

Fric et al. critiques: data curation

Elise Larsen & Vaughn Shirey

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Here we explore the occurrence data from Fric et al. (2020)

Parts of this code are duplicated in Larsen-Shirey2020_v3; this gives a more detailed account of getting from the raw data provided by Fric et al. to our cleaned datasets.

```
rm(list=ls())  
# Load libraries  
library(tidyverse)  
library(readxl)  
library(ggplot2)  
#Library(ggExtra)  
library(gridExtra)
```

Data Input

```

all.data <- readLines("fric_supplements/data.csv")

#identify header rows
all.header.rows<-grep("decimalLongitude", all.data)

#check headers for consistency
uniqueheaders<-unique(all.data[all.header.rows])

# 2 versions! -> Get row numbers for "header 1"
header.rows1<-grep(uniqueheaders[1], all.data)
#Get row numbers for "header 2"
header.rows2<-setdiff(all.header.rows, header.rows1)

#Create row identifiers:
#0 is a header row, 1 is format 1 data, 2 is format 2 data
j<-rep(0,length(all.data))
for (i in all.header.rows) {
  #set index to the next header if it's not the last header; otherwise set to end of datafile +
  1
  if(i<max(all.header.rows)) {
    next_index<-min(all.header.rows[all.header.rows>i])
  }else { next_index<-length(all.data)+1 }

  #for data between header rows, set row index
  j[(i+1):(next_index-1)]<-ifelse(i%in%header.rows1,1,2)
}

#need to add a row index to the header text for new data files
newheader1<-paste("row.index\\",'',uniqueheaders[1], sep="")
newheader2<-paste("row.index\\",'',uniqueheaders[2], sep="")

#write data file
formatteddatafile1<-file("data/fric_data_header_1.txt")
writeLines(c(newheader1,all.data[which(j==1)]), formatteddatafile1)
close(formatteddatafile1)

formatteddatafile2<-file("data/fric_data_header_2.txt")
writeLines(c(newheader2,all.data[which(j==2)]), formatteddatafile2)
close(formatteddatafile2)
rm(list=ls())

#read back in the formatted data
data1<-read_csv("data/fric_data_header_1.txt")

```

```
## Parsed with column specification:
## cols(
##   row.index = col_double(),
##   name = col_character(),
##   decimalLongitude = col_double(),
##   decimalLatitude = col_double(),
##   year = col_double(),
##   month = col_double(),
##   country = col_character(),
##   day = col_double(),
##   SuccDay = col_double(),
##   rndLat = col_double(),
##   alt = col_double()
## )
```

```
data2<-read_csv("data/fric_data_header_2.txt")
```

```
## Parsed with column specification:
## cols(
##   row.index = col_double(),
##   name = col_character(),
##   decimalLongitude = col_double(),
##   decimalLatitude = col_double(),
##   year = col_double(),
##   month = col_double(),
##   day = col_double(),
##   country = col_character(),
##   SuccDay = col_double(),
##   rndLat = col_double(),
##   alt = col_double()
## )
```

```
paste( nrow(data1), "records in format 1;", nrow(data2), "records in format 2")
```

```
## [1] "49243 records in format 1; 233201 records in format 2"
```

```
alldata<-rbind(data1,data2)
rm(data1,data2)
```

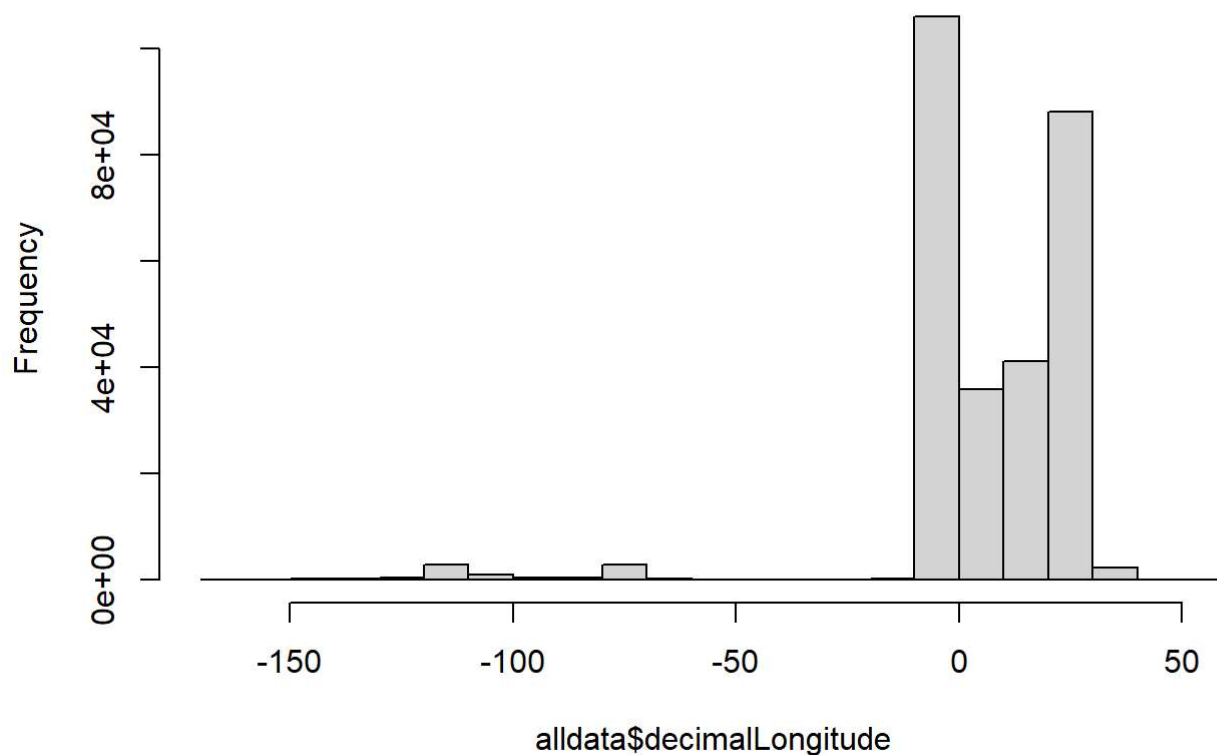
alldata now contains the raw data provided by Fric et al. in a usable format. **### Data exploration 1** Now we assign region, reconcile names that don't match between the data file and results files provided in the original supplement, and filter the Fric dataset to remove first day of the month records to obtain the dataset used in Fric et al.

```
summary(alldata)
```

```
##      row.index      name      decimalLongitude      decimalLatitude
## Min.      :    1  Length:282444      Min.      :-162.559      Min.      : 5.787
## 1st Qu.: 2367   Class :character      1st Qu.:  -2.782      1st Qu.:52.781
## Median : 7006   Mode  :character      Median :    9.398      Median :55.628
## Mean    :14816                                     Mean    :    6.298      Mean    :56.267
## 3rd Qu.:20210                                     3rd Qu.:  23.573      3rd Qu.:60.624
## Max.    :85273                                     Max.    :   59.333      Max.    :71.216
##
##      year      month      country      day
## Min.    :1616   Min.    : 1.000   Length:282444   Min.    : 1.00
## 1st Qu.:1992   1st Qu.: 6.000   Class :character 1st Qu.: 9.00
## Median :2002   Median : 7.000   Mode  :character Median :16.00
## Mean    :1996   Mean    : 6.517                                     Mean    :16.15
## 3rd Qu.:2009   3rd Qu.: 7.000                                     3rd Qu.:24.00
## Max.    :2015   Max.    :12.000                                     Max.    :31.00
## NA's    :58
##      SuccDay      rndLat      alt
## Min.    : 2.0     Min.    : 6.00   Min.    :-2666.74
## 1st Qu.:163.0     1st Qu.:53.00   1st Qu.:  23.21
## Median :186.0     Median :56.00   Median :   64.33
## Mean    :181.6     Mean    :56.21   Mean    :  114.25
## 3rd Qu.:202.0     3rd Qu.:61.00   3rd Qu.:  111.09
## Max.    :361.0     Max.    :71.00   Max.    : 4305.17
##
```

```
##Fric et al identifies datasets by region (N. America, Europe), but the data file does not include this information. We label data by region using Longitude:
## visualize data density by Longitude
hist(alldata$decimalLongitude, main="Data density by Longitude")
```

