Appendix S2: Estimating abundance with interruptions in data collection using open population spatial capture-recapture models Ecosphere

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This script performs a data set simulation and OPSCR modelling in the presence of sampling interruption with NIMBLE (NIMBLE Development Team 2019; Valpine et al. 2017). All details about the procedure are provided in Milleret et al. Estimating abundance with interruptions in data collection using open population spatial capture-recapture models. Ecosphere.

I. Load Libraries

```
library(rgdal)
library(raster)
library(rgeos)
library(sp)
library(nimble)
library(abind)
library(boot)
library(coda)
```

Download the .R data file Containing the R functions here, the Nimble functions here, here and here is the R script.

Set working directory where the *SourceRFunctions.R*, *SourceNimblePointProcess.R* and *SourceNimbleObservationModel.R* are located and source the files.

```
setwd("YourWorkingdirectory")
source("SourceRFunctions.R")
source("SourceNimblePointProcess.R")
source("SourceNimbleObservationModel.R")
```

II.SET SIMULATION PARAMETERS

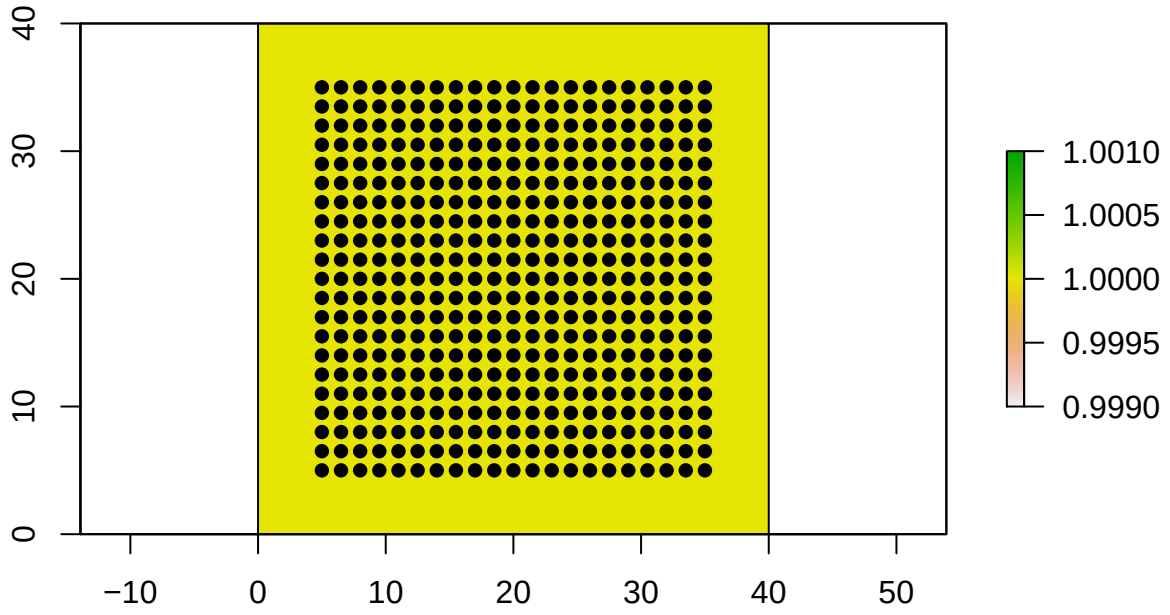
```
# HABITAT EXTENT
buffer <- 5
grid.size <- 30
# DETECTOR SPACING
detector.spacing <- 1.5
# DETECTION FUNCTION SURVEY CHARACTERISTICS
p0 <- 0.25          # p0 FOR THE HALFNORMAL DETECTION FUNCTION
```

```r
sigma <-  2         # SIGMA FOR THE HALFNORMAL DETECTION FUNCTION
n.occasions <- 5    # NB OCCASIONS

# POPULATION CHARACTERISTICS
N1 <- 50        # N INDIVIDUALS AT FIRST OCCASION
phi <- c(0.85) # SURVIVAL
rho <- c(0.15) # PER CAPITA RECRUITMENT
sd.phi <- c(0) # SD OF THE SURVIVAL (IF STOCHASTICITY)
sd.rho <- c(0) # SD OF THE PER CAPITA (IF STOCHASTICITY)
p.repro <- 1    # PROBABILITY OF INDIVIDUALS REPRODUCING (if = 1, ASSUME ALL INDIVIDUALS REPRODUCE)
tau <- 3 # TAU(DISPERSAL SIGMA)

# SAMPLING INTERUPTION
toggle.interuption <- c(1,1,1,1,1)# WHETHER INTERUPTION OCCUR (1) OR NOT (0) AT EACH OCCASION
# LEVEL OF AUGMENTATION
augmentation <- 1.2 # DATASET IS AUGMENTED BY N AUGMENTED INDIVIDUALS THAT EQUALS TO:
#SUPERPOPULATION SIZE * augmentation

# NIMBLE RUN CHARACTERISTICS
nburnin <- 2000    # BURN-IN
niter <- 10000      # N ITERATIONS
nchains <- 3       # N CHAINS
```

III.CREATE SIMULATED DATASET

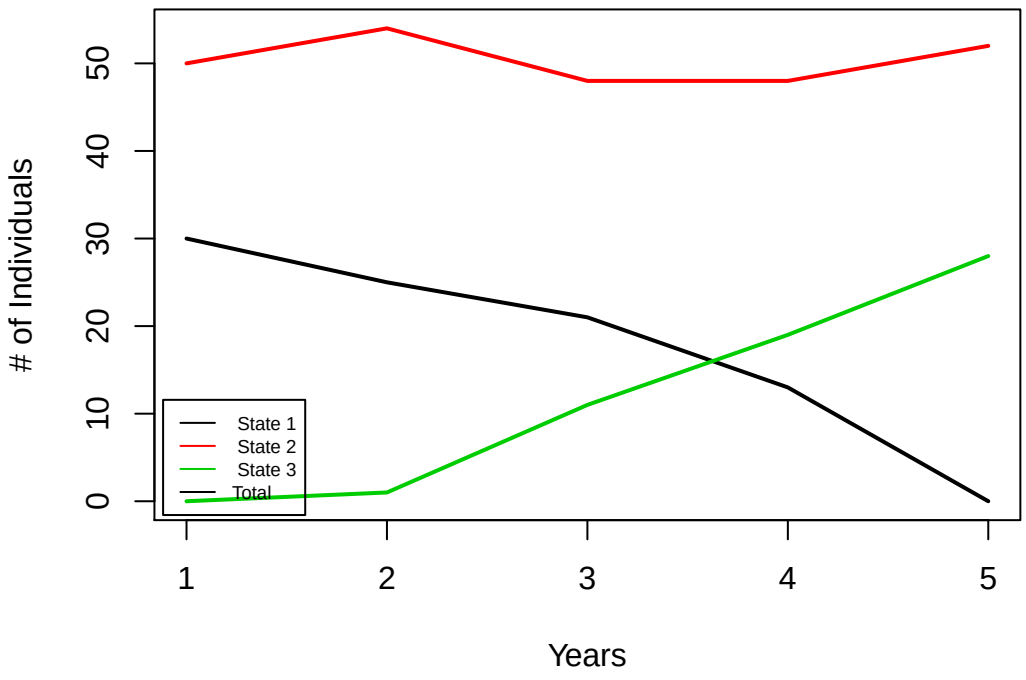
```r
### ==== 1.CREATE A SQUARE SPATIAL DOMAIN WHERE DETECTORS WILL BE PLACED  ====
coords <- matrix(c(0                    , 0                    ,
                   grid.size + buffer*2, 0                    ,
                   grid.size + buffer*2, grid.size + buffer*2,
                   0                    , grid.size + buffer*2,
                   0                    , 0
), ncol = 2, byrow = TRUE)

P1 <- Polygon(coords)
myStudyArea <-  SpatialPolygons(list(Polygons(list(P1), ID = "a")),
proj4string=CRS("+proj=utm +zone=33 +ellps=WGS84 +datum=WGS84 +units=m +no_defs"))
### ====  1.1. HABITAT OBJECTS  ====
r <- raster(nrow=4, ncol=4, xmn=0, xmx=grid.size + buffer*2, ymn=0, ymx=grid.size + buffer*2)

# HABITAT QUALITY VALUES, WE ASSUME HOMOGENEOUS HABITAT QUALITY
habitatQuality <- r[] <- 1
proj4string(r) <- CRS(proj4string(myStudyArea))
resolution <- res(r)
lowerCoords <- coordinates(r) - resolution/2
upperCoords <- coordinates(r) + resolution/2
habitatQuality <- r[]

### ==== 2.GENERATE DETECTORS  ====
co <- seq(buffer,grid.size+buffer, by=detector.spacing)
x <- rep(co, length(co))
y <- sort(rep(co, length(co)), decreasing = T)
detectors.xy <- cbind(x, y)
detectors.sp <- SpatialPoints(detectors.xy,
```

```
                                proj4string = CRS(proj4string(myStudyArea)))
# PLOT CHECK
plot(r)
plot(myStudyArea,add=T)
points(detectors.sp, col="black", pch=16)
```



