Mark-recapture distance sampling using R

CREEM, Univ. of St. Andrews 2016 Advanced distance sampling workshop

August 2016

This document is designed to give you some pointers so that you can perform the Mark-Recapture Distance Sampling practical directly using the `mrds` package in R, rather than via the Distance visual interface. I assume you have some knowledge of R, the `mrds` package, and Distance.

1 Golf tee survey

Luckily for us, the golf tee dataset is provided aspart of the mrds package, so we don't have to worry about obtaining the data from the Distance GolfteesExercise project.

Open R and load the mrds library and golf tee dataset.

```
library(mrds)
data(book.tee.data)
#investigate the structure of the dataset
str(book.tee.data)
```

```
List of 4
 $ book.tee.dataframe:'data.frame': 324 obs. of  7 variables:
  ..$ object  : num [1:324] 1 1 2 2 3 3 4 4 5 5 ...
  ..$ observer: Factor w/ 2 levels "1","2": 1 2 1 2 1 2 1 2 1 2 ...
  ..$ detected: num [1:324] 1 0 1 0 1 0 1 0 1 0 ...
  ..$ distance: num [1:324] 2.68 2.68 3.33 3.33 0.34 0.34 2.53 2.53 1.46 1.46 ...
  ..$ size    : num [1:324] 2 2 2 2 1 1 2 2 2 2 ...
  ..$ sex     : num [1:324] 1 1 1 1 0 0 1 1 1 1 ...
  ..$ exposure: num [1:324] 1 1 0 0 0 0 1 1 0 0 ...
 $ book.tee.region   :'data.frame': 2 obs. of  2 variables:
  ..$ Region.Label: Factor w/ 2 levels "1","2": 1 2
  ..$ Area        : num [1:2] 1040 640
 $ book.tee.samples  :'data.frame': 11 obs. of  3 variables:
  ..$ Sample.Label: num [1:11] 1 2 3 4 5 6 7 8 9 10 ...
  ..$ Region.Label: Factor w/ 2 levels "1","2": 1 1 1 1 1 1 2 2 2 2 ...
  ..$ Effort      : num [1:11] 10 30 30 27 21 12 23 23 15 12 ...
 $ book.tee.obs      :'data.frame': 162 obs. of  3 variables:
  ..$ object      : int [1:162] 1 2 3 21 22 23 24 59 60 61 ...
  ..$ Region.Label: int [1:162] 1 1 1 1 1 1 1 1 1 1 ...
  ..$ Sample.Label: int [1:162] 1 1 1 1 1 1 1 1 1 1 ...
```

```
#extract the list elements from the dataset into easy-to-use objects
detections <- book.tee.data$book.tee.dataframe
#make sure sex and exposure are factor variables
detections$sex <- as.factor(detections$sex)
detections$exposure <- as.factor(detections$exposure)
region <- book.tee.data$book.tee.region
samples <- book.tee.data$book.tee.samples
obs <- book.tee.data$book.tee.obs
```

We'll start by fitting the initial full independence model, with only distance as a covariate - just as was done in the "FI - MR dist" model in Distance. Indeed, if you did fit that model in Distance, you can look in the Log tab at the R code Distance generated, and compare it with the code we use here.

Feel free to use ? to find out more about any of the functions used – e.g., `?ddf` will tell you more about the ddf function.

