Comparing performance of multiple non-invasive genetic capture–recapture methods for abundance estimation: a case study with the Sonoran pronghorn *Antilocapra americana sonoriensis*

SUSANNAH P. WOODRUFF, PAUL M. LUKACS and LISETTE P. WAITS

SUPPLEMENTARY MATERIAL 1 *R* code for mark-recapture simulations in *capwire* and *RMark*.

```
# Mark-recapture simulation in R
# First in capwire

library(capwire)
#create population with 2 different deposition rates
#with binomial distribution
dep <- function(n, m) {
  samp <- rpois(n,m)
  samp
}
################################################
n.sessions <- 1 #Number of sessions required—always 1 in capwire
#x, k and j change depending on the total number of individuals.
Always 2 males to 1 female
x <- 198 #females
k <- 102 #males
j <- x+k

for(i in 1:100){

  for(i in 1:n.sessions){
    #dep.pop <- data.frame(Ind.ID=1:200,
Captures=sample(c(0:14),400, replace=TRUE))
    #Create vector holding the number of scats deposited per
individual where n = 200 individuals and 0-14 depositions could
occur
    #Generate dep.pop data for a single 7 day session
    dep.pop.f <- dep(n=x, m=7) #This is #females x 7 days with
#pp/day=1

    dep.pop.f <- as.matrix(dep.pop.f, nrow=x, ncol=1)
    rownames(dep.pop.f) <- (1:x)

    dep.pop.f <- cbind(Ind.ID=c(1:x), dep.pop.f) #add column
called Ind.ID
    rownames(dep.pop.f) <- NULL #remove column called "rownames"
```

```
    #Males
    dep.pop.m <- dep(n=k, m=14)  #this # males  x 7 days Mean pp/
day=2
    dep.pop.m <- as.matrix(dep.pop.m, nrow=k, ncol=1)
    rownames(dep.pop.m) <- (x+1:k)

    dep.pop.m <- cbind(Ind.ID=c(x+1:k), dep.pop.m) #add column
called Ind.ID
    rownames(dep.pop.m) <- NULL #remove column called "rownames"

    dep.pop <- rbind(dep.pop.f, dep.pop.m) #combine into single
data frame of xxx individuals

    colnames(dep.pop) <- c("Ind.ID","Captures")

    dep.pop1 <- dep.pop #make new dataframe to sample from to
keep dep.pop with total captures

    samples.collected <- 0  #Initialize the number of samples
collected in that session to 0
    samples.desired <- 150  #Identify the number of samples
desired (this could be changed to another loop if you desired
different amounts in each session)
    session <- NULL

    if(samples.desired >= sum(dep.pop1[, 2])){
      print("Error: there are insufficient scats deposited to
meet the desired sample size")
      print(paste('session', i, " capture data not generated",
sep=""))
    } else{
      while(samples.collected < samples.desired){
        sample.i <- sample(dep.pop1[,1], 1, replace=TRUE,
prob=dep.pop1[,2])
        if(dep.pop1[sample.i,'Captures']!=0){            #If
there are scats to sample
          samples.collected <- samples.collected+1       #Collect
a sample - increase the # of samples collected
          session <- append(session, dep.pop1[sample.i,'Ind.ID'])
#Record the Ind.ID of the sample collected
          dep.pop1[sample.i,'Captures'] <-
(dep.pop1[sample.i,'Captures']-1) #Decrease the number available
from that individual
```

```
        }  #If there are no scats to sample (from the individual
selected), do nothing.
      }
    }
    assign(paste('session', i, sep=""), session)
  }

  #change into table showing number of times each individual was
caught by session (always a single session in capwire)

  sess.1 <- sort(sess.1 <- (session1))
  Total <- c(sess.1)

  Total <- table(Total)
  Total <- table(Total)

  CAPWIRE <- as.data.frame.table(Total)
  colnames(CAPWIRE) <-  c("capture.class", "No.ind") #add column
names

  # Fit tirm to the simulated capture histories
  model <- list()
  for(i in 1:1){
    res.tirm <- fitTirm(data =CAPWIRE, max.pop=400)
    model[[i]] <- res.tirm
  }

  # Calculate confidence intervals (CI) for each simulated
capture history
