Ramírez-Mejía et al. (2021) Activity and habitat use by understory birds in a native Andean forest and a eucalypt plantation. The Wilson Journal of Ornithology.

Actividad y uso de hábitat de aves de sotobosque en un bosque andino nativo y una reforestación de eucalipto

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This document's primary purpose is to facilitate access to the code from different devices, so I did not include a detailed explanation. I hope it is clear enough to understand the way I conducted the activity analysis. If you have any concerns, questions, or suggestions, feel free to contact me.

```r
#### aves bosques de la chec

library(tidyverse)


chec <- read.delim("bird_activity_data.txt")

str(chec)
```

```
## 'data.frame':    299 obs. of  3 variables:
##  $ species: chr  "brun" "brun" "brun" "brun" ...
##  $ forest : chr  "andean" "andean" "andean" "andean" ...
##  $ time   : num  0.304 0.347 0.656 0.442 0.281 ...
```

```r
for (i in 1:ncol(chec)) {
  if (is.character(chec[[i]])) {
    chec[[i]] <- as.factor(chec[[i]])
  } else {
    next
  }
}
```

```r
head(chec)
```

```
##   species forest      time
## 1    brun andean 0.3041667
## 2    brun andean 0.3472083
## 3    brun andean 0.6562500
## 4    brun andean 0.4423333
## 5    brun andean 0.2805417
## 6    brun andean 0.3770833
```

```
summary(chec)
```

```
##    species              forest           time
##  brun :49   andean        :224   Min.   :0.2389
##  frena:97   reforestation: 75   1st Qu.:0.3079
##  goud :53                        Median :0.4014
##  mille:28                        Mean   :0.4540
##  rufi :39                        3rd Qu.:0.6235
##  torq :33                        Max.   :0.7583
```

```
range(chec$time)
```

```
## [1] 0.2388750 0.7583333
```

```
timeRad <- chec$time * 2 * pi
table(chec$species,chec$forest)
```

```
##
##           andean reforestation
##    brun        15            34
##    frena       82            15
##    goud        44             9
##    mille       26             2
##    rufi        35             4
##    torq        22            11
```
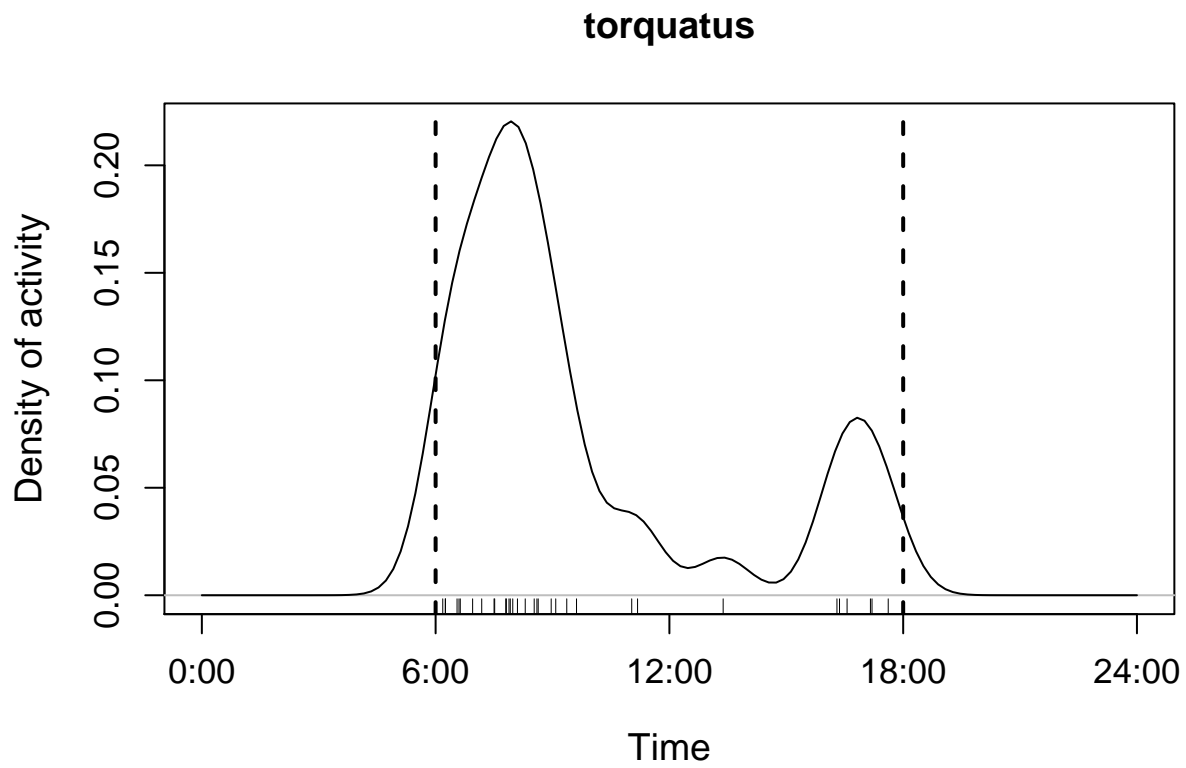
```
library(boot)
library(circular)
library(overlap)
library(cowplot)
library(gridExtra)
library(png)


#
#patrón de actividad por especie----
#

#Arremon torquatus
torquatus <- timeRad[chec$species == "torq"]
densityPlot(torquatus, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.2,
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```
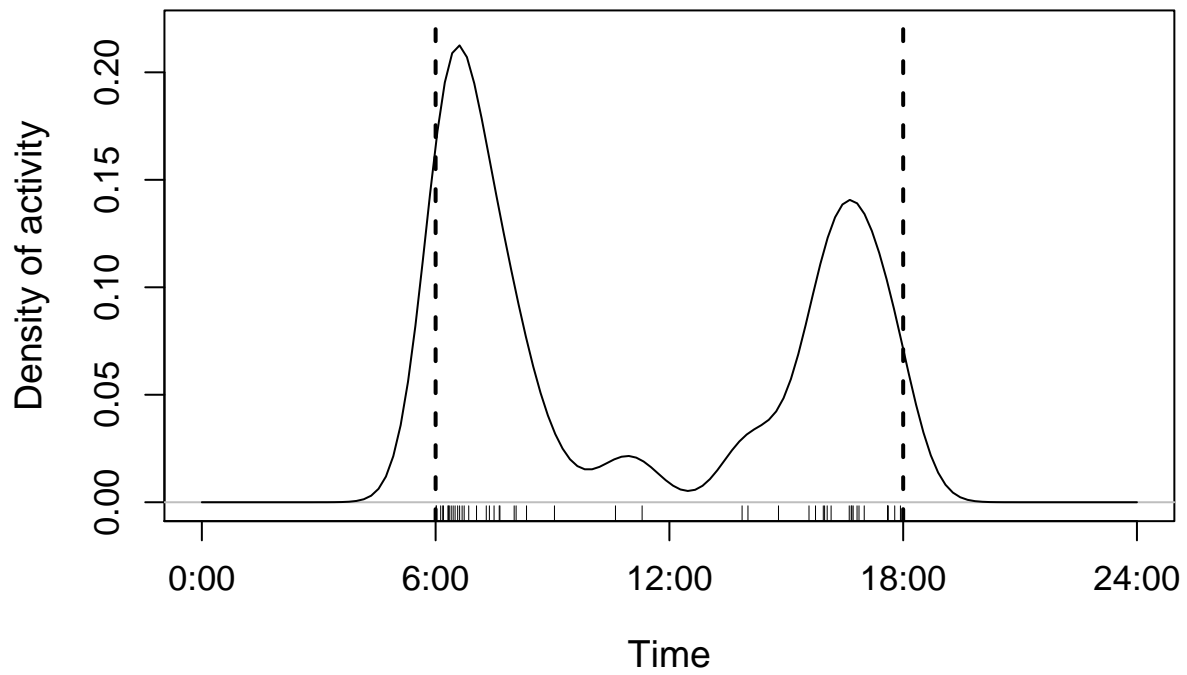
torquatus


