Capture-Recapture with Bayesian statistics

Loreleï Guéry

July 2020

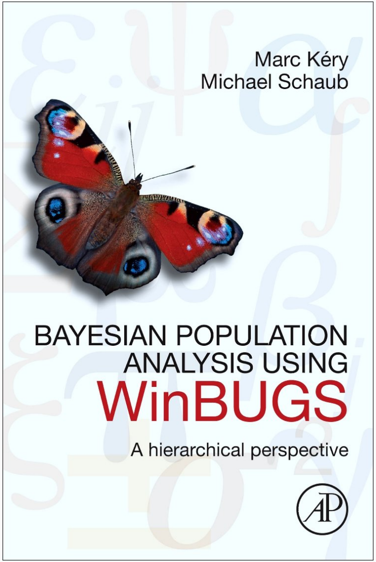
Slides, codes and data

- All material prepared with `R`.
- `R Markdown` used to write reproducible material.
- Material available via Github here.

Credits

- Workshops material shared by Andy Royle and the Biometrics Working Group there or there
- Materials shared by Olivier Gimenez, Murray Efford and Andy Royle here and there

The Bibles

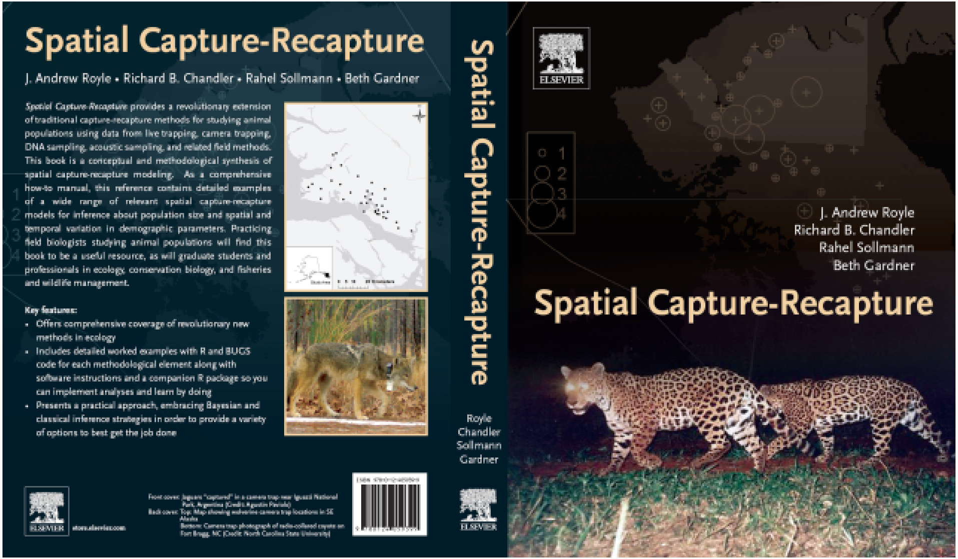


Marc Kéry
Michael Schaub

BAYESIAN POPULATION ANALYSIS USING WinBUGS

A hierarchical perspective

The Bibles



Spatial Capture-Recapture

J. Andrew Royle • Richard B. Chandler • Rahel Sollmann • Beth Gardner

Spatial Capture-Recapture provides a revolutionary extension of traditional capture-recapture methods for studying animal populations using data from live trapping, camera trapping, DNA sampling, acoustic sampling, and related field methods. This book is a conceptual and methodological synthesis of spatial capture-recapture modeling. As a comprehensive how-to manual, this reference contains detailed examples of a wide range of relevant spatial capture-recapture models for inference about population size and spatial and temporal variation in demographic parameters. Practicing field biologists studying animal populations will find this book to be a useful resource, as will graduate students and professionals in ecology, conservation biology, and fisheries and wildlife management.

Key features:

- Offers comprehensive coverage of revolutionary new methods in ecology
- Includes detailed worked examples with R and BUGS code for each methodological element along with software instructions and a companion R package so you can implement analyses and learn by doing
- Presents a practical approach, embracing Bayesian and classical inference strategies in order to provide a variety of options to best get the job done

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Front cover: Jaguars "captured" in a camera trap near Iguazú National Park, Argentina (Credit: Agustin Paviolo)
Back cover: Top: Map showing wolverine camera trap locations in SE Alaska
Bottom: Camera trap photograph of radio-collared coyote on Fort Bragg, NC (Credit: North Carolina State University)

ISBN [illegible]

Spatial Capture-Recapture

Royle
Chandler
Sollmann
Gardner

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Spatial Capture-Recapture

Outline

- Bayesian Capture-Recapture models in closed population
    - Example 1: Fit Model M0 to the bear data using JAGS and data augmentation
    - Example 2: Fit Model M0 to the bear data using MLE

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- Bayesian Capture-Recapture models in closed population
  - Example 1: Fit Model M0 to the bear data using JAGS and data augmentation
  - Example 2: Fit Model M0 to the bear data using MLE
- Spatially Explicit Capture Recapture (SECR) models in closed population
  - Example 3: Fit a basic SECR model in closed population with data augmentation
  - Example 4: Imagine an application of SECR to tuna fisheries

JAGS R Packages

Many different packages can be used to run JAGS from R such as:

- rjags
- jagsUI
- R2jags

SECR R Packages

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- secr developped by Murray Efford using MLE
- oSCR developed by Chris Sutherland, Andy Royle, and Dan Linden

Bayesian Capture-Recapture models in closed population

Capture-recapture, quésako?