  CI <- list()
  for(i in 1:1){
    boot.tirm <- bootstrapCapwire(x=model[[i]], bootstraps=10,
CI=c(0.025, 0.975))
    CI[[i]] <- boot.tirm
  }

  # Extract and calculate means across abundance and CI estimates
for each simulated capture history
  n <- list()
  lowCI <- list()
  highCI <- list()
  cap.ind <- list()
  for(i in 1:1){
    runs <- CI[[i]]
    pop.size <- runs$ml.pop.size
```

```
    ci <- runs$conf.int
    cap.ind <- res.tirm$cap.ind
    low <- ci[1]
    high <- ci[2]
    n[[i]] <- pop.size
    lowCI[[i]] <- low
    highCI[[i]] <- high
  }

  mean.n <- mean(as.numeric(n))
  mean.lowCI <- mean(as.numeric(lowCI))
  mean.highCI <- mean(as.numeric(highCI))
  mean.cap.ind <- mean(as.numeric(cap.ind))

  SOPH.sim <- cbind(mean.n,mean.lowCI,mean.highCI,mean.cap.ind)
  SOPH.sim

  Write.table(#output table of total captures to table)
}


# Then in Mark
library(RMark)
#create population with 2 different deposition rates
#with binomial distribution
dep <- function(n, m) {
  samp <- rpois(n,m)
  samp
}
################################################
n.sessions <- 2 #Set number of sessions required—2 or 3 in this
case
#x, k and j change depending on the total number of individuals.
Always 2 males to 1 female
x <- 132 #females
k <- 68 #males
j <- x+k

for(i in 1:100){

for(i in 1:n.sessions){
  #dep.pop <- data.frame(Ind.ID=1:200,
Captures=sample(c(0:14),400, replace=TRUE))
```

```
  #Create vector holding the number of scats deposited per
individual where n = 200 individuals and 0-14 depositions could
occur
  #Generate dep.pop data for a single 7 day session
  dep.pop.f <- dep(n=x, m=7) #This is #females x 7 days with #pp/
day=1

  dep.pop.f <- as.matrix(dep.pop.f, nrow=x, ncol=1)
  rownames(dep.pop.f) <- (1:x)

  dep.pop.f <- cbind(Ind.ID=c(1:x), dep.pop.f) #add column called
Ind.ID
  rownames(dep.pop.f) <- NULL #remove column called "rownames"

  #Males
  dep.pop.m <- dep(n=k, m=14)  #this # males  x 7 days Mean
pp/day=2
  dep.pop.m <- as.matrix(dep.pop.m, nrow=k, ncol=1)
  rownames(dep.pop.m) <- (x+1:k)

  dep.pop.m <- cbind(Ind.ID=c(x+1:k), dep.pop.m) #add column
called Ind.ID
  rownames(dep.pop.m) <- NULL #remove column called "rownames"

  dep.pop <- rbind(dep.pop.f, dep.pop.m) #combine into single
data frame of 200 individuals

  colnames(dep.pop) <- c("Ind.ID","Captures")

  #dep.pop$Ind.ID <- as.numeric(dep.pop$Ind.ID)
  #write.table(dep.pop,"path to table.txt", sep="\t") #output
table of total captures

  dep.pop1 <- dep.pop #make new dataframe to sample from to keep
dep.pop with total captures

  samples.collected <- 0  #Initialize the number of samples
collected in that session to 0
  samples.desired <-  350 #Identify the number of samples desired
(this could be changed to another loop if you desired different
amounts in each session)
  session <- NULL

  if(samples.desired >= sum(dep.pop1[, 2])){
```

```
    print("Error: there are insufficient scats deposited to meet
the desired sample size")
    print(paste('session', i, " capture data not generated",
sep=""))
  } else{
    while(samples.collected < samples.desired){
      sample.i <- sample(dep.pop1[,1], 1, replace=TRUE,
prob=dep.pop1[,2])
      if(dep.pop1[sample.i,'Captures']!=0){ #If there are scats
to samples
        samples.collected <- samples.collected+1   #Collect a
sample - increase the # of samples collected
        session <- append(session, dep.pop1[sample.i,'Ind.ID'])
#Record the Ind.ID of the sample collected
        dep.pop1[sample.i,'Captures'] <-
(dep.pop1[sample.i,'Captures']-1)   #Decrease the number
available from that individual
      }  #If there are no scats to sample (from the individual
selected), do nothing.
    }
  }
  assign(paste('session', i, sep=""), session)
}

#change into table showing number of times each individual was
