Decreasing trends of chinstrap penguin breeding colonies in a region of major and ongoing environmental change: a statistical critique and reanalysis of Krüger (2023)

Reanalysis of Krüger (2023)

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2023-10-05

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 fully reproducible R code for that study's analyses. We use that code here to replicate the original results. In addition, we provide additional analyses that cautions that the analyses 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:

```
# Humphries et al. (2017) Mapping Application for Penguin Populations
# and Projected Dynamics (MAPPD): 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
```

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

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

```
# 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.

```
# 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 = 0.196
## 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.

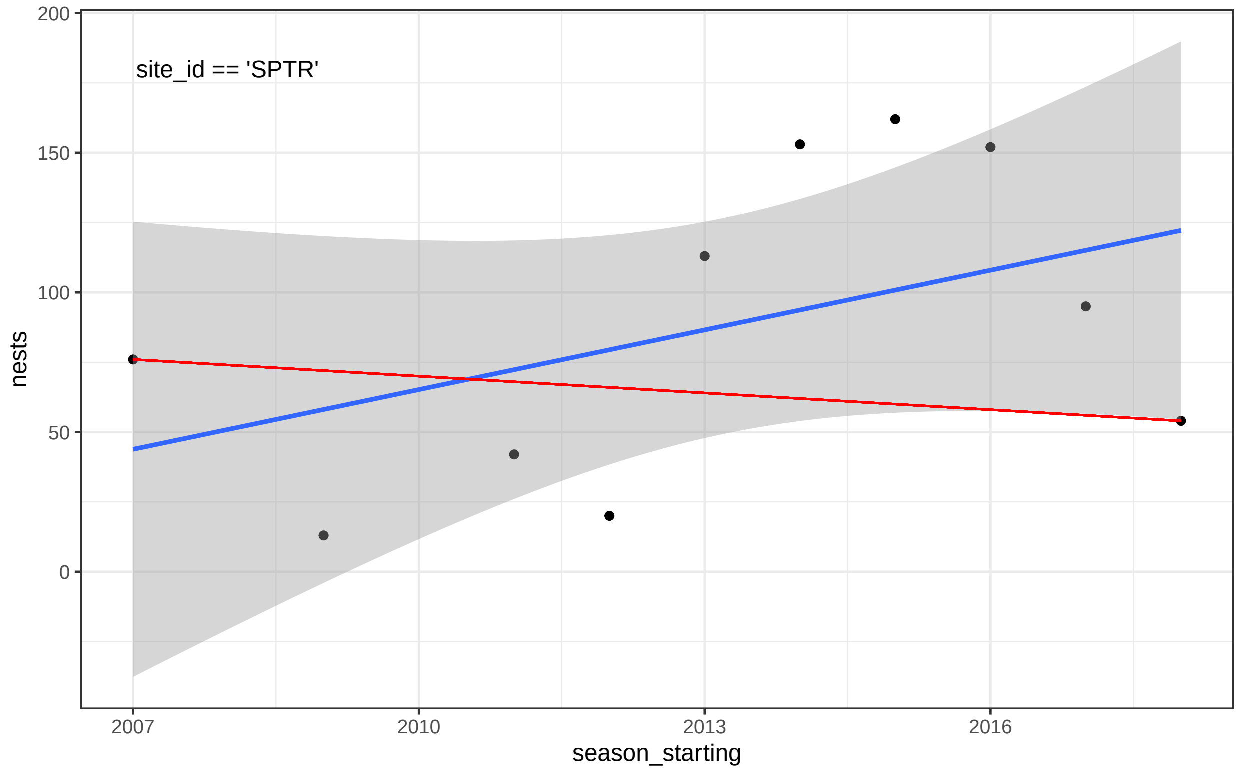
1.3 Calculate the mean slope of the decrease per site (glm)

```
# 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

```
# 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)
```

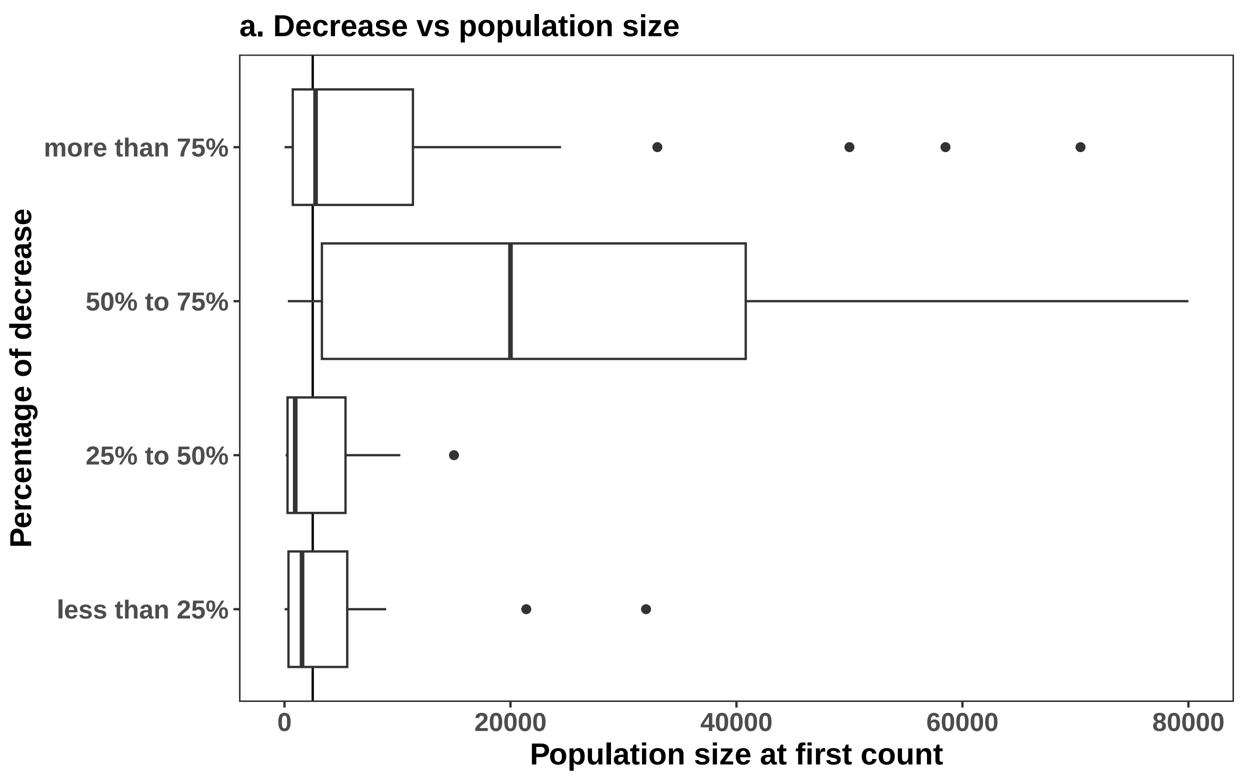
```r
decr$decrCat[decr$PercDecr<=25]<-"less than 25%"
decr$decrCat[decr$PercDecr>25 & decr$PercDecr<=50]<-"25% to 50%"
decr$decrCat[decr$PercDecr>50 & decr$PercDecr<=75]<-"50% to 75%"
# WCO: CODING ERROR / BUG. SELECTS >55 %, NOT 75%
decr$decrCat[decr$PercDecr>55]<-"more than 75%"
decr$decrCat<-factor(decr$decrCat,levels=c("less 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
```

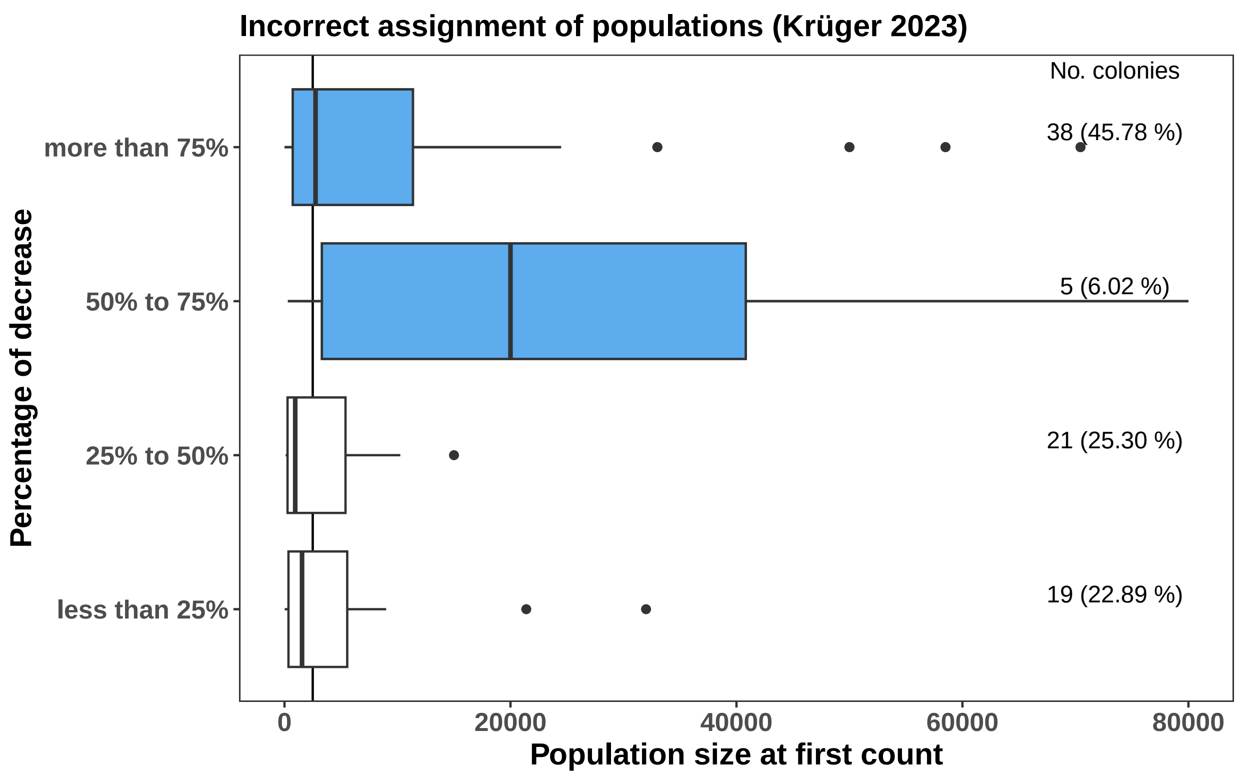
```r
sum(n$N) # check number of pops
```

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

```r
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 (Krüger 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

```
# 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
```

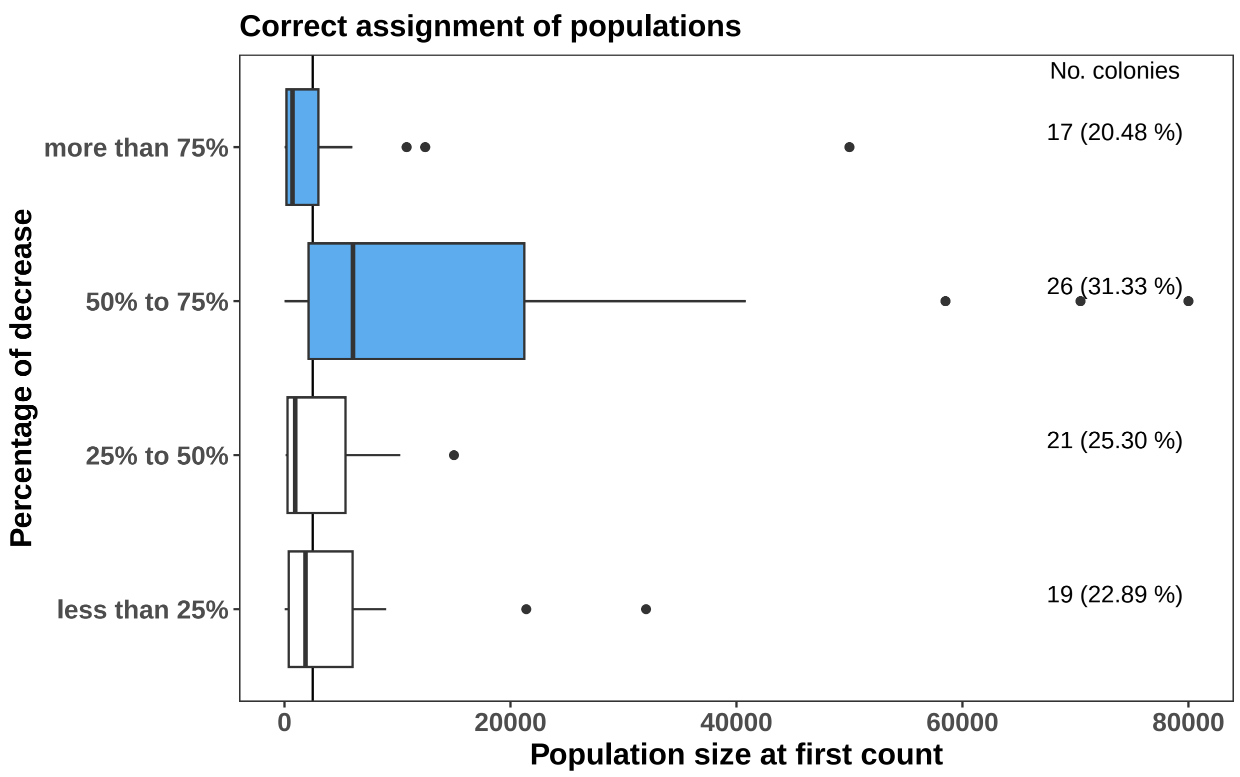
```
#sum(n$N) # check number of pops

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
```



```
# 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

```
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 = 0.000365
##
##                        MCMC iteration = 1000
##
##  Acceptance ratio for liability set 1 = 0.223979
##
##                        MCMC iteration = 2000
##
##  Acceptance ratio for liability set 1 = 0.286367
##
##                        MCMC iteration = 3000
##
##  Acceptance ratio for liability set 1 = 0.312578
##
##                        MCMC iteration = 4000
##
##  Acceptance ratio for liability set 1 = 0.324109
##
##                        MCMC iteration = 5000
##
##  Acceptance ratio for liability set 1 = 0.323727
##
##                        MCMC iteration = 6000
##
##  Acceptance ratio for liability set 1 = 0.324180
##
##                        MCMC iteration = 7000
##
##  Acceptance ratio for liability set 1 = 0.324311
##
```

```
##                         MCMC iteration = 8000
##
##  Acceptance ratio for liability set 1 = 0.324415
##
##                         MCMC iteration = 9000
##
##  Acceptance ratio for liability set 1 = 0.323468
##
##                         MCMC iteration = 10000
##
##  Acceptance ratio for liability set 1 = 0.324480
##
##                         MCMC iteration = 11000
##
##  Acceptance ratio for liability set 1 = 0.324106
##
##                         MCMC iteration = 12000
##
##  Acceptance ratio for liability set 1 = 0.324086
##
##                         MCMC iteration = 13000
##
##  Acceptance ratio for liability set 1 = 0.324186
```

```
# Note: low ESS for random effects. Random effect ESS was 25-27 in Krüger (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: 4790.432
##
##  G-structure:  ~us(1 + Lat):site_id
##
##                                  post.mean  l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id  939.6276  0.009028 3306.796    15.71
## Lat:(Intercept).site_id           15.7108 -0.023500   53.630    15.96
## (Intercept):Lat.site_id           15.7108 -0.023500   53.630    15.96
## Lat:Lat.site_id                    0.2636  0.001010    0.874    16.22
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     0.295   0.2523   0.3477     1000
##
##  Location effects: nests ~ season_starting
##
##                 post.mean  l-95% CI  u-95% CI eff.samp  pMCMC
## (Intercept)     27.713764 21.159681 35.907070     1000 <0.001 ***
## season_starting -0.010426 -0.014592 -0.007267     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
```

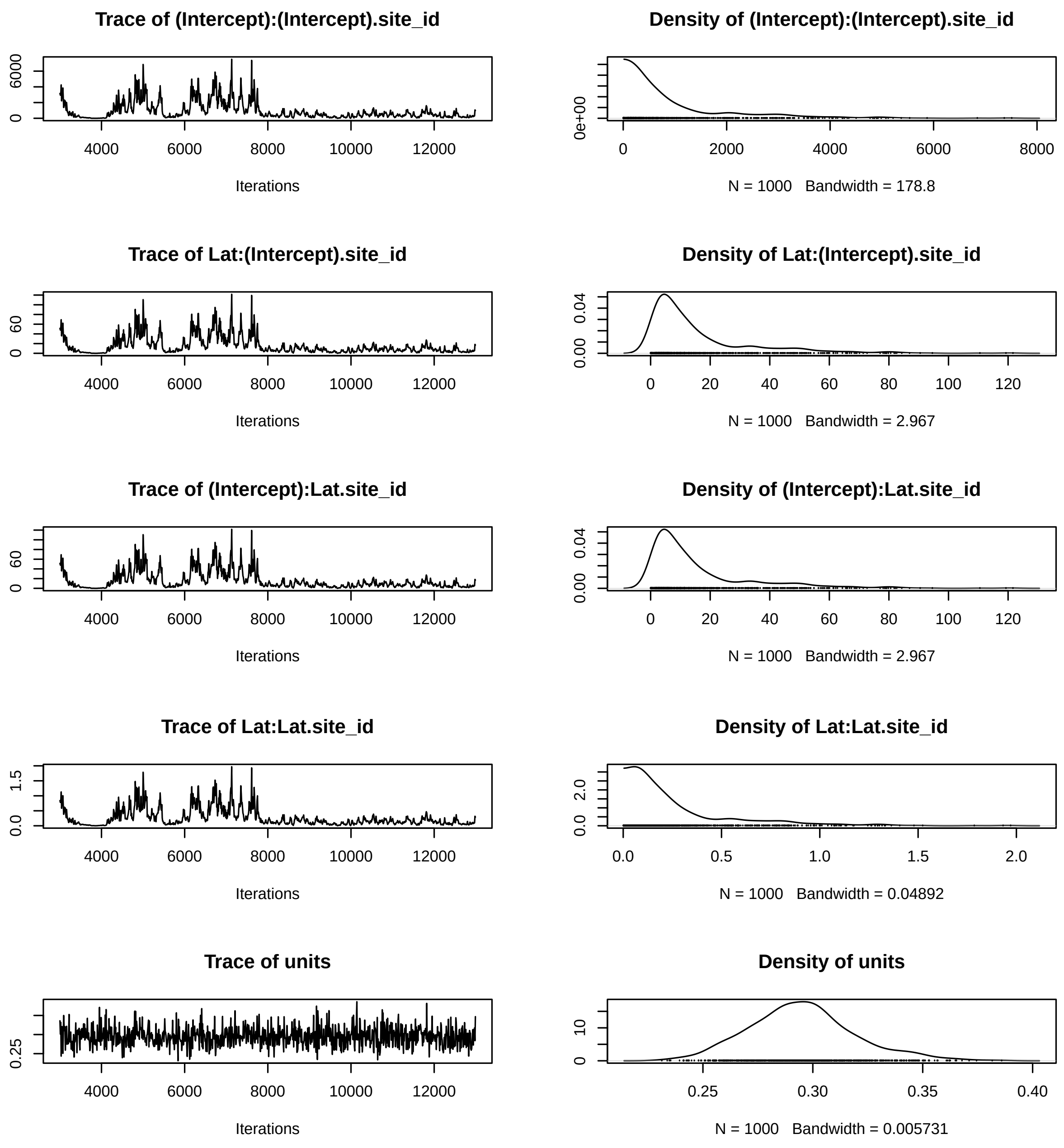
```r
length(unique(nestM3$site_id))
```

```
## [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
##                         15.71393                        15.95647
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                         15.95647                        16.22088
##                            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   -0.004623070
## Lag 50   -0.031880224
## Lag 100   0.019790683
## Lag 500   0.006792074
```

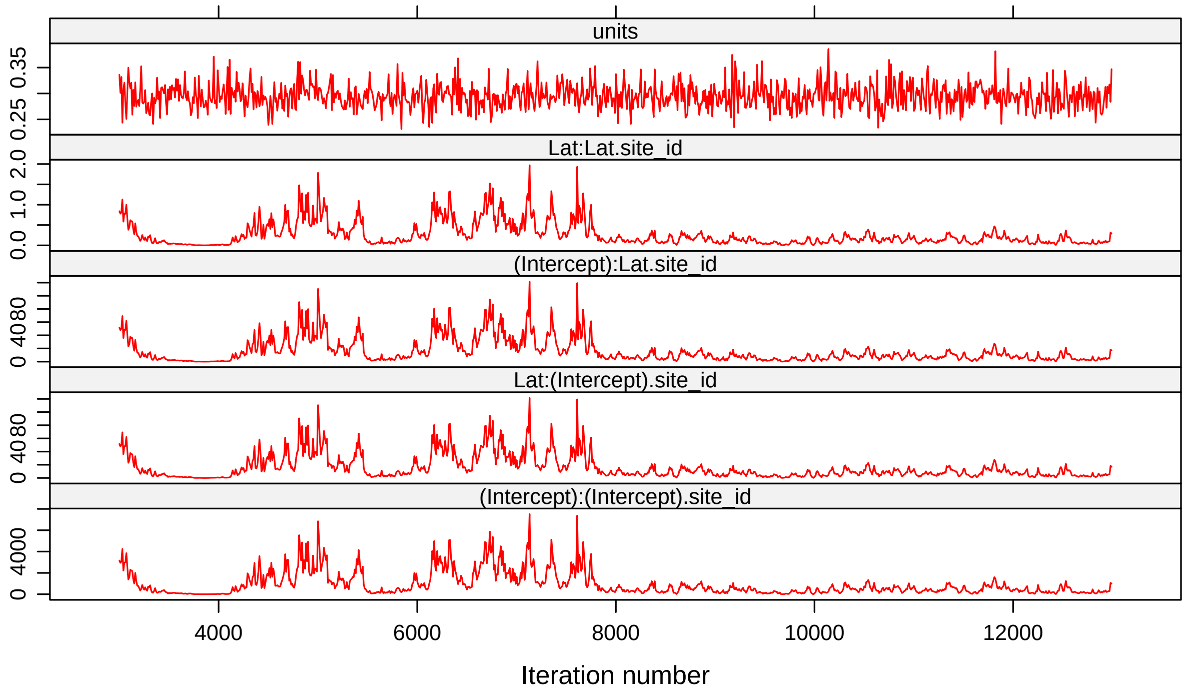
```
# from MCMC Course notes (page 60):
diag(autocorr(mc1$VCV)[2, , ])   # very high autocorrelation
```

```
## (Intercept):(Intercept).site_id         Lat:(Intercept).site_id
##                       0.83333754                      0.83045129
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                       0.83045129                      0.82731156
##                            units
##                       0.00837808
```

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

```
## (Intercept):(Intercept).site_id         Lat:(Intercept).site_id
##                         15.71393                        15.95647
##         (Intercept):Lat.site_id                 Lat:Lat.site_id
##                         15.95647                        16.22088
##                            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)

```
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. 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)

