

SUPPLEMENTARY ELECTRONIC MATERIAL

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FACTORS AFFECTING DIFFERENTIAL UNDERESTIMATES OF BIRD COLLISION FATALITIES AT ELECTRIC LINES: A CASE STUDY IN THE CANARY ISLANDS

FACTORES QUE AFECTAN A LA SUBESTIMACIÓN DIFERENCIAL DE LAS
COLISIONES DE AVES CON LÍNEAS ELÉCTRICAS: UN CASO DE ESTUDIO EN
LAS ISLAS CANARIAS

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APPENDIX 3.

R script (Código de R)

R script for the estimation of the proportion of large/very large carcasses (*i.e.* larger than an Eurasian Stone Curlew *Burhinus oedicanus* > 35cm) detected around high-voltage power lines, considering the dispersion patterns depicted in Figure 2 in the main document, and the detection probability presented in Figure 3 and Table 2.

```
library(fdrtool)

## "Those who can, do; those who can't - use computer simulation". George
## Bernard Shaw

set.seed(111)

## dispersion distances of corpses (Figure 2)
mean_distances <- 18.316
sd_distances <- 14.425
sd_distances / mean_distances    ## half-normal if the ratio is ca.
sqrt((pi-2)/2) = 0.7555
##
corpses_3 <- rhalfnorm(n=10000000, theta=1/mean_distances)
max(corpses_3)
hist(corpses_3)
corpses_2 <- subset(corpses_3, corpses_3<=50)
corpses <- c(-corpses_3, corpses_3)
##
b <- c(-50:50)
bins.corpses <- .bincode(corpses, b, TRUE)
table.corpses <- as.data.frame(aggregate(corpses ~ as.factor(bins.corpses),
FUN=length))
names(table.corpses)[1] <- "distance_m"
maximum <- max(table.corpses$corpses)
summatory <- sum(table.corpses$corpses)
table.corpses$probability <- table.corpses$corpses/maximum
table.corpses$percentage_2 <- table.corpses$corpses/summatory*100
table.corpses$percentage <- table.corpses$corpses/(summatory/2)*100
table.corpses$distance_m <- c(-50:-1, 1:50)
table.corpses

## detection distances of large carcasses (panels C and D in Figure 3)
mean_detections <- 8.295455
sd_detections <- 6.211149
sd_detections / mean_detections    ## half-normal if the ratio is ca.
sqrt((pi-2)/2) = 0.7555
##
carcasses_3 <- rhalfnorm(n=10000000, theta=1/mean_detections)
max(carcasses_3)
hist(carcasses_3)
carcasses_2 <- subset(carcasses_3, carcasses_3<=30)
carcasses <- c(-carcasses_3, carcasses_3)
##
b <- c(-50:50)
bins.carcasses <- .bincode(carcasses, b, TRUE)
```

```

table.carcasses <- as.data.frame(aggregate(carcasses ~
as.factor(bins.carcasses), FUN=length))
names(table.carcasses)[1] <- "distance_m"
maximum.c <- max(table.carcasses$carcasses)
table.carcasses$probability <- table.carcasses$carcasses/maximum.c
table.carcasses$distance_m <- c(-50:-1, 1:50)
table.carcasses

## with only ONE researcher below the power line axis
prop_corpses_detected <- table.carcasses$probability *
table.corpses$percentage
##
plot(table.corpses$distance_m, table.corpses$probability)
plot(table.carcasses$distance_m, table.carcasses$probability)
plot(table.corpses$distance_m, prop_corpses_detected)
##
sum(table.corpses$percentage)/2
sum(prop_corpses_detected)/2
plot(table.corpses$distance_m, table.corpses$percentage, col="blue",
xlim=c(-60, 60), cex=0, cex.main=2, cex.axis=1.5, main="CONTINUOUS: sampled
DOTTED: available")
lines(table.corpses$distance_m, table.corpses$percentage, col="blue",
lwd=4, lty=3)
lines(table.corpses$distance_m, prop_corpses_detected, col="red", lwd=6)

## with TWO researchers, both at D distance from the axis of the power line
D <- 15 ## put here the distance from the axis of the power line in
meters
##
## left and right researchers
table.carcasses.left <- table.carcasses
table.carcasses.left$distance_m <- table.carcasses.left$distance_m - D
table.carcasses.left <- subset(table.carcasses.left,
table.carcasses.left$distance_m >= -50)
table.carcasses.left.zeros <- data.frame(c((50-D+1):50), rep(0, times=D),
rep(0, times=D))
names(table.carcasses.left.zeros) <- names(table.carcasses.left)
table.carcasses.left <- rbind(table.carcasses.left,
table.carcasses.left.zeros)
##
table.carcasses.right <- table.carcasses
table.carcasses.right$distance_m <- table.carcasses.right$distance_m + D
table.carcasses.right <- subset(table.carcasses.right,
table.carcasses.right$distance_m <= 50)
table.carcasses.right.zeros <- data.frame(c(-50:(-50+D-1)), rep(0,
times=D), rep(0, times=D))
names(table.carcasses.right.zeros) <- names(table.carcasses.right)
table.carcasses.right <- rbind(table.carcasses.right.zeros,
table.carcasses.right)
## compound of probabilities
prob_corpses_detected.2 <- table.carcasses.left$probability + (1-
table.carcasses.left$probability)*table.carcasses.right$probability
prop_corpses_detected.2 <- prob_corpses_detected.2 *
table.corpses$percentage
##
sum(table.corpses$percentage)/2
sum(prop_corpses_detected.2)/2

