

# Applied Analysis 2

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The data set for this analysis is taken from the paper *Shifts in timing and duration of breeding for 73 boreal bird species over four decades*, Hållfors et al, PNAS vol. 117, no. 31, pages 18557–18565 (2020)

**Experiment** The data set consists of ringing records for birds across 73 species in Finland from year 1975–2017. Ringing is when a human volunteer places a metal ring on the leg of a bird living in the wild; these rings are marked and can be used to track the bird population. Ringing can only be performed on baby birds during a narrow window of age and is also dependent on conditions such as weather. This data set records the date, location, and bird species for all ringing events during the range of years studied. The dates of the ringing records can then be used to study the timing of the breeding season of the birds

**Statistical analysis** The paper studies how the breeding periods of the birds change with years. Specifically, the authors analyzed whether the breeding period is shifted/extended/shortened across species and locations, by using the ringing records of nestling in Finland from 1975 – 2017. Ringing data have been shown to be a reliable estimate for breeding phenology. Nestlings can only be ringed when a certain size (which is species-specific), so the range of the ringing time is treated in the paper as a representation of the breeding period. For the ringing records of each bird species, bioclimate zone and year, **the authors calculated three metrics: the 5% and 95% sample quantiles, and the difference between them.** Denoting one of the metrics as  $y_{ij,t}$  where  $i$  is a bioclimate zone,  $j$  is a species and  $t$  is a year. Then the paper proposes the following model

$$y_{ijs} = \beta_{js0} + \beta_{js1}x_i + u_{ij,s} + \epsilon_{ijs}$$

where  $x_i$  is the  $i$ -th year, and  $\beta_{js0}$  and  $\beta_{js1}$  are species-zone-specific coefficients. To borrow information across species, the authors added a prior on the  $\beta$ s, which takes the phylogenetic covariance matrix into account. The random effects  $u_{ij,s}$  account for the correlations among species, and the authors assumed that  $u_{ij} \sim MVN(0, \Omega)$  where  $\Omega$  is assumed to be a low-rank unknown covariance matrix. The random error terms  $\epsilon_{ijs} \sim N(0, \sigma^2)$  are independent entries. This hierarchical model is solved by MCMC.

After obtaining the posteriors of  $\beta_{js1}$ , the authors found that many of the coefficients  $\beta_{js1}$  for the two quantiles are significantly negative, uncovering a general advance of breeding with a strong phylogenetic signal but no systematic variation over space. For some species, the difference of the quantiles also have a negative trend, indicating that the breeding periods are more concentrated. In addition, these differences are more apparent in resident and short-distance migrating species that breed early in the season.

## Data Reading

```
#data reading
ring_data=read.csv("73_species.csv")
traits_info=read.csv("Traits_73_species.csv")
#looking at data
head(ring_data)
head(traits_info)
```

##	NestID	Species	XEUREF	YEUREF	BZ	Day	Month	Year	Dayofyear
## 1	A_001	ACCGEN	270000	6630000	HB	19	6	1979	170
## 2	A_002	ACCGEN	280000	6630000	HB	18	6	2001	169
## 3	A_003	ACCGEN	280000	6640000	HB	6	7	1984	188
## 4	A_004	ACCGEN	280000	6640000	HB	26	6	1987	177
## 5	A_005	ACCGEN	280000	6640000	HB	25	6	1995	176
## 6	A_006	ACCGEN	280000	6640000	HB	24	6	2010	175

##	Abbreviation	Scientific.name	Broods	Mig
## 1	PHACAR	Phalacrocorax carbo	1	S
## 2	ARDCIN	Ardea cinerea	1	S
## 3	SOMMOL	Somateria mollissima	1	S
## 4	BUCCLA	Bucephala clangula	1	S
## 5	PERAPI	Pernis apivorus	1	L
## 6	CIRAER	Circus aeruginosus	1	L

# 1 Possible Questions

## Problem 1

- Is i.i.d assumption of individual ringing events a reasonable one? Did the authors make this assumption?
- If we consider the above model (the one from paper) with upper/lower quantiles as our response, what aspects have been ignored in the model and how would you take care of it?

**Answer:** The ringing events may not be i.i.d. observations for a specific species, bioclimate zone and year as they are human behaviors, and aren't really done in a random manner.

The sample quantiles can have different uncertainty across years, as in some years there are much fewer observations. Such heterogeneity is ignored in the analysis. Quantiles in general might not have a linear relationship with years.

## Problem 2

In Figure 2 of Hallfors et al, left-hand panel, the authors show eight estimated densities (4 species in each of 2 different years) of ringing events across the seasons. Several of these estimated densities are multi-modal.

Attempt to produce versions of these eight plots from the same data, improving them where possible. Comment on whether the published density estimates accurately represent the raw observed data. Do you think the multi-modal features in the published density estimates likely represent clustering in the actual nesting behavior of the birds? Are there other possible explanations?