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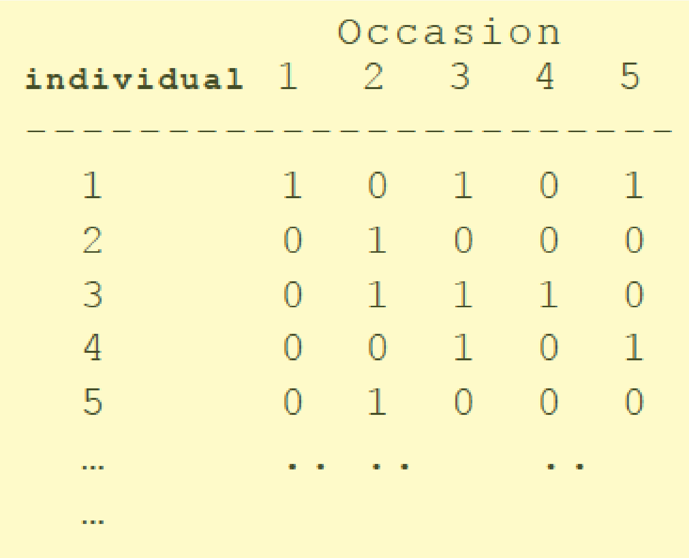
- Only a sample of individuals n is observed due to an encounter or detection probability p.
- To estimate or model p, studies to generate encounter history information are conducted.
- The statisitcal models to describe these encounter histories are capture-recapture (CR) models.

Individual encounter probability



	Occasion				
individual	1	2	3	4	5
1	1	0	1	0	1
2	0	1	0	0	0
3	0	1	1	1	0
4	0	0	1	0	1
5	0	1	0	0	0
...	. .	. .		. .	
...					

Starting point of CR

- Random sampling of individuals: detection is a Bernoulli trial (binomial distribution).

$$Pr(y_{ik} = 1) \sim Bernoulli(p_{ik})$$

```r
# Simulating Bernoulli trials
# Simulate random encounter events with p = 0.25 for an individual
# Outcome y = 1 means "captured" and y=0 means "not captured"
p <- 0.25
K <- 4 # sample occasions
# one encounter history
set.seed(1987)
rbinom(n=K, size=1, prob=p)
#> [1] 0 1 0 0
```

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- Random sampling of individuals: detection is a Bernoulli trial (binomial distribution).
- CR models are, one way or another, logistic regression models or GLMs where N is unknown.

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- Status of individuals is not known. You don't observe "all zero encounter histories".
- Initial CR models developped for geographically closed populations.
- Heterogeneity in p is important (bias in N) and CR models are all about modeling variation in p (Otis *et al.* 1978)

Classical closed population

- Demographic closure (no births, no deaths) and geographical closure (no entry, no exit)

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- Closed models characterization (Otis *et al.* 1978):
  - M0 = “the null model”, p is constant in all dimensions
  - Mt = p is a function of sample occasion , p(t)
  - Mb = behavioral response model. Trap happiness or shyness
  - Mh = individual heterogeneity
  - Mbt = time + behavior, or time*behavior
  - Mbh, Mth, Mbth

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- See Kery and Schaub (2012) Chapter 6 to go further

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- The main assumptions are:
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  - Encounters are independent among and within individuals
- Encounter observations are Bernoulli random variables
- Close to a binomial GLM or logistic regression but where N, size of some ideal data set, is unknown

Inference in closed population models

- Likelihood inference:
  - `R`: write custom likelihood function use `nlm()` or `optim()`
  - black box programs: e.g., Program MARK/RMark/ESURGE

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- Bayesian inference:
  - `R`: write a custom sampler
  - BUGS/JAGS
  - Stan, etc.

N unknown, so what?

- If N is known, Model M0 is a logistic regression.

```
model{
  p ~ dunif(0,1)
  for (i in 1:N){
    y[i] ~ dbin(p,K)
  }
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- Because N would be a parameter of the model and would be updated in the MCMC algorithm. The size of the data set would have to change, which is not possible with JAGS.

Data augmentation (DA), see Royle and Dorazio paper

- *Concept underlying DA is adding “observations” to create a dataset composed of a known number of individuals.*

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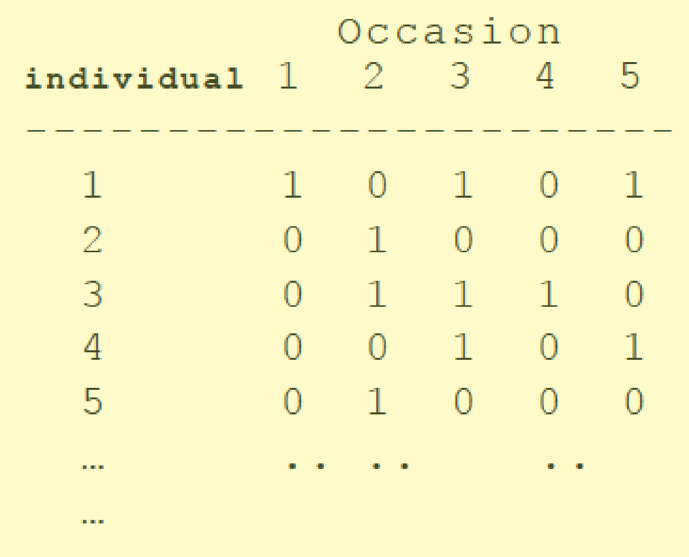
- *The model of the augmented dataset is a zero-inflated version of either a binomial or a multinomial base model.*

Data augmentation (DA), see Royle and Dorazio paper

- *Concept underlying DA is adding "observations" to create a dataset composed of a known number of individuals.*
- *For CR models, addition of a set of "all zero" encounter histories which are not observable in practice.*
- *The model of the augmented dataset is a zero-inflated version of either a binomial or a multinomial base model.*
- *Their use of DA provides a general approach for analyzing both closed and open population models of all types.*

DA and dataset



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...					

Example 1: Fit Model M0 to the bear data using JAGS and data augmentation

Instructions

- Material extracted from the day 1 of the SCR workshop in Athens in 2016 available here

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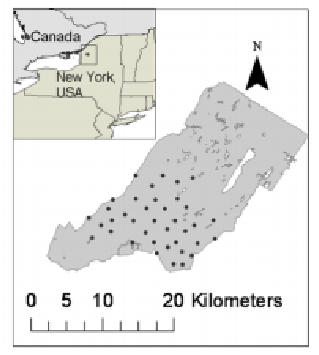
- Install the package scrbook there and get the bear data