Data density by Longitude



```
#We label everything East of -40 as Europe, the rest as N. America
alldata<-alldata %>%
  mutate(region=ifelse(decimalLongitude>=(-40),"Europe","N. America"))
```

```
#We expect 100 species names, based on the manuscript.
length(unique(alldata$name))
```

```
## [1] 108
```

```
#What are the names in the dataset?
data.names<-sort(unique(alldata$name))
#Which of these names shows up in the results?
result.names<-na.omit(read_excel("fric_supplements/Supplementary Table 2_final.xlsx", sheet="~latitude", range="A3:A113"))
result.names<-(strsplit(result.names$Species, " "))
result.names<-NULL
for(i in 1:length(result.names)) {
  result.names<-c(result.names,paste(result.names[[i]][1],result.names[[i]][2],sep=" "))
}
which(data.names%in%result.names)
```

```
## [1] 1 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
## [20] 21 22 23 25 26 27 28 29 31 32 33 34 35 36 37 38 39 40 41
## [39] 42 44 45 46 47 48 49 50 51 53 54 55 57 58 60 61 62 64 65
## [58] 67 68 69 70 72 73 74 75 76 78 79 80 81 82 83 84 85 86 87
## [77] 88 89 90 91 92 93 94 97 98 100 101 102 103 105 106 107
```

```
names_1<-data.names[which(!data.names%in%result.names)]
names_2<-result.names[which(!result.names%in%data.names)]
```

```
# We can link the following results names to similar data names
nmatch<-c(3,14,13,12,9,16,1,7)
```

#Of the remaining 8 names, Incisalia augustinus should be combined with Callophrys augustinus, Lycaeides idas should be combined with Plebejus idas, Maculinea arion should be combined with Phengaris arion. It is unclear if any others should be combined.

```
nmatch<-c(nmatch,8,10:11)
name_changes<-as.data.frame(cbind(result.name=c(names_2,sort(unique(result.names))[c(26,90,86)]),data.name=c(names_1[nmatch])))
print(name_changes)
```

##	result.name	data.name
## 1	Callophrys polia	Callophrys polios
## 2	Icaricia saepiolus	Plebejus saepiolus
## 3	Phyciodes cocyta	Phyciodes tharos
## 4	Phyciodes pratensis	Phyciodes campestris
## 5	Satyrodes eurydice	Lethe eurydice
## 6	Thymelicus lineolus	Thymelicus lineola
## 7	Vacciniina optilete	Agriades optilete
## 8	Argynnis adippe	Fabriciana adippe
## 9	Callophrys augustinus	Incisalia augustinus
## 10	Plebejus idas	Lycaeides idas
## 11	Phengaris arion	Maculinea arion

```
write.csv(name_changes, file="data/name_changes.csv")
# this file can now be used for correcting names in the main file

for(namei in 1:nrow(name_changes)) {
  alldata$name[alldata$name==name_changes$data.name[namei]]<-name_changes$result.name[namei]
}
write.csv(alldata, file="data/all_data_formatted.csv")

fricdata<-alldata %>% filter(alldata$name %in% result.names)
rm(name_changes, resultnames, result.names, data.names, namei, names_1, names_2, nmatch)

#Fric et al removed all 1st of month observations.
fricdata<-filter(fricdata, day!=1)

summary(fricdata)
```

```
##      row.index      name      decimalLongitude      decimalLatitude
## Min.      :    1 Length:257972 Min.      :-162.559 Min.      : 5.787
## 1st Qu.: 2341 Class :character 1st Qu.:  -2.676 1st Qu.:52.711
## Median : 7274 Mode  :character Median :    9.551 Median :55.638
## Mean    :15624 Mean    :    6.529 Mean    :56.296
## 3rd Qu.:22563 3rd Qu.: 23.672 3rd Qu.:60.649
## Max.    :85273 Max.    :   59.333 Max.    :71.216
##
##      year      month      country      day
## Min.    :1616 Min.    : 1.000 Length:257972 Min.    : 2.00
## 1st Qu.:1992 1st Qu.: 6.000 Class :character 1st Qu.: 9.00
## Median :2002 Median : 7.000 Mode  :character Median :16.00
## Mean    :1996 Mean    : 6.519 Mean    :16.19
## 3rd Qu.:2009 3rd Qu.: 7.000 3rd Qu.:24.00
## Max.    :2015 Max.    :12.000 Max.    :31.00
## NA's    :53
##      SuccDay      rndLat      alt      region
## Min.    : 2.0 Min.    : 6.00 Min.    : -2666.74 Length:257972
## 1st Qu.:165.0 1st Qu.:53.00 1st Qu.: 23.25 Class :character
## Median :187.0 Median :56.00 Median : 64.24 Mode  :character
## Mean    :181.8 Mean    :56.23 Mean    : 114.26
## 3rd Qu.:202.0 3rd Qu.:61.00 3rd Qu.: 109.48
## Max.    :361.0 Max.    :71.00 Max.    : 4305.17
##
```

```
#Save formatted and filtered occurrence data used by Fric et al.
save(fricdata,file="data/occurrences_FricAnalysis.RData")
```

Data exploration: altitude (elevation)

(We defer to the Fric et al use of “altitude” for clarity)

Early on in data exploration we were concerned with the range of altitude values in the data. One aspect of our data exploration for altitude involved examining outliers and spot-checking specific occurrence records in GBIF, which were either below 0m or in the top quartile of altitudes. Looking at these records led us to understand that

- 1. GIS coordinates had often been assigned by placename, or were otherwise inaccurate, and
- 2. 2. altitudes obtained by using the Google API to extract altitude for coordinates did not provide reliable altitudes for the underlying occurrences.

