# CHIS ASSP Banding Sheet QA/QC

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This document explains the QA/QC conducted on the Banding sheet of the CHIS ASSP Mistnetting Database. This work was completed in collaboration with Emily Kelsey, USGS.

#### Load libraries

```
library(tidyverse)
library(lubridate)
```

#### Set-up data for analysis

Read in Banding data sheet (copied/pasted from database version 3/24/2020). Use "na.strings" function to change "ND" values to be read as "NA" so that morphometric data is interpreted as as integers rather than characters.

```
banding <- read.csv("bandingQAQC.csv", header = TRUE, na.strings = c("NA", "ND"))</pre>
```

Filter data to ASSP species and banded individuals only.

```
ASSP <- group_by(.data = banding) %>%
filter(species == "ASSP") %>%
filter(band_no != "notbanded") %>%
ungroup()
```

#### Summarize band numbers and capture rates.

Summarize data by band number and determine capture rate for each band number (e.g., each individual).

```
summary <- group_by(.data = ASSP, band_no) %>%
summarise(no_captures = n()) %>%
ungroup()
```

There are 3644 unique band numbers.

Summarize capture rates.

```
summarycaptures <- group_by(summary, no_captures) %>%
summarise(count = n()) %>%
ungroup()
show(summarycaptures)
```

Summarize recapture rates.

```
recap <- group_by(.data = ASSP, recapture) %>%
   summarise(no_captures = n()) %>%
   ungroup()

show(recap)
```

```
## # A tibble: 3 x 2
## recapture no_captures
## <fct> <int>
## 1 N 3607
## 2 SNR 41
## 3 Y 196
```

The recapture rates will not necessarily match the unique band numbers because we might have encountered individuals only as a recapture (i.e., we did not band them).

How else can we proof these data?

[1] 22 23 0 1 2 3 4 21 20 11 10 12

#### Capture time

```
#Change data type of time stamp and pull out hour as new field
ASSP$capture_time <- mdy_hm(ASSP$capture_time, tz="US/Pacific")
ASSP$cap_hour <- hour(ASSP$capture_time)
unique(ASSP$cap_hour)</pre>
```

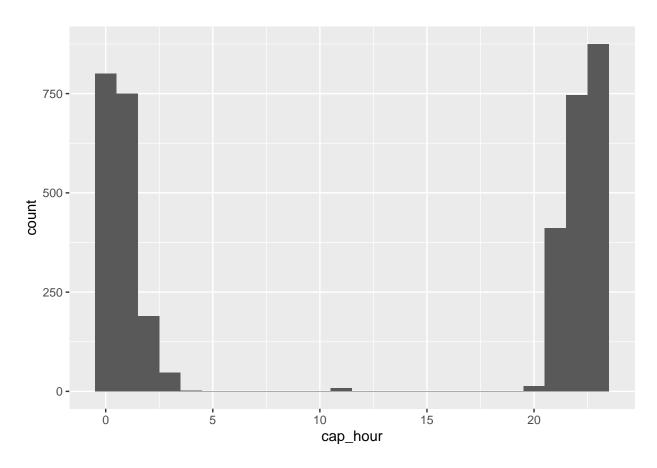
```
#Some problematic data, unique values at 11, 10, 12
#4 also seems like a really late morning capture time, but plausible, double-check.

summary(ASSP$cap_hour)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.00 1.00 21.00 12.18 22.00 23.00
```

```
#No NA's in capture time. Double-checked database, this is correct.
#They were filtered out (destroyed/lost bands).

ggplot(data = ASSP) +
   geom_histogram(mapping = aes(x = cap_hour), binwidth = 1)
```



```
#Appears that some time stamps were not entered in military time

captimesite <- arrange(ASSP, site_code, capture_time)
#Unsure how to check min/sec of capture time without preservation of data entry order

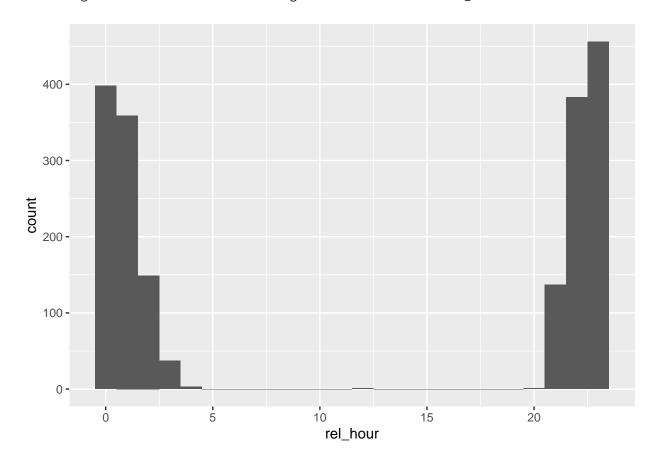
#Isolate questionable data
cap_hour_chk <- group_by(.data = ASSP, cap_hour) %>%
    filter(cap_hour %in% c(4, 10, 11, 12)) %>%
    ungroup()

write.csv(cap_hour_chk, "captimeQAQC.csv")
#Verified capture times with raw data and changed any mistakes. Tracked changes in csv.
```