caught by session
sess.1 <- sort(sess.1 <- (session1))
sess.2 <- sort(sess.2 <- (session2))
#sess.3 <- sort(sess.3 <- (session3))


####################################

#creating MARK encounter history
#put into ascending order and rename
sort(sess.1 <- unique(session1))
sort(sess.2 <- unique(session2))
#sort(sess.3 <- unique(session3))

y <-  matrix(NA, j, n.sessions) #create empty matrix--change

indx <- 1:j #index 1-200 since these are all possible numbers
that could be in there
```

```
for (i in 1:length(indx)) {    #create matrix where like values
line up
  y[i,1] <- ifelse(indx[i] %in% sess.1, indx[i], NA)
  y[i,2] <- ifelse(indx[i] %in% sess.2, indx[i], NA)
  #y[i,3] <- ifelse(indx[i] %in% sess.3, indx[i], NA)
}

#All.sess <- c(sess.1, sess.2, sess.3) #3 sessions
All.sess <- c(sess.1, sess.2) #2 sessions
##insert closed capture likelihood here


All.sess <- as.data.frame(y) #convert to data frame


All.sess[All.sess==1:j] <- 1 #replace all values (except NA with
1)
All.sess <- All.sess[rowSums(is.na(All.sess)) != ncol(All.sess),]
#remove rows with all NA to avoid 000 EH

All.sess[is.na(All.sess)] <- 0

#colnames(All.sess) <- c("sess1", "sess2", "sess3") #add column
names-- 3 sessions
colnames(All.sess) <- c( "sess1", "sess2") #add column names--2
sessions

All.sess <- cbind(Ind.ID=as.numeric(row.names(All.sess)),
All.sess)


All.sess$newcol <- ";"
All.sess$newcol1 <- "/*"
All.sess$newcol2 <- "*/"

All.sess$newcol3 <- ifelse(All.sess$Ind.ID<=x, 1, 0)
All.sess$newcol4 <- ifelse(All.sess$Ind.ID>x, 1, 0)
All.sess$newcol5 <- " "
All.sess$newcol6 <- " "

All.sess <- data.frame(All.sess, row.names=NULL)

#All.sess <- All.sess[,c("sess1", "sess2", "sess3", "newcol5",
"newcol3", "newcol5", "newcol4", "newcol", "newcol1", "Ind.ID",
"newcol2") ] #3 sessions
```

```
All.sess <- All.sess[,c("sess1", "sess2", "newcol5", "newcol3",
"newcol5", "newcol4", "newcol", "newcol1", "Ind.ID", "newcol2") ]
#2 sessions

write.table(All.sess,"MARK_sim.inp", sep="", quote=FALSE,
col.names=FALSE, row.names=FALSE) #output .inp for MARK


input <- convert.inp("MARK_sim",  group.df =
data.frame(sex=c("Female", "Male")), covariates = NULL,
                   use.comments = TRUE)

input.model=mark(input, model="Closed")

input.processed <- process.data(input, model="Closed",
groups=("sex"))


  psex=list(formula=~sex, share=TRUE) #p by sex

  p.sex <- mark(input.processed, model.parameters=list(p=psex))


#input.results #shows output of model like in MARK with AIC
values, weights, deviance, etc
#input.results$p.sex #page pops up with all results
#input.results$p.sex$results$real #to view real parameter results
from the model
#input.results$p.sex$results$derived #show results of N for this
model

#parameter.mod.avg <- model.average(input.results, vcv=FALSE)
#model average p, c, and f0
p.female <- p.sex$results$real$estimate[1]
p.lcif <- p.sex$results$real$lcl[1]
p.ucif <- p.sex$results$real$ucl[1]

p.male <- p.sex$results$real$estimate[2]
p.lcim <- p.sex$results$real$lcl[2]
p.ucim <- p.sex$results$real$lcl[2]

#std errors for each are

sqrt(diag(p.sex$results$derived.vcv$`N Population Size`))
```

```
# total abundance is
n <- sum(p.sex$results$derived$`N Population Size`$estimate)
p.sex$results$derived$`N Population Size`$estimate #show estimate

# se for total abundance is square root of sum of variances and
covariances
sqrt(sum(p.sex$results$derived.vcv$`N Population Size`))

lci <- n - sqrt(sum(p.sex$results$derived.vcv$`N Population
Size`))
uci <- n + sqrt(sum(p.sex$results$derived.vcv$`N Population
Size`))


MARKout.sim <- cbind(n, lci, uci, p.female, p.lcif, p.ucif,
p.male, p.lcim, p.ucim)
write.table(MARKout.sim,path_to_table,  append=TRUE,
col.names=FALSE) #output table of total captures
}
```