```
#Arremon brunneinucha
brunneinucha <- timeRad[chec$species == "brun"]
densityPlot(brunneinucha, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```

brunneinucha


```r
#Grallaria ruficapilla
ruficapilla <- timeRad[chec$species == "rufi"]
densityPlot(ruficapilla, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```
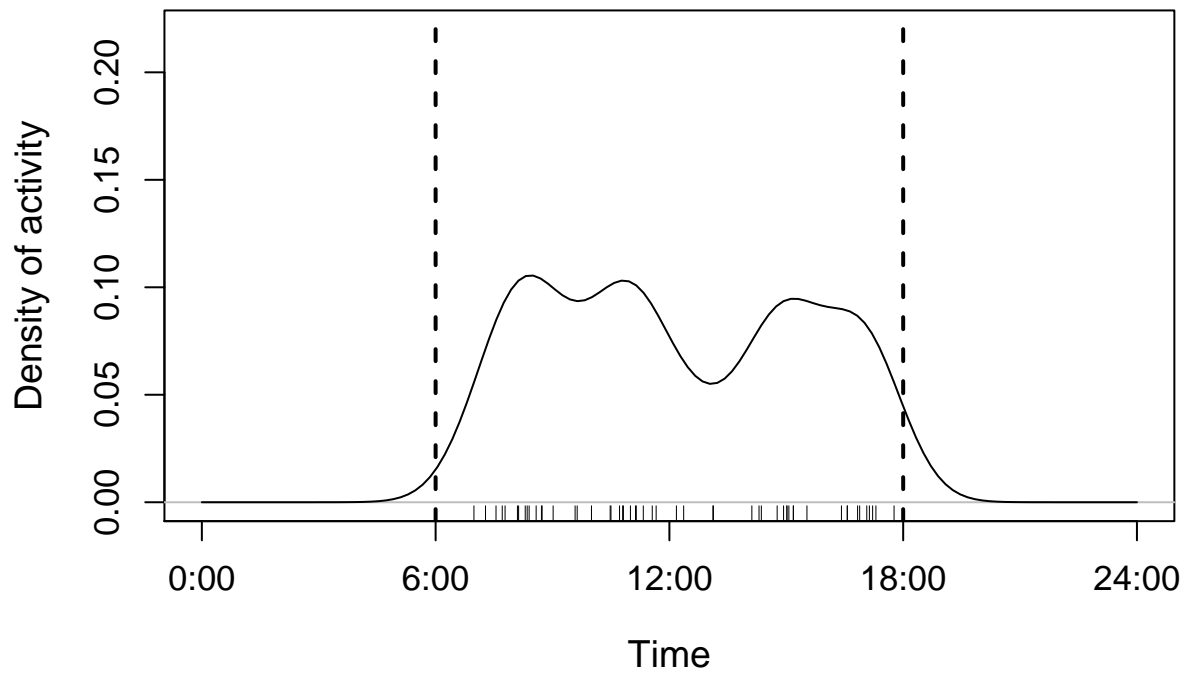
ruficapilla
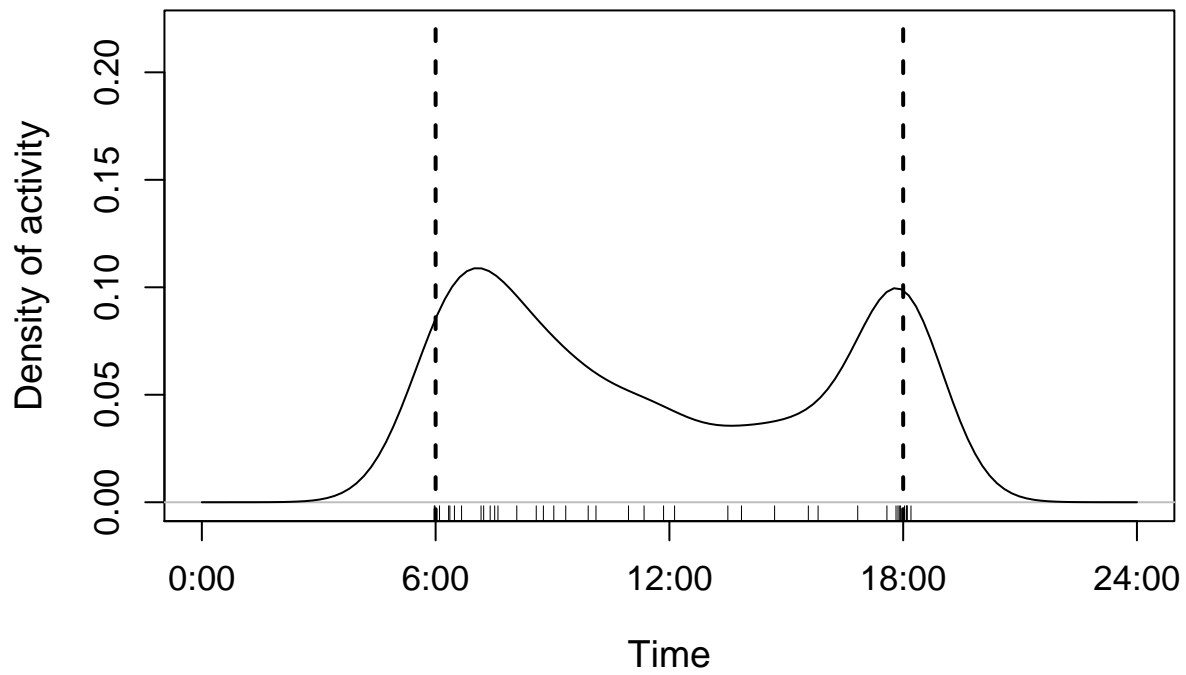