```
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

# WCO: Add lower and upper prediction intervals to the data used for inference
popy$lwr<-popypred$lwr
popy$upr<-popypred$upr
```

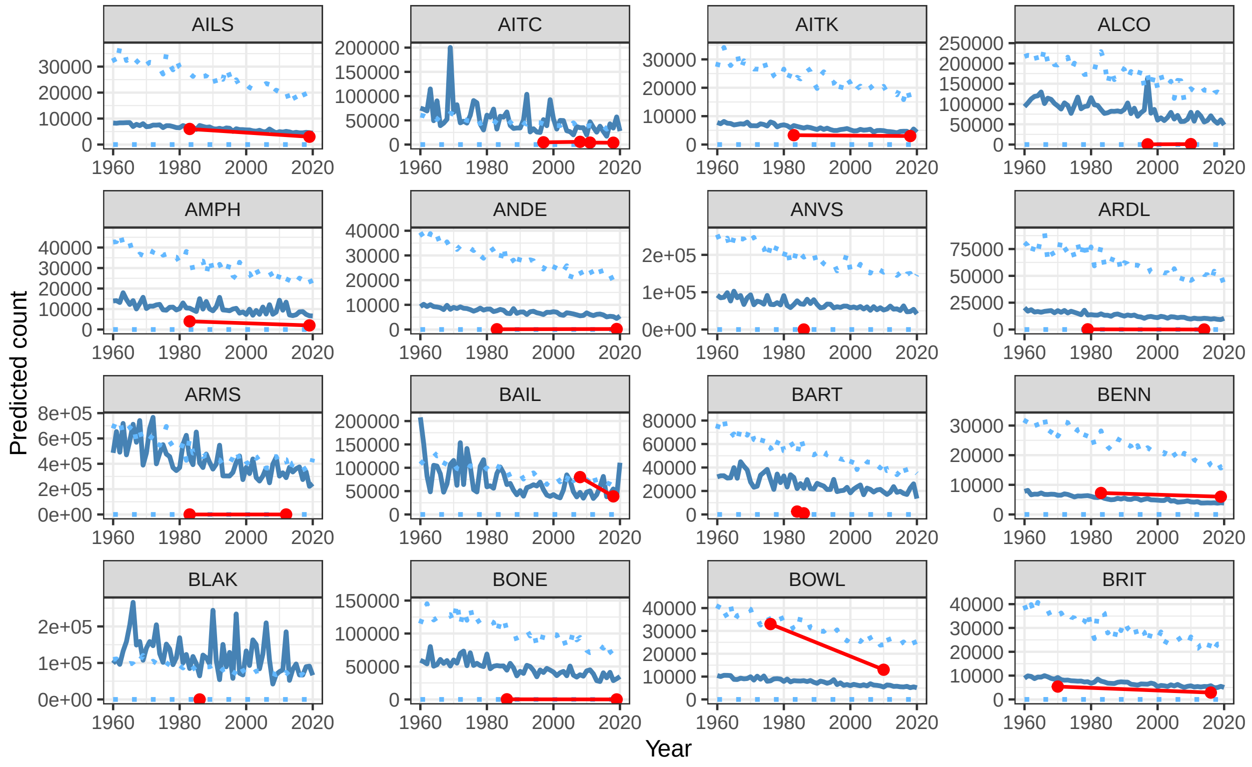
The prediction above contains a high degree of uncertainty, which was ignored in Krüger (2023). The uncertainty is the lwr and upr columns, which is the Highest Posterior Density intervals, I believe, from coda::HPDinterval. https://rdrr.io/cran/MCMCglmm/src/R/predict.MCMCglmm.R*

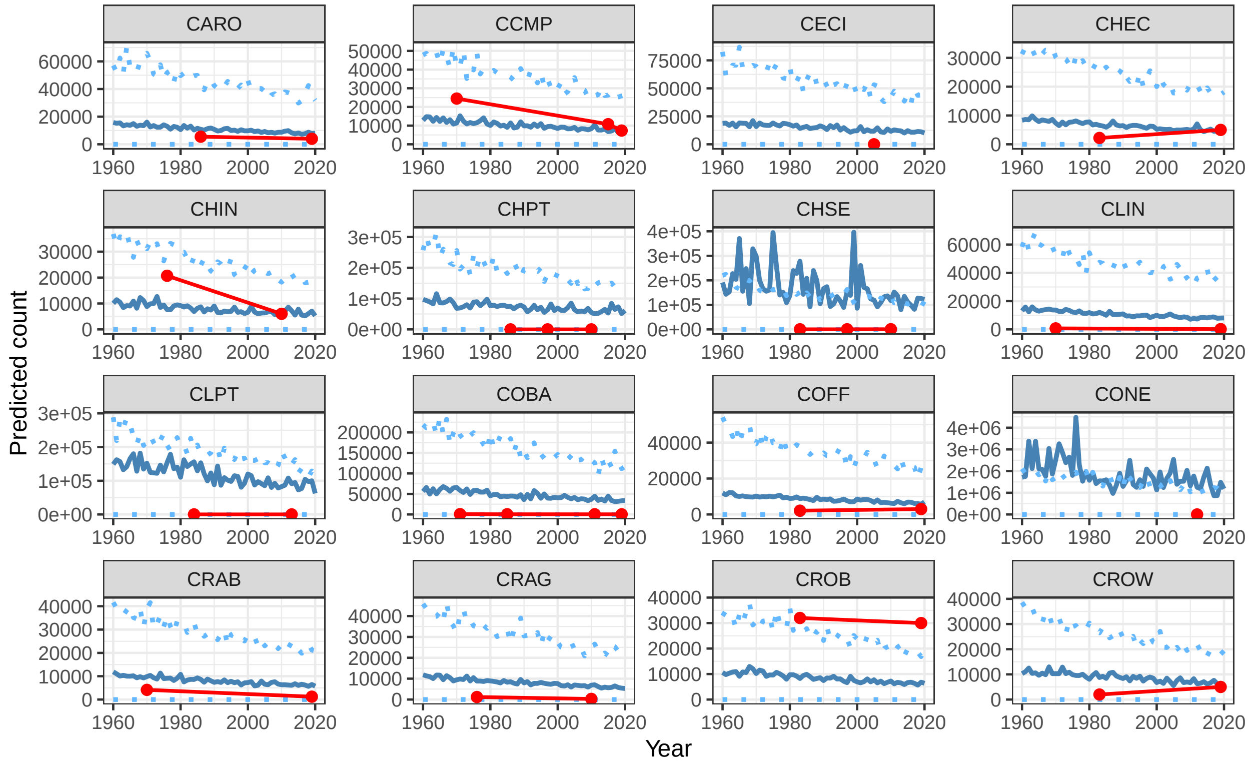
Here, the syntax marginal=mc1*Random*formula was used. This means random effects were marginalized (see simulation study). posterior="mean" also should not be used, but rather posterior="all".

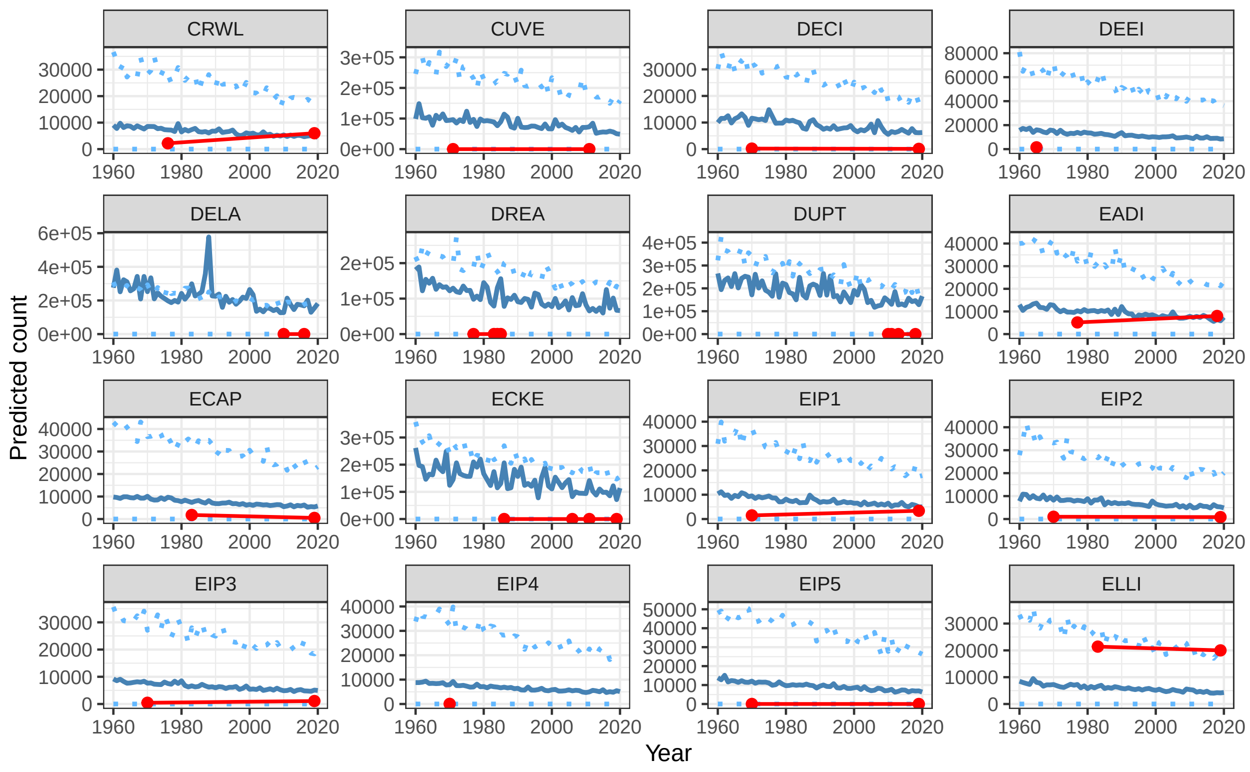
1.14 How accurate are the predictions relative to observed data?

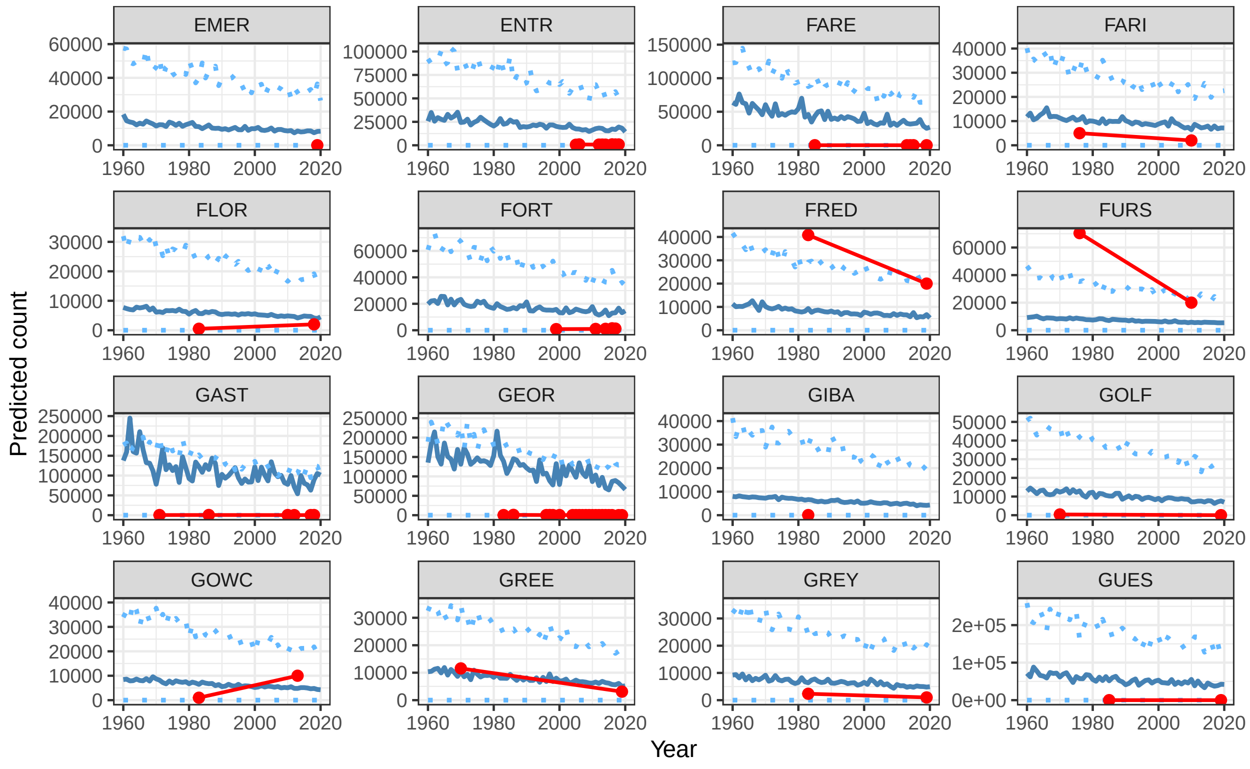
Let us plot the observed data against predicted data, per site, to see whether observed data and predicted data agree.

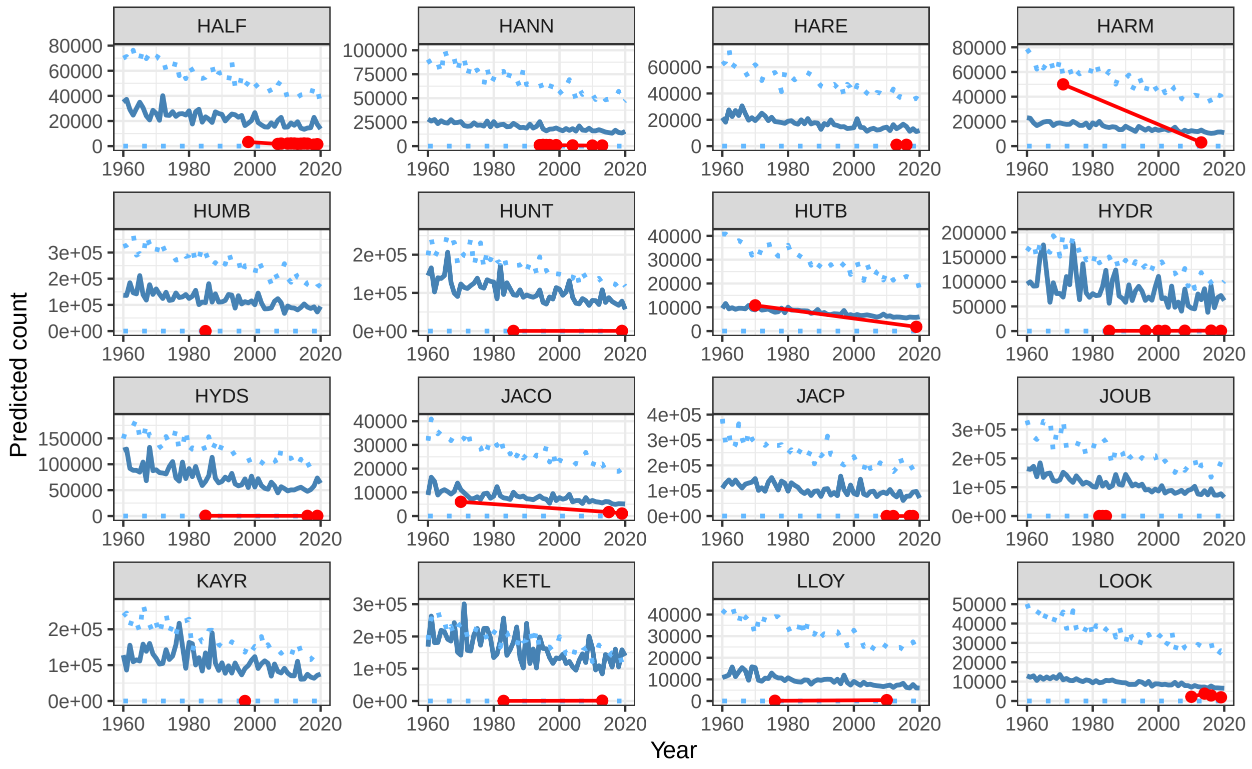
```r
required_n_pages = round(133/16)+1

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'))}
```



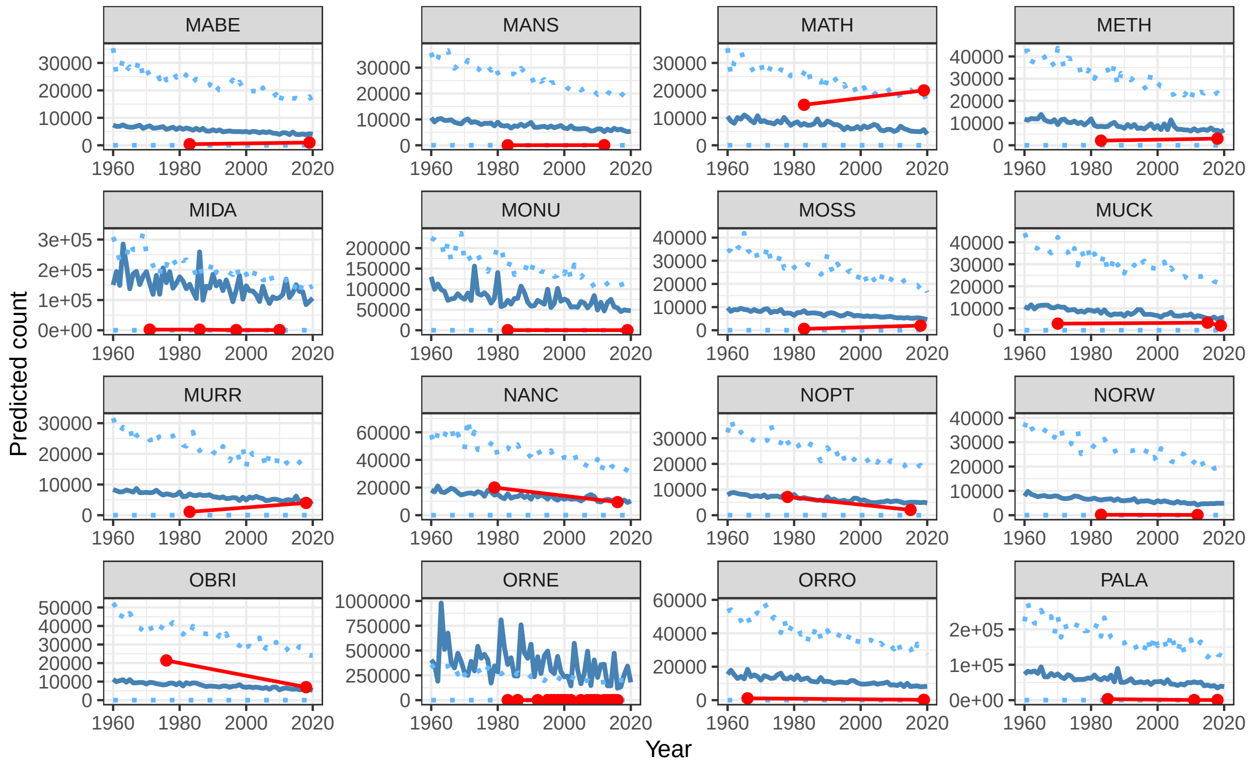



CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

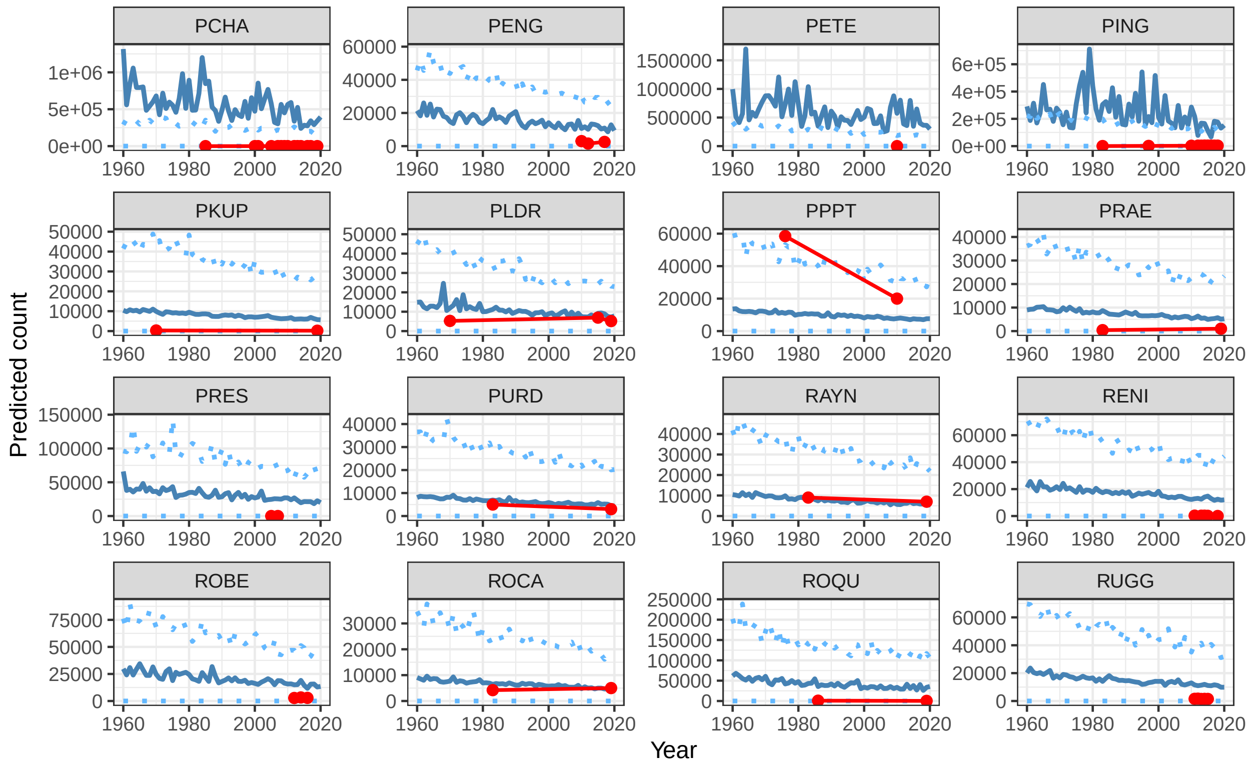

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year

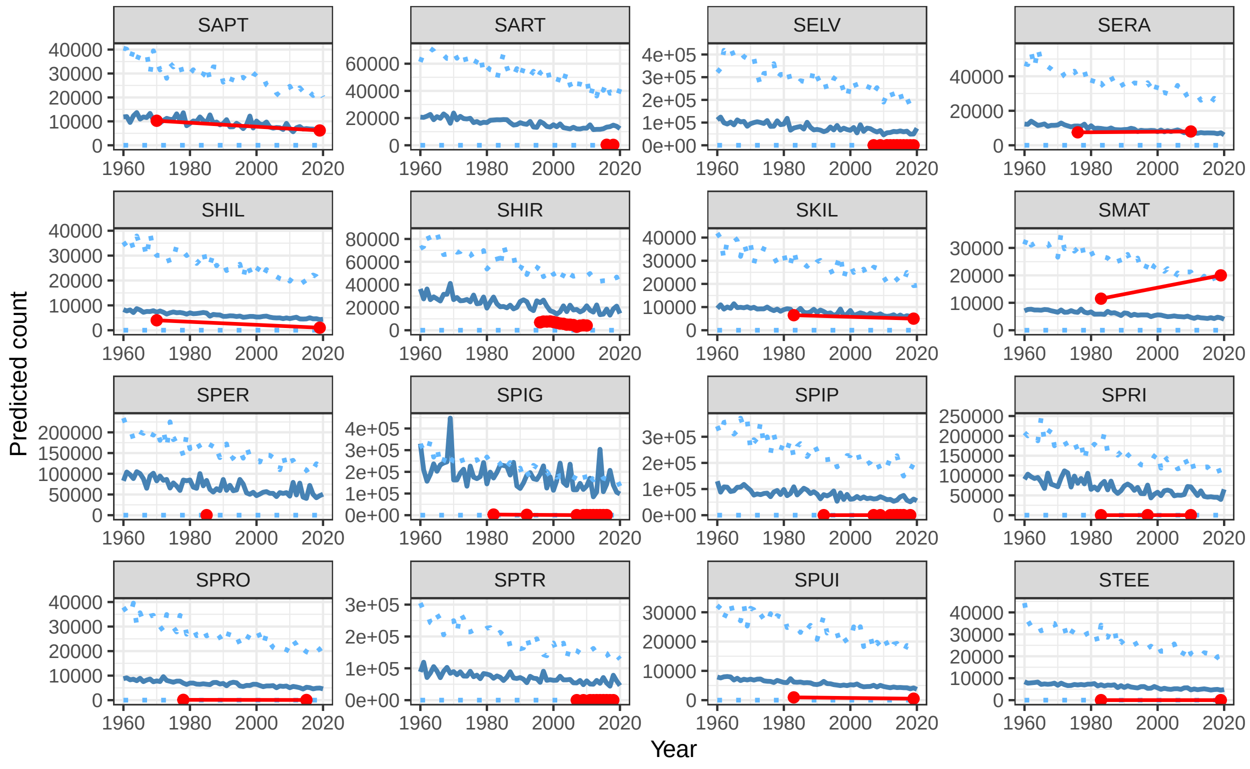


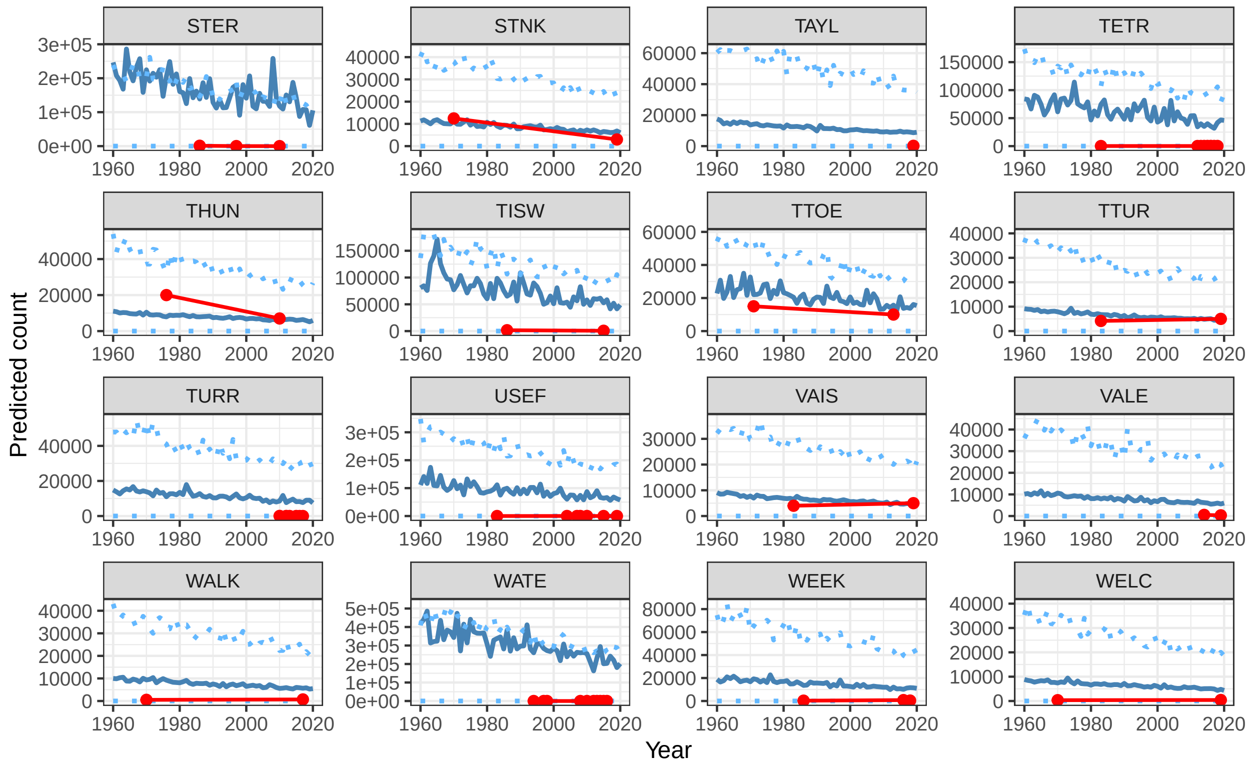
HALF
HANN
HARE
HARM
HUMB
HUNT
HUTB
HYDR
HYDS
JACO
JACP
JOUB
KAYR
KETL
LLOY
LOOK
Predicted count
Year



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

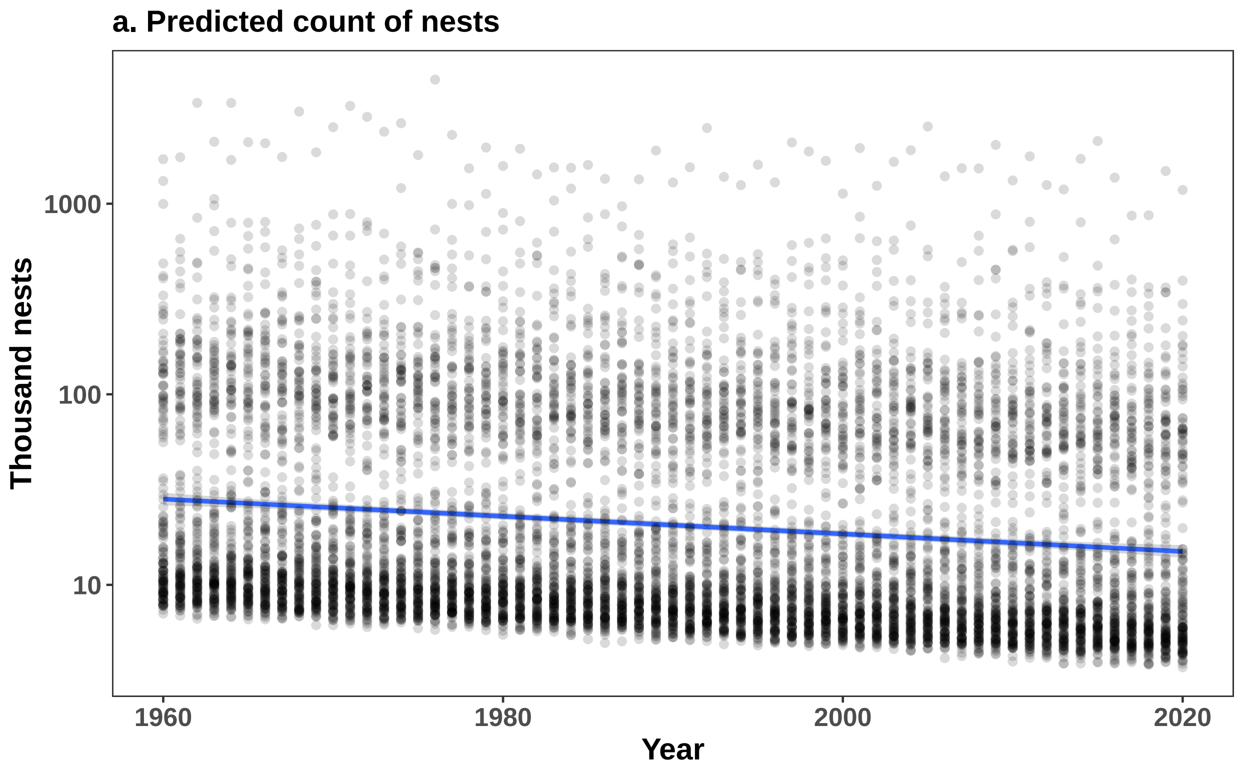


