

# Ramírez-Mejía & Sánchez (2016). Activity patterns and habitat use of mammals in an Andean forest and a Eucalyptus reforestation in Colombia. *Hystrix* 27

Patrones de actividad y uso de hábitat de mamíferos, en un bosque andino y una reforestación de eucalipto en Colombia

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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.

```
mammals <- read.delim("mammal_activity.txt", header = T)
```

```
for (i in seq_along(mammals)) {  
  if (is.character(mammals[[i]])) {  
    mammals[[i]] <- as.factor(mammals[[i]])  
  } else {  
    next  
  }  
}
```

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

```
##  
##           andean reforestation  
## dasypus      30           10  
## didelphis    7            5  
## mazama       8           13  
## nasua        48           23  
## nasuella     10           42  
## sciurus      13            9
```

```
library(overlap)  
library(boot)  
library(circular)
```

```
##  
## Attaching package: 'circular'
```

```
## The following objects are masked from 'package:stats':
```

```
##  
## sd, var
```

```
timeRad <- mammals$time * 2 * pi
```

```
levels(mammals$species)
```

```
## [1] "dasypus" "didelphis" "mazama" "nasua" "nasuella" "sciurus"
```

```
#####-  
# ===== Comparison between forest =====  
#####-
```

```
# ===== Dasypus novemcinctus =====  
#####overlap dasypus
```

```
dasypus_A <- timeRad[mammals$forest == "andean" & mammals$species == "dasypus"]  
dasypus_R <- timeRad[mammals$forest == "reforestation" & mammals$species == "dasypus"]  
min(length(dasypus_A), length(dasypus_R))
```

```
## [1] 10
```

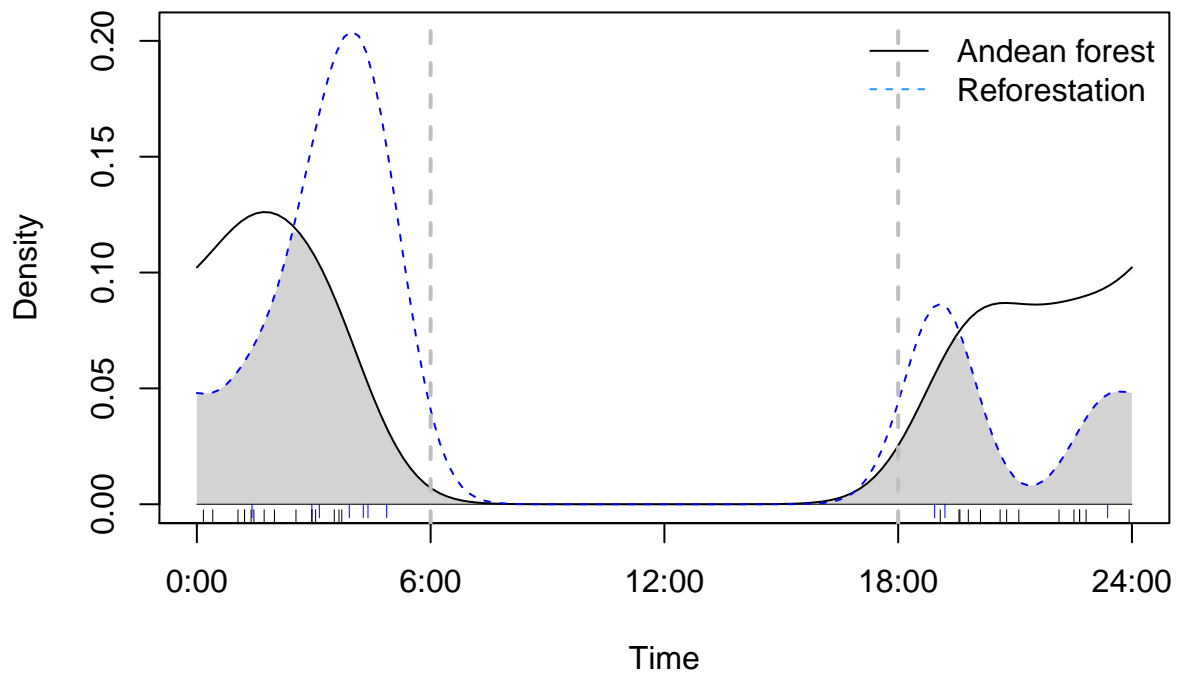
```
overlapEst(dasypus_A, dasypus_R)
```

```
##      Dhat1      Dhat4      Dhat5  
## 0.6069357 0.6058597 0.7000000
```

```
#####plot activity overlap
```

```
overlapPlot(dasypus_A, dasypus_R, xscale = 24, main = "", rug = T)  
legend("topright", c("Andean forest", "Reforestation"), lty = c(1,2), col = c(1,4), bty = "n")  
title(expression(italic("Dasypus novemcinctus")))  
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)  
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Dasypus novemcinctus*



```
##### bootstrap
```

```
dasypus_bootA <- resample(dasypus_A, 10000)
```

```
dasypus_bootR <- resample(dasypus_R, 10000)
```

```
dim(dasypus_bootA); dim(dasypus_bootR)
```

```
## [1] 30 10000
```

```
## [1] 10 10000
```

```
##### overlap estimates by bootstrap
```

```
dasypus_overlapp <- bootEst(dasypus_bootA, dasypus_bootR, adjust = c(1, 1, 1))
```

```
dim(dasypus_overlapp)
```

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

```
dasypues_mean <- colMeans(dasypus_overlapp)
```

```
dasypues_mean
```

```
## Dhat1 Dhat4 Dhat5
```

```
## 0.6127697 0.5905746 0.5240000
```

```
##### calculation of CI
dasypusCI <- dasypus_overlapp[, 1]
bootCI(overlapEst(dasypus_A, dasypus_R)[1], dasypusCI)

##           lower      upper
## norm    0.3527533 0.8494503
## norm0    0.3585872 0.8552843
## basic    0.3738175 0.8556688
## basic0    0.3523687 0.8342200
## perc     0.3582027 0.8400540