```
#Grallaria milleri
milleri <- timeRad[chec$species == "mille"]
densityPlot(milleri, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.2, e
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```

milleri
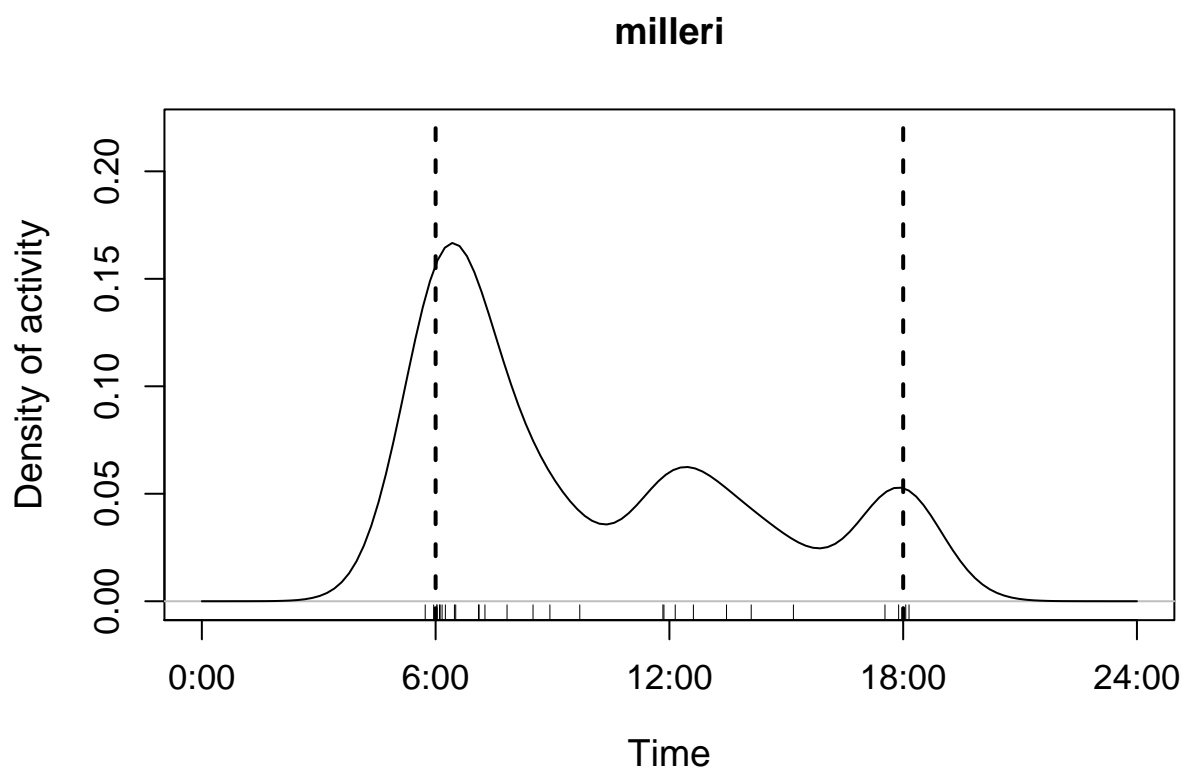

```
#Chamaepetes goudotii
goudotii <- timeRad[chec$species == "goud"]
densityPlot(goudotii, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.2, 
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```

goudotii
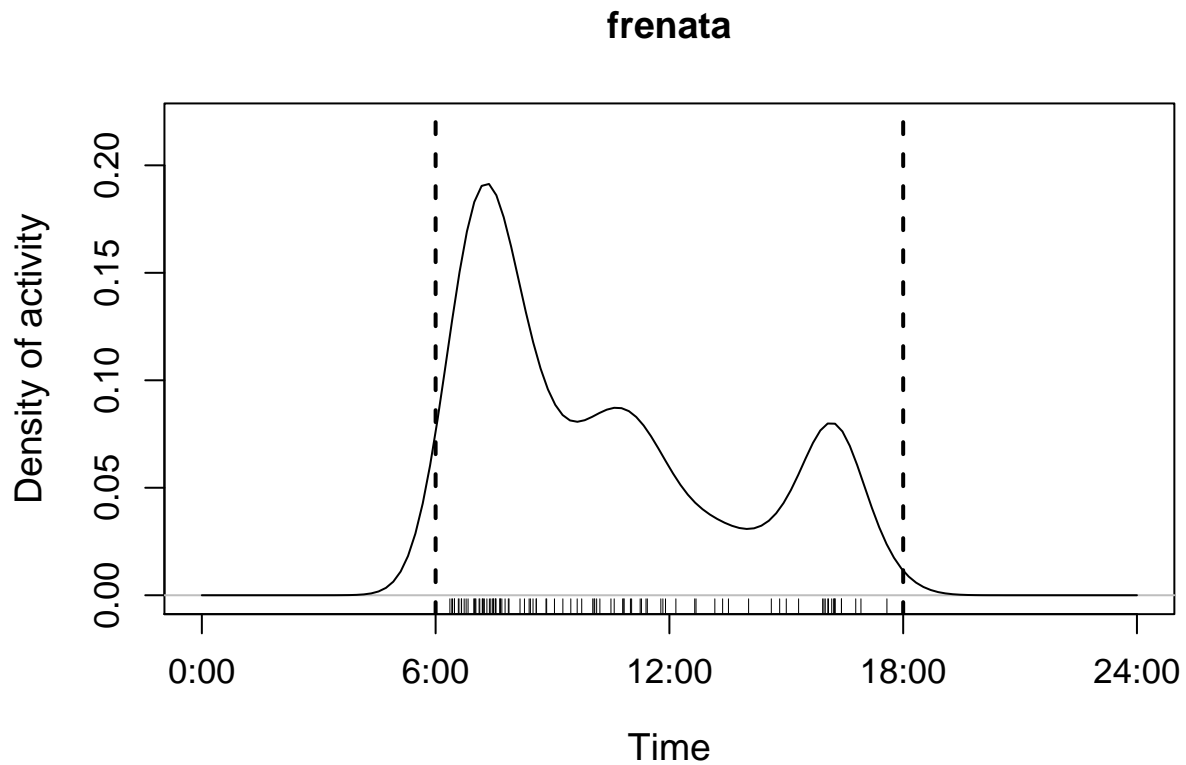


