Supporting documentation: Unreliable inferences about chinstrap penguin population trends: a statistical critique and reanalysis

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Contents

1 Krüger (2023) reanalysis

This script provides a reanalysis of chinstrap penguin population trends, in the context 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.).

- To reduce extrapolation beyond the range of observed data, this revised analysis restricted predictions of population trends between 1980 and 2019.
- This script evaluated the 30-year population change between 1990 and 2019 at all sites (n = 91) with at least two counts (with accuracy < 5) between 1980 and 2019

2 Load packages and set plotting theme

```r
# Load packages
library(tidyverse)
library(MCMCglmm)
library(scales)
library(ggforce)

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

3 Load and process MAPPPD data for area 48.1 and 48.2:

```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 data to chinstrap penguins only
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
# subset to use only nest counts
nests <- subset(chins,count_type=="nests")
dim(nests)
```

```
## [1] 1104   15
```

```r
# subset to cammlr_region 48.1 and 48.2
nests <- subset(nests,cammlr_region =="48.1" | cammlr_region =="48.2")
dim(nests)
```

```
## [1] 1103   15
```

```r
# remove the most uncertain counts (could be very inaccurate - an order of magnitude)
# This is a choice we made for the current analysis.
# Comment this line of code out to run analysis including uncertain counts
nests <- subset(nests, accuracy < 5)
dim(nests)
```

```
## [1] 944  15
```

```r
nests = subset(nests, nests$season_starting> 1979)

which(colSums(is.na(nests))>0)
```

```
##   day month
##     7     8
```

```r
# some populations had multiple counts over the same season:
# this code summarises the count with the maximum nests
nestM = nests %>%
          group_by(site_id, season_starting) %>%
          slice(which.max(penguin_count)) %>%      # take only maximum counts
          dplyr::rename(Lat = latitude_epsg_4326,
                        Lon = longitude_epsg_4326,
                        nests = penguin_count) %>%
          dplyr::select(season_starting, site_id, nests, Lat, Lon)

dim(nestM)
```

```
## [1] 764   5
```

4 Processed data summary

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

```
##   site_id     Lat     Lon ncounts minseason maxseason interval
## 1    ACUN -60.761 -44.637       2      1983      2004       21
## 2    AILS -60.780 -44.631       1      1983      1983        0
## 3    AITC -62.407 -59.752       4      1997      2018       21
## 4    AITK -60.738 -44.525       1      1983      1983        0
## 5    ALCO -64.240 -61.127       3      1989      2010       21
## 6    AMPH -60.684 -45.339       1      1983      1983        0
```

```r
summary(as.factor(countsN$ncounts)) # most populations are only counted once
```

```
##   1   2   3   4   5   6   7   8   9  10  11  12  15  16  22  23  24  28  30  31
## 152  35  13   7   4   5   1   4   2   5   2   2   1   1   2   1   1   2   1   1
##  33
##   1
```

```r
npops=length(countsN$ncounts[countsN$ncounts>1])
npops # number of populations with more than 2 counts
```

```
## [1] 91
```

```r
nestM2 <- merge(nestM,countsN) # add number of counts for each population to nestM2

# Subset to sites with more than 1 count:
nestm3 = subset(nestM2, ncounts>1)
#nestm3 = subset(nestm3, nestm3$interval > 9)
#nestm3 = subset(nestm3, nestm3$minseason < 2005 & nestm3$maxseason > 2004)

nestM3 <- nestm3

countspersite = nestM3 %>%
      group_by(site_id) %>%
      summarise(counts = mean(ncounts))

summary(countspersite$counts)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   2.000   2.000   3.000   6.725   8.000  33.000
```

5 Oosthuizen et al data distribution figures

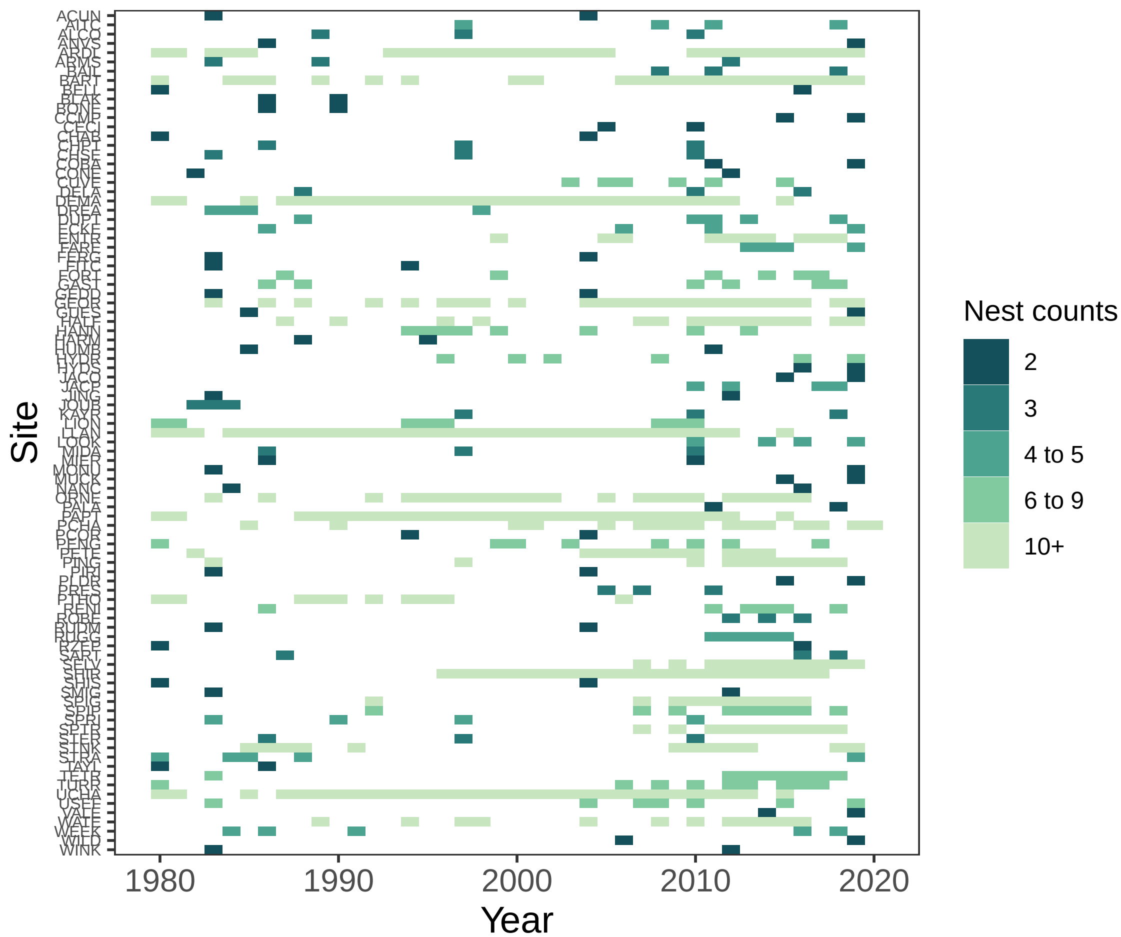
```r
# This shows that there are some 1-count sites in the data being analysed
# (n = 146, not n = 133)
samplesize = nestM3 %>% group_by(site_id, ncounts) %>% tally()
length(unique(nestM3$site_id))
```

```
## [1] 91
```

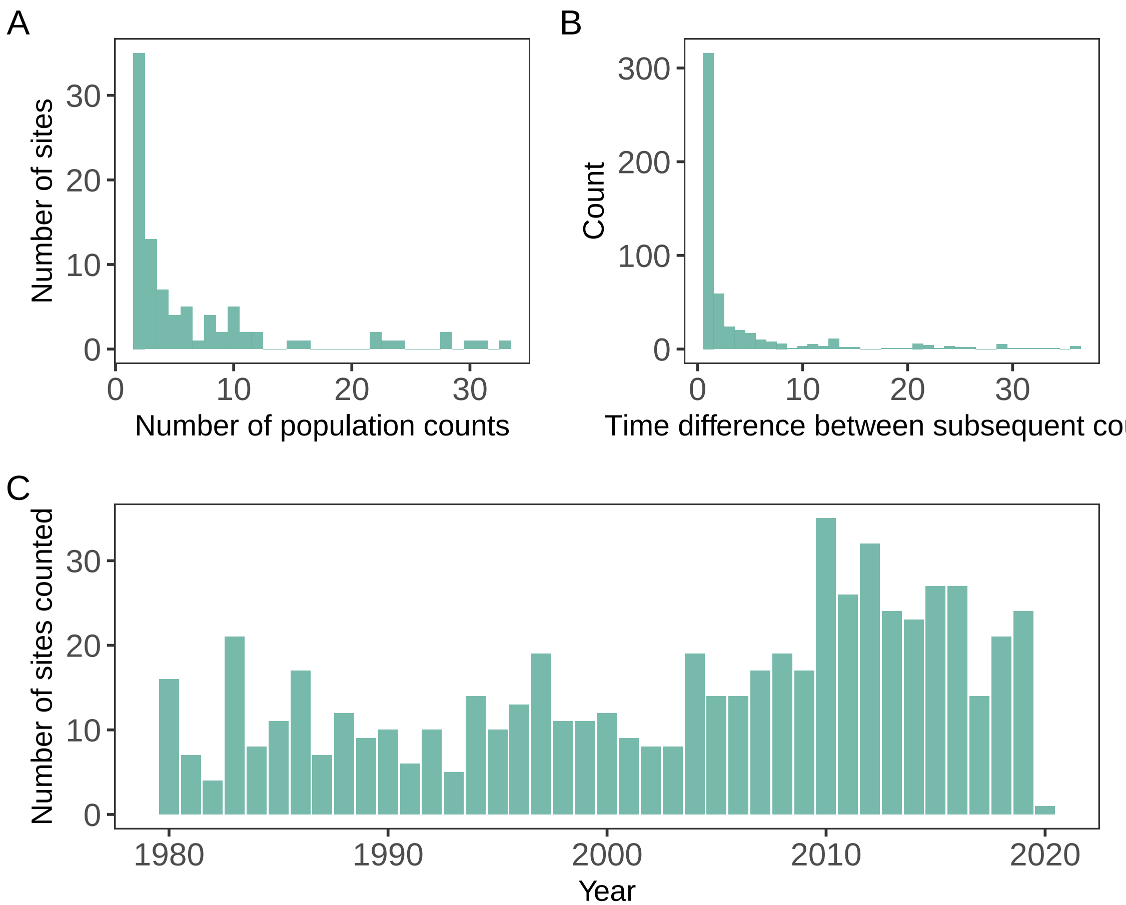
```r
samplesize.plot <- samplesize %>%
  ggplot(aes(x=n)) +
  geom_histogram(binwidth=1, fill="#69b3a2",  alpha=0.9) +
  theme_bw()+
  ylab("Number of sites")+
  xlab("Number of population counts") +
  theme(axis.text=element_text(size=12),
        panel.grid.major = element_blank(),
        panel.grid.minor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

```r
# samplesize.plot

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

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

# 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("Time difference 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

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),
```

