

Giant anteater revisions (adult)

2024-01-25

```
# Load packages
library(ctmm)
library(dplyr)
library(tidyverse)
library(glmmTMB)
library(lme4)
```

The pre-print analyses contained 23 range-resident giant anteaters. Within the 23 individuals contained 12 males (8 adults, 4 subadults) and 11 females (all adults). This script is based on adult giant anteaters only. Subadults have been removed.

```
#import data, cleaned giant anteater GPS tracking data, containing no outliers
COLLAR_DATA <- read.csv("data/Anteaters_NoOutliers.csv")
```

```
#correct mismatch ID entries
COLLAR_DATA$ID[COLLAR_DATA$ID == "Larry 267"] <- "Larry"
```

```
COLLAR_DAT <- data.frame(timestamp = COLLAR_DATA$timestamp,
                        ID = COLLAR_DATA$ID,
                        GPS.Latitude = COLLAR_DATA$GPS.Latitude,
                        GPS.Longitude = COLLAR_DATA$GPS.Longitude,
                        GPS.Horizontal.Dilution =
COLLAR_DATA$GPS.Horizontal.Dilution,
                        OUT = COLLAR_DATA$OUT,
                        Road = COLLAR_DATA$Road)
```

```
#subset to the 20 adult range-resident individuals
anteater_data <- COLLAR_DAT[which(COLLAR_DAT$ID
                                %in% c("Alexander", "Annie", "Beto",
                                "Bumpus", "Cate",
                                "Christoffer", "Elaine",
                                "Hannah", "Jackson", "Jane",
                                "Larry", "Luigi", "Makao",
                                "Margaret", "Maria",
                                "Puji", "Rodolfo", "Sheron",
                                "Thomas")),]
```

```
anteater_data <- readRDS("data/anteater_data_adults.rds")
```

```
#import supplementary data containing biological information
DATA_META <- read.csv("data/Anteater_Results_Final.csv")
```

```
#subset biological data from supplementary data
```

```

bio_data <- DATA_META[which(DATA_META$ID
                             %in% c("Alexander", "Annie", "Beto", "Bumpus",
"Kate",
                             "Christoffer", "Elaine",
"Hannah", "Jackson", "Jane",
                             "Larry", "Luigi", "Makao", "Margaret",
"Maria",
                             "Puji", "Rodolfo", "Sheron",
"Thomas")), c(1:5)]

#add site location
bio_data$Site[bio_data$Road == "MS-040"] <- 1
bio_data$Site[bio_data$Road == "BR_267"] <- 2

#add bio data
anteater_data <- merge(anteater_data, bio_data, all = TRUE)

#convert dataset to a telemetry object
DATA_TELEMETRY <- as.telemetry(anteater_data)

#import movement models
load("data/anteater_fit.rda")

#subset to adults only
FIT <- FIT[-c(3,12,14,20)]

#import home-range estimates
load("data/anteater_AKDE.rda")

#subset to adults only
AKDE <- AKDE[-c(3,12,14,20)]

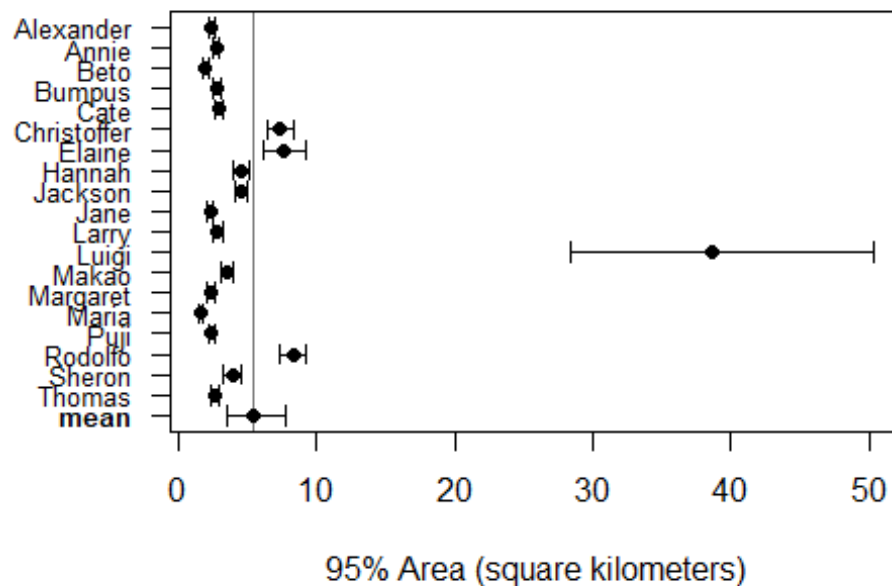
```