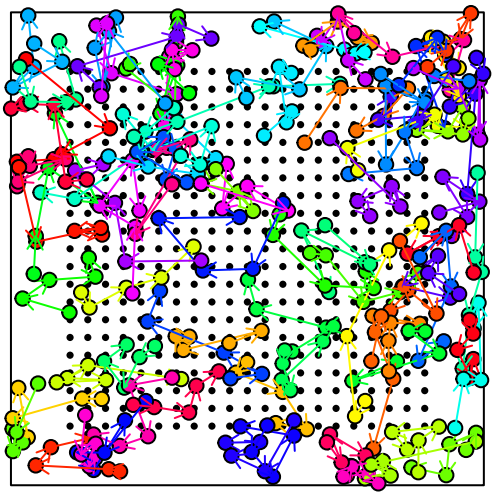

```
### ==== 3.SIMULATE INDIVIDUAL STATE MATRIX ===
### ====  3.1 DEFINE PHI AND RHO ARRAYS ====
# CREATE ARRAYS SO PHI AND RHO CAN VARRY OVER TIME AND STOCHASTICITY IN VITAL RATES CAN BE ADDED (t)
PHI.arr <- array(NA, c(2,2, n.occasions))
REPRO.arr <- array(NA, c(2,2, n.occasions))
FEC.mat <- matrix(NA, nrow=2, ncol=n.occasions)
phit <- 0
fect <- 0

for(t in 1:n.occasions){
   # DEFINE THE PHI MATRIX
   # two states: ALIVE/DEAD
   # DRAW PHI FROM NORMAL DISTRIB AND APPLY LOGIT
   phit[t]  <-   inv.logit(rnorm(1, mean=logit(phi), sd=sd.phi))
   PHI.arr[,,t] <-  matrix(c(phit[t]       , 0,
                             1-phit[t] , 1 ), ncol=2, nrow=2, byrow = TRUE)
   # DEFINE REPRO MATRIX (p of reproducing)
   # THIS DEFINES THE PROBABILITY OF INDIVIDUALS TO REPRODUCE (ASSUME ALL INDIVIDUALS REPRODUCE HERE)
   REPRO.arr[,,t] = matrix(c( p.repro, 0,
                              0      , 0 ), ncol=2, nrow=2, byrow = TRUE)
```

```
   # DEFINE PER CAPITA RECRUITMENT. GIVEN THAT INDIVIDUAL REPRODUCES, HOW MANY ARE RECRUITED
   fect[t] <-   inv.logit(rnorm(1, mean=logit(rho), sd=sd.rho))
   FEC.mat[,t] = c(fect[t], 0)
}



### ====  3.2 SIMULATE Z ====
z.mx <- SimulateZ( N0 = N1,
                       n.occasions = n.occasions-1,
                       PHI = PHI.arr,
                       REPRO = REPRO.arr,
                       FEC = FEC.mat,
                       init.state = 1)
myZ <- z.mx$z
# ADD THE NOT ENTERED STATE
# 1: NOT ENTERERD
# 2: ALIVE
# 3: DEAD
myZ <- myZ+1
myZ[is.na(myZ)] <- 1

# GET POP COMPOSITION AND PLOT IT
z.levels <- unique(na.omit(unlist(apply(myZ, 1, unique))))
z.levels <- z.levels[order(z.levels)]
Pop.Compo <- list()
for(l in 1:length(z.levels)){
   Pop.Compo[[l]] <- apply(myZ, 2, function(x){length(which(x == z.levels[l]))})
}#l

# PLOT CHECK
plot(1:dim(myZ)[2], Pop.Compo[[1]], type="l", col=1, lwd=2,
     ylim=c(0, max(unlist(Pop.Compo))),
     xlab = "Years", ylab = "# of Individuals")

for(l in 2:length(Pop.Compo)){
   points(1:dim(myZ)[2],Pop.Compo[[l]], type="l", col=l, lwd=2)
}#l
legend("bottomleft"
       , legend =  c(unlist(lapply(z.levels, function(x){paste(" State", x)})), "Total")
       , col = 1:length(Pop.Compo)
       , lwd = 1
       , cex = 0.6
       , inset = 0.01)
```




```
### ==== 4.SIMULATE INDIVIDUAL AC LOCATIONS ====
### ====  4.1 FIRST OCCASION ====
# CREATE EMPTY OBJECTS
mySimulatedACs <- list()
tempCoords <- matrix(NA,nrow=dim(myZ)[1], ncol=2)

# SIMULATE UNIFORM LOCATION OF ACS
for(i in 1:dim(myZ)[1]){
   tempCoords[i,] <- rbinomPPSingle(
     n = 1
, lowerCoords = lowerCoords
, upperCoords = upperCoords
, intensityWeights = habitatQuality
, areAreas = 1
, numWindows = nrow(lowerCoords)
   )
}#i

# STORE ACS IN A SP OBJECT
mySimulatedACs[[1]] <- SpatialPointsDataFrame( tempCoords
                                               , data.frame( x = tempCoords[, 1]
                                                           , y = tempCoords[, 2]
                                                           , Id = 1:nrow(tempCoords))
                                               , proj4string = CRS(proj4string(r)))
### ====  4.2 FOLLWOWING YEARS ====
# DRAW SUBSEQUENT INDIVIDUAL ACS FROM A NORMAL DISTRIBUTION CENTERED AROUND THE SOURCE COORDINATE
```

```
# WITH A SD EQUAL TO "tau"
# THERE IS THE POSSIBILITY TO DEFINE A HABITAT QUALITY SURFACE
# FOR THE PUPORSE OF THE STUDY, HABITAT QUALITY WAS UNIFORM (SET TO 1 EVERYWHERE)
for(t in 2:dim(myZ)[2]){
   for(i in 1:nrow(tempCoords)){
      tempCoords[i,]  <- rbinomMNormSourcePPSingle(
          n = 1
        , lowerCoords = lowerCoords
        , upperCoords = upperCoords
        , sourceCoords = tempCoords[i,]
        , normSD = tau
        , intensityWeights = habitatQuality
        , areAreas = 1
        , numWindows = nrow(lowerCoords)
      )
   }
   # STORE ACS IN A SP OBJECT
   mySimulatedACs[[t]] <- SpatialPointsDataFrame(
     tempCoords
    , data.frame( x = tempCoords[, 1]
                , y = tempCoords[, 2]
                , Id = 1:nrow(tempCoords))
    , proj4string = CRS(proj4string(mySimulatedACs[[t-1]]))
   )
}#t

# PLOT CHECK
plot(aggregate(rasterToPolygons(r,fun = function(x){x>0})))
points(detectors.sp, pch=16, cex=0.5)
col <- rainbow(length(mySimulatedACs[[1]]))
points(mySimulatedACs[[1]], pch=21, bg=col)

for(t in 2:length(mySimulatedACs)){
   points(mySimulatedACs[[t]], pch=21, bg=col)
   arrows( x0 = coordinates(mySimulatedACs[[t]])[ ,1]
           , x1 = coordinates(mySimulatedACs[[t-1]])[ ,1]
           , y0 = coordinates(mySimulatedACs[[t]])[ ,2]
           , y1 = coordinates(mySimulatedACs[[t-1]])[ ,2], col = col, length = 0.08)
}#t
```



