

# 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.

```
#### 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 ...
```

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

```
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)
```

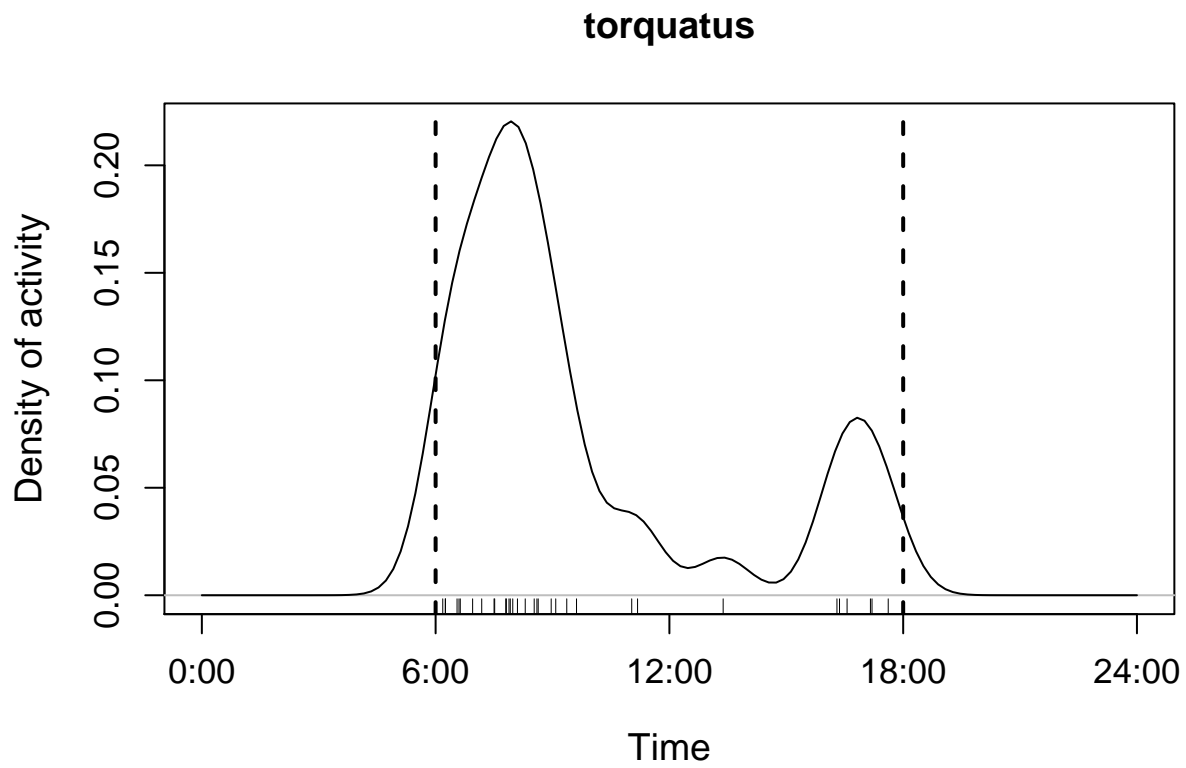
```
##
##      andean reforestation
## brun      15           34
## frena     82           15
## goud      44            9
## mille     26            2
## rufi      35            4
## torq      22           11
```

```
library(boot)
library(circular)
library(overlap)
library(cowplot)
library(gridExtra)
library(png)
```

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

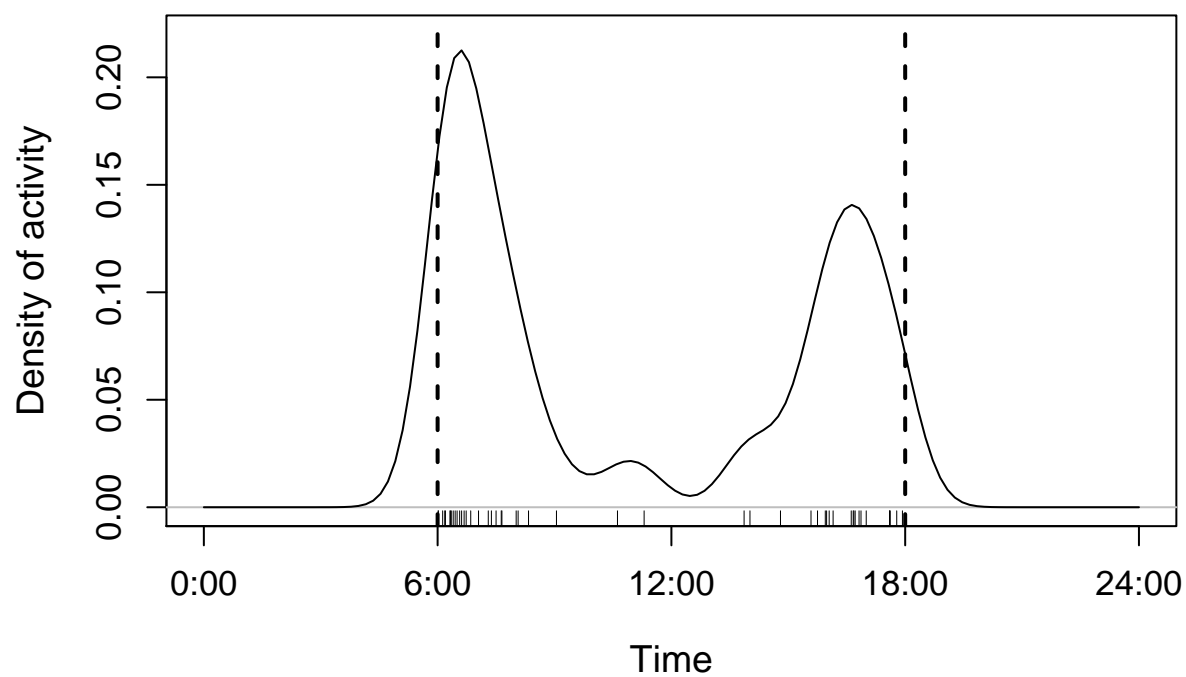
```
#Arremon torquatus
```

```
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)
```