Home-range results

#Mean HR size...

```
meta(AKDE)
```

```
##                ΔAICc
## inverse-Gaussian    0.000
## Dirac-δ            1671.981
```



```
##               low      est      high
## mean (km²)  3.5554087 5.3982357 7.852936
## CoV² (RVAR) 0.2798331 0.7412662 1.423521
## CoV (RSTD)  0.5394160 0.8779329 1.216623
```

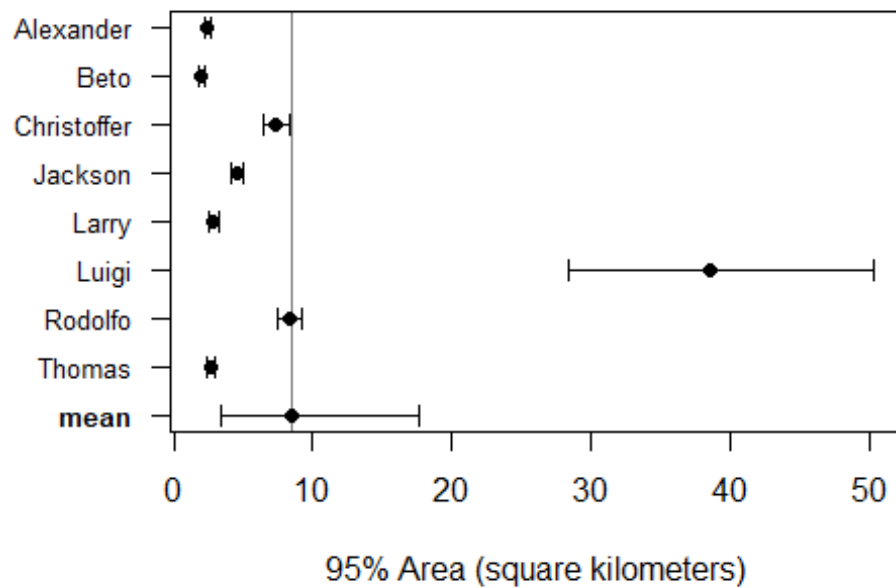
#Compare between sex...

```
AKDE_male <- AKDE[c("Alexander", "Beto", "Christoffer", "Jackson", "Larry",
                    "Luigi", "Rodolfo", "Thomas")]
AKDE_female <- AKDE[c("Annie", "Bumpus", "Cate", "Elaine", "Hannah",
                     "Jane", "Makao", "Margaret", "Maria", "Puji",
                     "Sheron")]
```