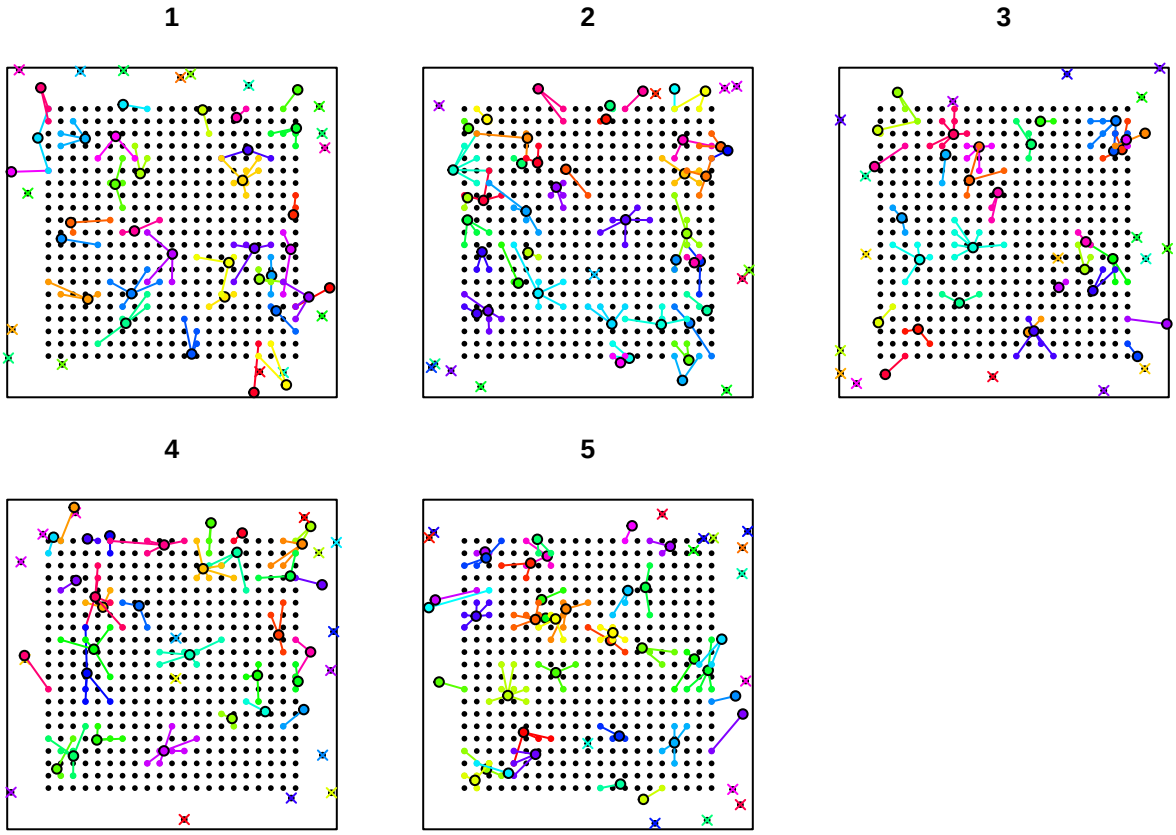
```
### ==== 5.SIMULATE DETECTION ====
### ====  5.1 DETECTION ARRAY ====
z.not.alive <- apply(myZ, 2, function(x){which(x %in% c(1,3))})
Y <- array(NA, c(dim(myZ)[1], length(detectors.sp), dim(myZ)[2]))

for(t in 1:dim(myZ)[2]){
   D <- gDistance(detectors.sp, mySimulatedACs[[t]], byid=TRUE)
   # OBTAIN Y DETECTION MATRIX USING HALF NORMAL DETECTION FUNCTION (EQN 7 IN MAIN TEXT)
   fixed.effects <- rep(log(p0), length(detectors.sp))
   pzero <- exp(fixed.effects)
   p <- pzero * exp(-D*D/(2*sigma*sigma))
   Y[,,t] <- apply(p, c(1,2), function(x) rbinom(1, 1, x))
   # individuals not alive can't be detected
   Y[z.not.alive[[t]],,t] <- 0

}#t
### ====  5.1 PLOT CHECK ====
par(mfrow=c(2,3), mar=c(0,0,3,0))
for(t in 1:dim(myZ)[2]){
   plot(myStudyArea)
   title(t)
   points(detectors.sp, pch=16, cex=0.6)
   detections <- apply(Y[,,t],1, function(x) which(x>0))
   col <- rainbow(dim(Y)[1])[sample(dim(Y)[1])]
   for(i in 1:length(detections)){
      if(!i %in% z.not.alive[[t]]){
```

```
         if(length(detectors.sp[detections[[i]],])==0){
            points(mySimulatedACs[[t]][i,],bg=col[i], pch=21, cex=0.5)
            points(mySimulatedACs[[t]][i,], col=col[i], pch=4)

         }else{
            points(detectors.sp[detections[[i]],],col=col[i], pch=16, cex=0.7)
            ac <- coordinates(mySimulatedACs[[t]][i,])
            dets <- coordinates(detectors.sp[detections[[i]],])
            segments(x0=ac[1,1], x1=dets[,1] , y0=ac[1,2], y1=dets[,2], col=col[i])
            points(mySimulatedACs[[t]][i,],bg=col[i], pch=21)

         }#else
      }#if
   }#i
}#t

### ==== 6.AUGMENT DATA SET ====
# REMOVE UNDETECTED IDS
detected.time <- apply(Y, c(1,3), function(x) any(x >= 1))
detected <- apply(detected.time, c(1), function(x) sum(x==1)>0)
Y <- Y[detected,,]

#AUGMENTATION=  "augmentation" x N OF THE SUPER POPULATION
y.aug <- array(0,c(  nrow(myZ)*augmentation - dim(Y)[1] ,dim(Y)[2:3]))
y <- abind(Y , y.aug, along = 1)
dim(y)
```

```
## [1]  96 441   5
```

```
### ==== 7.ADD INTERUPTION ====
interuptions <- which(toggle.interuption==0)
if(length(interuptions)>0){
   # ZERO DETECTIONS DURING INTERUPTIONS
   y[,,interuptions] <- 0
}

### ==== 8.RECONSTRUCT z VALUES ====
z <- apply(y, c(1,3), function(x) any(x>0))
z <- ifelse(z, 2, NA)

z <- t(apply(z, 1, function(zz){
   if(any(!is.na(zz))){
      range.det <- range(which(!is.na(zz)))
      zz[range.det[1]:range.det[2]] <- 2
   }
   return(zz)
}))

### ==== 9.GENERATE z INITIAL values====
z.init <- t(apply(z, 1, function(zz){
   out <- zz
   out[] <- 1
   if(any(!is.na(zz))){
      range.det <- range(which(!is.na(zz)))
```

```
      if(range.det[1]>1)zz[1:(range.det[1]-1)] <- 1
      if(range.det[2]<length(zz))zz[(range.det[2]+1):length(zz)] <- 3
      out[] <- zz
   }
   return(out)
}))

z.init <- ifelse(!is.na(z), NA, z.init)
```



