Introduction to Resampling in R

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Friday, November 06, 2015

Ecological studies often suffer from limited resource availability, including time, money, and people power. Oversampling not only taxes these resources needlessly, but may also negatively influence the system being studied; for example, through lethal collections of organisms or unnecessary handling of non-target species. Projects relying on data collection over multiple field seasons may benefit from resampling algorithms that can identify efficient collection protocols if oversampling is known or thought to have occurred.

We'll be using a mock data set of tagged and non-tagged eels captured in a small lake to estimate population size, then build a resampling algorithm to explore the sensitivity of using varying numbers of traps and sampling events.

- 50 American eels were captured from a small lake, marked with an external tag, and released back into the lake
- 15 traps were checked 20 times over a season
- number of tagged and non-tagged eels in each trap was recorded

Load Required Packages

```
library(dplyr)
library(FSA)
library(ggplot2)
library(digest)
library(lubridate)
```

You can find the dataset here: https://github.com/DanielleQuinn/RLessons/blob/master/SensitivityAnalysis/recapture_data.csv

```
df.data<-read.csv("recapture_data.csv")
```

First, take a look at the data frame `df.data`

```
head(df.data)

  X trap check present tag
1 1    1     1       1   1
2 2    1     1       1   0
3 3    1     1       1   0
4 4    1     1       1   0
5 5    1     1       1   0
6 6    1     1       1   0

str(df.data)
```

```
'data.frame':	150036 obs. of  5 variables:
 $ X      : int  1 2 3 4 5 6 7 8 9 10 ...
 $ trap   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ check  : int  1 1 1 1 1 1 1 1 1 2 ...
 $ present: int  1 1 1 1 1 1 1 1 1 1 ...
 $ tag    : int  1 0 0 0 0 0 0 0 0 1 ...
```

Baseline Population Size Estimate

We'll be using the `mrClosed()` function from the `FSA` package to estimate the population size using the Schnabel method. Without getting into too much detail, the Schnbabel method is used when we have multiple sampling occassions and assumes a closed population. The function requires specific input, including:

- `n`: the number of captured animals
- `m`: the number of recaptured marked animals
- `M`: the number of extant marked animals prior to the sample

Step 1: Build cmr data frame

```
df.cmr<-data.frame(df.data%>%
                     group_by(check)%>%
                     summarise(date=unique(check),n=sum(present), m=sum(tag),
M=50)%>%
                     select(n,m,M))
```

Step 2: Estimate population size

```
pop.est<-summary(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel"))) #From
FSA package
pop.low<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[1] #
Confidence intervals #
pop.high<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[2] #
Confidence intervals #
baseline<-data.frame(pop.est, pop.low, pop.high)
baseline

    N pop.low pop.high
1 152     151      154
```

We see that using all of the data avilable (50 traps each checked 20 times), our population estimate is 152, with confidence intervals of 151 and 154.

Because the lake is very small, we're fairly certain that oversampling may have occurred, and our goal is to design a sampling protocol for the next year that maximizes the efficiency of our sampling effort. We want to know the minimum number of traps and the minimum number of checks that we can do that will result in a realistic estimate of population size.

Sample 10 Random Traps

```
all_traps<-unique(df.data$trap) # A vector of all available traps
use_traps<-sample(all_traps, 10) # Choose 10 random traps
```

Subset the data to include only those traps, then create `df.cmr` and use `mrClosed()` to estimate population size.

```
my_subset<-data.frame(df.data%>%
  filter(trap %in% use_traps))

df.cmr<-data.frame(my_subset%>%
                     group_by(check)%>%
                     summarise(date=unique(check),n=sum(present), m=sum(tag),
M=50)%>%
                     select(n,m,M))

pop.est<-summary(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel"))) #From
FSA package
pop.low<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[1] #
Confidence intervals #
pop.high<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[2] #
Confidence intervals #
results<-data.frame(pop.est, pop.low, pop.high)
results

    N pop.low pop.high
1 163     159      167
```

Sample X Random Traps

Repeat this analysis using varying numbers of traps and see how our results vary from the baseline population estimates. We are going to resample from 10 to 50 random traps and apply to analysis for each subset.