```

```

plot(table.corpses$distance_m, table.corpses$percentage, col="blue",
xlim=c(-60, 60), cex=0, cex.main=2, cex.axis=1.5, main="CONTINUOUS: sampled
DOTTED: available")
lines(table.corpses$distance_m, table.corpses$percentage, col="blue",
lwd=4, lty=3)
lines(table.corpses$distance_m, prop_corpses_detected.2, col="red", lwd=6)

```

```

## with THREE researchers, one below the power line axis, and two at D
distance from the axis of the power line
D <- 25 ## put here the distance from the axis of the power line in
meters
##
## central researcher
table.carcasses$probability
##
## left and right researchers
table.carcasses.left <- table.carcasses
table.carcasses.left$distance_m <- table.carcasses.left$distance_m - D
table.carcasses.left <- subset(table.carcasses.left,
table.carcasses.left$distance_m >= -50)
table.carcasses.left.zeros <- data.frame(c((50-D+1):50), rep(0, times=D),
rep(0, times=D))
names(table.carcasses.left.zeros) <- names(table.carcasses.left)
table.carcasses.left <- rbind(table.carcasses.left,
table.carcasses.left.zeros)
##
table.carcasses.right <- table.carcasses
table.carcasses.right$distance_m <- table.carcasses.right$distance_m + D
table.carcasses.right <- subset(table.carcasses.right,
table.carcasses.right$distance_m <= 50)
table.carcasses.right.zeros <- data.frame(c(-50:(-50+D-1)), rep(0,
times=D), rep(0, times=D))
names(table.carcasses.right.zeros) <- names(table.carcasses.right)
table.carcasses.right <- rbind(table.carcasses.right.zeros,
table.carcasses.right)
##
## compound of probabilities
prob_corpses_detected.2 <- table.carcasses.left$probability + (1-
table.carcasses.left$probability)*table.carcasses.right$probability
prob_corpses_detected.3 <- table.carcasses$probability + (1-
table.carcasses$probability)*prob_corpses_detected.2
prop_corpses_detected.3 <- prob_corpses_detected.3 *
table.corpses$percentage
##
sum(table.corpses$percentage)/2
sum(prop_corpses_detected.3)/2
plot(table.corpses$distance_m, table.corpses$percentage, col="blue",
xlim=c(-60, 60), cex=0, cex.main=2, cex.axis=1.5, main="CONTINUOUS: sampled
DOTTED: available")
lines(table.corpses$distance_m, table.corpses$percentage, col="blue",
lwd=4, lty=3)
lines(table.corpses$distance_m, prop_corpses_detected.3, col="red", lwd=6)

```