

Supplementary material for paper van der Heijden, Whittaker, Cruyff, Bakker and van der Vliet.

Estimation in R

This document provides an example of the estimation procedure and the corresponding R-code to fit a log-linear model and obtain a confidence interval for the estimate of the population size N . The example involves the log-linear model $[AX2][BX1]$ to the data presented in Table 5 in the paper. In this example where A and B are the two incomplete registers, with covariate $X1$ measured in A but not in B and covariate $X2$ measured in B but not in A . The data are supposed to be in an SPSS file called "data.sav", with the missing values on the covariates coded as system missing.

The estimation procedure:

Step 1: reading the data into R

Step 2: fitting the log-linear model to the data with the missing covariates

Step 3: obtain data with imputation of the missing values of the covariates

Step 4: fitting the log-linear to the imputed data to obtain an estimate of N

Step 5: calculation of the fit statistics

Step 6: parametric bootstrap to obtain the confidence interval for the estimate of N

R-code:

loading the necessary libraries

```
library(cat)
library(foreign)
```

step 1: reading the data into R

```
datafile      <- read.spss("data.sav",use.value.labels=FALSE,to.data.frame=TRUE)
colnames(datafile) <- c("A","B","X1","X2")
```

```
a <- 1
b <- 2
x1 <- 3
x2 <- 4
```

specification of the log-linear model $[AX2][BX1]$,

```
MODEL      <- Freq~A*X2+B*X1
MARGINS    <- c(a,x2,0,b,x1)
MAXMODEL   <- Freq~A*X2+B*X1+X1*X2
```

step 2: fitting the log-linear model to the data with the missing covariates

```
table.miss <- as.data.frame(table(datafile))
observed   <- ifelse(table.miss[,1] == 2 & table.miss[,2] == 2, 0, 1)
table.miss <- cbind(table.miss,observed)
dcat       <- prelim.cat(as.matrix(datafile))
```

```

struc.zero      <- array(observed, dim = dcat$d)/sum(observed)
dcat.saturated  <- em.cat(dcat,start=struc.zero,showits=FALSE)
dcat.model      <- ecm.cat(dcat,start=struc.zero,margins=MARGINS,showits=FALSE,eps= 1e-7)

```

Step 3: obtain data with imputation of the missing values covariates

```

table.complete      <- table.miss
table.complete$Freq <- as.numeric(dcat.model*dcat$n)

```

Step 4: fitting the log-linear to the imputed data to obtain an estimate of N

```

glm.complete      <- glm(MODEL,family=poisson,subset=(observed ==1), data = table.complete)
model.frame.complete <- model.frame(MODEL, data = table.complete)
fitted.complete    <- predict(glm.complete, model.frame.complete, type = "response")
hatN               <- sum(fitted.complete)

```

Step 5: calculation of the fit statistics

```

deviance.model     <- -2*(logpost.cat(dcat,dcat.model)-logpost.cat(dcat,dcat.saturated))
glm.maxmodel       <- glm(MAXMODEL, family = poisson, subset = (observed == 1),
                          data = table.complete)
df.adjusted        <- glm.complete$df.residual-glm.maxmodel$df.residual
aic                <- deviance.model+2*(glm.complete$df.null-glm.complete$df.residual+1)

```

printing the results

```

results            <- cbind(deviance.model,df.adjusted,aic,hatN)
colnames(results)  <- c("Deviance","df","AIC","Pop.size")
rownames(results)  <- c(MODEL)
print(results)

```

Step 6: parametric bootstrap to obtain the confidence interval for the estimate of N

```

nreps             <- 1000
boot.result       <- matrix(0,nreps,1)

for(i in 1:nreps){
  boot.data      <- table.complete[,1:(length(table.complete)-2)]
  Freq           <- rmultinom(n=1,size=round(hatN,0),
                             prob=fitted.complete/sum(fitted.complete))
  boot.data      <- cbind(boot.data,Freq)
  obs            <- ifelse(boot.data$A== 2 & boot.data$B == 2, 0, 1)
  boot.fit       <- glm(MODEL,family=poisson,subset=(obs==1),data=boot.data)
  boot.matrix    <- model.frame(MODEL, data = boot.data)
  boot.pred      <- predict(boot.fit, boot.matrix, type = "response")
  boot.result[i] <- sum(boot.pred)
}

```

```

CI_Nhat <- quantile(boot.result[,1], probs = c(0.025,0.975))

```