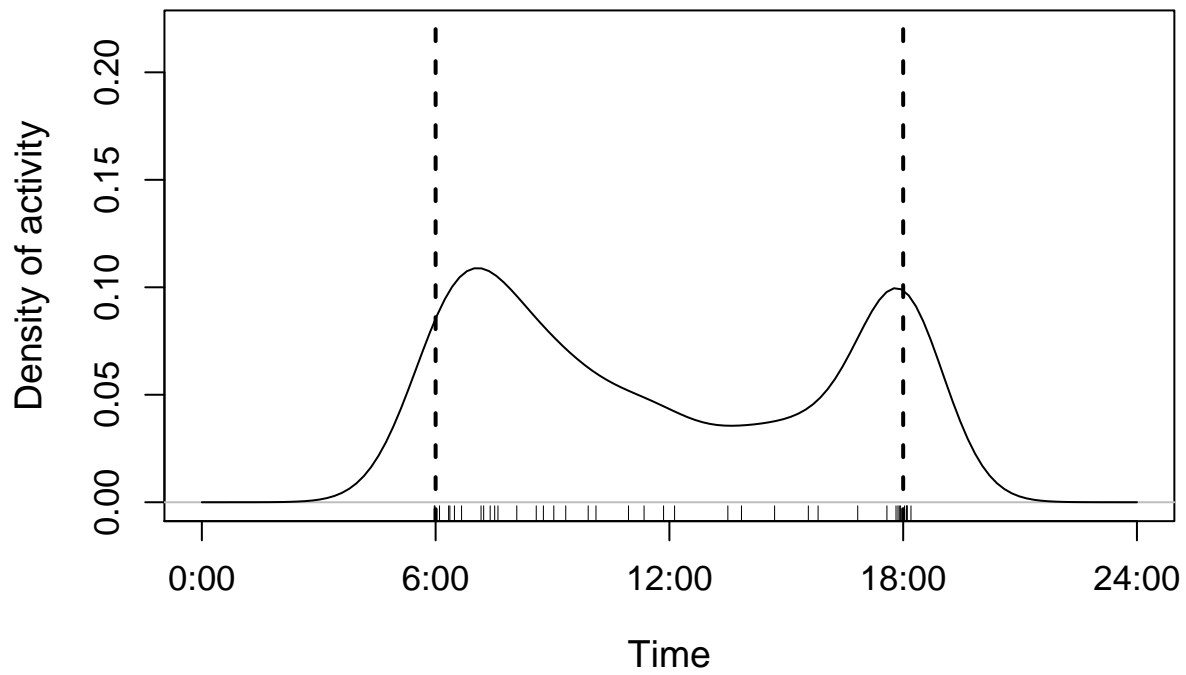
```
#Arremon brunneinucha
brunneinucha <- timeRad[chech$species == "brun"]
densityPlot(brunneinucha, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.1)
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```

## brunneinucha



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

## ruficapilla

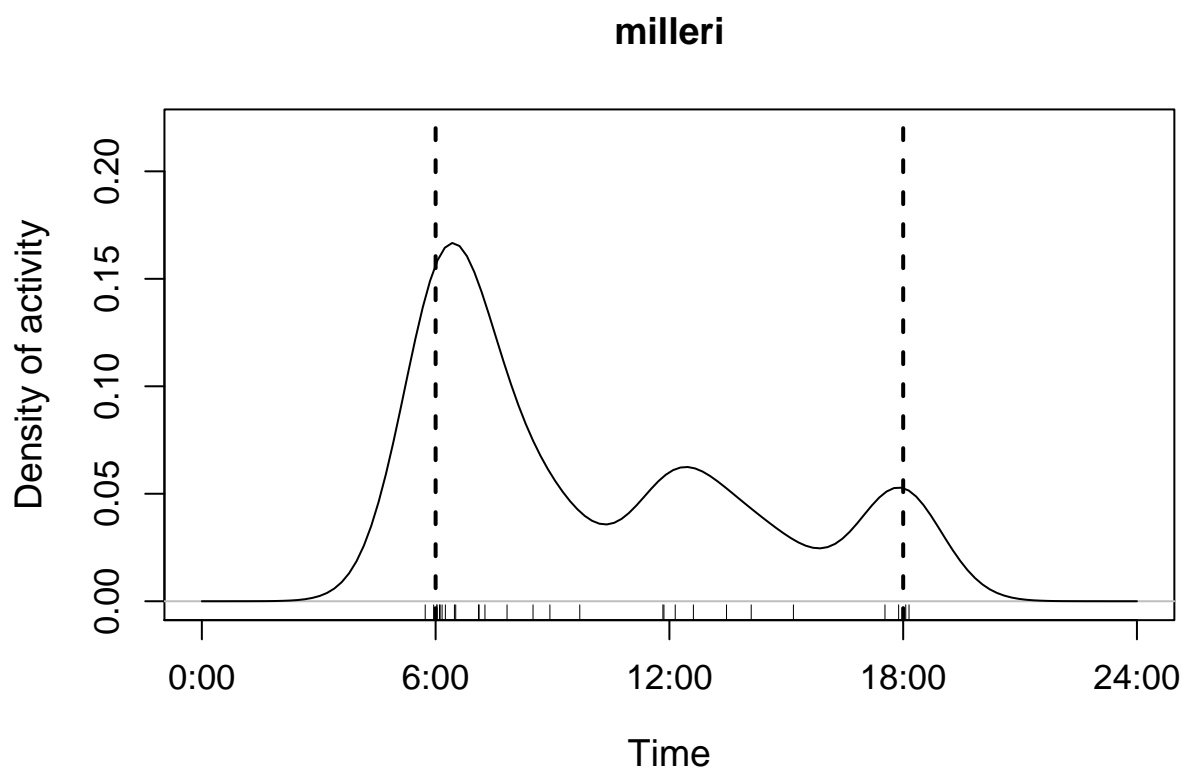