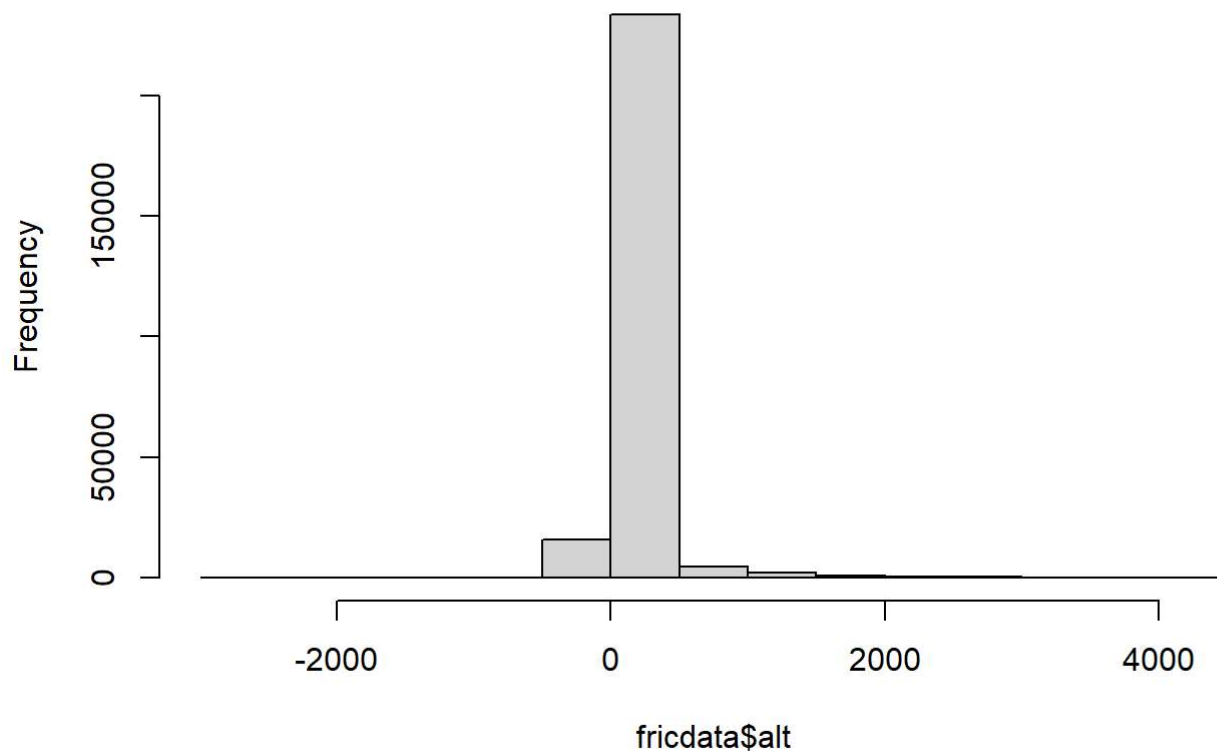
Here we examine broad patterns and specific outlier cases.

```
#basic range & frequency in data
summary(fricdata$alt)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -2666.74  23.25   64.24   114.26  109.48  4305.17
```

```
hist(fricdata$alt)
```

Histogram of fricdata\$alt



#how many records below 0?

```
print(paste(nrow(filter(fricdata,alt<0)), "records below sea level represent", round(nrow(filter(fricdata,alt<0))/nrow(fricdata)*100,2), "percent of all occurrence records. We examined lat/long for many of these records and all examined locations were in bodies of water.", sep=" "))
```

```
## [1] "9974 records below sea level represent 3.87 percent of all occurrence records. We examined lat/long for many of these records and all examined locations were in bodies of water."
```

#how many records are above 500m?

```
print(paste(nrow(filter(fricdata,alt>500)), "records above 500m represent", round(nrow(filter(fricdata,alt>500))/nrow(fricdata)*100,2), "percent of all occurrence records. We examined lat/long and location for a small subset of high altitude records and found vague place names had been used for geolocation.", sep=" "))
```

```
## [1] "8629 records above 500m represent 3.34 percent of all occurrence records. We examined lat/long and location for a small subset of high altitude records and found vague place names had been used for geolocation."
```

#How many in the 0-500m range

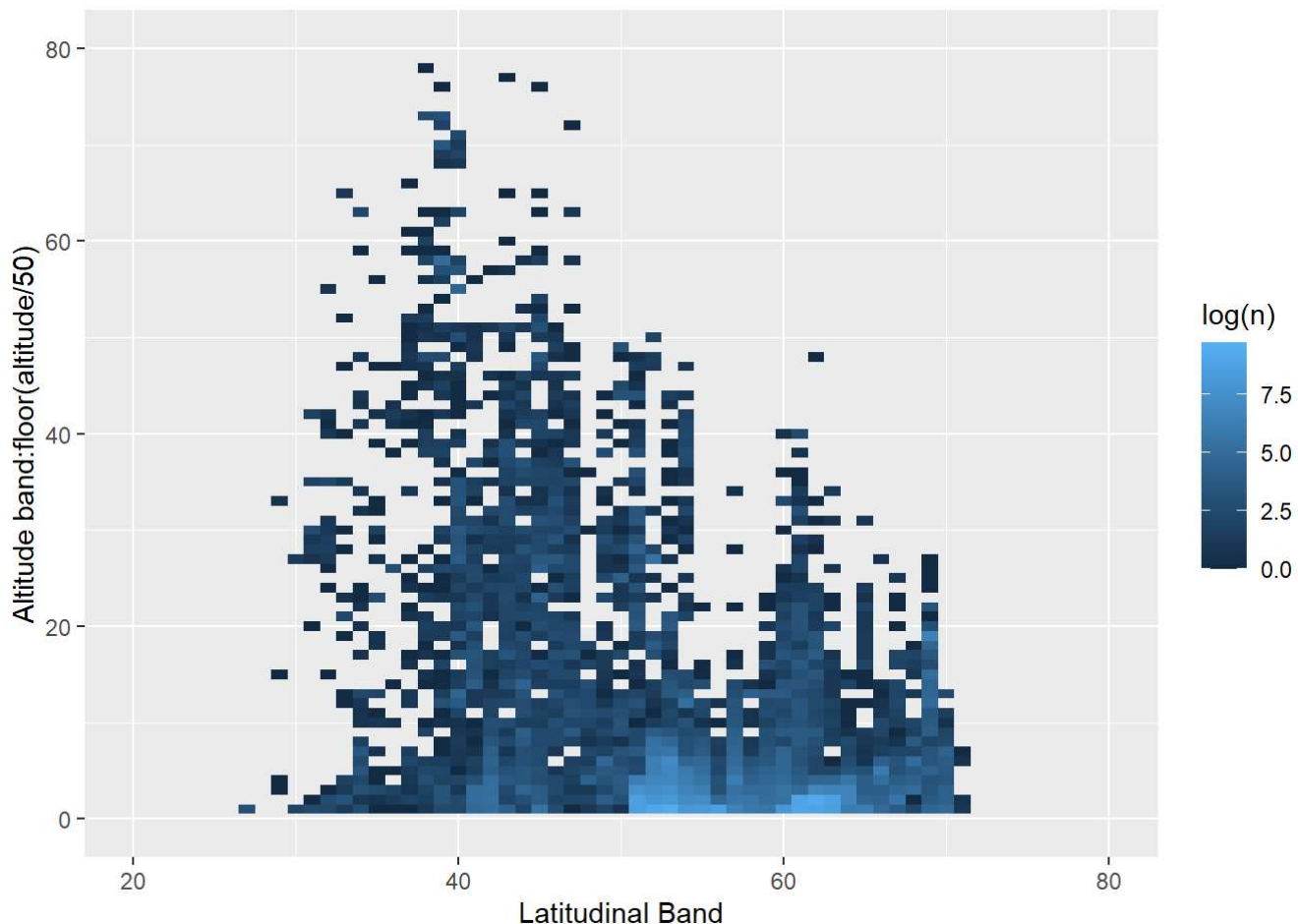
```
print(paste(nrow(filter(fricdata,between(alt,0,500))), "records within 0-500m represent", round(nrow(filter(fricdata,between(alt,0,500))/nrow(fricdata)*100,2), "percent of all occurrence records. For reanalysis, we can constrain data to these records with minimal impact on data density.", sep=" "))
```



```
## [1] "239369 records within 0-500m represent 92.79 percent of all occurrence records. For reanalysis, we can constrain data to these records with minimal impact on data density. "
```

```
altdata<-fricdata %>% mutate(alt.grp=floor(alt/50)) %>%
  group_by(alt.grp, rndLat) %>% tally()
# Heatmap
ggplot(altdata, aes(rndLat, alt.grp, fill= log(n))) +
  geom_tile() + labs(x="Latitudinal Band", y="Altitude band:floor(altitude/50)") +
  xlim(20,80) + ylim(0,80)
```

```
## Warning: Removed 37 rows containing missing values (geom_tile).
```