Step 1: Build a function that creates the cmr data frame and produces the population estimate and confidence intervals

```
my_cmr<-function(my_subset)
{
  # Build cmr data frame
  df.cmr<-data.frame(my_subset%>%
                       group_by(check)%>%
                       summarise(date=unique(check),n=sum(present),
m=sum(tag), M=50)%>%
                       select(n,m,M))

  # Estimate Population Size
  pop.est<<-summary(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))
#From FSA package
  pop.low<<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[1] #
Confidence intervals #
  pop.high<<-
stats::confint(with(df.cmr,mrClosed(n=n,m=m,M=M,method="Schnabel")))[2] #
Confidence intervals #
}
```

Step 2: Set up a data frame to handle the output of the analyses We want a data frame that has information about how many traps were used, and the results of our analysis. In this case, we're going to have 41 sets of output.

```
results<-data.frame(traps=c(10:50), pop.est=NA, pop.low=NA, pop.high=NA)
results

   traps pop.est pop.low pop.high
1     10      NA      NA       NA
2     11      NA      NA       NA
3     12      NA      NA       NA
4     13      NA      NA       NA
5     14      NA      NA       NA
6     15      NA      NA       NA
7     16      NA      NA       NA
8     17      NA      NA       NA
9     18      NA      NA       NA
10    19      NA      NA       NA
11    20      NA      NA       NA
12    21      NA      NA       NA
13    22      NA      NA       NA
14    23      NA      NA       NA
15    24      NA      NA       NA
16    25      NA      NA       NA
17    26      NA      NA       NA
18    27      NA      NA       NA
19    28      NA      NA       NA
20    29      NA      NA       NA
21    30      NA      NA       NA
22    31      NA      NA       NA
23    32      NA      NA       NA
24    33      NA      NA       NA
25    34      NA      NA       NA
26    35      NA      NA       NA
27    36      NA      NA       NA
28    37      NA      NA       NA
29    38      NA      NA       NA
30    39      NA      NA       NA
31    40      NA      NA       NA
32    41      NA      NA       NA
33    42      NA      NA       NA
34    43      NA      NA       NA
35    44      NA      NA       NA
```

```
36    45       NA       NA        NA
37    46       NA       NA        NA
38    47       NA       NA        NA
39    48       NA       NA        NA
40    49       NA       NA        NA
41    50       NA       NA        NA
```