```
#Grallaria milleri
```

```
milleri <- timeRad[chech$species == "mille"]
```

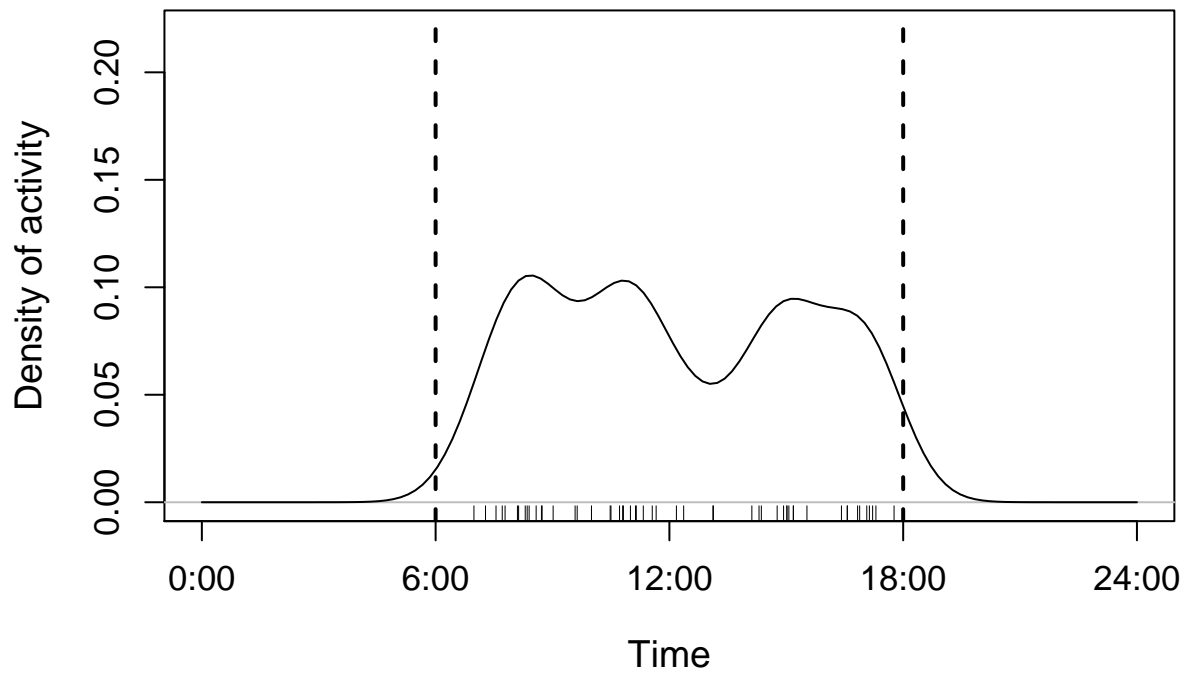
```
densityPlot(milleri, rug=TRUE, ylim=c(0,0.22), ylab="Density of activity", cex.axis=1.1, cex.lab=1.2, e
```