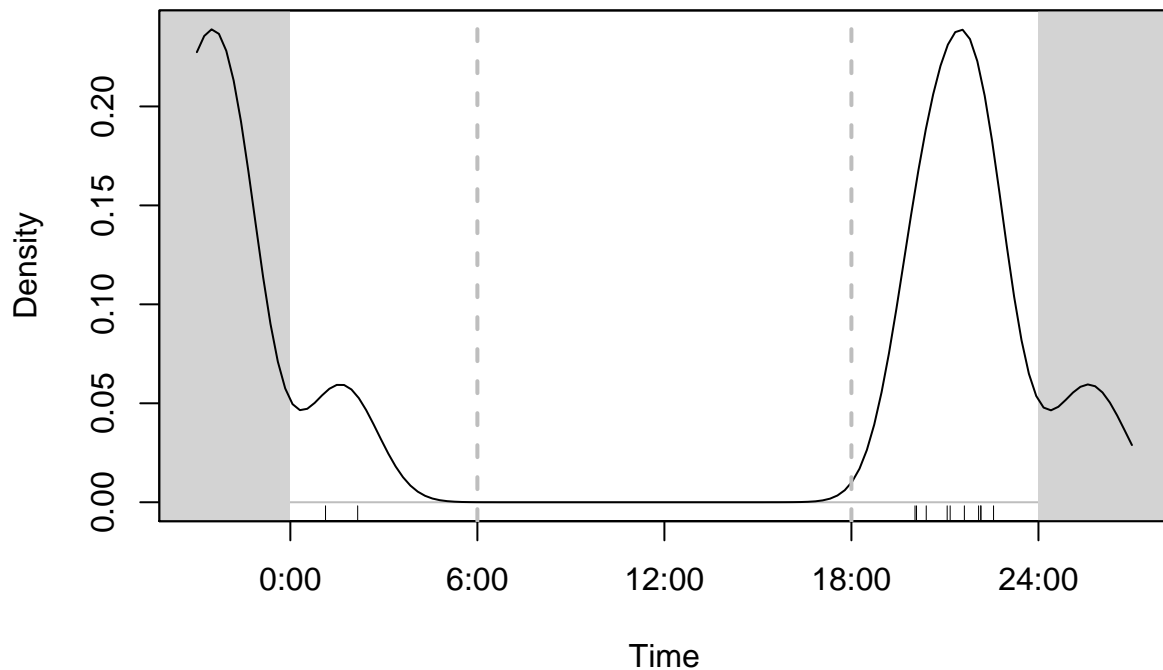
bootCIlogit(overlapEst(dasypus_A, dasypus_R)[1], dasypusCI)

##           lower      upper
## norm    0.3189565 0.8183277
## norm0    0.3323967 0.8272505
## basic    0.3122266 0.8103173
## basic0    0.3442571 0.8316580
## perc     0.3582027 0.8400540

# ===== Didelphis pernigra =====
#####overlap didelphis
didelphis_A <- timeRad[mammals$species == "didelphis"]

#####plot activity overlap
densityPlot(didelphis_A, xscale = 24, main = "", rug = T)
title(expression(italic("Didelphis pernigra")))
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Didelphis pernigra*



```
# ===== Mazama rufina =====
#####overlap mazama
mazama_A <- timeRad[mammals$forest == "andean" & mammals$species == "mazama"]
mazama_R <- timeRad[mammals$forest == "reforestation" & mammals$species == "mazama"]
min(length(mazama_A), length(mazama_R))

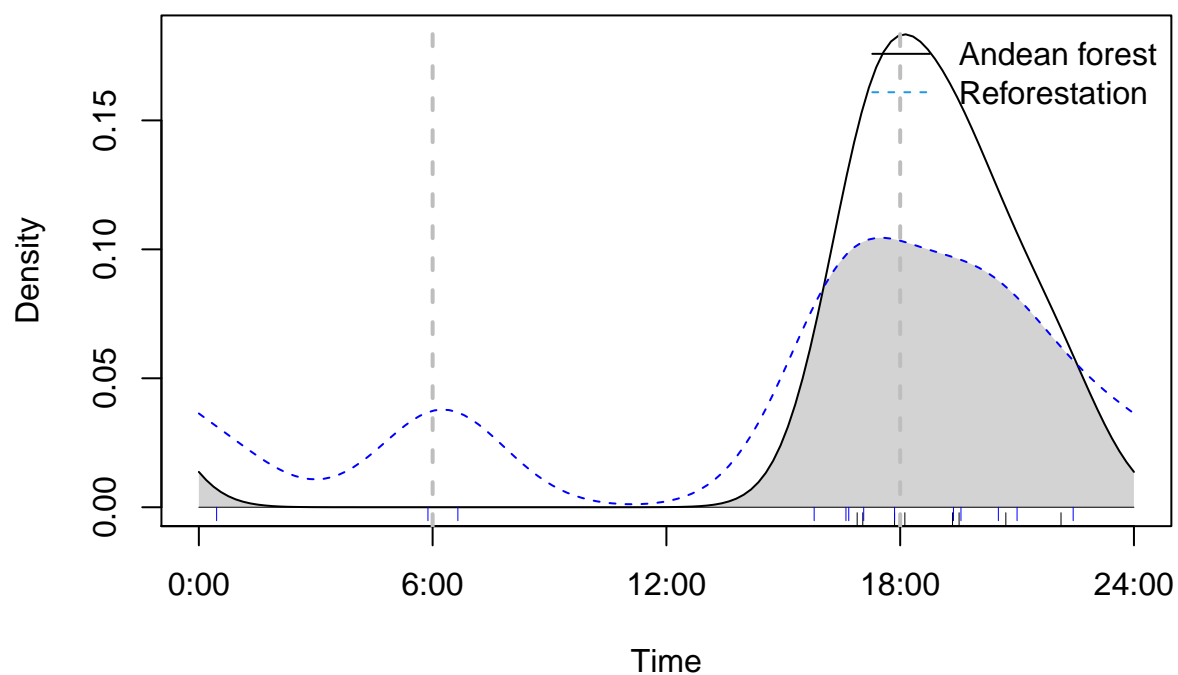
## [1] 8

overlapEst(mazama_A, mazama_R)

##      Dhat1      Dhat4      Dhat5
## 0.7070903 0.7215979 0.7692308

#####plot activity overlap
overlapPlot(mazama_A, mazama_R, xscale = 24, main = "", rug = T)
legend("topright", c("Andean forest", "Reforestation"), lty = c(1,2), col = c(1,4), bty = "n")
title(expression(italic("Mazama rufina")))
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Mazama rufina*



```
##### bootstrap
```

```
mazama_bootA <- resample(mazama_A, 10000)
```

```
mazama_bootR <- resample(mazama_R, 10000)
```

```
dim(mazama_bootA); dim(mazama_bootR)
```

```
## [1]      8 10000
```

```
## [1]     13 10000
```

```
##### overlap estimates by bootstrap
```

```
mazama_overlapp <- bootEst(mazama_bootA, mazama_bootR, adjust = c(1, 1, 1))
```

```
dim(mazama_overlapp)
```

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

```
dasypues_mean <- colMeans(mazama_overlapp)
```

```
dasypues_mean
```

```
##      Dhat1      Dhat4      Dhat5
```

```
## 0.6320326 0.6132633 0.5495375
```

```
##### calculation of CI
```

```
mazamaCI <- mazama_overlapp[, 1]
```

```
bootCI(overlapEst(mazama_A, mazama_R)[1], mazamaCI)
```

```
##           lower      upper
## norm    0.5369777 1.0273184
## norm0   0.4619200 0.9522607
## basic   0.5619658 1.0468607
## basic0  0.4423776 0.9272725
## perc    0.3673199 0.8522148
```

```
bootCIlogit(overlapEst(mazama_A, mazama_R)[1], mazamaCI)
```

```
##           lower      upper
## norm    0.5108433 0.9102514
## norm0   0.4365021 0.8826698
## basic   0.5026273 0.9093991
## basic0  0.4390591 0.8860314
## perc    0.3673199 0.8522148
```