```
#Zentrigon frenata
frenata <- timeRad[chec$species == "frena"]
densityPlot(frenata, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.2, e
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```

frenata


```
levels(chec$species)
```

```
## [1] "brun"  "frena" "goud"  "mille" "rufi"  "torq"
```

```
table(chec$species, chec$forest)
```

```
##
##          andean reforestation
##   brun       15            34
##   frena      82            15
##   goud       44             9
##   mille      26             2
##   rufi       35             4
##   torq       22            11
```

```
#
#
#
#coeficiente de solapamiento----

#C. goudotti ----
#overlap calculation
bosq <- timeRad[chec$species == "goud" & chec$forest == "andean"]
plant <- timeRad[chec$species == "goud" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

```
## [1] 9
```

```
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
##     Dhat1     Dhat4     Dhat5
## 0.7271702 0.7294513 0.6666667
```

```
#plot activity overlap
#png("c_goudotti1.png", height = 10 , width = 15, units = 'cm', res = 300)
par(mar=c(2.8,4.1,1,1))
torq <- overlapPlot(bosq, plant, ylim=c(0,0.29), ylab="Density of activity", cex.axis=1.4, cex.lab=1.4,
                    rug = T, linecol = c("black", "black"), linewidth = c(1,1), main='', extend = NULL)
a <- readPNG(paste(getwd(), "/c_goudotti.png", sep = ""))
rasterImage(a, xleft=18.2, xright=24.9, ybottom=0.155, ytop=0.27)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
text(21.5,0.125,expression(n == 53), cex = 0.95);text(21.5,0.148,expression(paste(italic("C. goudotti")
text(12,0.28, expression(hat(Delta) == 0.71  (0.58 - 0.96)), cex = 1.2)
```
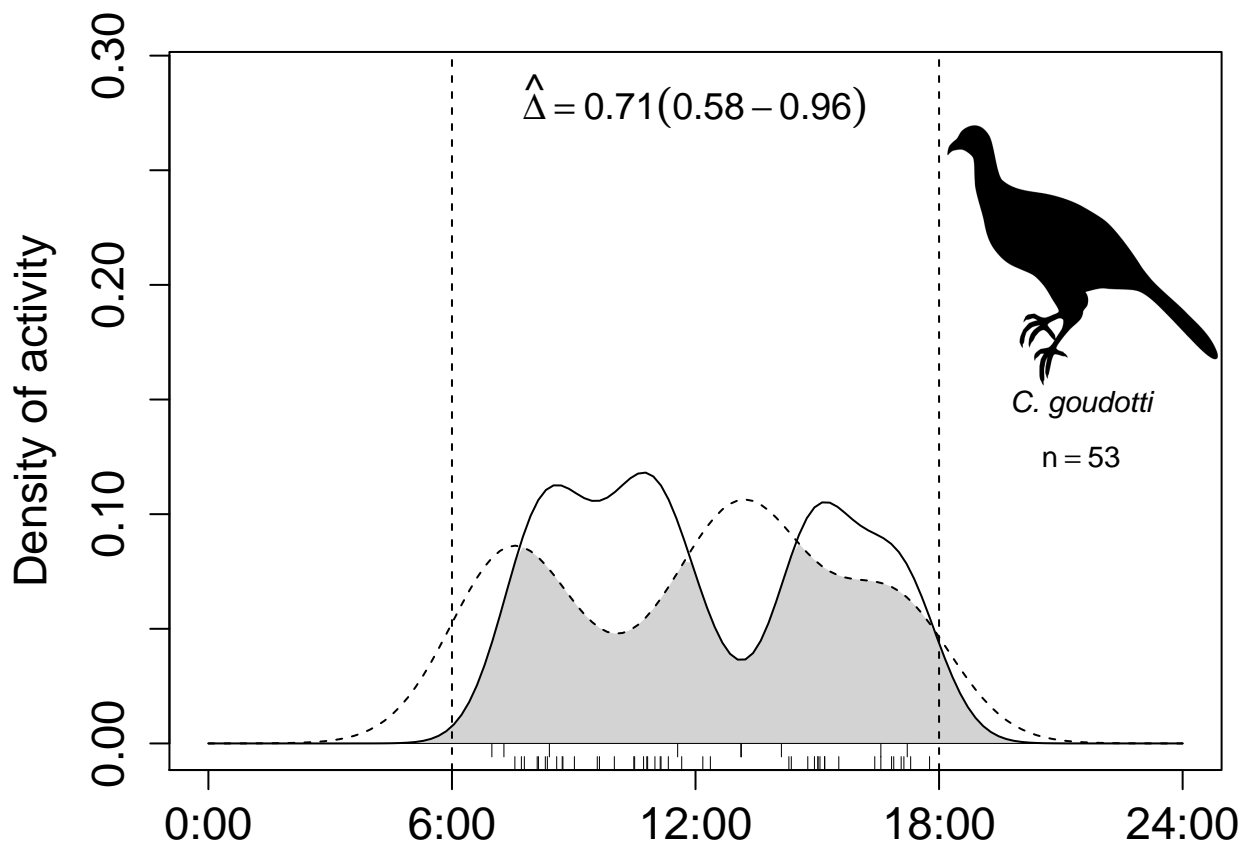


```
#dev.off()
#legend("topleft", c("Andean ", "G. ruficapilla"), lty=c(1,2), col=c(1,4), bty="n")
#bootstrap
bosqboot <- resample(bosq, 10000)
dim(bosqboot)
```

```
## [1]    44 10000
```

```
plantboot <- resample(plant, 10000)
dim(plantboot)
```

```
## [1]     9 10000
```

```
#overlap estimates by boostrap
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

```
## [1] 10000     3
```

```
BSmean <- colMeans(BosqPlant)
BSmean
```

```
##     Dhat1     Dhat4     Dhat5
## 0.7071672        NA        NA
```

```
#calculation of CI
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
##             lower     upper
## norm    0.5521387 0.9422075
## norm0   0.5321357 0.9222046
## basic   0.5834191 0.9659841
## basic0  0.5083591 0.8909241
## perc    0.4883562 0.8709212
```

```
tmp <- BosqPlant[, 1] # Extract the required column of the matrix
bootCIlogit(BosqPlantMILLE[1], tmp)
```

```
##             lower     upper
## norm    0.5126446 0.8817988
## norm0   0.5002048 0.8765119
## basic   0.5128711 0.8815518
## basic0  0.5007966 0.8764137
## perc    0.4883562 0.8709212
```

```
#Z. frenata ----
#overlap calculation
bosq <- timeRad[chec$species == "frena" & chec$forest == "andean"]
plant <- timeRad[chec$species == "frena" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