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



6 Analysis for Oosthuizen et al. (current)

6.1 Fit a better GLMM

```
# How is this model different to Kruger (2023)?
# 1) We used a different model specification for fixed and random effects
# 2) We z-standardized the covariates before running the model
# 3) We 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)

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))))
```

```r
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=30000, thin=10, burnin=10000, pr=T,
              pl=FALSE, verbose=F, DIC=TRUE, singular.ok=FALSE, saveX=TRUE,
              prior=prior, saveZ=TRUE, saveXL=TRUE, slice=FALSE,
              ginverse=NULL, trunc=FALSE)
```

```r
summary(mc2)
```

```
##
##  Iterations = 10001:29991
##  Thinning interval  = 10
##  Sample size  = 2000
##
##  DIC: 5611.676
##
##  G-structure:  ~us(1 + Zseason_starting):site_id
##
##                                             post.mean l-95% CI u-95% CI eff.samp
## (Intercept):(Intercept).site_id                8.1138   5.7002   10.756   1618.8
## Zseason_starting:(Intercept).site_id           1.8688   1.0181    2.798    784.5
## (Intercept):Zseason_starting.site_id           1.8688   1.0181    2.798    784.5
## Zseason_starting:Zseason_starting.site_id      0.9741   0.5821    1.409    973.6
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.1151  0.09472   0.1379     1264
##
##  Location effects: nests ~ Zseason_starting * ZLat
##
##                         post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)               5.15608  4.54116  5.78297   1870.8 <5e-04 ***
## Zseason_starting         -0.44085 -0.66476 -0.22455   1372.0 <5e-04 ***
## ZLat                      1.55919  1.05830  2.09081   2000.0 <5e-04 ***
## Zseason_starting:ZLat    -0.20078 -0.40464 -0.01164    741.1  0.033 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

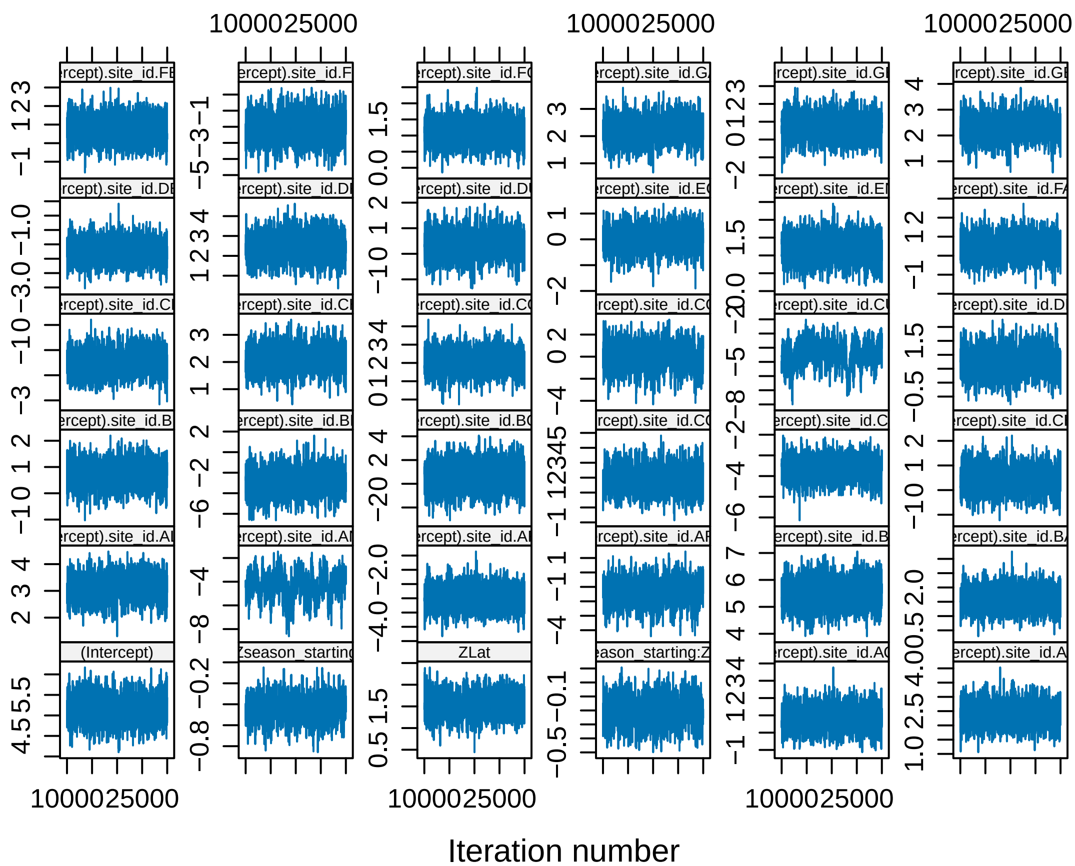
6.2 MCMCglmm diagnostics for mc2

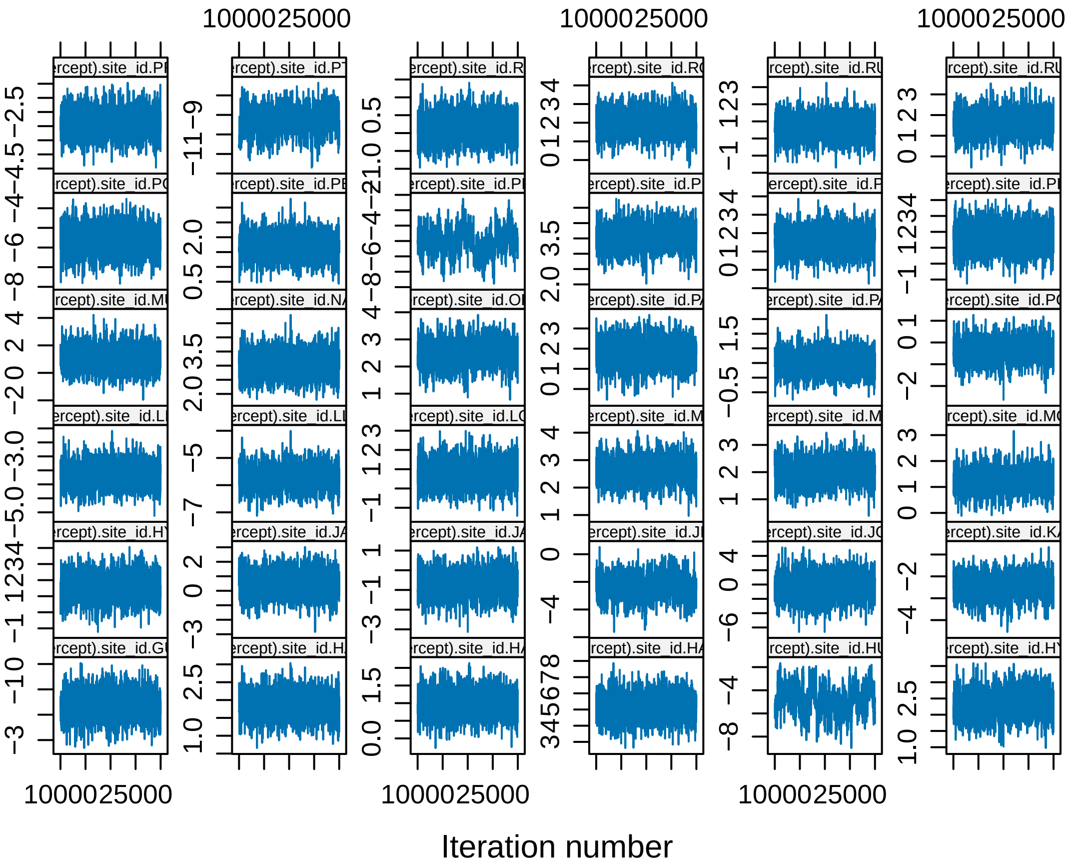
```r
# Assessing model convergence. We do this separately for both fixed
# and random effects. The trace plot should look like a fuzzy caterpillar

