

NZ SRW Calving interval Report

Anthony Davidson

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Raw data

The data is then converted into intervals for each of the years 2010, 2011, 2012 and 2013.

A table of the raw results as the year increase

year	n	mY	low.qt	high.qt	sd
2010	3	2.666667	1.605851	3.727482	0.5773503
2011	15	2.866667	2.673022	3.060312	0.3518658
2012	25	3.240000	2.919170	3.560830	0.7788881
2013	45	3.311111	3.056488	3.565734	0.8480518

Raw data plots

The raw intervals can be presented as different means and confidence intervals as the length of the study increases:

We can also plot these as bar charts that show this more obviously:

What is interesting is that in 2011 there were more intervals that subsequently reduced the standard error of the estimate and the precision increased.

My idea of why this has happened is as follows:

At the time of collection in 2011 the number of possible intervals greater than 5 was very unlikely (as there were only 5 years of research). This meant that the overall error of the estimate was reduced as there was very few “chances” of obtaining a calving interval of 5 or 6 even though there may have been quite a few. The following estimates then picked these up and the error in the estimate increased again.

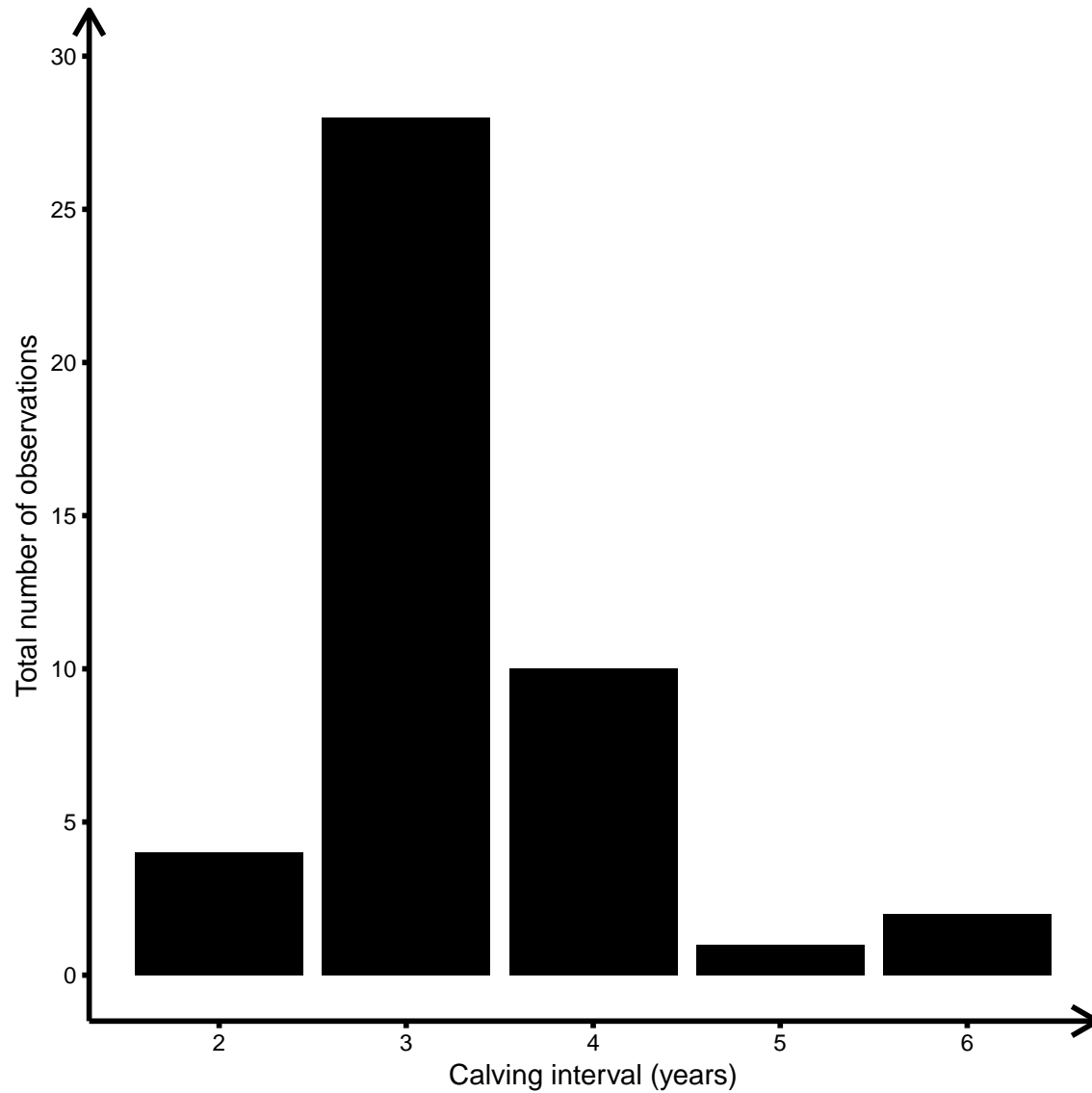
The upgrade for publication standard: **working in the R enviroment**

```
## pdf
```