```
abline(v=6, lty="dashed", col="black", lwd=2); abline(v=18, lty="dashed", col="black", lwd=2)
```



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

## **goudotii**

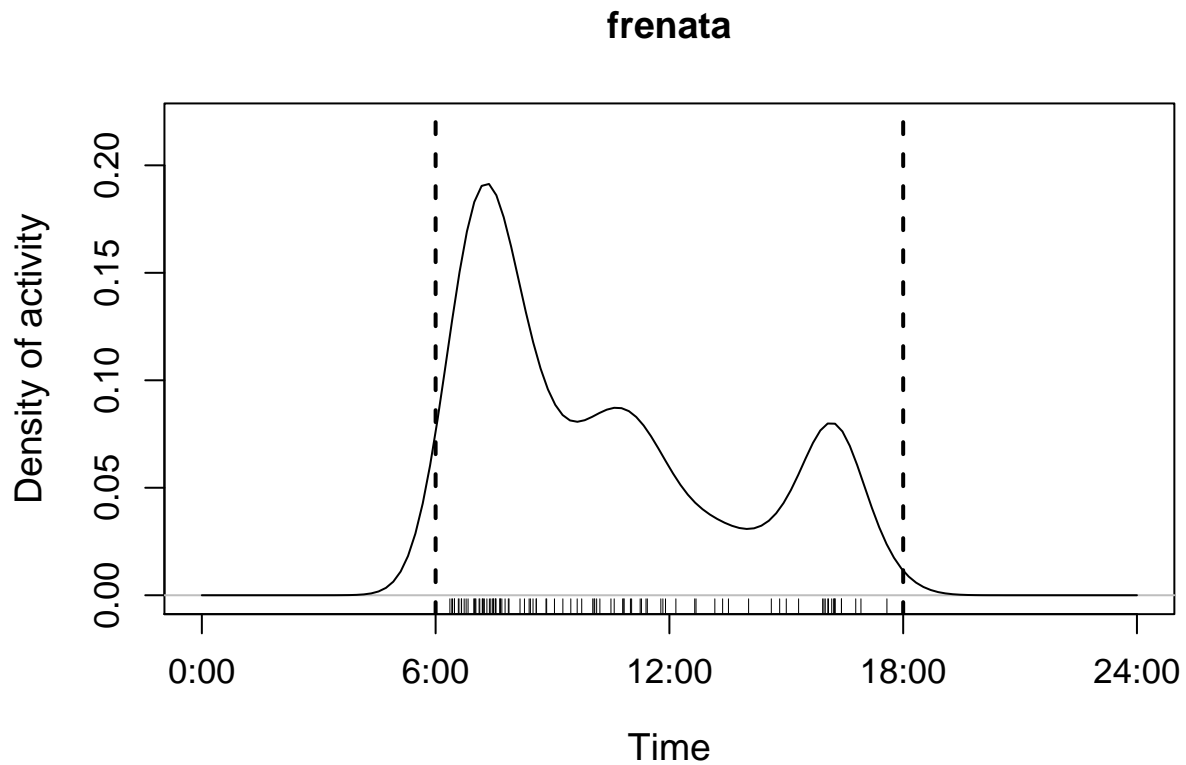


```
#Zentrignon frenata
```

```
frenata <- timeRad[chech$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)
```



```
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))
```

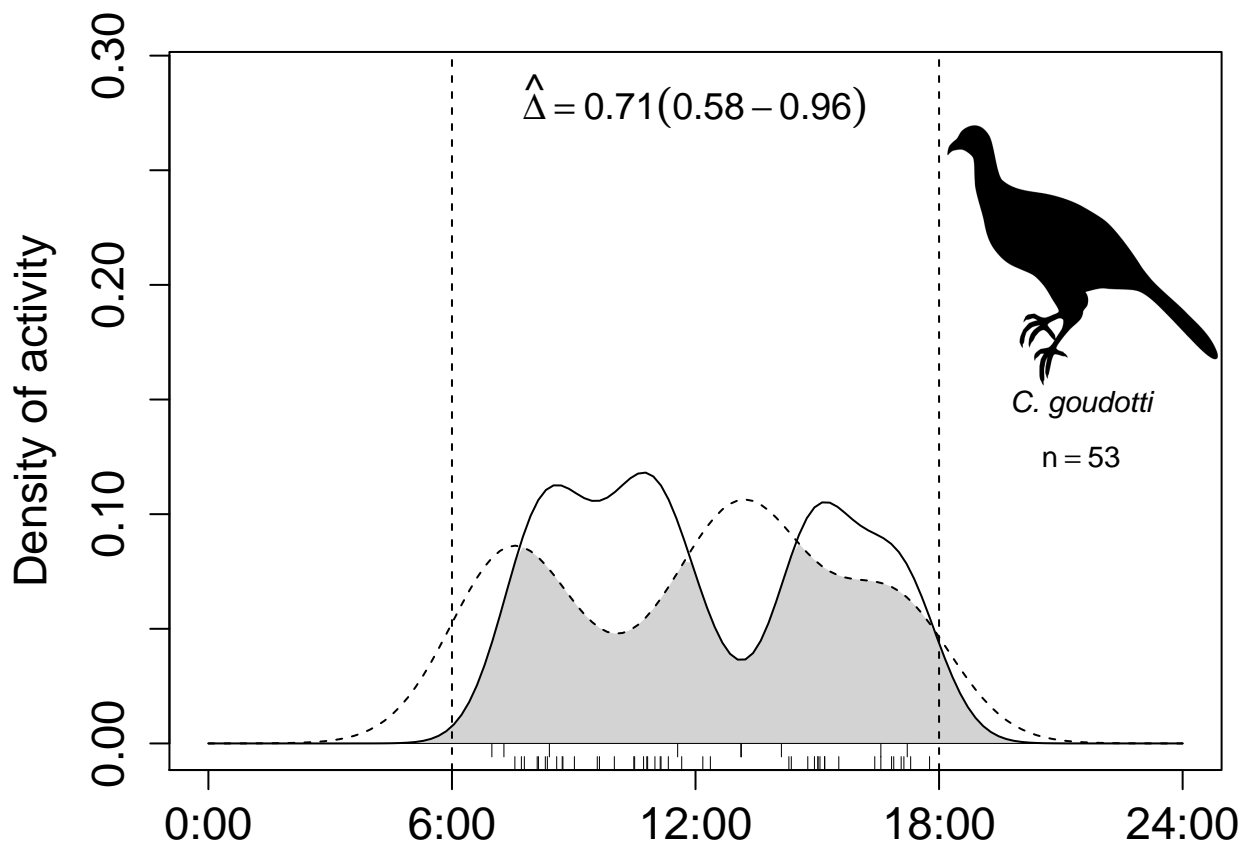