#### Release time

```
#Change data type of release time stamp and pull out hour as new field
ASSP$release_time <- mdy_hm(ASSP$release_time, tz="US/Pacific")
ASSP$rel_hour <- hour(ASSP$release_time)
unique(ASSP$rel_hour)
## [1] NA 23 0 1 2 21 22 3 4 12 20
#Problematic data: 12
\#Double\mbox{-}check\ 3am\ and\ 4am\ also
summary(ASSP$rel_hour)
##
      Min. 1st Qu. Median
                              Mean 3rd Qu.
                                               Max.
                                                       NA's
##
              1.00
                     21.00
                             11.75
                                      22.00
                                              23.00
                                                       1920
#1920 NA's
#Min and max make sense
ggplot(data = ASSP) +
  geom_histogram(mapping = aes(x = rel_hour), binwidth = 1)
```

## Warning: Removed 1920 rows containing non-finite values (stat\_bin).



```
#Also appears to be data not entered in military time

#Isolate questionable data
rel_hour_chk <- group_by(.data = ASSP, rel_hour) %>%
  filter(rel_hour %in% c(3, 4, 12)) %>%
  ungroup()

write.csv(rel_hour_chk, "reltimeQAQC.csv")

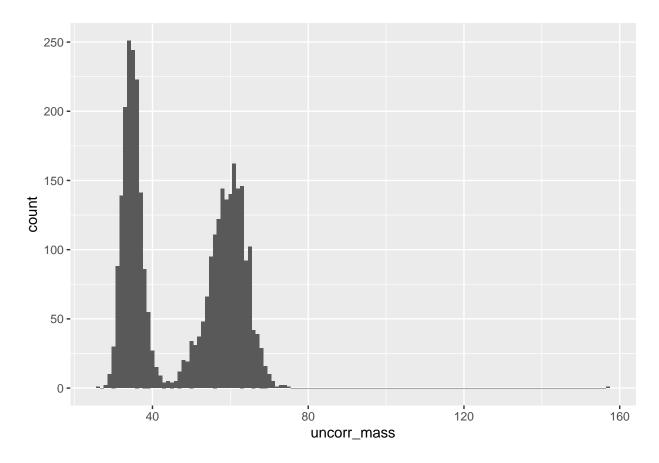
#Verified with raw data and changed any mistakes. Tracked changes in csv.
```

#### **Brood** patch

```
unique(ASSP$BP)
                                                                  pd
## [1] 4
            1.5 0
                    1
                           3
                                5
                                     <NA> 2
                                                    PD
                                                         В
                                                                      d
                                                                            4.5
## Levels: 0 1 1.5 2 3 4 4.5 5 b B d D pd PD
#Fix lowercase values
#All in range of values included in data dictionary
#Not sure how else to QAQC?
```

#### Mass

```
## Mass(uncorrected)
unique(ASSP$uncorr_mass)
  [1]
            36 34 32
                       33
                           35
                               37
                                   38
                                       39
                                           62
                                              61
                                                  60
                                                     NA
                                                              40
                                                                      26
                                                                         44
                                                                             68
## [20]
       47
            48 50 59
                       63
                           51
                               55 64
                                       69
                                          75 42 65 67
                                                          57 49 54 66 56
                                                                             70
## [39]
        30
           53 72 71 52
                           46
                               45 74 73 43 29
                                                  28 157
summary(ASSP$uncorr_mass)
##
     Min. 1st Qu. Median
                            Mean 3rd Qu.
                                            Max.
                                                   NA's
##
    26.00
           35.00
                   52.00
                           48.14
                                  60.00 157.00
                                                    493
#Large range between 26 - 157 but it's uncorrected data
#493 NAs
ggplot(data = ASSP) +
 geom_bar(mapping = aes(x = uncorr_mass), binwidth =1)
## Warning: `geom_bar()` no longer has a `binwidth` parameter. Please use
## `geom_histogram()` instead.
## Warning: Removed 493 rows containing non-finite values (stat_bin).
```