# effective sample size
coda::effectiveSize(mc2$VCV)
```

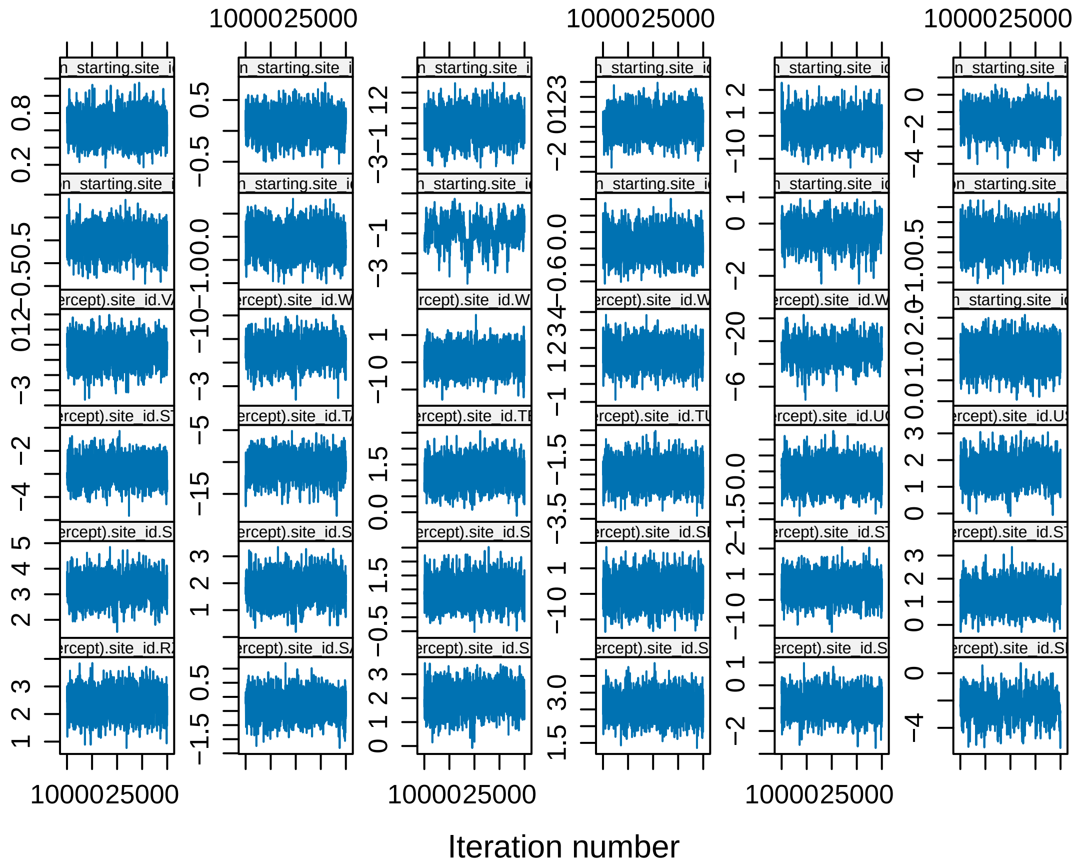
```
##           (Intercept):(Intercept).site_id
```

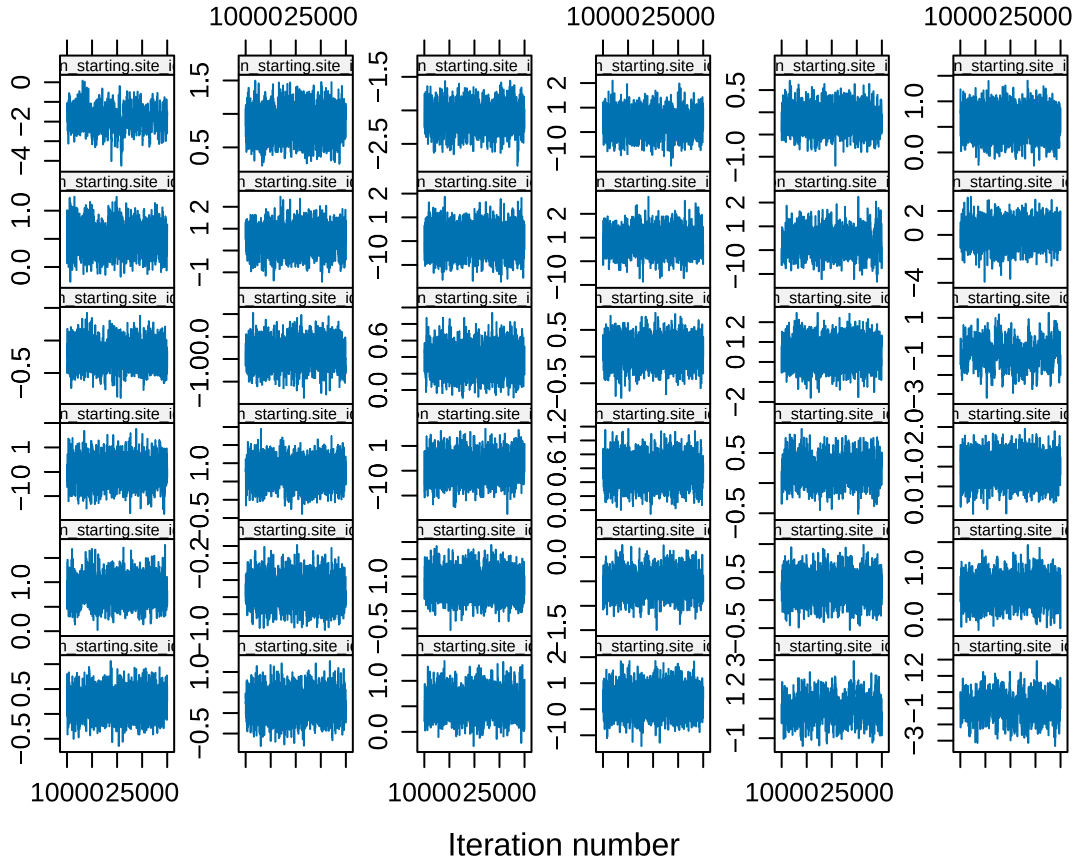
```
##                                  1618.8231
##       Zseason_starting:(Intercept).site_id
##                                   784.4808
##       (Intercept):Zseason_starting.site_id
##                                   784.4808
## Zseason_starting:Zseason_starting.site_id
##                                   973.5844
##                                      units
##                                  1263.7352
```

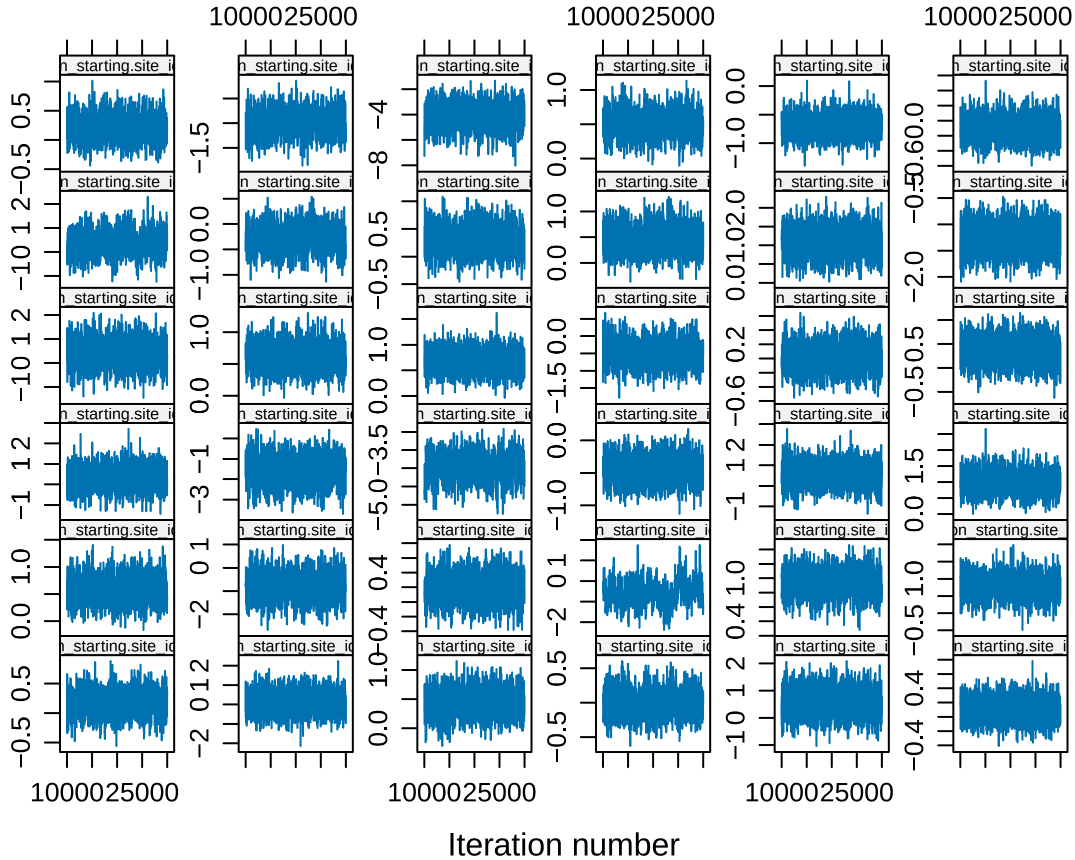
```r
# check that the mcmc chain is mixing well - should be "white noise"
lattice::xyplot(as.mcmc(mc2$Sol), layout=c(6,6), par.strip.text=list(cex=0.5))
```

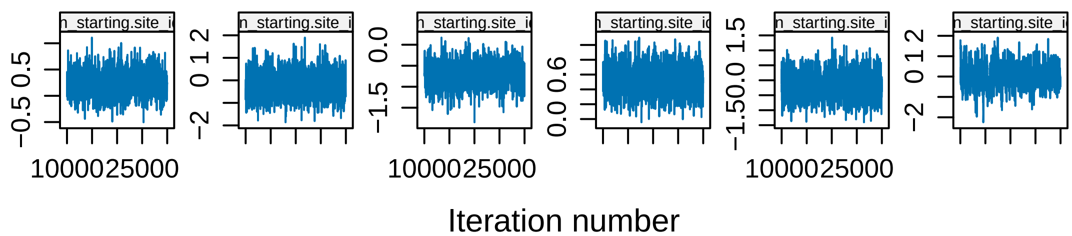



Iteration number

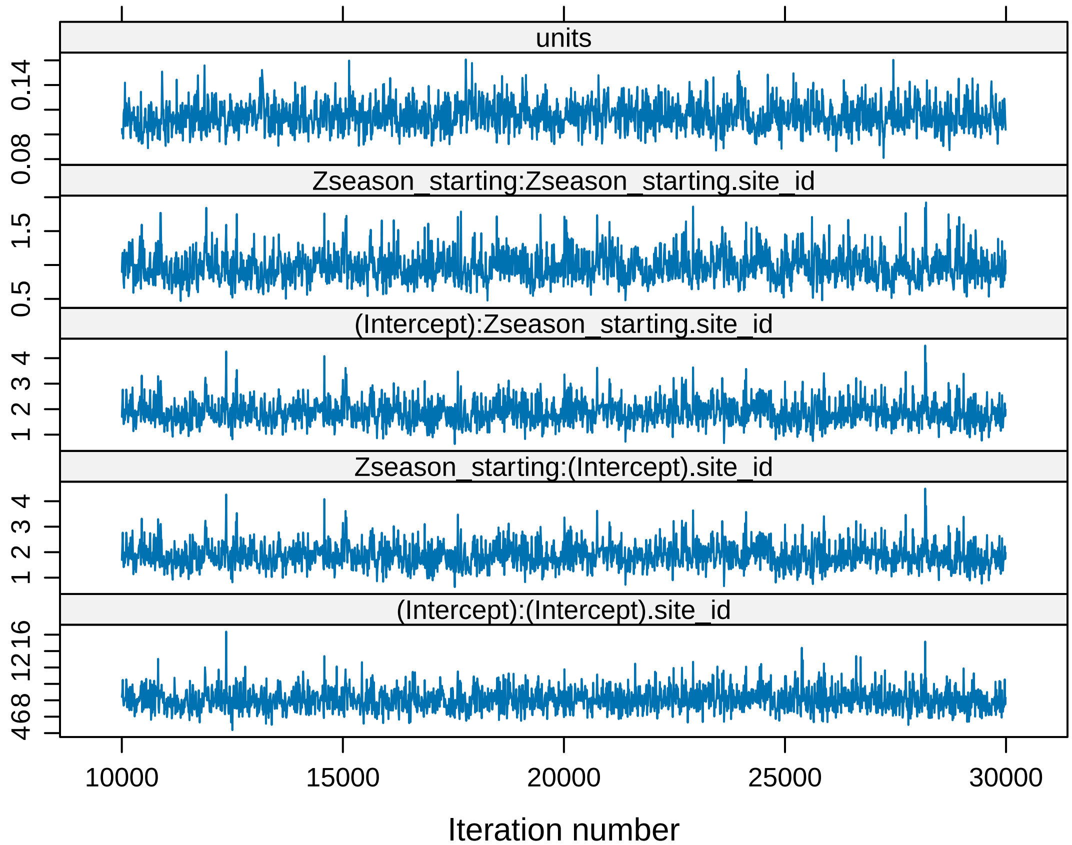

1000025000
Iteration number


Iteration number


1000025000
Iteration number




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




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