```
## [1] 9
```

```
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 bootstrap
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

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

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

```
## Dhat1 Dhat4 Dhat5
## 0.7068009 NA NA
```

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

```
## lower upper
## norm 0.5549973 0.9400816
## norm0 0.5346280 0.9197123
## basic 0.5828007 0.9649856
## basic0 0.5097240 0.8919089
## perc 0.4893547 0.8715396
```

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

```
## lower upper
## norm 0.5156063 0.8810935
## norm0 0.5025305 0.8755014
## basic 0.5114940 0.8811339
## basic0 0.5024340 0.8772846
## perc 0.4893547 0.8715396
```

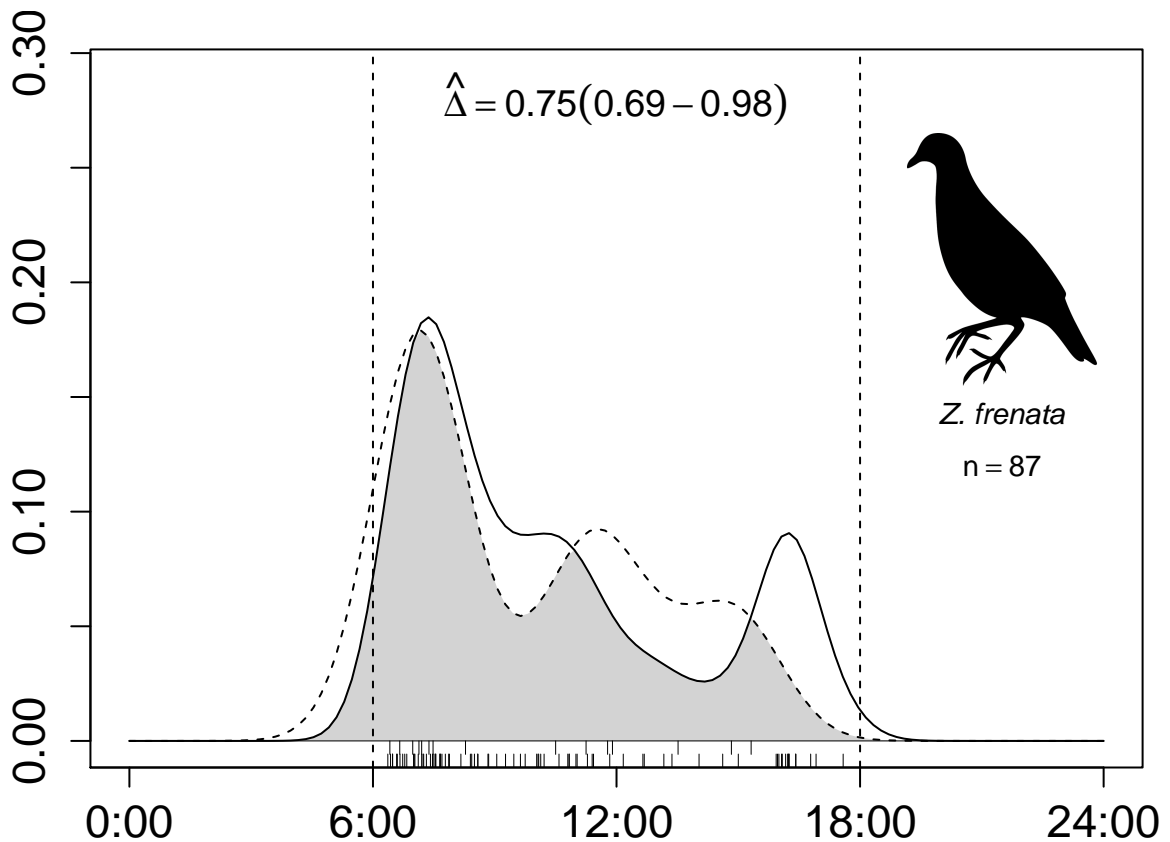
```
#Z. frenata ----
#overlap calculation
bosq <- timeRad[chech$species == "frena" & chec$forest == "andean"]
plant <- timeRad[chech$species == "frena" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

```
## [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 bootstrap
```

```
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

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

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

```
## Dhat1 Dhat4 Dhat5
## 0.7586201 NA NA
```

```
#calculation of CI
```

```
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
## lower upper
## norm 0.6812542 0.9631428
## norm0 0.6494650 0.9313536
## basic 0.6988382 0.9787548
## basic0 0.6338530 0.9137696
## perc 0.6020638 0.8819805
```

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

```
## lower upper
## norm 0.6623453 0.9057561
## norm0 0.6301439 0.8930188
## basic 0.6555372 0.9038468
## basic0 0.6352951 0.8958787
## perc 0.6020638 0.8819805
```

```
#A. brunneinucha ----
```

```
#overlap calculation
```

```
bosq <- timeRad[chech$species == "brun" & chec$forest == "andean"]
plant <- timeRad[chech$species == "brun" & chec$forest == "reforestation"]
min(length(bosq), length(plant))
```