```
# Blue solid lines are the predicted abundance (posterior mean) used by Krüger (2023)
# to predict regional declines. Light blue dots are the 95 % Highest Posterior Density
# interval for this prediction. Red points are the observed counts
# (connected with a red line).
```

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 this figure looks the same as that in Krüger (2023). In other model runs the y-axis scale is much larger (e.g. to 1e+05). In other words, the model is very unstable (simply re-run and plot the same model multiple times to confirm this fact).

1.16 In the above plots, why are the predicted abundance so 'wiggly'?

The predictions per site is very 'wiggly', which is unexpected for a GLMM model. In addition, the estimated count is sometimes not included in the interval between popy$lwr < -popypred$lwr and popy$upr < -popypred$upr. Why is this so? Let use review the code used for predicion:

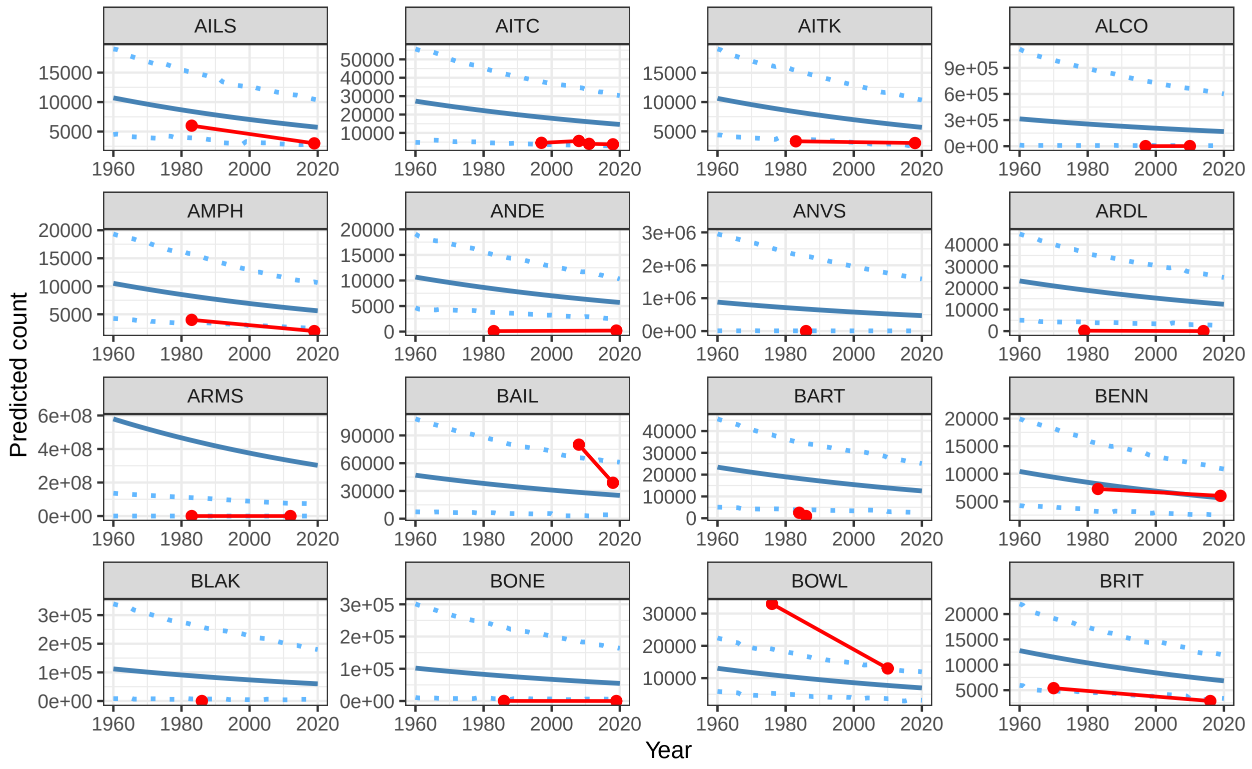
popypred<-data.frame(predict(mc1,newdata=popy,type="response", marginal=mc1$Random$formula, interval="prediction", posterior="mean"))

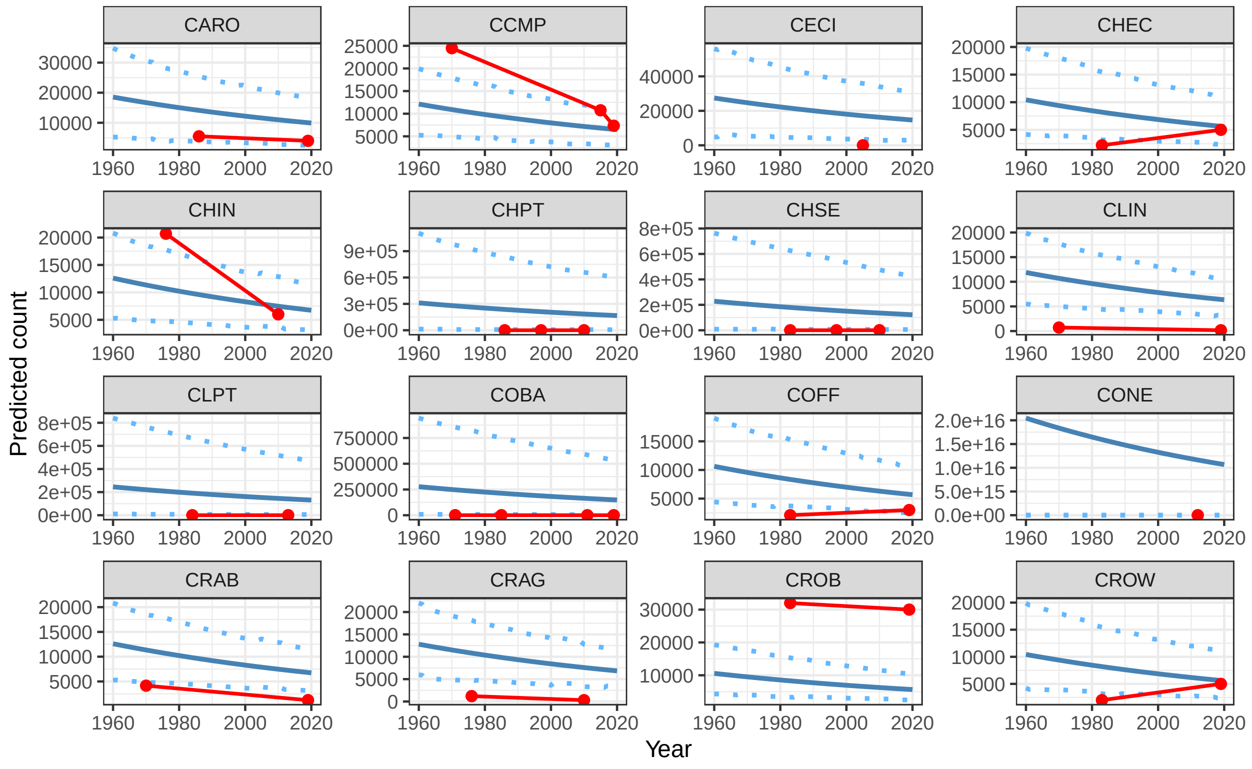
It is the prediction interval specification that leads to having very 'wiggly' predictions. Prediction intervals are obtained through posterior predictive simulation. Note, however, that in the reanalysis (below) we also specify prediction intervals (to agree with this code) but in that case the predictions do not have such extreme wiggliness, and well-behaved credible intervals.

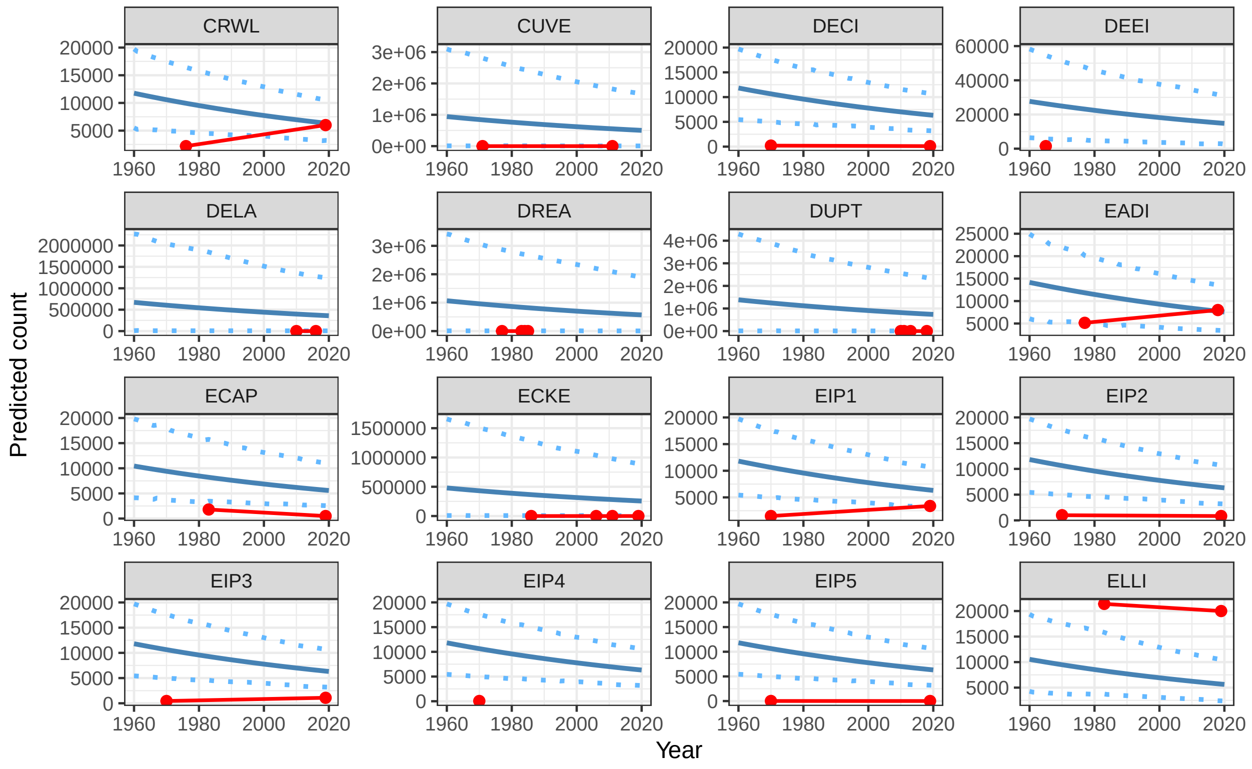
Let us plot "confidence" (credible intervals) rather than prediction intervals https://www.rdocumentation.org/packages/MCMCglmm/versions/2.35/topics/predict.MCMCglmm

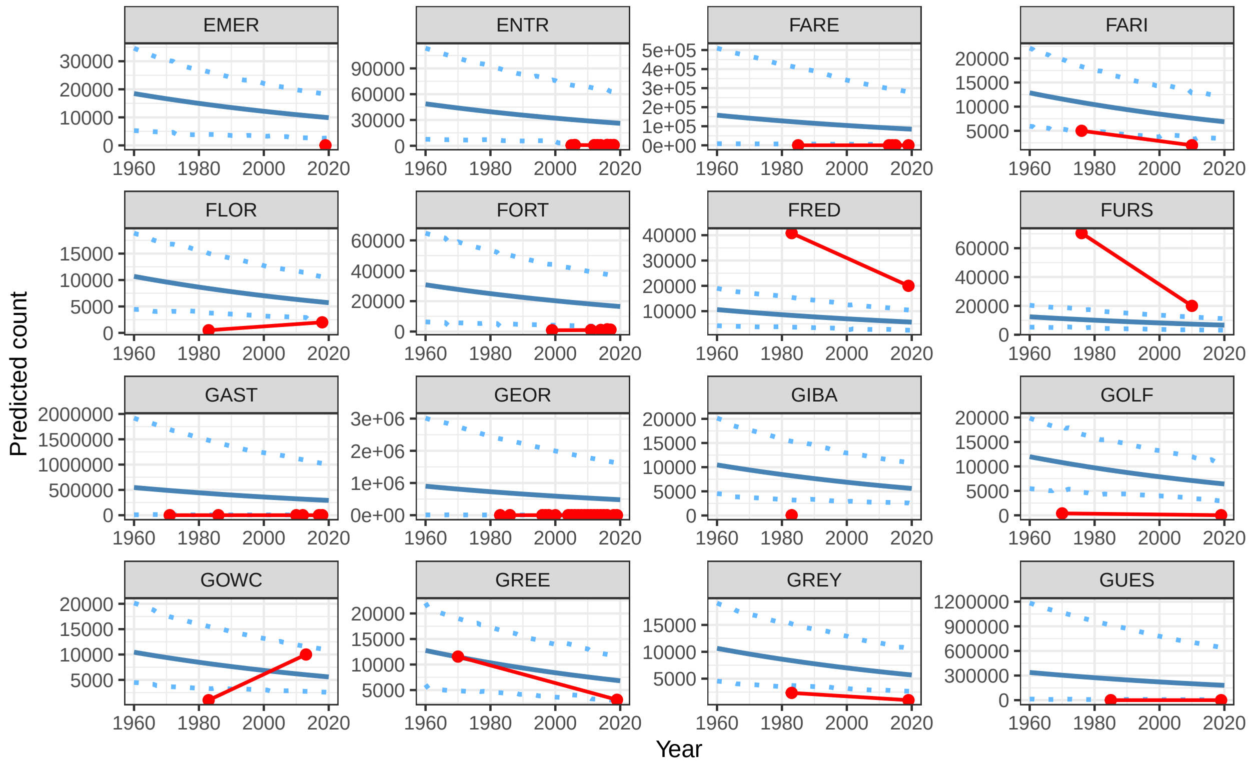
1.17 Change prediction to 'confidence' (i.e., credible) interval

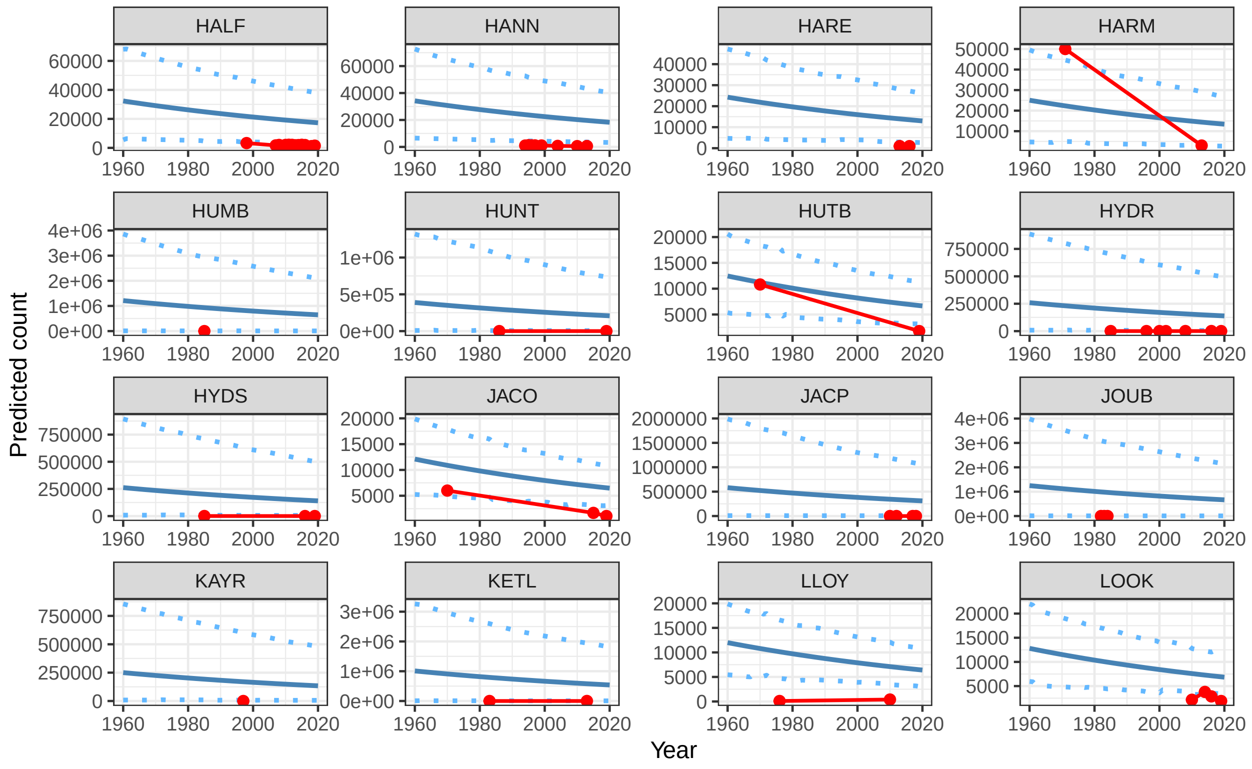
```r
# you have to change posterior="mean" to posterior="mean" when using interval="confidence", otherwise
# there is an error about HPDinterval.mcmc(mcmc(post.pred), prob = level) : obj must have nsamp > 1
popypred_cr <-data.frame(predict(mc1,newdata=popy,type="response",
                            marginal=mc1$Random$formula,
                            interval="confidence", posterior="all"))

popy$fit_cr<-popypred_cr$fit
# Add lower and upper prediction intervals to the data used for inference
popy$lwr_cr<-popypred_cr$lwr
popy$upr_cr<-popypred_cr$upr