```
##            (Intercept):(Intercept).site_id
##                                 0.04448942
##       Zseason_starting:(Intercept).site_id
##                                 0.13271737
##       (Intercept):Zseason_starting.site_id
##                                 0.13271737
## Zseason_starting:Zseason_starting.site_id
##                                 0.16923137
##                                      units
##                                 0.18540852
```

6.3 Predict using MCMCglmm mc2

```r
# construct an hypothetical dataframe to predict to

# need to predict to z-standardized variables
Z1 = dplyr::select(nestM3, season_starting, Lat)
```

```r
Z2 <- scale(Z1)
attr(Z2,"scaled:center")
```

```
## season_starting             Lat
##      2003.25817       -63.15355
```

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

```
## season_starting             Lat
##       11.628821        1.291479
```

```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(1980:2019)) # 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    ACUN -60.761            1980     0        -2.000045  1.8525633
## 2    AITC -62.407            1980     0        -2.000045  0.5780551
## 3    ALCO -64.240            1980     0        -2.000045 -0.8412484
## 4    ANVS -64.661            1980     0        -2.000045 -1.1672314
## 5    ARDL -62.213            1980     0        -2.000045  0.7282705
## 6    ARMS -65.884            1980     0        -2.000045 -2.1142080
```

```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: 91 x 3
##    site_id minyear maxyear
##    <chr>     <int>   <int>
##  1 ARDL       1980    2019
##  2 BART       1980    2019
##  3 BELL       1980    2016
```

```
## 4 CHAB        1980    2004
## 5 DEMA        1980    2015
## 6 LION        1980    2010
## 7 LLAN        1980    2015
## 8 PAPT        1980    2015
## 9 PENG        1980    2017
## 10 PTHO       1980    2006
## # i 81 more rows
```

```
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] 91
```

```
popypred <- 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"))

head(popypred)
```

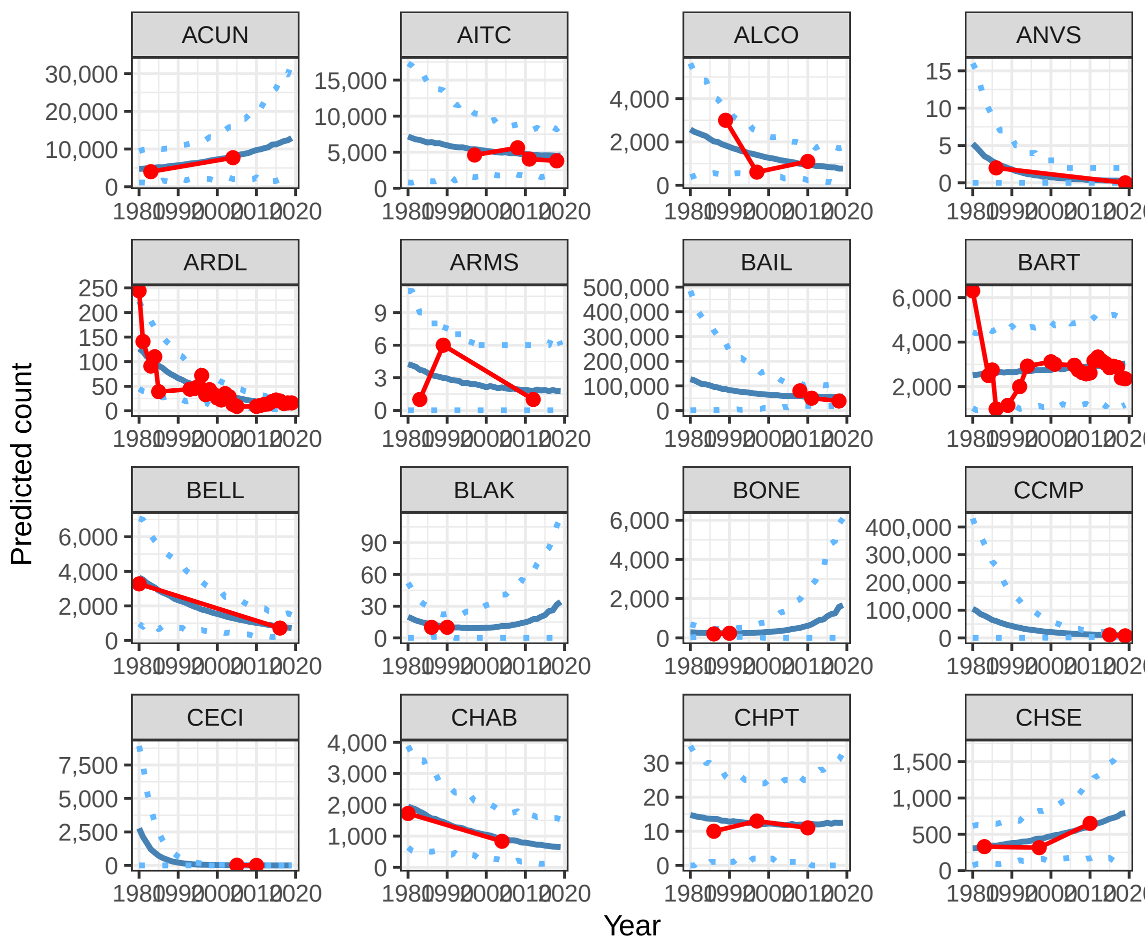
```
##          fit  lwr   upr
## 1  4762.095 1111  9448
## 2  5062.144 1468  9815
## 3  5526.481 1262 10168
## 4  5978.181 1741 11167
## 5  6333.770 2038 11699
## 6 12321.150 1252 29759
```

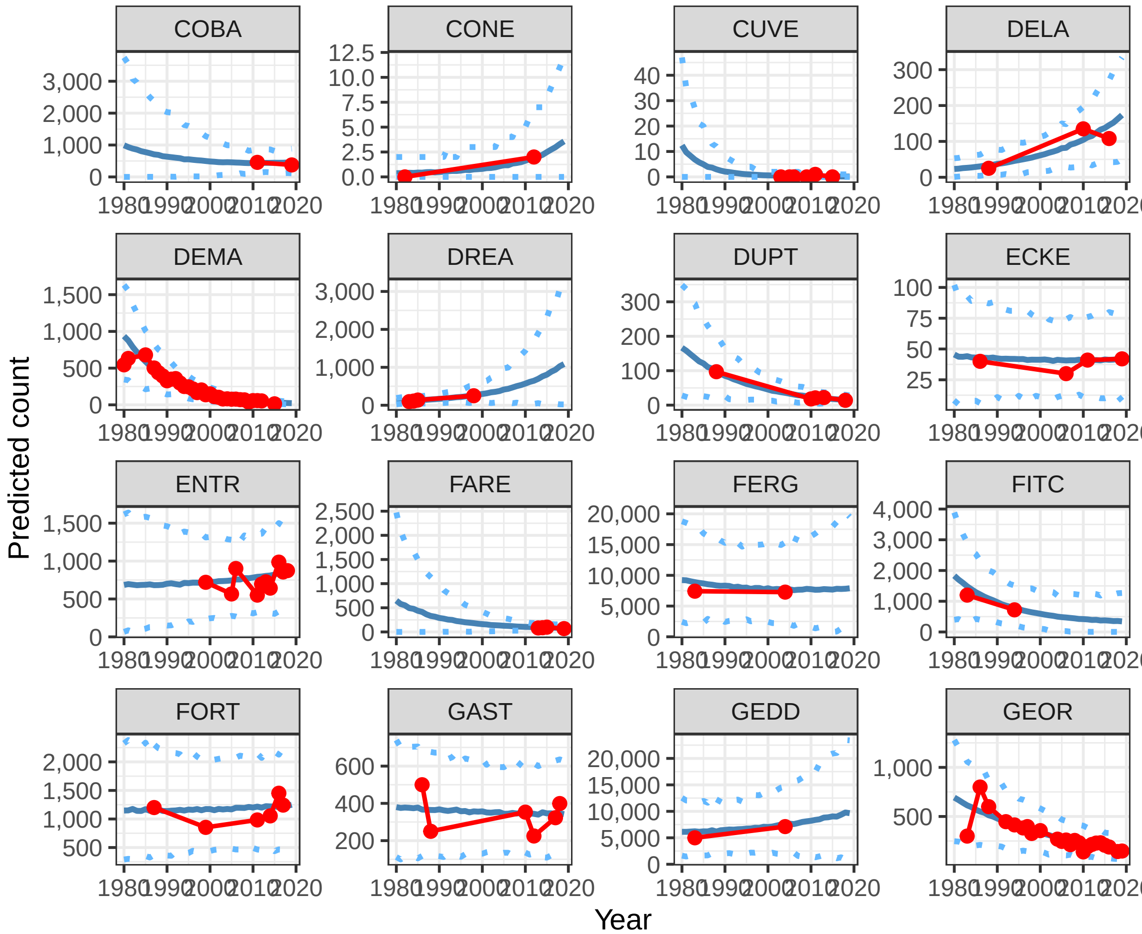
```
popy$Zfit = popypred$fit
popy$Zlwr = popypred$lwr
popy$Zupr = popypred$upr