#calculate mean home range sizes for male

```
meta(AKDE_male)
```

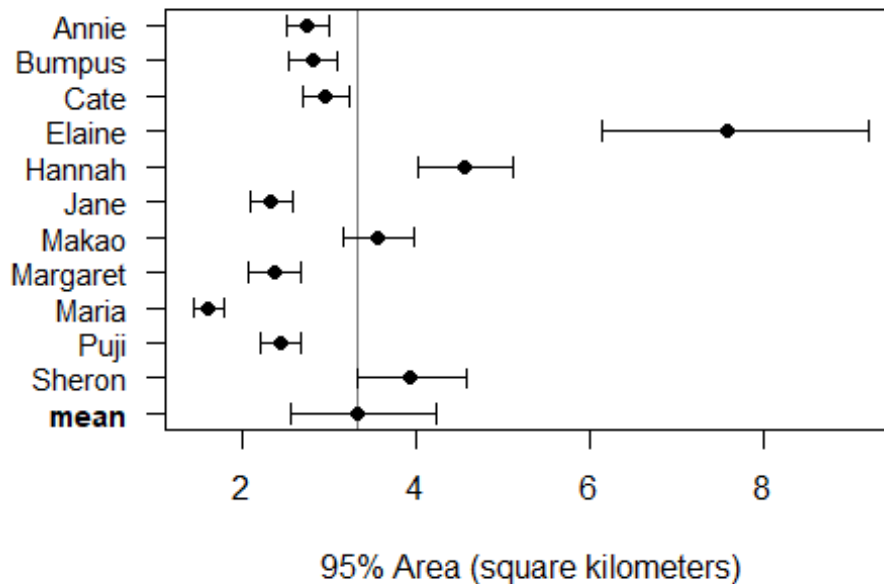
```
##               ΔAICc
## inverse-Gaussian    0.000
## Dirac-δ             1018.877
```



```
##               low      est      high
## mean (km²)  3.4269511 8.473694 17.647143
## CoV² (RVAR) 0.2042960 1.471644  3.963360
## CoV  (RSTD) 0.4770962 1.280494  2.101396
```

#calculate mean home range sizes for female
meta(AKDE_female)

```
##               ΔAICc
## inverse-Gaussian  0.0000
## Dirac-δ           288.9002
```



```
##               low      est      high
## mean (km²)  2.56403337 3.3229336 4.2340253
## CoV² (RVAR) 0.05286222 0.1735890 0.3647910
## CoV  (RSTD) 0.23610030 0.4278435 0.6202202
```

#female/male ratio of mean home-range areas

```
AKDE_sex_compare <- list(male = AKDE_male,
                          female = AKDE_female)
```

```
meta(AKDE_sex_compare, col = c("#004488", "#A50026"), sort = TRUE)
```

* Sub-population male

```
##               ΔAICc
## inverse-Gaussian 0.000
## Dirac-δ         1018.877
```

* Sub-population female

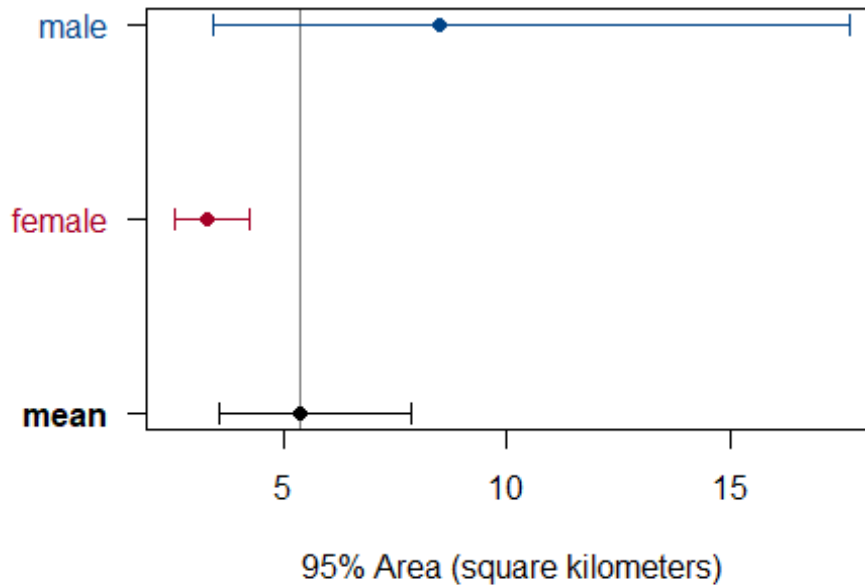
```
##               ΔAICc
## inverse-Gaussian 0.0000
## Dirac-δ         288.9002
```

* Joint population

```
##               ΔAICc
## inverse-Gaussian 0.000
## Dirac-δ         1671.981
```

```
## * Joint population versus sub-populations (best models)
```

```
##           $\Delta AIC_c$   
## Sub-population 0.000000  
## Joint population 3.607806
```



```
## , , low  
##  
##          /male  /female  
## male/    1.000000 0.8082377  
## female/  0.1107186 1.0000000  
##  
## , , est  
##  
##          /male  /female  
## male/    1.000000 2.507956  
## female/  0.3169989 1.000000  
##  
## , , high  
##  
##          /male  /female  
## male/    1.000000 5.262085  
## female/  0.8380671 1.000000
```