**Answer:**

```
library(kdensity)
#plotting densities
spcs_1="FICHYP"
spcs_2="VANVAN"
spcs_3="PASDOM"
spcs_4="BUTBUT"
#plotting data for a sepcific species
plot_spcs_density=function(spcs,zone,years,rng){
  data=ring_data[which(ring_data$Species==spcs & ring_data$BZ==zone),]
  data_old=data[which(data$Year==years[1]),]$Dayofyear
  data_new=data[which(data$Year==years[2]),]$Dayofyear
  m_old=mean(data_old);sd_old=sd(data_old)
  m_new=mean(data_new);sd_new=sd(data_new)
  kde_old=kdensity((data_old-m_old)/sd_old,kernel="gaussian")
  kde_new=kdensity((data_new-m_new)/sd_new,kernel="gaussian")
  years_to_plot=seq(rng[1],rng[2],0.1)
  plot(years_to_plot,kde_old((years_to_plot-m_old)/sd_old),ty="l",ylim=c(0,0.6),
  xlab="day of year",ylab="density value",main=spcs)
  lines(years_to_plot,kde_new((years_to_plot-m_new)/sd_new),col="blue")
}
par(mfrow=c(2,2))
plot_spcs_density(spcs_1,"NB",c(1977,1999),c(170,210))
legend("topright",legend=c(1977,1999),col=c("black","blue"),lty=rep(1,2),cex=0.8)
plot_spcs_density(spcs_2,"MB",c(1980,2015),c(130,210))
legend("topright",legend=c(1980,2015),col=c("black","blue"),lty=rep(1,2),cex=0.8)
plot_spcs_density(spcs_3,"SB",c(1979,2000),c(140,220))
legend("topright",legend=c(1979,2000),col=c("black","blue"),lty=rep(1,2),cex=0.8)
plot_spcs_density(spcs_4,"HB",c(1980,2013),c(160,195))
legend("topright",legend=c(1980,2013),col=c("black","blue"),lty=rep(1,2),cex=0.8)
```

```
par(mfrow=c(2,2))
#FICHYP
data=ring_data[which(ring_data$Species=="FICHYP" & ring_data$BZ=="NB"),]
data_old=data[which(data$Year==1977),]$Dayofyear
```

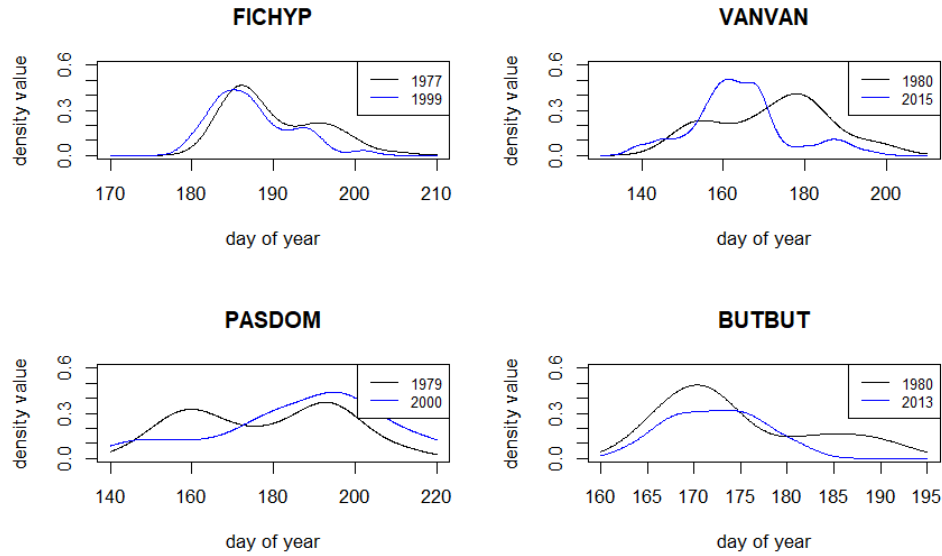


Figure 1: Caption

```
data_new=data[which(data$Year==1999),]$Dayofyear
m_old=mean(data_old);sd_old=sd(data_old)
m_new=mean(data_new);sd_new=sd(data_new)
kde_old=kdensity((data_old-m_old)/sd_old,kernel="gaussian")
kde_new=kdensity((data_new-m_new)/sd_new,kernel="gaussian")
hist(data_old,breaks=seq(170,210,by=1),main="FICHYP_old",freq=F)
hist(data_new,breaks=seq(170,210,by=1),main="FICHYP_new",freq=F)

#PASDOM
data=ring_data[which(ring_data$Species=="PASDOM" & ring_data$BZ=="SB"),]
data_old=data[which(data$Year==1979),]$Dayofyear
data_new=data[which(data$Year==2000),]$Dayofyear
m_old=mean(data_old);sd_old=sd(data_old)
m_new=mean(data_new);sd_new=sd(data_new)
kde_old=kdensity((data_old-m_old)/sd_old,kernel="gaussian")
kde_new=kdensity((data_new-m_new)/sd_new,kernel="gaussian")
hist(data_old,breaks=seq(130,230,by=1),main="PASDOM_old",freq=F)
hist(data_new,breaks=seq(130,230,by=1),main="PASDOM4_new",freq=F)
```

Questions: Is the conclusion of multi-modality correct based on above histograms? What we can do as a solution? Additionally, how to check whether the multimodality is actually an effect of clustering of birds, using the data given?

reduce smoothing; using the x-y co-ordinates somehow?

