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

JAGS R Packages

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

- rjags
- jagsUI
- R2jags

SECR R Packages

Different packages can be used to run SECR models from R such as:

- scrbook from the Spatial Capture-Recapture book by Andy Royle, Richard Chandler, Rahel Sollmann and Beth Gardner

SECR R Packages

Different packages can be used to run SECR models from R such as:

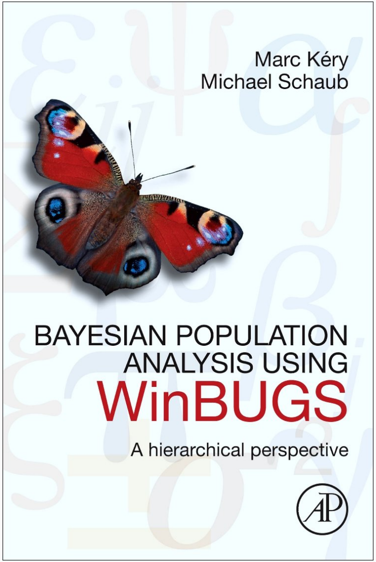
- scrbook from the Spatial Capture-Recapture book by Andy Royle, Richard Chandler, Rahel Sollmann and Beth Gardner
- secr developped by Murray Efford

SECR R Packages

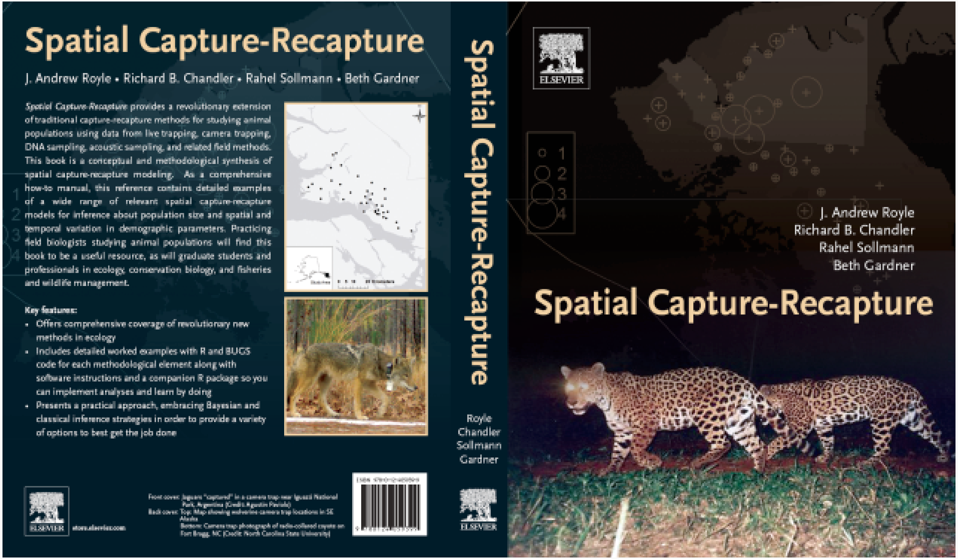
Different packages can be used to run SECR models from R such as:

- scrbook from the Spatial Capture-Recapture book by Andy Royle, Richard Chandler, Rahel Sollmann and Beth Gardner
- secr developped by Murray Efford
- oSCR developed by Chris Sutherland, Andy Royle, and Dan Linden

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
ELSEVIER
Spatial Capture-Recapture
Royle
Chandler
Sollmann
Gardner
ELSEVIER
ELSEVIER
1
2
3
4
J. Andrew Royle
Richard B. Chandler
Rahel Sollmann
Beth Gardner
Spatial Capture-Recapture

Outline

1. Bayesian Capture-Recapture models in closed population

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

2. Spatially Explicit Capture Recapture (SECR) models

Bayesian Capture-Recapture models in closed population

Capture-recapture, quésako?

- Information on N or density D is the main interest.

Capture-recapture, quésako?

- Information on N or density D is the main interest.
- Only a sample of individuals n is observed due to an encounter or detection probability p.

Capture-recapture, quésako?

- Information on N or density D is the main interest.
- 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.

Capture-recapture, quésako?

- Information on N or density D is the main interest.
- 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)

Starting point of CR

- 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.