Estimating home-range overlap

#subset home range overlap based on site location

```
AKDE_1 <- AKDE[c("Alexander", "Bumpus", "Cate", "Christoffer",
```

```

      "Elaine", "Jackson", "Makao",
      "Puji", "Rodolfo"]])

AKDE_2 <- AKDE[c("Annie", "Beto", "Hannah", "Jane", "Larry",
               "Luigi", "Margaret", "Maria", "Sheron",
               "Thomas")]

#calculate 95% AKDE home range overlap for a pairwise comparison for each site
overlap1 <- overlap(AKDE_1, level = 0.95)
overlap2 <- overlap(AKDE_2, level = 0.95)

overlap_data <- readRDS("data/home_range/overlap_data_adults.rds")

```

Home-range overlap results

#Is sex a factor?...

#rescale the values

```

min_val <- min(overlap_data$overlap_est)
max_val <- max(overlap_data$overlap_est)
squeeze_min <- 0.001
squeeze_max <- 0.999
overlap_data$overlap_est_squeezed <- ((overlap_data$overlap_est - min_val) /
(max_val - min_val)) * (squeeze_max - squeeze_min) + squeeze_min

```

#compare model with and without sex as a variable

```

HRO_test <- glmmTMB(overlap_est_squeezed ~ sex_comparison + (1|site),
                  family = beta_family(link = "logit"), data =
overlap_data)
HRO_test2 <- glmmTMB(overlap_est_squeezed ~ 1 + (1|site),
                  family = beta_family(link = "logit"), data =
overlap_data)
HRO_test_results <- anova(HRO_test, HRO_test2)
HRO_test_results

```

```
## Data: overlap_data
```

```
## Models:
```

```
## HRO_test2: overlap_est_squeezed ~ 1 + (1 | site), zi=~0, disp=~1
```

```
## HRO_test: overlap_est_squeezed ~ sex_comparison + (1 | site), zi=~0,
disp=~1
```

```
##           Df      AIC      BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
## HRO_test2  3 -267.69 -260.51 136.84  -273.69
## HRO_test   5 -264.82 -252.85 137.41  -274.82 1.1323      2      0.5677
```

#calculate sex impact via likelihood ratio test

```

HRO_test_pvalue <- round(HRO_test_results$`Pr(>Chisq)`[2], 2)
HRO_test_pvalue

```

```
## [1] 0.57
```

```

#Home range overlap results based on sex comparisons (i.e.. male-male,
female-female, and female-male).

#number of home range overlap in each sex comparison category
table(overlap_data$sex_comparison)

##
## female-female    female-male    male-male
##           25           44           12

#calculate mean home range overlap and the range based on sex comparisons
round(mean(overlap_data$overlap_est[overlap_data$sex_comparison == "male-
male"]), 2)

## [1] 0.14

round(min(overlap_data$overlap_est[overlap_data$sex_comparison == "male-
male"]), 2)

## [1] 0

round(max(overlap_data$overlap_est[overlap_data$sex_comparison == "male-
male"]), 2)

## [1] 0.69

round(mean(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
female"]), 2)

## [1] 0.14

round(min(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
female"]), 2)

## [1] 0

round(max(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
female"]), 2)

## [1] 0.87

round(mean(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
male"]), 2)

## [1] 0.19

round(min(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
male"]), 2)

## [1] 0

round(max(overlap_data$overlap_est[overlap_data$sex_comparison == "female-
male"]), 2)