## Problem 3

In Supplementary Text *S2*, entitled “Assessing change in ringer behavior”, the authors discuss whether ringer behavior and effort may change over time. In particular they examined changes in wing length (Fig 3) [the data for which are not included in the dataset we used here]. Why the authors examined changes in wing length over time?

**Answer:** They are essentially checking for protocol changes that might lead to ringers ringing birds later (when they are bigger) because such changes in protocol could obviously lead to shifts in the distributions of ringing events of the kind they are looking for. That is they want to make sure the effects they identify are changes in “bird” behavior, not ringing behavior.

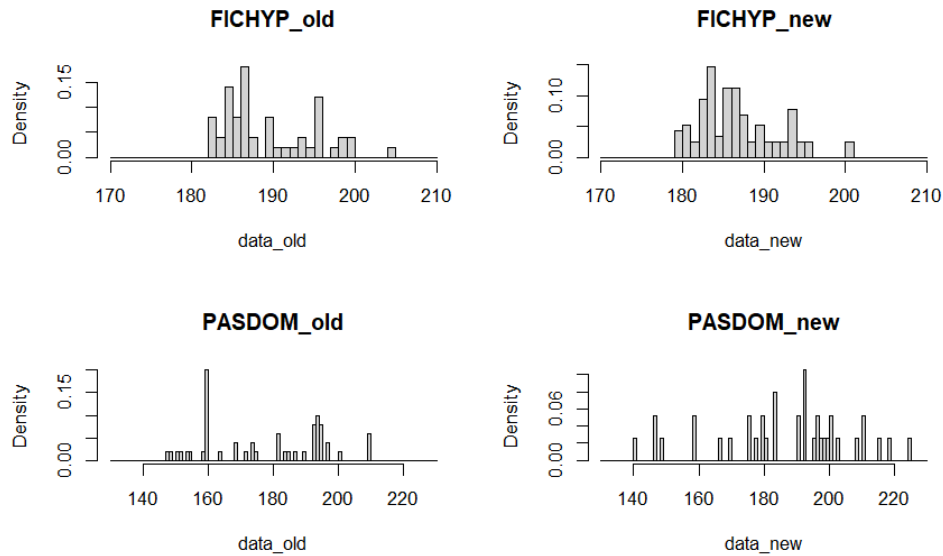


Figure 2: Caption

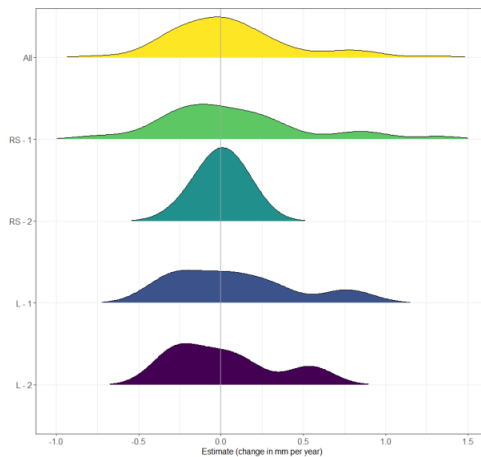


Figure 3: Figure S7 from supplement

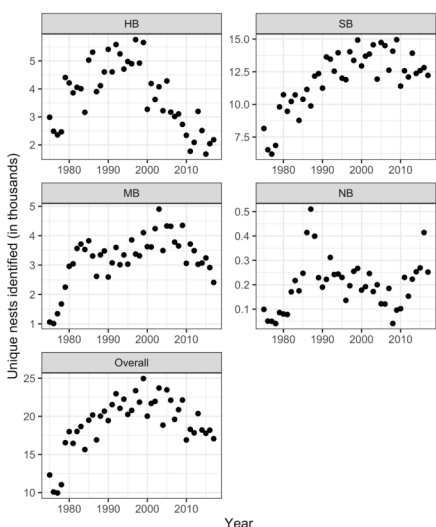
## Problem 4

They also analyzed changes in total numbers of ringing events as a proxy to ringing effort (Figures 4a,4b) over the years of the study. Explain how changes in ringing effort over time, if they existed, could impact the main results and conclusions of the study. Authors argue

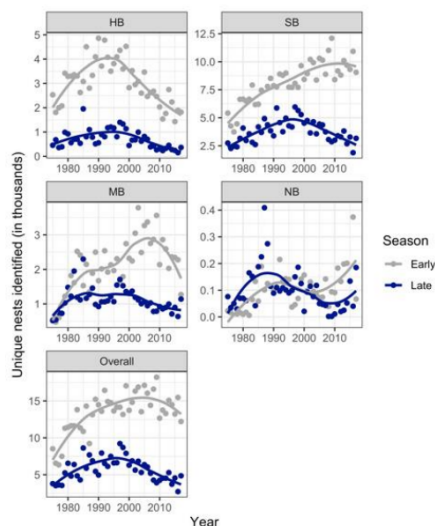
- Annual effort levels stabilized in all zones by 1990 and remained relatively constant thereafter. There are sufficient samples (in thousands) late in the breeding season to accurately identify the end of the breeding.
- While there is variation in the number of nests observed in each year over the study period, the proportions of nests observed in the beginning and end of the breeding season are relatively constant over the study period

Discuss the strengths and limitations of their argument. What assumptions would make it possible to

distinguish changes in ringing effort from changes in bird behavior?