```r
library(scrbook)
data(beardata)
```

Analysis of the Fort Drum bear data

- Hair snare study
  - J = 38 hair snares
  - K = 8 weeks of sampling
  - n = 47 individuals captured



Step 1: Create a text file with the model description, written in the BUGS language

```
cat("
model {
psi ~ dunif(0, 1)
p ~ dunif(0,1)
for (i in 1:M){
   z[i] ~ dbern(psi)

   for(k in 1:K){
     tmp[i,k] <- p*z[i]
     y[i,k] ~ dbin(tmp[i,k],1)
      }
     }
N <- sum(z[1:M])
}
",file="code/modelM0.txt")
```

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```
cat("
model {
psi ~ dunif(0, 1) # DA parameter
p ~ dunif(0,1) # prior distribution
for (i in 1:M){
   z[i] ~ dbern(psi) # binary DA latent variables which indicates if individual i is
                     # a member of the population - Abundance is just the sum of
                     # these binary latent variables
   for(k in 1:K){
     tmp[i,k] <- p*z[i]
     y[i,k] ~ dbin(tmp[i,k],1) # likelihood
      }
     }
N <- sum(z[1:M])
}
",file="code/modelM0.txt")
```

Step 2: Store the different values of interest

```
M = 175 # number of all individuals (encountered and DA)
nind <- dim(beardata$bearArray)[1] # number of encounter histories (individuals)
ntraps <- dim(beardata$bearArray)[2] # number of traps
K <- dim(beardata$bearArray)[3] # number of occasions

# How many "all zero" encounter histories are there?
nz <- M-nind

nz
#> [1] 128
```

Step 3: Set up the data augmentation and create the 2-d matrix “individual x occasions”

```r
# Fill up an array with zeros
Yaug <- array(0, dim=c(M,ntraps,K))

# Store the real data into the first nind slots
Yaug[1:nind,,] <- beardata$bearArray

# Because traditional CR models ignore space create a 2-d matrix
# "individuals x occasions"  of 0/1 data where 1 = "captured" 0 = "not captured"

y <- apply(Yaug,c(1,3),sum) # summarize by ind * occ
y[y>1] <- 1                 # make sure that multiple encounters do not occur
```

Step 4: Set input and output

- Format your data in R as a named list

```r
set.seed(2020)
data <- list(y=y,M=M,K=K)
```

- Make an object containing the names of the parameters that you are interested in

```r
params <- c("psi","p","N")
```

Step 5: Initial values

- Create a function to generate random initial values

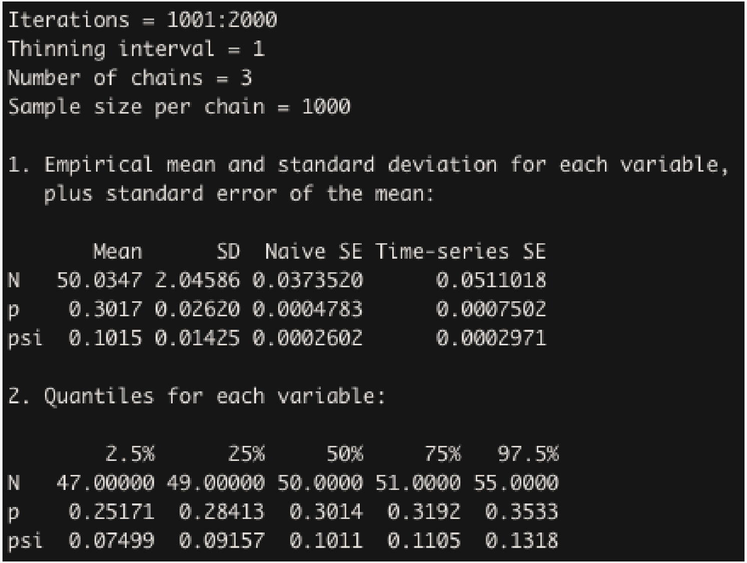
```
zst = c(rep(1,nind),rbinom(M-nind, 1, .5))
inits =  function(){list(z=zst, psi=runif(1), p=runif(1))}
```

Step 6: Run

- Compile the model and obtain posterior samples

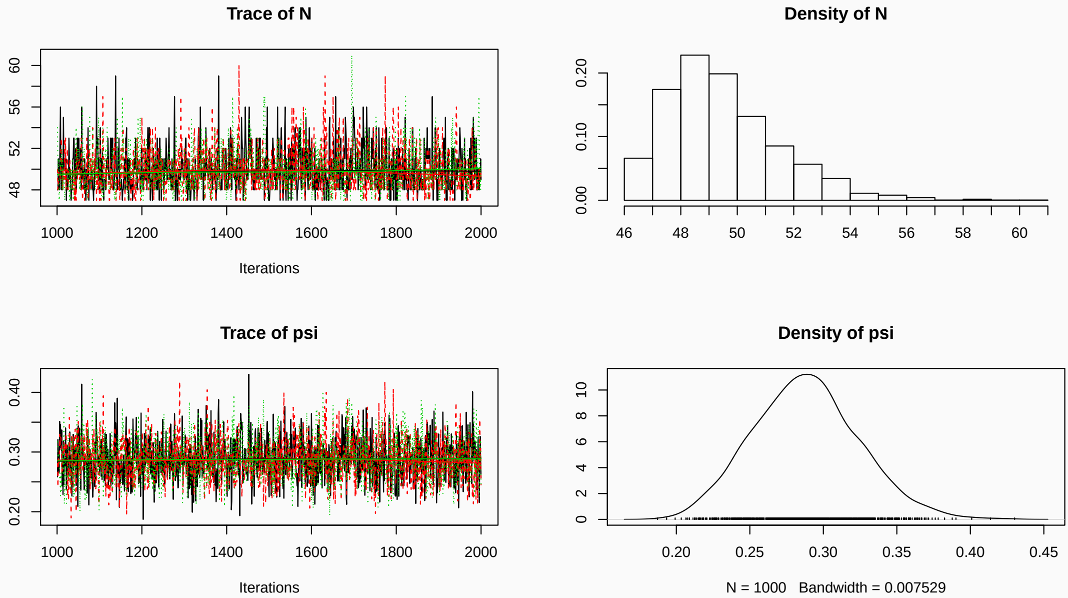
```
# Package rjags
library(rjags)
jm <- jags.model("code/modelM0.txt", data=data, inits=inits, n.chains=3, n.adapt=1000)
fit0j <- coda.samples(jm, params, n.iter=1000)

# Package jagsUI
library(jagsUI)
fit0j = jags(data, inits, params, model.file="code/modelM0.txt",n.chains=3,
             n.iter=2000, n.burnin=1000, n.thin=1)
```

