no_re$pop.last)
# names(pred_last_noRE) = "pred_last"
#---------------------------------------------------------------------------
pop_predict.p +
  geom_point(data = pred_first, aes(x = year1, y = pred_first), col = "red") +
  geom_point(data = pred_last, aes(x = year2, y = pred_last), col = "red")
```


Total predicted counts across all sites
Data source
Model predicted count
Total population count
Year