```



```
## [1] 0.96
```

Estimating proximity ratio

```
#import proximity data
proximity_data <- readRDS("data/proximity/proximity_df.rds")
proximity_data <- as.data.frame(proximity_data)

#remove subadults from proximity data
proximity_data <- proximity_data[!(proximity_data$anteater_A %in% "Anthony" |
proximity_data$anteater_B %in% "Anthony"),]
proximity_data <- proximity_data[!(proximity_data$anteater_A %in% "Kyle" |
proximity_data$anteater_B %in% "Kyle"),]
proximity_data <- proximity_data[!(proximity_data$anteater_A %in%
"Little_Rick" | proximity_data$anteater_B %in% "Little_Rick"),]
proximity_data <- proximity_data[!(proximity_data$anteater_A %in% "Reid" |
proximity_data$anteater_B %in% "Reid"),]

#combine overlap and proximity data
overlap_data <- merge(overlap_data, proximity_data, all = TRUE)
```

Proximity ratio results

```
#test for significance in sex, compare model with and without sex as a
variable
proximity_test <- glmer(proximity_est ~ sex_comparison + (1|site),
                        family = Gamma(link = "log"), data = overlap_data)

## boundary (singular) fit: see help('isSingular')

proximity_test2 <- glmer(proximity_est ~ 1 + (1|site),
                        family = Gamma(link = "log"), data = overlap_data)

## boundary (singular) fit: see help('isSingular')

proximity_test_results <- anova(proximity_test, proximity_test2)

#calculate sex impact on proximity ratio via likelihood ratio test
proximity_test_pvalue <- round(proximity_test_results$`Pr(>Chisq)`[2], 2)
proximity_test_pvalue

## [1] 0.12

#compare model with and without overlap as a variable
prox_overlap_test <- glmer(proximity_est ~ overlap_est + (1|site),
                        family = Gamma(link = "log"), data = overlap_data)

## boundary (singular) fit: see help('isSingular')
```

```

prox_overlap_test2 <- glmer(proximity_est ~ 1 + (1|site),
                           family = Gamma(link = "log"), data =
overlap_data)
## boundary (singular) fit: see help('isSingular')
prox_overlap_test_results <- anova(prox_overlap_test, prox_overlap_test2)

#calculate home-range overlap impact via likelihood ratio test
prox_overlap_test_pvalue <- round(prox_overlap_test_results$ Pr(>Chisq)`[2],
2)
prox_overlap_test_pvalue
## [1] 0.02

```

Estimating encounters

Encounter results

```

#calculate the number of encounters based on threshold of 15m
sum(overlap_data$encounter_count)
## [1] 1209

sum(overlap_data$encounter_count[overlap_data$sex_comparison == "male-male"])
## [1] 16

sum(overlap_data$encounter_count[overlap_data$sex_comparison == "female-
female"])
## [1] 145

sum(overlap_data$encounter_count[overlap_data$sex_comparison == "female-
male"])
## [1] 1048

#effect of sex and overlap on encounter rates and does not include 0
encounter counts
encounter_test <- glmer(encounter_count ~ overlap_est + sex_comparison +
(1|site),
                      family = poisson(link = "log"),
                      data = overlap_data, subset = encounter_count > 0)
encounter_test2 <- glmer(encounter_count ~ 1 + (1|site),
                        family = poisson(link = "log"),
                        data = overlap_data, subset = encounter_count > 0)
encounter_test_results <- anova(encounter_test, encounter_test2)
encounter_test_results

```

```

## Data: overlap_data
## Subset: encounter_count > 0
## Models:
## encounter_test2: encounter_count ~ 1 + (1 | site)
## encounter_test: encounter_count ~ overlap_est + sex_comparison + (1 |
site)
##               npar      AIC      BIC    logLik deviance  Chisq Df Pr(>Chisq)
## encounter_test2      2 2134.8 2137.3 -1065.38   2130.8
## encounter_test      5 1429.3 1435.6  -709.66   1419.3 711.44  3  < 2.2e-16
***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#calculate sex impact on encounters via likelihood ratio test
encounter_test_pvalue <- round(encounter_test_results$`Pr(>Chisq)`[2], 2)
encounter_test_pvalue

## [1] 0

#amount of home range overlap and the number of observed encounters
summary(encounter_test)

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: encounter_count ~ overlap_est + sex_comparison + (1 | site)
## Data: overlap_data
## Subset: encounter_count > 0
##
##      AIC      BIC    logLik deviance df.resid
## 1429.3   1435.6  -709.7   1419.3        21
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.3616 -5.2131 -2.4377 -0.5606 28.1608
##
## Random effects:
## Groups Name      Variance Std.Dev.
## site (Intercept) 0.005524 0.07433
## Number of obs: 26, groups: site, 2
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.94374    0.13669  14.220  < 2e-16 ***
## overlap_est      1.95462    0.12774  15.302  < 2e-16 ***
## sex_comparisonfemale-male 1.24952    0.09199  13.583  < 2e-16 ***
## sex_comparisonmale-male  -1.19742    0.26718  -4.482 7.41e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:

```

```
##           (Intr) ovrlp_ sx_cmprsnf-
## overlap_est -0.690
## sx_cmprsnf- -0.722  0.236
## sx_cmprsnm- -0.305  0.164  0.324
```

Deviated pairs

```
#import identified deviated pairs (7 pairs)
proximity_identified_pairs_df <-
readRDS("data/proximity/proximity_identified_adult_pairs_df.rds")

#number of pairs with a deviated proximity ratio based on sex comparison
table(proximity_identified_pairs_df$sex_comparison)

##
## female-female   female-male
##              3             4

#test for significance in sex, compare model with and without sex as a
variable
proximity_test_pairs <- glmer(proximity_est ~ sex_comparison + (1|site),
                             family = Gamma(link = "log"),
                             data = proximity_identified_pairs_df)
proximity_test2_pairs <- glmer(proximity_est ~ 1 + (1|site),
                              family = Gamma(link = "log"),
                              data = proximity_identified_pairs_df)

## boundary (singular) fit: see help('isSingular')

proximity_test_results_pairs <- anova(proximity_test_pairs,
proximity_test2_pairs)
proximity_test_results_pairs

## Data: proximity_identified_pairs_df
## Models:
## proximity_test2_pairs: proximity_est ~ 1 + (1 | site)
## proximity_test_pairs: proximity_est ~ sex_comparison + (1 | site)
##
##           npar    AIC    BIC  logLik deviance  Chisq Df
Pr(>Chisq)
## proximity_test2_pairs    3 11.042 10.88 -2.5211    5.0423
## proximity_test_pairs    4 10.746 10.53 -1.3730    2.7460 2.2963  1
0.1297

#calculate sex impact via likelihood ratio test
proximity_test_pvalue_pairs <-
round(proximity_test_results_pairs$`Pr(>Chisq)`[2], 2)
proximity_test_pvalue_pairs

## [1] 0.13
```

```

#test for significance in home range overlap, compare model with and without overlap as a variable
prox_overlap_test_pairs <- glmer(proximity_est ~ overlap_est + (1|site),
                                family = Gamma(link = "log"),
                                data = proximity_identified_pairs_df)

## boundary (singular) fit: see help('isSingular')

prox_overlap_test2_pairs <- glmer(proximity_est ~ 1 + (1|site),
                                family = Gamma(link = "log"),
                                data = proximity_identified_pairs_df)

## boundary (singular) fit: see help('isSingular')

prox_overlap_test_results_pairs <- anova(prox_overlap_test_pairs,
prox_overlap_test2_pairs)
prox_overlap_test_results_pairs

## Data: proximity_identified_pairs_df
## Models:
## prox_overlap_test2_pairs: proximity_est ~ 1 + (1 | site)
## prox_overlap_test_pairs: proximity_est ~ overlap_est + (1 | site)
##
##      npar    AIC    BIC  logLik deviance  Chisq Df
## prox_overlap_test2_pairs    3 11.042 10.880 -2.5211    5.0423
## prox_overlap_test_pairs    4 11.492 11.275 -1.7458    3.4916 1.5506  1
##
##      Pr(>Chisq)
## prox_overlap_test2_pairs
## prox_overlap_test_pairs      0.213

#calculate home-range overlap impact via likelihood ratio test
prox_overlap_test_pvalue_pairs <-
round(prox_overlap_test_results_pairs$`Pr(>Chisq)`[2], 2)
prox_overlap_test_pvalue_pairs

## [1] 0.21

```