Electronic Supplementary Information (ESM)

Estimating the abundance of rare and elusive carnivores from photographic-sampling data when the population size is very small

Brian D. Gerber[1], Jacob S. Ivan[2], and Kenneth P. Burnham[3]

[1]Colorado Cooperative Fish and Wildlife Research Unit, Department of Fish, Wildlife and Conservation Biology, Colorado State University, Fort Collins, CO 80523, USA.

[2]Colorado Division of Parks and Wildlife, Wildlife Research Center, 317 West Prospect Road, Fort Collins, Colorado 80526-2097, USA

[3]Professor Emeritus, Department of Fish, Wildlife, and Conservation Biology, Colorado State University, Fort Collins, CO 80523, USA.

Corresponding Author:

Brian D. Gerber, Colorado Cooperative Fish and Wildlife Research Unit Department of Fish, Wildlife and Conservation Biology, Colorado State University, Fort Collins, CO 80523, USA.

bgerber@colostate.edu

R code for simulations

```
######################################
#Simulate heterogeneous capture-recapture
#data to examine how many individuals will
#likely be detected and secondly, to
#estimate abundance using the M0-unconditional
#likelihood C-R estimator and quantify uncertainty
#with profile-likelihood confidence intervals
##############################################
#Author: Brian D. Gerber
#Contact: bgerber@colostate.edu
#Last Modified: 8/22/2012
#############################################


###########################
#Load Functions and Libraries
###########################
library(RMark)
library(gregmisc)

  expit = function (logit){
    exp(logit)/(1+exp(logit))
  }

  logit = function (expit){
    log(expit/(1-expit))
  }

###########################
#Setup Variables
###########################
  J=30   #J will be the number of sampling occasions, identified as t in manuscript
  N=10  #True abundance- animals that have some chance of capture
  sets=100 #Number of datasets to simulate
  l=0
  num_capt=rep(0,sets) #number of animals detected- M(t+1)
  M0_N=M0_se=M0_lcl=M0_ucl=rep(0,sets) # Store abundance estimates
  #Set the heterogeneity for detection probability- logit(p) as
  mu=0.1
  sigma=0.1

###############################################################
#Plot heterogeneity of p
```

```
################################################################

  plot(1, type="n", axes=T, xlab="", ylab="", xlim=c(0,1), ylim=c(0,4))
  curve(dnorm(x,mu,sigma),col=2,lwd=2,add=TRUE)

########################
#Create heterogeneity
#C-R Data and start simulation
########################

  while (l<sets){
    if(l%%10==0)cat("Simulation # ",l,"\n"); flush.console()
      mat=data.frame(matrix(0,N,J))
        for (q in 1:N){
          detection=expit(rnorm(1,logit(mu),sigma))
          for (r in 1:J){
            sample_unif=runif(1,0,1)
            if(sample_unif<=detection){
           mat[q,r]=1}
            else{mat[q,r]=0}
          }
        }



    #Drop the capture histories with no detections
    Rcapture_input=as.matrix(mat[rowSums(mat) != 0, , drop=FALSE])


    #Create input for RMARK
    mark_input=mat[rowSums(mat) != 0, , drop=FALSE]
    mark_input=as.data.frame(apply(mark_input,1,paste,collapse=""))
    mark_input <- data.frame(lapply(mark_input, as.character), stringsAsFactors=FALSE)
    colnames(mark_input)= c("ch")
    num_capt_temp=dim(Rcapture_input)[1]

    #With low p and N, sum C-H will have zero animals
    #or some C-H will be too small, such as 2 animals, which
    #can't be used to estimate N

    if(num_capt_temp<=2){
      next}
    else{
      l=l+1
      num_capt[l]=dim(Rcapture_input)[1]  #this is the number of animals caught
```

```
      #Define Null model
      pdotshared=list(formula=~1,share=TRUE)

      #Run model through RMARK- M0-unconditional with profile likelihood CI.
      m0=try(mark(mark_input,model="Closed",profile.int =
TRUE,adjust=FALSE,model.parameters=list(p=pdotshared), brief=FALSE,output=FALSE,
delete=TRUE, invisible=TRUE), silent=TRUE)

      #Save estimates in simulation
      M0_N[l]=as.numeric(m0$results$real[2,1]) #Abundance only
      M0_se[l]=as.numeric(m0$results$real[2,2]) #Abundance SE
      M0_lcl[l]=as.numeric(m0$results$real[2,3]) #LCL
      M0_ucl[l]=as.numeric(m0$results$real[2,4]) #UCL
#      if(!is.na(M0_se[l])){if(M0_se[l]>N*inflation){M0_lcl[l]=M0_ucl[l]=NA
#                                                  M0_se[l]= NA}}


  }
}
#########################################################
M0_N=as.numeric(M0_N)
M0_se=as.numeric(M0_se)
M0_lcl=as.numeric(M0_lcl)
M0_ucl=as.numeric(M0_ucl)
M0_se[M0_se=="NaN"]=NA
M0=cbind(M0_N,M0_se,M0_lcl,M0_ucl)

#Display frequency of captures by individual
rowSums(Rcapture_input)
mean(rowSums(Rcapture_input)) #Mean frequency of detection

# Plot the histogram of individuals detected
hist(num_capt, xlim=c(0,(N+10)), freq=FALSE)
abline(v=N, lwd=2, col=2) #Plots truth

# Plot proportion of population detected
hist((num_capt/N), xlim=c(0,1), freq=FALSE)

#Plot histogram of abundance estimates
hist(M0_N, breaks=10, main="Abundance Estimate", xlim=c(0,(N+10)),freq=FALSE)
abline(v=mean(M0_N), col=1, lwd=2) #Expected value of N-hat
abline(v=N, col=2, lwd=2) #N-truth


#Expected_bias
mean(M0_N)-N
```

```
#Plot all simulations- abundance estimates and profile condidence intervals
win.graph()
plotCI(seq(1,sets,1), M0_N, pch=16,ui=M0_ucl, li=M0_lcl,xlim=c(1,sets), ylim=c(0,50), gap=0,
xlab="Simulation #",ylab=expression(hat(N)))
abline(h=N, lwd=2, col=2)
```