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_cr), col = "steelblue",linewidth=1.04) +
    geom_line(aes(x = season_starting, y = lwr_cr), col = "steelblue1",
              linetype="dotted", linewidth = 1.02) +
    geom_line(aes(x = season_starting, y = upr_cr), 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'))}
```

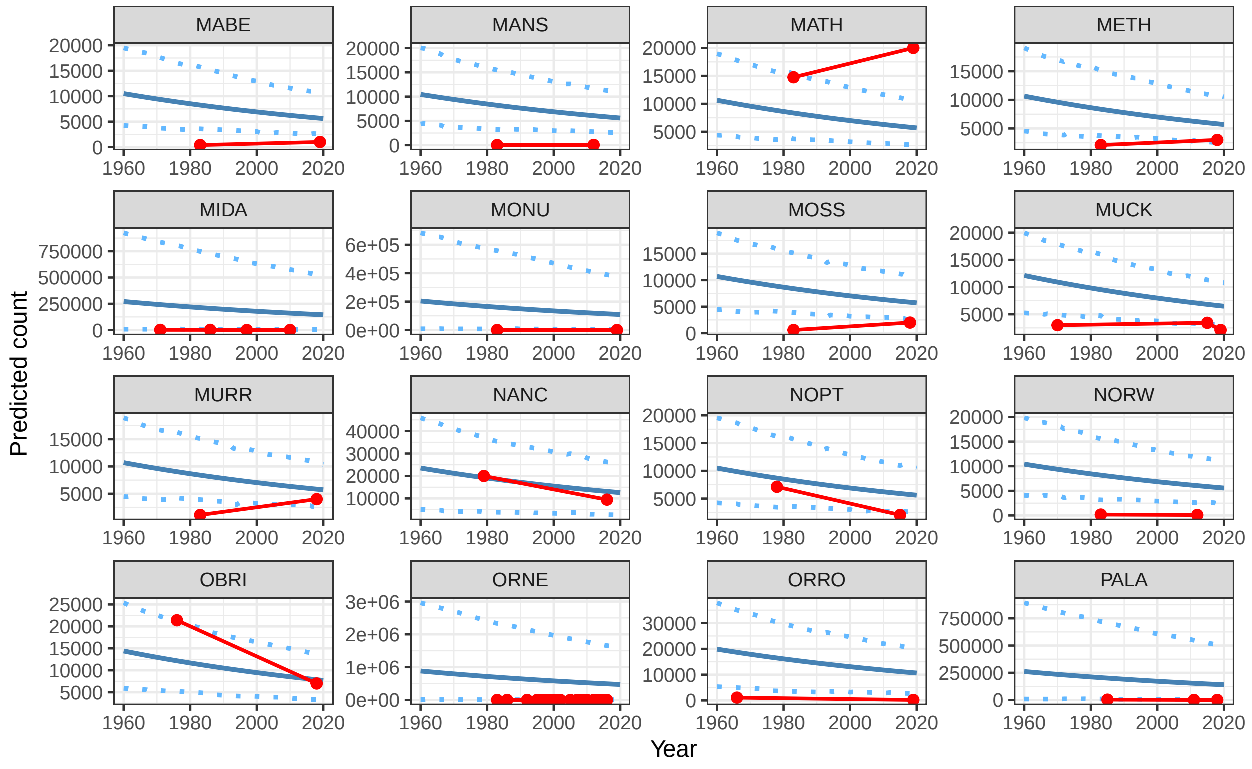

AILS
AITC
AITK
ALCO
AMPH
ANDE
ANVS
ARDL
ARMS
BAIL
BART
BENN
BLAK
BONE
BOWL
BRIT
Predicted count
Year

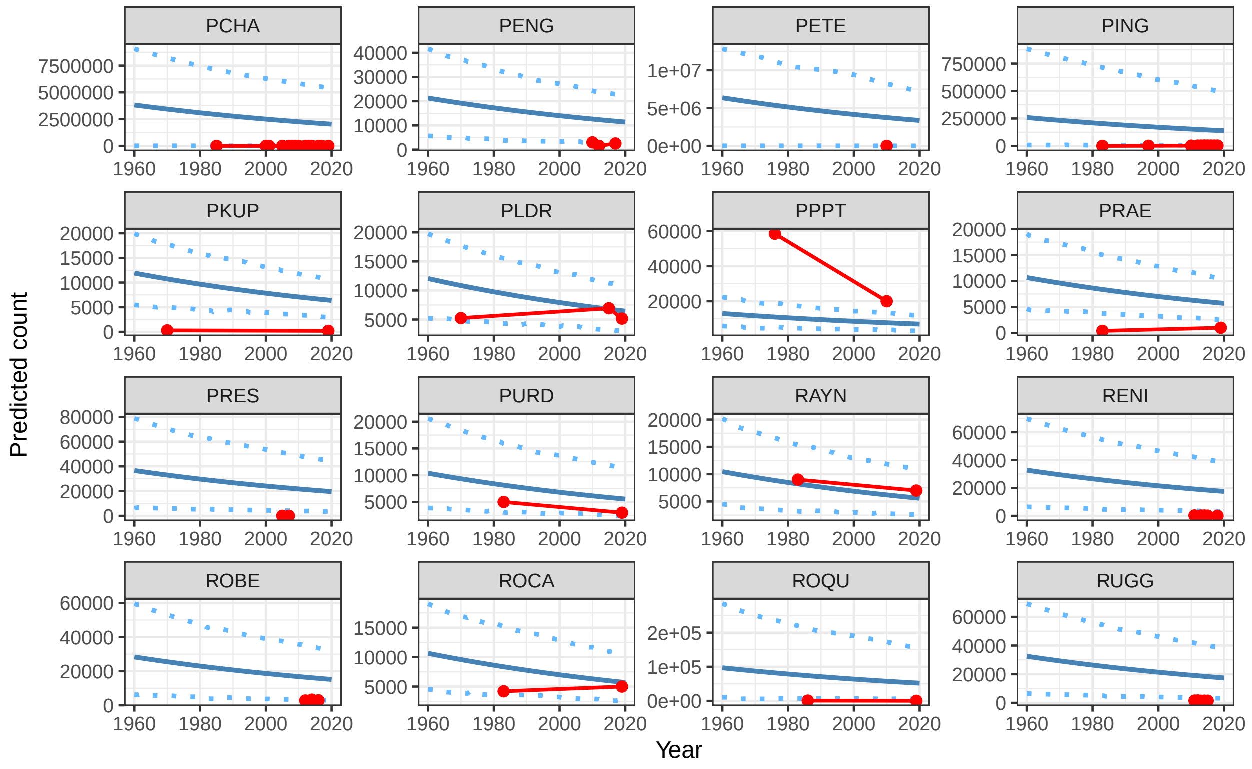

CARO
CCMP
CECI
CHEC
CHIN
CHPT
CHSE
CLIN
CLPT
COBA
COFF
CONE
CRAB
CRAG
CROB
CROW
Predicted count
Year

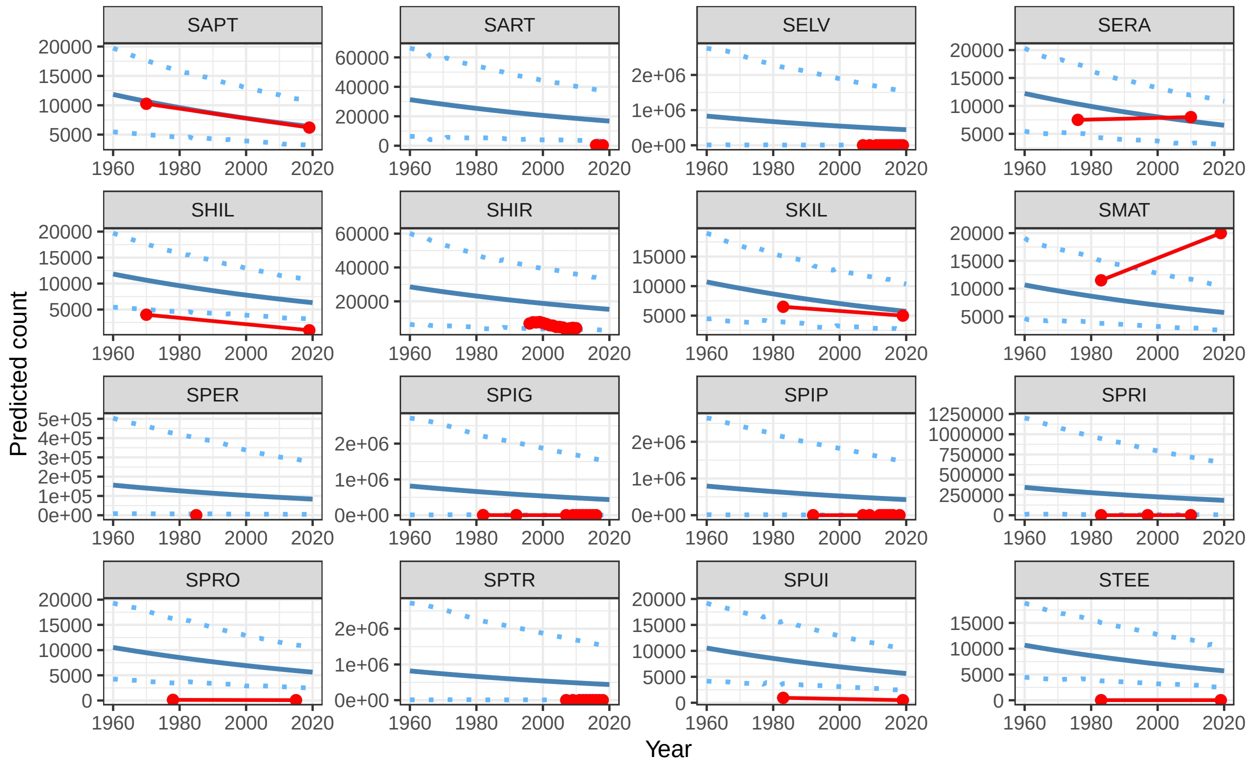

CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

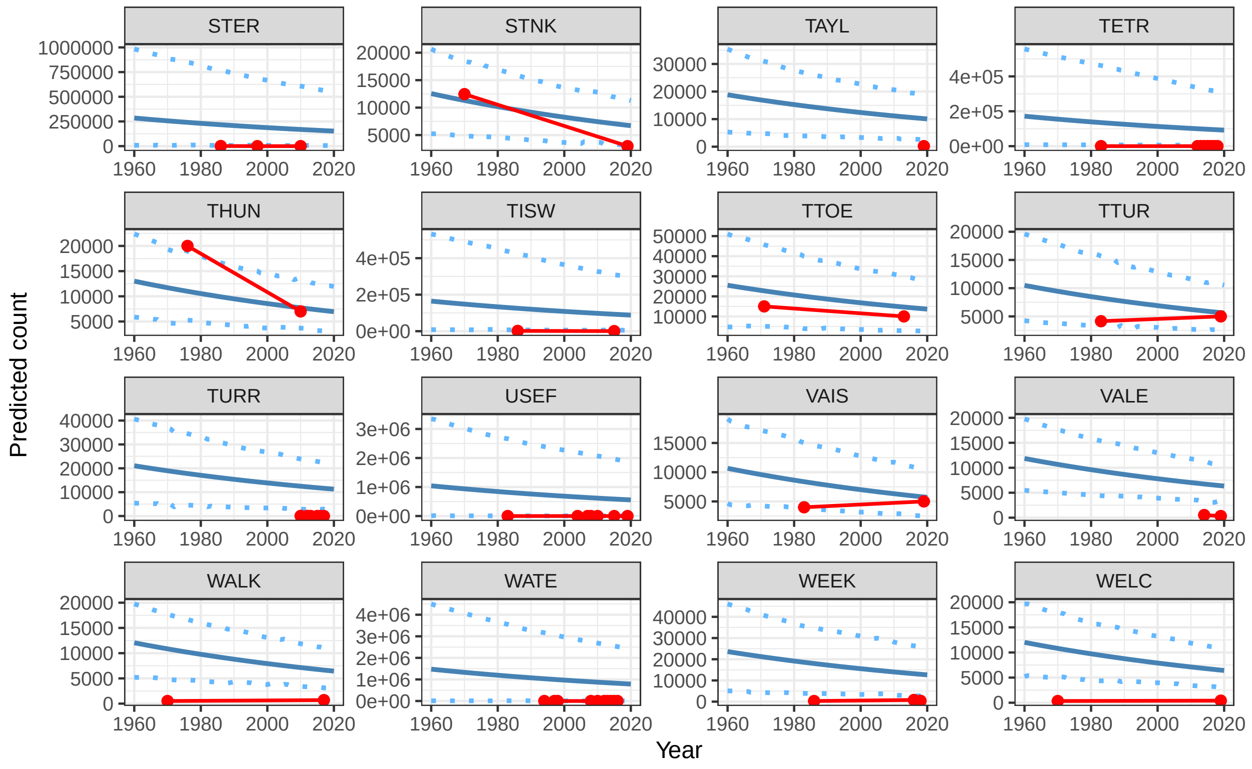

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year


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


MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year
1960
1980
2000
2020


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



```
# 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).

# Extreme / strange values for prediction intervals should perhaps be expected given the large
# l-95% CI u-95% CI in the model:
summary(mc1)
```

```
##
##  Iterations = 3001:12991
##  Thinning interval  = 10
##  Sample size  = 1000
##
##  DIC: 4790.432
##
##  G-structure:  ~us(1 + Lat):site_id
##
##                                    post.mean  l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id   939.6276  0.009028 3306.796    15.71
## Lat:(Intercept).site_id            15.7108 -0.023500   53.630    15.96
## (Intercept):Lat.site_id            15.7108 -0.023500   53.630    15.96
## Lat:Lat.site_id                     0.2636  0.001010    0.874    16.22
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units     0.295   0.2523   0.3477     1000
```

```
##
##  Location effects: nests ~ season_starting
##
##                 post.mean  l-95% CI  u-95% CI eff.samp  pMCMC
## (Intercept)     27.713764 21.159681 35.907070     1000 <0.001 ***
## season_starting -0.010426 -0.014592 -0.007267     1000 <0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

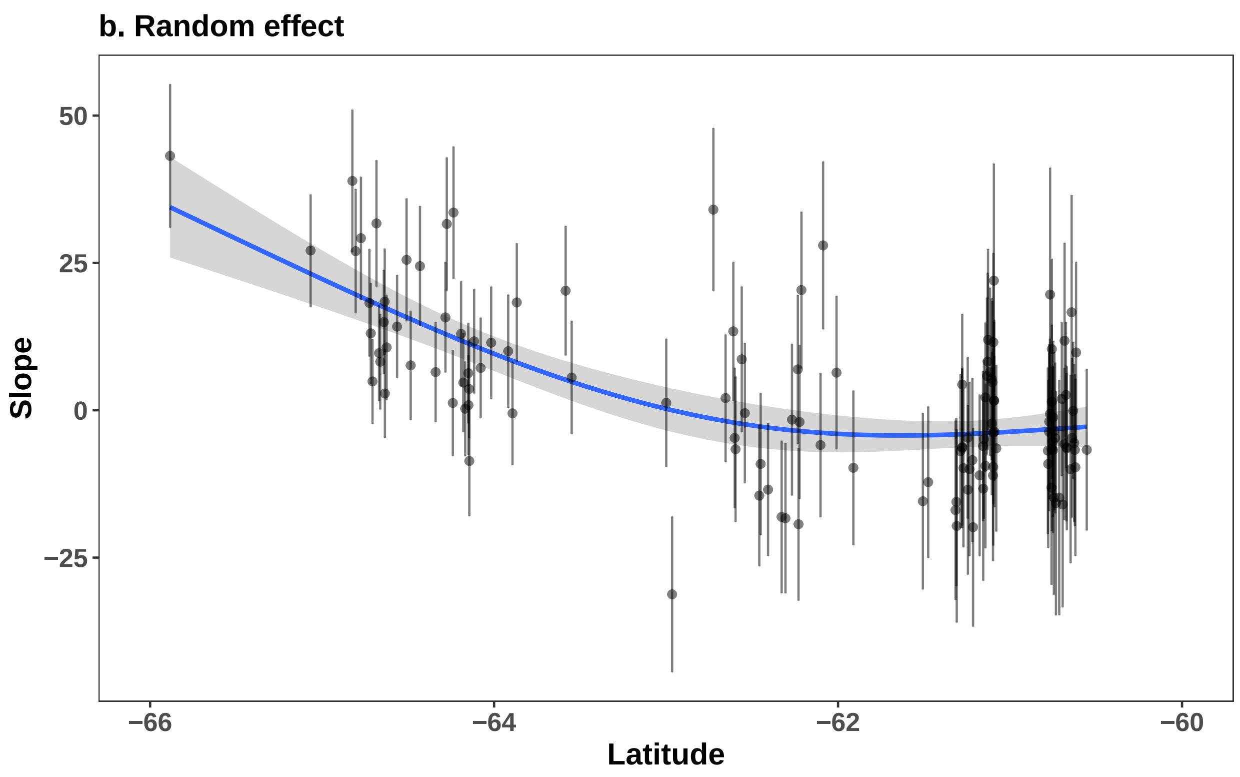
1.18 Figure 3B (Krüger 2023): Latitude

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
```

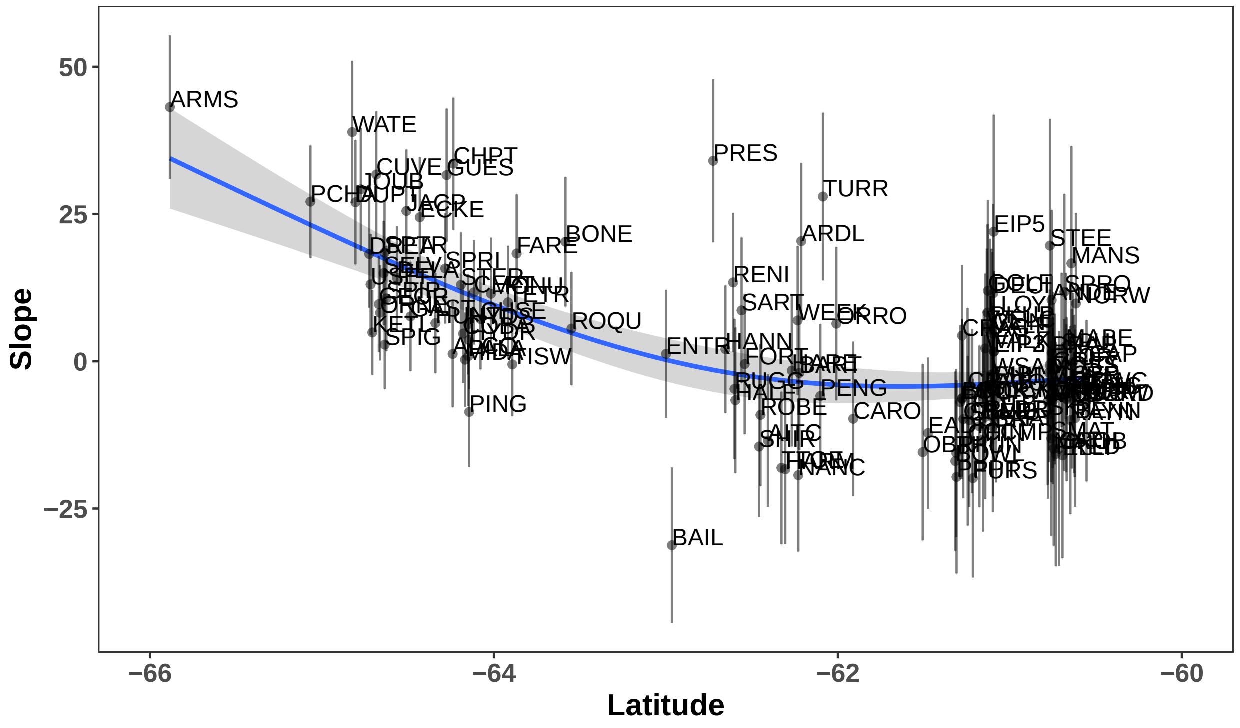
```
## Warning in smooth.construct.tp.smooth.spec(object, dk$data, dk$knots): basis dimension, k, increased
```



```r
# Add text labels to these points
ggplot(subset(rlat,Lat>(-67)),aes(Lat,int,label = site_id))+
  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") +
  geom_text(hjust=0, vjust=0)
```

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

## Warning: The following aesthetics were dropped during statistical transformation: label
## i This can happen when ggplot fails to infer the correct grouping structure in
##   the data.
## i Did you forget to specify a ‘group‘ aesthetic or to convert a numerical
##   variable into a factor?
```

b. Random effect



```
# 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
```

1.19 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. Furthermore, these calculations do not account for any uncertainty in the predicted abundance, which is not a good protocol to follow.

```
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    fit_cr
## 1    AILS -60.780           1960     0  8278.281   1  33376  10716.16
## 2    AITC -62.407           1960     0 75170.955   1  60657  27294.21
## 3    AITK -60.738           1960     0  7773.358   2  27353  10621.85
## 4    ALCO -64.240           1960     0 93541.040   0 217001 313945.31
## 5    AMPH -60.684           1960     0 13939.745   4  42650  10520.13
## 6    ANDE -60.757           1960     0  9257.283   1  39327  10662.89
##      lwr_cr     upr_cr
## 1  4494.554   19002.50
## 2  4852.482   55625.59
## 3  4385.670   19063.07
## 4 12863.101 1116923.05
## 5  4251.126   19330.98
## 6  4646.556   19100.18
```

```
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 12417063      NA       NA       NA       NA
## 1961-01-01 1961 11278069      NA       NA       NA       NA
## 1962-01-01 1962 12497234      NA       NA       NA       NA
## 1963-01-01 1963 12438713      NA       NA       NA       NA
## 1964-01-01 1964 14091813      NA       NA       NA       NA
## 1965-01-01 1965 12253854      NA       NA       NA       NA
## 1966-01-01 1966 11778134      NA       NA       NA       NA
## 1967-01-01 1967 10548747      NA       NA       NA       NA
## 1968-01-01 1968 12278594      NA       NA       NA       NA
## 1969-01-01 1969 11296979      NA       NA       NA       NA
## 1970-01-01 1970 11353738      NA       NA       NA       NA
## 1971-01-01 1971 12111838      NA       NA       NA       NA
## 1972-01-01 1972 11923300      NA       NA       NA       NA
## 1973-01-01 1973 10721321      NA       NA       NA       NA
## 1974-01-01 1974 11639853      NA       NA       NA       NA
## 1975-01-01 1975 10767587      NA       NA       NA       NA
## 1976-01-01 1976 13110375      NA       NA       NA       NA
## 1977-01-01 1977 11506680      NA       NA       NA       NA
## 1978-01-01 1978  9758525      NA       NA       NA       NA
## 1979-01-01 1979 10933877      NA       NA       NA       NA
## 1980-01-01 1980 10102442      NA       NA       NA       NA
## 1981-01-01 1981 10086276       NA       NA       NA       NA
## 1982-01-01 1982  9444311       NA       NA       NA       NA
## 1983-01-01 1983 10317203       NA       NA       NA       NA
## 1984-01-01 1984  9993046       NA       NA       NA       NA
## 1985-01-01 1985  9624675       NA       NA       NA       NA
## 1986-01-01 1986  9344641       NA       NA       NA       NA
## 1987-01-01 1987  9213076 12417063       NA       NA       NA
## 1988-01-01 1988  9593693 11278069 12417063       NA       NA
## 1989-01-01 1989  8549964 12497234 11278069 12417063       NA
## 1990-01-01 1990  8774361 12438713 12497234 11278069 12417063
## 1991-01-01 1991  8865351 14091813 12438713 12497234 11278069
## 1992-01-01 1992  9501039 12253854 14091813 12438713 12497234
## 1993-01-01 1993  8238987 11778134 12253854 14091813 12438713
## 1994-01-01 1994  8075273 10548747 11778134 12253854 14091813
## 1995-01-01 1995  8786803 12278594 10548747 11778134 12253854
## 1996-01-01 1996  7552304 11296979 12278594 10548747 11778134
## 1997-01-01 1997  9240879 11353738 11296979 12278594 10548747
## 1998-01-01 1998  8517206 12111838 11353738 11296979 12278594
## 1999-01-01 1999  8923665 11923300 12111838 11353738 11296979
## 2000-01-01 2000  7634422 10721321 11923300 12111838 11353738
## 2001-01-01 2001  9155041 11639853 10721321 11923300 12111838
## 2002-01-01 2002  8070564 10767587 11639853 10721321 11923300
## 2003-01-01 2003  8380623 13110375 10767587 11639853 10721321
## 2004-01-01 2004  8162844 11506680 13110375 10767587 11639853
## 2005-01-01 2005  8707623  9758525 11506680 13110375 10767587
## 2006-01-01 2006  7219652 10933877  9758525 11506680 13110375
## 2007-01-01 2007  7089783 10102442 10933877  9758525 11506680
## 2008-01-01 2008  7816324 10086276 10102442 10933877  9758525
## 2009-01-01 2009  8598017  9444311 10086276 10102442 10933877
## 2010-01-01 2010  7369227 10317203  9444311 10086276 10102442
## 2011-01-01 2011  8283976  9993046 10317203  9444311 10086276
## 2012-01-01 2012  6850137  9624675  9993046 10317203  9444311
## 2013-01-01 2013  6663641  9344641  9624675  9993046 10317203
## 2014-01-01 2014  7750571  9213076  9344641  9624675  9993046
## 2015-01-01 2015  7636482  9593693  9213076  9344641  9624675
## 2016-01-01 2016  6814559  8549964  9593693  9213076  9344641
## 2017-01-01 2017  6133122  8774361  8549964  9593693  9213076
## 2018-01-01 2018  6175958  8865351  8774361  8549964  9593693
## 2019-01-01 2019  6649998  9501039  8865351  8774361  8549964
## 2020-01-01 2020  6266990  8238987  9501039  8865351  8774361
```

```
# 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.
## -0.44932 -0.31049 -0.27408 -0.26766 -0.22205 -0.08961
```

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

```
##        95%
## -0.1491117
```

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

```
##         5%
## -0.3718116
```

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

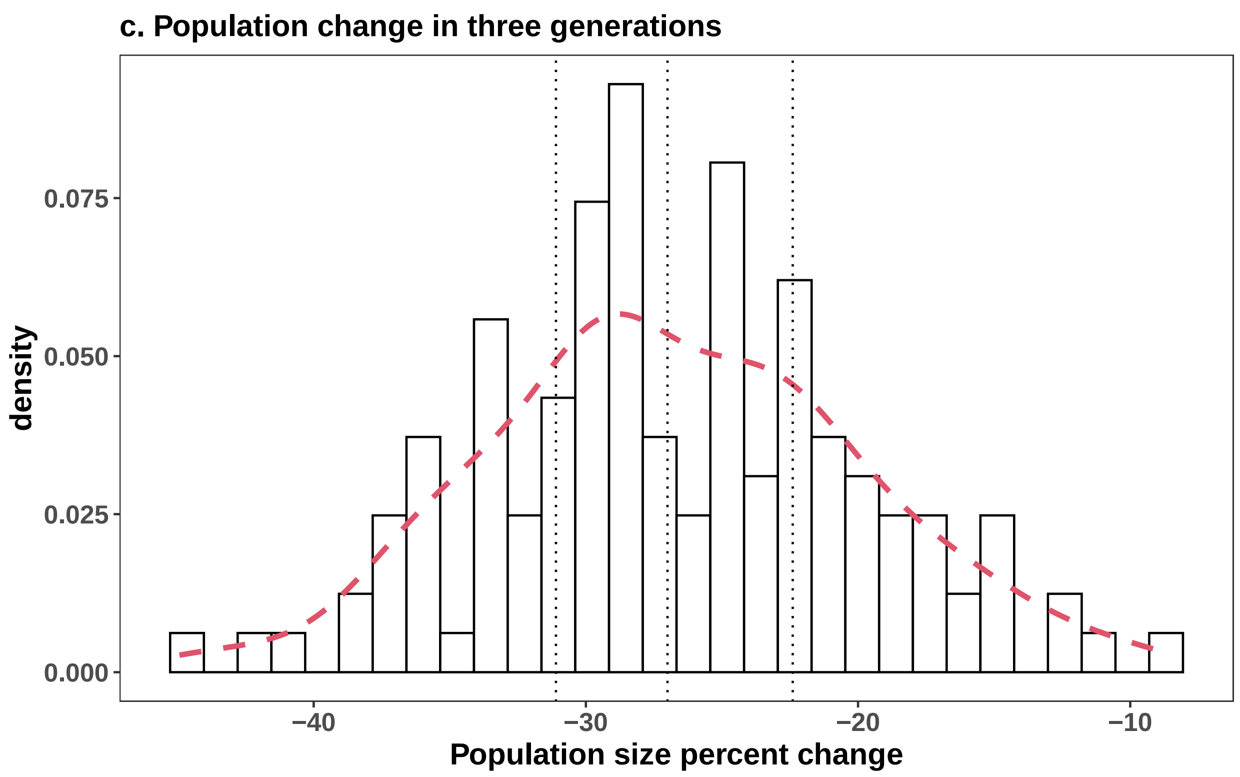
```
## [1] -0.2676584
```

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

```
## [1] 0.06866281
```

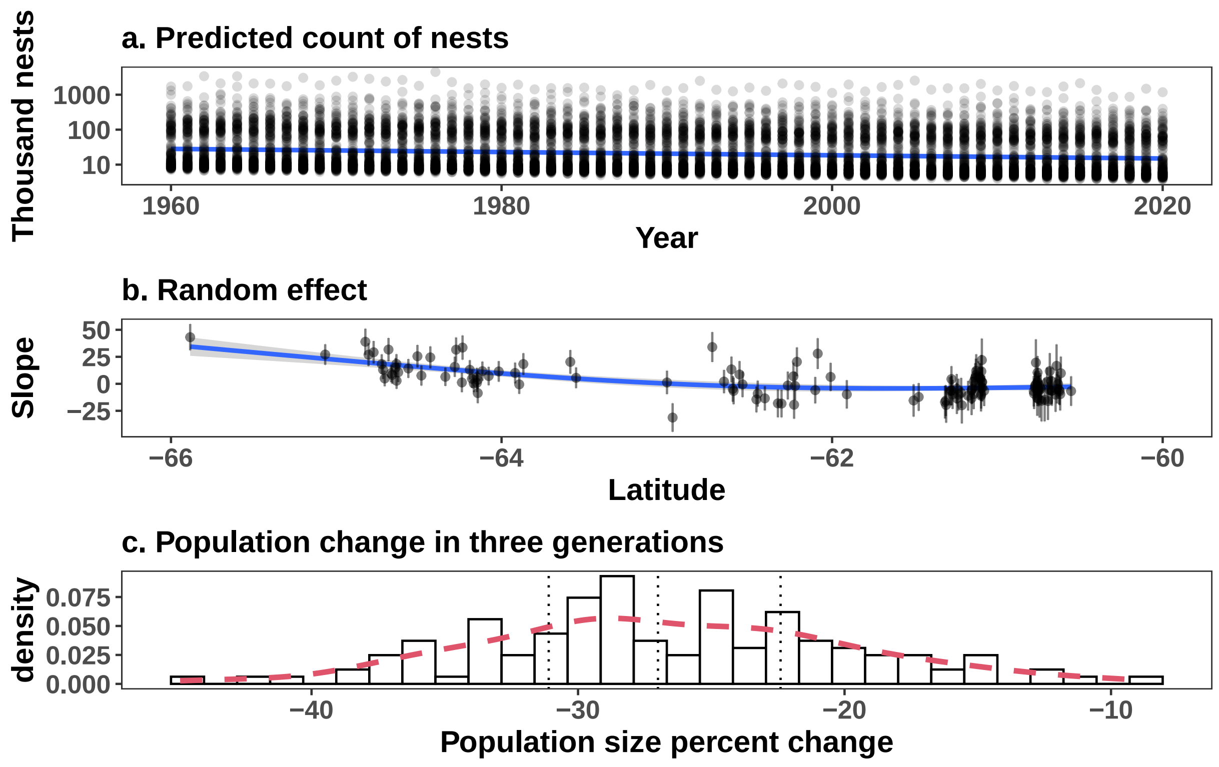
```
p3<-ggplot(chm,aes(value*100))+
  geom_histogram(aes(y = ..density..), colour = 1, fill = "white") +
  geom_density(lwd = 1.2, linetype = 2,colour = 2)+
  theme_bw()+th+
  geom_vline(xintercept = c(-22.4,-27.0,-31.1),linetype="dotted")+
  xlab("Population size percent change")+
  ggtitle(label="c.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

p3
```