Results: summary



```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

       Mean      SD  Naive SE Time-series SE
N   50.0347 2.04586 0.0373520      0.0511018
p    0.3017 0.02620 0.0004783      0.0007502
psi  0.1015 0.01425 0.0002602      0.0002971

2. Quantiles for each variable:

        2.5%      25%     50%     75%   97.5%
N   47.00000 49.00000 50.0000 51.0000 55.0000
p    0.25171  0.28413  0.3014  0.3192  0.3533
psi  0.07499  0.09157  0.1011  0.1105  0.1318
```

Results: plot



Trace of N

Density of N

Trace of psi

Density of psi

Your turn

- Try different values of M: 50 and 400.

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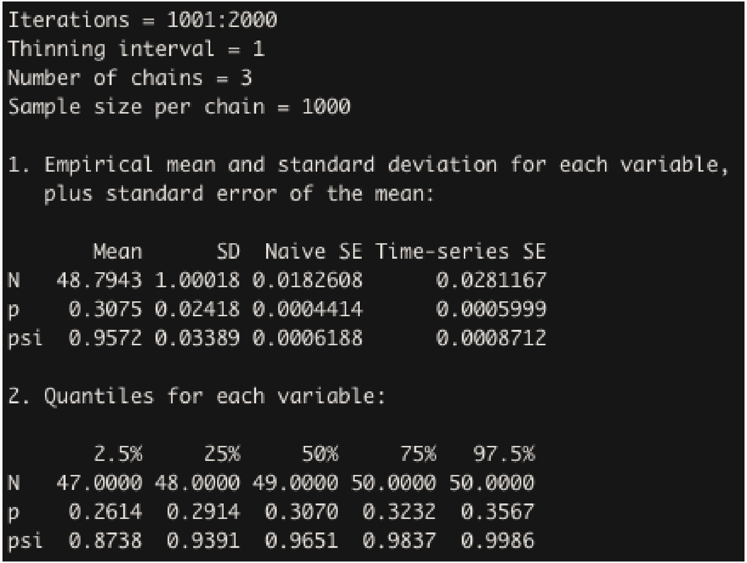
- Compare estimates (with summary function)

Your turn

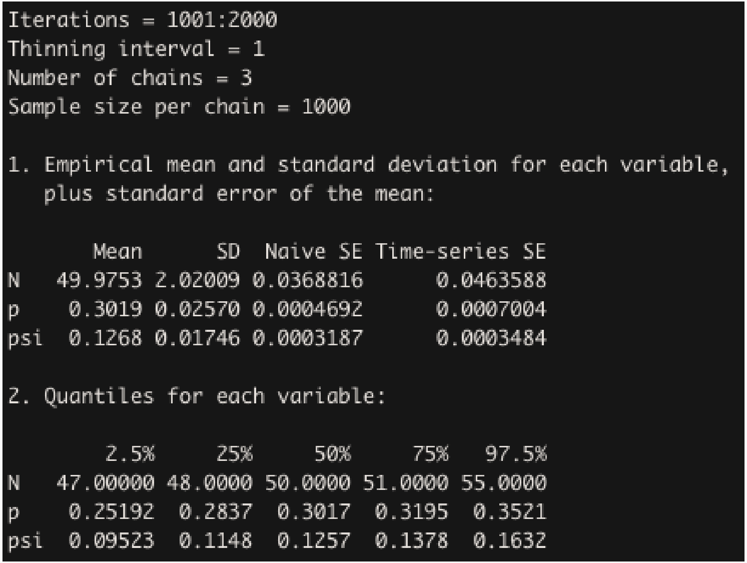
- Try different values of M: 50 and 400.
- Compare estimates (with summary function)
- Make a plot of the posterior distribution of N for both of them

Solution M = 50



```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

       Mean      SD  Naive SE Time-series SE
N   48.7943 1.00018 0.0182608      0.0281167
p    0.3075 0.02418 0.0004414      0.0005999
psi  0.9572 0.03389 0.0006188      0.0008712

2. Quantiles for each variable:

       2.5%     25%     50%     75%   97.5%
N   47.0000 48.0000 49.0000 50.0000 50.0000
p    0.2614  0.2914  0.3070  0.3232  0.3567
psi  0.8738  0.9391  0.9651  0.9837  0.9986
```

Solution M = 400



```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

       Mean      SD  Naive SE Time-series SE
N   49.9753 2.02009 0.0368816      0.0463588
p    0.3019 0.02570 0.0004692      0.0007004
psi  0.1268 0.01746 0.0003187      0.0003484

2. Quantiles for each variable:

        2.5%     25%     50%     75%   97.5%
N   47.00000 48.0000 50.0000 51.0000 55.0000
p    0.25192  0.2837  0.3017  0.3195  0.3521
psi  0.09523  0.1148  0.1257  0.1378  0.1632
```

Example 2: Fit Model M0 to the bear data using MLE

Define a log-likelihood function for model M0

```
M0.lik <-function(parameters){
  p <- plogis(parameters[1])
  n0 <- exp(parameters[2])
  N <- n + n0
  loglik.part1 <- lgamma(N+1) - lgamma(n0+1)
  loglik.part2 <- matrix(NA, n, K)
  for(i in 1:n){
    for(k in 1:K){
      loglik.part2[i,k] <- sum( Y[i,k]*log(p) + (1-Y[i,k])*log(1-p) )
    }
  }
  loglik.part3 <- n0 * sum(rep(log(1-p),K))
  -1 * (loglik.part1 + sum(loglik.part2) + loglik.part3)
  }
```