```
# ===== Nasua nasua =====
#####overlap nasua
nasua_A <- timeRad[mammals$forest == "andean" & mammals$species == "nasua"]
nasua_R <- timeRad[mammals$forest == "reforestation" & mammals$species == "nasua"]
min(length(nasua_A), length(nasua_R))
```

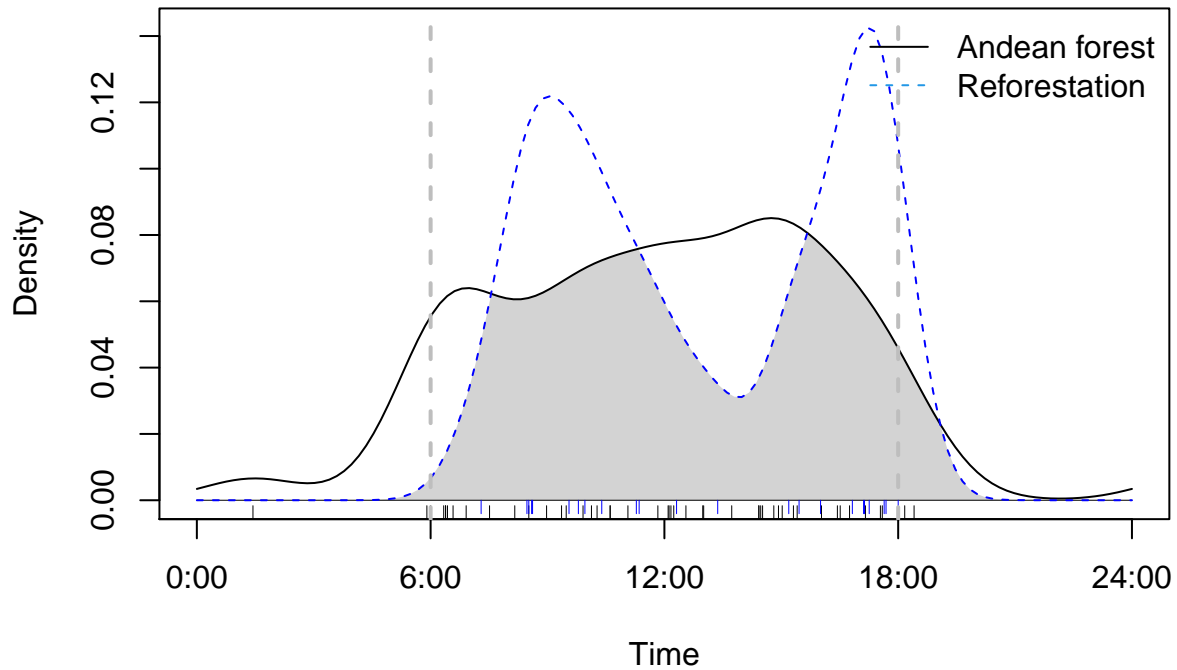
```
## [1] 23
```

```
overlapEst(nasua_A, nasua_R)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.7029960 0.6907816 0.5661232
```

```
#####plot activity overlap
overlapPlot(nasua_A, nasua_R, xscale = 24, main = "", rug = T)
legend("topright", c("Andean forest", "Reforestation"), lty = c(1,2), col = c(1,4), bty = "n")
title(expression(italic("Nasua nasua")))
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Nasua nasua*



```
##### bootstrap
```

```
nasua_bootA <- resample(nasua_A, 10000)
nasua_bootR <- resample(nasua_R, 10000)
dim(nasua_bootA); dim(nasua_bootR)
```

```
## [1] 48 10000
```

```
## [1] 23 10000
```

```
##### overlap estimates by bootstrap
```

```
nasua_overlapp <- bootEst(nasua_bootA, nasua_bootR, adjust = c(1, 1, 1))
dim(nasua_overlapp)
```

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

```
dasympues_mean <- colMeans(nasua_overlapp)
dasympues_mean
```

```
## Dhat1 Dhat4 Dhat5
## 0.7082534 0.6907486 0.6265841
```

```
##### calculation of CI
```

```
nasuaCI <- nasua_overlapp[, 1]
bootCI(overlapEst(nasua_A, nasua_R)[1], nasuaCI)
```



```
##           lower      upper
## norm    0.5384254 0.8570518
## norm0    0.5436828 0.8623092
## basic    0.5501857 0.8648178
## basic0    0.5359168 0.8505489
## perc     0.5411741 0.8558063
```

```
bootCIlogit(overlapEst(nasua_A, nasua_R)[1], nasuaCI)
```

```
##           lower      upper
## norm    0.4975096 0.8337394
## norm0    0.5126080 0.8419446
## basic    0.4855851 0.8260864
## basic0    0.5261427 0.8481910
## perc     0.5411741 0.8558063
```

```
# ===== Nasuella olivacea =====
#####overlap nasuella
nasuella_A <- timeRad[mammals$forest == "andean" & mammals$species == "nasuella"]
nasuella_R <- timeRad[mammals$forest == "reforestation" & mammals$species == "nasuella"]
min(length(nasuella_A), length(nasuella_R))
```

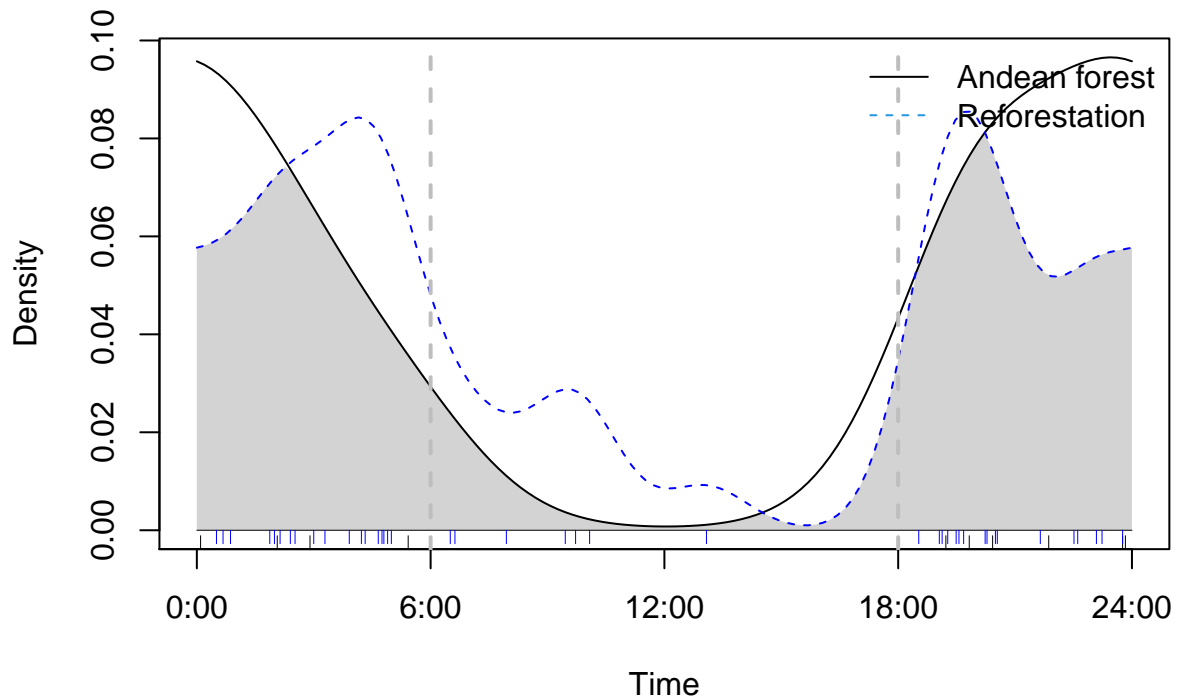
```
## [1] 10
```

```
overlapEst(nasuella_A, nasuella_R)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.7708026 0.7965027 0.8619048
```

```
#####plot activity overlap
overlapPlot(nasuella_A, nasuella_R, xscale = 24, main = "", rug = T)
legend("topright", c("Andean forest", "Reforestation"), lty = c(1,2), col = c(1,4), bty = "n")
title(expression(italic("Nasuella olivacea")))
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Nasuella olivacea*