III.NIMBLE

```
### ==== 1.MODEL CODE ====
modelCode <- nimbleCode({
  ##-------------------------------------------------------------------------------
  ##-----------------------------##
  ##------ SPATIAL PROCESS ------##
  ##-----------------------------##
  tau ~ dgamma(0.001, 0.001)

  for(i in 1:n.individuals){
    sxy[i, 1:2, 1] ~ dbinomPPSingle(lowerHabCoords[1:n.cells, 1:2],
                                    upperHabCoords[1:n.cells, 1:2],
                                    mu[1:n.cells], 1, n.cells)
    for(t in 2:n.years){
      sxy[i, 1:2, t] ~ dbinomMNormSourcePPSingle(lowerHabCoords[1:n.cells, 1:2]
```

```
                                                    , upperHabCoords[1:n.cells, 1:2]
                                                    , sxy[i, 1:2, t - 1]
                                                    , tau
                                                    , mu[1:n.cells]
                                                    , 1
                                                    , n.cells,-1)

  }#t
}#i


##------------------------------------------------------------------------------
##------------------------------##
##----- DEMOGRAPHIC PROCESS -----##
##------------------------------##
psi ~ dunif(0, 1)
phi ~ dunif(0, 1)
rho ~ dunif(0, 5)
for (t in 2:n.years) {
  gamma[t - 1] <- (N[t - 1] * rho)/n.available[t - 1]
} #t
omeg1[1] <- 1 - psi
omeg1[2] <- psi
omeg1[3] <- 0
for (t in 1:(nyears1)) {
  # NOT ENTERED
  omega[1, 1, t] <- 1 - gamma[t]
  omega[1, 2, t] <- gamma[t]
  omega[1, 3, t] <- 0
  # ALIVE
  omega[2, 1, t] <- 0
  omega[2, 2, t] <- phi
  omega[2, 3, t] <- 1 - phi
  # DEAD
  omega[3, 1, t] <- 0
  omega[3, 2, t] <- 0
  omega[3, 3, t] <- 1
} #t
for (i in 1:n.individuals) {
  z[i, 1] ~ dcat(omeg1[1:3])
  for (t in 1:(nyears1)) {
    z[i, t + 1] ~ dcat(omega[z[i, t], 1:3, t])
  } #t
}

##------------------------------------------------------------------------------
##------------------------------##
##----- DETECTION PROCESS -----##
##------------------------------##
sigma ~ dunif(0,5)
p0 ~ dunif(0,1)
for(i in 1: n.individuals){
  for(t in 1:n.years){
```

```
      y[i,1:nMaxDetectors,t] ~ dbin_LESSCachedAllSparse(
        pZero = p0 * toggle[t]
      , sxy = sxy[i,1:2,t]
      , sigma = sigma
      , nbDetections[i,t]
      , yDets = yDets[i,1:nMaxDetectors,t]
      , detector.xy =  detector.xy[1:n.detectors,1:2]
      , trials = trials[1:n.detectors]
      , detectorIndex = detectorIndex[1:n.cellsSparse,1:maxNBDets]
      , nDetectorsLESS = nDetectorsLESS[1:n.cellsSparse]
      , ResizeFactor = ResizeFactor
      , maxNBDets = maxNBDets
      , habitatID = habitatIDDet[1:y.maxDet,1:x.maxDet]
      , maxDist = maxDist
      , indicator = z[i,t]==2)
    }#t
  }#i


  ##------------------------------------------------------------------------
  ##---------------------------------------##
  ##---------- DERIVED PARAMETERS ----------##
  ##---------------------------------------##
  for(t in 1:n.years){
    N[t] <- sum(z[1:n.individuals, t]==2)
    n.available[t] <- sum(z[1:n.individuals, t]==1)
  }#t
})

### ==== 2.NIMBLE DATA ====
nimDims <- list(  "omeg1" = 3
                , "omega" = c(3,3,4)
                , "z" = c(dim(y)[1], dim(y)[3]))

params <- c("N", "tau"
            ,"p0", "phi", "sigma","rho","z","sxy")


nimConstants <- list( n.individuals = dim(y)[1]
                    , n.detectors = dim(y)[2]
                    , n.years = dim(y)[3]
                    , nyears1 = dim(y)[3]-1
                    , n.cells = nrow(lowerCoords))


myScaledDetectors  <- UTMToGrid(grid.sp = SpatialPoints(coordinates(r)),
                                data.sp = detectors.sp,
                                plot.check = F)


nimData <- list( z = z
                , y = y
                , toggle = toggle.interuption
```

```
                  , detector.xy = myScaledDetectors$data.scaled.xy
                  , lowerHabCoords = myScaledDetectors$grid.scaled.xy - 0.5
                  , upperHabCoords = myScaledDetectors$grid.scaled.xy + 0.5
                  , mu = habitatQuality)

sxy <- MakeInitsXY(  y= y
                     , detector.xy = detectors.xy
                     , habitat.r = r
                     , dist.move = 3)

for( t in 1:dim(sxy)[3]){
  sxy[,,t] <- UTMToGrid(grid.sp = SpatialPoints(coordinates(r)),
                        data.sp = SpatialPoints(sxy[,,t]),
                        plot.check = F
  )$data.scaled.xy
}


nimInits <- list(z = z.init, rho = rho, phi = phi, sigma = sigma,
                 psi = 0.1, p0 = p0, sxy = sxy, tau = tau)
```

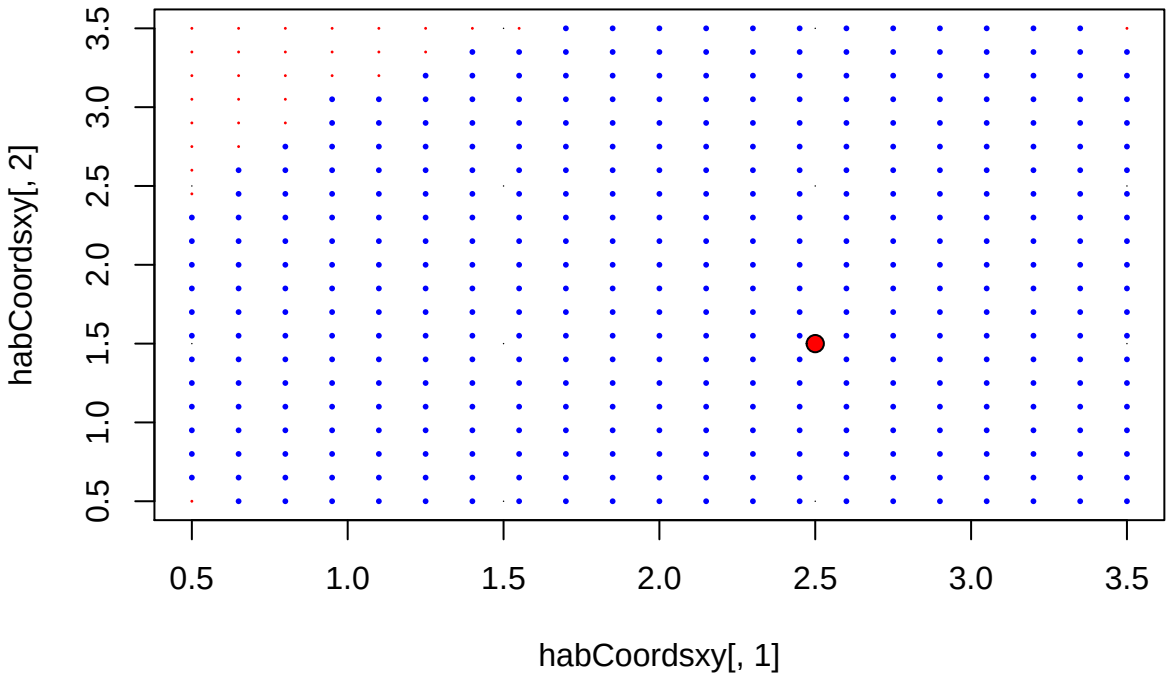
III.NIMBLE TRICKS

Here we need to create a few objects that are necessary to make the computation of OPSCR models more efficient. The first step consists in performing a local evaluation of the state space (LESS) (Milleret et al. 2019). This means that detectors that are further away than a certain distance from a given individual activity center are not evaluated. If the distance threshold is large enough, it should not cause any bias (see Milleret et al. (2019) for further details).