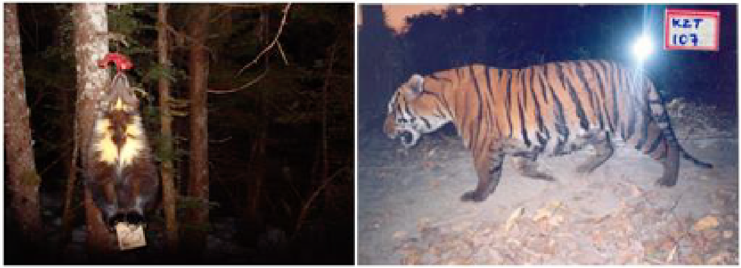
Find the MLEs for the bear data

```
# Set up the data

Y <- apply(beardata$bearArray,c(1,3),max)
n <- nrow(Y)
K <- ncol(Y)

# fit the model
fm.M0 <- nlm(M0.lik,rep(0,2),hessian=TRUE)

# estimated p
(phat <- plogis(fm.M0$est[1]))
#> [1] 0.3049265

# estimated N
(Nhat <- n+exp(fm.M0$est[2]))
#> [1] 49.19216
```

Spatially Explicit Capture Recapture (SECR) models in closed population

Why SECR models?

- New technologies producing vast quantities of encounter history data



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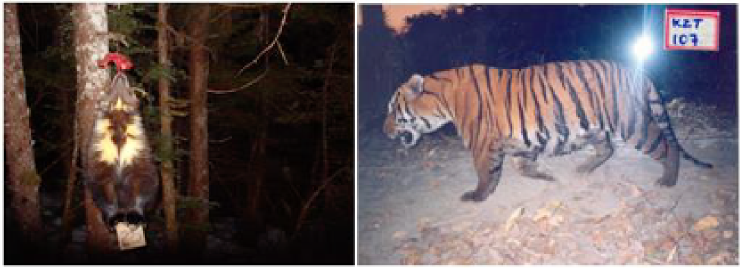

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- DNA sampling (Scat picked up by searching space, Urine on scent sticks or in snow, Tissue samples from treed individuals, Hair snares. . .)
- Acoustic sampling (whales, birds, bats)

Main Goals

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- Extension of CR (Improvement of Mx) to make use of encounter location data in order to study spatial aspects of animal populations
- Examples of applications: spatial variation in animal density, resource selection or animal movement
- Models developed to deal explicitly with 2 main problems associated with density estimation in trapping studies
  - Unknown sample area varies with trap layout – home range size
  - Heterogeneity in capture probability associated with spatial location of individuals (heterogeneity in p) relative to traps

Spatial point process model

- Spatial distribution of organisms is naturally described by point process models

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- In the CR context, Efford (2004, Oikos) described two concepts:
  - Concept 1: the biological or state process
  - Concept 2: the observation process

Concept 1: Biological or state process

Describe how individuals are distributed in space = a point process model for “activity centers” or home range centers:

- s_i = coordinates of the activity center or home range center for individual i

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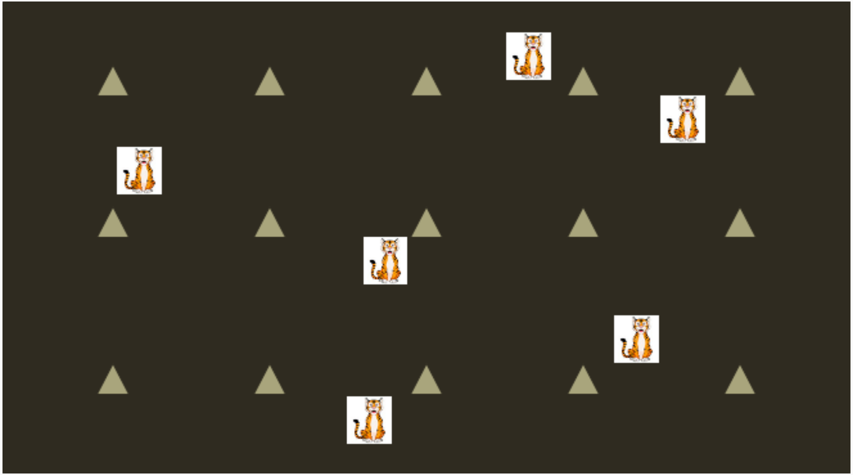
- s_i = coordinates of the activity center or home range center for individual i
- $s_1, s_2, ..., s_N$ = realization of a point process
- $s_i \sim Uniform(S); S$ = state-space of point process, i.e. the spatial region where the N activity centers occur (the frequentist literature tends to call it a “mask”). Activity centers are distributed independent of one another and uniformly in the plane = homogeneous point process

Concept 1: Biological or state process



Concept 2: Observation process

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- $p(x_j, s_i) = p_0 * exp(-d_{ij}^2(x_j, s_i)/\sigma^2)$

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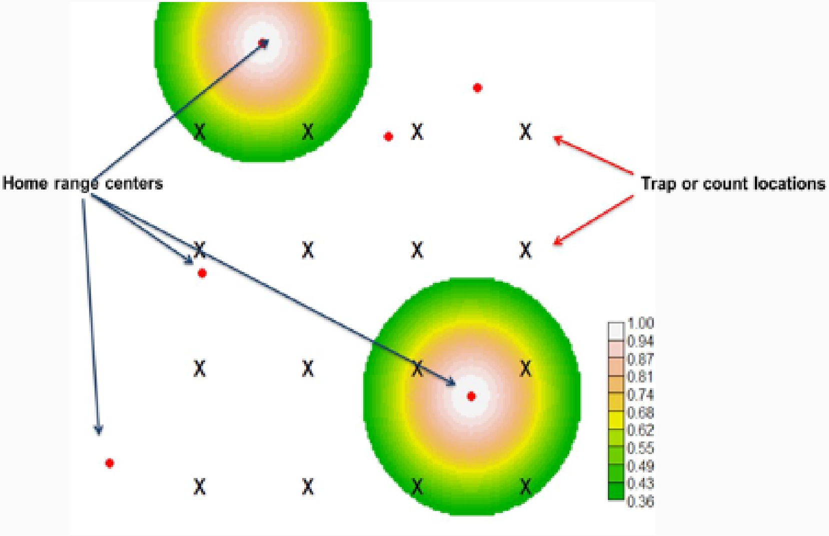
Describe p(encounter in trap) conditional on where an individual lives (s_i)