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

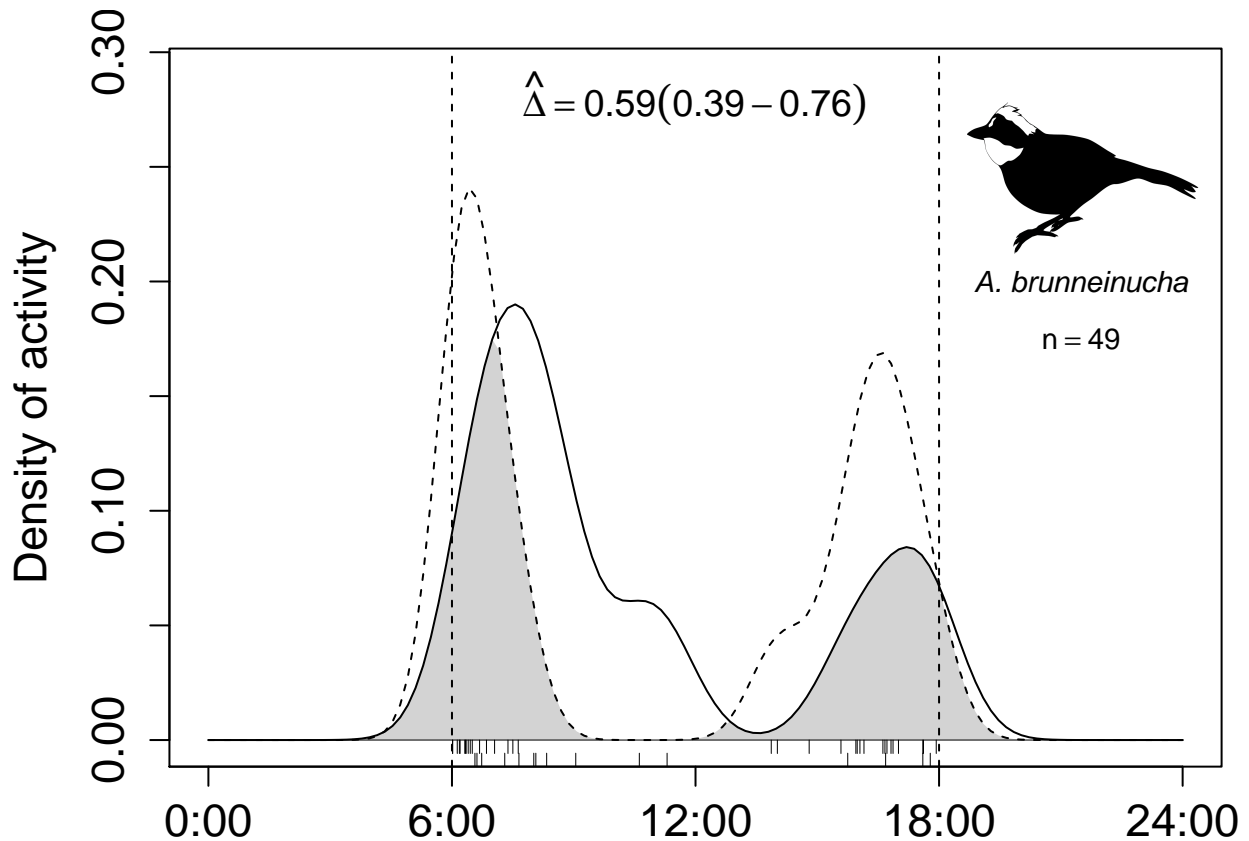
```
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
## 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 bootstrap
```

```
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))  
dim(BosqPlant)
```

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

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

```
##      Dhat1      Dhat4      Dhat5  
## 0.5903134      NA      NA
```

```
#calculation of CI
```

```
tmp <- BosqPlant[, 1]  
bootCI(BosqPlantMILLE[1], tmp)
```

```
##          lower      upper  
## norm    0.3956814 0.7592237  
## norm0   0.4021118 0.7656541  
## basic   0.4004344 0.7624131  
## basic0  0.3989225 0.7609011  
## perc    0.4053529 0.7673315
```

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

```
##          lower      upper  
## norm    0.3807753 0.7468053  
## norm0   0.3904982 0.7544867  
## basic   0.3738264 0.7428201  
## basic0  0.3955000 0.7599241  
## perc    0.4053529 0.7673315
```

```
#A. torquatus ----
```

```
#overlap calculation
```

```
bosq <- timeRad[chech$species == "torq" & chec$forest == "andean"]  
plant <- timeRad[chech$species == "torq" & chec$forest == "reforestation"]  
min(length(bosq), length(plant))
```