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## 2
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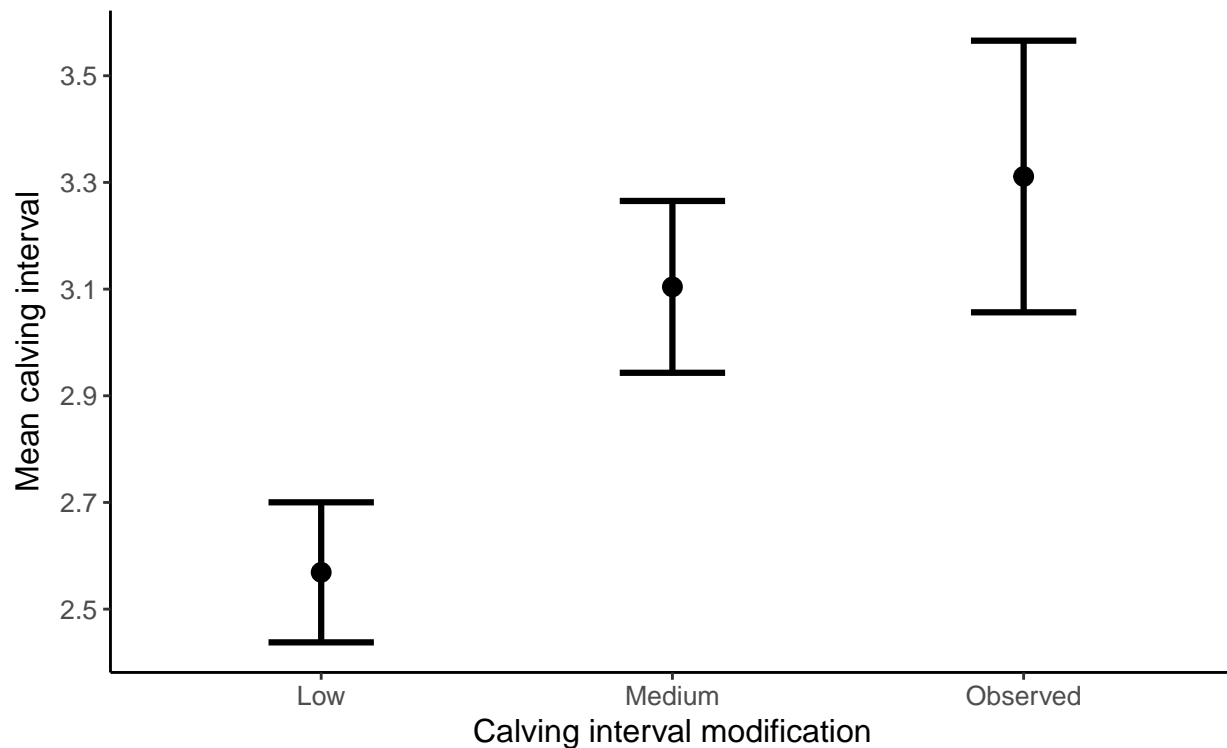
```
## pdf
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## 2
```



Missing intervals (Bradford et al. 2008)

This is a way to see what the calving interval might be if we had in fact missed calving events that happened before or after the study period.