- $y_{i,j}|s_i \sim Bern(p(x_j, s_i))$
- $x_j = traplocation$
- $p(x_j, s_i) = p_0 * exp(-d_{ij}^2(x_j, s_i)/\sigma^2)$
- $d_{ij} = ||s_i \breve{ } x_j|| = \sqrt{(s_{1i} \breve{ } x_{1i})^2 + (s_{2i} \breve{ } x_{2i})^2}$

Concept 2: Observation process



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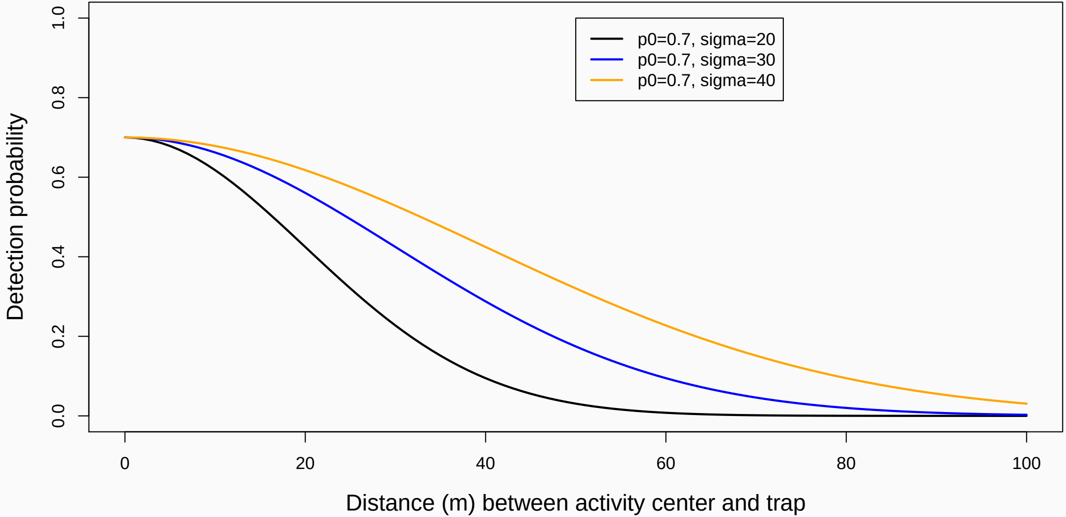

Distributions for observation model

- Binomiale (hare snare): The individual can be encountered maximum once in each trap but in different traps in the same occasion

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- Poisson (camera trap): The individual can be encountered several times by trap in each occasion occasion

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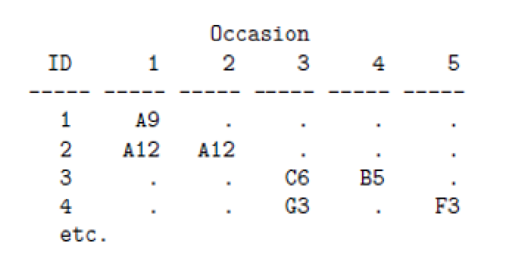
- Other references on hierarchical MCMC approach: Gardner *et al.* (2009, 2010)

Ingredients

SCR is a model of 3-dimensional encounter histories (i, j, k):

- Encounter data: Available individual IDs

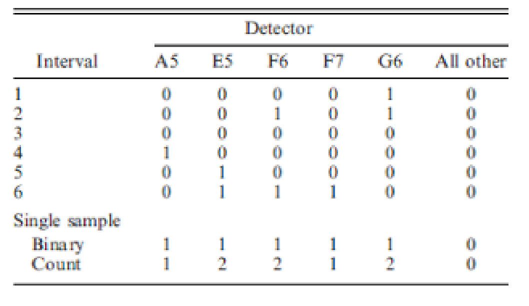


```
               Occasion
 ID      1     2     3     4     5
----- ----- ----- ----- ----- -----
 1      A9     .     .     .     .
 2     A12   A12     .     .     .
 3       .     .    C6    B5     .
 4       .     .    G3     .    F3
 etc.
```

Ingredients

SCR is a model of 3-dimensional encounter histories (i, j, k):

- Trap data: Network of fixed detectors in 2D with known localisations



	Detector					
Interval	A5	E5	F6	F7	G6	All other
1	0	0	0	0	1	0
2	0	0	1	0	1	0
3	0	0	0	0	0	0
4	1	0	0	0	0	0
5	0	1	0	0	0	0
6	0	1	1	1	0	0
Single sample						
Binary	1	1	1	1	1	0
Count	1	2	2	1	2	0

Example 3: Fit a basic SECR model in closed population with data augmentation

Instructions

- Import the encounter history data

```
#>   animalID trapID   occasion
#> 1       a6     t1 2020-01-01
#> 2       a6     t2 2020-01-01
#> 3       a6     t3 2020-01-01
#> 4       a8     t4 2020-01-01
```

Instructions

- Import the encounter history data

```
#>   animalID trapID   occasion
#> 1       a6     t1 2020-01-01
#> 2       a6     t2 2020-01-01
#> 3       a6     t3 2020-01-01
#> 4       a8     t4 2020-01-01
```

- Import trap coordinates

```
#>     x1  x2
#> t1 0.3 0.3
#> t2 0.3 0.4
#> t3 0.3 0.5
#> t4 0.3 0.6
```