## [1] 0 NA 27 13 26 14 25 23 30 22 31 33 35 29 28 17 24 32 12 21 16 36 20 15 10 ## [26] 18 19 9 11

```
summary(ASSP$mass_tare)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's ## 0.0 0.0 16.0 12.7 25.0 36.0 494
```

# unique(ASSP\$mass\_corr) ## [1] 31 36 34 32 33 35 37 38 39 62 61 60 NA 58 40 41 26 44 43 ## [20] 42 29 30 23 17 28 22 48 45 6 7 135 20 27 24 46

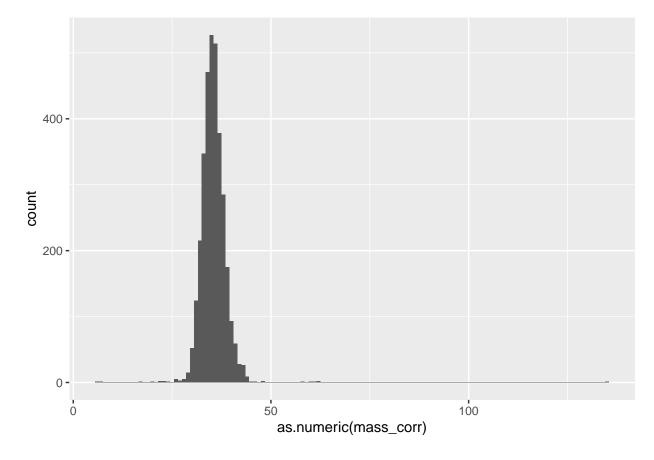
```
summary(ASSP$mass_corr)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## 6.00 34.00 35.00 35.45 37.00 135.00 494
```

```
#494 NAs
#large range between 6 - 135
#mean 35.45
#median 35

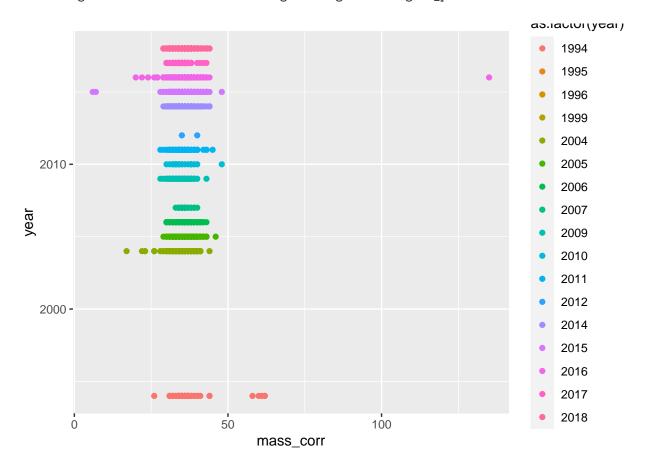
ggplot(data = ASSP) +
   geom_histogram(mapping = aes(x = as.numeric(mass_corr)), binwidth = 1)
```

## Warning: Removed 494 rows containing non-finite values (stat\_bin).



```
ggplot(data = ASSP) +
geom_point(mapping = aes(x = mass_corr, y = year, color = as.factor(year)))
```

## Warning: Removed 494 rows containing missing values (geom\_point).



```
#Need to double-check outliers

#Re Adams 2016 paper, Mass (g) 36.1 +/- 2.8 (f) and 34.7 +/- 2.1 (m)

#Isolate questionable data
mass_corr_chk <- filter(ASSP, mass_corr < 25 | mass_corr > 50)

write.csv(mass_corr_chk, "masscorrQAQC.csv")
#Verified with raw data and changed any mistakes. Tracked changes in csv.
```