(a) Figure S9 from supplement



(b) Figure S10 from supplement

Figure 4: Supplement pictures

**Answer:** If the change in ringing efforts over time exists, any estimated phenological shifts over time might be partially caused by the change in ringing efforts and any conclusion without considering this effect of ringing efforts might be severely flawed.

I think the most obvious answer would be to assume that changes in ringing behavior affect data on all species similarly, whereas changes in bird behavior are potentially species-specific (and perhaps correlated across similar species?). One could formally encode this kind of assumption into the model, for example by including a “ringing” effect that is shared across all species as well a species-specific effect. However, any overall change across species would then go into the ringing effect...

## Problem 5

For this question, we will work with the duration of the breeding season as the response variable, which(as in the paper) is defined as the number of days between the 5th and 95th percentile of ringing events. For the species CORRAX, use a linear regression to assess whether the duration of the breeding season is showing a decrease in length over time. (For this problem, you should treat duration as the observed response, and ignore the fact that it was computed based on individual ringing events. However, you may choose to include other information such as boreal zone in your analysis.) Discuss your findings. **Answer:**

```
#duration estimates for each species-zone combo
duration_spcs_zone=function(spcs,zone){
  duration=vector();year=vector()
  data=ring_data[ring_data$Species==spcs & ring_data$BZ==zone,]
  for(i in 1975:2017){
    if(sum(data$Year==i)>0){
      data_i=data[which(data$Year==i),]$Dayofyear
      duration=c(duration,quantile(data_i,probs=0.95)-quantile(data_i,probs=0.05))
      year=c(year,i)
    }
  }
}
```

```

    }
  }
  return(cbind(duration,year,zone))
}
#duration estimate for each species
duration_spcs=function(spcs){
  duration=vector();year=vector();zone=vector()
  data=ring_data[which(ring_data$Species==spcs),]
  for(i in 1975:2017){
    if(sum(data$Year==i)>0){
      data_i=data[which(data$Year==i),]$Dayofyear
      duration=c(duration,quantile(data_i,probs=0.95)-quantile(data_i,probs=0.05))
      zone=c(zone,sum(data[data$Year==i,]$BZ=="SB")/dim(data[data$Year==i,])[1])
      year=c(year,i)
    }
  }
  return(cbind(duration,year,zone))
}

```

```

#fitting a linear regression for CORRAX data and doing the test
corrax_data=as.data.frame(duration_spcs("CORRAX"))
model_all=lm(duration~year,data=corrax_data)
summary(model_all)
library(ggplot2)
ggplot(corrax_data,aes(x=year,y=duration))+
  geom_point(shape=21,size=1.3)+
  geom_smooth(method = "lm", fill = NA)

```

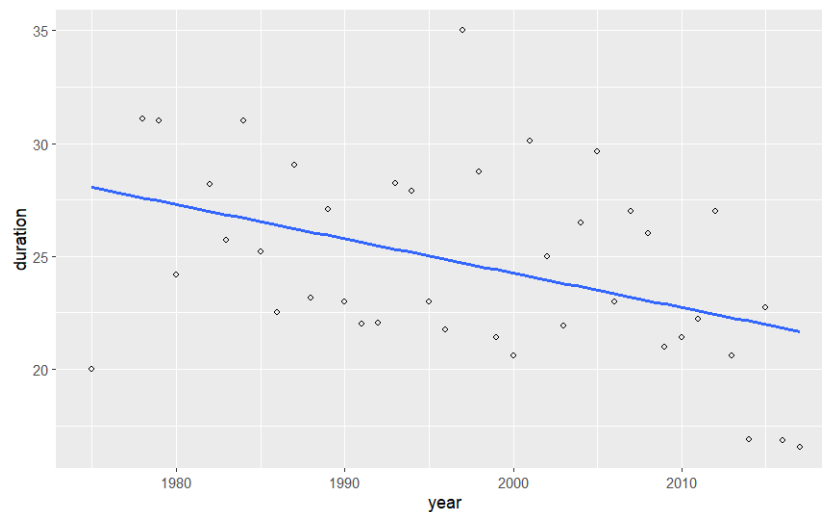


Figure 5: Caption

```

##
## Call:
## lm(formula = duration ~ year, data = corrax_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.0529 -3.0285 -0.7607  2.9388 10.2893
##
## Coefficients:

```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 328.09809  104.78351   3.131  0.00334 **
## year        -0.15192    0.05246  -2.896  0.00624 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.913 on 38 degrees of freedom
## Multiple R-squared:  0.1808, Adjusted R-squared:  0.1592
## F-statistic: 8.386 on 1 and 38 DF,  p-value: 0.006237
```

