

WEB APPENDIX FOR CAPTURE-RECAPTURE ABUNDANCE ESTIMATION USING A SEMI-COMPLETE DATA LIKELIHOOD APPROACH

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In this web appendix we provide sample JAGS code for model M_h considered in Section 4.1 (Appendix A) and the SECR model considered in Section 4.2 (Appendix B). For each example we provide the model specification component of the JAGS code for the four different model-fitting algorithms: (i) semi-complete data likelihood specifying Jeffreys' prior on N (SCD1); (ii) semi-complete data likelihood specifying the posterior conditional distribution on $N - n$, induced by Jeffreys' prior on N (SCD2); (iii) super-population complete data likelihood approach of [Royle et al. \(2007\)](#) (CD:R) and (iv) super-population complete data likelihood approach of [Durban and Elston \(2005\)](#) (CD:DE).

APPENDIX A: JAGS CODE FOR MODEL M_H

In this web appendix we provide sample JAGS code for model M_h considered in Section 4.1.

A.1. First semi-complete data likelihood approach - SCD1. The model component of the JAGS code is provided here for the semi-complete data likelihood approach using the Jeffreys' prior specification for N .

```
model{
  Pi <- 3.14159265359
  # Priors:
  alpha ~ dnorm(0.0,0.01)
  tau ~ dgamma(0.01,0.01)
  sigma <- 1/sqrt(tau)

  for (i in 1:n) {
    y[i] ~ dbin(p[i],T)
    logitp[i] ~ dnorm(alpha,tau)
    logit(p[i]) <- logitp[i]
  }

  # Calculate probability of not being observed using Gauss-Hermite quadrature
  # q = number of quadrature points
  # weights and nodes correspond to q quadrature points; entered as data

  for(i in 1:q){
    probi[i] <- 1/sqrt(Pi)*weights[i]*(1/(1+exp(sqrt(2)*sigma*nodes[i]+alpha)))^T
  }
  prob<- sum(probi[])

  # Prior for N: Jeffreys' prior - this is incorporated in the zero trick below
  # in specifying the likelihood term
  # However a prior distribution is needed to be specified on N
```

```

43 # Use a discrete Uniform prior so the only influence on the posterior
44 # distribution is the upper limit
45
46 n00 ~ dcat(prior[]) # prior = rep(1/(M+1-n),M+1-n); entered as data
47 n0 <- n00 - 1
48 N <- n + n0
49
50 # Use zero trick for model likelihood
51 # Note loggam(N) instead of loggam(N+1) because of Jeffreys' prior for N
52
53 logzeroprob <- loggam(N) - loggam(n0+1) - loggam(n+1) + n0*log(prob)
54 lambda <- -logzeroprob + 100000
55 dummy ~ dpois(lambda) # dummy = 0; entered as data
56 }

```

57 **A.2. Second semi-complete data likelihood approach - SCD2.** The model component
58 of the JAGS code is provided here for the semi-complete data likelihood approach, specifying the
59 posterior conditional distribution of $N - n$ to be of Negative-Binomial form.

```

60 model{
61   Pi <- 3.14159265359
62   # Priors:
63   alpha ~ dnorm(0.0,0.01)
64   tau ~ dgamma(0.01,0.01)
65   sigma <- 1/sqrt(tau)
66   for (i in 1:n) {
67     y[i] ~ dbin(p[i],T)
68     logitp[i] ~ dnorm(alpha,tau)
69     logit(p[i]) <- logitp[i]
70   }
71
72   # Posterior conditional distribution for N-n (and hence N):
73
74   n0 ~ dnegbin(pstar,n)
75   N <- n + n0
76
77   # Calculate probability of not being observed using Gauss-Hermite quadrature
78   # q = number of quadrature points
79   # weights and nodes correspond to q quadrature points; entered as data
80   for(i in 1:q){
81     probi[i] <- 1/sqrt(Pi)*weights[i]*(1/(1+exp(sqrt(2)*sigma*nodes[i]+alpha)))^T
82   }
83   pstar <- 1-sum(probi[])
84
85   # Use zero trick for initial 1/(pstar)^n
86
87   loglikterm <- -n*log(pstar)
88   lambda <- -loglikterm + 100000
89   dummy ~ dpois(lambda) # dummy = 0; entered as data
90 }

```

91 **A.3. Super-population complete data likelihood approach - CD:R.** The model com-
 92 ponent of the JAGS code for the super-population complete data likelihood approach of [Royle et](#)
 93 [al. \(2007\)](#).

```

94 model{
95   # Priors:
96   psi ~ dbeta(0.001,1)
97   alpha ~ dnorm(0.0,0.01)
98   tau ~ dgamma(0.01,0.01)
99   sigma <- 1/sqrt(tau)
100
101   # Complete data likelihood:
102   for(i in 1:M){
103     y[i] ~ dbin(pi[i],T)
104     pi[i] <- z[i]*p[i]
105     z[i] ~ dbern(psi)
106     logit(p[i]) <- logitp[i]
107     logitp[i] ~ dnorm(alpha,tau)
108   }
109
110   # Calculate N:
111   N <- sum(z[1:M])
112 }
```