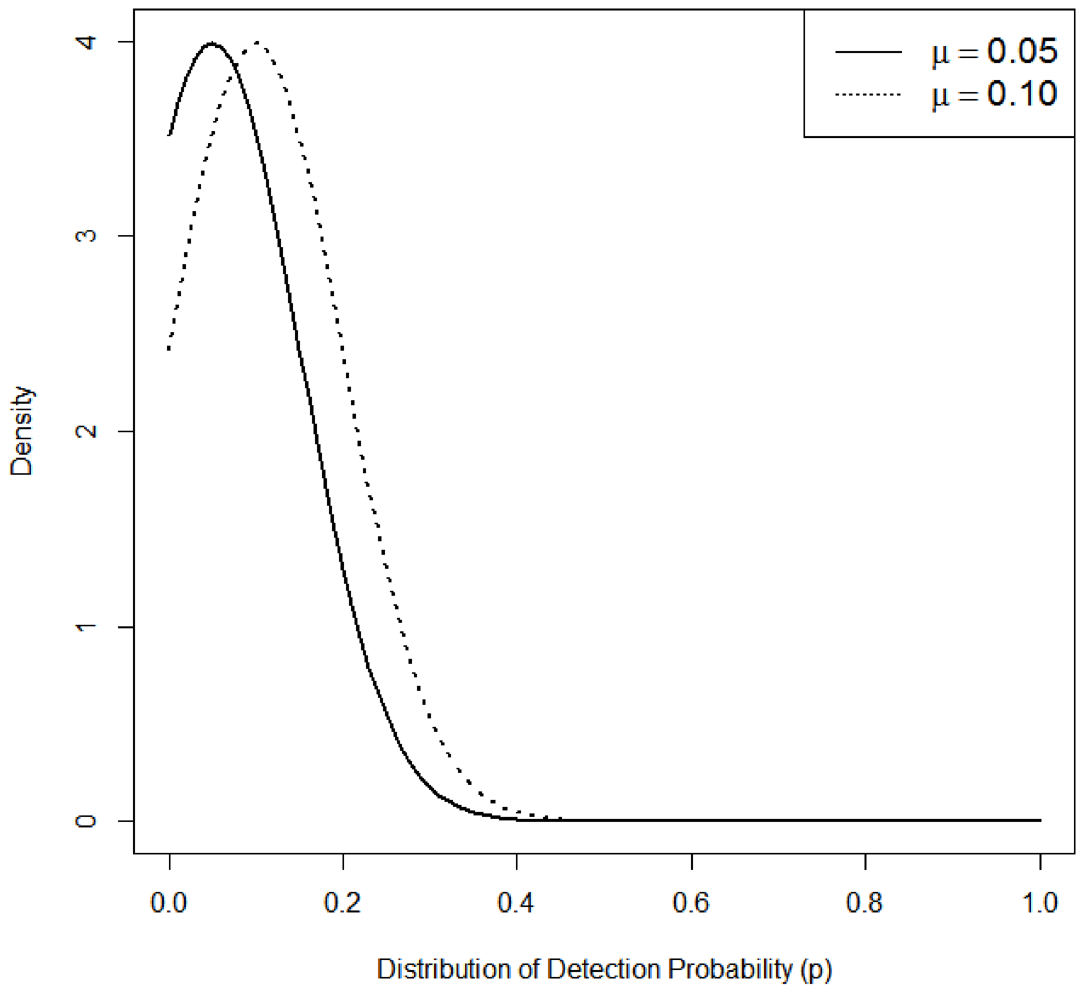