```
ggplot(corrax_data,aes(x=year,y=duration,color=zone))+
  geom_point(shape=21,size=1.3)+
  geom_smooth(method = "lm", fill = NA)
```

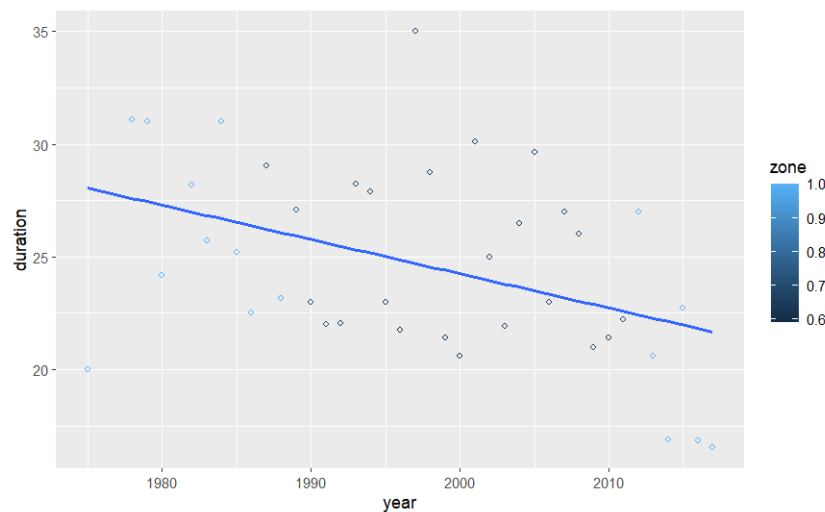


Figure 6: Caption

```
corrax_zonal_data=as.data.frame(rbind(duration_spcs_zone("CORRAX", "SB"),duration_spcs_zone("CORRAX", "MB")))

corrax_zonal_data$year=as.numeric(corrax_zonal_data$year)
corrax_zonal_data$duration=as.numeric(corrax_zonal_data$duration)
model_zone=lm(duration~year*zone, data=corrax_zonal_data)
summary(model_zone)

ggplot(corrax_zonal_data,aes(x=year,y=duration,color=zone))+
  geom_point(shape=21,size=1.3)+
  geom_smooth(method = "lm", fill = NA)

model_zone_only=lm(duration~zone, data=corrax_zonal_data)
anova(model_zone_only,model_zone)
anova(model_zone,lm(duration~year, data=corrax_zonal_data))
```

```
##
## Call:
## lm(formula = duration ~ year * zone, data = corrax_zonal_data)
##
## Residuals:
```



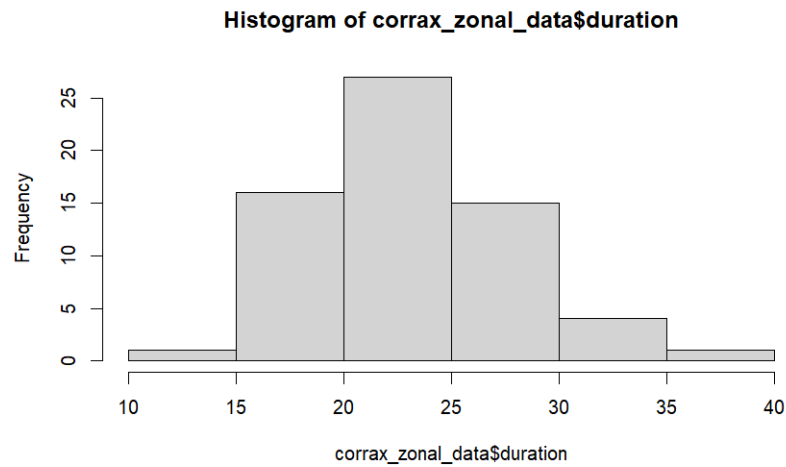


Figure 7: Caption

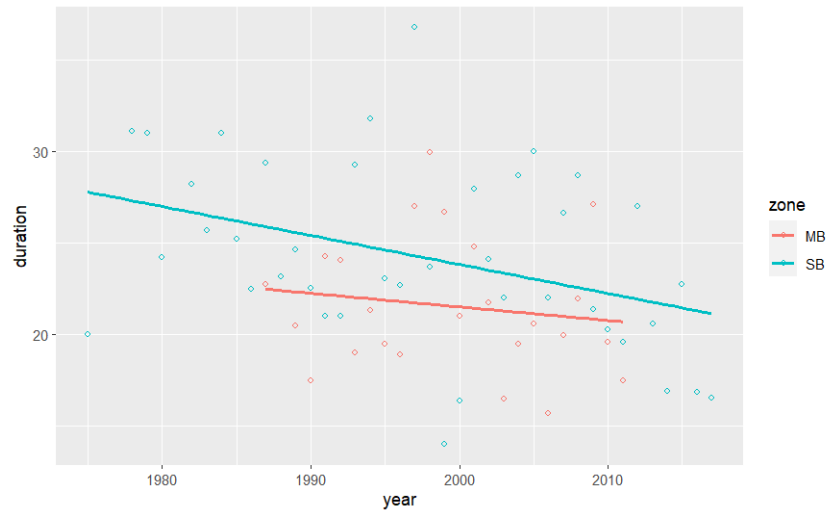


Figure 8: Caption