```
## [1] 15
```

```
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
##     Dhat1     Dhat4     Dhat5
## 0.7904093 0.8246503 0.8617886
```

```
#plot activity overlap
#png("z_frenata1.png", height = 10 , width = 15, units = 'cm', res = 300)
par(mar=c(2.8,4.1,1,1))
torq <- overlapPlot(bosq, plant, ylim=c(0,0.29), ylab="", cex.axis=1.4, cex.lab=1.4, cex.main= 1.4, xlab
                    rug = T, linecol = c("black", "black"), linewidth = c(1,1), main = "", extend = NULL
a <- readPNG(paste(getwd(), "/z_frenata.png", sep = ""))
rasterImage(a, xleft=19, xright=24, ybottom=0.155, ytop=0.265)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
text(21.5,0.12,expression(n == 87), cex = 0.95);text(21.5,0.143,expression(paste(italic("Z. frenata")))
text(12,0.28,expression(hat(Delta) == 0.75  (0.69 - 0.98)), cex = 1.2)
```
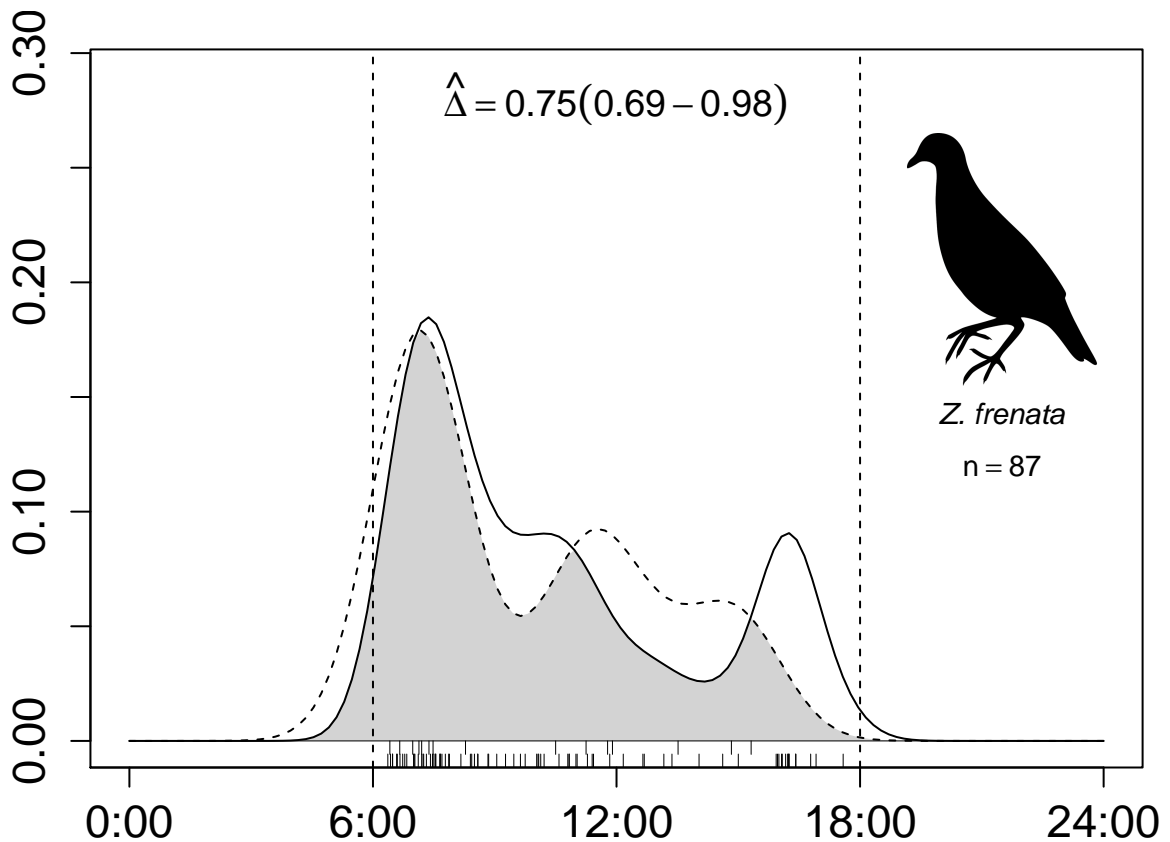


```
#dev.off()
#legend("topleft", c("Andean ", "G. ruficapilla"), lty=c(1,2), col=c(1,4), bty="n")
#bootstrap
bosqboot <- resample(bosq, 10000)
dim(bosqboot)
```

```
## [1]    82 10000
```

```
plantboot <- resample(plant, 10000)
dim(plantboot)
```

```
## [1]    15 10000
```

```
#overlap estimates by boostrap
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

```
## [1] 10000     3
```

```
BSmean <- colMeans(BosqPlant)
BSmean
```

```
##    Dhat1    Dhat4    Dhat5
## 0.7579262       NA       NA
```

```
#calculation of CI
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.6822096 0.9635752
## norm0  0.6497265 0.9310921
## basic  0.7001644 0.9829856
## basic0 0.6303161 0.9131373
## perc   0.5978330 0.8806542
```

```
tmp <- BosqPlant[, 1] # Extract the required column of the matrix
bootCIlogit(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.6648884 0.9055784
## norm0  0.6317125 0.8923735
## basic  0.6583947 0.9053679
## basic0 0.6322844 0.8951279
## perc   0.5978330 0.8806542
```

```
#A. brunneinucha ----
#overlap calculation
bosq <- timeRad[chec$species == "brun" & chec$forest == "andean"]
plant <- timeRad[chec$species == "brun" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

```
## [1] 15
```

```
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
##    Dhat1    Dhat4    Dhat5
## 0.5838830 0.5863419 0.5549020
```