TABLE S1 Simulation results in *capwire* and *MARK*.

No. of sampling sessions	True abundance	No. of samples/ session[1]	Total no. of samples	N hat	Lower 95% CI	Upper 95% CI	SE	CV	CI coverage	RMSE[2]
capwire										
1	300	150	150	343	320.99	397.27	19.45804	0.057	0.33	6.16
1	300	200	200	350	344.80	397.22	13.37423	0.038	0.13	8.33
1	300	250	250	349	348.00	397.00	12.50000	0.036	0.07	8.00
1	300	300	300	360	363.00	399.00	9.18367	0.026	0.01	12.00
1	300	350	350	364	363.00	398.00	8.92857	0.025	0.01	13.65
1	300	400	400	359	355.00	397.00	10.71429	0.030	0.03	11.60
1	300	450	450	347	349.00	397.00	12.24490	0.035	0.02	7.36
1	300	500	500	339	346.00	392.00	11.73469	0.035	0.00	5.07
1	300	550	550	341	342.00	385.00	10.96939	0.032	0.00	5.60
1	300	600	600	340	339.71	379.16	10.06365	0.030	0.00	5.31
1	250	125	125	286	263.00	378.00	29.33673	0.103	0.39	5.18
1	250	200	200	298	298.00	379.00	20.66327	0.069	0.02	9.22
1	250	250	250	300	300.00	372.00	18.36735	0.061	0.01	10.00
1	250	300	300	303	300.00	364.00	16.32653	0.054	0.03	11.24
1	250	350	350	297	291.00	349.00	14.79592	0.050	0.04	8.84
1	250	400	400	285	291.00	352.00	15.56122	0.055	0.02	4.90
1	250	450	450	282	283.00	327.00	11.22449	0.040	0.01	4.10
1	250	500	500	282	279.00	318.00	9.94898	0.035	0.02	4.10
1	250	600	600	279	274.00	308.00	8.67347	0.031	0.02	3.36
1	250	750	750	264	257.00	278.00	5.35714	0.020	0.21	0.78
1	200	100	100	226	205.00	330.00	31.88776	0.141	0.49	3.38
1	200	150	150	236	227.00	324.00	24.74490	0.211	0.18	6.48
1	200	200	200	239	232.00	305.00	18.62245	0.162	0.09	7.61
1	200	250	250	240	235.00	289.00	13.77551	0.124	0.02	8.00
1	200	300	300	230	226.00	281.00	14.03061	0.134	0.08	4.50
1	200	350	350	226	225.00	271.00	11.73469	0.052	0.01	3.38