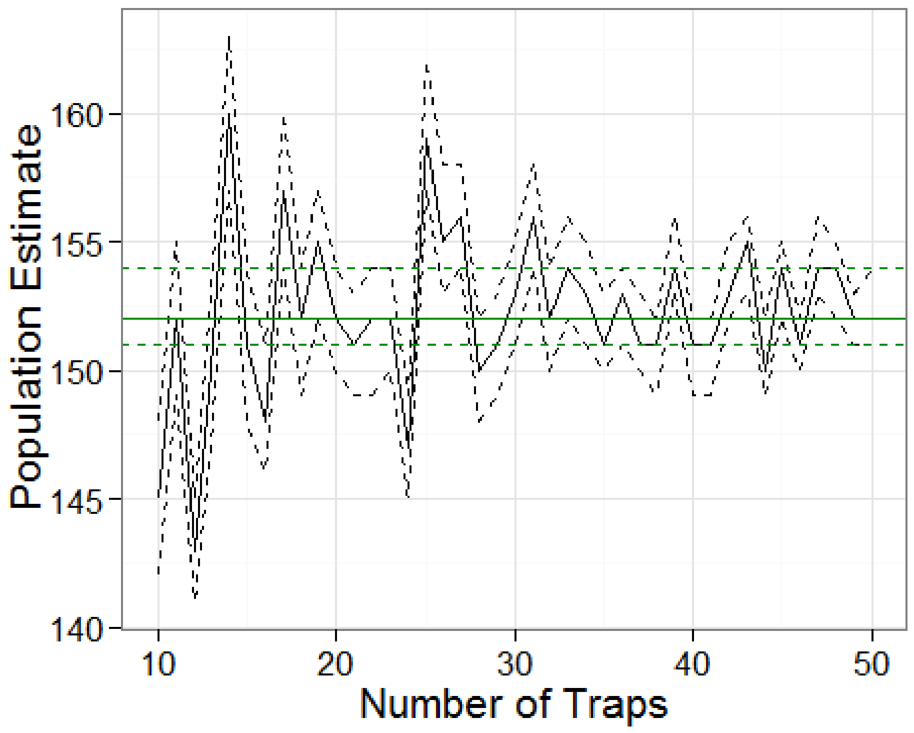
Step 3: Resample the data and fill in the results data frame

```
for(i in 1:nrow(results)) # For each row in our results data frame
{
  use_traps<-sample(all_traps, results$traps[i]) # Sample x number of random
traps
  my_subset<-data.frame(df.data%>%filter(trap %in% use_traps)) # Subset the
data to only include those traps
  my_cmr(my_subset) # Apply our my_cmr function to the subset
  results$pop.est[i]<-pop.est # Fill in our results
  results$pop.low[i]<-pop.low
  results$pop.high[i]<-pop.high
}
results

   traps pop.est pop.low pop.high
1     10     145     142      148
2     11     152     149      155
3     12     143     141      145
4     13     150     147      153
5     14     160     157      163
6     15     151     148      154
7     16     148     146      151
8     17     157     154      160
9     18     152     149      154
10    19     155     152      157
11    20     152     150      154
12    21     151     149      153
13    22     152     149      154
14    23     152     150      154
15    24     147     145      149
16    25     159     157      162
17    26     155     153      158
18    27     156     154      158
19    28     150     148      152
20    29     151     149      153
21    30     153     151      155
22    31     156     154      158
23    32     152     150      154
24    33     154     152      156
25    34     153     151      155
26    35     151     150      153
27    36     153     151      154
28    37     151     150      153
```

```
29    38     151     149      152
30    39     154     153      156
31    40     151     149      152
32    41     151     149      152
33    42     153     152      155
34    43     155     153      156
35    44     150     149      152
36    45     154     152      155
37    46     151     150      152
38    47     154     153      156
39    48     154     152      155
40    49     152     151      153
41    50     152     151      154
```

Step 4: Visualize results

```
ggplot(results)+
  geom_line(aes(x=traps, y=pop.est))+
  geom_line(aes(x=traps, y=pop.low), linetype='dashed')+
  geom_line(aes(x=traps, y=pop.high), linetype='dashed')+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Traps")+ylab("Population Estimate")
```



Because random traps are selected each time, your results will look slightly different. However, you should see the same amount of variation in population estimates. Why is there so much variation? It's because we're only randomly selecting each number of traps a single time. To really get an idea of the overall sensitivity of the population estimate to the number of traps used, we'll repeat this resampling algorithm many times.

Bootstrapping

Repeat this algorithm 25 times, but instead of varying the number of traps to be 1 to 50, we'll limit those options to be 10, 15, 20, ...50.

Step 1: Build a function - already done!

Step 2: Set up a data frame to handle the output of the analyses In this case, we're going to have 9 (different numbers of traps to select) x 25 (repeats) outputs:

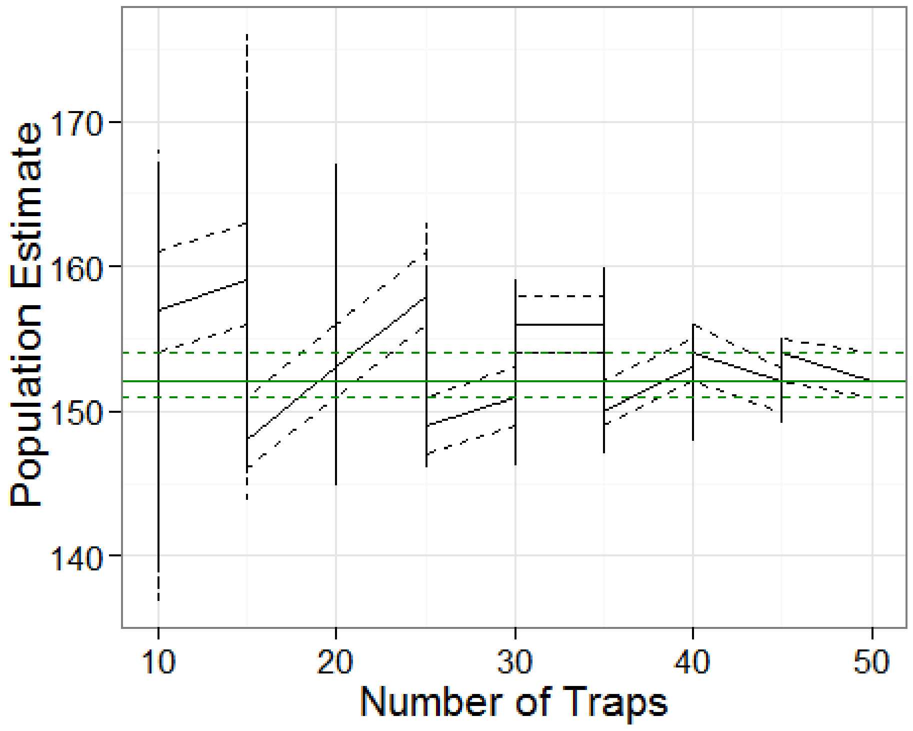
```
results<-data.frame(traps=rep(seq(from=10, to=50, by=5),25), pop.est=NA,
pop.low=NA, pop.high=NA)
head(results)

  traps pop.est pop.low pop.high
1    10      NA      NA       NA
2    15      NA      NA       NA
3    20      NA      NA       NA
4    25      NA      NA       NA
5    30      NA      NA       NA
6    35      NA      NA       NA
```

Step 3: Resample and fill in the results data frame In addition, we'll set up a means of keeping track of how long the resampling takes, and how long each iteration takes to complete.

```
starttime=Sys.time() # What time does the resampling begin?
for(i in 1:nrow(results))
{
  use_traps<-sample(all_traps, results$traps[i])
  my_subset<-data.frame(df.data%>%filter(trap %in% use_traps))
  my_cmr(my_subset)
  results$pop.est[i]<-pop.est
  results$pop.low[i]<-pop.low
  results$pop.high[i]<-pop.high
}
totaltime<-difftime(Sys.time(),starttime, unit="secs") #How long did it take?
totaltime

Time difference of 5.752329 secs

paste(round(as.numeric(totaltime)/nrow(results),2),"seconds per iteration") #
How long did each iteration take?

[1] "0.03 seconds per iteration"
```

Step 4: Visualize results

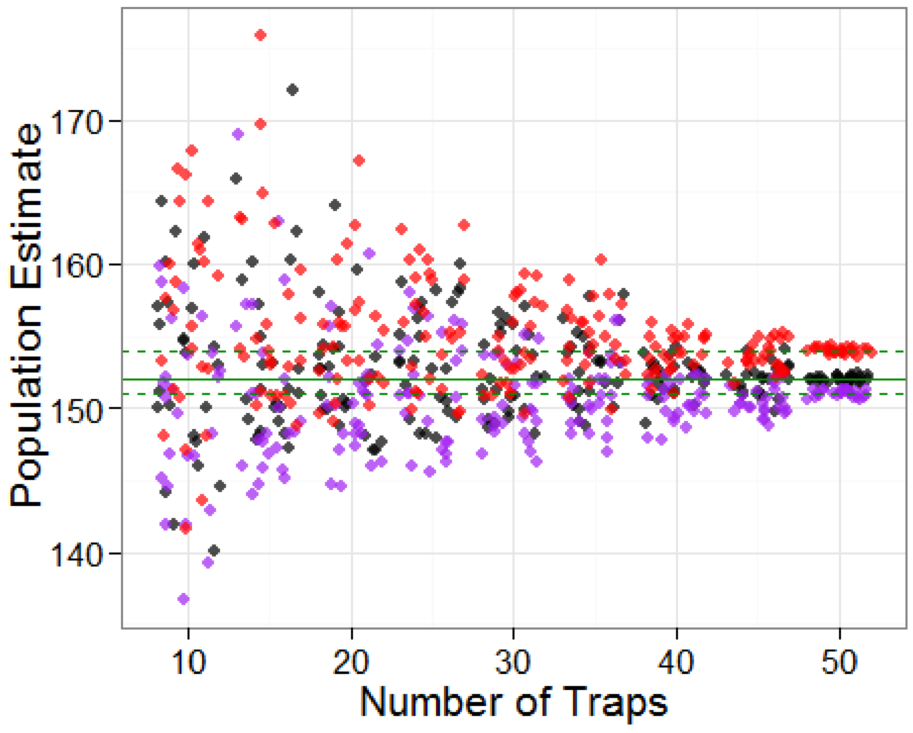
```
ggplot(results)+
  geom_line(aes(x=traps, y=pop.est))+
  geom_line(aes(x=traps, y=pop.low), linetype='dashed')+
  geom_line(aes(x=traps, y=pop.high), linetype='dashed')+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Traps")+ylab("Population Estimate")
```