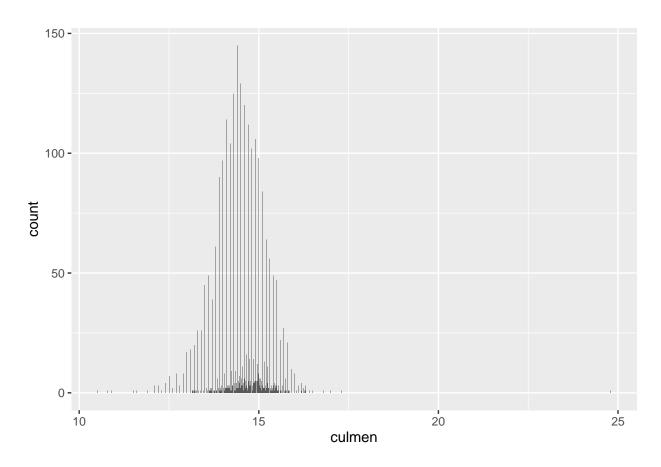
#### Culmen

```
summary(ASSP$culmen)
##
      Min. 1st Qu. Median
                              Mean 3rd Qu.
                                                      NA's
                                              Max.
                    14.50
##
     10.50
           14.10
                             14.51
                                     14.99
                                             24.80
                                                       1253
#Large range between 10.50 - 24.80
#Mean at 14.51
#Medium at 14.50
```

```
#Larger values seen incongruous

ggplot(data = ASSP) +
  geom_bar(mapping = aes(x = culmen))
```

## Warning: Removed 1253 rows containing non-finite values (stat\_count).



```
#Re Adams 2016 paper, Bill length (mm) 14.9 ? 0.5 (f) and 14.6 ? 0.8 (m)
#Re Pyle guide, 13.1-15.2 (95% CI)

#Isolate questionable data
culmen_chk <- filter(ASSP, culmen < 13 | culmen > 16)

write.csv(culmen_chk, "culmenQAQC.csv")
#Verified with raw data and changed any mistakes. Tracked changes in csv.
#Seems like the range I picked (13-16) was too narrow. Most were not typos.
#Assumed values w/in (12-16.9) were not typos after reviewing data.
```

#### Skull length

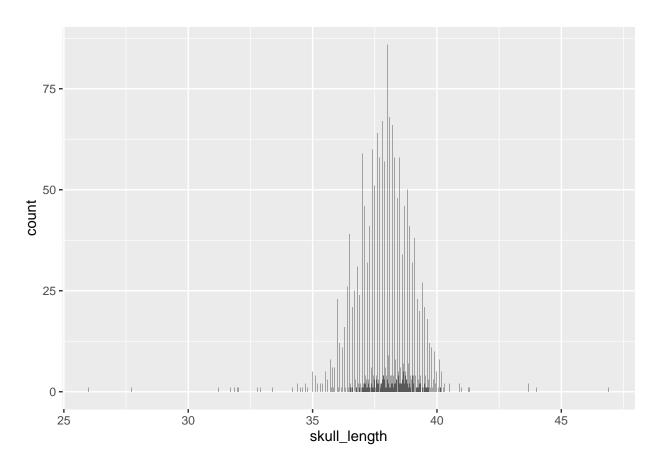
```
summary(ASSP$skull_length)
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## 26.00 37.30 38.00 37.93 38.65 46.90 1805
```

```
#Range between 26 - 46.90
#Mean at 37.93
#Median at 38
#Lower values seen incongruous

ggplot(data = ASSP) +
   geom_bar(mapping = aes(x = skull_length))
```

## Warning: Removed 1805 rows containing non-finite values (stat\_count).



```
#Re Adams 2016 paper, skull length (mm) 38.1 ? 1.1 (f) and 37.9 ? 0.8 (m)
#No info in Pyle guide

#Isolate questionable data
skull_chk <- filter(ASSP, skull_length < 35 | skull_length > 41)

write.csv(skull_chk, "skullQAQC.csv")
```

#### **Tarsus**

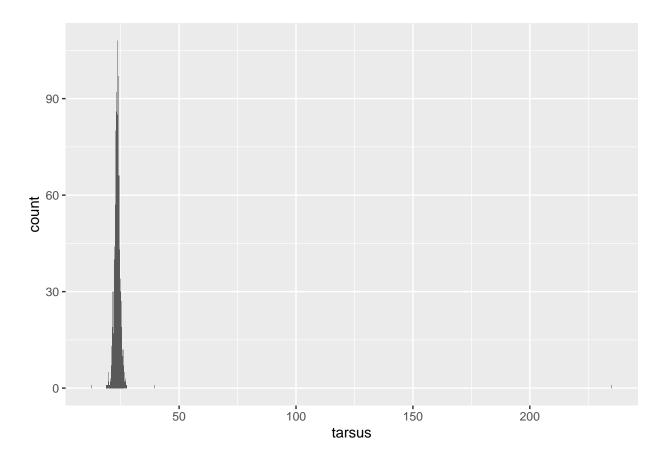
#### summary(ASSP\$tarsus)

```
## Min. 1st Qu. Median Mean 3rd Qu. Max. NA's ## 12.60 22.80 23.45 23.55 24.10 235.00 1252
```

```
#Range between 12.60 - 235
#Mean at 23.55
#Median at 23.45

ggplot(data = ASSP) +
  geom_bar(mapping = aes(x = tarsus))
```