No. of sampling sessions	True abundance	No. of samples/ session[1]	Total no. of samples	N hat	Lower 95% CI	Upper 95% CI	SE	CV	CI coverage	RMSE[2]
1	200	400	400	225	222.00	255.00	8.41837	0.042	0.05	3.13
1	200	500	500	223	216.00	245.00	7.39796	0.033	0.11	2.65
1	200	600	600	212	205.00	225.00	5.10204	0.033	0.18	0.72
1	150	75	75	176	150.00	281.00	33.41837	0.190	0.61	4.51
1	150	150	150	176	170.44	230.89	15.41939	0.098	0.35	4.51
1	150	200	200	179	170.35	217.94	12.13865	0.068	0.12	5.67
1	150	250	250	167	165.00	212.00	11.98980	0.072	0.08	1.93
1	150	300	300	170	165.00	193.00	7.14286	0.042	0.11	2.67
1	150	350	350	167	162.00	187.00	6.37755	0.038	0.10	1.93
1	150	400	400	166	157.00	186.00	7.39796	0.045	0.29	1.71
1	150	450	450	158	151.00	169.00	4.59184	0.029	0.36	0.43
1	100	50	50	111	91.00	197.00	27.04082	0.244	0.73	1.21
1	100	100	100	119	111.00	159.00	12.24490	0.103	0.24	3.61
1	100	150	150	117	110.00	148.00	9.69388	0.083	0.30	2.89
1	100	200	200	115	111.00	136.00	6.37755	0.055	0.11	2.25
1	100	250	250	111	103.00	125.00	5.61224	0.051	0.38	1.21
1	100	300	300	105	100.00	114.00	3.57143	0.034	0.51	0.25
Mark										
3	300	150	450	276	264.06	287.95	6.09572	0.022	0.19	1.920
3	300	200	600	279	271.44	286.69	3.88853	0.014	0.07	1.461
3	300	250	750	283	277.55	287.91	2.64060	0.009	0.03	0.994
3	300	300	900	287	283.14	290.52	1.88342	0.007	0.03	0.578
3	300	350	1050	289	286.56	291.65	1.29739	0.004	0.02	0.396
3	300	400	1200	292	290.14	293.85	0.94745	0.003	0.03	0.214
3	300	450	1350	294	292.37	294.85	0.63380	0.002	0.02	0.138
3	300	500	1500	295	295.16	295.66	0.12651	0.000	0.02	0.070
3	300	550	1650	297	296.91	296.92	0.00086	0.000	0.03	0.033
3	300	600	1800	298	297.77	297.77	0.00027	0.000	0.08	0.017

No. of sampling sessions	True abundance	No. of samples/ session[1]	Total no. of samples	N hat	Lower 95% CI	Upper 95% CI	SE	CV	CI coverage	RMSE[2]
3	250	83	249	229	210.44	248.44	9.69254	0.042	0.4	1.691
3	250	125	375	232	221.00	243.00	5.61224	0.024	0.29	1.296
3	250	200	600	235	229.76	239.96	2.60299	0.011	0.07	0.917
3	250	250	750	239	235.22	241.79	1.67596	0.007	0.06	0.528
3	250	300	900	241	239.14	243.56	1.12863	0.005	0.04	0.299
3	250	350	1050	244	242.29	245.23	0.74958	0.003	0.05	0.156
3	250	400	1200	246	245.31	245.97	0.16896	0.001	0.06	0.077
3	250	450	1350	247	246.93	246.93	0.00047	0.000	0.03	0.037
3	250	500	1500	248	248.35	248.35	0.00021	0.000	0.23	0.011
3	200	67	201	180	164.00	196.47	8.28497	0.046	0.39	1.953
3	200	100	300	185	175.20	194.97	5.04321	0.027	0.32	1.112
3	200	150	450	187	182.06	192.39	2.63475	0.014	0.08	0.816
3	200	200	600	191	187.85	193.84	1.52808	0.008	0.1	0.419
3	200	250	750	193	191.55	195.03	0.88704	0.005	0.06	0.225
3	200	300	900	195	195.02	196.02	0.25690	0.001	0	0.102
3	200	350	1050	197	197.18	197.19	0.00039	0.000	0.12	0.039
3	200	400	1200	199	198.61	198.61	0.00018	0.000	0.24	0.010
3	150	50	150	138	123.26	153.42	7.69365	0.056	0.53	0.906
3	150	75	225	136	128.12	144.64	4.21436	0.031	0.29	1.237
3	150	100	300	138	133.02	143.47	2.66593	0.019	0.13	0.921
3	150	150	450	142	139.87	144.76	1.24678	0.009a	0.08	0.394
3	150	200	600	145	144.08	146.10	0.51591	0.004	0.07	0.161
3	150	250	750	148	147.48	147.48	0.00023	0.000	0.09	0.041
3	150	300	900	149	148.85	148.85	0.00011	0.000	0.36	0.009
3	100	50	150	91	84.16	97.62	3.43272	0.038	0.36	0.830
3	100	75	225	93	89.01	96.13	1.81533	0.020	0.19	0.552