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

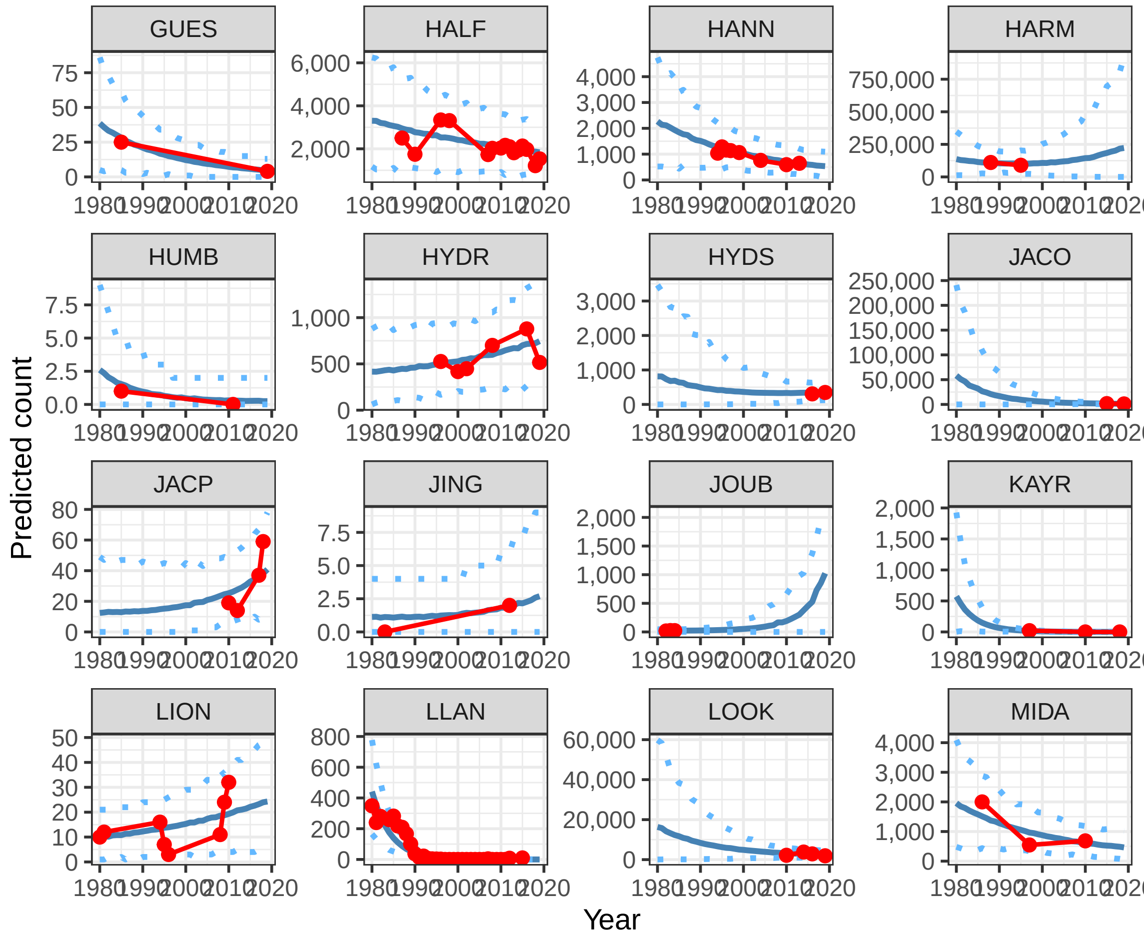
6.4 Conditional model predictions

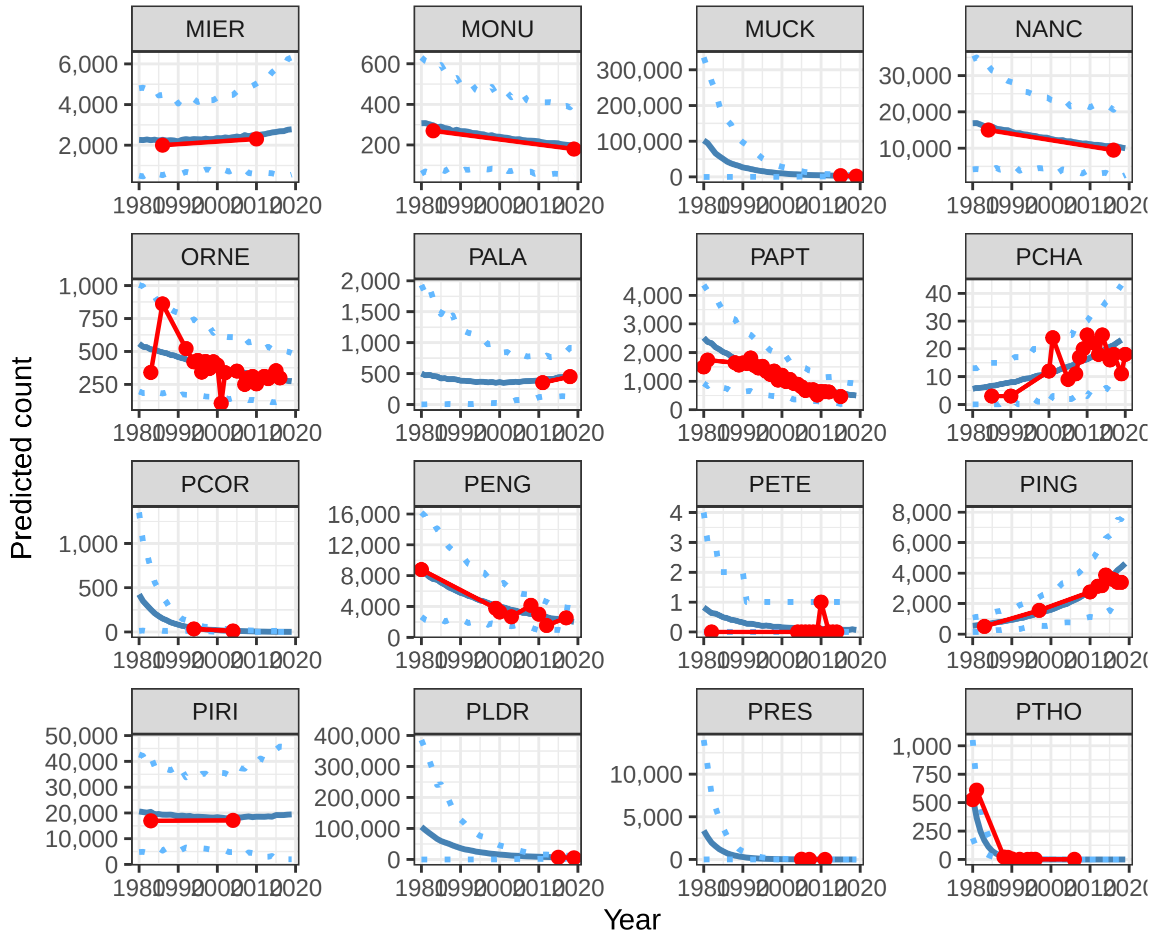
```
#required_n_pages = round(101/16)+1
required_n_pages = round(80/16)+1
for(i in 1:required_n_pages){
```

```r
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") +
    scale_y_continuous(label = comma)+
  #  theme(strip.text = element_text(size = 1.5)) +
    facet_wrap_paginate(~ site_id, ncol = 4, nrow = 4,
                        page = i,
                        scales = 'free'))}
```