Step 0: Create 3D capture history array using the table function

Add missing traps and occasions in the levels to have a complete 3D array and order

```
nocapTraps <- setdiff(rownames(traps), encounters$trapID)
nocapTraps
#> [1] "t5"  "t9"  "t13" "t14" "t15" "t17" "t19" "t24"
levels(encounters$trapID) <- c(levels(encounters$trapID), nocapTraps)
levels(encounters$trapID) # All trapIDs should be here now
#>  [1] "t1"  "t10" "t11" "t12" "t16" "t18" "t2"  "t20" "t21" "t22" "t23" "t25"
#> [13] "t3"  "t4"  "t6"  "t7"  "t8"  "t5"  "t9"  "t13" "t14" "t15" "t17" "t19"
#> [25] "t24"

y3D <- table(encounters$animalID, encounters$trapID,
             encounters$occasion)
```

Step 0: Create 3D capture history array using the table function

```
y3D[1:4,1:10,1] ## Data on first 4 ind at first 10 trap on k=1
#>
#>        t1 t10 t11 t12 t16 t18 t2 t20 t21 t22
#>   a1    0   0   0   0   0   0  0   0   0   0
#>   a10   0   0   1   0   0   0  0   0   0   0
#>   a11   0   0   0   0   0   0  0   0   0   0
#>   a2    0   0   0   0   0   0  0   0   0   0

all(rownames(traps)==colnames(y3D))  ## Not good
#> [1] FALSE
y3D <- y3D[,rownames(traps),]        ## Re-order
all(rownames(traps)==colnames(y3D))  ## Good
#> [1] TRUE
```

Step 1: Create a text file with the model description

```
cat("
model {
p0 ~ dunif(0, 1) # baseline encounter probability
sigma ~ dunif(0, 2) # scale parameter of encounter function
psi ~ dunif(0, 1) # DA parameter: E(N) = M*psi

for(i in 1:M) {
z[i] ~ dbern(psi) # Is individual real?
s[i,1] ~ dunif(xlim[1], xlim[2]) # x-coordinate of activity center
s[i,2] ~ dunif(ylim[1], ylim[2]) # y-coordinate

for(j in 1:J) {
# dist between activity center and trap
d[i,j] <- sqrt((s[i,1] - x[j,1])^2 + (s[i,2] - x[j,2])^2)
p[i,j] <- p0*exp(-d[i,j]^2/(2*sigma^2)) # capture prob at trap j

...
```

Step 1: Create a text file with the model description

```
cat("
...

for(k in 1:K) {
y[i,j,k] ~ dbern(p[i,j]*z[i]) # model for data
}
}
}

N <- sum(z) # realized abundance
EN <- M*psi # expected abundance
A <- (xlim[2]-xlim[1])*(ylim[2]-ylim[1]) # area of state-space
D <- N/A # realized density
ED <- EN/A # expected density
}
",file="code/SECR0.txt")
```

Step 2: Store the different values of interest

```r
M <- 50 # number of all individuals (encountered and DA)
J <- dim(y3D)[2] # number of traps
K <- dim(y3D)[3] # number of occasions
n0 <- nrow(y3D) # number of encounter histories, i.e. encountered individuals
```

Step 3: Set up the data augmentation

```r
# Fill up an array with zeros
yz <- array(0, c(M, J, K))

# Store the real data into the first nind slots
yz[1:n0,,] <- y3D
```

Step 4: Set input and output

- Format your data in R as a named list

```r
set.seed(2020)
jd <- list(y=yz, J=J, K=K, M=M, x=traps, xlim=c(0,1), ylim=c(0,1))
```

Step 4: Set input and output

- Format your data in R as a named list

```
set.seed(2020)
jd <- list(y=yz, J=J, K=K, M=M, x=traps, xlim=c(0,1), ylim=c(0,1))
```

- Make an object containing the names of the parameters that you are interested in

```
jp <- c("N", "p0", "sigma")
```

Step 5: Initial values

- Create a function to generate random initial values

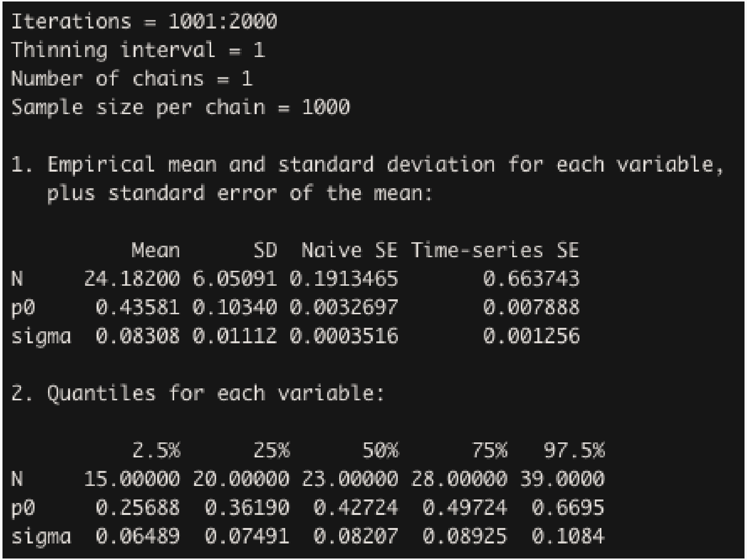
```r
ji <- function() list(z=rep(1,M), p0=runif(1), sigma=runif(1))
```