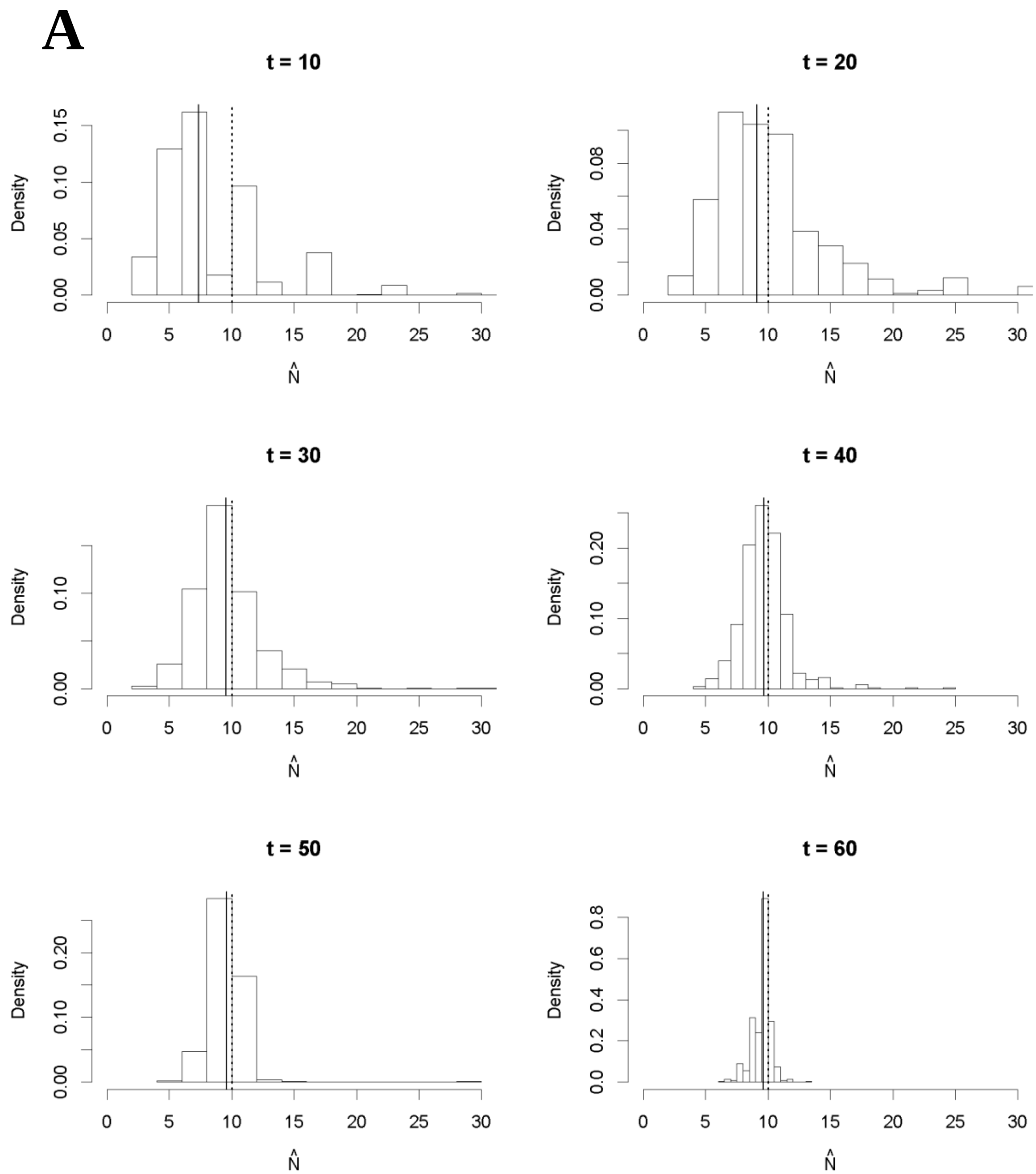