The error gets smaller as the variance in the estimate decreases. We are artificially doing this here by modifying data to match what is more biologically possible.

interval	n	mY	low.qt	high.qt	sd
Low	58	2.568966	2.437666	2.700265	0.4995461
Medium	48	3.104167	2.943089	3.265244	0.5550382
Observed	45	3.311111	3.056488	3.565734	0.8480518

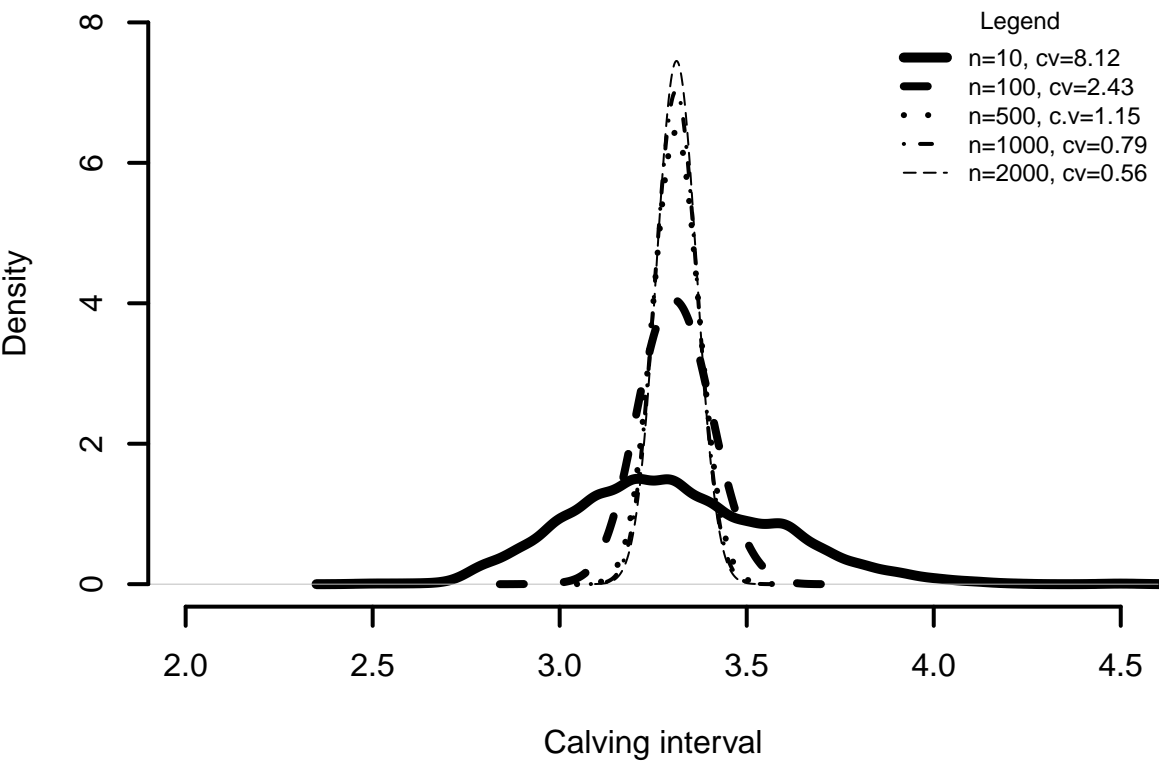
Bootstrapping

Table of parameters: This is taken directly from my Master's thesis. There may be updated estimates that need to be checked here.