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



```
p1v2/p2/p3
```

```
## 'geom_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```



2 Reanalysis of Krüger (2023) data

2.1 Fit a better GLMM

How is this model different to Krüger (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

```
# 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)
```

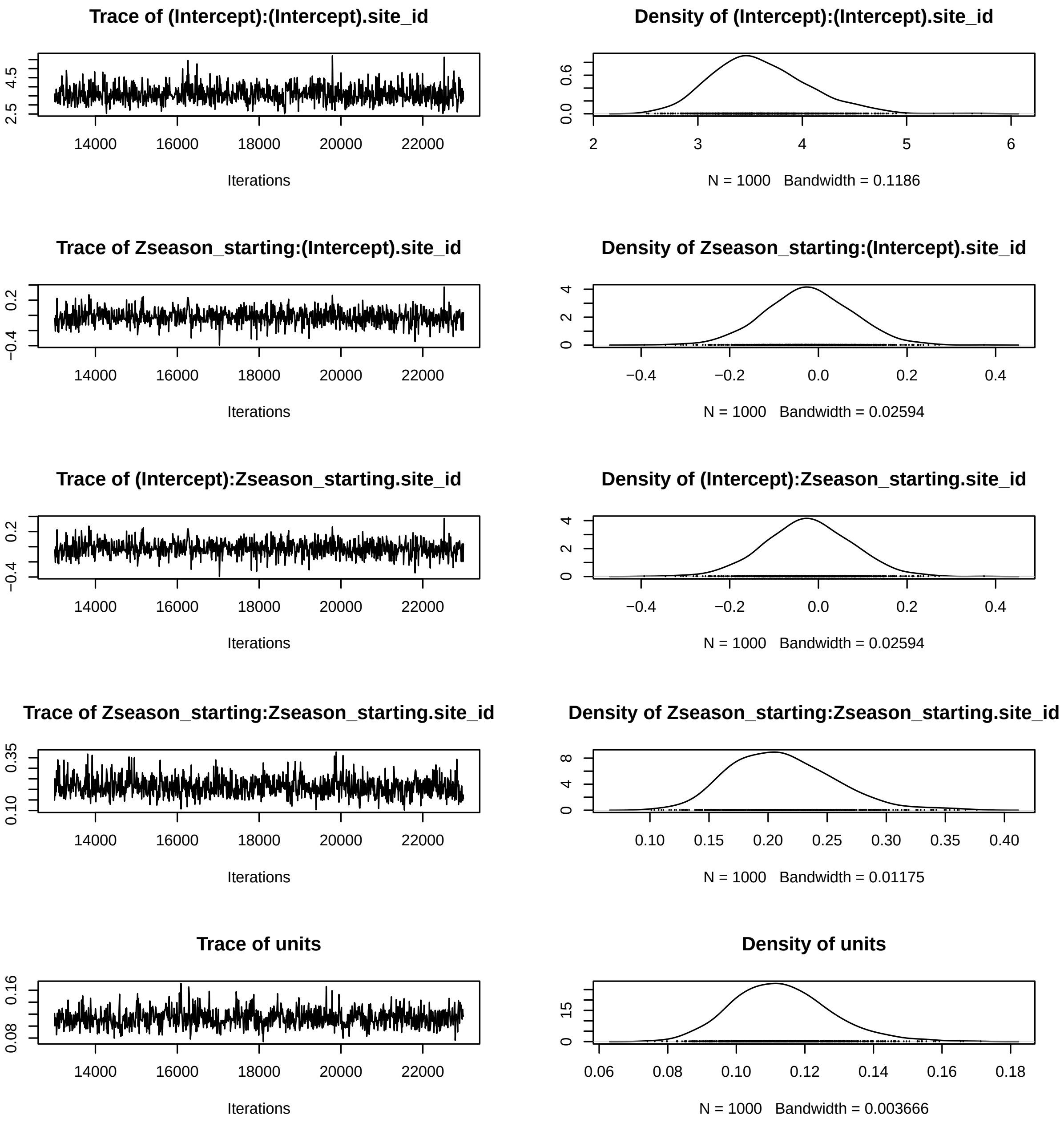
```
summary(mc2)
```

```
##
##  Iterations = 13001:22991
##  Thinning interval  = 10
##  Sample size  = 1000
##
##  DIC: 4792.052
##
##  G-structure:  ~us(1 + Zseason_starting):site_id
##
##                                             post.mean l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id              3.59738   2.8325   4.6023   1000.0
## Zseason_starting:(Intercept).site_id        -0.02254  -0.2138   0.1701    887.9
## (Intercept):Zseason_starting.site_id        -0.02254  -0.2138   0.1701    887.9
## Zseason_starting:Zseason_starting.site_id    0.21200   0.1270   0.2935    868.4
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.1132  0.08481   0.1399    739.8
##
##  Location effects: nests ~ Zseason_starting * ZLat
##
##                         post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)               5.81530  5.47823  6.17278    803.2 <0.001 ***
## Zseason_starting         -0.17970 -0.28552 -0.07475    847.0  0.004 **
## ZLat                      1.43158  1.12282  1.76493    785.5 <0.001 ***
## Zseason_starting:ZLat     0.04959 -0.04280  0.14374    871.4  0.314
## ---
## 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)
```



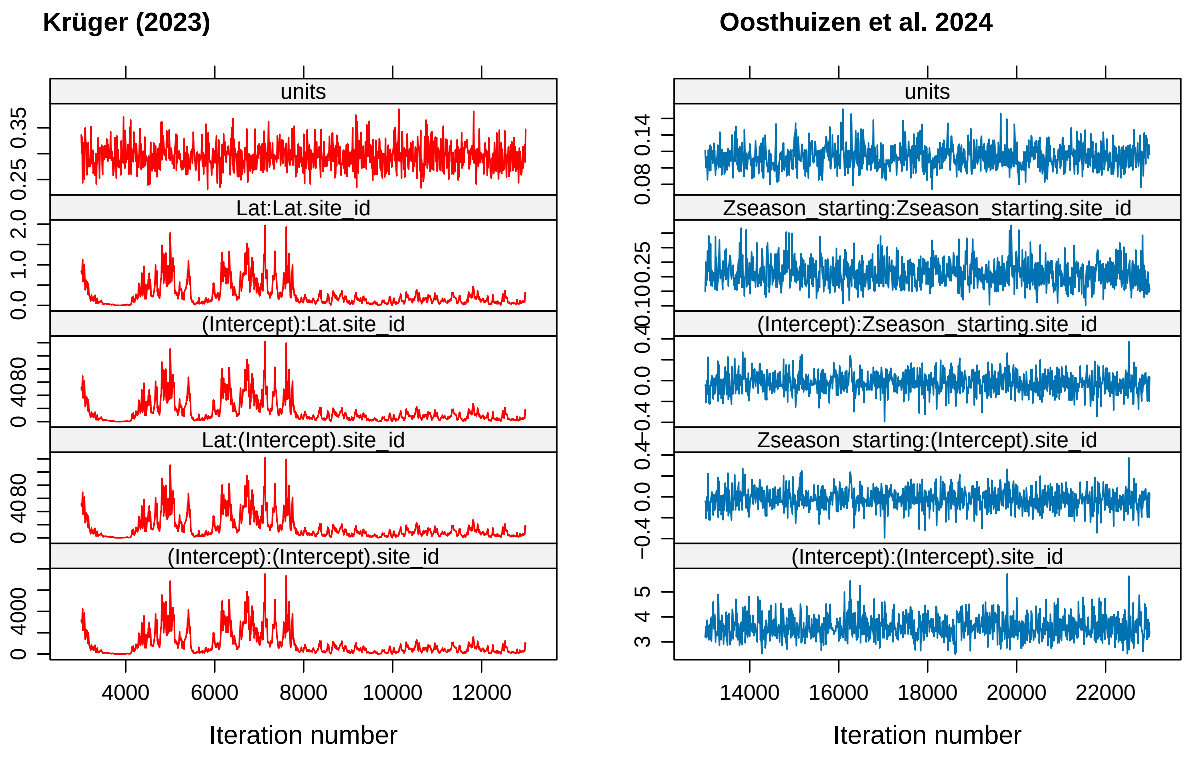
```r
# what are the effective sample size for the random effects?
coda::effectiveSize(mc2$VCV)
```

```
##             (Intercept):(Intercept).site_id
##                                   1000.0000
##      Zseason_starting:(Intercept).site_id
##                                    887.9219
##      (Intercept):Zseason_starting.site_id
##                                    887.9219
## Zseason_starting:Zseason_starting.site_id
##                                    868.4266
##                                       units
##                                    739.7818
```

```
# The effective sample size is large

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

```
##           (Intercept):(Intercept).site_id
##                                -0.001762195
##      Zseason_starting:(Intercept).site_id
##                                 0.058866878
##      (Intercept):Zseason_starting.site_id
##                                 0.058866878
## Zseason_starting:Zseason_starting.site_id
##                                 0.069921085
##                                       units
##                                 0.149079871
```

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

cowplot::plot_grid(traceK, trace2, labels = c('Krüger (2023)', 'Oosthuizen et al. 2024'), ncol = 2, labe
```



```
# 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

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)

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)
```

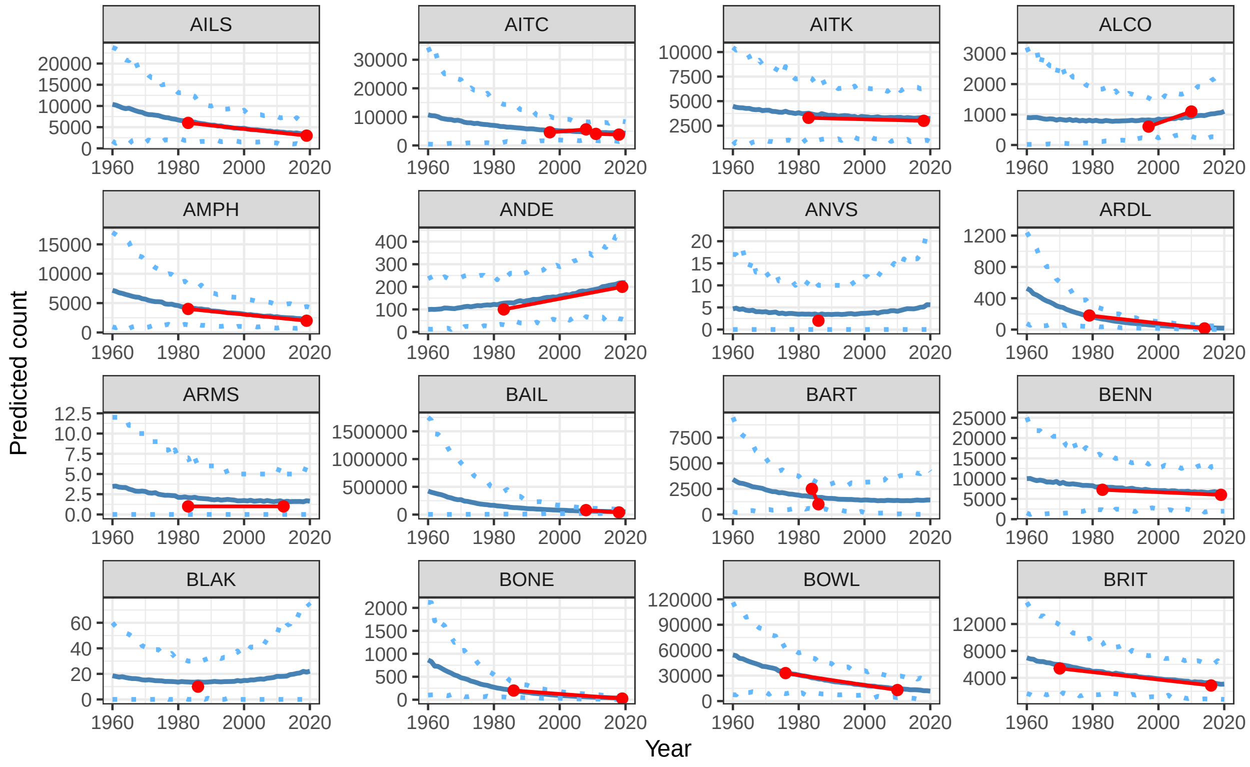
```
##          fit  lwr   upr
## 1 10376.781 1720 23803
## 2  5758.052 1637 10672
## 3  9477.298 1018 20666
## 4  8147.767 1429 18271
## 5  7476.230 1495 14982
## 6  4382.271 1491  7931
```

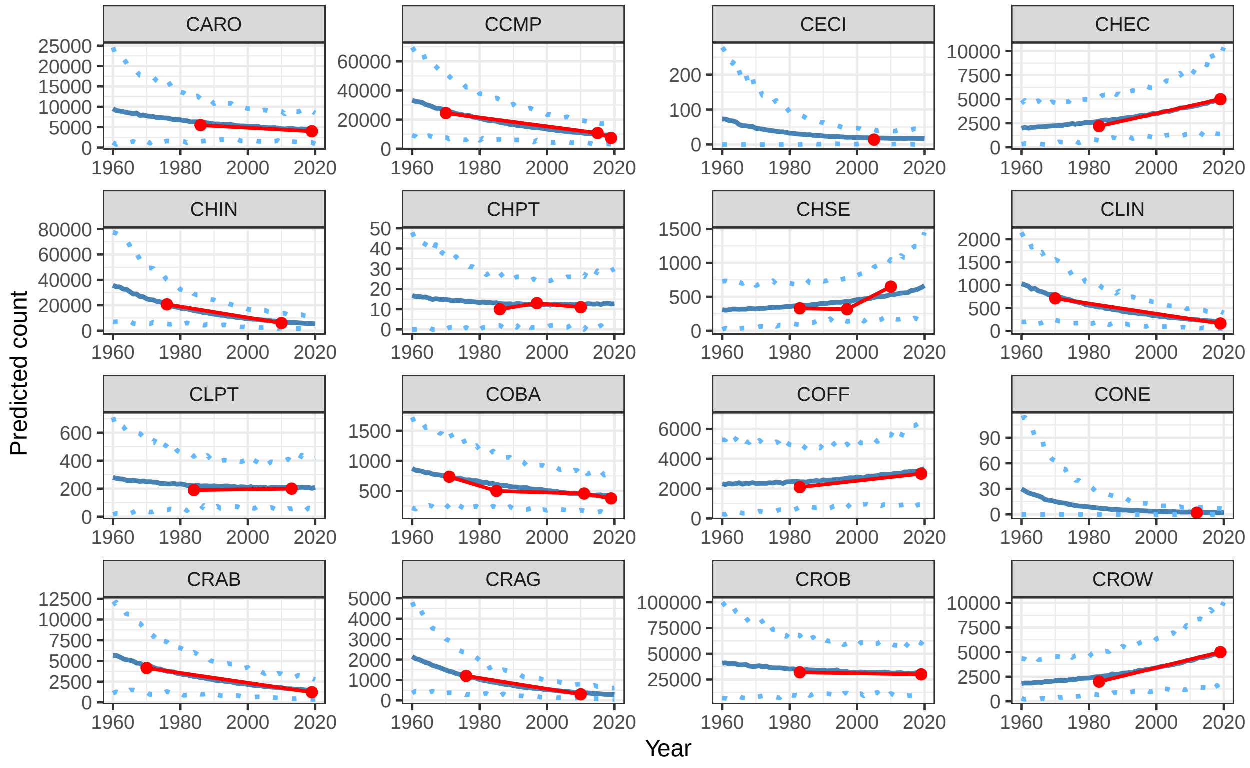
```
popy$Zfit = popypred$fit
popy$Zlwr = popypred$lwr
popy$Zupr = popypred$upr

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

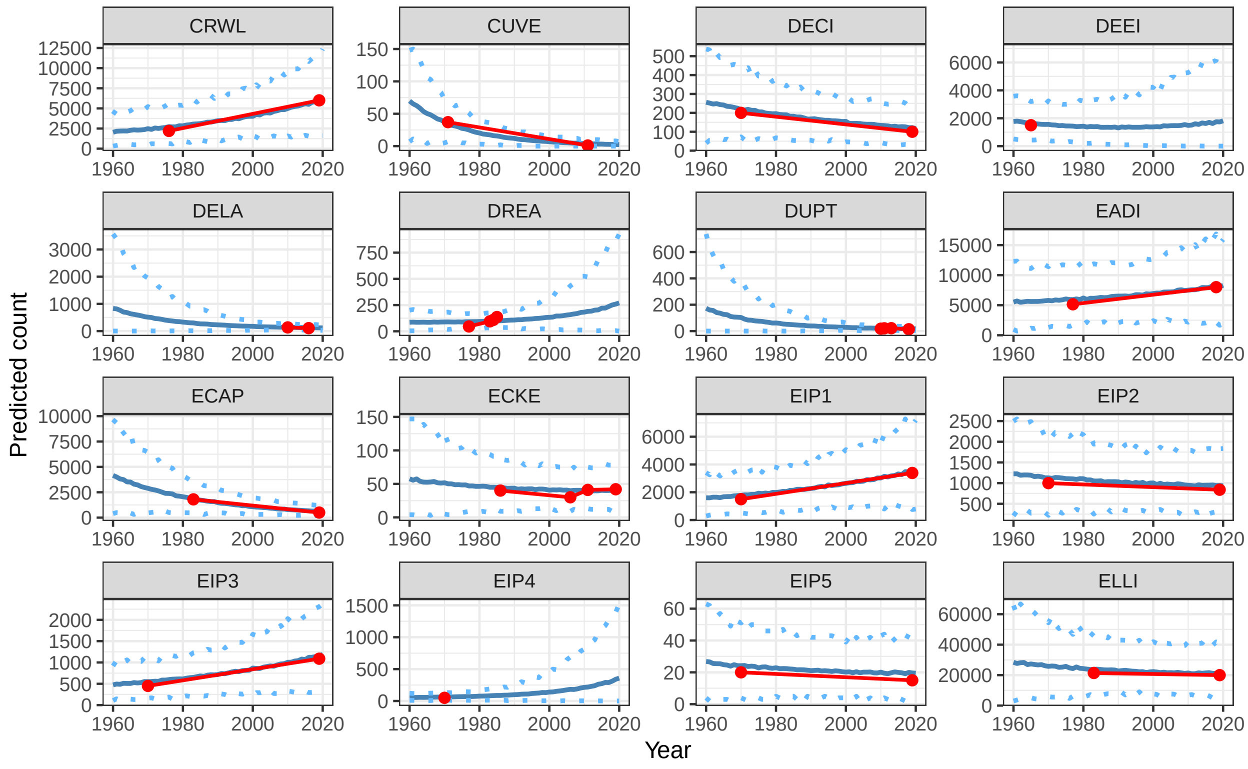
2.4 Conditional model predictions

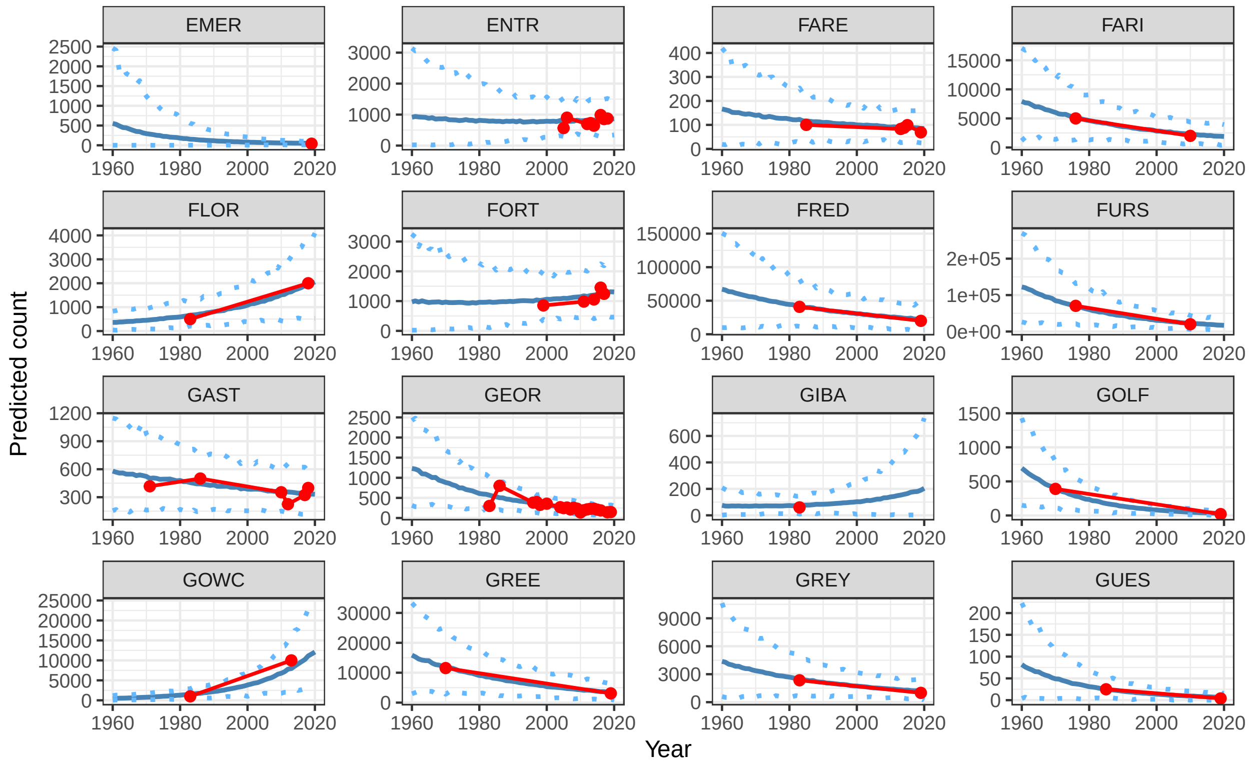
Plot the observed data against predicted data, per site, to see whether observed data and predicted data agree for the revised analysis

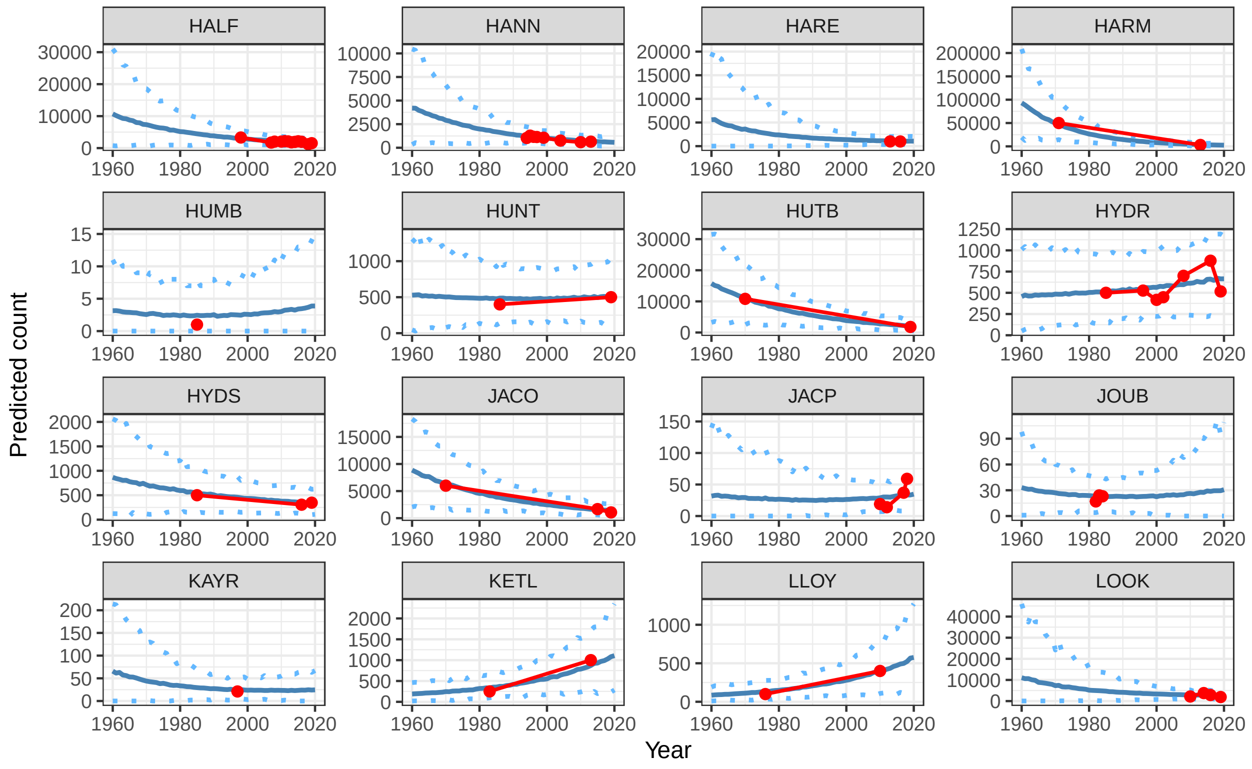
```
required_n_pages = round(133/16)+1

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'))}
```

