



Lecture 12

Estimating abundance: Closed-population
capture-mark-recapture

WILD6900 (Spring 2020)

Readings

Kéry & Schaub 134-170

Powell & Gale chp. 8

Estimating abundance

Unbiased estimates of N require estimating p

Many methods available:

- Mark-recapture
- Removal sampling
- Distance sampling
- Double observer
- N-mixture models

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Capture-mark-recapture

Capture-mark-recapture (CMR)

CMR includes a **wide** variety of related techniques and models

Traditionally, CMR referred to methods of capturing, marking, and then recapturing individuals at some point in the future

This results in a **capture-history** for each individual:

Individual 1: 101101

Individual 2: 011001

From the capture-histories, possible to estimate p

With p , possible to estimate N

$$N = \frac{C}{p}$$

Capture-mark-recapture

From capture-histories, we can estimate:

- abundance
- detection probability
- survival
- movement
- recruitment
- individual growth
- populations trends

Capture-mark-recapture

CMR methods are not restricted to physical captures and recaptures



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What ties all of these methods together is that we have individual-level capture-histories

Capture-mark-recapture

Key to closed CMR is that because individuals do not enter or leave the population, we assume any 0 in the capture history is non-detection
 $(1 - p)$

- in simplest model, easy to translate capture history into probabilistic statements based only on p :

Individual 1: 101101

$$p(1 - p)pp(1 - p)p$$

Individual 2: 011001

$$(1 - p)pp(1 - p)(1 - p)p$$

In the CMR literature, the constant p model is known at the M_0 model
(Otis et al. (1978))

The M_0 model in JAGS

In all closed CMR models, N is unknown

- we know n but how many individuals were not detected at all?
- data augmentation!

Data augmentation

Data augmentation

Imagine an occupancy study:

- M sites are surveyed
 - N sites are occupied ($z = 1$)
 - $M - N$ sites are unoccupied ($z = 0$)
- species is detected ($y_i = 1$) at n sites
 - species is not detected ($y_i = 0$) at $M - n$ sites

$$y_i \sim Bernoulli(z_i p)$$

Data augmentation

Imagine an occupancy study:

How many sites are actually occupied (N)?

- if ψ is the probability of occupancy

$$z_i \sim \text{Bernoulli}(\psi)$$

- and

$$N = \sum_{i=1}^M z_i$$

Data augmentation

These ideas can be applied to CMR studies

Imagine a CMR study:

- n individuals were detected during the study
- $N - n$ individuals were not detected
 - how do we know how many individuals were not detected?
- Add $M - n$ individuals to the data
 - Choose $M \gg N$
 - All of these "augmented" individuals have $y = 0$

$$z_i \sim \text{Bernoulli}(\psi)$$

$$N = \sum_{i=1}^M z_i$$

The M_0 model in JAGS

In all closed CMR models, N is unknown

- we know n but how many individuals were not detected at all?
- data augmentation!

$$z_i \sim Bernoulli(\psi)$$

$$y_{ik} \sim Bernoulli(z_i p)$$

$$\psi \sim beta(1, 1)$$

$$p \sim beta(1, 1)$$

$$N = \sum_{i=1}^M z_i$$

The M_0 model in JAGS

```
model{
  omega ~ dbeta(1, 1)
  p ~ dbeta(1, 1)

  for(i in 1:M){
    z[i] ~ dbern(psi)

    for(t in 1:T){
      y[i, t] ~ dbern(p * z[i])
    } # end t
  } # end i

  N <- sum(z[1:M])
}
```

Capture-mark-recapture

In addition to the M_0 model, Otis et al. 1978 outlined 3 other basic *closed CMR* "models":

- M_t : variation in p among occasions

$$p_1(1 - p_2)p_3p_4(1 - p_5)p_6$$

- M_h : variation in p among individuals

$$p_i(1 - p_i)p_ip_i(1 - p_i)p_i$$

- M_b : behavioral responses (trap happiness/shyness)

$$p(1 - c)cc(1 - c)c$$

[1] David Otis was a post-doc at USU in the Coop Unit when he wrote this seminal paper

Capture-mark-recapture

Otis et al. 1978 was seminal because it clarified ways that p might vary

However, M_0, M_t, M_h, M_b are not single models but instead families of models that allow p to vary for different reasons

In modern Bayesian analysis of closed CMR models, we can use the tools you learned so far in this course to model complex variation in p

- group effects
- hierarchical structure
- continuous covariates (via GLM)

The M_t model in JAGS

How do we model p as a function of occasion?

```
model{
  omega ~ dbeta(1, 1)
  for(t in 1:T){
    p[t] ~ dbeta(1, 1)
  }

  for(i in 1:M){
    z[i] ~ dbern(psi)

    for(t in 1:T){
      y[i, t] ~ dbern(p[t] * z[i])
    } # end t
  } # end i

  N <- sum(z[1:M])
}
```

The M_t model in JAGS

```
model{
  omega ~ dbeta(1, 1)
  for(t in 1:T){
    lp[t] ~ dnorm(mu.p, tau.p)
    logit(p[t]) <- lp[t]
  }
  mu.p ~ dnorm(0, 0.1)
  tau.p ~ dgamma(0.25, 0.25)
  for(i in 1:M){
    z[i] ~ dbern(psi)

    for(t in 1:T){
      y[i, t] ~ dbern(p[t] * z[i])
    } # end t
  } # end i
}
```

- What is the difference between this model and the previous? How will this change influence estimates of p_t ?

Model M_b

Behavioral responses are common in studies that require physical captures

- probability of capture \neq probability of recapture (c)
- individuals learn to avoid traps (trap shy; $p > c$)
- individuals learn to seek out traps (trap happy; $c > p$)

In the M_b models, p depends on whether an individual has previously been captured

- response can be permanent or ephemeral

Model M_b in JAGS

```
model{
  omega ~ dbeta(1, 1)
  p ~ dbeta(1, 1)
  c ~ dbeta(1, 1)

  for(i in 1:M){
    z[i] ~ dbern(psi)

    y[i, 1] ~ dbern(p * z[i])

    for(t in 2:T){
      y[i, t] ~ dbern(z[i] * ((1 - y[i, t-1]) * p + y[i, t-1] * c))
    } # end t
  } # end i

  N <- sum(z[1:M])
  trap.response <- c - p
}
```

Model M_h

Individual heterogeneity not captured by covariates

- treat individuals as random effect

$$\text{logit}(p_i) \sim \text{normal}(\text{logit}(\mu_p), \tau_p)$$

- models with heterogeneity are not always identifiable
 - different assumptions about p_i will give different estimates of N but model selection does not differentiate between models
 - however, *not* modeling individual heterogeneity leads to known bias
 - assuming constant p underestimates N

Model M_h in JAGS

```
model{
  omega ~ dbeta(1, 1)
  mean.p ~ dbeta(1, 1)
  mean.lp <- log(mean.p) - log(1 - mean.p)
  tau.p ~ dgamma(0.25, 0.25)

  for(i in 1:M){
    z[i] ~ dbern(psi)
    logit(p[i]) ~ dnorm(mean.lp, tau.p)T(-5, 5)

    y[i] ~ dbin(p[i] * z[i], T)
  } # end i

  N <- sum(z[1:M])
}
```

Extensions of the Otis et al. models

Many extensions possible

- M_{tb}
- M_{th}
- M_{tjh}
- and many more limited only by your data and your modeling skills

As additional variation is added, more data is needed to estimate parameters

- all else equal, each new parameter results in lower precision for N (no free lunch!)