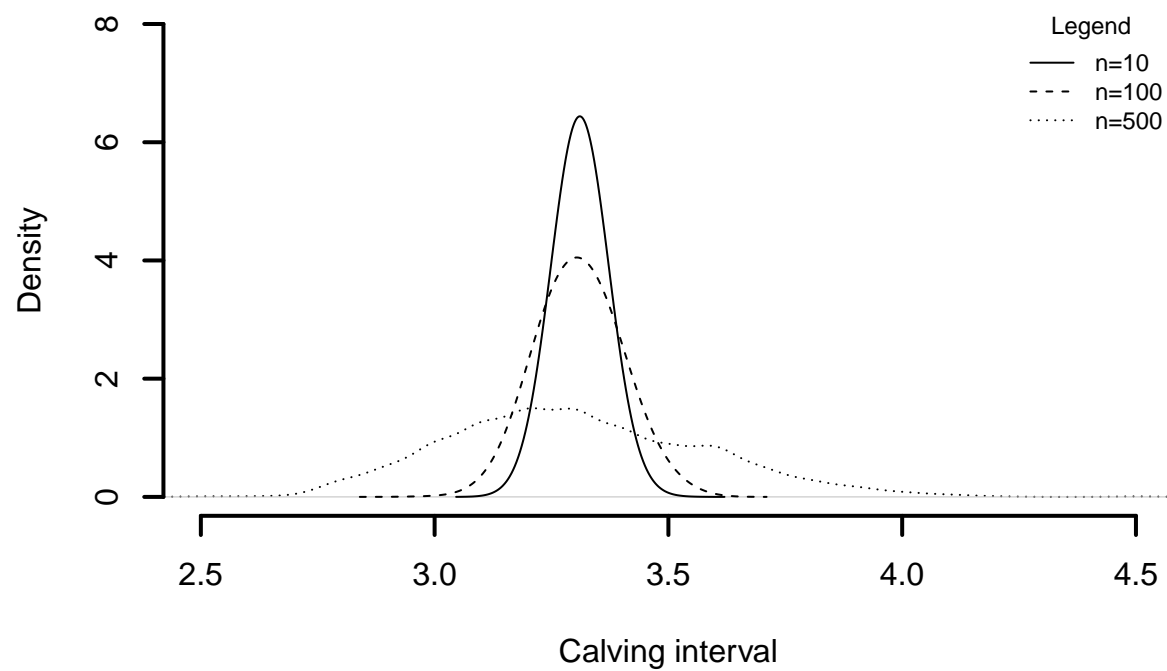
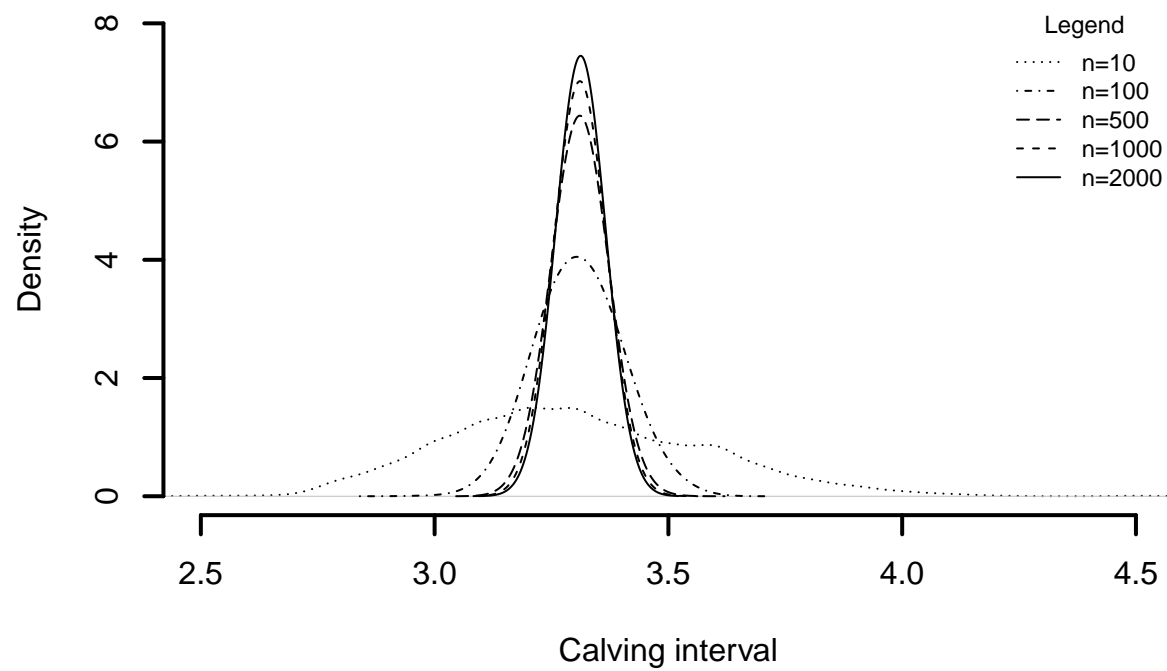
n	interval	low.qt	high.qt	se.pub	author	location
NA	3.12	3.07	3.17	NA	Best et al. 2001	South Africa
1504	3.15	3.11	3.18	NA	Best et al. 2005	South Africa (1971-2003 Updated)
NA	3.16	3.13	3.19	NA	Brandao et al 2010	South Africa (1971-2006 Updated)
NA	3.35	NA	NA	0.05	Cooke et al. 2001	Argentina
749	3.42	NA	NA	0.11	Cooke et al. 2003	Argentina
NA	3.63	NA	NA	0.13	Burnell 2001	Australia