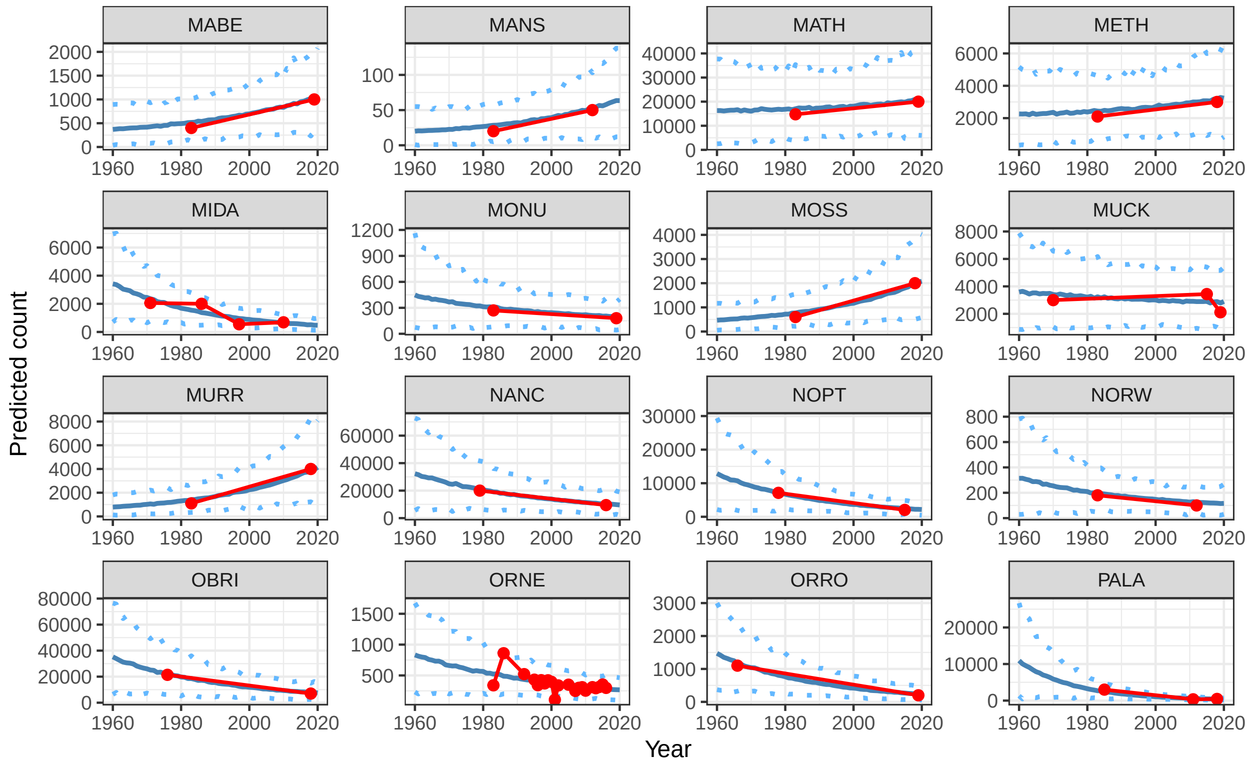


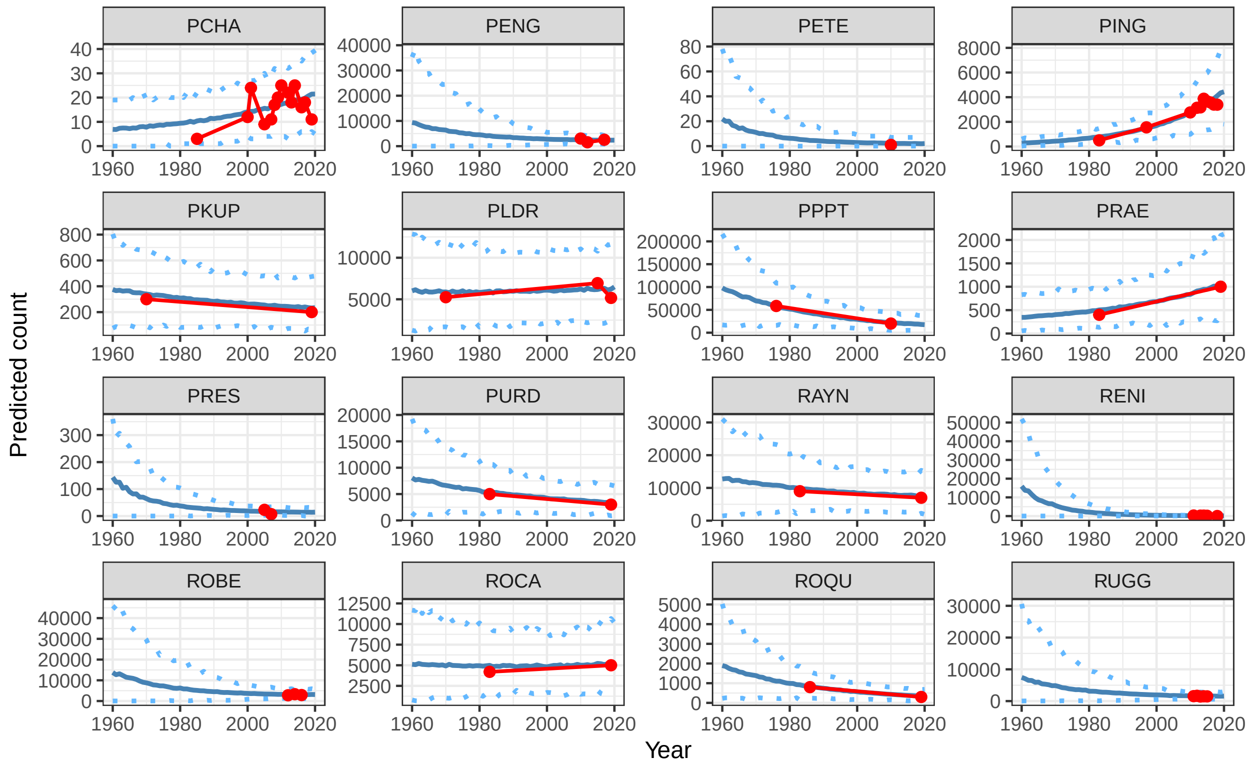



CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year

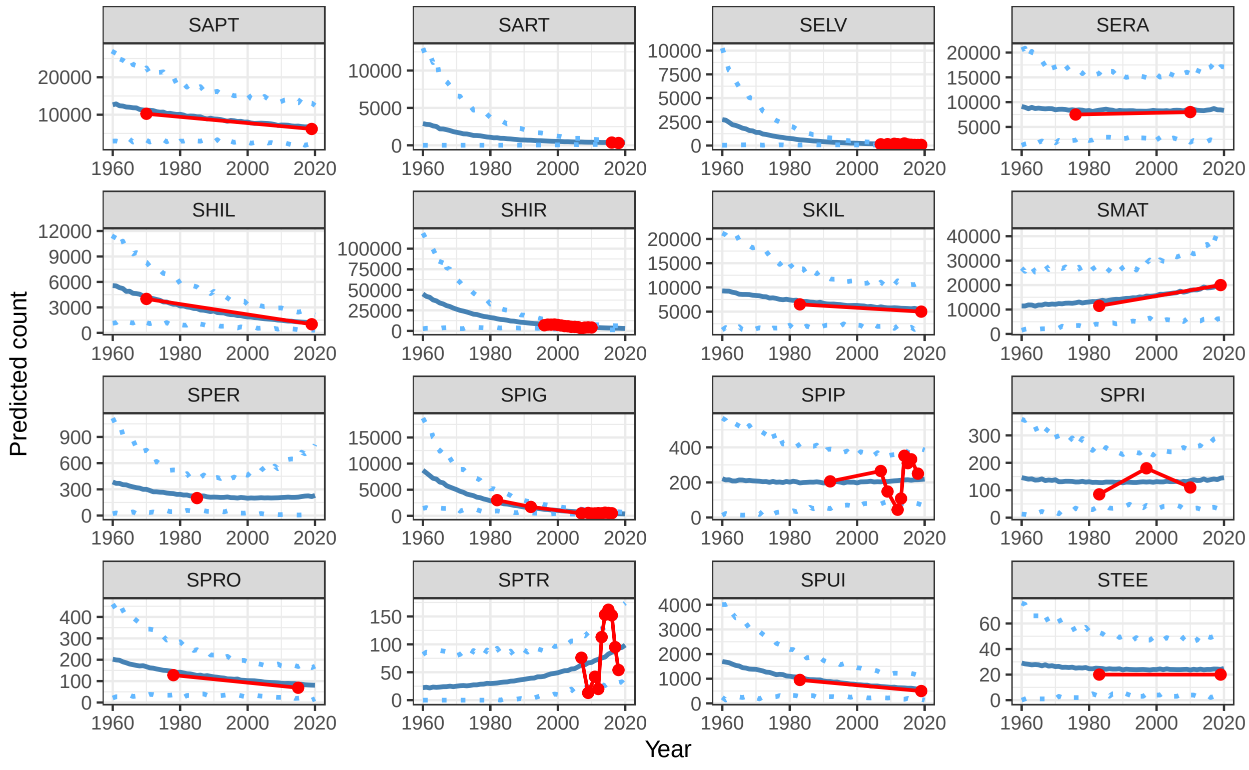

EMER
ENTR
FARE
FARI
FLOR
FORT
FRED
FURS
GAST
GEOR
GIBA
GOLF
GOWC
GREE
GREY
GUES
Predicted count
Year


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

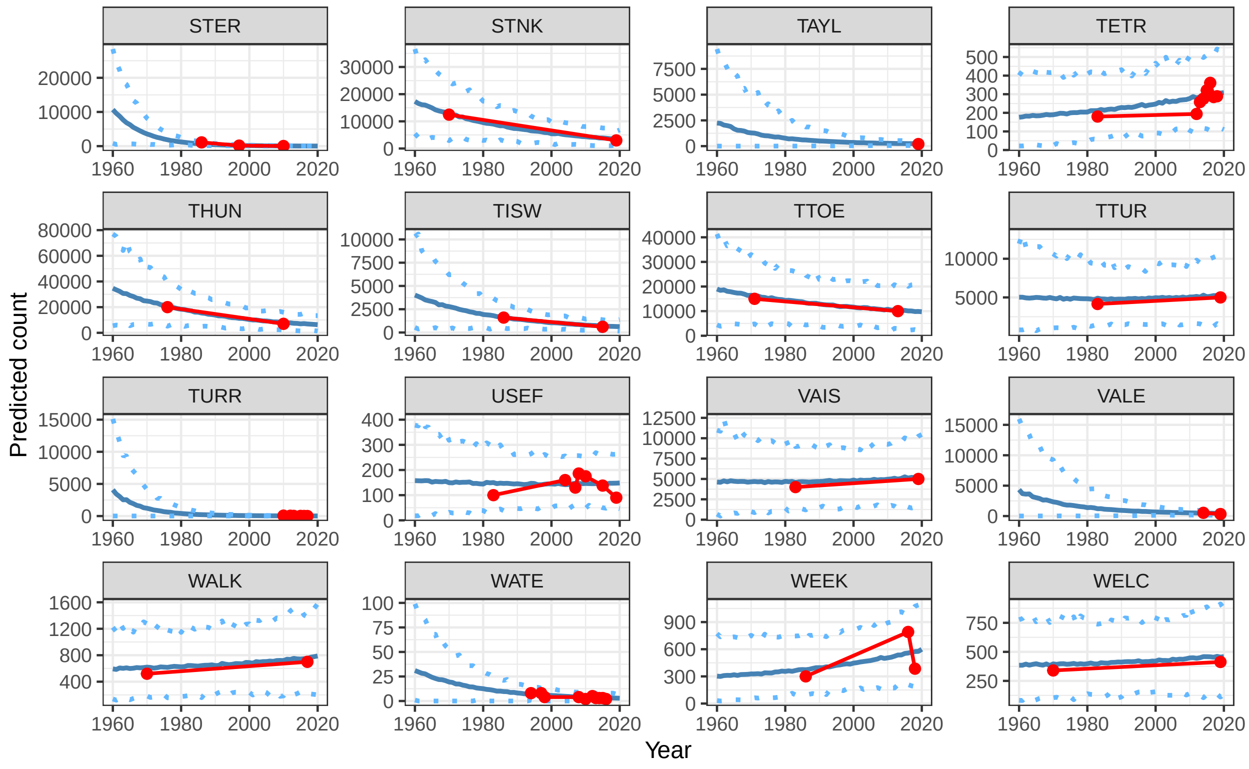

MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year



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

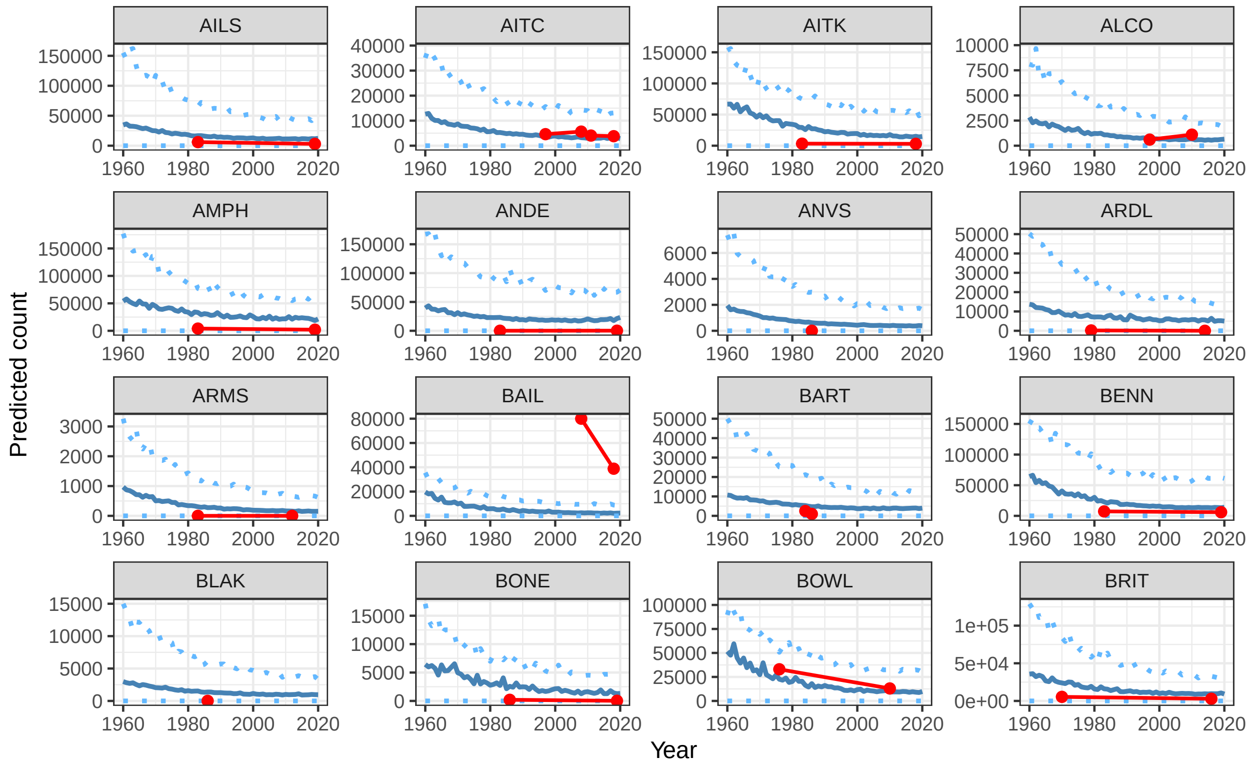


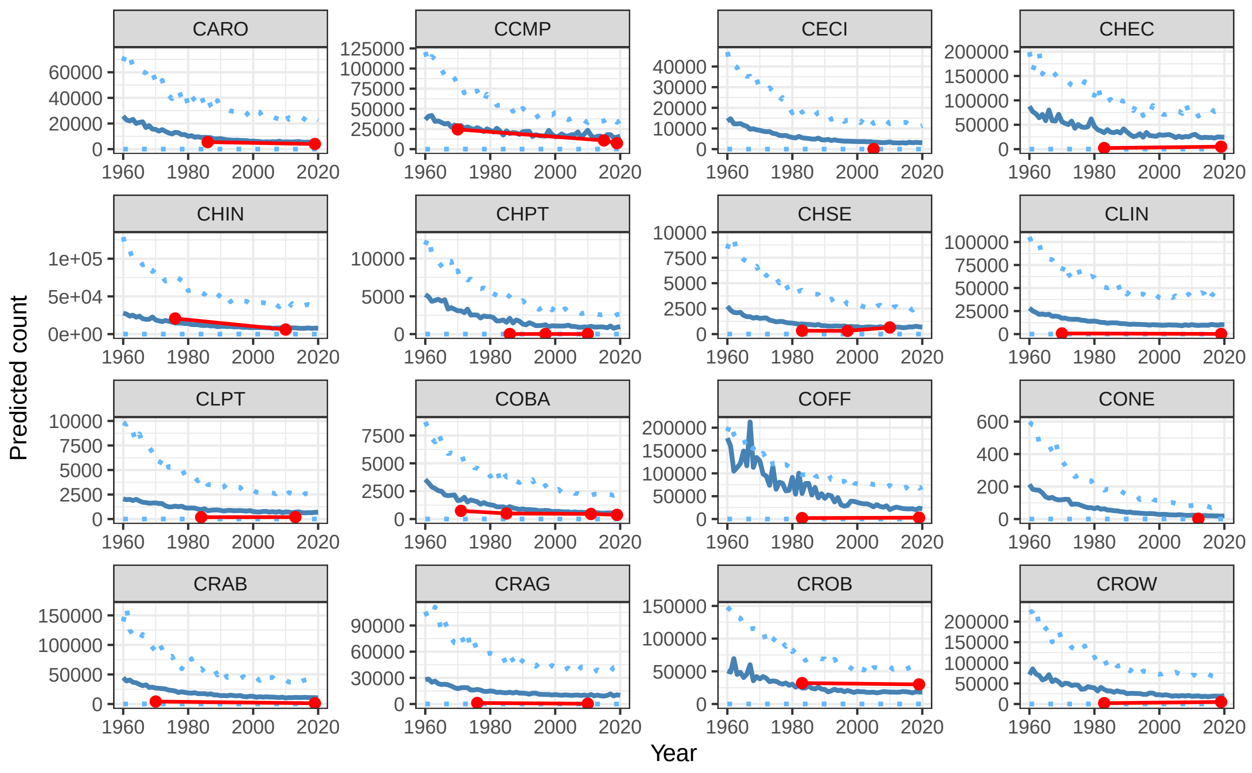
```r
# Predictions are good, although back-predicting to 1960 is extrapolation
# (there are only 2 counts prior to 1970) so uncertainty (prediction intervals)
# is high.
```

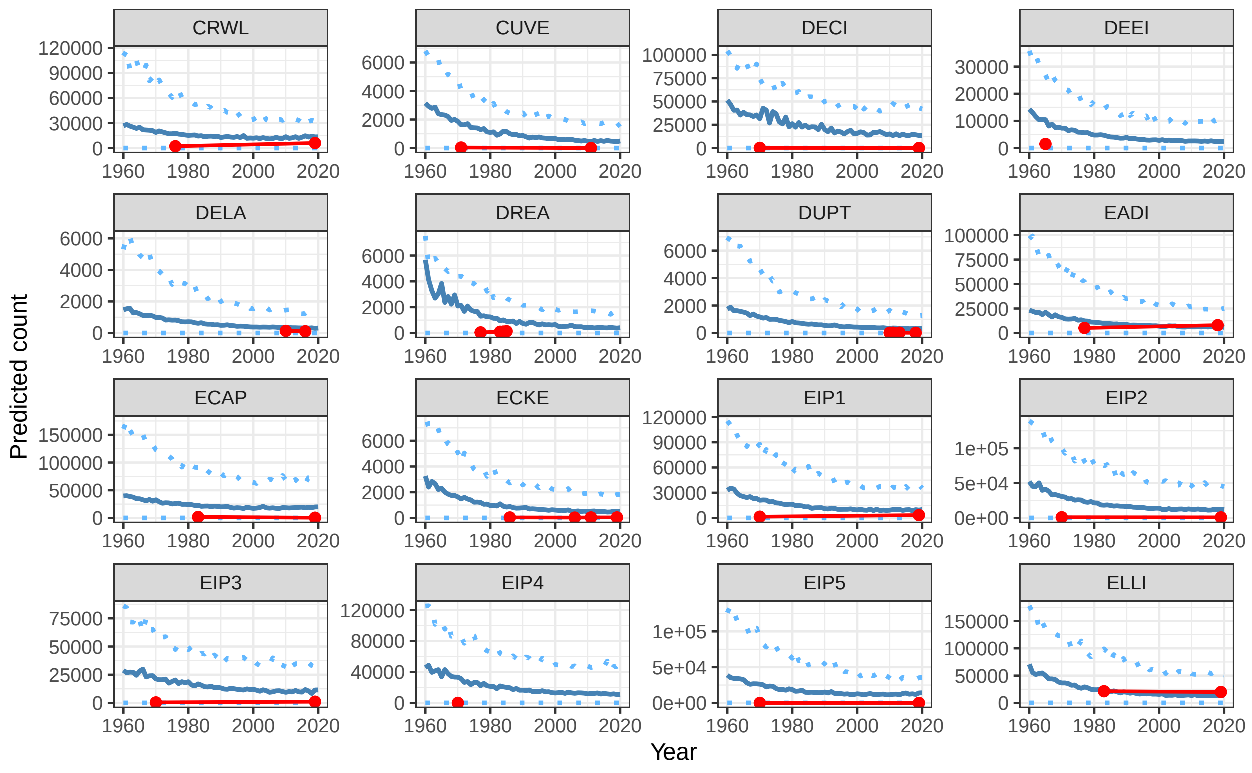
2.5 Marginal model predictions

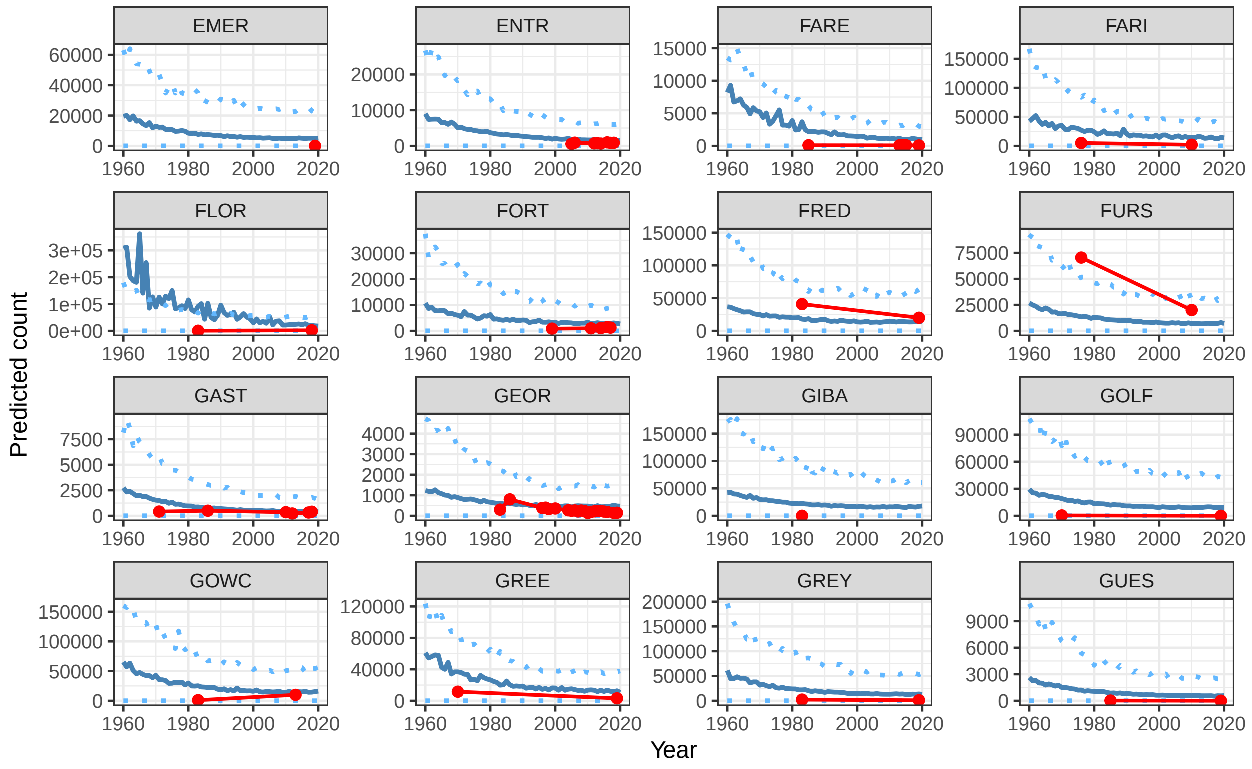
```r
# This predicts the population average response - i.e., a similar prediction at all sites.
# If you are adding up the individual sites, as Krüger 2023 did to calculate popT,
# then you are adding predictions of the average response every time.
popypred_marg <- data.frame(predict(mc2,
                                    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){
```