Why do we have jagged lines? It's because each value of traps has 25 points associate with it. There are different ways to deal with this.

Option 1: Don't use a line to represent the resampled data.

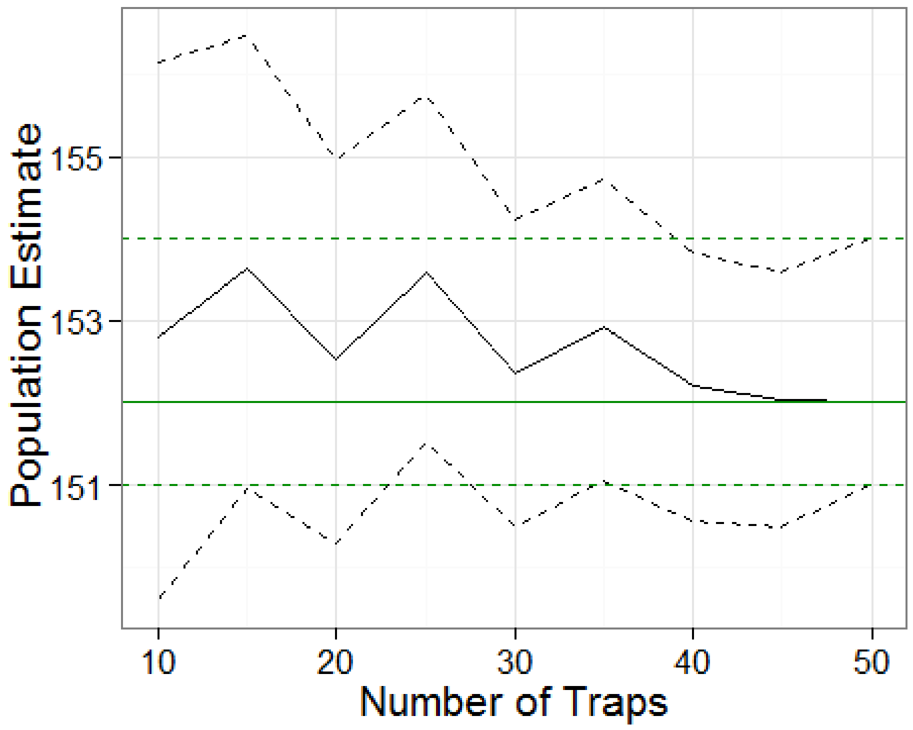
```
ggplot(results)+
  geom_jitter(aes(x=traps, y=pop.est), alpha=0.7)+
  geom_jitter(aes(x=traps, y=pop.low), col='purple', alpha=0.7)+
  geom_jitter(aes(x=traps, y=pop.high), col='red', alpha=0.7)+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Traps")+ylab("Population Estimate")
```



You can start to see that when few traps are used, the population estimates are much more variable than if many traps are used.