The function GetDetectorIndex identifies the set of detectors that are within a certain distance from each habitat cell center. The distance value should be large enough so that for any particular individual, the sxy values of the initial activity center restrict the calculation of p0 to all detectors with positive detections. Here, we use maxDist=2.2.

When the dimensions of the habitat matrix is large, we can resize it to lower dimensions. This may help reducing the number of habitat cells for which we have to identify the set of detectors that are within a certain distance from the cell center. The ResizeFactor argument which corresponds to the the fact argument used internally in raster::disaggregate. The goal is to create the object DetectorIndex$detectorIndex of the smallest dimension possible.

```
### ==== 1. CREATE CACHED DETECTORS OBJECTS ====
DetectorIndexLESS <- GetDetectorIndexLESS(habitat.mx = as.matrix(r),
                                          detectors.xy = myScaledDetectors$data.scaled.xy,
                                          maxDist = 2.2,
                                          ResizeFactor = 1,
                                          plot.check = TRUE)
```




```
nimConstants$maxNBDets <- DetectorIndexLESS$maxNBDets
nimConstants$y.maxDet <- dim(DetectorIndexLESS$habitatID)[1]
nimConstants$x.maxDet <- dim(DetectorIndexLESS$habitatID)[2]
nimData$detectorIndex<- DetectorIndexLESS$detectorIndex
nimData$habitatIDDet<- DetectorIndexLESS$habitatID

nimData$nDetectorsLESS <- DetectorIndexLESS$nDetectorsLESS
nimConstants$n.cellsSparse <- dim(DetectorIndexLESS$detectorIndex)[1]
nimConstants$ResizeFactor <- DetectorIndexLESS$ResizeFactor
nimConstants$maxDist <- 2.2
```

Last, we re-express the detection matrix y to reduce its size. We use a new representation, where each row (corresponding to one individual) contains the detector identification numbers (values of j) which detected that individual.

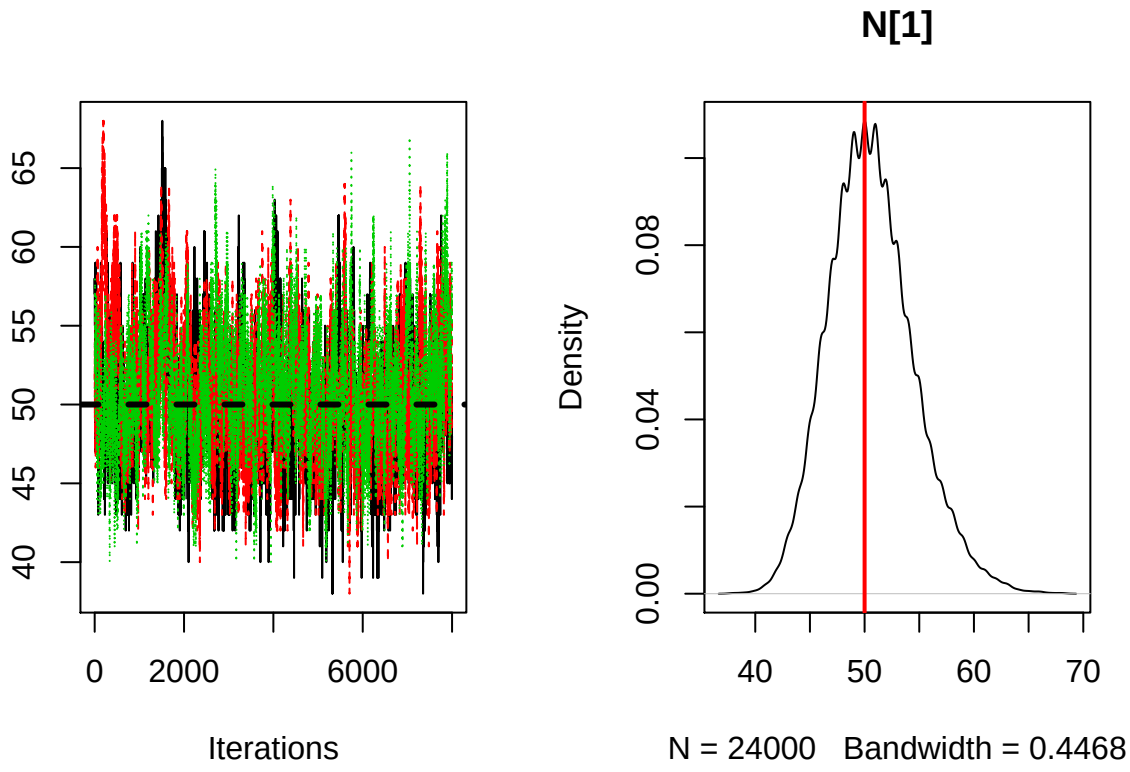
A second matrix of identical dimension was also created, containing the number of detections occurring at each detector. The second matrix would be necessary for modelling non-binary detections.

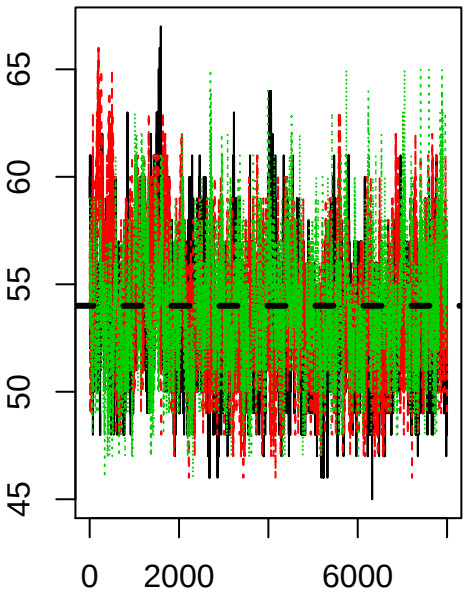
```
### ==== 2. CREATE SPARSE MATRICES ====

SparseY <- GetSparseY(nimData$y)


# ADD TO NIMDATA
nimData$y = SparseY$y ## Detection array
nimData$yDets = SparseY$yDets
nimData$nbDetections = SparseY$nbDetections
```

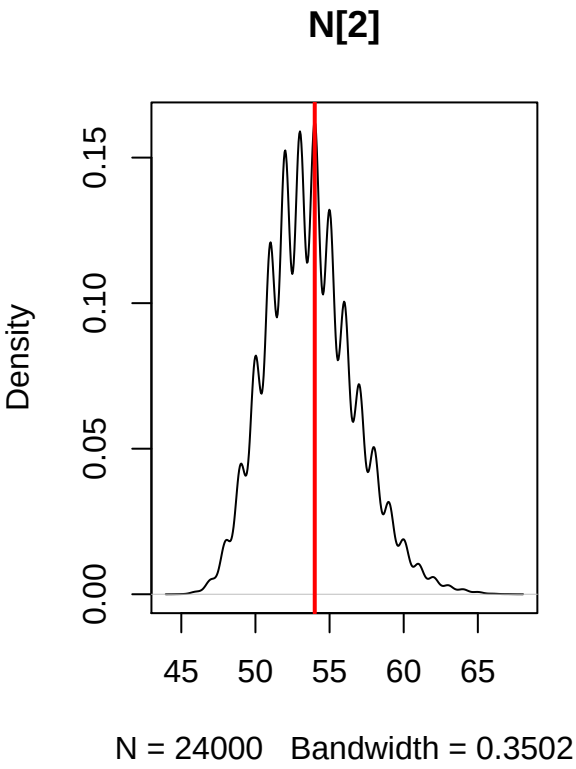
```
nimData$trials = rep(1, nimConstants$n.detectors)

nimConstants$nMaxDetectors = SparseY$nMaxDetectors
```