```
##      Min      1Q  Median      3Q      Max
## -9.997 -2.826 -0.910  3.568 12.486
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 170.61613  254.43709   0.671   0.505
## year        -0.07455   0.12725  -0.586   0.560
## zoneSB       170.40970  279.94855   0.609   0.545
## year:zoneSB  -0.08404   0.14004  -0.600   0.551
##
## Residual standard error: 4.36 on 60 degrees of freedom
## Multiple R-squared:  0.1833, Adjusted R-squared:  0.1425
## F-statistic: 4.489 on 3 and 60 DF,  p-value: 0.00658
```

IS the year effect necessary?

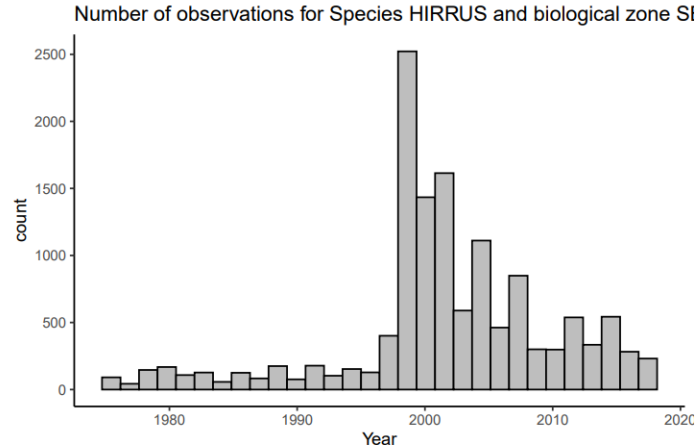


Figure 9: Number of ringing events per year for HIRRUS species

```
## Analysis of Variance Table
##
## Model 1: duration ~ zone
## Model 2: duration ~ year * zone
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      62 1287.0
## 2      60 1140.6  2    146.45 3.8518 0.02668 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Is the zone effect necessary?

## Analysis of Variance Table
##
## Model 1: duration ~ year * zone
## Model 2: duration ~ year
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      60 1140.6
## 2      62 1232.9 -2    -92.33 2.4284 0.0968 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Problem 6

For this question, we will also work with the duration of the breeding season as the response variable, and consider the linear regression model

$$y_i = \beta_0 + \beta_1 x_i + \epsilon_i$$

where  $y_i$  is the estimated duration of the breeding season for year  $i$  and  $x_i$  is corresponding time variable for the  $i$ -th year (e.g.,  $x_i = 1990$ ). We focus on fitting this model for the species HIRRUS in the south boreal zone. The following histogram reveals that, for this species-zone combination, the number of observed ringing events in each year has a dramatic increase after year 1997. Explain why this fact might call into question the use of ordinary least squares (OLS) for fitting the model above. Propose and implement an alternative approach, and compare the results with those from OLS. In what scenarios might this kind of issue be a serious concern in practice?

**Answer:**

```

hirrus_data=as.data.frame(duration_spcs_zone("HIRRUS","SB"))
hirrus_data$duration=as.numeric(hirrus_data$duration)
hirrus_data$year=as.numeric(hirrus_data$year)
#plotting
plot(hirrus_data[,2],hirrus_data[,1],xlab="Year",ylab="Breeding Duration",
main="scatterplot for HIRRUS duration data")

```

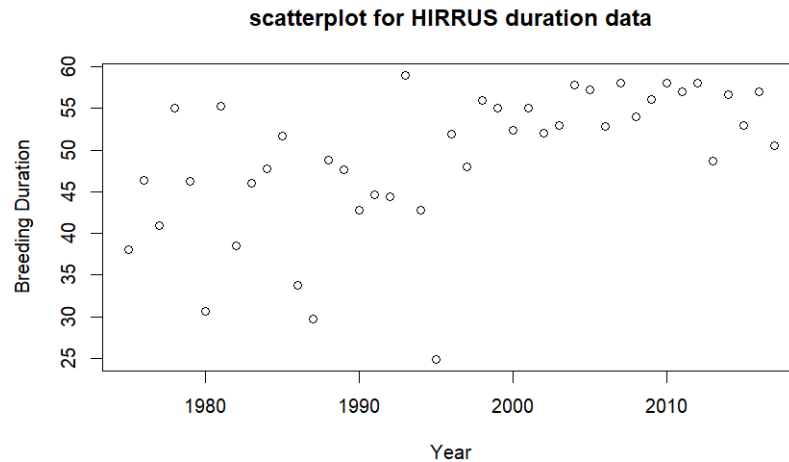


Figure 10: Caption

```

#normal OLS regression
model_ols=lm(duration~year, data=hirrus_data)
summary(model_ols)
plot(model_ols$residuals)

```

```

##
## Call:
## lm(formula = duration ~ year, data = hirrus_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.909  -3.201   1.208   3.786  12.684
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -707.39446  173.19153  -4.084   2e-04 ***
## year          0.37902    0.08677   4.368 8.32e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.061 on 41 degrees of freedom
## Multiple R-squared:  0.3176, Adjusted R-squared:  0.301
## F-statistic: 19.08 on 1 and 41 DF,  p-value: 8.322e-05