```
##### bootstrap
```

```
nasuella_bootA <- resample(nasuella_A, 10000)
nasuella_bootR <- resample(nasuella_R, 10000)
dim(nasuella_bootA); dim(nasuella_bootR)
```

```
## [1] 10 10000
```

```
## [1] 42 10000
```

```
##### overlap estimates by bootstrap
```

```
nasuella_overlapp <- bootEst(nasuella_bootA, nasuella_bootR, adjust = c(1, 1, 1))
dim(nasuella_overlapp)
```

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

```
dasypues_mean <- colMeans(nasuella_overlapp)
dasypues_mean
```

```
## Dhat1 Dhat4 Dhat5
## 0.7008674 0.6753722 0.5968676
```

```
##### calculation of CI
```

```
nasuellaCI <- nasuella_overlapp[, 1]
bootCI(overlapEst(nasuella_A, nasuella_R)[1], nasuellaCI)
```

```
##           lower      upper
## norm    0.6485685 1.0329070
## norm0   0.5786333 0.9629718
## basic   0.6746653 1.0518294
## basic0  0.5597109 0.9368750
## perc    0.4897758 0.8669398
```

```
bootCIlogit(overlapEst(nasuella_A, nasuella_R)[1], nasuellaCI)
```

```
##           lower      upper
## norm    0.6381360 0.9233240
## norm0   0.5627412 0.8978355
## basic   0.6344903 0.9217669
## basic0  0.5680958 0.8992715
## perc    0.4897758 0.8669398
```

```
# ===== Sciurus granatensis =====
#####overlap sciurus
sciurus_A <- timeRad[mammals$forest == "andean" & mammals$species == "sciurus"]
sciurus_R <- timeRad[mammals$forest == "reforestation" & mammals$species == "sciurus"]
min(length(sciurus_A), length(sciurus_R))
```

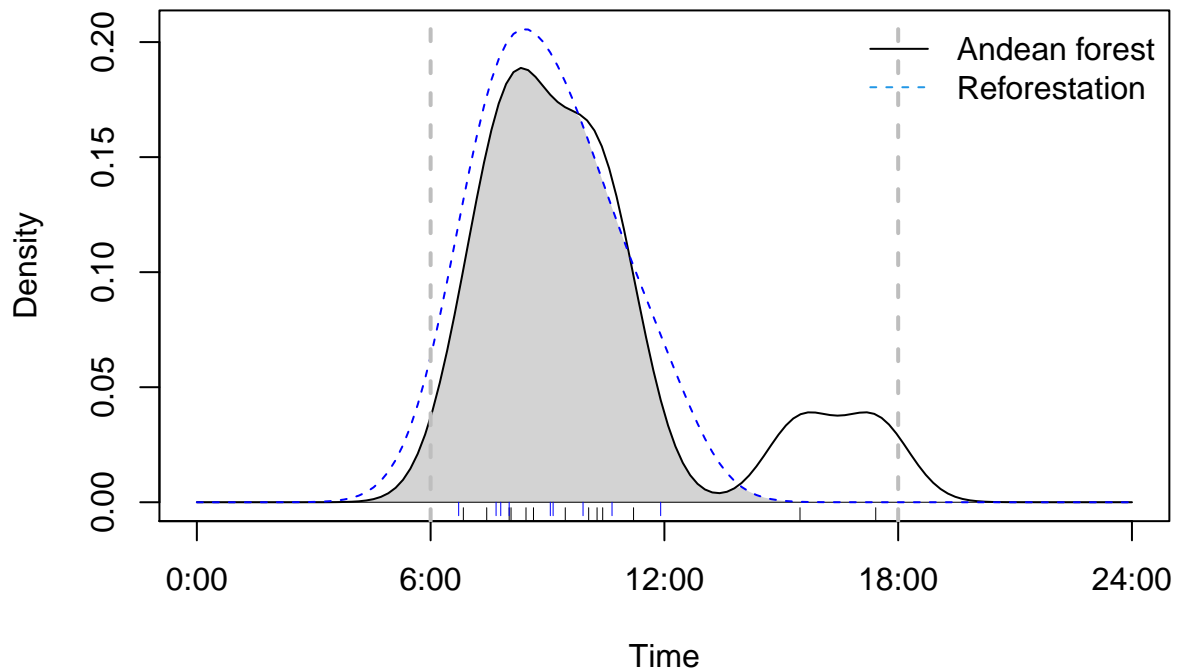
```
## [1] 9
```

```
overlapEst(sciurus_A, sciurus_R)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.8314321 0.8528366 0.8717949
```

```
#####plot activity overlap
overlapPlot(sciurus_A, sciurus_R, xscale = 24, main = "", rug = T)
legend("topright", c("Andean forest", "Reforestation"), lty = c(1,2), col = c(1,4), bty = "n")
title(expression(italic("Sciurus granatensis")))
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## *Sciurus granatensis*



```
##### bootstrap
```

```
sciurus_bootA <- resample(sciurus_A, 10000)
sciurus_bootR <- resample(sciurus_R, 10000)
dim(sciurus_bootA); dim(sciurus_bootR)
```

```
## [1] 13 10000
```

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

```
##### overlap estimates by bootstrap
```

```
sciurus_overlap <- bootEst(sciurus_bootA, sciurus_bootR, adjust = c(1, 1, 1))
dim(sciurus_overlap)
```