```
#plot activity overlap
#png('a_brunneinucha1.png', width = 15, height = 10, units = "cm", res = 300)
par(mar=c(2.8,4.1,1,1))
torq <- overlapPlot(bosq, plant, ylim=c(0,0.29), ylab="Density of activity", cex.axis=1.4, cex.lab=1.4,
                    rug = T, linecol = c("black", "black"), linewidth = c(1,1), main='', extend = NULL)
a <- readPNG(paste(getwd(), "/a_brunneinucha.png", sep = ""))
rasterImage(a, xleft=18.7, xright=24.4, ybottom=0.21, ytop=0.28)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
text(21.5,0.175,expression(n == 49), cex = 0.95);text(21.5,0.20,expression(paste(italic("A. brunneinucha
text(12,0.28,expression(hat(Delta) == 0.59  (0.39 - 0.76)), cex = 1.2)
```
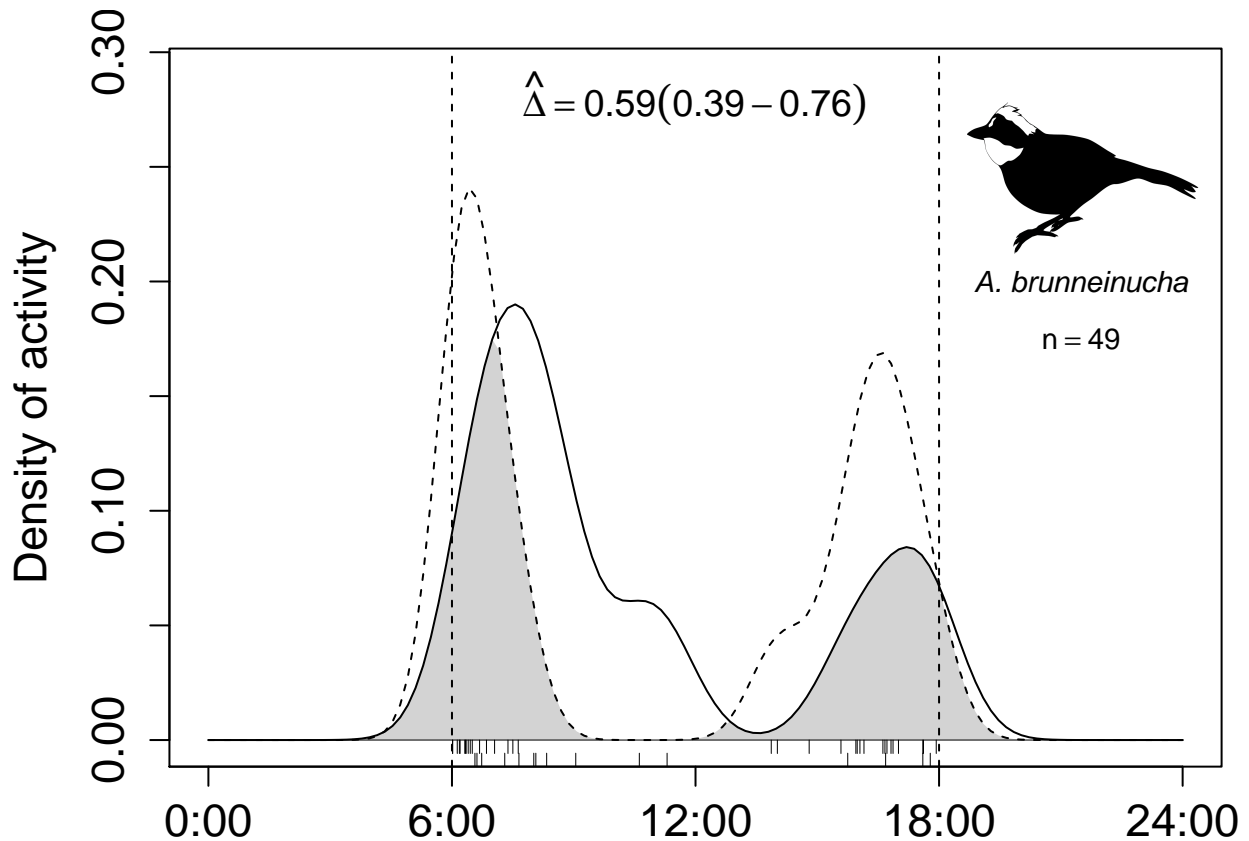


```
#dev.off()
#legend("topleft", c("Andean ", "G. ruficapilla"), lty=c(1,2), col=c(1,4), bty="n")
#bootstrap
bosqboot <- resample(bosq, 10000)
dim(bosqboot)
```

```
## [1]    15 10000
```

```
plantboot <- resample(plant, 10000)
dim(plantboot)
```

```
## [1]    34 10000
```

```
#overlap estimates by boostrap
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

```
## [1] 10000      3
```

```
BSmean <- colMeans(BosqPlant)
BSmean
```

```
##    Dhat1     Dhat4     Dhat5
## 0.5893745       NA        NA
```

```
#calculation of CI
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.3977566 0.7590262
## norm0  0.4032482 0.7645178
## basic  0.4019457 0.7612592
## basic0 0.4010151 0.7603287
## perc   0.4065067 0.7658203
```

```
tmp <- BosqPlant[, 1] # Extract the required column of the matrix
bootCIlogit(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.3828474 0.7466934
## norm0  0.3916140 0.7536177
## basic  0.3758055 0.7419050
## basic0 0.3976246 0.7591292
## perc   0.4065067 0.7658203
```

```
#A. torquatus ----
#overlap calculation
bosq <- timeRad[chec$species == "torq" & chec$forest == "andean"]
plant <- timeRad[chec$species == "torq" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

```
## [1] 11
```

```
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
##    Dhat1     Dhat4     Dhat5
## 0.6849370 0.6993380 0.9090909
```