Fig. S1 Distributions of detection probability used to model individual heterogeneity, where logit(p_i) = N(expit(μ), σ) and σ = 0.1.


A
t = 10
t = 20
t = 30
t = 40
t = 50
t = 60
Density
N̂

B

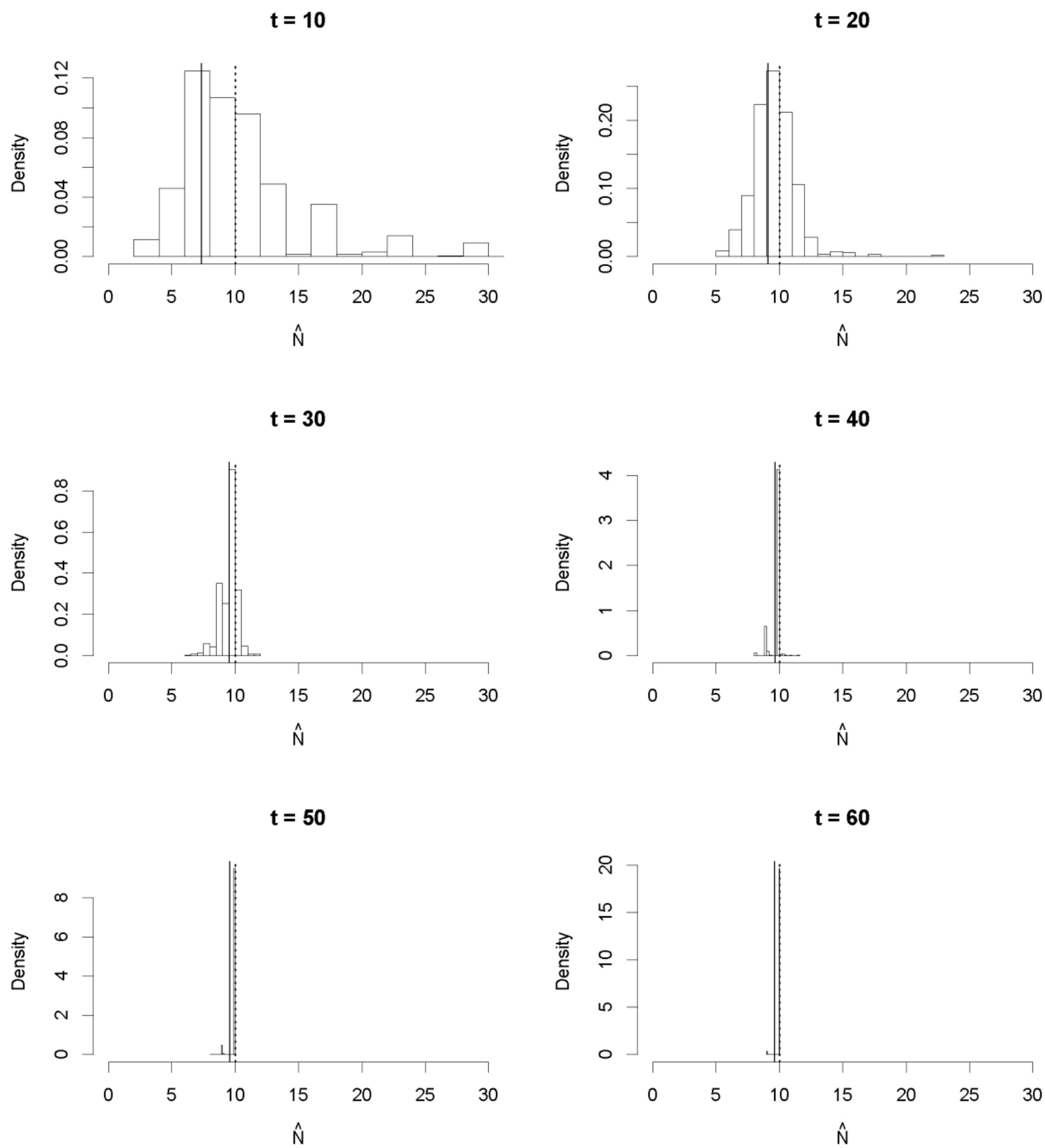


Fig. S2 Empirical distributions of abundance estimates ($\widehat{N}$) using the M_0 (null, constant p) closed-capture recapture estimator and simulated heterogeneous data where A) logit(p_i) = N(expit(μ = 0.05), σ = 0.1) and B) logit(p_i) = N(expit(μ = 0.10), σ = 0.1) over sampling occasions (t) of 10-60; the dotted line at N = 10 indicates true abundance and the solid line is E[N].