```

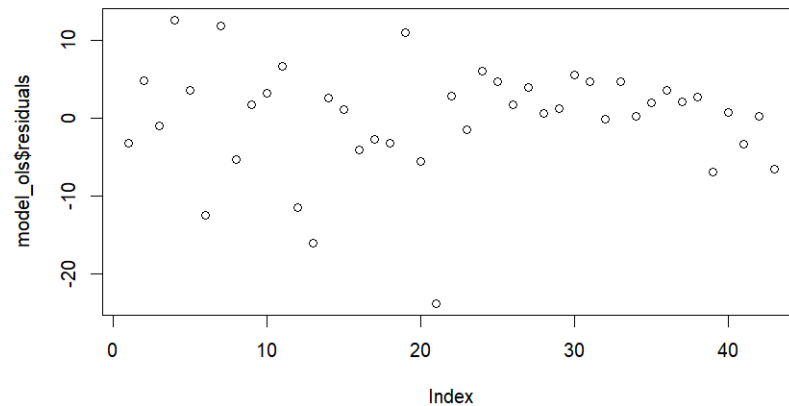


Figure 11: Caption

```
##weighted least square regression
sd_lm=lm(abs(model_ols$residuals)~hirus_data$year)
weights_1=1/(sd_lm$fitted.values^2)
model_wls1=lm(duration~year,data=hirus_data,weights=weights_1)
summary(model_wls1)

plot(hirus_data$year, hirus_data$duration)
abline(model_ols,col="red")
abline(model_wls1,col="blue")
```

```
##
## Call:
## lm(formula = duration ~ year, data = hirus_data, weights = weights_1)
##
## Weighted Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7025 -0.5808  0.3214  0.9554  2.0251
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -643.21730   157.60896  -4.081 0.000202 ***
## year          0.34692    0.07867   4.410 7.31e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.365 on 41 degrees of freedom
## Multiple R-squared:  0.3217, Adjusted R-squared:  0.3052
## F-statistic: 19.45 on 1 and 41 DF,  p-value: 7.305e-05
```

```
par(mfrow=c(1,2))
plot(hirus_data$year,studres(model_ols))
plot(hirus_data$year,studres(model_wls1))
```

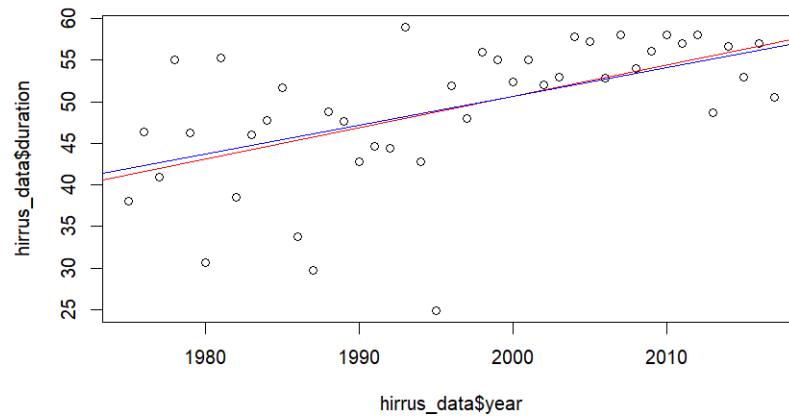


Figure 12: Caption

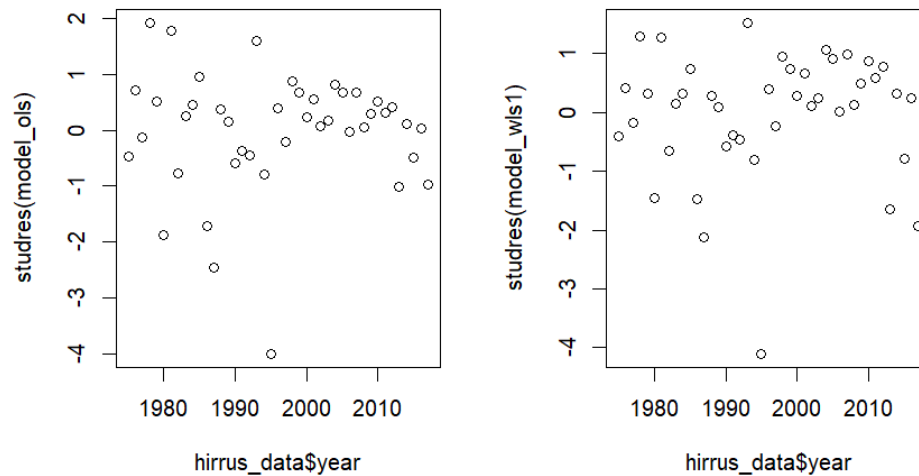


Figure 13: Caption

## Problem 7

In this question we consider an alternative way of measuring shifts in the breeding season than the quantile-based approaches used in the paper. Specifically, for each year  $i$ , let  $p_{ijs}$  denote the proportion of ringing events that occur before Day 170 of the year for species  $j$  in bioclimatic zone  $s$ . Changes in  $p_{ijs}$  with year would suggest shifts in the breeding season (for species  $j$  in zone  $s$ ). Devise analyses to estimate how  $p_{ijs}$  changes with year  $i$ , and whether there are differences in this year effect among species. Further, assess whether year effects differ among species that have different numbers of broods or migration types. Clearly explain the models you use, the results of the analyses, and your conclusions.

