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")

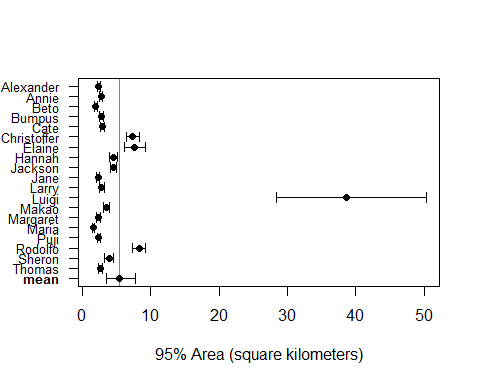
#import supplementary data containing biological information  
DATA\_META <- read.csv("data/Anteater\_Results\_Final.csv")  
  
#subset biological data from supplementary data  
bio\_data <- DATA\_META[which(DATA\_META$ID   
 %in% c("Alexander", "Annie", "Beto", "Bumpus", "Cate",   
 "Christoffer","Elaine", "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)

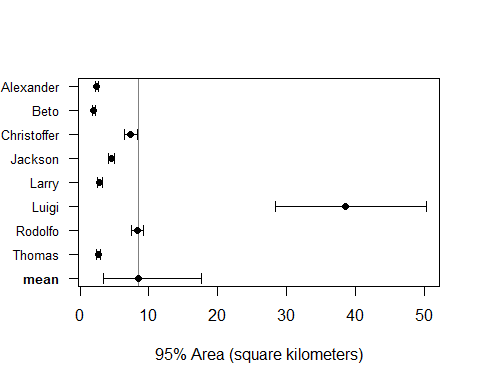
## ΔAICc  
## inverse-Gaussian 0.000  
## Dirac-δ 1671.981



## 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)

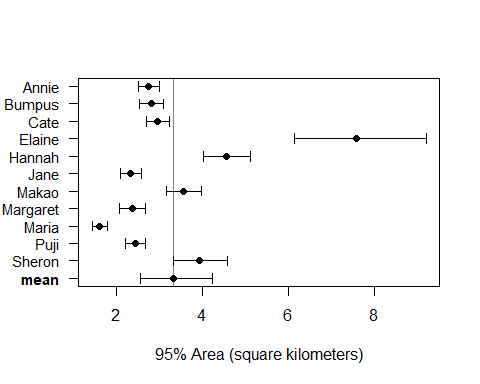
## ΔAICc  
## inverse-Gaussian 0.000  
## Dirac-δ 1018.877



## 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

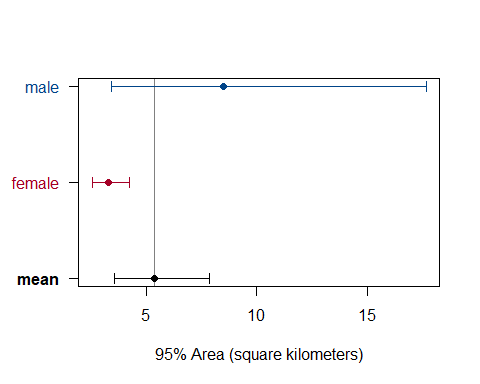
## ΔAICc  
## inverse-Gaussian 0.0000  
## Dirac-δ 288.9002

## \* Joint population

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

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

## ΔAICc  
## Sub-population 0.000000  
## Joint population 3.607806



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