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

```
dasypues_mean <- colMeans(sciurus_overlap)
dasypues_mean
```

```
## Dhat1 Dhat4 Dhat5
## 0.7091774 0.6992689 0.6164744
```

```
##### calculation of CI
```

```
sciurusCI <- sciurus_overlap[, 1]
bootCI(overlapEst(sciurus_A, sciurus_R)[1], sciurusCI)
```

```
##           lower    upper
## norm    0.7467425 1.160631
## norm0    0.6244877 1.038377
## basic    0.7766473 1.189707
## basic0    0.5954119 1.008472
## perc     0.4731572 0.886217
```

```
bootCIlogit(overlapEst(sciurus_A, sciurus_R)[1], sciurusCI)
```

```
##           lower    upper
## norm    0.7649988 0.9645557
## norm0    0.6304391 0.9344731
## basic    0.7574876 0.9643978
## basic0    0.6315118 0.9369588
## perc     0.4731572 0.8862170
```

```
#####-
# ===== Species comparison =====
#####-

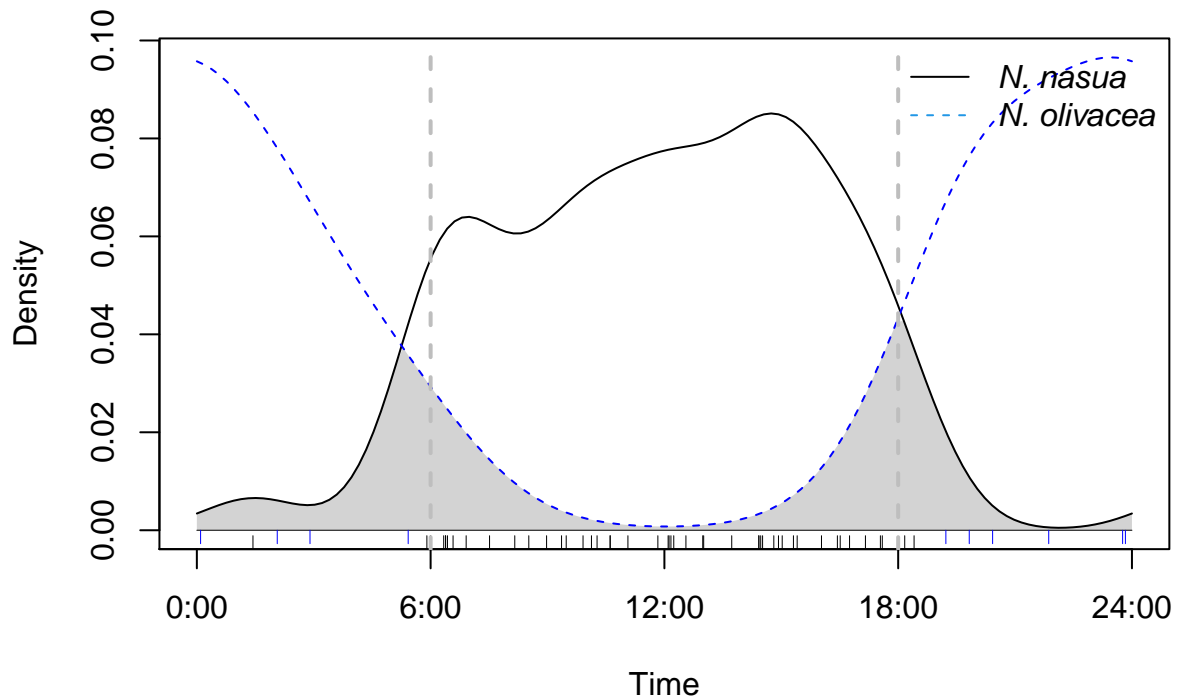
# ===== N. olivacea - N. nasua, andean=====
#####overlap
```

```
overlapEst(nasua_A, nasuella_A)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.2295215 0.1987673 0.0625000
```

```
#####plot activity overlap
overlapPlot(nasua_A, nasuella_A, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. nasua")),
                        expression(italic("N. olivacea"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Andean forest")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## Andean forest



```
##### overlap estimates by bootstrap
```

```
NasuaNasuella_overlapp_A <- bootEst(nasua_bootA, nasuella_bootA, adjust = c(1, 1, 1))
dim(NasuaNasuella_overlapp_A)
```

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

```
NasuaNasuella_mean_A <- colMeans(NasuaNasuella_overlapp_A)
NasuaNasuella_mean_A
```

```
##      Dhat1      Dhat4      Dhat5
## 0.2950613 0.2563494 0.2080704
```

```
##### calculation of CI
```

```
NasuaNasuellaCI_A <- NasuaNasuella_overlapp_A[, 1]
bootCI(overlapEst(nasua_A, nasuella_A)[1], NasuaNasuellaCI_A)
```

```
##           lower      upper
## norm  -0.01942157 0.3473848
## norm0   0.04611830 0.4129246
## basic -0.03021416 0.3320980
## basic0  0.06140510 0.4237172
## perc   0.12694497 0.4892571
```

```
bootCIlogit(overlapEst(nasua_A, nasuella_A)[1], NasuaNasuellaCI_A)
```

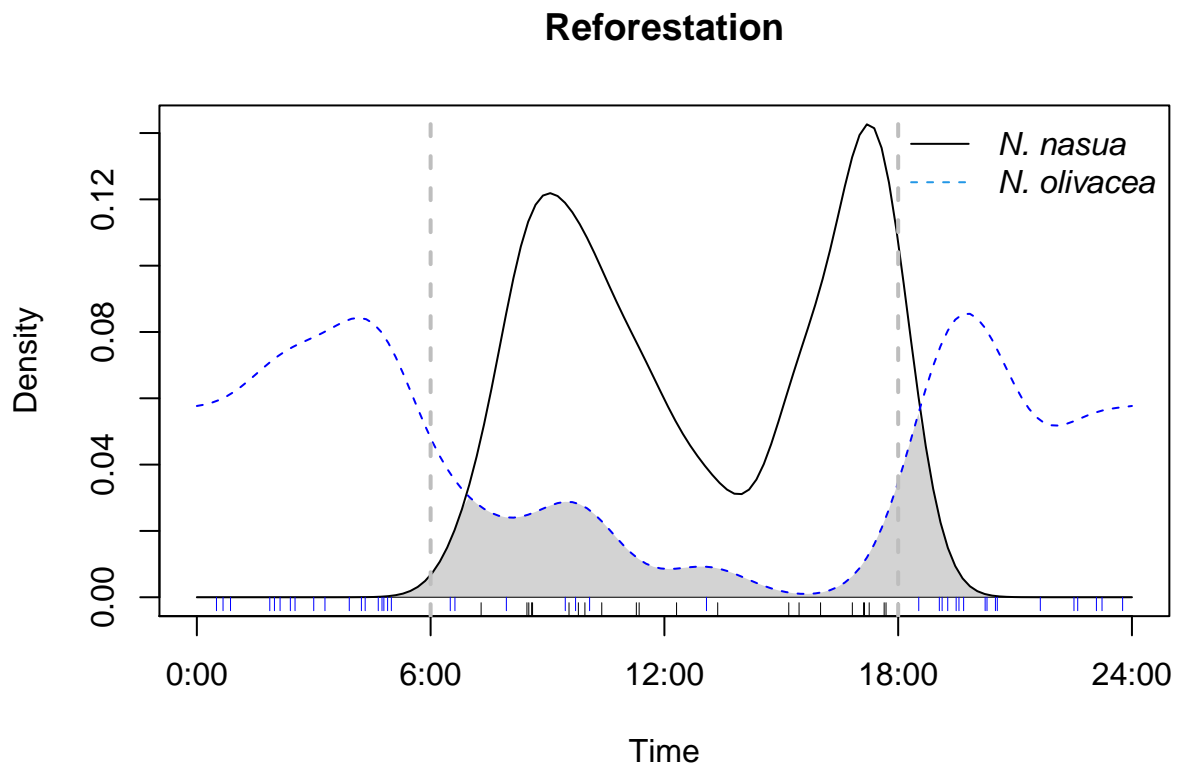
```
##           lower      upper
## norm    0.07918146 0.3647612
## norm0    0.10336369 0.4349621
## basic    0.08478408 0.3790022
## basic0    0.09784787 0.4167566
## perc     0.12694495 0.4892571
```