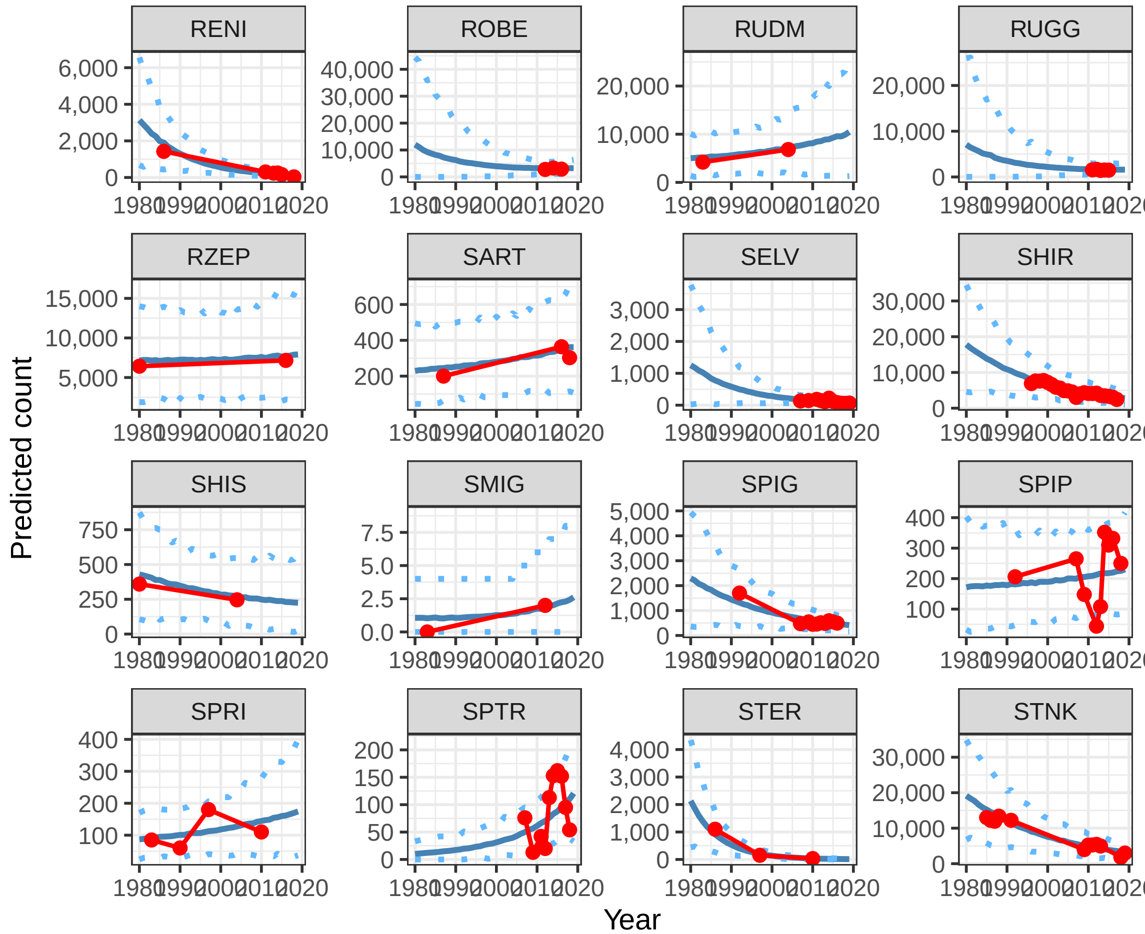


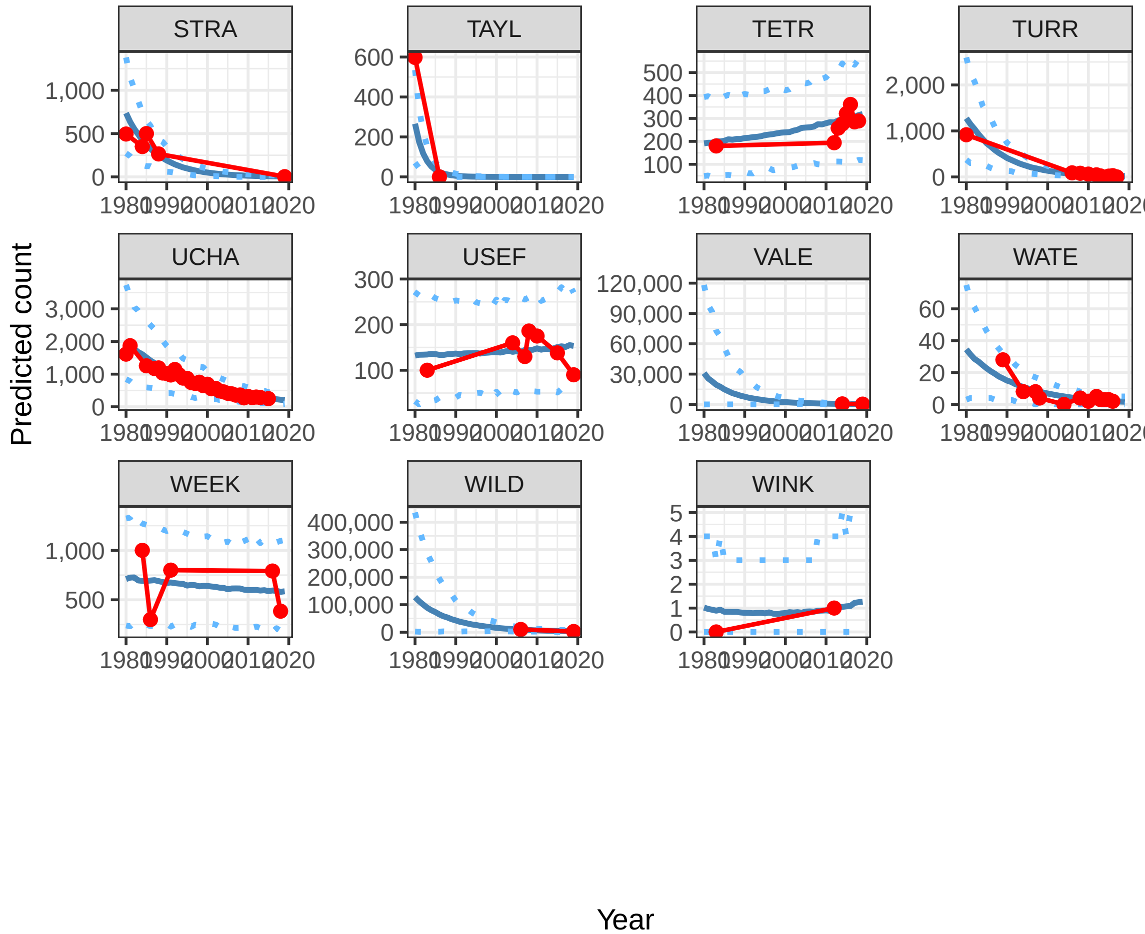

COBA
CONE
CUVE
DELA
DEMA
DREA
DUPT
ECKE
ENTR
FARE
FERG
FITC
FORT
GAST
GEDD
GEOR
Predicted count
Year


GUES
HALF
HANN
HARM
HUMB
HYDR
HYDS
JACO
JACP
JING
JOUB
KAYR
LION
LLAN
LOOK
MIDA
Predicted count
Year



MIER
MONU
MUCK
NANC
ORNE
PALA
PAPT
PCHA
PCOR
PENG
PETE
PING
PIRI
PLDR
PRES
PTHO
Predicted count
Year

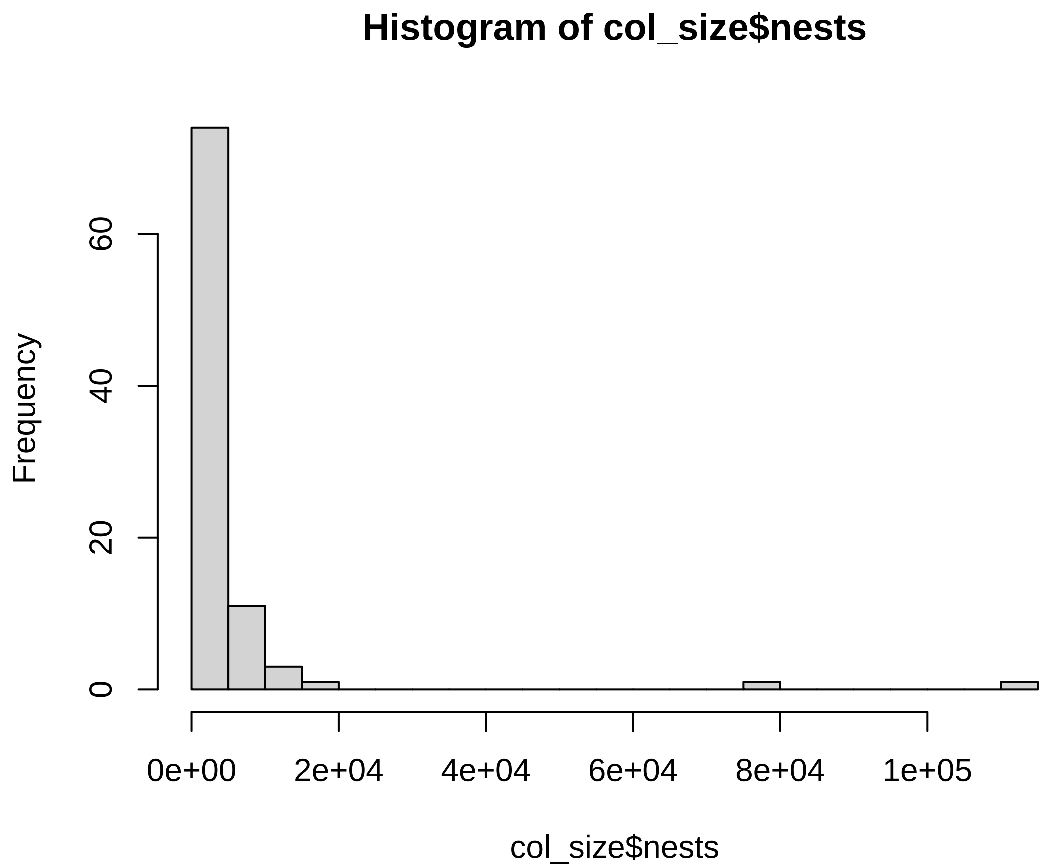

RENI
ROBE
RUDM
RUGG
RZEP
SART
SELV
SHIR
SHIS
SMIG
SPIG
SPIP
SPRI
SPTR
STER
STNK
Predicted count
Year




```r
# Predictions are generally good, but back-predicting to 1960 is extrapolation
# (there are only 1 or 2 counts prior to 1970) so uncertainty (prediction intervals)
# is high.


# Look at some sites with temporally sparse data and strong extrapolation
nestM3 %>% dplyr::filter(site_id == "MUCK")
```

```
##   site_id     Lat    Lon season_starting nests ncounts minseason maxseason
## 1    MUCK -61.157 -54.86            2015  3438       2      2015      2019
## 2    MUCK -61.157 -54.86            2019  2114       2      2015      2019
##   interval Zseason_starting     ZLat
## 1        4         1.009718 1.545938
## 2        4         1.353691 1.545938
```

```r
col_size = nestM3 %>%
           group_by(site_id) %>%
           slice(which.max(nests))

hist(col_size$nests, breaks = 30)
```




```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)
```