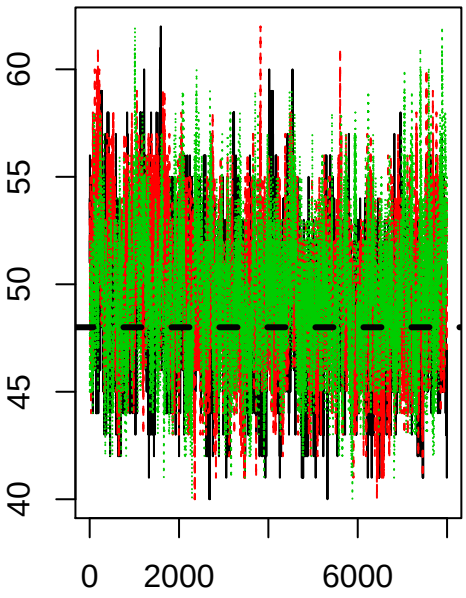
V.PLOT OUTPUT

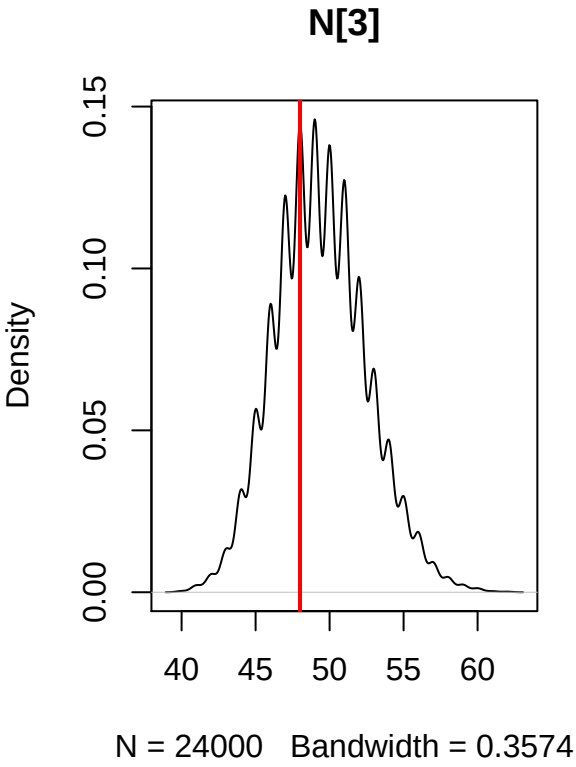
```
# N
for(t in 1:n.occasions){
  PlotParams(myNimbleOutput, params= paste("N[",t,"]", sep=""), sim.values=Pop.Compo[[2]][t])
}
```