113 **A.4. Super-population complete data likelihood approach - CD:DE.** The model com-
 114 ponent of the JAGS code for the super-population complete data likelihood approach of [Durban](#)
 115 [and Elston \(2005\)](#).

```

116 model{
117   # Priors:
118   alpha ~ dnorm(0.0,0.01)
119   tau ~ dgamma(0.01,0.01)
120   sigma <- 1/sqrt(tau)
121
122   # Prior for N: (Jeffrey's prior over {n,n+1,...,M} following Link 2013).
123
124   n00 ~ dcat(prior[]) # prior = rep(1/(M+1-n),M+1-n); entered as data
125   n0 <- n00 - 1
126   N <- n+n0
127
128   # Use zero trick for factorial term
129   # Note loggam(N) instead of loggam(N+1) because of Jeffrey's prior for N
130
131   logzeroprob <- loggam(N) - loggam(n0+1) - loggam(n+1)
132   lambda <- -logzeroprob + 1000
133   dummy ~ dpois(lambda) # dummy = 0; entered as data
134
135   # Complete data likelihood:
136
137   for (i in 1:M){
138     y[i] ~ dbin(pi[i],T)
```

```

139   pi[i] <- z[i]*p[i]
140   z[i] <- step(N-i)
141   logit(p[i]) <- z[i]*logitp1[i] + (1-z[i])*logitp2[i]
142
143   logitp1[i] ~ dnorm(alpha,tau)
144   logitp2[i] ~ dnorm(alphaprior,tauprior)
145
146   # alpha prior and tauprior are pseudo-prior parameters entered as data
147
148 }
149 }
```

APPENDIX B: JAGS CODE FOR SECR MODEL

In this web appendix we provide sample JAGS code for the SECR models considered in Section 4.2.

B.1. First semi-complete data likelihood approach - SCD1. The model component of the JAGS code is provided here for the semi-complete data likelihood approach using the Jeffreys' prior specification for N .

```

155 model{
156   # Priors:
157   sigma ~ dunif(0,10)
158   tau <- 1/(sigma*sigma)
159   for(i in 1:n){
160     X[i] ~ dunif(xlim[1], xlim[2])
161     Y[i] ~ dunif(ylim[1], ylim[2])
162   }
163
164   # pdot = probability of being detected at least once (given location)
165   # Calculate esa numerically using the integration grid
166
167   for(i in 1:G){ # G = number of points on integration grid
168     for(s in 1:S){
169       for(k in 1:K){
170         one_minus_detprob[i,s,k] <- 1 - exp(-dist2[i,k]*tau/2)
171       }
172     }
173     pdot.temp[i] <- 1 - prod(one_minus_detprob[i,,])
174     pdot[i] <- max(pdot.temp[i], 1.0E-10)
175   }
176   esa <- sum(pdot[])*a # a = size of grid square in numerical integration
177   pstar <- esa / A
178
179   # Prior for N: Jeffreys' prior - this is incorporated in the zero trick below
180   # in specifying the likelihood term
181   # However a prior distribution is needed to be specified on N
182   # Use a discrete Uniform prior so the only influence on the posterior
183   # distribution is the upper limit
184 }
```

```

185 n00 ~ dcat(prior[]) # prior = rep(1/(M+1-n),M+1-n); entered as data
186 n0 <- n00 - 1
187 N <- n + n0
188
189 # Zero trick for likelihood component for unobserved individuals
190 logzeroprob <- loggam(N) - loggam(n0+1) - loggam(n+1) + n0*log(1-pstar)
191 lambda <- -logzeroprob + 1000
192 dummy ~ dpois(lambda) # dummy = 0; entered as data
193
194 # Model for capture histories of observed individuals:
195 for(i in 1:n){
196   for(k in 1:K){
197     for(s in 1:S){
198       capthist[i,s,k] ~ dbern(detprob[i,s,k])
199       detprob[i,s,k] <- exp(-r2[i,k] * tau/2 )
200     }
201     r2[i,k] <- pow(X[i] - traps[k,1], 2) + pow(Y[i] - traps[k,2], 2)
202   }
203 }
204 }

```

205 **B.2. Second semi-complete data likelihood approach - SCD2.** The model component
 206 of the JAGS code is provided here for the semi-complete data likelihood approach, specifying the
 207 posterior conditional distribution of $N - n$ to be of Negative-Binomial form.

```

208 model{
209   # Priors:
210   sigma ~ dunif(0,10)
211   tau <- 1/(sigma*sigma)
212   for(i in 1:n){
213     X[i] ~ dunif(xlim[1], xlim[2])
214     Y[i] ~ dunif(ylim[1], ylim[2])
215   }
216
217   # Posterior conditional distribution for N-n (and hence N):
218
219   n0 ~ dnegbin(pstar,n)
220   N <- n + n0
221
222   # pdot = probability of being detected at least once (given location)
223   # calculate esa numerically using the integration grid
224
225   for(i in 1:G){ # G = number of points on integration grid
226     for(s in 1:S){
227       for(k in 1:K){
228         one_minus_detprob[i,s,k] <- 1 - exp(-dist2[i,k] * tau/2)
229       }
230     }
231     pdot.temp[i] <- 1 - prod(one_minus_detprob[i,,])
232     pdot[i] <- max(pdot.temp[i], 1.0E-10)
233   }