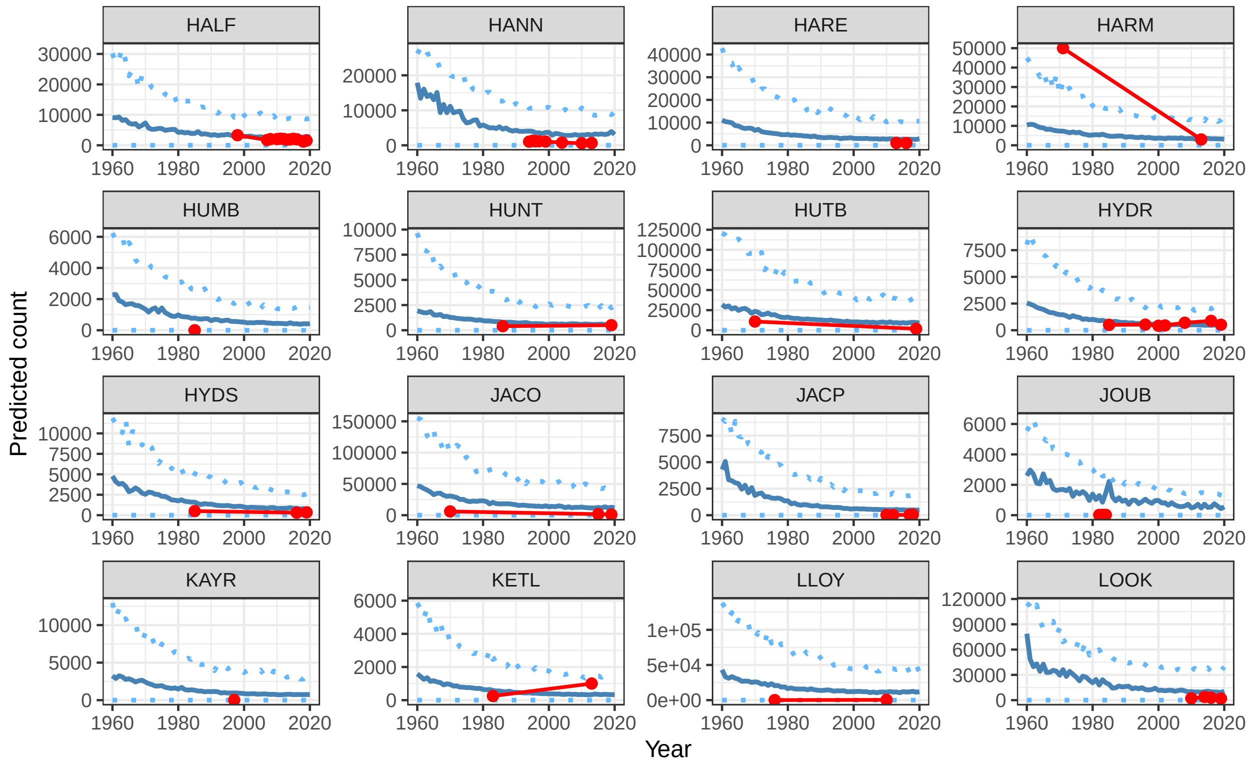
```
print(ggplot(data = popy) +
    geom_line(aes(x = season_starting, y = Zfit_marg),
              col = "steelblue", linewidth=1.04) +
    geom_line(aes(x = season_starting, y = Zlwr_marg),
              col = "steelblue1", linetype="dotted", linewidth = 1.02) +
    geom_line(aes(x = season_starting, 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",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'))}
```

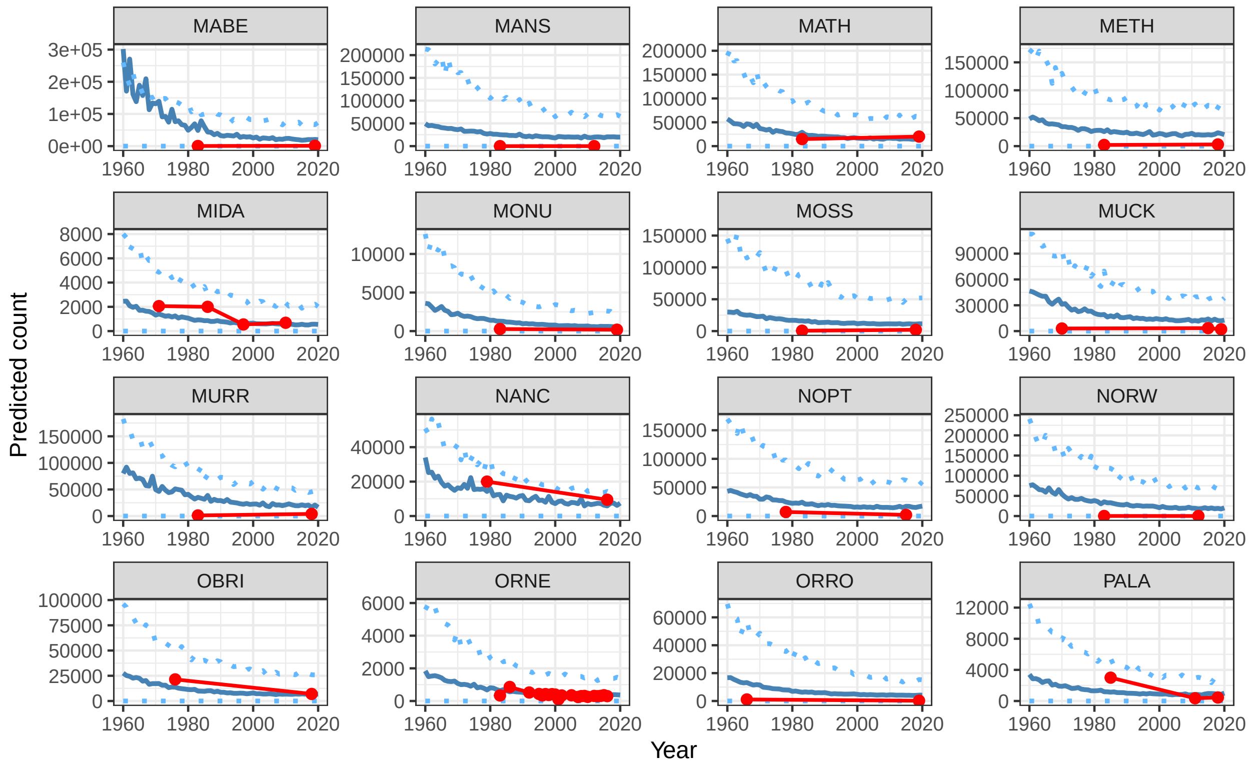



CARO
CCMP
CECI
CHEC
CHIN
CHPT
CHSE
CLIN
CLPT
COBA
COFF
CONE
CRAB
CRAG
CROB
CROW
Predicted count
Year

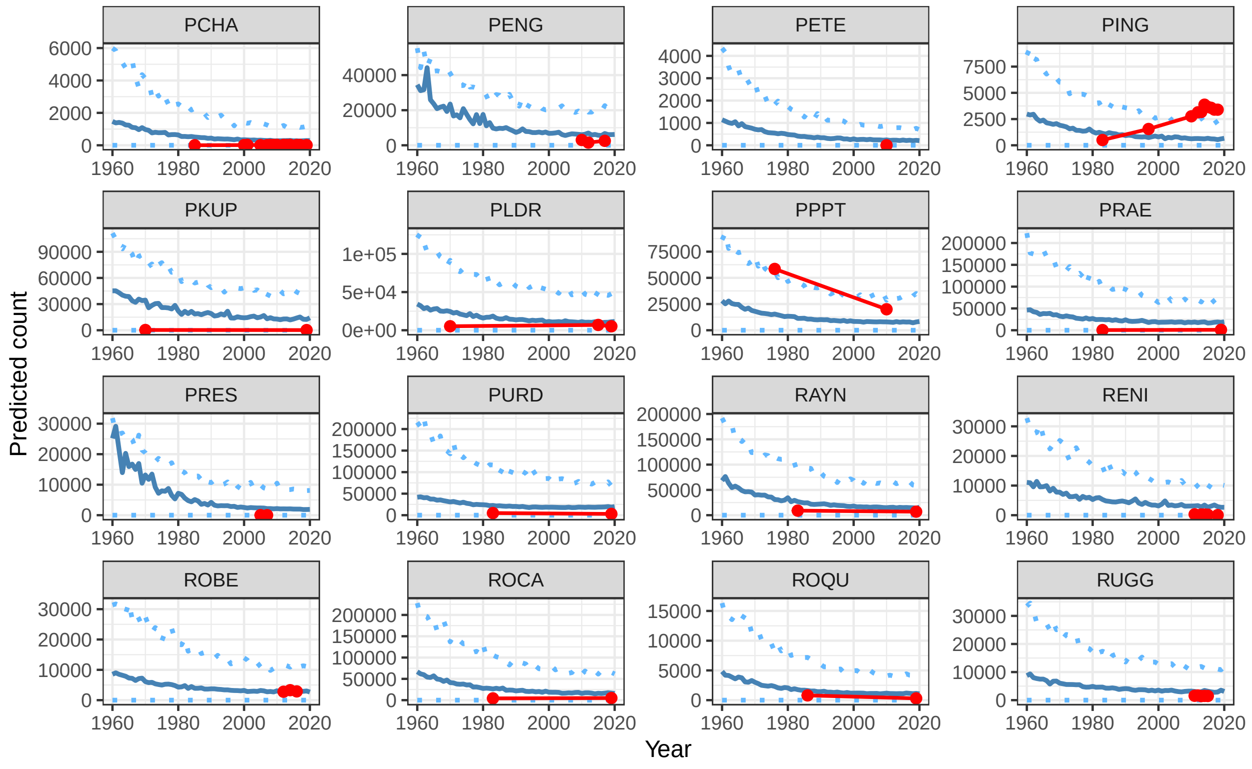

CRWL
CUVE
DECI
DEEI
DELA
DREA
DUPT
EADI
ECAP
ECKE
EIP1
EIP2
EIP3
EIP4
EIP5
ELLI
Predicted count
Year


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

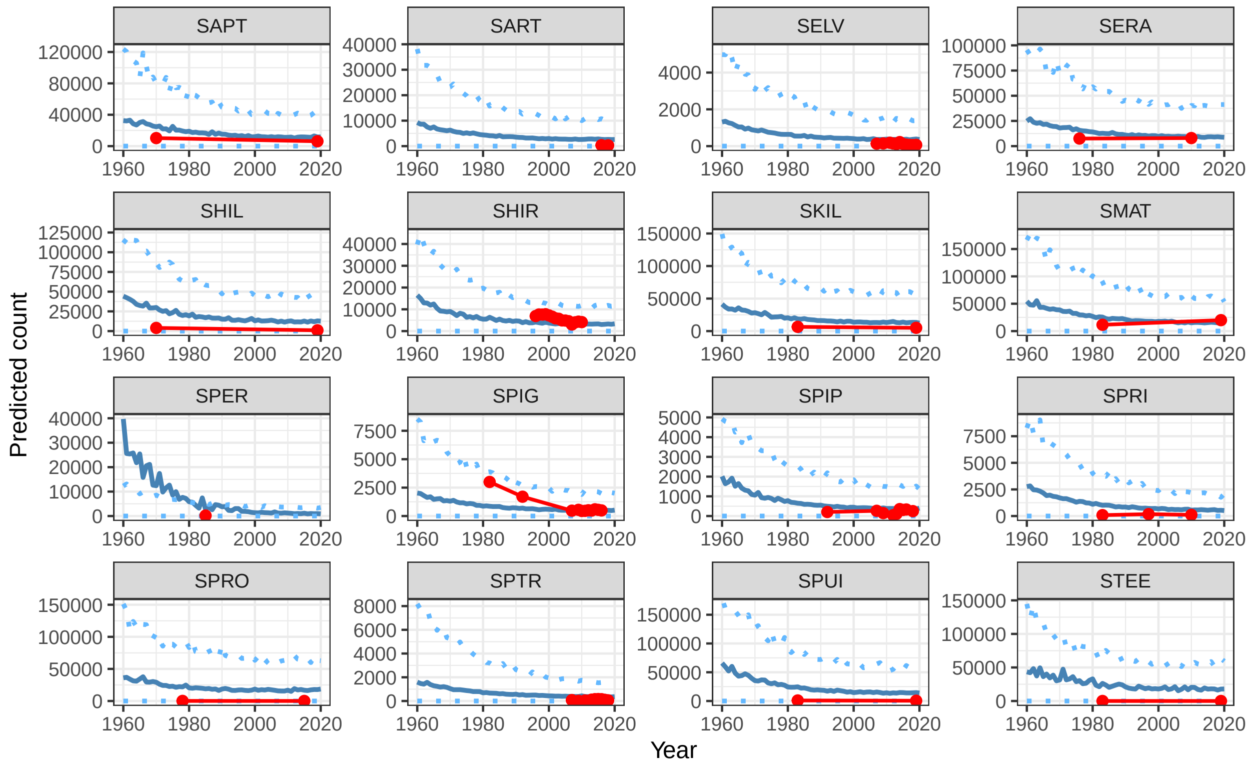

HALF
HANN
HARE
HARM
HUMB
HUNT
HUTB
HYDR
HYDS
JACO
JACP
JOUB
KAYR
KETL
LLOY
LOOK
Predicted count
Year

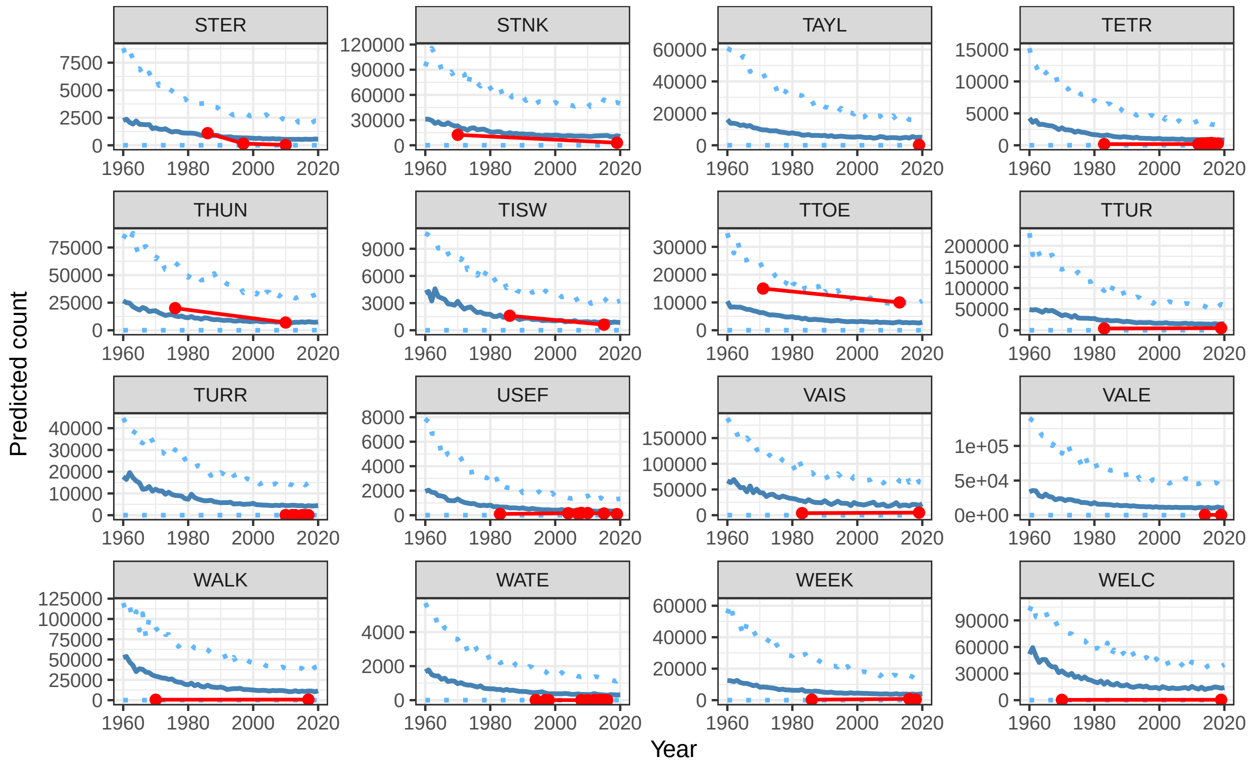


MABE
MANS
MATH
METH
MIDA
MONU
MOSS
MUCK
MURR
NANC
NOPT
NORW
OBRI
ORNE
ORRO
PALA
Predicted count
Year



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
1960
1980
2000
2020


STER
STNK
TAYL
TETR
THUN
TISW
TTOE
TTUR
TURR
USEF
VAIS
VALE
WALK
WATE
WEEK
WELC
Predicted count
Year
1960
1980
2000
2020

2.6 Revised plots of latitude and slope (population change)

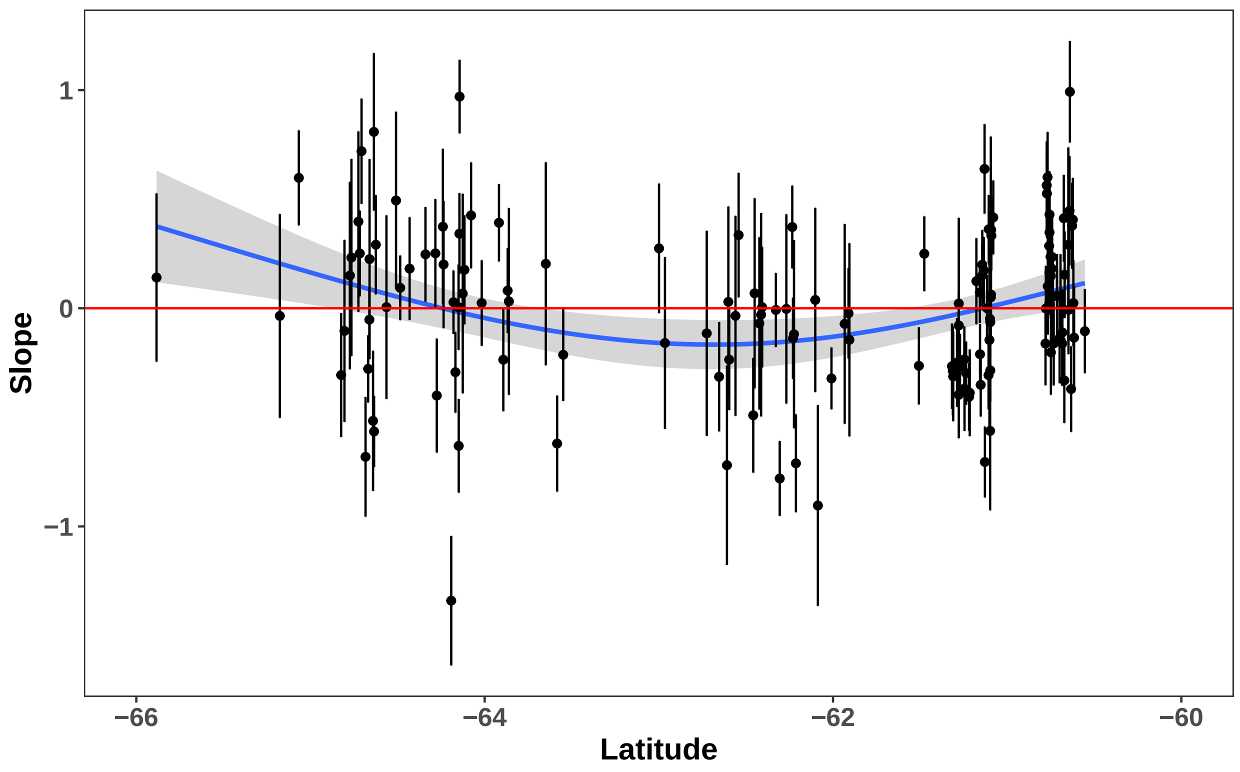
```
# extract random effects from MCMCglmm
# https://stackoverflow.com/questions/64562052/extract-random-effects-from-mcmcglmm
library(broom.mixed)

re = tidy(mc2, effects="ran_vals")
unique(re$group)
```

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

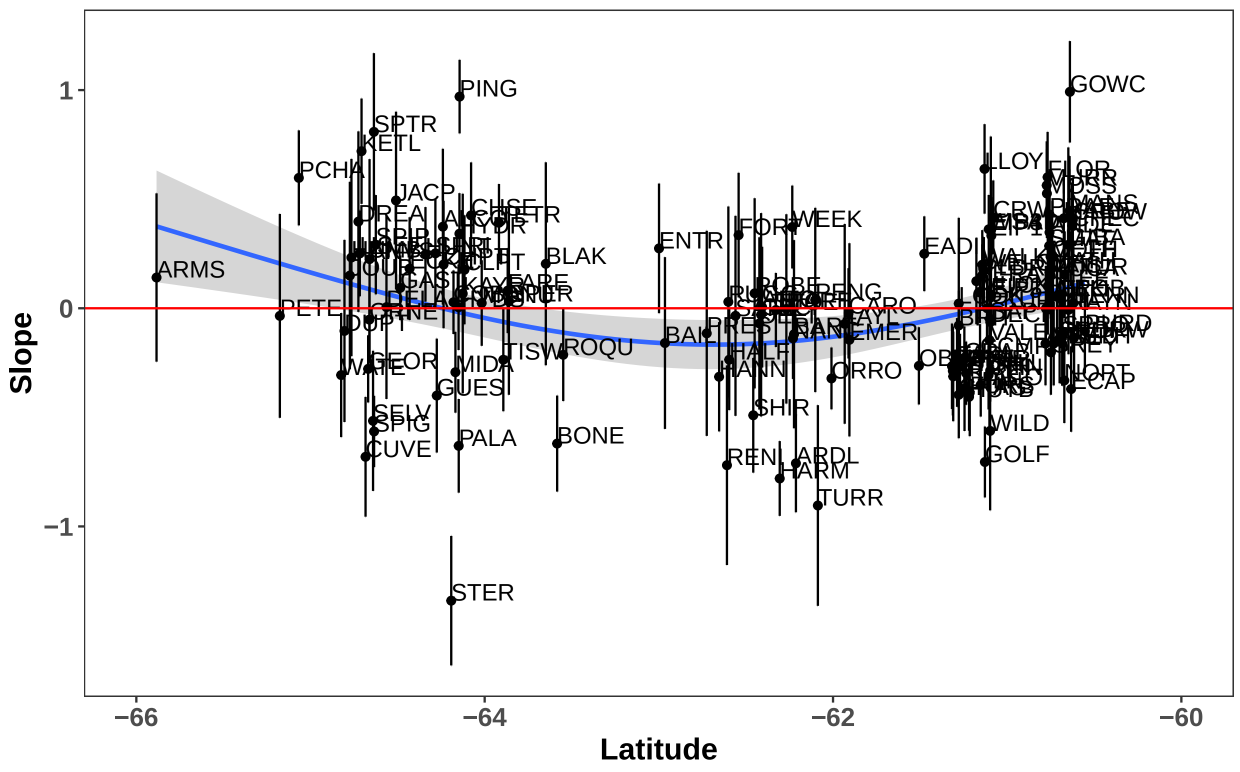
```
re = re %>%
    dplyr::select(-group, -effect) %>%
    pivot_wider(names_from = term, values_from = c(estimate, std.error))

head(re)
```

```
## # A tibble: 6 x 5
##   level `estimate_(Intercept)` estimate_Zseason_starting `std.error_(Intercept)`
##   <chr>                  <dbl>                     <dbl>                   <dbl>
## 1 AILS                  0.513                   -0.162                     0.329
## 2 AITC                  2.11                     0.00502                   0.253
## 3 AITK                  0.228                    0.0537                    0.317
## 4 ALCO                  2.00                     0.374                     0.345
## 5 AMPH                  0.0494                  -0.162                     0.325
## 6 ANDE                 -2.75                     0.348                     0.320
## # i 1 more variable: std.error_Zseason_starting <dbl>
```

```
# 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")
```