```
# ===== N. olivacea - N. nasua, reforestation=====
#####overlap
```

```
overlapEst(nasua_R, nasuella_R)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.2179979 0.1870992 0.1428571
```

```
#####plot activity overlap
overlapPlot(nasua_R, nasuella_R, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. nasua")),
                        expression(italic("N. olivacea"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Reforestation")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```



```
##### overlap estimates by bootstrap
```

```
NasuaNasuella_overlapp_R <- bootEst(nasua_bootR, nasuella_bootR, adjust = c(1, 1, 1))
dim(NasuaNasuella_overlapp_R)
```

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

```
NasuaNasuella_mean_R <- colMeans(NasuaNasuella_overlapp_R)
NasuaNasuella_mean_R
```

```
##      Dhat1      Dhat4      Dhat5
## 0.2893678 0.2555954 0.2150157
```

```
##### calculation of CI
```

```
NasuaNasuellaCI_R <- NasuaNasuella_overlapp_R[, 1]
bootCI(overlapEst(nasua_R, nasuella_R)[1], NasuaNasuellaCI_R)
```

```
##           lower      upper
## norm    0.02250099 0.2707550
## norm0    0.09387088 0.3421249
## basic    0.01841950 0.2662282
## basic0    0.09839774 0.3462064
## perc     0.16976763 0.4175763
```

```
bootCIlogit(overlapEst(nasua_R, nasuella_R)[1], NasuaNasuellaCI_R)
```

```
##           lower      upper
## norm    0.09468046 0.2664698
## norm0    0.13011318 0.3419119
## basic    0.09779105 0.2753853
## basic0    0.12508897 0.3339101
## perc     0.16976762 0.4175763
```

```
# ===== N. olivacea - D. novemcinctus, reforestation=====
#####overlap
```

```
overlapEst(nasuella_R, dasypus_R)
```

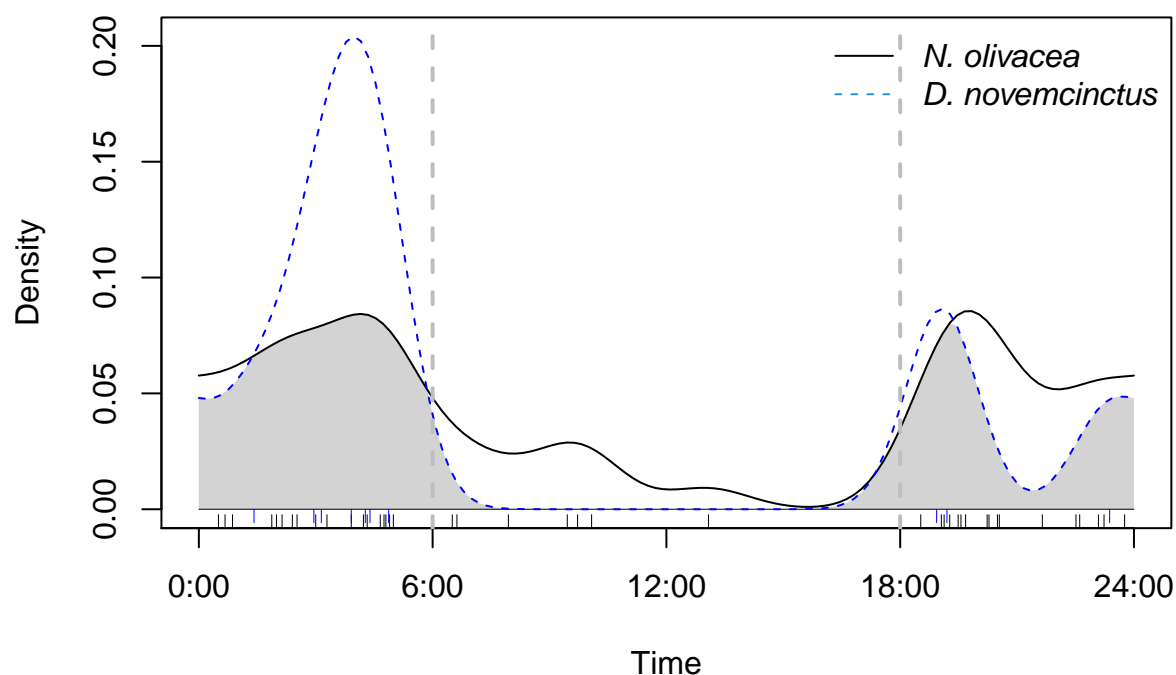
```
##      Dhat1      Dhat4      Dhat5
## 0.6855628 0.6840338 0.7761905
```

```
#####plot activity overlap
```

```
overlapPlot(nasuella_R, dasypus_R, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. olivacea")),
                      expression(italic("D. novemcinctus"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Reforestation")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```



## Reforestation



```
##### overlap estimates by bootstrap
```

```
DasypusNasuella_overlapp_R <- bootEst(dasypus_bootR, nasuella_bootR, adjust = c(1, 1, 1))
dim(DasypusNasuella_overlapp_R)
```

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

```
DasypusNasuella_mean_R <- colMeans(DasypusNasuella_overlapp_R)
DasypusNasuella_mean_R
```

```
##      Dhat1      Dhat4      Dhat5
## 0.6279094 0.6012674 0.5389105
```

```
##### calculation of CI
```

```
DasypusNasuellaCI_R <- DasypusNasuella_overlapp_R[, 1]
bootCI(overlapEst(dasypus_R, nasuella_R)[1], DasypusNasuellaCI_R)
```

```
##      lower      upper
## norm  0.5129802 0.9734522
## norm0 0.4553268 0.9157988
## basic 0.5364422 0.9879022
## basic0 0.4408769 0.8923368
## perc  0.3832234 0.8346834
```