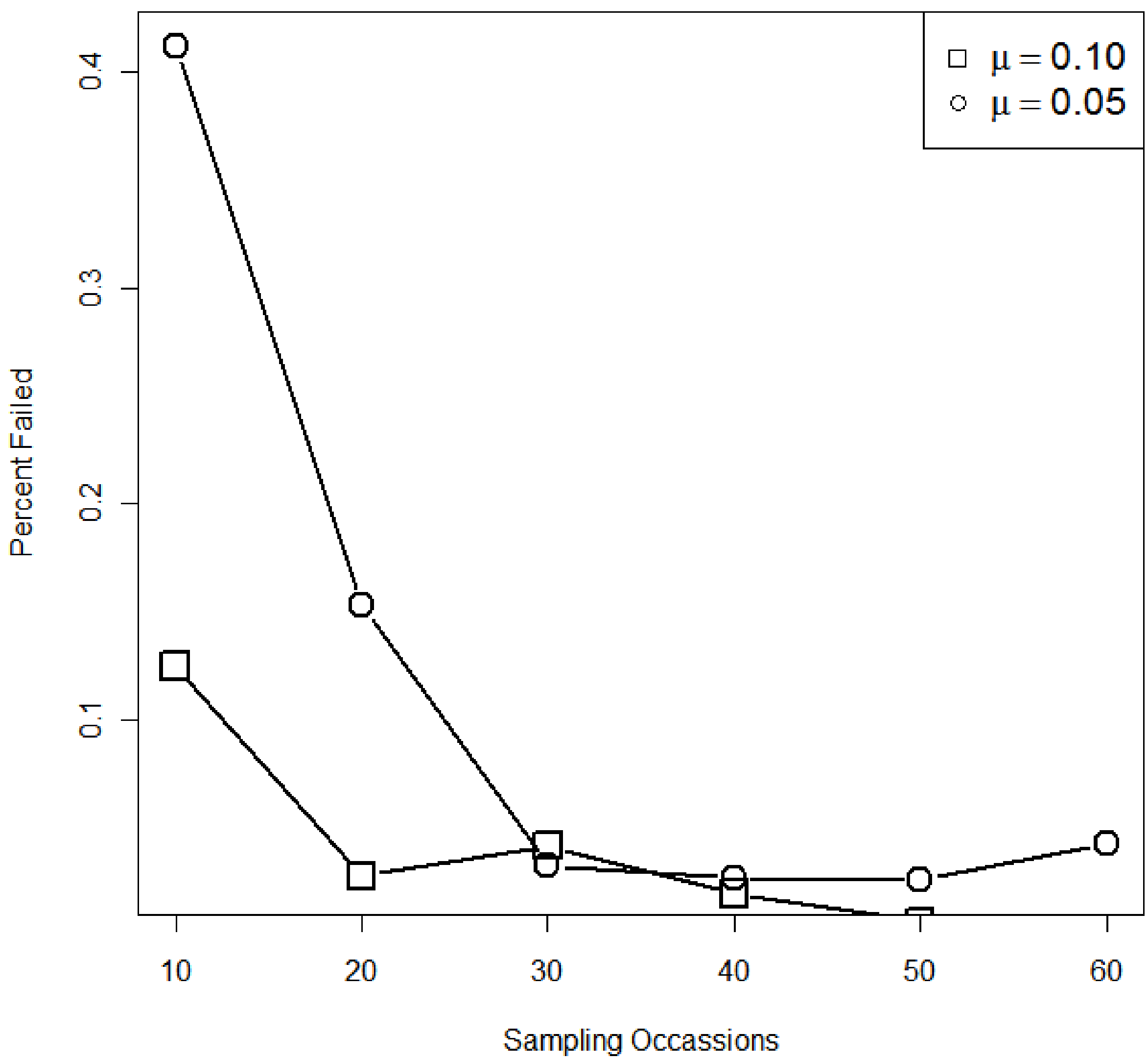


Fig. S3 Percentage of failed point or standard error estimates from simulated heterogeneous capture-recapture data where logit(p_i) = N(expit(μ), σ) where μ = 0.05 or 0.1 and σ = 0.1 over sampling occasions of 10-60.