Outliers appear to be a problem with altitude. Reviewing GBIF records, this appears to be primarily due to the assumption by Fric et al. that the GIS coordinates are precise and that the google API would provide accurate and reliable altitude metrics. Based on the records we spot-checked, when GBIF includes elevation, the values do not match those used in the analysis.

A few examples including the lowest and highest alt records, as well as some additional records selected arbitrarily from the extreme quantiles of altitude:

- 1953 *Anthocharis sara* record (row.index 166; altitude -525.96m) is from <https://www.gbif.org/occurrence/1039154960> (<https://www.gbif.org/occurrence/1039154960>); geocoordinates were assigned via vertnet in 2015. These coordinates are located in the ocean. The GBIF record traces to <https://collections.peabody.yale.edu/search/Record/YPM-ENT-729028> (<https://collections.peabody.yale.edu/search/Record/YPM-ENT-729028>) which simply gives a locality of

“North America; USA; California; Los Angeles County; Rolling Hills”. Rolling Hills, CA is ~10km east of the given lat/long according to our estimation using googlemaps.

- 1991 *Parnassius smintheus* record (row.index 38; altitude 4048m) is from <https://www.gbif.org/occurrence/1039027733> (<https://www.gbif.org/occurrence/1039027733>) (which gives elevation of 3810m). The GBIF record traces to <https://collections.peabody.yale.edu/search/Record/YPM-ENT-430824> (<https://collections.peabody.yale.edu/search/Record/YPM-ENT-430824>) which gives a locality of “North America; USA; Colorado; Summit County; Loveland Pass, 3810 m”. The actual collection altitude is provided by the source, and is different than that used in the analysis.
- 1918 *Euphydryas chalcedona* record (row.index 139; altitude 4305m) is the highest record in the data. It's from <https://www.gbif.org/occurrence/1039181223> (<https://www.gbif.org/occurrence/1039181223>). The GBIF record traces to <https://collections.peabody.yale.edu/search/Record/YPM-ENT-819202> (<https://collections.peabody.yale.edu/search/Record/YPM-ENT-819202>) which gives a locality of “North America; USA; California; Siskiyou County; Mount Shasta” There is a city named Mount Shasta, CA that incorporated in 1905 that is at elevation 1100m and the peak of Mount Shasta is 4320. It is unclear whether the locality refers to the mountain or to the city; either way it is unlikely that an altitude so close to the peak of the mountain is the best choice for this specimen.

So far those examples are all North America - does this problem exist in Europe too?

- A *Lycaena hippothoe* record from 1995 (row.index 2160; altitude 3274m) is from <https://www.gbif.org/occurrence/2570253925> (<https://www.gbif.org/occurrence/2570253925>) which lists an inferred elevation of 2000m.
- A *Lycaena virgaureae* record from 2002 (row.index 4501; altitude -85.8m) appears to match <https://www.gbif.org/occurrence/173651704> (<https://www.gbif.org/occurrence/173651704>) which is located in the Gulf of Bothnia, though GBIF assigns an elevation of 0m. Considering the lat/long are (65,23) most likely those coordinates are imprecise.