Step 6: Run

- Compile the model and obtain posterior samples

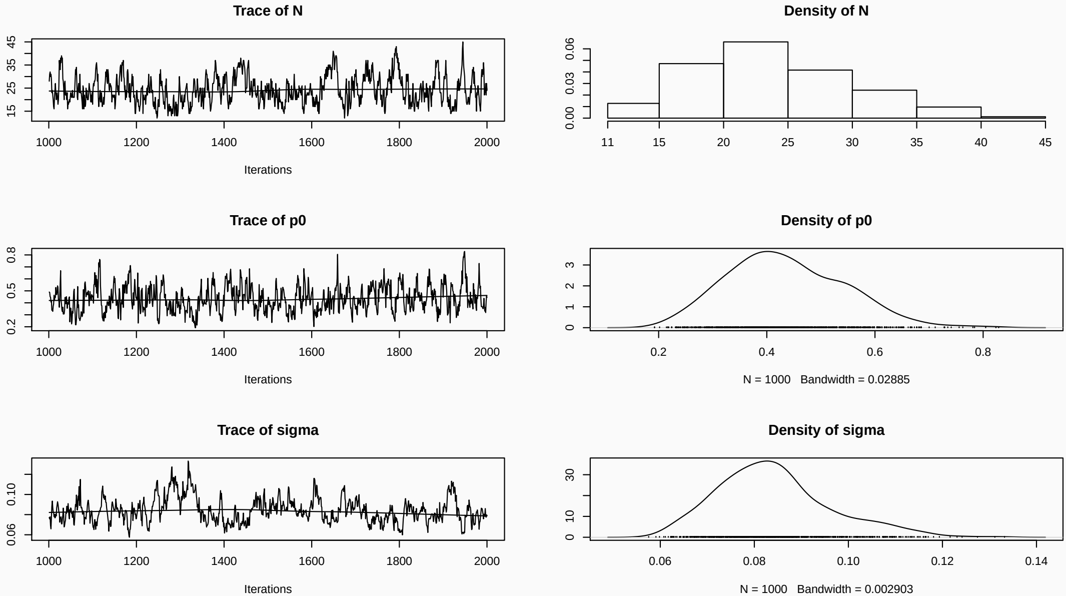
```r
# Package rjags
library(rjags)
jm <- jags.model("code/SECR0.txt", jd, ji, n.chains=1, n.adapt=1000)
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 5000
#>    Unobserved stochastic nodes: 153
#>    Total graph size: 32475
#>
#> Initializing model
jc <- coda.samples(jm, jp, 1000)
```

Results: summary



```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean      SD  Naive SE Time-series SE
N     24.18200 6.05091 0.1913465       0.663743
p0     0.43581 0.10340 0.0032697       0.007888
sigma  0.08308 0.01112 0.0003516       0.001256

2. Quantiles for each variable:

          2.5%      25%      50%      75%   97.5%
N     15.00000 20.00000 23.00000 28.00000 39.0000
p0     0.25688  0.36190  0.42724  0.49724  0.6695
sigma  0.06489  0.07491  0.08207  0.08925  0.1084
```

Results: plot



Example 4: Imagine an application of SECR to tuna fisheries

Your turn

- Story: Purse senners fishing tropical tunas under drifting Fish Aggregating Devices (dFAD)
- Goal: Imagine how to use SECR to estimate dFADs density

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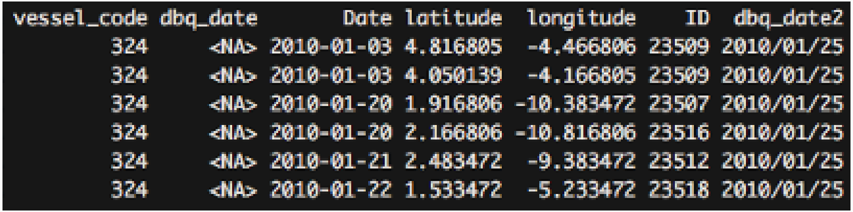
Your turn

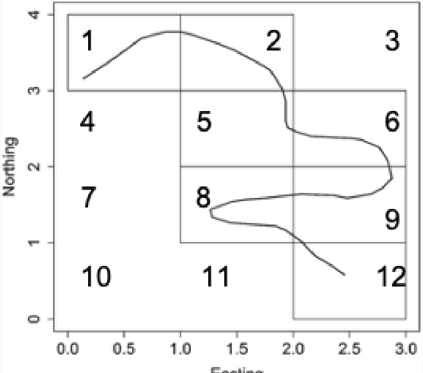
- Hint on available data:
  - Fishing activities (grid with activities locations)
  - dFADs IDs
  - Boats trajectories



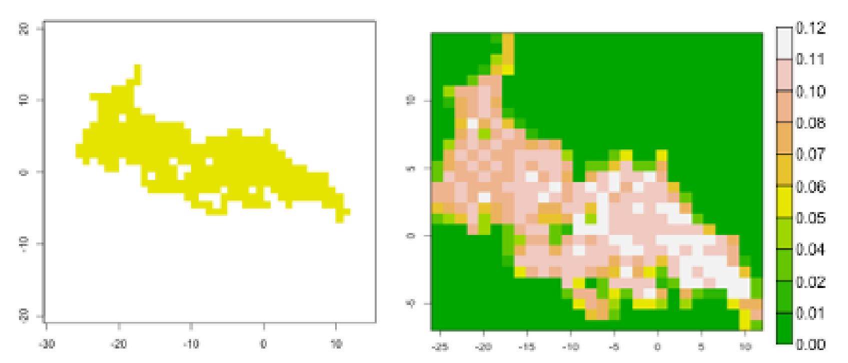
```
vessel_code dbq_date        Date latitude  longitude    ID  dbq_date2
        324     <NA> 2010-01-03 4.816805  -4.466806 23509 2010/01/25
        324     <NA> 2010-01-03 4.050139  -4.166805 23509 2010/01/25
        324     <NA> 2010-01-20 1.916806 -10.383472 23507 2010/01/25
        324     <NA> 2010-01-20 2.166806 -10.816806 23516 2010/01/25
        324     <NA> 2010-01-21 2.483472  -9.383472 23512 2010/01/25
        324     <NA> 2010-01-22 1.533472  -5.233472 23518 2010/01/25
```

Solution

- Transfer the method to estimate non-tracked buoys density considering:
  - dFADs as animals
  - Traps = square/cell of 1*1 degree
  - Detectors = vessels with activities on dFADs
  - Occasion = Day



What you could obtain



More complex models

- Open population ouverte (survival, recruitment. . .)

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- Open population ouverte (survival, recruitment. . .)
- Time and/or sex effect
- Variation in effort, e.g. duration of trap activity
- Habitat mask
- Mobile activity centers
- Mixing count data with SECR data