Distance sampling: Methods and applications

Lure point transect case study: Scottish crossbills

Contents

The Scottish crossbill is Britain's only endemic bird species. A lure point transect survey was used to estimate its population size (Summers and Buckland 2011). In this case study, we work through the analyses reported in Section 10.2.1 of the book. We do not attempt to recreate those analyses exactly; instead, we simplify the analyses, while retaining the essential elements to allow the approach to be adapted to other studies.

1 The trials

The trials data are in file `lure trials.csv`. We first read the data:

```
xbill <- read.table("lure trials.csv", header = T, sep = ",")
attach(xbill)
```

We next specify a distance (in metres) beyond which it is reasonable to assume that no crossbill will respond to the lure:

```
w <- 850
```

There are several covariates in the data that might affect probability that a bird responds to the lure: day (days from 1st January); time (hour of the day); habitat (1 = plantation, 2 = native pinewood); behavcode (1 = perching and feeding, 2 = giving excitement calls, 3 = singing); numbirds (flock size); and dist (distance of birds from the point when the lure was played). We can fit all these covariates as follows.

```
habitat <- factor(habitat)
behavcode <- factor(behavcode)
model1 <- glm(response ~ dist + numbirds + day + time + habitat + behavcode,
    family = binomial)
summary(model1)
```

```
Call:
glm(formula = response ~ dist + numbirds + day + time + habitat +
    behavcode, family = binomial)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9526  -0.8708   0.5563   0.8168   2.0009

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.641601   1.301148   2.030   0.0423 *
```

```
dist        -0.010086   0.002323  -4.342 1.41e-05 ***
numbirds     0.076882   0.081172   0.947   0.3436
day         -0.008597   0.007405  -1.161   0.2456
time        -0.020251   0.113258  -0.179   0.8581
habitat2    -0.263713   0.574532  -0.459   0.6462
behavcode2   0.070903   0.495256   0.143   0.8862
behavcode3   0.962426   0.614541   1.566   0.1173
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 219.23  on 166  degrees of freedom
Residual deviance: 169.10  on 159  degrees of freedom
  (8 observations deleted due to missingness)
AIC: 185.1

Number of Fisher Scoring iterations: 5
```

```
anova(model1)
```

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: response

Terms added sequentially (first to last)

          Df Deviance Resid. Df Resid. Dev
NULL                        166     219.23
dist       1   44.961       165     174.27
numbirds   1    1.514       164     172.76
day        1    0.825       163     171.93
time       1    0.115       162     171.82
habitat    1    0.022       161     171.80
behavcode  2    2.694       159     169.10
```

We see that only `dist` has a coefficient that is significantly different from zero. Experiment with dropping non-significant terms. Using a backwards stepping procedure, you should find that other covariates remain non-significant, so we can use the simple model:

```
model2 <- glm(response ~ dist, family = binomial)
summary(model2)
```

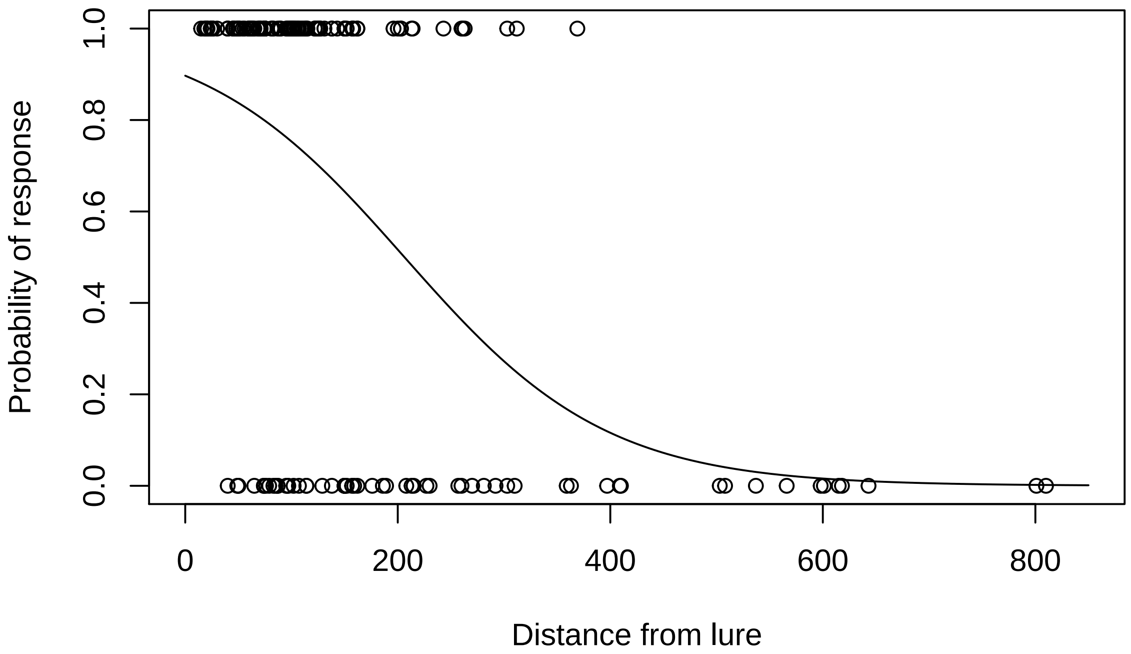
```
Call:
glm(formula = response ~ dist, family = binomial)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9521  -0.8066   0.5957   0.7618   1.9355