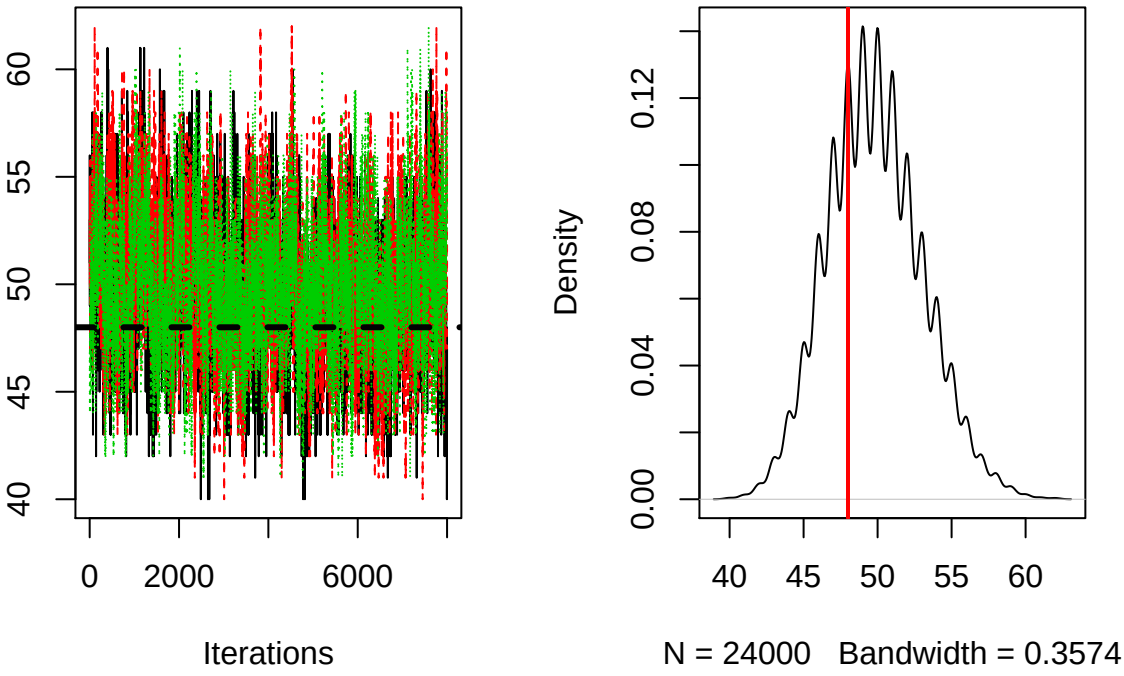


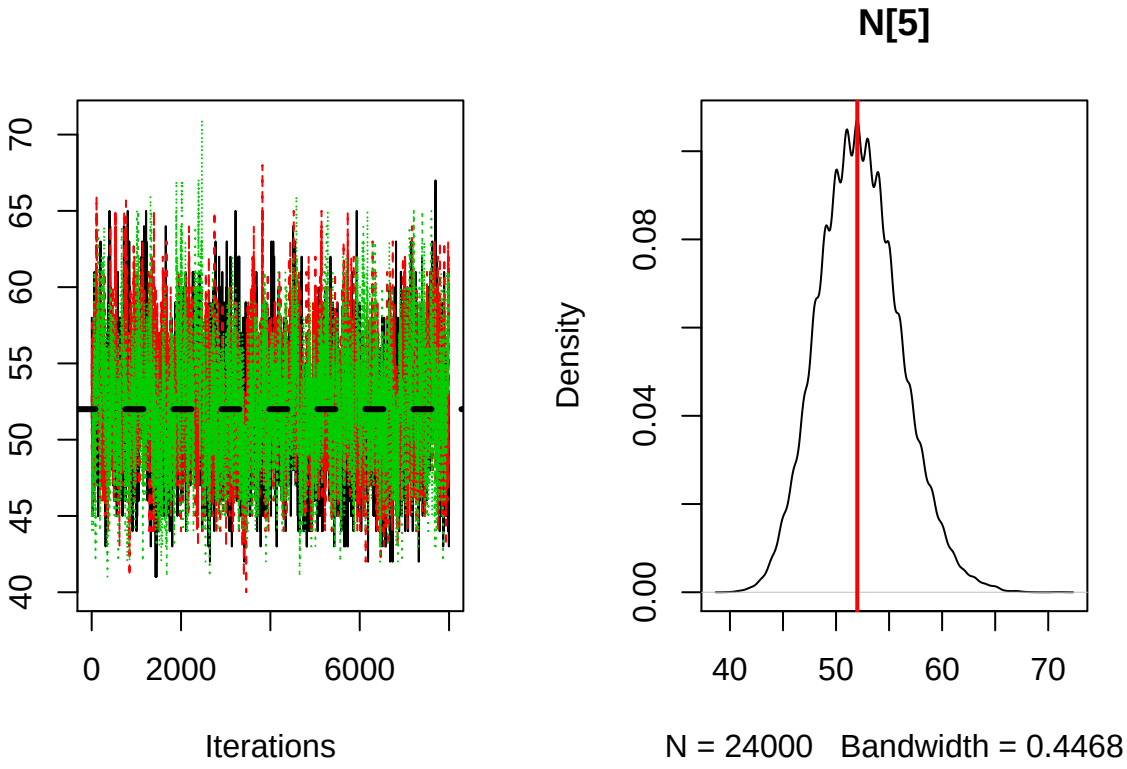

45
50
55
60
65
0
2000
6000
Iterations


N[2]
Density
0.00
0.05
0.10
0.15
45
50
55
60
65
N = 24000 Bandwidth = 0.3502

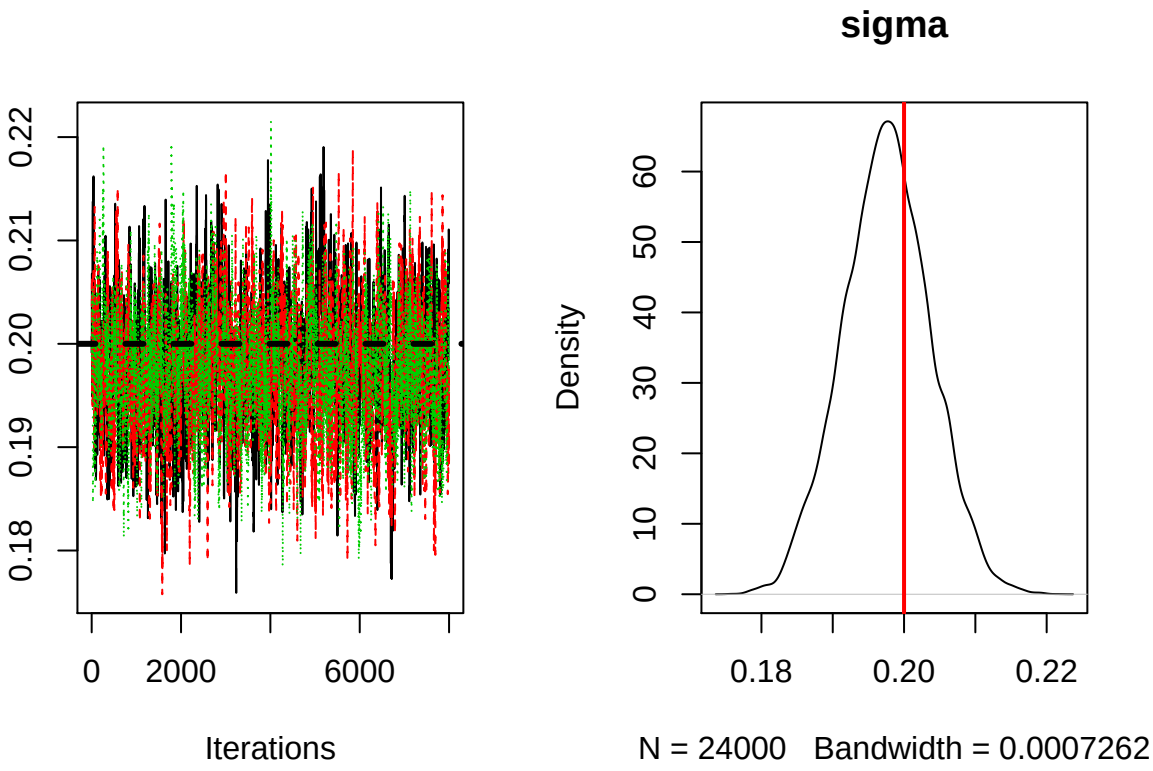

40
45
50
55
60
0
2000
6000
Iterations


N[3]
Density
0.00
0.05
0.10
0.15
40
45
50
55
60
N = 24000 Bandwidth = 0.3574

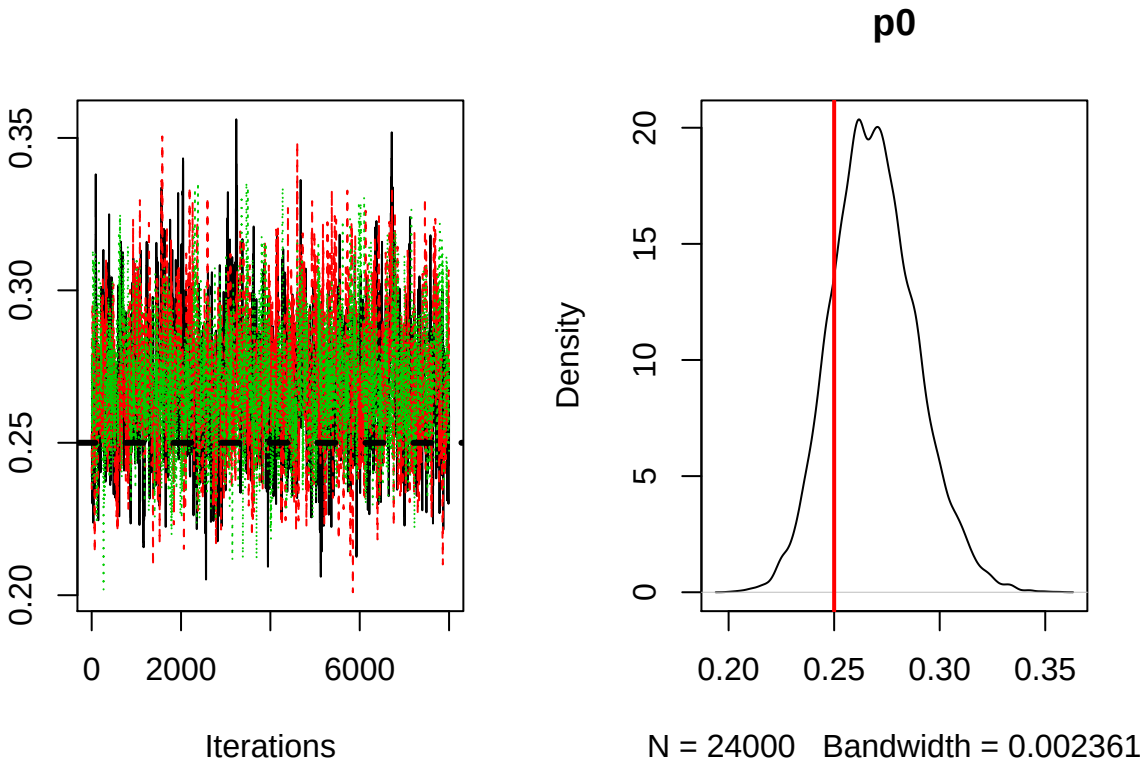

N[4]
40
45
50
55
60
0
2000
6000
Iterations
Density
0.00
0.04
0.08
0.12
40
45
50
55
60
N = 24000 Bandwidth = 0.3574



