

**Murray G. Efford. 2011. Estimation of population density by spatially explicit capture–recapture analysis of data from area searches. *Ecology* 92:2202-2207.**

Appendix C. R code for likelihood-based analyses of horned lizard data and simulations.

This code uses version 2.1 of the R package ‘secr’ that may be obtained from <http://cran.r-project.org/>. See the package for source code and detailed documentation. The software uses ‘g0’ for the parameters  $p_{\infty}$  and  $\lambda_{\infty}$ , and defaults to a half-normal detection function ( $g$ ) (i.e., a Gaussian kernel).

1. Table 1. Flat-tailed horned lizard example. The example dataset `hornedlizardCH` is built into the R package from version 2.0. ‘`distribution = binomial`’ ensures that the estimates are spatially conditional, approximating Royle and Young (2008) (see Appendix A).

```
library(secr)
FTHL.fit <- secr.fit( capthist = hornedlizardCH,
                     details = list(distribution = "binomial") )
FTHL.fit
```

2. Bias and coverage, simulating data from fitted model for flat-tailed horned lizards

```
extrfn <- function(x) unlist(predict(x)[,2:5]) ## save estimate, SE, lcl, ucl
temp <- sim.secr(FTHL.fit, n = 1000, hessian = TRUE, extractfn = extrfn)
temp <- temp[temp$estimate3 < 100,] ## drop row(s) with invalid estimate
true <- predict(FTHL.fit)['D', 'estimate']
mean((temp$estimate1 - true)/true) ## bias
sd(temp$estimate1) / sqrt(nrow(temp)) / true ## sd(bias)
sum((temp$lcl1 < true) & (temp$ucl1 > true)) / nrow(temp) ## coverage
```

3. Table 2. Simulations for comparison with Royle and Young (2008) and Marques et al. (2011). Distances are in meters and density in animals  $\text{ha}^{-1}$ . The argument 'nx' determines the number of grid cells in x- and y-directions and hence their size.

```

runsim <- function (simtraps, outfile, nrepl = 100, nx = 64,
                    D = c(0.234, 0.352, 0.469, 0.586, 0.781),
                    g0 = 0.25, sigma = c(100,200,400), nocc = 5) {
  nd <- length(D)
  ns <- length(sigma)
  out <- array (dim=c(nrepl, nd, ns, 6))
  masklist <- lapply(sigma, function(b) make.mask(simtraps, buffer=3*b, nx = nx))
  dimnames(out) <- list(1:nrepl, D, sigma, c('n', 'capts', 'D-hat',
      'se-Dhat', 'lcl', 'ucl'))
  for (r in 1:nrepl) {
    for (d in 1:nd) {
      for (s in 1:ns) {
        pop <- sim.popn (core = simtraps, D = D[d], buffer = sigma[s]*3,
          Ndist = 'fixed')
        tempcapt <- sim.caphist(simtraps, pop, detectpar = list(g0 = g0,
          sigma = sigma[s]), noccasions = nocc)
        out[r,d,s,1:2] <- c(nrow(tempcapt), sum(tempcapt))
        if (nrow(tempcapt)>0) {
          ## set start to avoid any problem with automatic start values
          tempfit <- secr.fit(tempcapt, mask = masklist[[s]],
            details = list(distribution = 'binomial'),
            start=c(log(0.5), log(0.2), log(200)), trace=F)
          out[r,d,s,3:6] <- unlist(predict(tempfit) ['D',-1])
        }
      }
    }
    cat ('completed replicate',r,' ',date(),'\n')
    flush.console()
    save (out, D, sigma, ns, nd, nrepl, simtraps, file = outfile)
  }
  out
}

bias <- function() {
  true <- rep(rep(D,rep(100,5)),3)
  out[,,,3][out[,,,3]>10] <- NA
  b <- (out[,,,3] - true) / true
  N <- apply(b, 2:3, function(x) sum(!is.na(x)))
  SE <- function (x) sd(x,na.rm=T)/sqrt(sum(!is.na(x)))
  list(N=N, bias = round(apply(b, 2:3, mean, na.rm = TRUE),3),

```

```

        sebias = round(apply(b, 2:3, SE),3))
    }
    coverage <- function () {
        true <- rep(rep(D,rep(100,5)),3)
        OK <- apply((out[,,,5] < true) & (out[,,,6] > true), 2:3, sum, na.rm=T)
        N <- apply((out[,,,5] < true) & (out[,,,6] > true), 2:3,
            function (x) sum(!is.na(x)))
        list(N=N, coverage=round(OK/N,3))
    }
    ## Run simulations and summarize
    library(secr)
    simtrap <- make.poly(exclusive = TRUE, x=c(0,1,1,0)*1000, y=c(0,0,1,1)*1000)
    out <- runsim (simtraps = simtrap, outfile = 'simulations.RData')
    bias()
    coverage()

```

## Literature cited

- Marques, T. A., L. Thomas, and J. A. Royle. 2011. A hierarchical model for spatial capture–recapture data: comment. *Ecology* 92: 526–528.
- Royle, J. A., and K. V. Young. 2008. A hierarchical model for spatial capture–recapture data. *Ecology* 89:2281–2289.