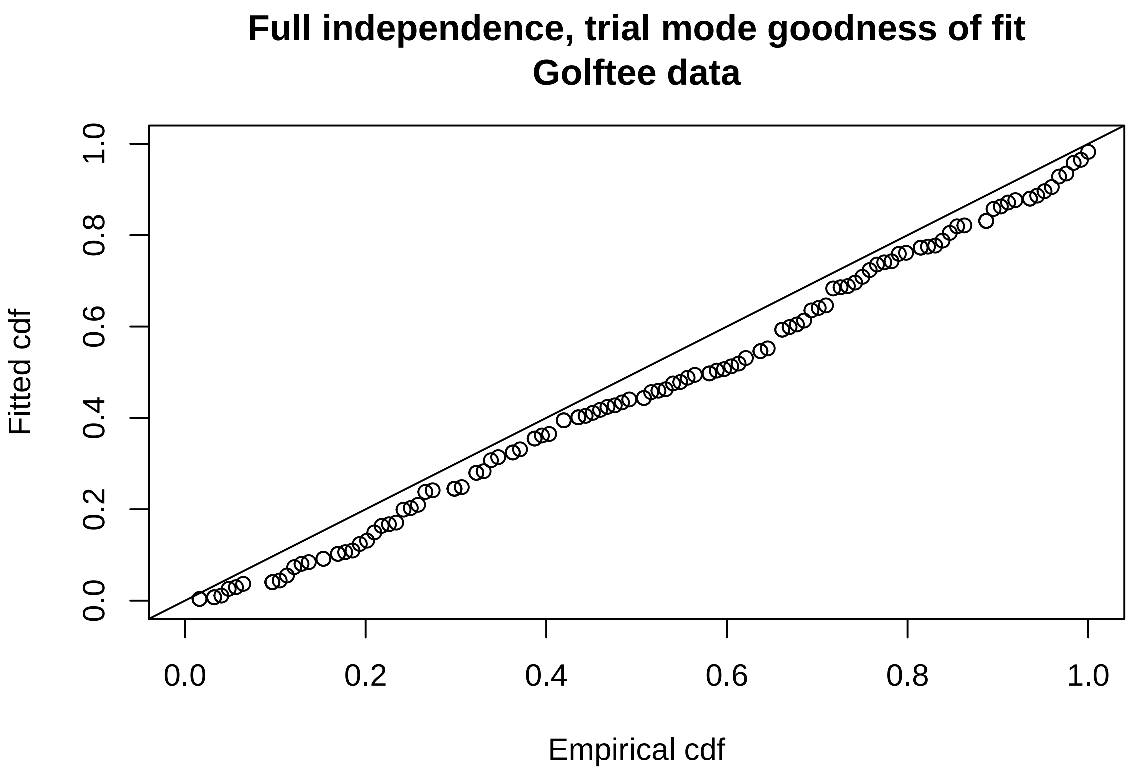
```r
#Fit the model
fi.mr.dist <- ddf(method='trial.fi',mrmodel=~glm(link='logit',formula=~distance),
                 data=detections,meta.data=list(width=4))
#Create a set of tables summarizing the double observer data (this is what Distance does)
detection.tables <- det.tables(fi.mr.dist)
#Print these detection tables
detection.tables
```

```
Observer 1 detections
           Detected
            Missed Detected
  [0,0.4]        1       25
  (0.4,0.8]      2       16
  (0.8,1.2]      2       16
  (1.2,1.6]      6       22
  (1.6,2]        5        9
  (2,2.4]        2       10
  (2.4,2.8]      6       12
  (2.8,3.2]      6        9
  (3.2,3.6]      2        3
  (3.6,4]        6        2

Observer 2 detections
           Detected
            Missed Detected
  [0,0.4]        4       22
  (0.4,0.8]      1       17
  (0.8,1.2]      0       18
  (1.2,1.6]      2       26
  (1.6,2]        1       13
  (2,2.4]        2       10
  (2.4,2.8]      3       15
  (2.8,3.2]      4       11
  (3.2,3.6]      2        3
  (3.6,4]        1        7

Duplicate detections

  [0,0.4] (0.4,0.8] (0.8,1.2] (1.2,1.6]   (1.6,2]   (2,2.4] (2.4,2.8]
       21        15        16        20         8         8         9
(2.8,3.2] (3.2,3.6]   (3.6,4]
        5         1         1

Observer 1 detections of those seen by Observer 2
          Missed Detected Prop. detected
[0,0.4]        1       21      0.9545455
(0.4,0.8]      2       15      0.8823529
(0.8,1.2]      2       16      0.8888889
(1.2,1.6]      6       20      0.7692308
(1.6,2]        5        8      0.6153846
(2,2.4]        2        8      0.8000000
(2.4,2.8]      6        9      0.6000000
(2.8,3.2]      6        5      0.4545455
(3.2,3.6]      2        1      0.3333333
(3.6,4]        6        1      0.1428571
```

```r
# They could also be plotted, but I've not done so in the interest of space
# plot(detection.tables)

#Produce a summary of the fitted detection function object
summary(fi.mr.dist)
```

```
Summary for trial.fi object
Number of observations               :  162
Number seen by primary               :  124
Number seen by secondary (trials)    :  142
Number seen by both (detected trials):  104
AIC                                  :  452.8094


Conditional detection function parameters:
             estimate        se
(Intercept)  2.900233 0.4876238
distance    -1.058677 0.2235722

                        Estimate          SE         CV
Average p              0.6423252  0.04069409 0.06335434
Average primary p(0)   0.9478579  0.06109655 0.06445750
N in covered region  193.0486185 15.84826458 0.08209468
```

```r
#Produce goodness of fit statistics and a qq plot
gof.result <- ddf.gof(fi.mr.dist,
                      main="Full independence, trial mode goodness of fit\nGolftee data")
```




```r
chi.distance <- gof.result$chisquare$chi1$chisq
chi.markrecap <- gof.result$chisquare$chi2$chisq
chi.total <- gof.result$chisquare$pooled.chi
```

Abbreviated χ^2 goodness of fit assessment shows the χ^2 contribution from the distance sampling model to be 11.5 and the χ^2 contribution from the mark-recapture model to be 3.4. The combination of these elements produces a total χ^2 of 14.9 with 17 degrees of freedom, resulting in a P-value of 0.604

```
#Calculate density estimates using the dht function
tee.abund <- dht(fi.mr.dist,region,samples,obs)
kable(tee.abund$individuals$summary, digits=2,
      caption="Survey summary statistics for golftees")
```