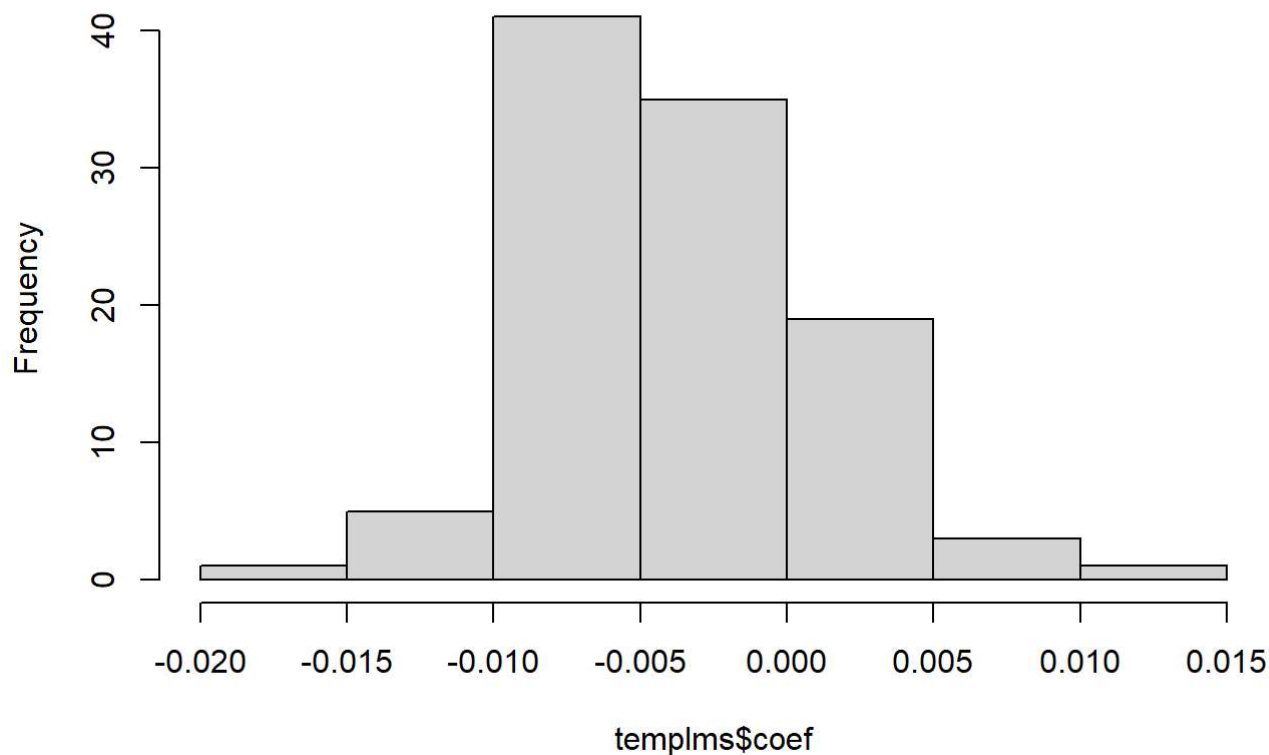
Altitude ~ Latitude collinearity

Fric et al. used regression of residuals for corrected analyses. Regression of residuals is not recommended, particularly if there could be collinearity among explanatory variables. We examined the collinearity between altitude and latitude, which would indicate the regression of residuals analysis would produce biased parameter estimates.

```
#Additional issues with altitude
#Given the use of regression of residuals, we were concerned that collinearity among independent
variables could have led to biased results.

#How many datasets have significant collinearity between altitude and latitude?
templms<-NULL
datasets<-fricdata %>% group_by(name, region) %>% tally()
for (spi in 1:nrow(datasets)) {
  tempdata<-fricdata %>% filter(name==datasets$name[spi],region==datasets$region[spi])
  spilm<-summary(lm(rndLat~alt, data=tempdata))
  templms<-rbind(templms,c(nrow(tempdata), spilm$coefficients[2,1], spilm$coefficients[2,4], sp
ilm$r.squared))
}
templms<-as.data.frame(templms)
names(templms)<-c("n","coef","pval","r2")
hist(templms$coef)
```

Histogram of templms\$coef



```
summary(templms)
```

```
##          n          coef          pval          r2
## Min.   : 15   Min.   :-0.019376   Min.   :0.00000   Min.   :0.0000222
## 1st Qu.: 78   1st Qu.: -0.006861   1st Qu.:0.00000   1st Qu.:0.0280076
## Median : 189  Median :-0.004516   Median :0.00000   Median :0.1909175
## Mean   : 2457  Mean   :-0.003832   Mean   :0.06654   Mean   :0.2824787
## 3rd Qu.: 1067 3rd Qu.: -0.001088   3rd Qu.:0.00851   3rd Qu.:0.5261002
## Max.   :51819  Max.   : 0.014635   Max.   :0.86050   Max.   :0.8487862
```

```
round(nrow(filter(templms,pval<0.05))/nrow(templms),2)
```

```
## [1] 0.85
```

```
#How many datasets have significant collinearity
print(paste(nrow(filter(templms,pval<0.05)),"datasets have significant collinearity, representing", round(nrow(filter(templms,pval<0.05))/nrow(templms)*100,1),"percent of all datasets. For datasets with significant collinearity, the mean coefficient is",round(mean(templms$coef[templms$pval<0.05]),3),"(which translates to a slope of", round(1/mean(templms$coef[templms$pval<0.05]),0),"meters per degree latitude) and mean r-squared is",round(mean(templms$r2[templms$pval<0.05]),3)," - therefore regression of residuals is likely producing bias parameters.",sep=" "))
```

```
## [1] "89 datasets have significant collinearity, representing 84.8 percent of all datasets. For datasets with significant collinearity, the mean coefficient is -0.004 (which translates to a slope of -224 meters per degree latitude) and mean r-squared is 0.33 - therefore regression of residuals is likely producing bias parameters."
```

Data exploration: data density

- In Fric et al. (2020), datasets were analysed with as few as 15 occurrence records.
- We examine the prevalence of singleton occurrences, when just one occurrence was available in a latitudinal band.

```
lat.summary1<-fricdata %>%
  group_by(name, region, rndLat) %>%
  summarize(lat.samplesize=n(),singleton=ifelse(lat.samplesize==1,1,0),dur=max(SuccDay)-min(SuccDay))
```

```
## `summarise()` regrouping output by 'name', 'region' (override with `.groups` argument)
```

```
lat.summary2<-lat.summary1 %>%
  group_by(name,region) %>%
  summarize(samplesize=sum(lat.samplesize),latspan=max(rndLat)-min(rndLat),nlats=length(unique(rndLat)),n.singletons=sum(singleton),prop.singletons=n.singletons/nlats)
```

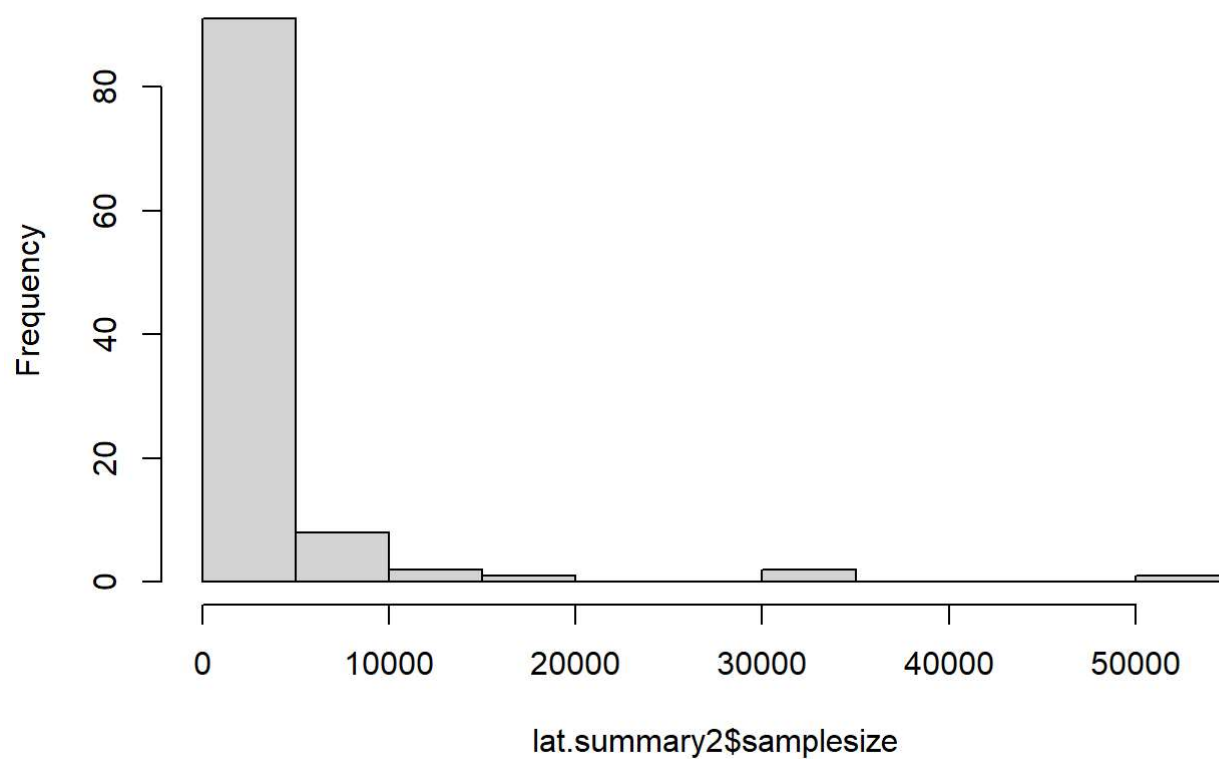
```
## `summarise()` regrouping output by 'name' (override with `.groups` argument)
```

```
summary(lat.summary2)
```

```
##      name      region      samplesize      latspan
## Length:105      Length:105      Min.   : 15      Min.   :10.0
## Class :character Class :character 1st Qu.: 78      1st Qu.:24.0
## Mode  :character Mode  :character Median : 189      Median :27.0
##                                     Mean  : 2457      Mean   :26.3
##                                     3rd Qu.: 1067      3rd Qu.:30.0
##                                     Max.   :51819      Max.   :64.0
##      nlats      n.singletons      prop.singletons
## Min.   : 5.0      Min.   : 0.000      Min.   :0.00000
## 1st Qu.:13.0      1st Qu.: 2.000      1st Qu.:0.09375
## Median :18.0      Median : 3.000      Median :0.19048
## Mean   :18.9      Mean   : 3.429      Mean   :0.20831
## 3rd Qu.:25.0      3rd Qu.: 5.000      3rd Qu.:0.33333
## Max.   :33.0      Max.   :10.000      Max.   :0.60000
```