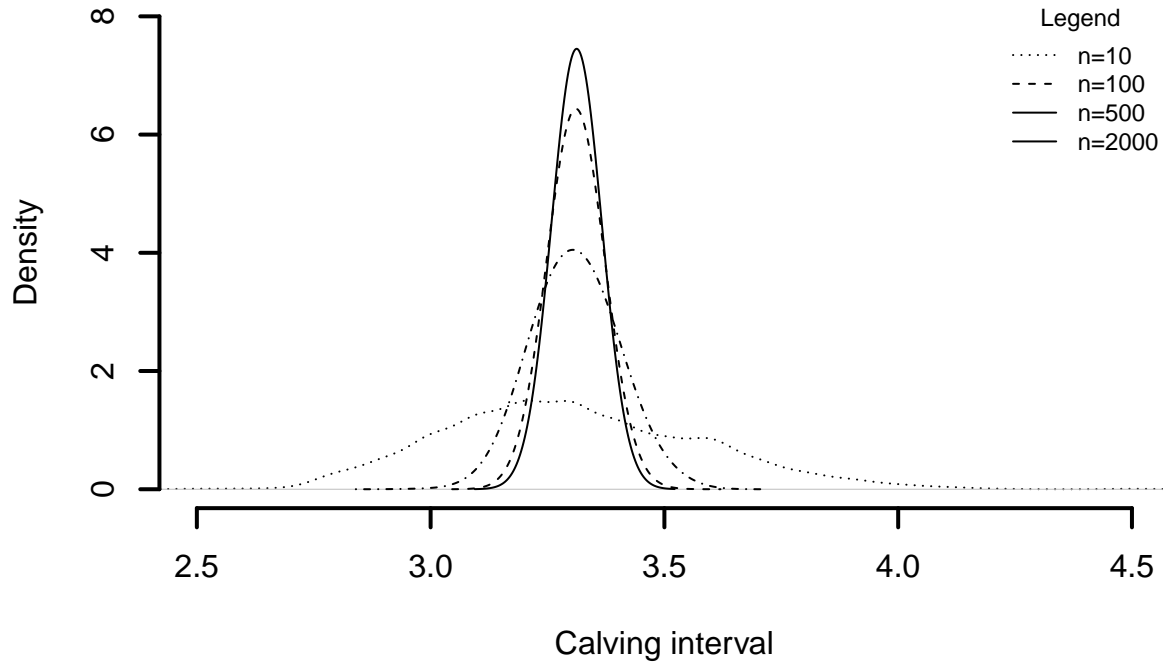
Bootstrap mean calving interval 1000 times and save the mean for each bootstrap sample. Here I investigate the effect of a sample size of 10,100,1000,2000 from the observed NZ calving interval.