Option 2: Summarize the data.

```
results.sum<-data.frame(results%>%
  group_by(traps)%>%
  summarise(mean.pop=mean(pop.est), mean.low=mean(pop.low),
mean.high=mean(pop.high)))

ggplot(results.sum)+
  geom_line(aes(x=traps, y=mean.pop))+
  geom_line(aes(x=traps, y=mean.low), linetype='dashed')+
  geom_line(aes(x=traps, y=mean.high), linetype='dashed')+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Traps")+ylab("Population Estimate")
```



More Bootstrapping

Recall that each trap was checked 20 times. Imagine all of the time and effort that would be saved if we could sample traps fewer times and still be confident in our population estimates! In addition to exploring the sensitivity of the number of traps, let's add another level to this analysis and include a varying number of checks. We'll say that we want to see what would happen if 10 to 20 checks were done.

```
all_checks<-unique(df.data$check)
```

Because we've been keeping track of how long each iteration takes (approx. 0.03 sec, depending on the processing power of your computer), we know that we can easily do more iterations within a reasonable time frame. We'll do 40 repeats this time.

Step 1: Build a function - already done!

Step 2: Set up a data frame to handle the output of the analyses In this case, we're going to have 9 (different numbers of traps to select) x 11 (different numbers of checks to select) x 40 (repeats) outputs. Using `expand.grid()` will be useful here; it creates a dataframe of every combination of each argument you give it.

```
results<-expand.grid(traps=seq(from=10, to=50, by=5), checks=c(10:20),
repeats=c(1:40))
nrow(results) # How many iterations?

[1] 3960

nrow(results)*0.03/60 # It should take roughly 2 minutes
```

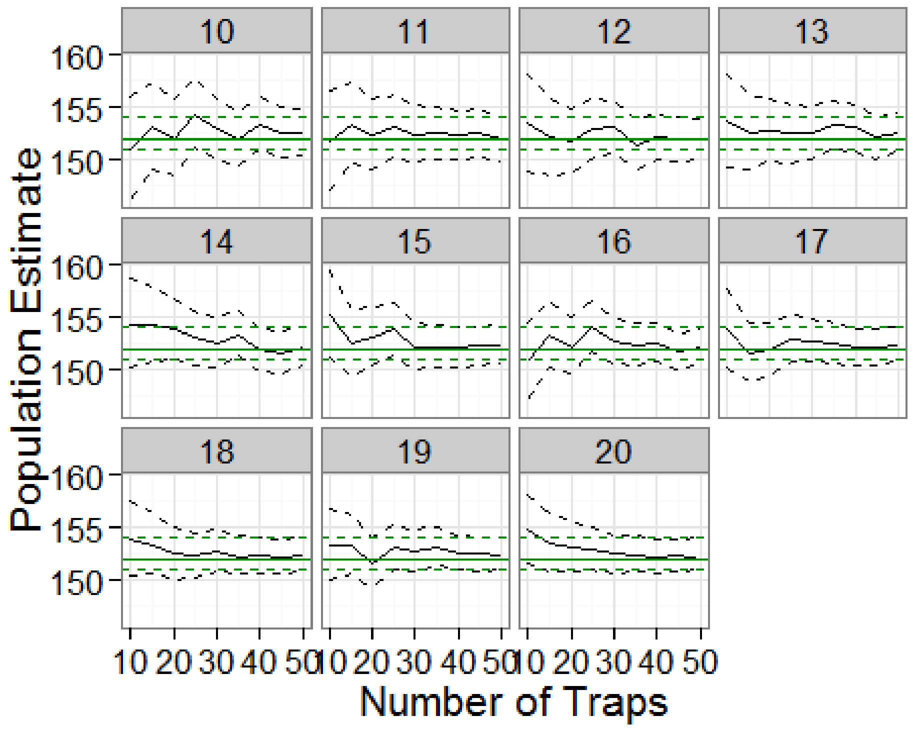
```
[1] 1.98

# We can get rid of the repeats column
results<-results[,-3]

# And need to add the pop.est, pop.low, and pop.high columns
results$pop.est<-NA
results$pop.low<-NA
results$pop.high<-NA
```