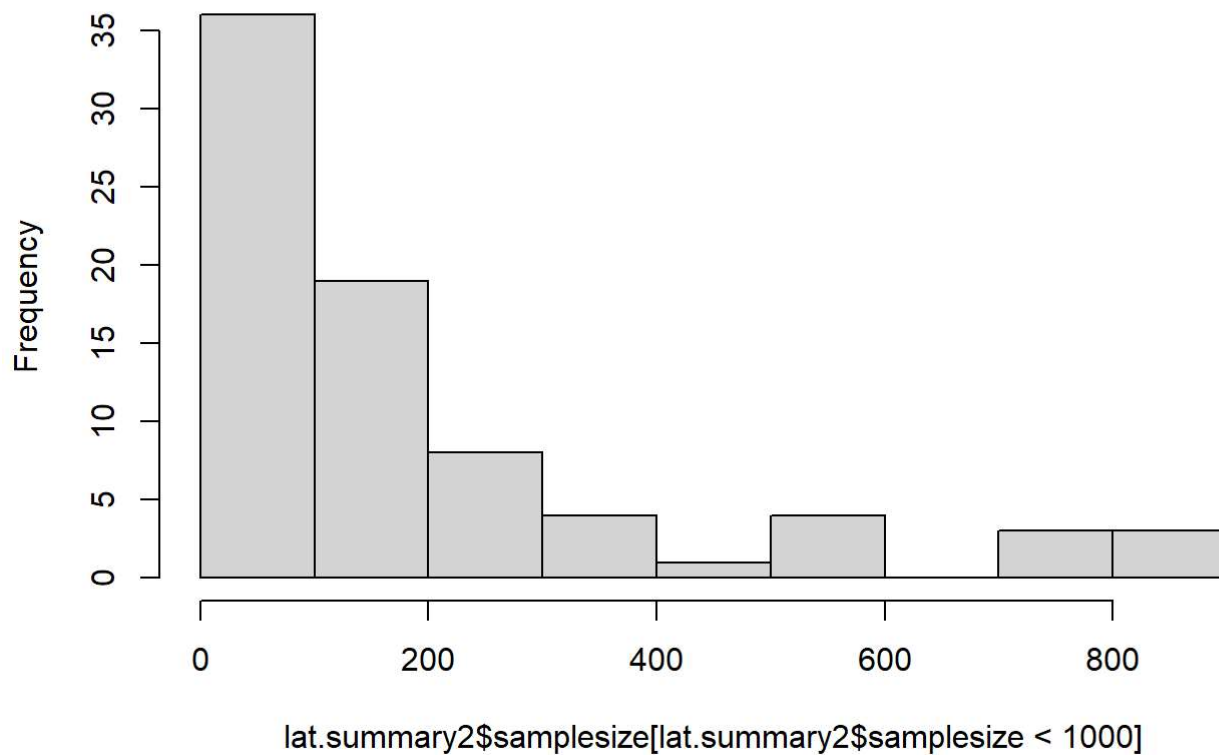
```
#Visualize range of sample sizes
hist(lat.summary2$samplesize, main="Sample size distribution")
```

Sample size distribution



```
#Look at the lower end of sample sizes, where most datasets are  
hist(lat.summary2$samplesize[lat.summary2$samplesize<1000], main="Sample size distribution up to  
1k records")
```

Sample size distribution up to 1k records



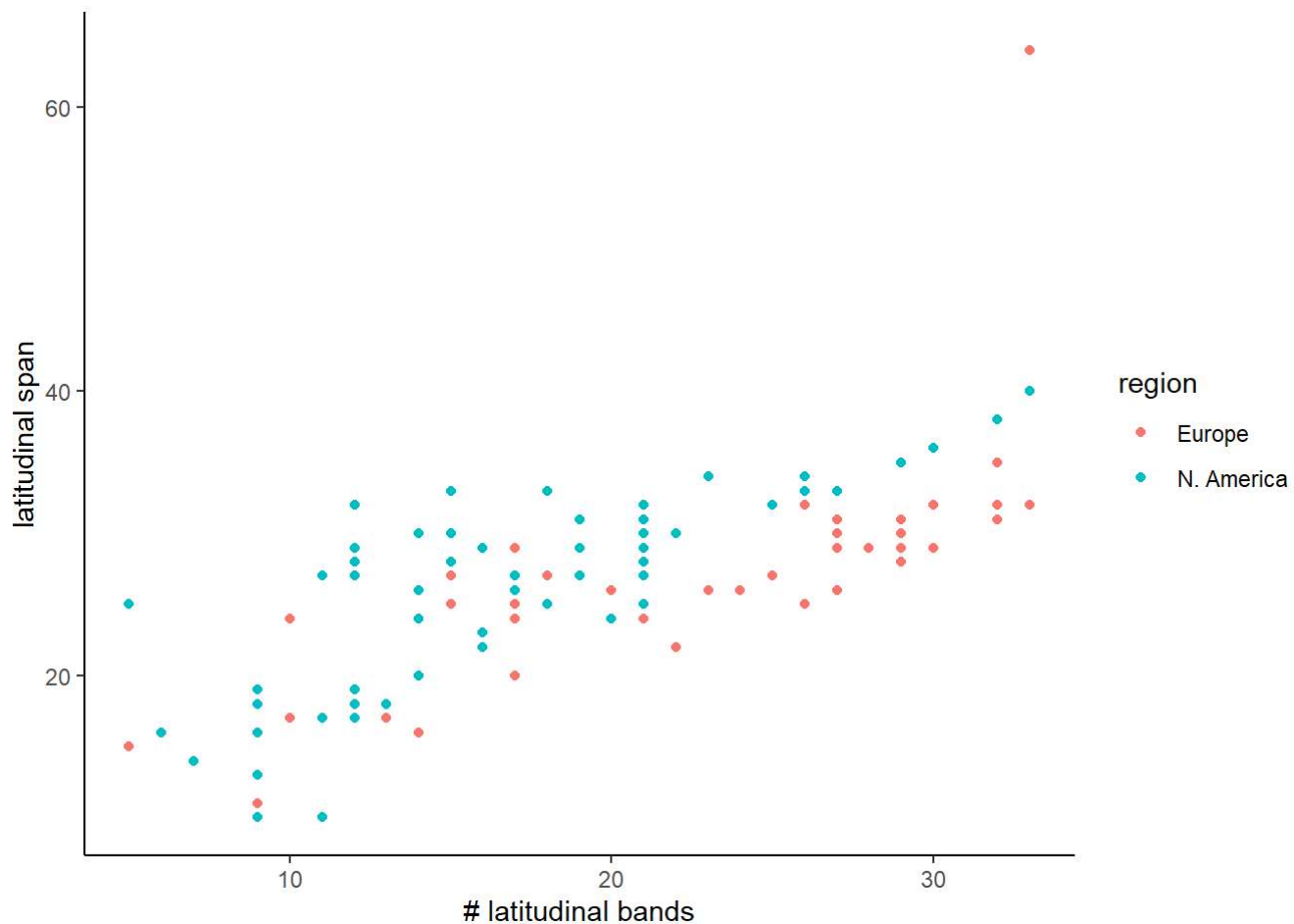
```
nrow(lat.summary2 %>% filter(samplesize<100))
```

```
## [1] 36
```