```
#plot activity overlap
#png('a_torquatus1.png', width = 15, height = 10, units = 'cm', res = 300)
par(mar=c(2.8,4.1,1,1))
torq <- overlapPlot(bosq, plant, ylim=c(0,0.29), ylab="", cex.axis=1.4, cex.lab=1.4, cex.main= 1.4, xlal
                    rug = T, linecol = c("black", "black"), linewidth = c(1,1), main='', extend = NULL)
a <- readPNG(paste(getwd(), "/a_torquatus.png", sep = ""))
rasterImage(a, xleft=18.3, xright=24.8, ybottom=0.21, ytop=0.28)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
text(21.5,0.175,expression(n == 33), cex = 0.95);text(21.5,0.20,expression(paste(italic("A. torquatus")
text(12,0.28,expression(hat(Delta) == 0.63  (0.53 - 0.94)), cex = 1.2)
```
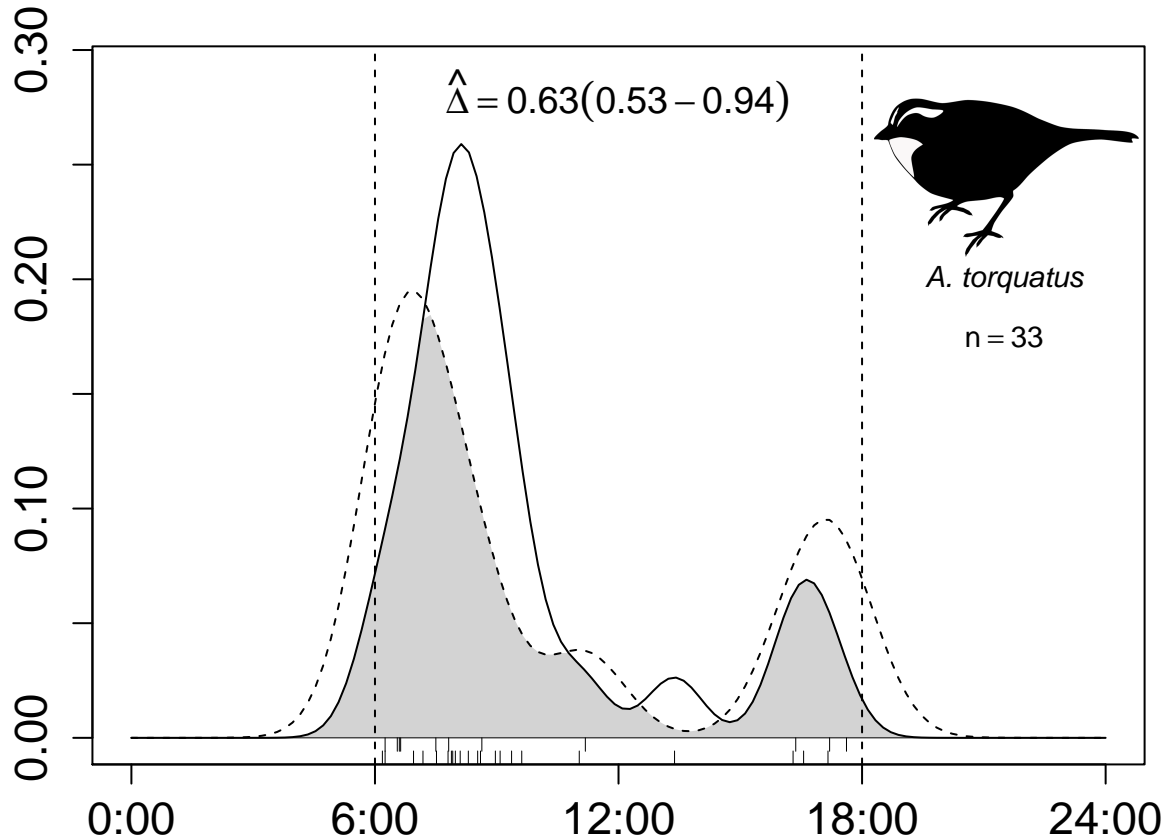


```
#dev.off()
#legend("topleft", c("Andean ", "G. ruficapilla"), lty=c(1,2), col=c(1,4), bty="n")