No. of sampling sessions	True abundance	No. of samples/ session[1]	Total no. of samples	N hat	Lower 95% CI	Upper 95% CI	SE	CV	CI coverage	RMSE[2]
3	100	100	300	95	92.95	97.12	1.06257	0.011	0.22	0.246
3	100	150	450	97	97.43	97.51	0.02061	0.000	0.08	0.064
3	100	200	600	99	99.20	99.20	0.00007	0.000	0.46	0.007
2	300	150	300	275	251.86	298.84	11.98688	0.044	0.48	2.025
2	300	200	400	277	260.39	292.82	8.27331	0.030	0.33	1.824
2	300	250	500	278	266.72	289.90	5.91335	0.021	0.21	1.568
2	300	300	600	280	271.20	288.46	4.40154	0.016	0.14	1.356
2	300	350	700	283	275.77	289.39	3.47547	0.012	0.14	1.011
2	300	400	800	285	280.13	290.69	2.69399	0.009	0.08	0.709
2	300	450	900	286	282.19	290.21	2.04478	0.007	0.07	0.635
2	300	500	1000	288	284.89	291.22	1.61590	0.006	0.03	0.476
2	300	550	1100	290	287.60	292.73	1.30770	0.005	0.05	0.322
2	300	600	1200	291	289.38	293.45	1.03602	0.004	0.03	0.249
2	250	83	166	230	193.79	266.40	18.52152	0.080	0.49	1.585
2	250	125	250	226	204.97	246.28	10.53704	0.047	0.33	2.376
2	250	200	400	232	220.97	243.76	5.81432	0.025	0.36	1.244
2	250	250	500	231	223.66	239.21	3.96774	0.017	0.13	1.379
2	250	300	600	236	230.40	242.23	3.01704	0.013	0.19	0.749
2	250	350	700	237	232.77	241.28	2.17157	0.009	0.07	0.673
2	250	400	800	239	236.00	242.35	1.61924	0.007	0.08	0.468
2	250	450	900	241	239.07	243.79	1.20305	0.005	0.06	0.294
2	250	500	1000	243	241.04	244.47	0.87512	0.004	0	0.210
2	200	67	134	182	150.18	213.86	14.15000	0.077	0.55	1.450
2	200	75	150	183	155.10	210.56	9.25756	0.052	0.4	2.189
2	200	100	200	179	160.93	197.22	9.25756	0.052	0.4	2.189
2	200	150	300	184	173.38	195.54	5.65130	0.031	0.42	1.208
2	200	200	400	185	178.14	191.81	3.48766	0.019	0.2	1.129