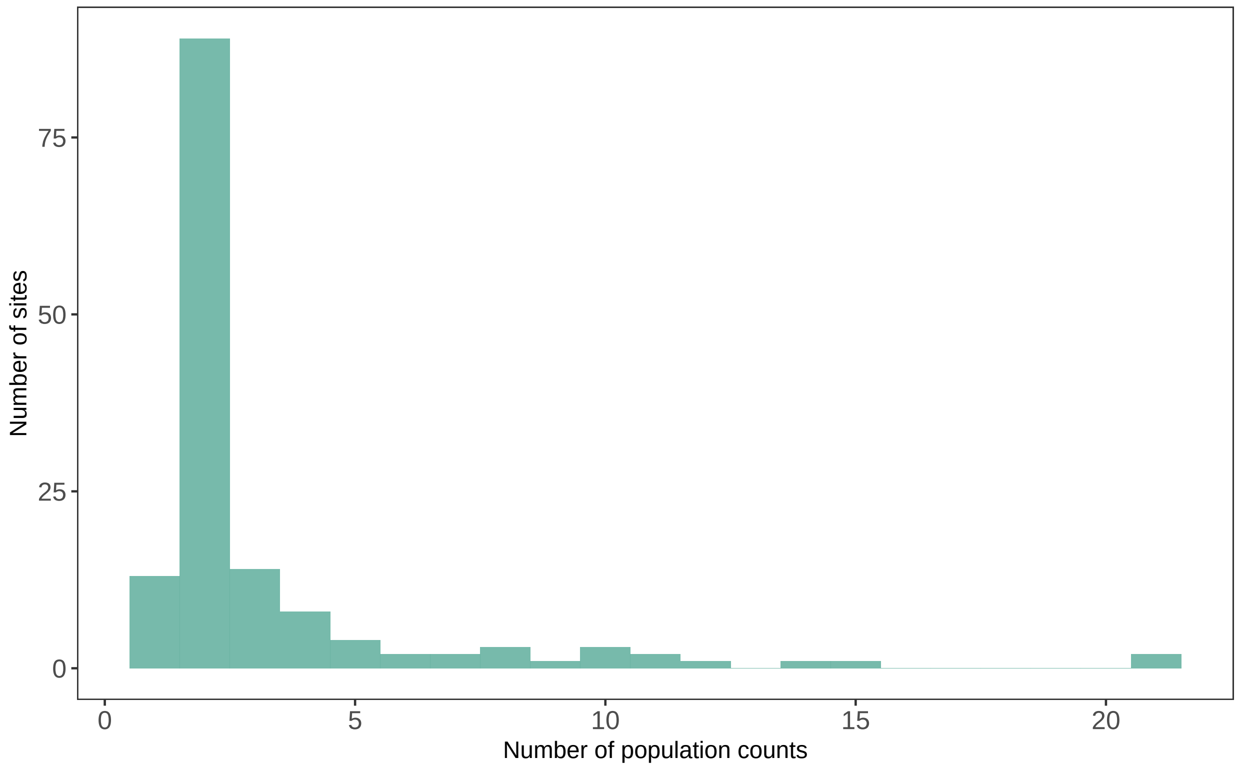
The following figures plot the data from the original study

3 Oosthuizen et al - data distribution figures

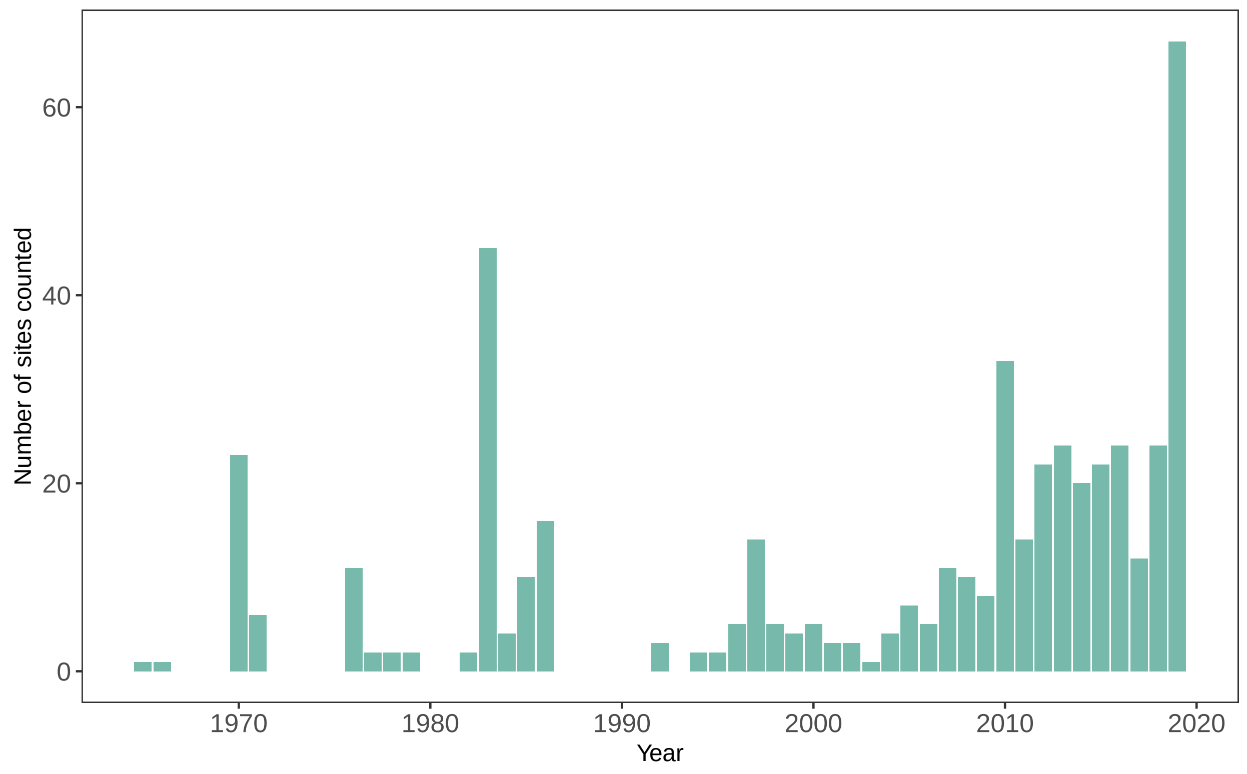
```
# This shows that there are some 1-count sites in the data being analysed
# (n = 146, not n = 133)
samplesize = nestM3 %>% group_by(site_id, ncounts) %>% tally()
length(unique(nestM3$site_id))
```

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

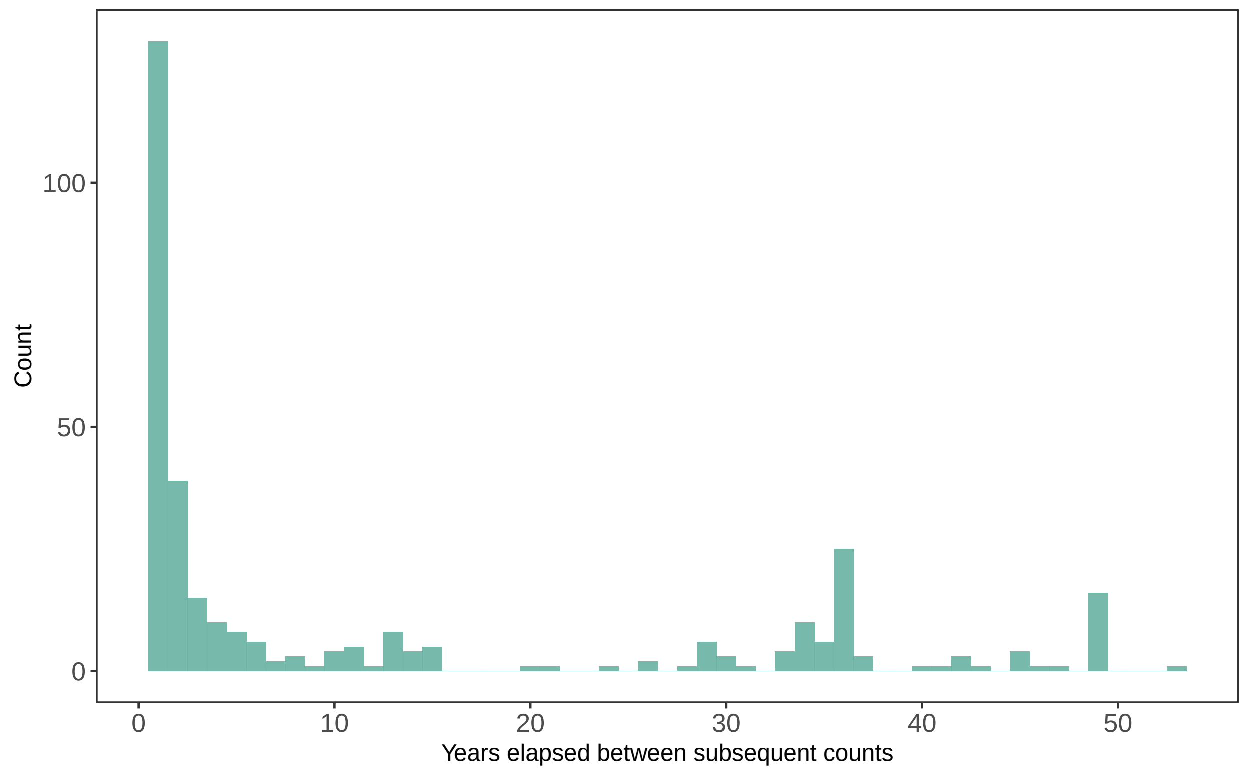
```
samplesize.plot <- samplesize %>%
  ggplot(aes(x=n)) +
  geom_histogram(binwidth=1, fill="#69b3a2",  alpha=0.9) +
  theme_bw()+
  ylab("Number of sites")+
  xlab("Number of population counts") +
  theme(axis.text=element_text(size=12),
        panel.grid.major = element_blank(),
        panel.grid.minor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

samplesize.plot
```



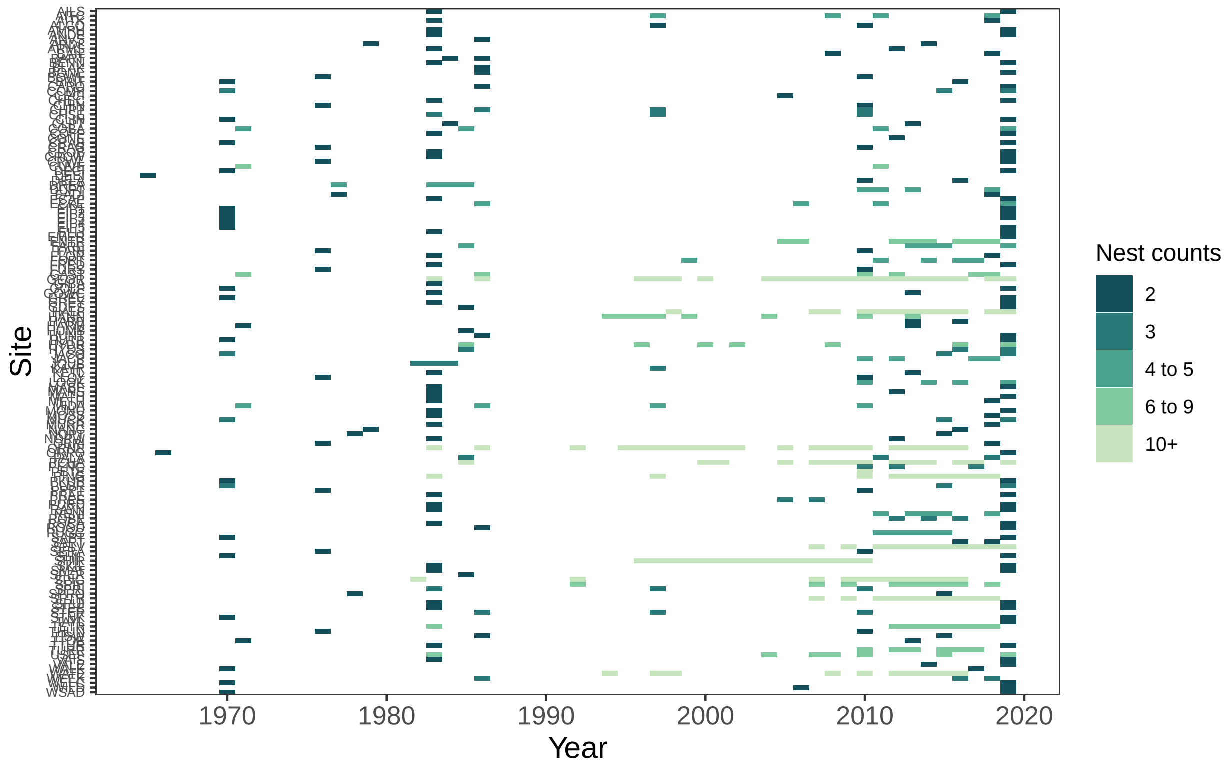
```
## Save Plot
# pdf("./Figure samplesize.pdf",
#     useDingbats = FALSE, width = 4, height = 4)
# samplesize.plot
# dev.off()

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
```



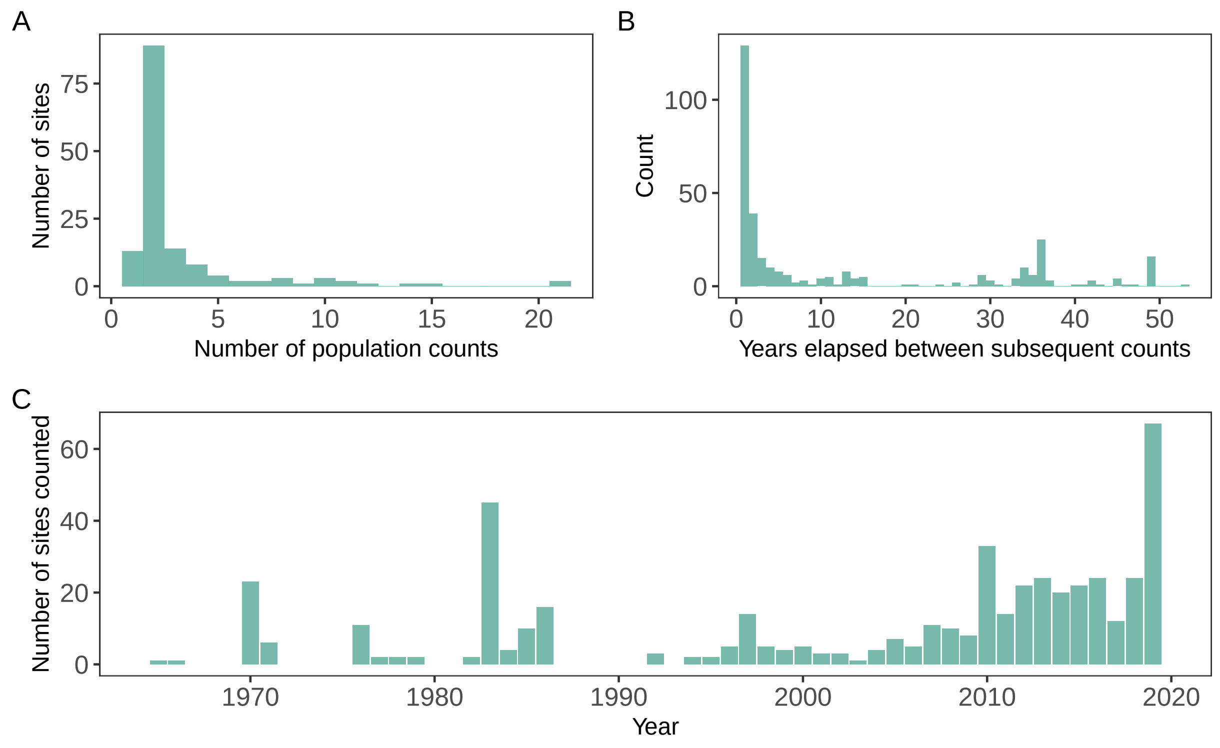
```
## Save Plot
# pdf("./Figure samplesizeYear.pdf",
#     useDingbats = FALSE, width = 6, height = 4)
# samplesizeYear.plot
# dev.off()

# 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
```



```r
## 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
```



```r
## 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
```



```r
## Save Plot
# pdf("./figure/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?)

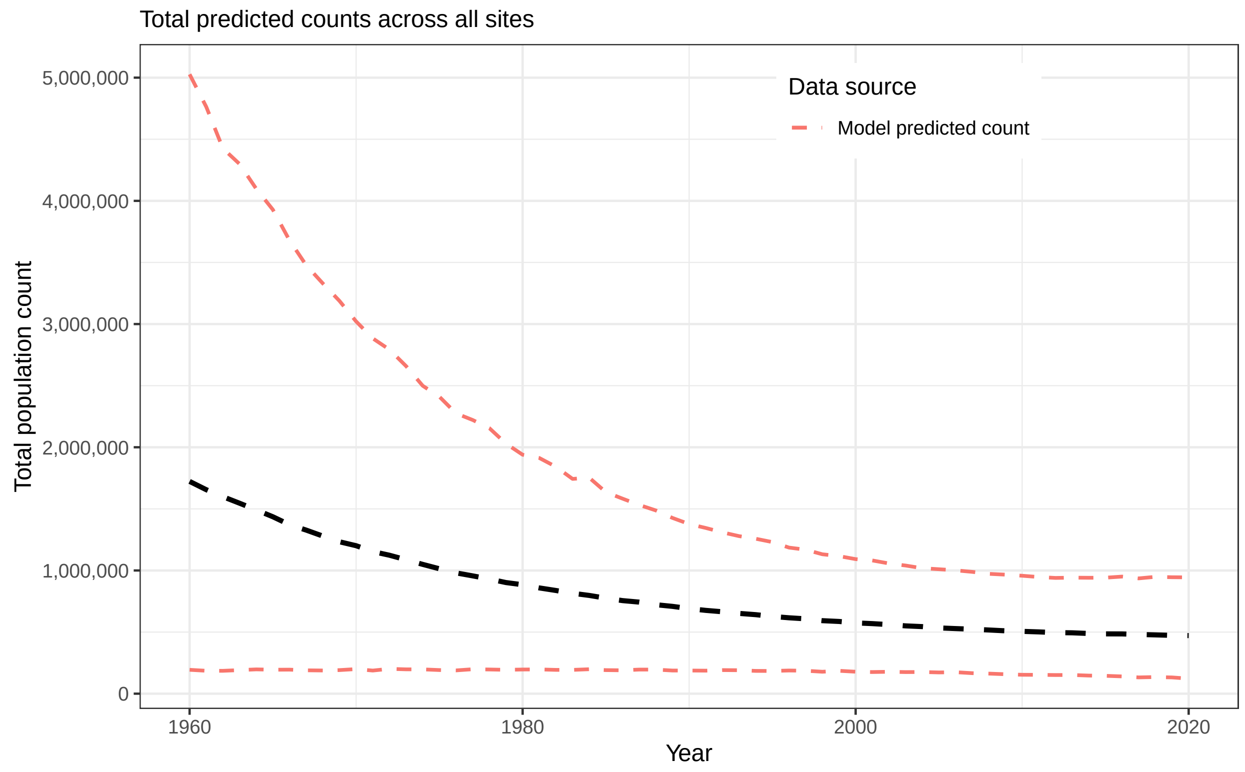
```r
head(popy)
```

```
##   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 10376.781 1720 23803  34582.09         0    155103
## 2    2019  5758.052 1637 10672  16037.88         2     62417
## 3    2019  9477.298 1018 20666  30140.19         1    114384
## 4    2019  8147.767 1429 18271  24930.19         2    117409
## 5    2019  7476.230 1495 14982  19568.98         3     88914
## 6    2019  4382.271 1491  7931  12434.09         2     45729
```

```
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))
```

```
## 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.
```

```
pop_predict.p
```



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

```
##   total_pred
## 1  -72.63636
```

5 Oosthuizen et al - Predicting population change

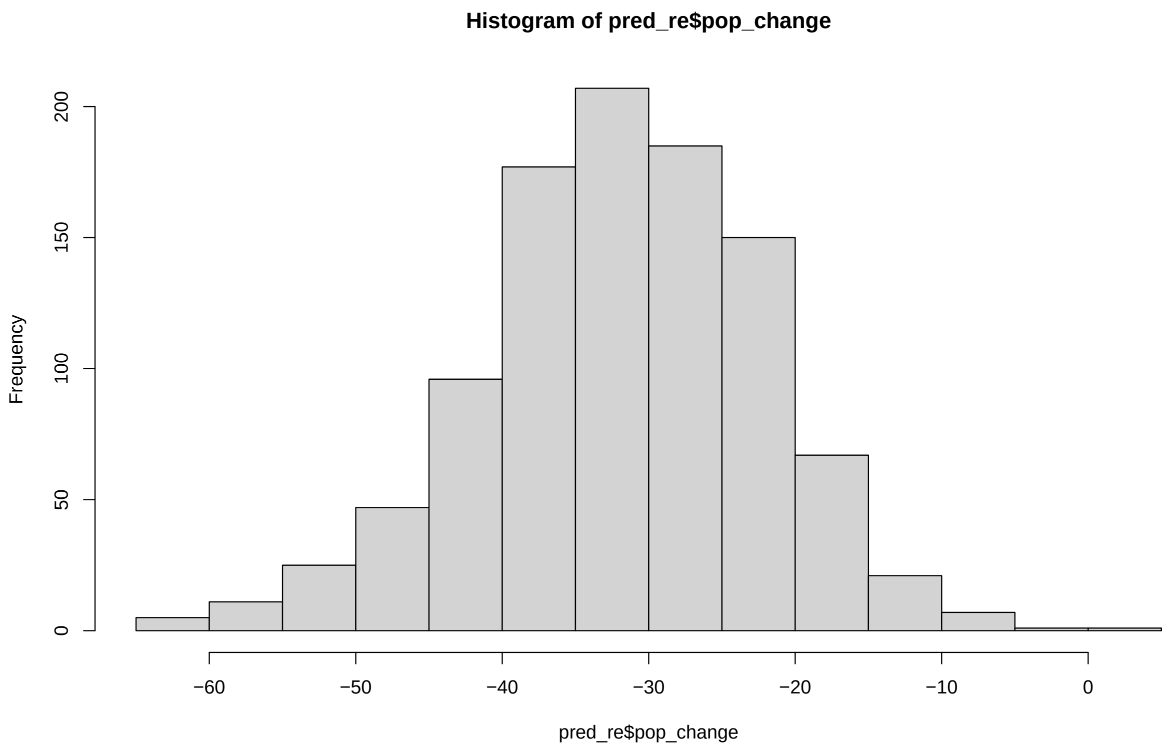
Calculate population change over a 30 year period (~ 3 generations according to the original study)

```r
# 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, use 1990 as the first year and 2019 as the last year  (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,
                            last_year,
                            use_random_effects = FALSE) {
  # matrices for predictions at each site in year 1 and year 2
  # 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 +
```

```r
        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)
```

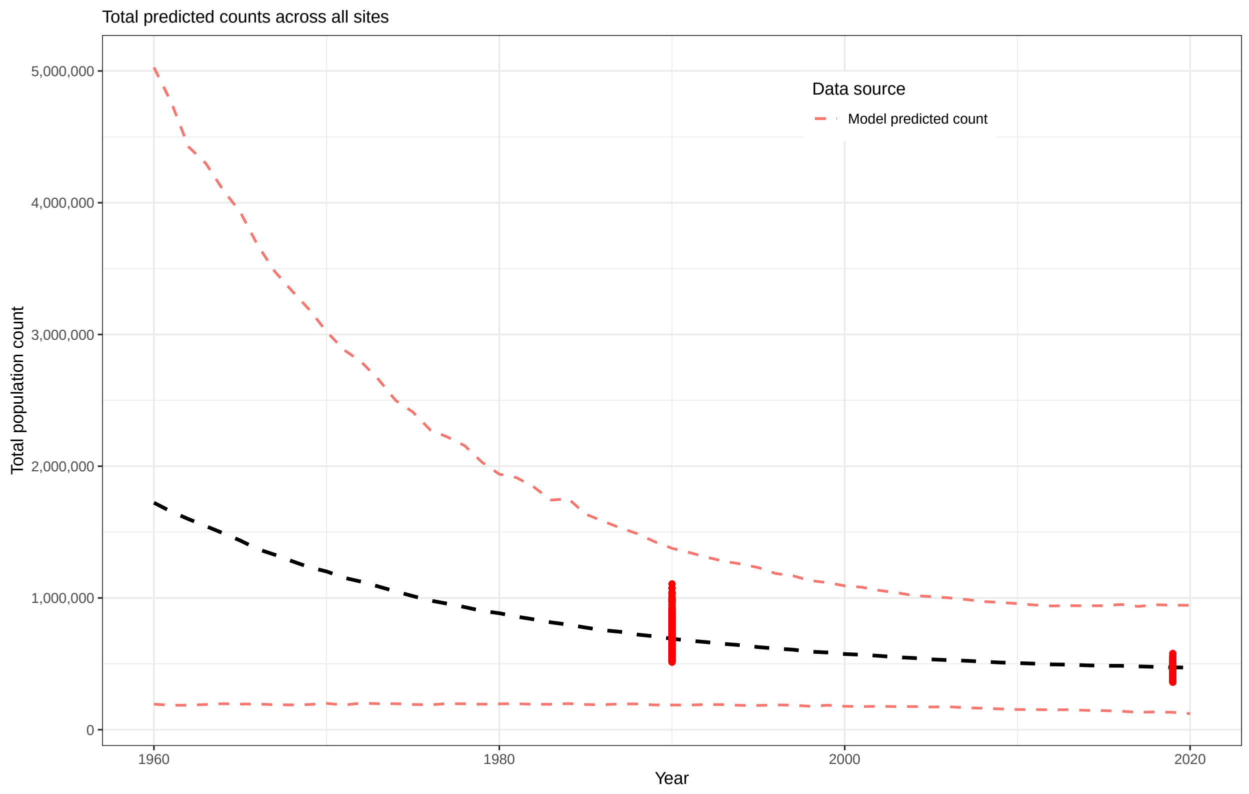


```r
# can calculate the probability that the population has decreased by
# at least thirty percent with
mean(pred_re$pop_change < -30)
```

```
## [1] 0.568
```

```r
# 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)

#----------------------------------------------------------------------------
# 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"
#
```

```r
# # 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")
```



> Note of Caution. When modeling counts using the Poisson distribution with a log link, the link scale is linear, while the response scale is exponential. So extrapolating backwards in time (without many observations) can lead to large (exponential) model predicted increases in populations counts.