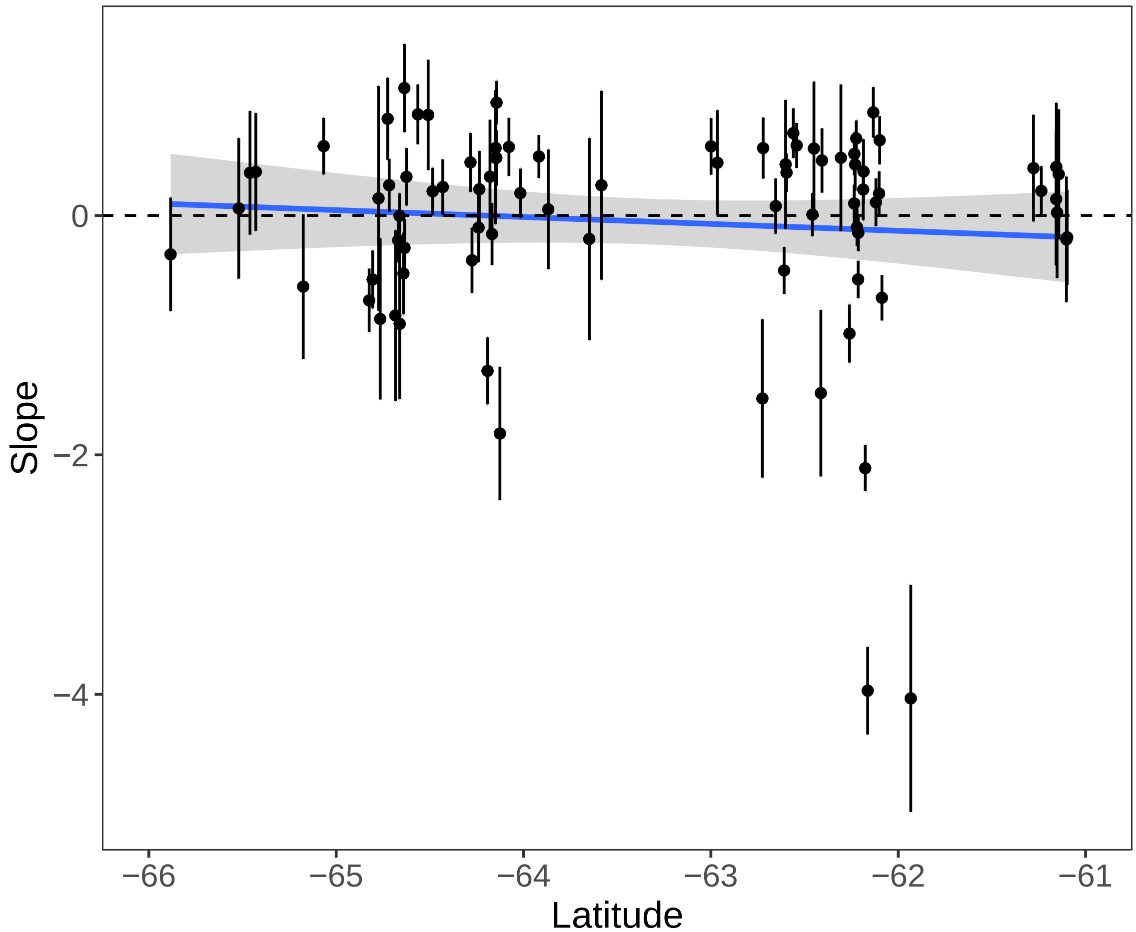
```
## [1] "site_id"
```

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

head(re)
```

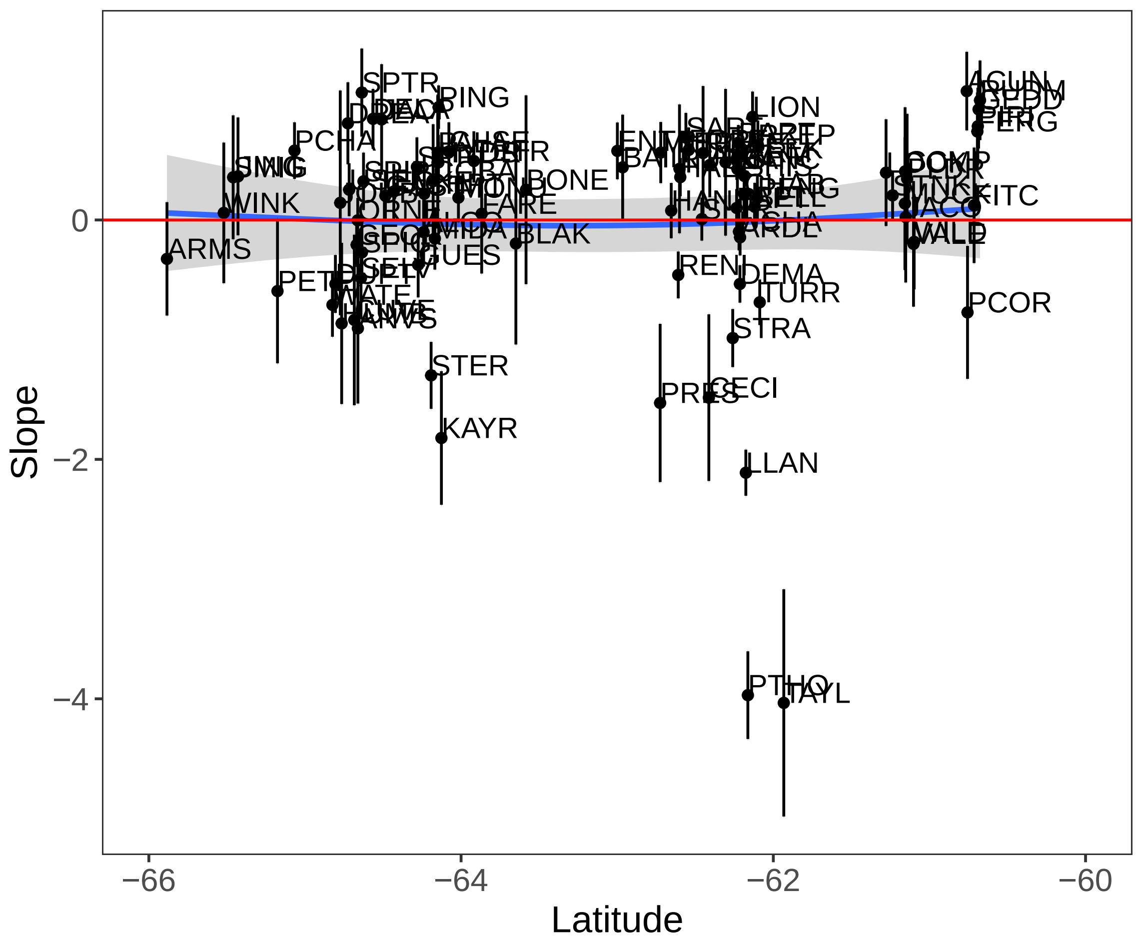
```
## # A tibble: 6 x 5
##   level `estimate_(Intercept)` estimate_Zseason_starting `std.error_(Intercept)`
##   <chr>                  <dbl>                     <dbl>                   <dbl>
## 1 ACUN                   0.813                     1.08                    0.660
## 2 AITC                   2.39                      0.459                   0.406
## 3 ALCO                   3.13                     -0.101                   0.444
## 4 ANVS                  -4.31                     -0.906                   1.10
## 5 ARDL                  -2.99                     -0.145                   0.384
```

```
## 6 ARMS                  -1.32                    -0.325                    0.880
## # 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

lat_plot = 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")+
  scale_x_continuous(lim = c(-66,-61), breaks = seq(-66, -61, by = 1))+
  xlab("Latitude")+
  geom_hline(yintercept=0,
             color = "black", lty = 2)

lat_plot
```




```
## Save Plot
# pdf("./figures/MS_Latitude.pdf",
#       useDingbats = FALSE, width = 5, height = 4)
# plot(lat_plot)
# dev.off()

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")
```



7 Oosthuizen et al Population change:

```r
# How many penguins were there, per year, across all sites?
# We don't know, as we only have intermittent counts.