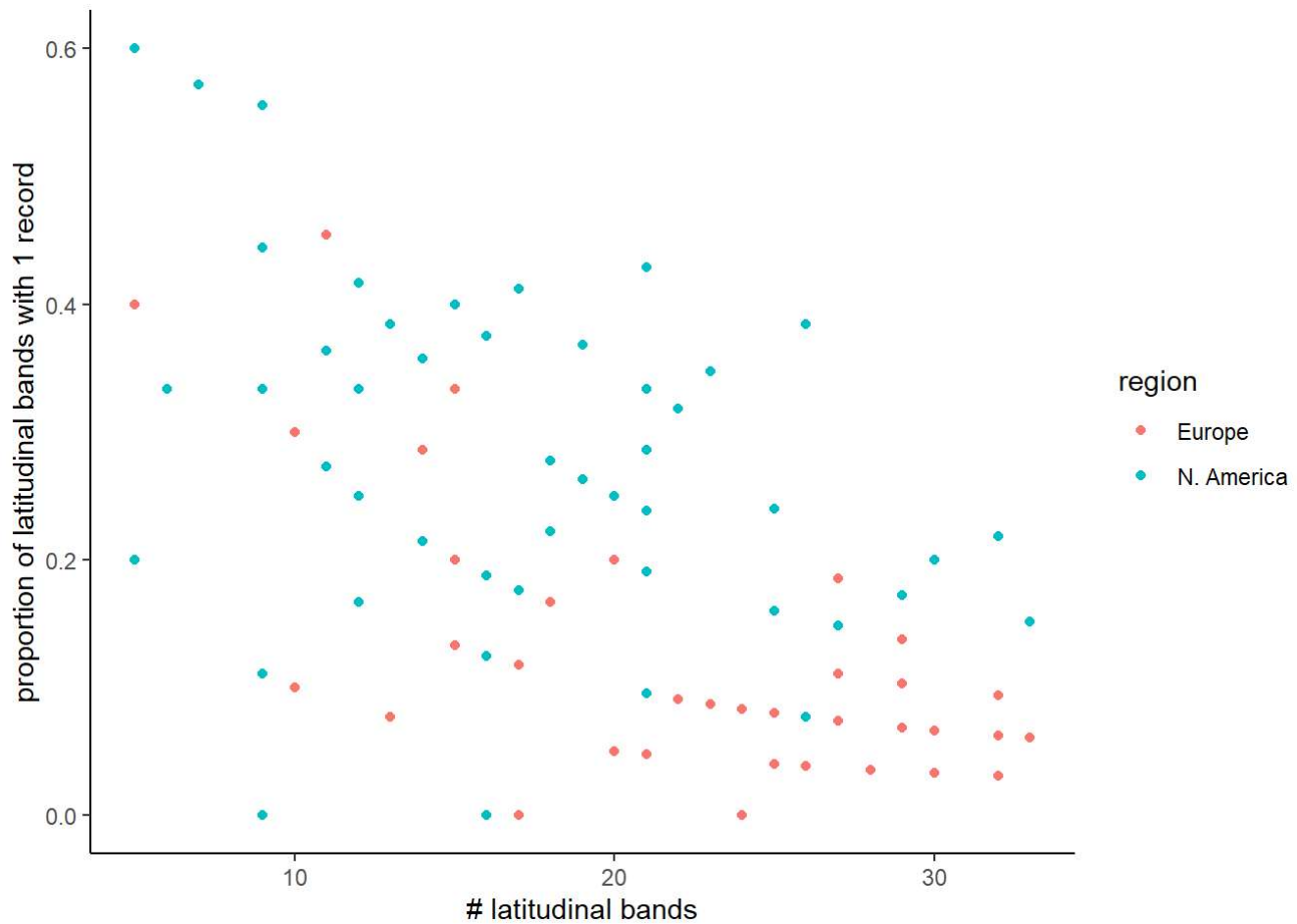
```
print(paste(nrow(lat.summary2 %>% filter(samplesize<100)), "datasets have less than 100 occurrence records."))
```

```
## [1] "36 datasets have less than 100 occurrence records."
```

```
ggplot(data=lat.summary2, aes(x=nlat, y=latspan, color=region)) + geom_point() + theme_classic() +
  labs(x="# latitudinal bands", y="latitudinal span")
```