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

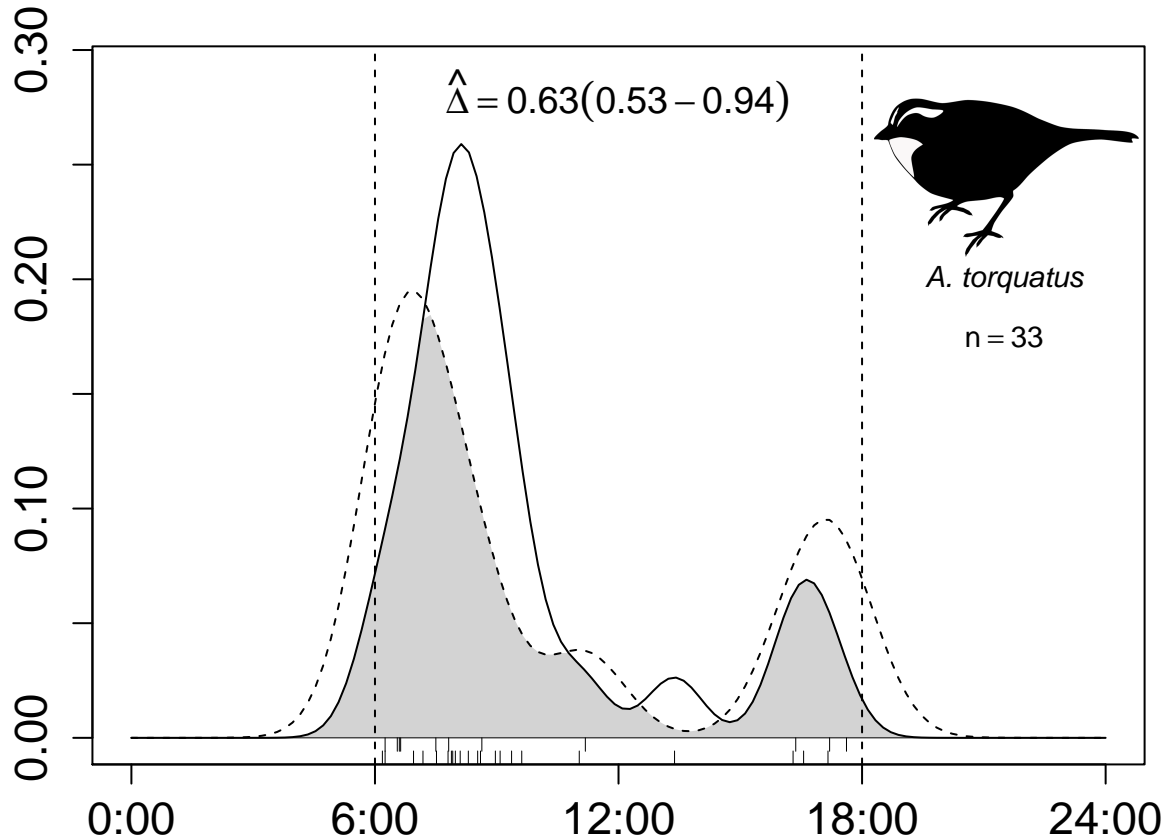
```
BosqPlantMILLE <- overlapEst(bosq, plant)  
BosqPlantMILLE
```

```
##      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, xlab=
                    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 bootstrap
```

```
BosqPlant <- bootEst(bosqboot, plantboot, adjust = c(1, NA, NA))
dim(BosqPlant)
```

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

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

```
##      Dhat1      Dhat4      Dhat5
## 0.6475237      NA      NA
```

```
#calculation of CI
```

```
tmp <- BosqPlant[, 1]
bootCI(BosqPlantMILLE[1], tmp)
```

```
##          lower      upper
## norm    0.5116997 0.9330010
## norm0    0.4742864 0.8955876
## basic    0.5366586 0.9525157
## basic0    0.4547716 0.8706287
## perc     0.4173583 0.8332154
```

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

```
##          lower      upper
## norm    0.4852195 0.8677134
## norm0    0.4517851 0.8515196
## basic    0.4861335 0.8683829
## basic0    0.4503378 0.8510564
## perc     0.4173583 0.8332154
```

```
#G. ruficapilla ----
```

```
#overlap calculation
```

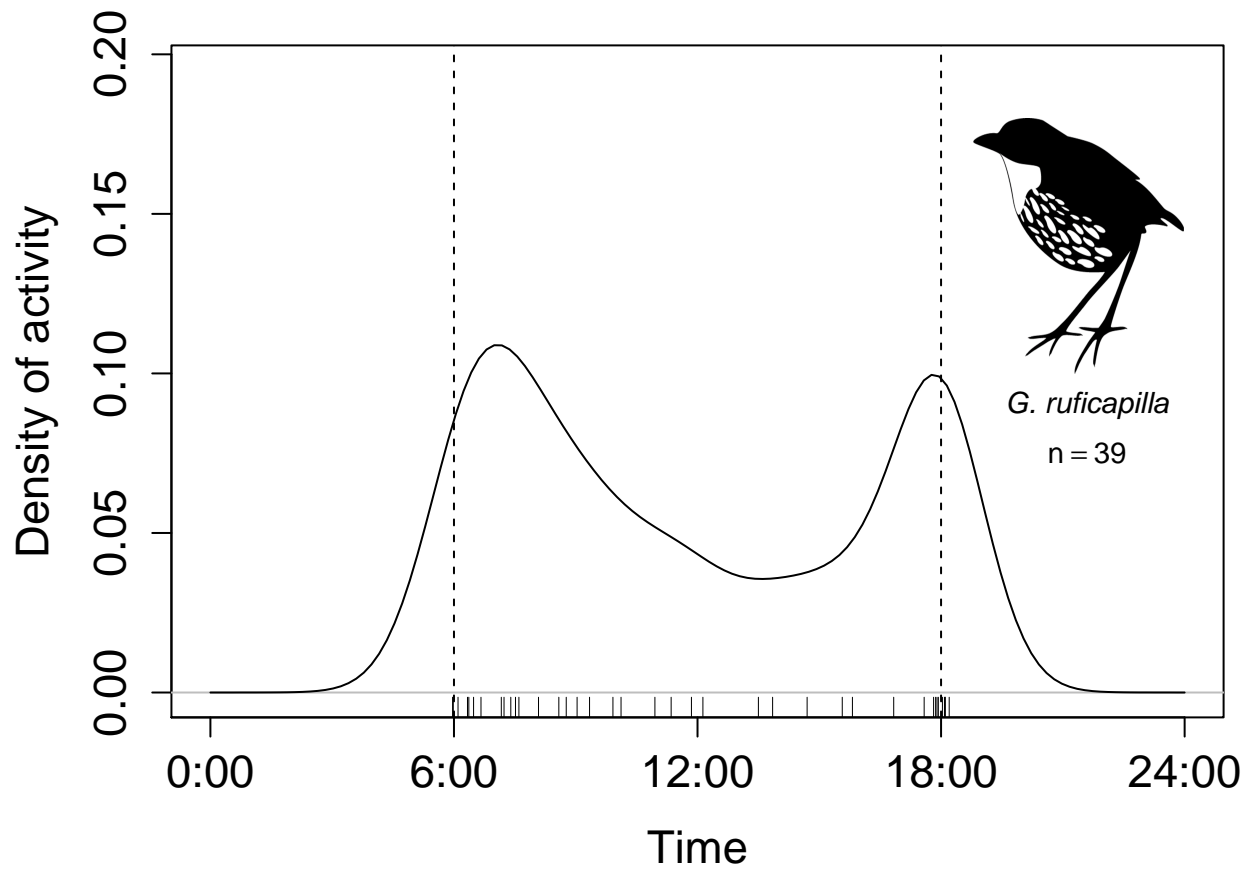
```
bosq <- timeRad[chech$species == "rufi"]
#plant <- timeRad[chech$species == "mille" & chec$forest == 2]
#min(length(bosq), length(plant))
BosqPlantMILLE <- overlapEst(bosq, plant)
BosqPlantMILLE
```

```
#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.m
                      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
```