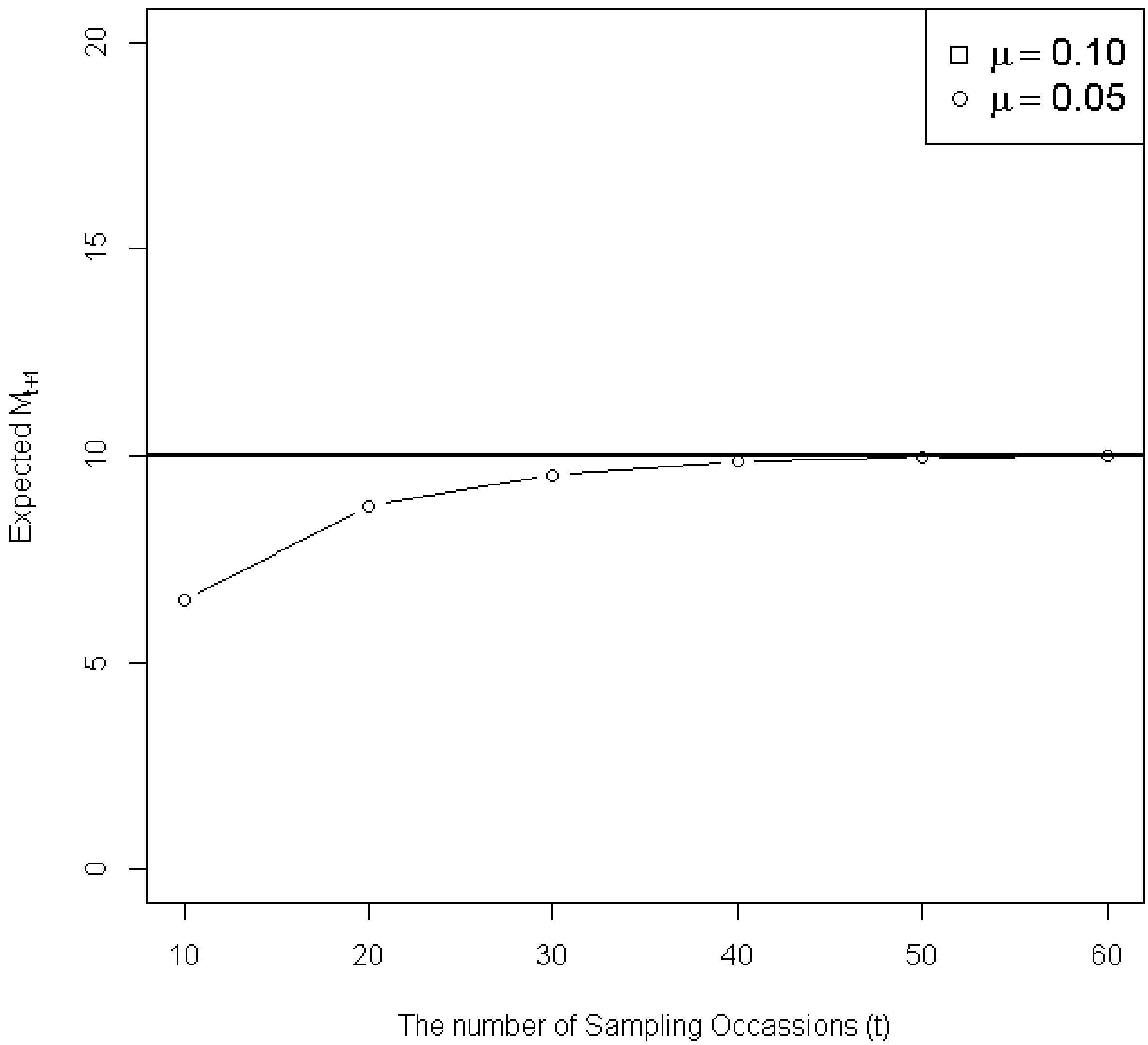


Fig. S4 The expected number of unique individuals detected (M_{t+1}) from simulated heterogeneous capture-recapture data where logit(p_i) = N(expit(μ), σ) where μ = 0.05 or 0.1 and σ = 0.1 over sampling occasions of 10-60.