## Warning: Removed 1252 rows containing non-finite values (stat\_count).



```
#Re Adams 2016 paper, tarsus (mm) 23.2 ? 0.9 (f) and 23.1 ? 0.8 (m)
#Re Pyle guide, 21-25 (95% CI)

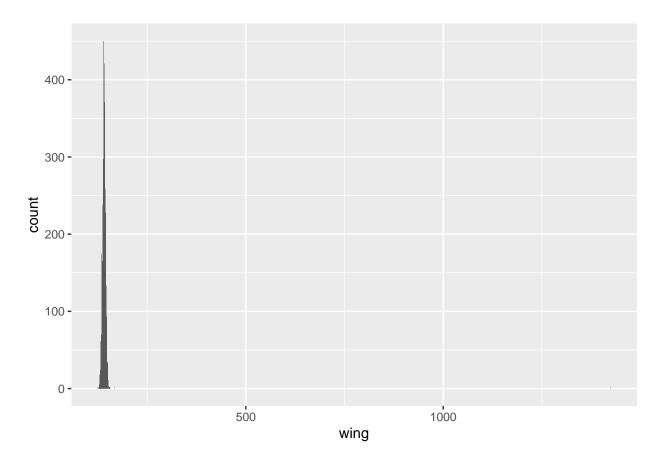
#Isolate questionable data
tarsus_chk <- filter(ASSP, tarsus < 19 | tarsus > 27)

write.csv(tarsus_chk, "tarsusQAQC.csv")
```

## Wing

```
summary(ASSP$wing)
##
     Min. 1st Qu. Median
                              Mean 3rd Qu.
                                                      NA's
                                              Max.
##
       123
               138
                       141
                               141
                                       143
                                              1425
                                                        161
#Range between 123 - 1425
#Mean at 141
#Median at 141
ggplot(data = ASSP) +
geom_bar(mapping = aes(x = wing))
```

## Warning: Removed 161 rows containing non-finite values (stat\_count).



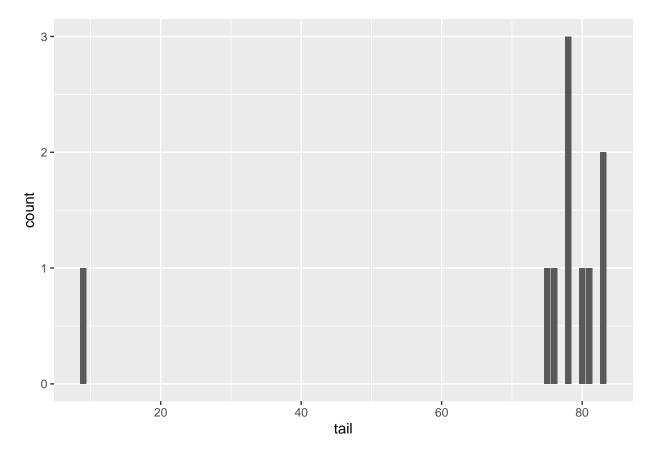
```
#Re Adams 2016, max flat wing (mm) 142.7 ? 2.8 (f) and 140.4 ? 3.3 (m)
#Re Pyle guide, wing chord 132-148 (95% CI)

#Isolate questionable data
wing_chk <- filter(ASSP, wing < 130 | wing > 150)
write.csv(wing_chk, "wingQAQC.csv")
```

### Tail

```
summary(ASSP$tail)
##
     Min. 1st Qu. Median
                             Mean 3rd Qu.
                                             Max.
                                                     NA's
##
     9.00 76.50
                   78.00
                            72.10 80.75
                                            83.00
                                                     3834
\#Range\ between\ 9 - 83
#Mean 72.10
#Median 78
ggplot(data = ASSP) +
 geom_bar(mapping = aes(x = tail))
```

## Warning: Removed 3834 rows containing non-finite values (stat\_count).



```
#Re Pyle, 72-84 (95% CI)

#Isolate questionable data
tail_chk <- filter(ASSP, tail < 71 | tail > 85)

write.csv(tail_chk, "tailQAQC.csv")
```