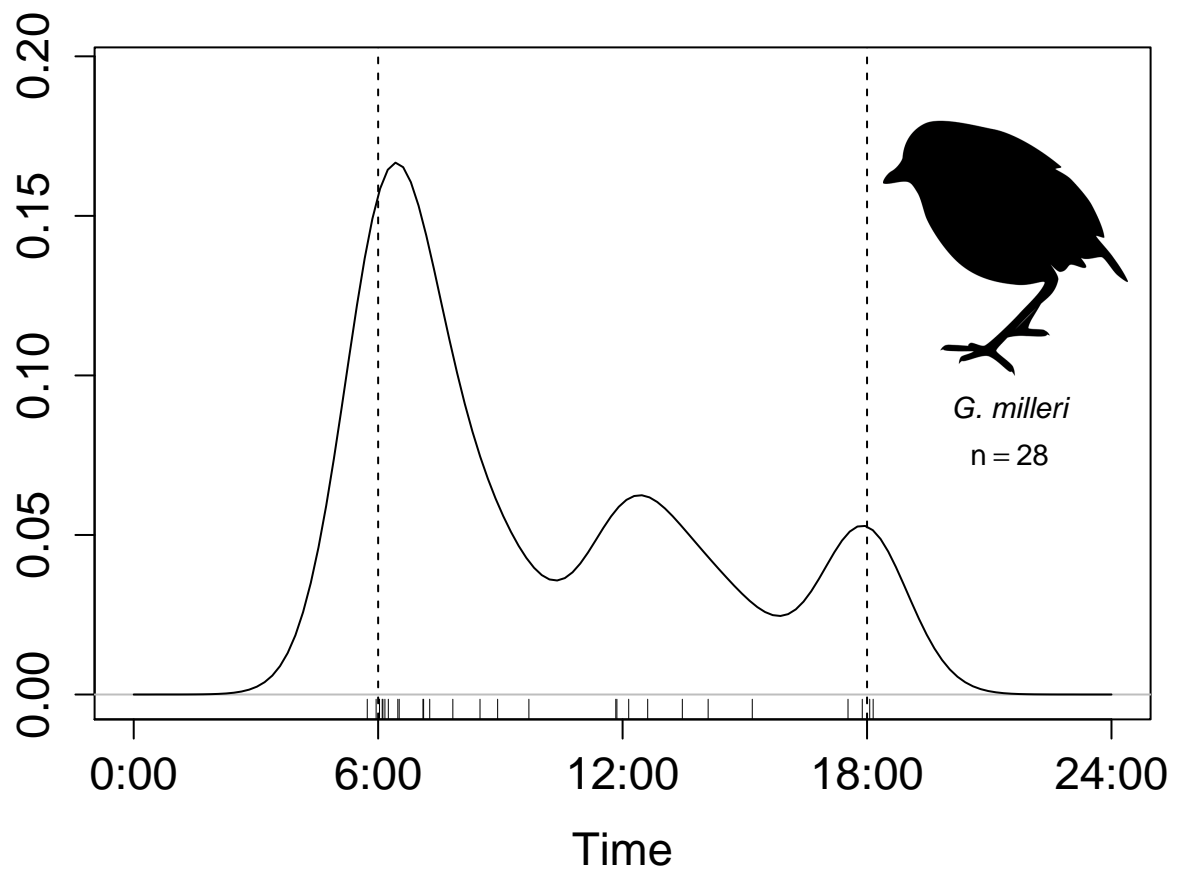




```
#dev.off()

#G. milleri ----
#overlap calculation
bosq <- timeRad[chech$species == "mille"]
#plant <- timeRad[chech$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"))))
```



`#dev.off()`