#bootstrap
bosqboot <- resample(bosq, 10000)
dim(bosqboot)
```

```
## [1]    22 10000
```

```
plantboot <- resample(plant, 10000)
dim(plantboot)
```

```
## [1]    11 10000
```

```
#overlap estimates by boostrap
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

```
## [1] 10000     3
```

```
BSmean <- colMeans(BosqPlant)
BSmean
```

```
##     Dhat1     Dhat4     Dhat5
## 0.6471335        NA        NA
```

```
#calculation of CI
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.5091562 0.9363248
## norm0  0.4713527 0.8985213
## basic  0.5318935 0.9578906
## basic0 0.4497869 0.8757840
## perc   0.4119834 0.8379805
```

```
tmp <- BosqPlant[, 1] # Extract the required column of the matrix
bootCIlogit(BosqPlantMILLE[1], tmp)
```

```
##            lower     upper
## norm   0.4819130 0.8694055
## norm0  0.4483124 0.8532848
## basic  0.4774728 0.8708933
## basic0 0.4450578 0.8554980
## perc   0.4119834 0.8379805
```

```
#G. ruficapilla ----
#overlap calculation
bosq <- timeRad[chec$species == "rufi"]
#plant <- timeRad[chec$species == "mille" & chec$forest == 2]
#min(length(bosq), length(plant))
#BosqPlantMILLE <- overlapEst(bosq, plant)
#BosqPlantMILLE

#plot activity overlap
#png('g_ruficapilla1.png', height = 10, width = 15, units = 'cm', res = 300)
par(mar=c(4,4.1,1,1))
rufi <- densityPlot(bosq, ylim=c(0,0.195), ylab="Density of activity", cex.axis=1.4, cex.lab=1.4, cex.ma
                    rug = T, linecol = c("black", "black"), linewidth = c(1,1), main='', extend = NULL)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
a <- readPNG(paste(getwd(), "/g_ruficapilla.png", sep = ""))
rasterImage(a, xleft=18.8, xright=24, ybottom=0.10, ytop=0.18)
text(21.6,0.075,expression(n == 39), cex = 0.95);text(21.6,0.09,expression(paste(italic("G. ruficapilla
```
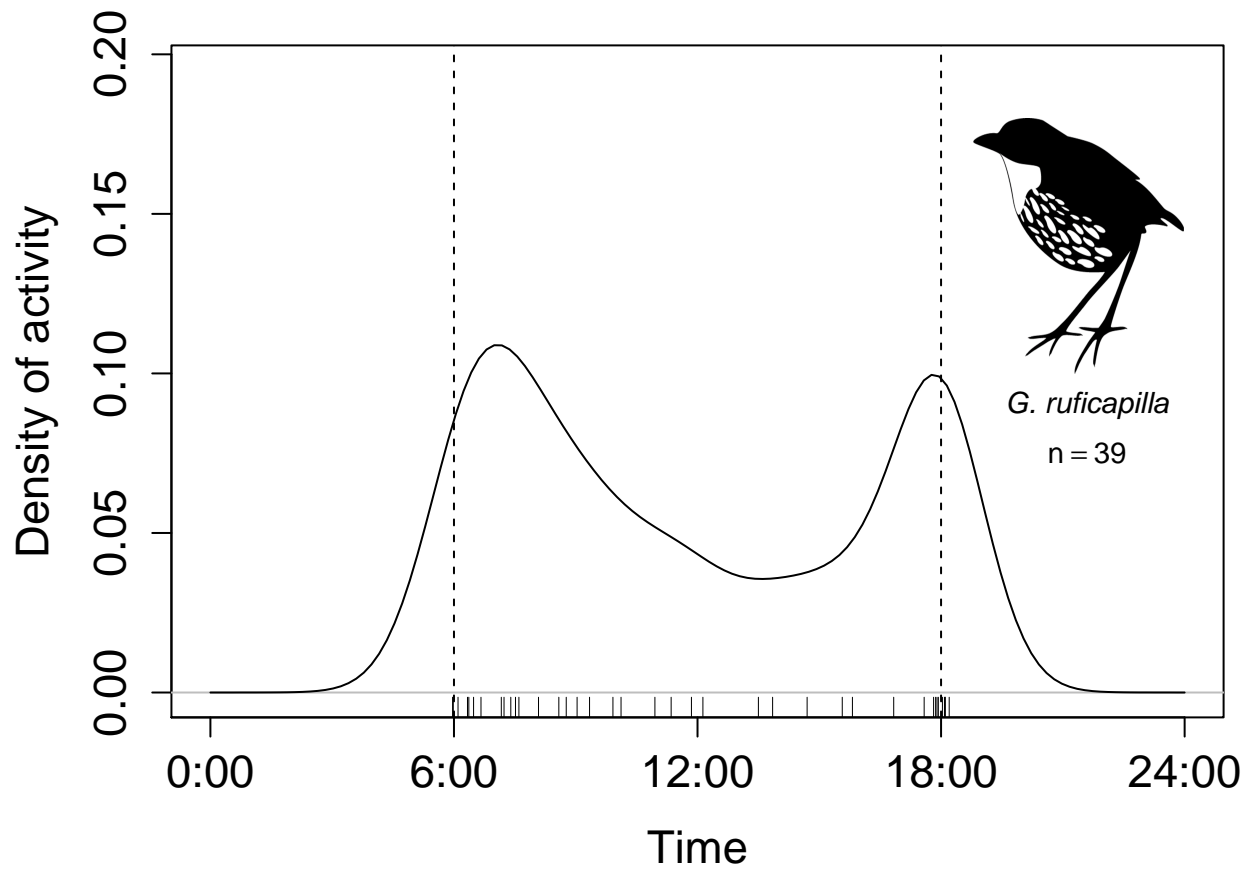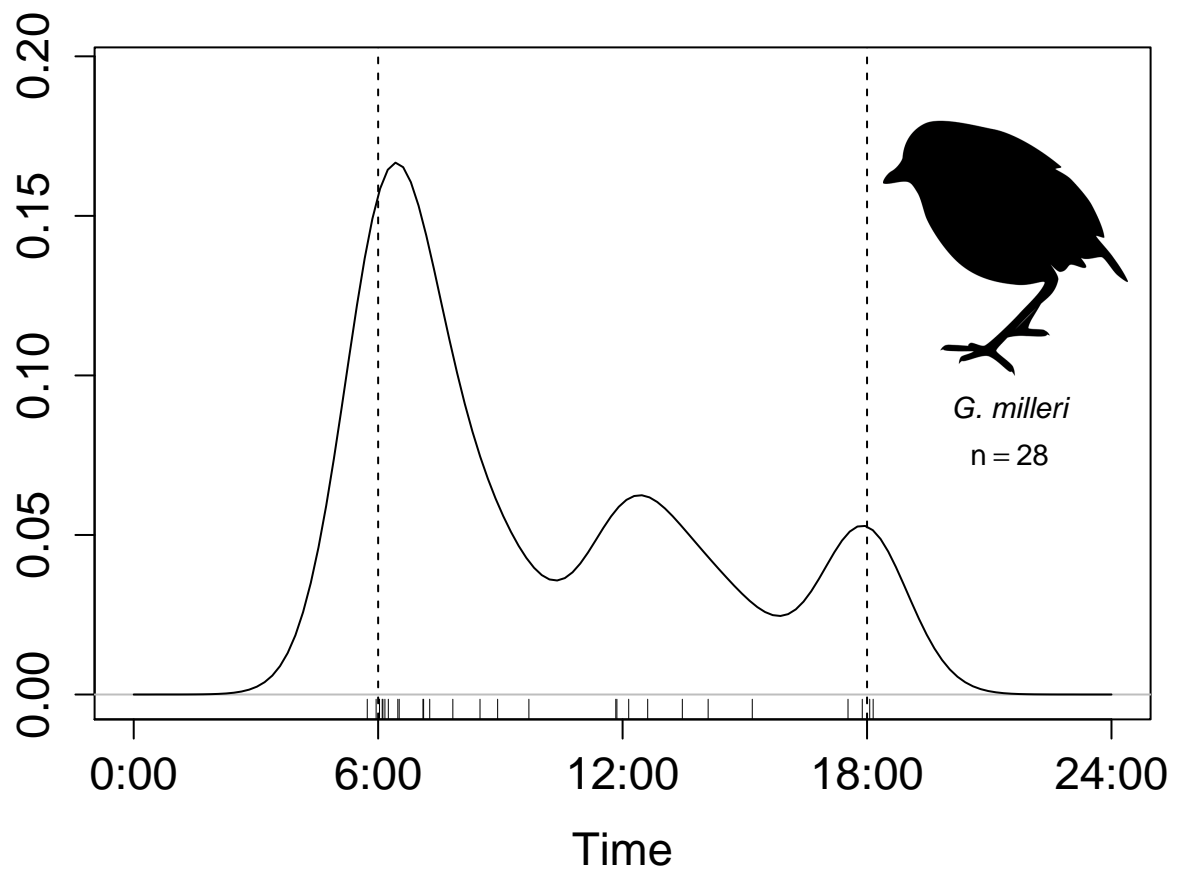
```
#dev.off()



#G. milleri ----
#overlap calculation
bosq <- timeRad[chec$species == "mille"]
#plant <- timeRad[chec$species == "mille" & chec$forest == 2]
#min(length(bosq), length(plant))
#BosqPlantMILLE <- overlapEst(bosq, plant)
#BosqPlantMILLE

#plot activity overlap
#png('g_milleri1.png', width = 15, height = 10, units = 'cm', res = 300)
par(mar=c(4,4,1,1))
mille <- densityPlot(bosq, ylim=c(0,0.195), ylab="", cex.axis=1.4, cex.lab=1.4, cex.main= 1.4,
          rug = T, linecol = c("black", "black"), linewidth = c(1,1), main='', extend = NULL)
abline(v=6, lty="dashed", col="black", lwd=1); abline(v=18, lty="dashed", col="black", lwd=1)
a <- readPNG(paste(getwd(), "/g_milleri.png", sep = ""))
rasterImage(a, xleft=18.4, xright=24.4, ybottom=0.10, ytop=0.18)
text(21.5,0.075,expression(n == 28), cex = 0.95);text(21.5,0.09,expression(paste(italic("G. milleri"))))
```

G. milleri

n = 28

Time

```
#dev.off()
```