```
bootCIlogit(overlapEst(dasypus_R, nasuella_R)[1], DasypusNasuellaCI_R)
```

```
##           lower      upper
## norm    0.4885068 0.8856908
## norm0    0.4335787 0.8613056
## basic    0.4849350 0.8844027
## basic0    0.4366905 0.8630047
## perc     0.3832234 0.8346834
```

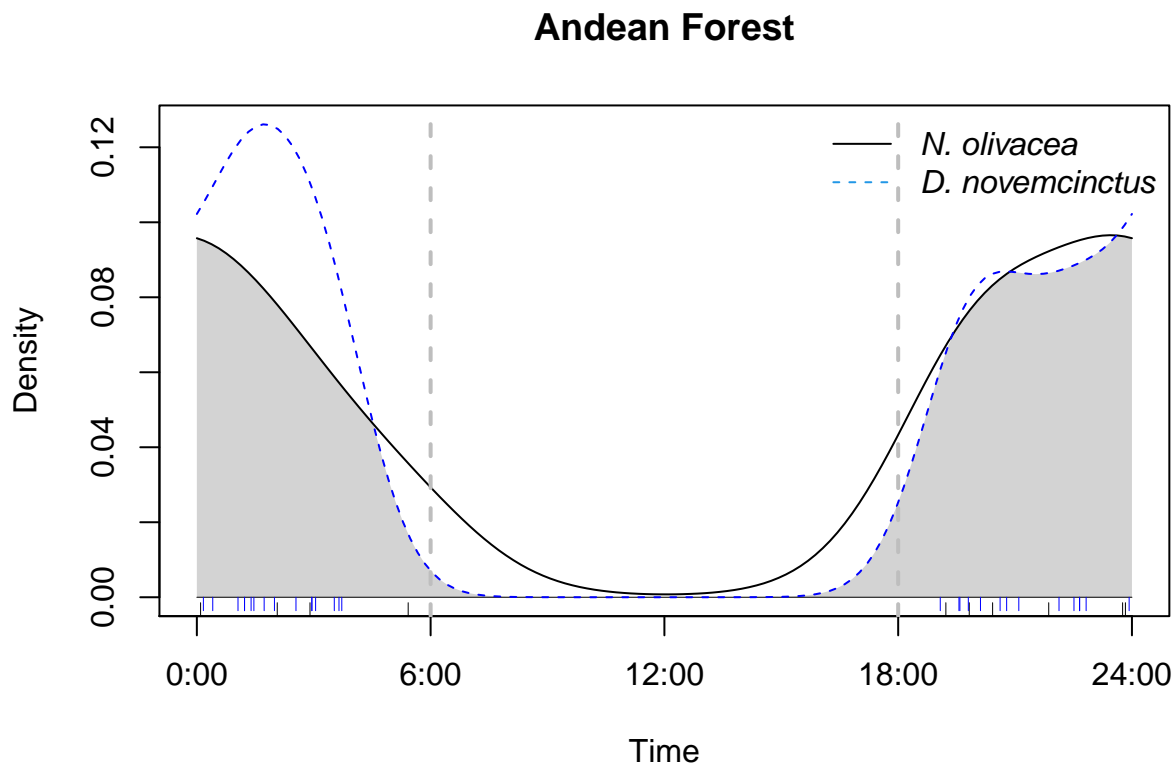
```
# ===== N. olivacea - D. novemcinctus, andean =====
#####overlap
```

```
overlapEst(nasuella_A, dasypus_A)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.8523122 0.8823674 0.9000000
```

```
#####plot activity overlap
```

```
overlapPlot(nasuella_A, dasypus_A, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. olivacea")),
                        expression(italic("D. novemcinctus"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Andean Forest")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```



```
##### overlap estimates by bootstrap
```

```
DasypusNasuella_overlapp_A <- bootEst(dasypus_bootA, nasuella_bootA, adjust = c(1, 1, 1))
dim(DasypusNasuella_overlapp_A)
```

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

```
DasypusNasuella_mean_A <- colMeans(DasypusNasuella_overlapp_A)
DasypusNasuella_mean_A
```

```
##      Dhat1      Dhat4      Dhat5
## 0.7411869 0.7261734 0.6449433
```

```
##### calculation of CI
```

```
DasypusNasuellaCI_A <- DasypusNasuella_overlapp_A[, 1]
bootCI(overlapEst(dasypus_A, nasuella_A)[1], DasypusNasuellaCI_A)
```

```
##           lower      upper
## norm    0.7729697 1.1539052
## norm0   0.6618444 1.0427800
## basic   0.7990330 1.1736002
## basic0  0.6421495 1.0167167
## perc    0.5310242 0.9055914
```

```
bootCIlogit(overlapEst(dasypus_A, nasuella_A)[1], DasypusNasuellaCI_A)
```

```
##           lower      upper
## norm    0.7906487 0.9690374
## norm0   0.6671919 0.9432242
## basic   0.7763895 0.9671197
## basic0  0.6808292 0.9475632
## perc    0.5310242 0.9055914
```

```
# ===== N. nasua - D. novemcinctus, andean =====
#####overlap
```

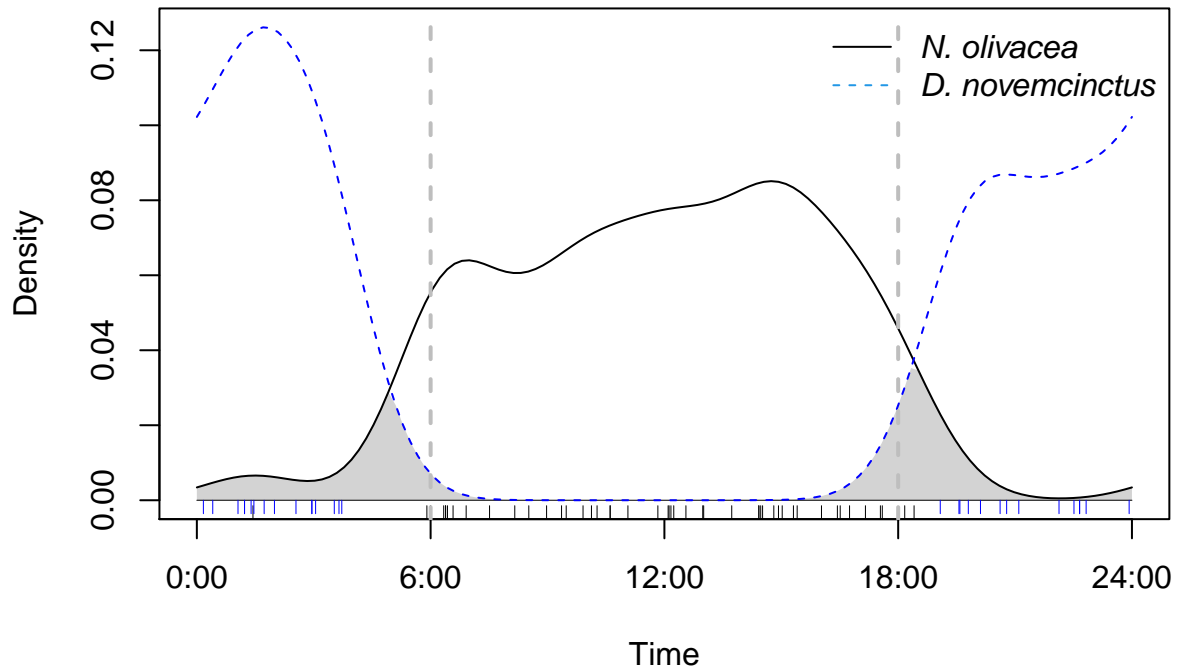
```
overlapEst(nasua_A, dasypus_A)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.11774214 0.07757358 0.04166667
```

```
#####plot activity overlap
```

```
overlapPlot(nasua_A, dasypus_A, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. olivacea")),
                      expression(italic("D. novemcinctus"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Andean Forest")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```

## Andean Forest