Step 3: Resample and fill in the results data frame

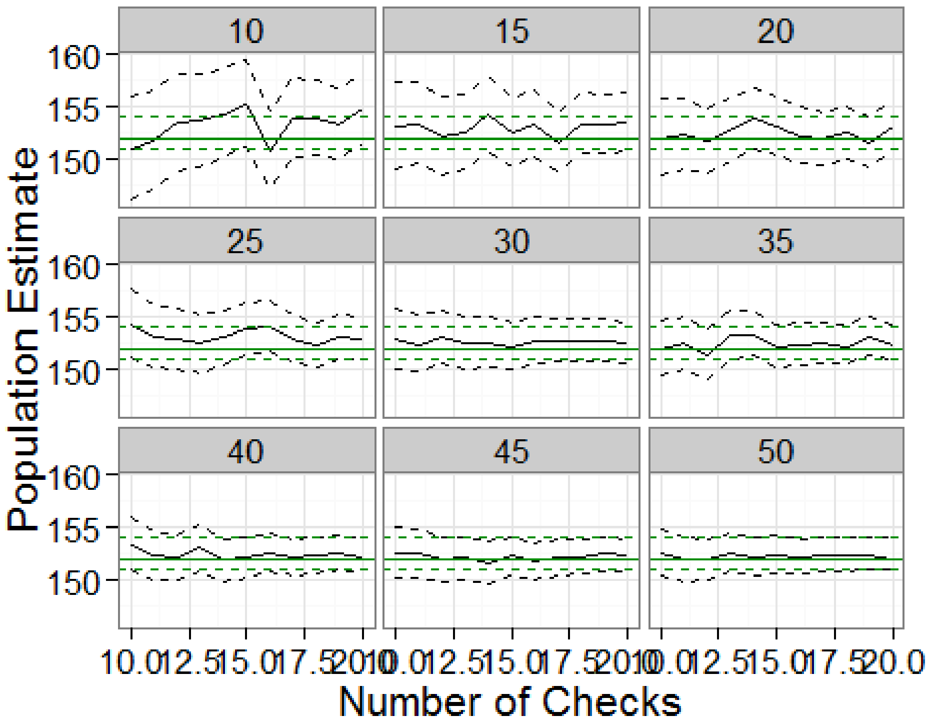
```
starttime=Sys.time()
for(i in 1:nrow(results))
{
  # print(paste(i/nrow(results)*100, "% Complete")) # This is useful for
keeping track of how many iterations have been completed
  use_traps<-sample(all_traps, results$traps[i])
  use_checks<-sample(all_checks, results$checks[i])
  my_subset<-data.frame(df.data%>%filter(trap %in% use_traps)%>%filter(check
%in% use_checks))
  my_cmr(my_subset)
  results$pop.est[i]<-pop.est
  results$pop.low[i]<-pop.low
  results$pop.high[i]<-pop.high
}
totaltime<-difftime(Sys.time(),starttime, unit="secs")
totaltime

Time difference of 109.2773 secs

paste(round(as.numeric(totaltime)/nrow(results),2),"seconds per iteration")

[1] "0.03 seconds per iteration"
```

Step 4: Visualize results

```
results.sum<-data.frame(results%>%
                          group_by(traps, checks)%>%
                          summarise(mean.pop=mean(pop.est),
mean.low=mean(pop.low), mean.high=mean(pop.high)))

ggplot(results.sum)+
  geom_line(aes(x=traps, y=mean.pop))+
  geom_line(aes(x=traps, y=mean.low), linetype='dashed')+
  geom_line(aes(x=traps, y=mean.high), linetype='dashed')+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Traps")+ylab("Population Estimate")+
  facet_wrap(~checks)
```



```
ggplot(results.sum)+
  geom_line(aes(x=checks, y=mean.pop))+
  geom_line(aes(x=checks, y=mean.low), linetype='dashed')+
  geom_line(aes(x=checks, y=mean.high), linetype='dashed')+
  geom_hline(yint=baseline$N, col='green4')+
  geom_hline(yint=baseline$pop.low, col='green4',linetype='dashed')+
  geom_hline(yint=baseline$pop.high, col='green4',linetype='dashed')+
  theme_bw(16)+xlab("Number of Checks")+ylab("Population Estimate")+
  facet_wrap(~traps)
```



You can use these plots to start identifying the number of traps and the number of checks that result in population estimates that you consider to be acceptable, and from there you can design more efficient sampling protocols for next year!