Table 1: Survey summary statistics for golftees

Region	Area	CoveredArea	Effort	n	ER	se.ER	cv.ER	mean.size	se.mean
1	1040	1040	130	229	1.76	0.12	0.07	3.18	0.21
2	640	640	80	152	1.90	0.33	0.18	2.92	0.23
Total	1680	1680	210	381	1.81	0.14	0.08	3.07	0.15

```
kable(tee.abund$individuals$N, digits=2,
      caption="Abundance estimates for golftee population with two strata")
```

Table 2: Abundance estimates for golftee population with two strata

Label	Estimate	se	cv	lcl	ucl	df
1	356.52	32.35	0.09	294.54	431.53	17.13
2	236.64	44.14	0.19	147.33	380.09	5.06
Total	593.16	60.38	0.10	478.32	735.57	16.06

Now, see if you can work out how to change the call to ddf to fit the other models mentioned in the exercise, and then write code to enable you to compare the models and select among them.

2 Crabeater seal survey

```
## Warning: package 'knitcitations' was built under R version 3.3.1
```

This analysis is described in Borchers et al. (2005) of aerial survey data looking for seals in the Antarctic pack ice. There were four observers in the plane, two on each side (front and back).

The data from the survey has been saved in a `.csv` file. This file can be easily read into R, and with the `checkdata()` function, the information to construct the region, sample, and observation table can be extracted. Note that these tables are only needed when estimating abundance by scaling up from the covered region to the study area.

```
library(Distance)
crabseal <- read.csv("crabbieMRDS.csv")
#  Half normal detection function, 700m truncation distance,
#        logit function for mark-recapture component
crab.ddf.io <- ddf(method="io", dsmodel=~cds(key="hn"),
                   mrmodel=~glm(link="logit", formula=~distance),
                   data=crabseal, meta.data=list(width=700))
summary(crab.ddf.io)
```

```
Summary for io.fi object
Number of observations   :  1740
Number seen by primary   :  1394
Number seen by secondary :  1471
Number seen by both      :  1125
AIC                      :  3011.463
```

```
Conditional detection function parameters:
                estimate           se
(Intercept)  2.107762345 0.0994391200
distance    -0.003087713 0.0003159216

                        Estimate          SE          CV
Average primary p(0)   0.8916554 0.009606428 0.010773701
Average secondary p(0) 0.8916554 0.009606428 0.010773701
Average combined p(0)  0.9882614 0.002081614 0.002106339


Summary for ds object
Number of observations :  1740
Distance range         :  0  -  700
AIC                    :  22314.4

Detection function:
 Half-normal key function

Detection function parameters
Scale coefficient(s):
            estimate        se
(Intercept) 5.828703 0.0268578

           Estimate         SE         CV
Average p 0.5845871 0.01247837 0.02134562


Summary for io object
Total AIC value :  25325.86

                        Estimate          SE         CV
Average p              0.5777249  0.01239179 0.02144929
N in covered region 3011.8139211 79.84197966 0.02650960
```

Goodness of fit could be examined in the same manner as the golf tees by the use of `ddf.gof(crab.ddf.io)` but I have not shown this step.

Following model criticism and selection, estimation of abundance ensues. the estimates of abundance for the study area are arbitrary because inference of the study was restricted to the covered region. Hence the estimates of abundance here are artificial, but if we wished to produce them, we would need to produce the region, sample, and observation tables and apply Horvitz-Thompson like estimators to produce estimates of $\hat{N}$. The use of `covert.units` adjusts the units of perpendicular distance measurement (m) to units of transect effort (km). Be sure to perform the conversion correctly or your abundance estimates will be off by orders of magnitude.

```
tables <- Distance:::checkdata(crabseal[crabseal$observer==1,])
crab.ddf.io.abund <- dht(region=tables$region.table,
                         sample=tables$sample.table, obs=tables$obs.table,
                         model=crab.ddf.io, se=TRUE, options=list(convert.units=0.001))
kable(crab.ddf.io.abund$individuals$summary, digits=3,
      caption="Summary information from crabeater seal aerial survey.")
```

Table 3: Summary information from crabeater seal aerial survey.

Region	Area	CoveredArea	Effort	n	ER	se.ER	cv.ER	mean.size	se.mean
1	1e+06	8594.082	6138.63	2053	0.334	0.033	0.097	1.18	0.013

```r
kable(crab.ddf.io.abund$individual$N, digits=3,
      caption="Crabeater seal abundance estimates for study area of arbitrary size.")
```

Table 4: Crabeater seal abundance estimates for study area of arbitrary size.

Label	Estimate	se	cv	lcl	ucl	df
Total	413493.2	41201.49	0.09964248	339670.9	503359.6	128.6257

References

Borchers, D. L., J. L. Laake, C. Southwell, and C. G. M. Paxton. 2005. "Accommodating Unmodeled Heterogeneity in Double-Observer Distance Sampling Surveys." *Biometrics* 62 (2). Wiley-Blackwell: 372–78. doi:10.1111/j.1541-0420.2005.00493.x.