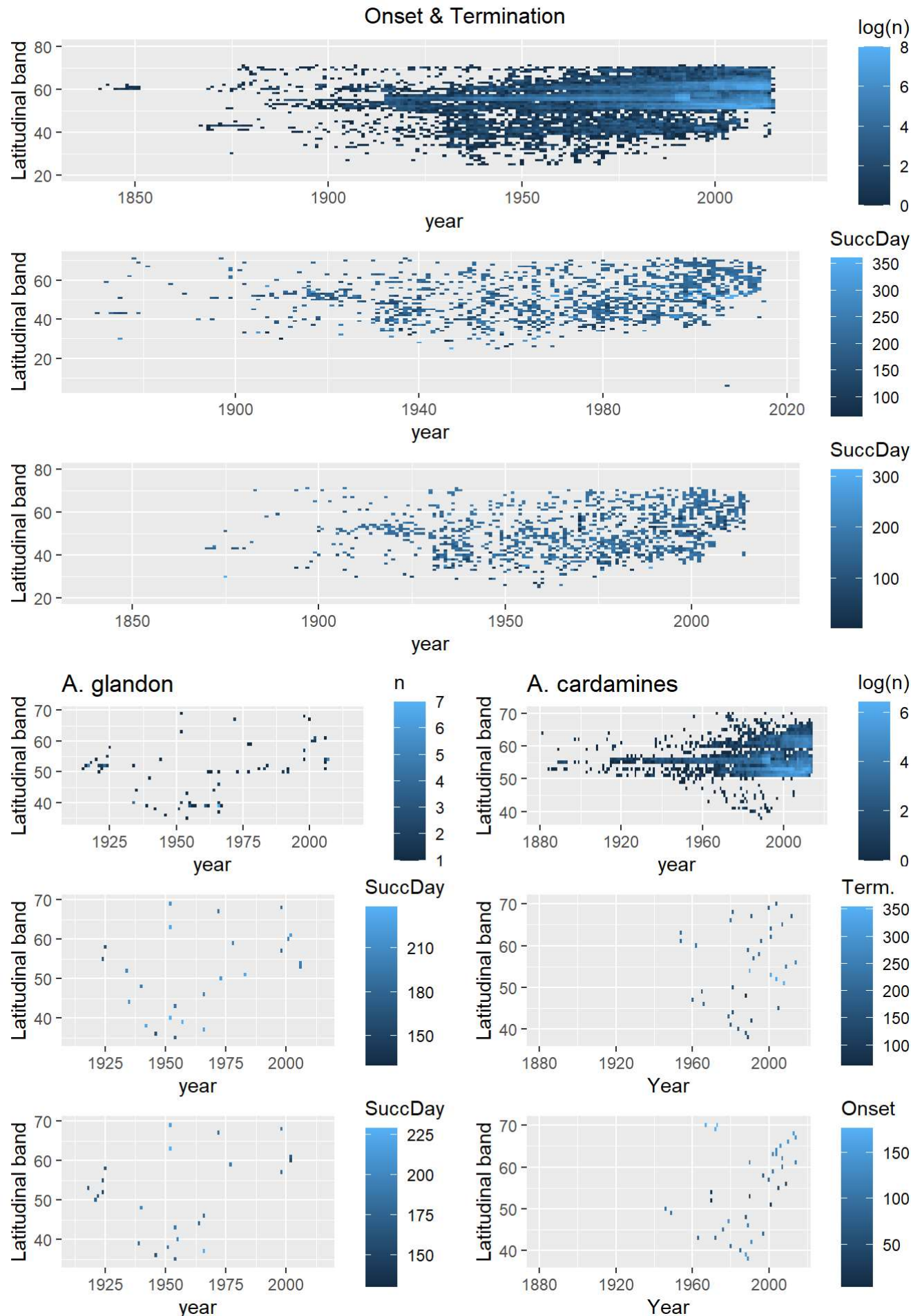
```
ggplot(data=lat.summary2, aes(x=nlat, y=prop.singletons, color=region)) + geom_point() + theme_
classic() +
  labs(x="# latitudinal bands", y="proportion of latitudinal bands with 1 record")
```

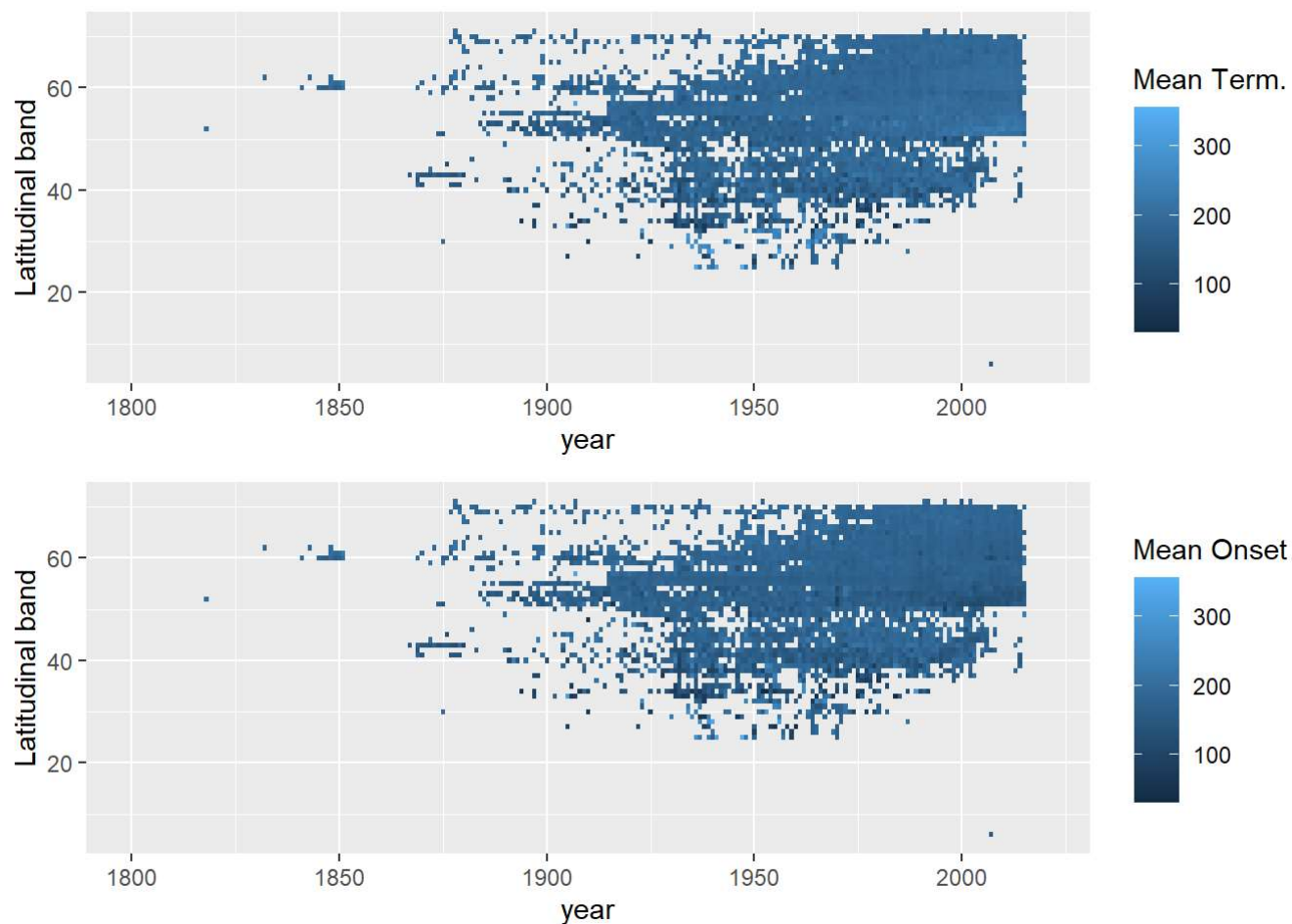


Data exploration: year

As expected, most data are quite recent. By selecting the min and max day of year per latitudinal band as onset & termination, the authors vastly decrease their sample size and remove most of the variation along the year and altitude axes

We arbitrarily selected two species, one with a low sample size and one with a large sample size, to visualize.





Recreate original results We also wanted to confirm that we understood correctly the Fric et al. analysis. We attempted to recreate the original Fric et al. analysis

```
## NEED TO ADD THIS CODE
```

End of File