No. of sampling sessions	True abundance	No. of samples/ session[1]	Total no. of samples	N hat	Lower 95% CI	Upper 95% CI	SE	CV	CI coverage	RMSE[2]
2	200	250	500	189	183.75	193.48	2.48124	0.013	0.14	0.648
2	200	300	600	191	187.66	194.19	1.66581	0.009	0.12	0.412
2	200	350	700	192	190.11	194.40	1.09567	0.006	0.1	0.300
2	200	400	800	194	192.73	195.56	0.72154	0.004	0.09	0.174
2	200	450	900	195	194.83	195.84	0.25628	0.001	0.1	0.108
2	150	75	150	136	119.24	152.37	8.45365	0.062	0.5	1.343
2	150	100	200	137	125.80	147.93	5.64650	0.041	0.54	1.150
2	150	150	300	139	132.96	145.18	3.11833	0.022	0.3	0.797
2	150	200	400	142	138.27	145.49	1.84110	0.013	0.27	0.440
2	150	250	500	144	141.57	145.71	1.05506	0.007	0.23	0.272
2	150	300	600	145	144.61	146.40	0.45583	0.003	0.15	0.137
2	150	350	700	147	146.76	146.96	0.05029	0.000	0.14	0.063
2	150	400	800	148	148.27	148.27	0.00022	0.000	0.22	0.020
2	150	450	900	149	148.61	148.61	0.00008	0.000	0.25	0.013
2	150	500	1000	149	149.31	149.31	0.00004	0.000	0.5	0.007
2	100	50	100	90	76.72	103.27	6.77363	0.075	0.44	1.001
2	100	100	200	91	86.77	96.15	2.39324	0.026	0.31	0.729
2	100	150	300	94	92.20	96.30	1.04730	0.011	0.14	0.331
2	100	200	400	97	96.43	97.07	0.16349	0.002	0.22	0.109
2	100	250	500	98	98.39	98.44	0.01384	0.000	0.2	0.026
2	100	300	600	99	99.21	99.21	0.00005	0.000	0.5	0.006

[1]Number of samples per session assuming all samples achieve a consensus genotype.

[2]Relative mean square error/

TABLE S2 Cost per sample (in USD) for non-invasive genetic (faecal pellet) sampling capture–recapture methods for Sonoran pronghorn abundance estimation in Arizona, USA. Sample collection includes envelope to store sample, tape, pens and silica desiccant. Species ID PCR is included for all samples for comparison to other studies, but in this study only samples not achieving consensus genotypes were run in Species ID. Individual ID includes six repetitions (average number needed to obtain genotype) of the microsatellite multiplex and corresponding analysis on ABI. The salary cost (USD 25/hour) includes time for sample collection and recording sample in database, DNA extraction and analysis, PCR set up and analysis for species and individual ID (i.e. allele calling and genotype matching). It does not include salary associated with travel time to and from sampling location because personnel are already traveling to sampling locations for pronghorn feeding and monitoring. The cost estimate does not include time spent generating population estimates in software.

Item/task	Cost (USD)
Sample collection	0.15
DNA extraction	5.65
Species ID PCR	0.55
Individual ID PCR	9.45
Salary	12.98
Total	28.78

TABLE S3 Comparison of the number of unique individuals (Min. count) identified in 2013 and 2014. There were no extra samples in Session 1. Sessions 2 and 3 (separately and combined) include individuals from single session sites because we were comparing estimates of reduced sessions, and a site with just a single visit would be included regardless of the timing of the sampling. Caps/ind. represents captures per individual in c*apwire* and *p* (m: male, f: female) is average capture probability in closed capture models (CCR).

	Year	2013			2013 + extra			2014		
Estimator	Session	Min. count	Caps/ ind.	*p*	Min. count	Caps/ind.	*p*	Min. count	Caps/ind.	*p*
capwire	1	51	2.49	--	51	2.50	--	83	2.60	--
	2	54	2.22	--	58	2.49	--	73	2.24	--
	3	68	2.59	--	70	3.30	--	77	2.00	--
capwire	1 & 2	67	3.54	--	68	3.70	--	100	3.68	--
CCR	1 & 2	67	--	m: 0.83 f: 0.44	68	--	m: 0.82 f: 0.42	100	--	m: 0.76 f: 0.64
capwire	2 & 3	80	3.58	--	84	4.31	--	96	3.29	--
CCR	2 & 3	80	--	m: 0.80 f: 0.71	84	--	m: 0.76 f: 0.69	96	--	m: 0.76 f: 0.67
capwire	ALL	88	5.38	--	91	5.21	--	110	4.63	--
CCR	ALL	88	--	m: 0.72 f: 0.49	91	--	m: 0. 71 f: 0.55	110	--	m: 0.73 f: 0.61