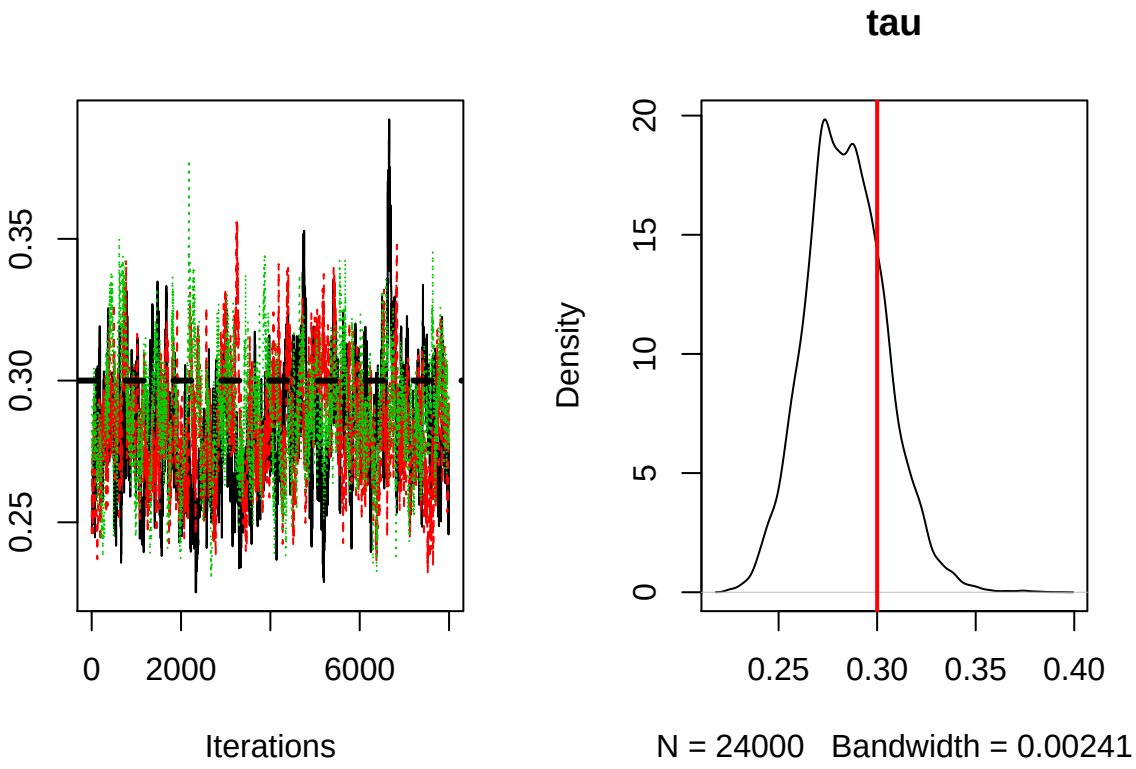

```
# SIGMA
PlotParams(myNimbleOutput, params= "sigma", sim.values=sigma/res(r))
```



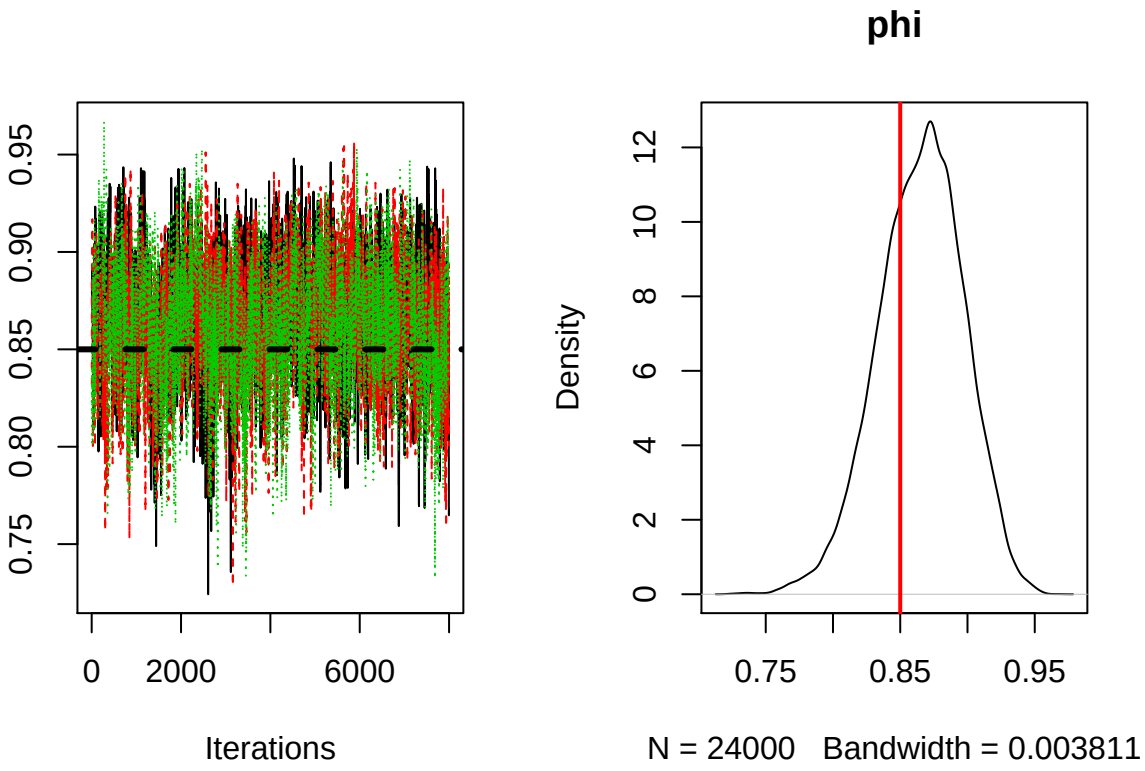

```
# p0
PlotParams(myNimbleOutput, params= "p0", sim.values=p0)
```



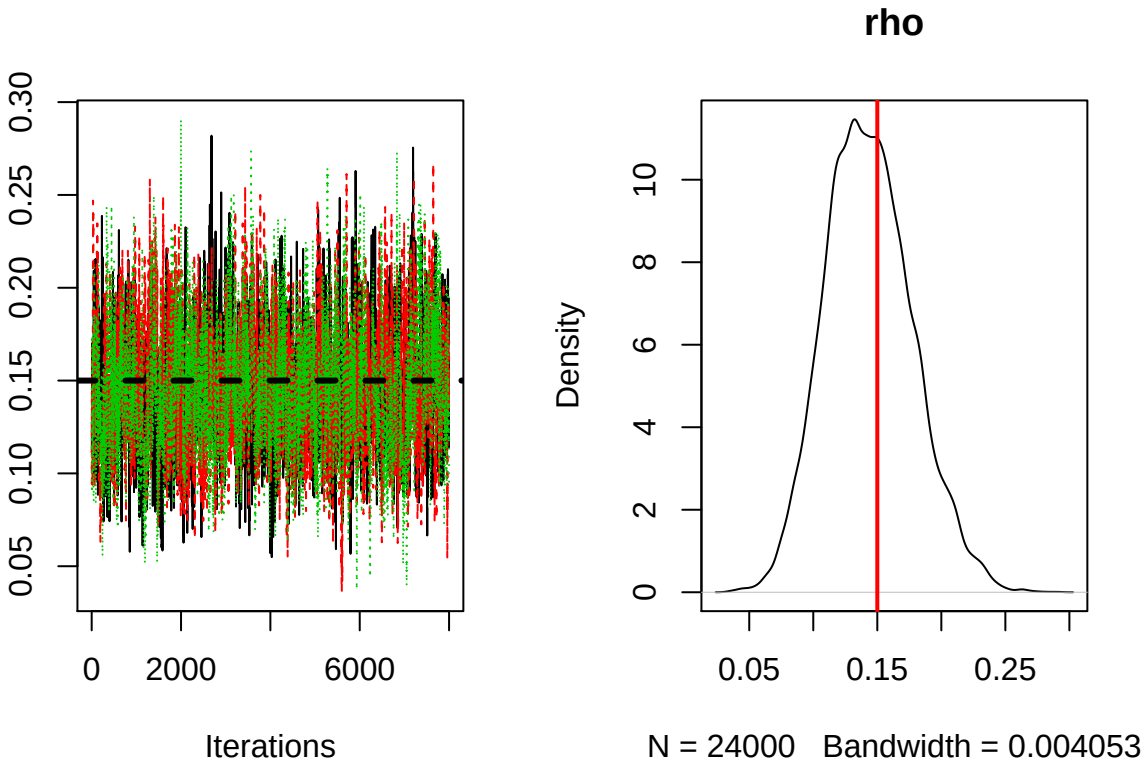

```
# tau
PlotParams(myNimbleOutput, params= "tau", sim.values=tau/res(r))
```




```
# phi
PlotParams(myNimbleOutput, params= "phi", sim.values=phi)
```




```
# rho
PlotParams(myNimbleOutput, params= "rho", sim.values=rho)
```



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