```

```

234 esa <- sum(pdot[])*a # a = size of grid square in numerical integration
235 pstar <- esa / A
236
237 # Zero trick for initial 1/pstar^n
238
239 loglikterm <- -n * log(pstar)
240 lambda <- -loglikterm + 1000
241 dummy ~ dpois(lambda) # dummy = 0; entered as data
242
243 # Model for capture histories of observed individuals:
244
245 for(i in 1:n){
246   for(k in 1:K){
247     for(s in 1:S){
248       capthist[i,s,k] ~ dbern(detprob[i,s,k])
249       detprob[i,s,k] <- exp(-r2[i,k] * tau/2 )
250     }
251     r2[i,k] <- pow(X[i] - traps[k,1], 2) + pow(Y[i] - traps[k,2], 2)
252   }
253 }
254 }

```

255 **B.3. Super-population complete data likelihood approach - CD:R.** The model com-
 256 ponent of the JAGS code for the super-population complete data likelihood approach.

```

257 model {
258   # Priors:
259   psi ~ dbeta(0.001,1)
260   sigma ~ dunif(0,10)
261   tau <- 1/(sigma*sigma)
262   for(i in 1:M){
263     z[i] ~ dbern(psi)
264     X[i] ~ dunif(xlim[1], xlim[2])
265     Y[i] ~ dunif(ylim[1], ylim[2])
266   }
267
268   # Complete data likelihood component:
269
270   for(i in 1:M){
271     for(k in 1:K){
272       for(s in 1:S){
273         capthist[i,s,k] ~ dbern(detprob[i,s,k])
274         detprob[i,s,k] <- z[i] * exp(-r2[i,k] * tau/2)
275       }
276       r2[i,k] <- pow(X[i] - traps[k,1], 2) + pow(Y[i] - traps[k,2], 2)
277     }
278   }
279
280   # Calculate N:
281   N <- sum(z[])
282 }

```

```

283 B.4. Super-population complete data likelihood approach - CD:DE. The model com-
284 ponent of the JAGS code for the super-population complete data likelihood approach.
285 model{
286
287   # Priors:
288   psi ~ dbeta(0.001,1)
289   sigma ~ dunif(0,10)
290   tau <- 1/(sigma*sigma)
291
292   # Data augmentation part - using Durban and Elston approach:
293
294   for(i in 1:M){
295
296     # Define the first N individuals to be in population of interest
297
298     z[i] <- step(N-i) # z = 1 if i \le N; z = 0 if i > N.
299
300     # Prior for home range centre for an individual in the population
301
302     X1[i] ~ dunif(xlim[1], xlim[2])
303     Y1[i] ~ dunif(ylim[1], ylim[2])
304
305     # Set pseudo-prior for home range centre for an individual in the population
306     # Independent Beta priors for (x,y) location scaled to be in specified region
307
308     Xtemp ~ dbeta(xprior[1],xprior[2]) # xprior - pseudo-prior parameters entered as data
309     Ytemp ~ dbeta(yprior[1],yprior[2]) # yprior - pseudo-prior parameters entered as data
310
311     X2[i] <- xlim[1] + Xtemp*xlim[2]
312     Y2[i] <- ylim[1] + Ytemp*ylim[2]
313
314     X[i] <- z[i] * X1[i] + (1 - z[i]) * X2[i]
315     Y[i] <- z[i] * Y1[i] + (1 - z[i]) * Y2[i]
316
317   }
318
319   # Prior for N: (Jeffrey's prior over {n,n+1,...,M} following Link 2013).
320
321   n00 ~ dcat(prior[]) # prior = rep(1/(M+1-n),M+1-n); entered as data
322   n0 <- n00 - 1
323   N <- n+n0
324
325   # Use zero trick for factorial term
326   # Note loggam(N) instead of loggam(N+1) because of Jeffrey's prior for N
327
328   logLik <- loggam(N) - loggam(n0 + 1) - loggam(n + 1)
329   phi <- -logLik + 100000
330   dummy ~ dpois(phi) # dummy = 0; entered as data
331

```

```

332   for(i in 1:M){
333     for(k in 1:K){
334       for(s in 1:S){
335         capthist[i,s,k] ~ dbern(detprob[i,s,k])
336         detprob[i,s,k] <- z[i] * exp(-r2[i,k] * tau/2)
337       }
338       r2[i,k] <- pow(X[i] - traps[k,1], 2) + pow(Y[i] - traps[k,2], 2)
339     }
340   }
341 }
342

```

REFERENCES

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|---|--|