Starting point of CR

- 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.
- Status of individuals is not known. You don't observe "all zero encounter histories".

Starting point of CR

- 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.
- Status of individuals is not known. You don't observe "all zero encounter histories".
- Initial CR models developped for geographically closed populations.

Starting point of CR

- 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.
- 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)

Closed population

- Demographic closure (no births, no deaths) and geographical closure (no entry, no exit)
- 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
- See Kery and Schaub (2012) Chapter 6 to go further

Basic model M0

- Model M0 can be considered as a null model
- The main assumptions are:
  - p is constant for all sample occasions and all individuals
  - 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

Data augmentation (DA)

- 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)
  }
}
```

Data augmentation (DA)

- 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)
  }
}
```

- But N is not known. Why couldn't we put a prior on N (e.g. N $\sim$ Dunif(0, 1000)) and analyze the model using standard methods of MCMC?

Data augmentation (DA)

- 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)
  }
}
```

- But N is not known. Why couldn't we put a prior on N (e.g. $N \sim \text{Dunif}(0, 1000)$) and analyze the model using standard methods of MCMC?
- 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.*

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.*

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.*

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.*

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

Instructions

- Install the package scrbook there and get the bear data

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

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

```
cat("
model {
psi ~ dunif(0, 1) # DA parameter
p ~ dunif(0,1) # prior distribution
for (i in 1:M){
   z[i] ~ dbern(psi) # DA latent variables
   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="modelM0.txt")
```

Step 2: Store the different values of interest

```r
M = 175 # number of all individuals (encountered and DA)
nind <- dim(beardata$bearArray)[1] # number of encounter histories, i.e. encountered indiv
ntraps <- dim(beardata$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”

```
# 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

```
set.seed(2013)
data <- list(y=y,M=M,K=K)
```

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

```
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

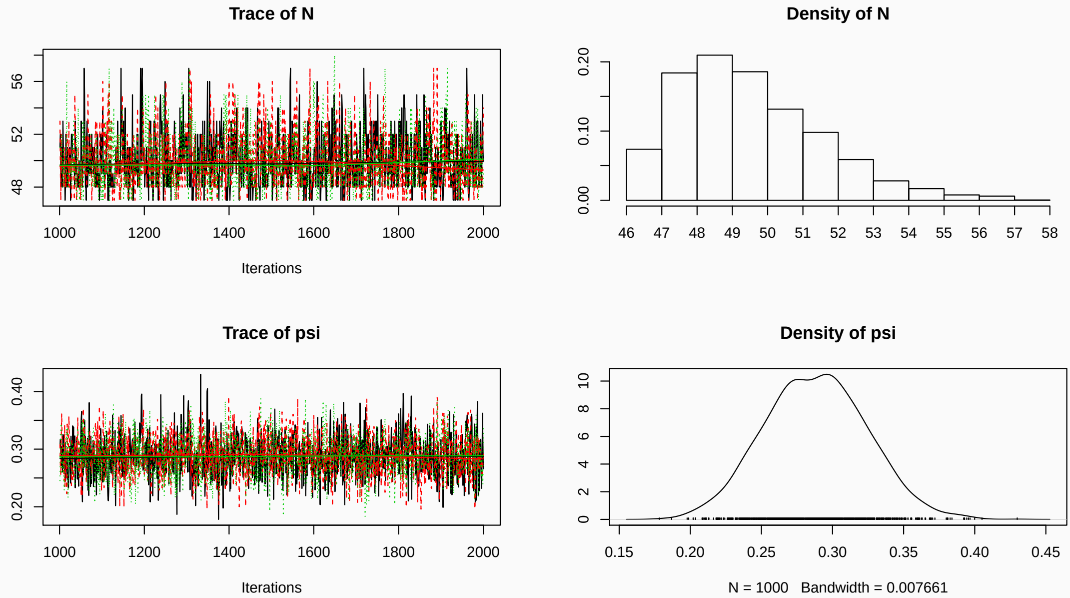
- Compile the model and obtain posterior samples

```
# Package rjags
library(rjags)
jm <- jags.model("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="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



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
```

Take home message

- Choose M sufficiently large

Spatially Explicit Capture Recapture (SECR) models