# calculate total population size predicted (how many penguins were there in all populations?)
head(popy)
```

```
##   site_id     Lat season_starting nests Zseason_starting     ZLat minyear
## 1    ACUN -60.761            1980     0       -2.0000454 1.852563    1983
## 2    ACUN -60.761            1984     0       -1.6560725 1.852563    1983
## 3    ACUN -60.761            1988     0       -1.3120995 1.852563    1983
## 4    ACUN -60.761            1992     0       -0.9681265 1.852563    1983
## 5    ACUN -60.761            1995     0       -0.7101468 1.852563    1983
## 6    ACUN -60.761            2018     0        1.2676978 1.852563    1983
##   maxyear     Zfit Zlwr  Zupr
## 1    2004 4762.095 1111  9448
## 2    2004 5062.144 1468  9815
## 3    2004 5526.481 1262 10168
## 4    2004 5978.181 1741 11167
```

```
## 5    2004  6333.770 2038 11699
## 6    2004 12321.150 1252 29759
```

```
pop_predict = popy %>%
#           dplyr::filter(site_id != "HARM") %>%
              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 = 1, linewidth = 1.1)+
  geom_line(aes(x = season_starting, y = min_pred), lty = 2, linewidth = 0.8)+
  geom_line(aes(x = season_starting, y = max_pred), lty = 2, linewidth = 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[40,2] - pop_predict[1,2]) / pop_predict[1,2]
# delta.y
```

8 Predicting population change with entire posterior distribution

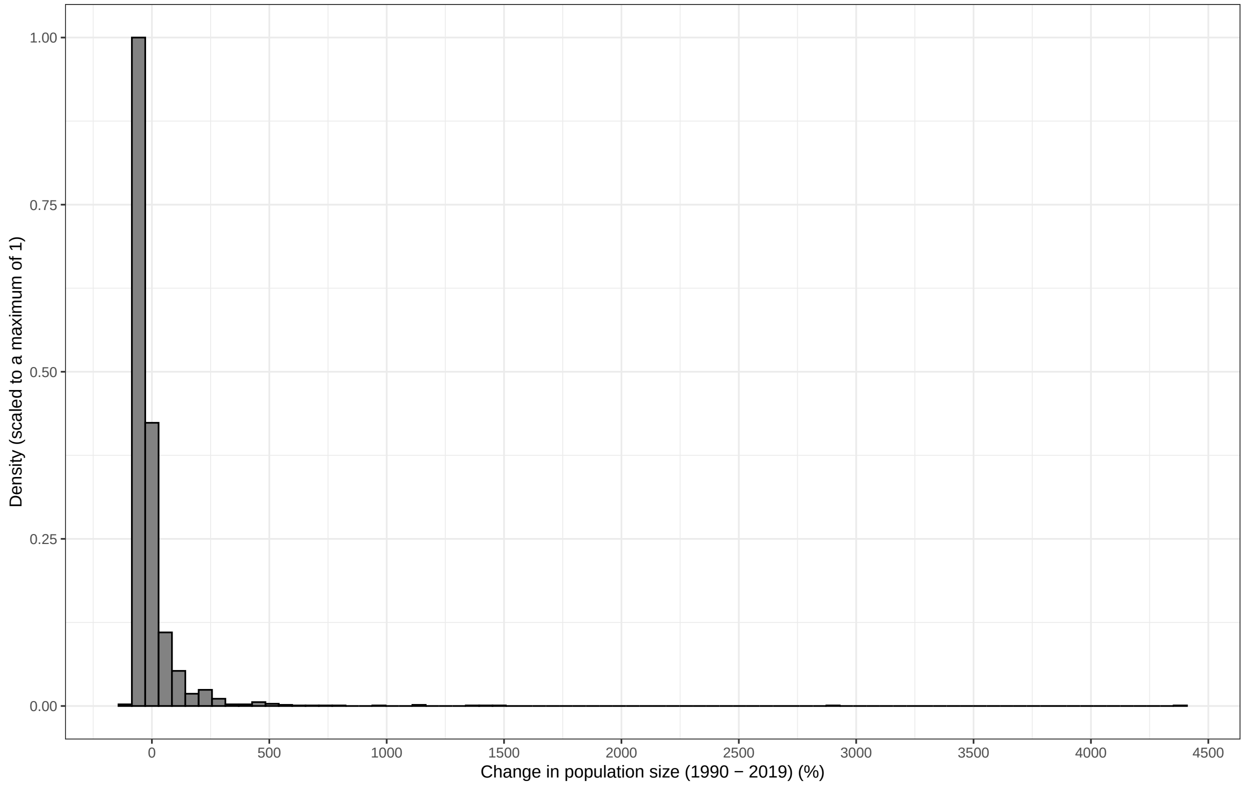
```
# extract posterior draws of fixed effects and random effects
posterior <- as.matrix(mc2$Sol)

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

site_and_lat
```

```
## # A tibble: 91 x 2
##    site_id ZLat[,1]
##    <chr>      <dbl>
##  1 ACUN       1.85
##  2 AITC       0.578
##  3 ALCO      -0.841
##  4 ANVS      -1.17
##  5 ARDL       0.728
##  6 ARMS      -2.11
##  7 BAIL       0.146
##  8 BART       0.720
```

```
##   9 BELL       0.801
## 10 BLAK      -0.384
## # i 81 more rows
```

```r
# 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(nestM3$season_starting)) / sd(nestM3$season_starting)
last_year <- (year2 - mean(nestM3$season_starting)) / sd(nestM3$season_starting)


# 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 (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 )
```

```r
    }
  }

  # 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
}

#------ Set Plotting theme----------------
gg_theme <- function () {
  theme_bw() %+replace%
    theme(
      axis.text = element_text(colour = "black", size = 11),
      axis.title = element_text(size=13),
      axis.ticks = element_line(colour = "black"),
    #  panel.grid = element_blank(),
    #  strip.background = element_blank(),
      panel.border = element_rect(colour = "black", fill = NA),
      axis.line = element_line(colour = "black"),
    legend.background = element_blank())
}
# 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_growth =
  ggplot(data = data.frame(pred_re$pop_change), aes(x = pred_re.pop_change,
                                                    after_stat(ndensity)))+
  geom_histogram(bins = 80, colour = "black", fill = "grey51")+
  theme_bw()+
  scale_x_continuous(n.breaks = 10)+
  labs(y= "Density (scaled to a maximum of 1)",
       x = "Change in population size (1990 - 2019) (%)")

hist_growth
```




```r
# can calculate the probability that the population has decreased by
# at least thirty percent with
sum(pred_re$pop_change < -30)/2000  # McElreath Chapter 3
```

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

```r
mean(pred_re$pop_change < -30)
```

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

```r
mean(pred_re$pop_change < 0)
```

```
## [1] 0.7825
```

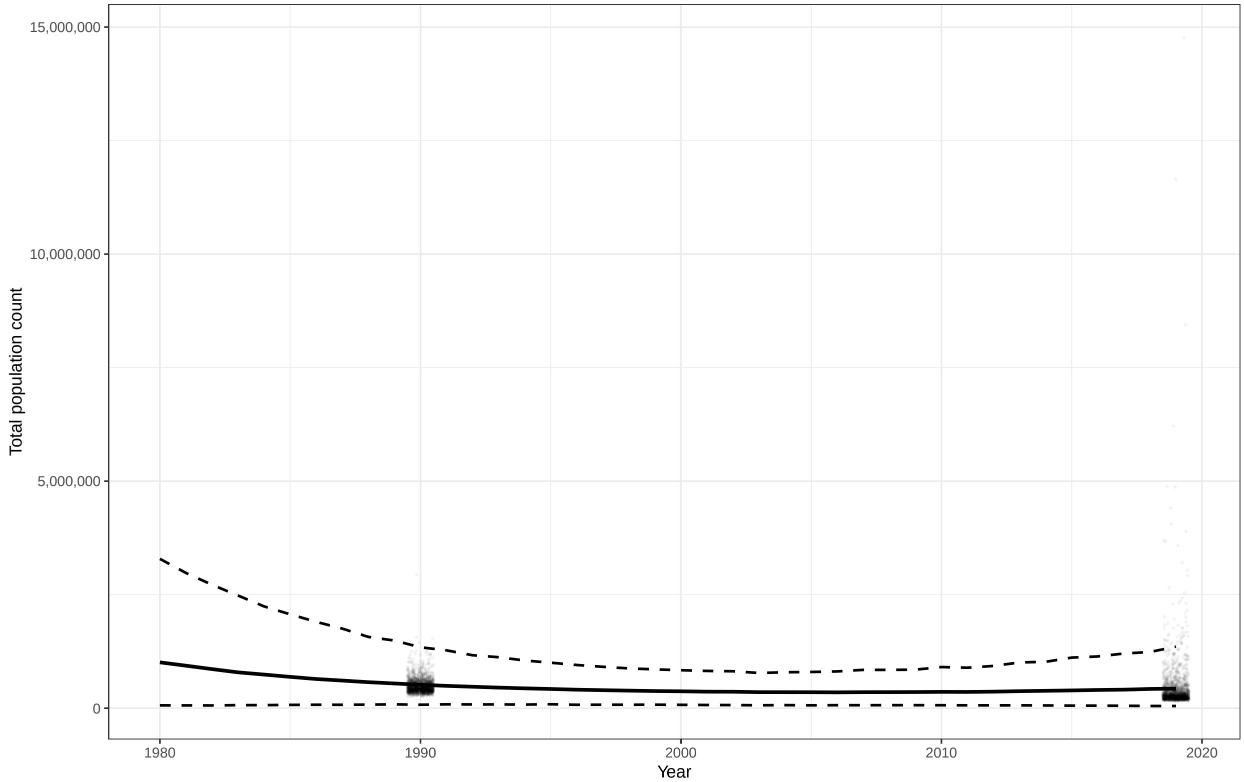
```r
quantile(pred_re$pop_change,c(0.05,0.95))
```

```
##        5%       95%
## -69.99381 135.88746
```

```r
length(unique(nestm3$site_id))
```

```
## [1] 91
```

```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"
#
# # 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 = pop_predict.p +
  geom_jitter(data = pred_first, aes(x = year1, y = pred_first),
             col = "black",size = 1, height = 0, width = 0.5,
              alpha = 0.05, stroke = NA) +
  geom_jitter(data = pred_last, aes(x = year2, y = pred_last),
             col = "black",size = 1, height = 0, width = 0.5,
              alpha = 0.05, stroke = NA)

pop_predict.p
```




```
## Save Plot
# pdf("./figures/MS_Population_change.pdf",
#       useDingbats = FALSE, width = 10, height = 4)
# cowplot::plot_grid(pop_predict.p, hist_growth, labels = c('A', 'B'), ncol = 2, label_size = 12)
# dev.off()
```