```
##### overlap estimates by bootstrap
```

```
DasypusNasua_overlapp_A <- bootEst(dasypus_bootA, nasua_bootA, adjust = c(1, 1, 1))
dim(DasypusNasua_overlapp_A)
```

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

```
DasypusNasua_mean_A <- colMeans(DasypusNasua_overlapp_A)
DasypusNasua_mean_A
```

```
##      Dhat1      Dhat4      Dhat5
## 0.2086849 0.1696278 0.1252058
```

```
##### calculation of CI
```

```
DasypusNasuaCI_A <- DasypusNasua_overlapp_A[, 1]
bootCI(overlapEst(dasypus_A, nasua_A)[1], DasypusNasuaCI_A)
```

```
##           lower      upper
## norm  -0.06998168 0.1235804
## norm0   0.02096108 0.2145232
## basic  -0.07387410 0.1188425
## basic0   0.02569897 0.2184156
## perc    0.11664173 0.3093584
```

```
bootCIlogit(overlapEst(dasypus_A, nasua_A)[1], DasypusNasuaCI_A)
```

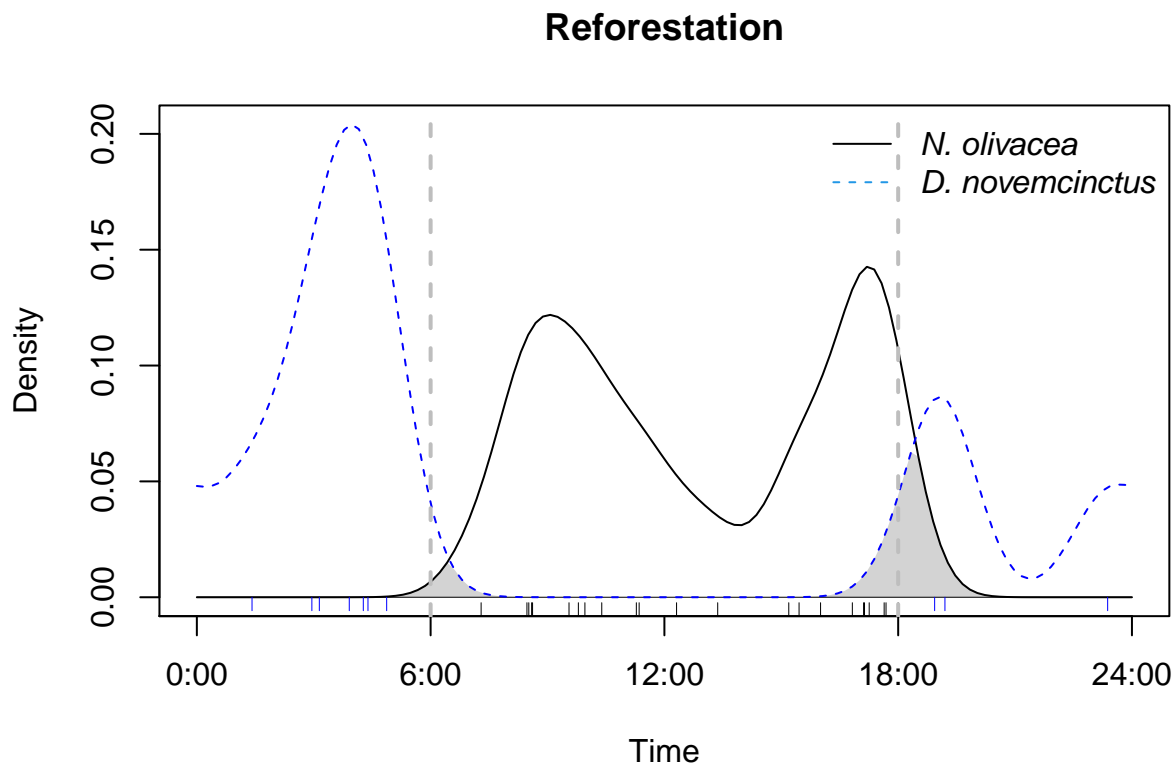
```
##           lower      upper
## norm  0.03643369 0.1130421
## norm0 0.06776480 0.1967973
## basic 0.03824105 0.1188515
## basic0 0.06427031 0.1889686
## perc  0.11664173 0.3093584
```

```
# ===== N. nasua - D. novemcinctus, reforestation =====
#####overlap
```

```
overlapEst(nasua_R, dasypus_R)
```

```
##      Dhat1      Dhat4      Dhat5
## 0.08438283 0.05279352 0.10000000
```

```
#####plot activity overlap
overlapPlot(nasua_R, dasypus_R, xscale = 24, main = "", rug = T)
legend("topright", c(expression(italic("N. olivacea")),
                        expression(italic("D. novemcinctus"))),
      lty = c(1,2), col = c(1,4), bty = "n")
title("Reforestation")
abline(v = 6, lty = "dashed", col = "gray", lwd = 2)
abline(v = 18, lty = "dashed", col = "gray", lwd = 2)
```



```
##### overlap estimates by bootstrap
```

```
DasypusNasua_overlapp_R <- bootEst(dasypus_bootR, nasua_bootR, adjust = c(1, 1, 1))  
dim(DasypusNasua_overlapp_R)
```

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

```
DasypusNasua_mean_R <- colMeans(DasypusNasua_overlapp_R)  
DasypusNasua_mean_R
```

```
##      Dhat1      Dhat4      Dhat5  
## 0.14890220 0.11599980 0.07939522
```

```
##### calculation of CI
```

```
DasypusNasuaCI_R <- DasypusNasua_overlapp_R[, 1]  
bootCI(overlapEst(dasypus_R, nasua_R)[1], DasypusNasuaCI_R)
```

```
##           lower      upper  
## norm    -0.12137951 0.1611064  
## norm0   -0.05686014 0.2256258  
## basic   -0.13262086 0.1473711  
## basic0  -0.04312479 0.2368672  
## perc     0.02139458 0.3013865
```

```
bootCIlogit(overlapEst(dasypus_R, nasua_R)[1], DasypusNasuaCI_R)
```

```
##           lower      upper  
## norm    0.01311505 0.1962173  
## norm0   0.02105005 0.2831498  
## basic   0.01930751 0.2797952  
## basic0  0.01333148 0.2104991  
## perc    0.02139458 0.3013865
```