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.16370    0.33944   6.374 1.84e-10 ***
dist        -0.01049    0.00210  -4.993 5.94e-07 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 227.52  on 174  degrees of freedom
Residual deviance: 179.44  on 173  degrees of freedom
AIC: 183.44

Number of Fisher Scoring iterations: 5
```

(Degrees of freedom change a little as some covariates have a few missing values.)

We can now plot the fitted detection function model:

```
fits <- fitted(model2)
plot(dist, response, xlim = c(0, w), xlab = "Distance from lure", ylab = "Probability of response")
dist2 <- 0:w
phat <- predict.glm(model2, newdata = data.frame(dist = dist2), type = "response")
lines(dist2, phat)
```



2 The survey

We need to specify the function $/pi(r), r/lew$, which represents the probability density function of distances of animals from the point. If we extend the study area out a distance w around the entire boundary, thus creating a bufferzone, and place our survey points at random throughout the area + bufferzone (or randomly place a systematic grid of points over the extended study area), we can assume that this density is triangular:

```
pi_r <- dist2/sum(dist2)
```

If the study area is fragmented, it may not be cost-effective to sample into the bufferzone. If points are restricted to within the boundaries of the study area, and the species of interest does not occur beyond the study area because habitat is unsuitable, we need to adjust $/pi(r)$ so that it reflects the amount of available habitat (averaged over points) with increasing distance from the point (Buckland et al. 2006). (Summers and Buckland 2011) estimated this availability function, but for the purposes of this case study, we use the above triangular distribution.

```
# Pa is prob of response, integrating r from 0 to w, assuming that phat is a
# function of distance alone (no z's in model)

(Pa <- sum(phat * pi_r))
```

```
[1] 0.09709381
```

Thus we estimate that just under 10% of birds within 850m of a point are detected. We now read in the data from the main survey. Note that detection distances are unknown in the main survey; instead, we have used the trials data to estimate the detection function, and hence the proportion of birds within 850m that are detected.

```
detections <- read.table("mainsurveydetections.csv", sep = ",", header = T)
attach(detections)
```

We now calculate the number of points kmain in the main survey, and the total area a within 850m of a point, converting from m^2 to km^2. (Note that, if we do not include unsuitable habitat as described above, this total area should also exclude that habitat.)

```
kmain <- length(point)
a <- kmain * pi * (w/1000)^2
A <- 3505.8  # size in km2 of study area
```

We can now estimate the size of the population as

```
(Nscot <- sum(nscottish) * A/(Pa * a))
```

```
[1] 10007.67
```

Thus we estimate that there are around 10,000 birds. (This does not agree with the estimate of 13,600 in (Summers and Buckland 2011), because we have opted to keep the case study simple, and have omitted corrections for unsuitable habitat on surveyed plots, for juveniles, for unidentified crossbills, for incubating or brooding females, and for flying birds. Correcting only for unsuitable habitat on surveyed plots increases the abundance estimate to 12,900 birds.)

3 Measure of precision

We can calculate a standard error for our estimate and a 95% confidence interval for true abundance by bootstrapping both trials and points:

```
index <- 1:kmain
nboot <- 999
bNscot <- vector(length = nboot)
m <- length(dist)
tindex <- 1:m
bdist <- vector(length = m)
bresponse <- vector(length = m)
```

```
for (i in 1:nboot) {
    # bootstrap trials
    btindex <- sample(tindex, m, replace = TRUE)
    for (l in tindex) {
        bdist[l] <- dist[btindex[l]]
        bresponse[l] <- response[btindex[l]]
    }
    bmodel <- glm(bresponse ~ bdist, family = binomial)
    bphat <- predict.glm(bmodel, newdata = data.frame(bdist = dist2), type = "response")
    bPa <- sum(bphat * pi_r)
    # bootstrap points
    rindex <- sample(index, kmain, replace = TRUE)
    bNscot[i] <- sum(nscottish[rindex]) * A/(bPa * a)
}
# calculate bootstrap standard error
seNscot <- sd(bNscot)
# calculate bootstrap percentile confidence limits
bNscot <- sort(bNscot)
alpha.over.2 <- 0.025
loNscot <- bNscot[round(alpha.over.2 * (nboot + 1))]
hiNscot <- bNscot[round((1 - alpha.over.2) * (nboot + 1))]
(c(Nscot, seNscot, loNscot, hiNscot))
```

```
[1] 10007.672  2855.774  5693.588 16793.749
```

Thus we estimate the population size to be 10008 birds with standard error 2856 and 95% confidence interval (5694, 16794).

References

Buckland, S. T., R. W. Summers, D. L. Borchers, and L. Thomas. 2006. Point transect sampling with traps or lures. Journal of Applied Ecology 43:377–384.

Summers, R. W., and S. T. Buckland. 2011. A first survey of the global population size and distribution of the Scottish Crossbill *loxia scotica*. Bird Conservation International 21:186–198.

This document describes a case study from

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See Case studies website

Also see Distance sampling website