**Answer:**

```

data=ring_data[,c("Species", "Year", "BZ", "Dayofyear")]
data$Dayofyear=data$Dayofyear<=170

#calculate proportion
proportion_data=aggregate(Dayofyear~Species+Year+BZ,data=data,FUN="mean")
total_number=aggregate(Dayofyear~Species+Year+BZ,data=data,FUN="length")
proportion_data=cbind(proportion_data,total_number[,4])

#add species information
proportion_data=cbind(proportion_data,0);proportion_data=cbind(proportion_data,0)
for(i in 1:dim(proportion_data)[1]){
  proportion_data[i,c(6,7)]=traits_info[which(traits_info$Abbreviation==proportion_data[i,1]),c(3,4)]
}
colnames(proportion_data)=c("Species", "Year", "Zone", "proportion", "total", "Brood", "Mig")
proportion_data$Year=(proportion_data$Year-mean(proportion_data$Year))/sd(proportion_data$Year)
head(proportion_data)

```

```

##   Species      Year Zone proportion total Brood Mig
## 1  ACCGEN -1.776804  HB  0.6153846    78     1    R
## 2  ALCTOR -1.776804  HB  0.0000000    36     1    S
## 3  BUTBUT -1.776804  HB  0.5312500    32     1    S
## 4  FICHYP -1.776804  HB  0.1343750   320     1    L
## 5  LARARG -1.776804  HB  0.8873917  1039     1    S
## 6  LARCAN -1.776804  HB  0.1104651   172     1    S

```

```

unique(proportion_data$Species)
model1=glmer(cbind(total*proportion, total*(1-proportion)) ~ Brood*Year +Mig*Year
              +(1|Species),data=proportion_data,family=binomial(link="logit"))
summary(model1)
model12=glmer(cbind(total*proportion, total*(1-proportion)) ~ Brood+Mig+Year
              +(1|Species),data=proportion_data,family=binomial(link="logit"))

```

```

## [1] "ACCGEN" "ALCTOR" "BUTBUT" "FICHYP" "LARARG" "LARCAN" "LARFUS" "LARMAR" "LARRID" "MOTALB"
## [11] "PARATE" "PARCAE" "PARMAJ" "STEAEA" "STECAS" "STEHIR" "STRALU" "STUVUL" "TURILI" "TURPIL"
## [21] "CEPGRY" "CORNIX" "HAEOST" "ACCNIS" "CHADUB" "APUAPU" "STECUS" "ARDCIN" "HIRRUS" "PHACAR"
## [31] "CORMON" "VANVAN" "AEGFUN" "ASIFLA" "FALTIN" "PARMON" "PHOPHO" "STRURA" "MUSSTR" "NUMARQ"
## [41] "LARMIN" "PICPIC" "CORRAX" "GLAPAS" "BUTLAG" "PARCIN" "ASIOTU" "CARERY" "CERFAM" "FRICOE"
## [51] "JYNTOR" "LANCOL" "PARCRI" "PHYLUS" "SAXRUB" "SYLBOR" "TURPHI" "TURNER" "SOMMOL" "PASDOM"
## [61] "RIPRIP" "DELURB" "DRYMAR" "PHYSIB" "SYLCOM" "MOTFLA" "PERAPI" "CIRAER" "BUCCLA" "FALSUB"
## [71] "PASMON" "DENMAJ" "GRUGRU"

```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
## Family: binomial ( logit )
## Formula: cbind(total * proportion, total * (1 - proportion)) ~ Brood *
##           Year + Mig * Year + (1 | Species)
## Data: proportion_data
##
##           AIC          BIC    logLik deviance df.resid
## 109980.2 110037.3 -54981.1 109962.2      4228
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -25.456  -2.145  -0.226   1.377  57.710
##
## Random effects:
## Groups Name          Variance Std.Dev.
## Species (Intercept) 6.93      2.632

```

```

## Number of obs: 4237, groups: Species, 73
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.159084   1.011739  -3.122 0.001794 **
## Brood       -0.554453   0.725799  -0.764 0.444915
## Year        0.150945   0.012771  11.820 < 2e-16 ***
## MigR        6.154843   0.798883   7.704 1.32e-14 ***
## MigS        3.036580   0.730007   4.160 3.19e-05 ***
## Brood:Year   0.077027   0.009594   8.029 9.84e-16 ***
## Year:MigR    0.045222   0.011901   3.800 0.000145 ***
## Year:MigS   -0.154541   0.009226 -16.751 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Brood  Year   MigR   MigS   Brd:Yr Yr:MgR
## Brood      -0.849
## Year        0.002 -0.002
## MigR       -0.263 -0.106  0.000
## MigS       -0.359 -0.031 -0.002  0.491
## Brood:Year -0.002  0.002 -0.785 -0.001  0.001
## Year:MigR   0.000 -0.001  0.020  0.001  0.001 -0.550
## Year:MigS  -0.001  0.001 -0.472  0.001  0.001 -0.075  0.611

## Data: proportion_data
## Models:
## model2: cbind(total * proportion, total * (1 - proportion)) ~ Brood + Mig + Year + (1 | Species)
## model1: cbind(total * proportion, total * (1 - proportion)) ~ Brood * Year + Mig * Year +
##(1 | Species)
##           npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## model2      6 111129 111167 -55559  111117
## model1      9 109980 110037 -54981  109962 1154.9  3 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```