Publication plot



1000 replicates





```
#final [plot]
#size defined by NZJFMR
# 195 mm (h) ? 148 mm (w).
#ylab(expression("Total"~"number"~"of"~"observations"~(italic("n")))) +

png("Figure_3_NZSRW_calving_interval_2017_lowres.png", width = 14.8, height = 14.8, units = 'cm', res = 300)

plot(density(sample10$mean10,bw = .05),col ="black", lty = 3, main = "", lwd = 1,ylim = c(0,8),xlim = c(2.5,4.5))
lines(density(sample100$mean100,bw = .05),col ="black", lty = 4, lwd = 1)
lines(density(sample500$mean500,bw = .05),col ="black", lty = 5, lwd = 1)
lines(density(sample1000$mean1000,bw = .05),col ="black", lty = 2, lwd = 1)
lines(density(sampleA$meanA,bw = .05),col ="black", lty = 1, lwd = 2)
legend(y = 8, x = 3.9,title = expression(bold("Sample size (n)")), c(expression(italic("n")~"="~"10"), c(expression(italic("n")~"="~"100"), c(expression(italic("n")~"="~"500"), c(expression(italic("n")~"="~"2000"))),
  lty = c(3,4,5,2,1), lwd = c(1,1,1,1,2), cex=1)
axis(1,lwd=2)
axis(2,lwd=2)
dev.off()

## pdf
## 2

png("Figure_3_NZSRW_calving_interval_2017_highres.png", width = 14.8, height = 14.8, units = 'cm', res = 300)

plot(density(sample10$mean10,bw = .05),col ="black", lty = 3, main = "", lwd = 1,ylim = c(0,8),xlim = c(2.5,4.5))
lines(density(sample100$mean100,bw = .05),col ="black", lty = 4, lwd = 1)
lines(density(sample500$mean500,bw = .05),col ="black", lty = 2, lwd = 1)
lines(density(sample1000$mean1000,bw = .05),col ="black", lty = 5, lwd = 1)
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```

lines(density(sampleA$meanA,bw = .05),col = "black", lty = 1, lwd = 2)
legend(y = 8, x = 3.9,title = expression(bold("Sample size (n)")), c(expression(italic("n")~"="~"10"), (
  lty = c(3,4,2,5,1), lwd = c(1,1,1,1,2), cex=1)
axis(1,lwd=2)
axis(2,lwd=2)
dev.off()

## pdf
## 2

# png("Figure_3_NZSRW_calving_interval_2017_highres_col.png", width = 14.8, height = 14.8, units = 'cm'
# plot(density(sample10$mean10,bw = .05),col = "black", lty = 3, main = "", lwd = 2,ylim = c(0,8),xlim =
# lines(density(sample100$mean100,bw = .05),col = "red", lty = 4, lwd = 2)
# lines(density(sample500$mean500,bw = .05),col = "orange", lty = 5, lwd = 2)
# lines(density(sample1000$mean1000,bw = .05),col = "darkolivegreen", lty = 2, lwd = 2)
# lines(density(sampleA$meanA,bw = .05),col = "royalblue", lty = 1, lwd = 2)
# legend(y = 8, x = 3.9,title = expression(bold("Sample size (n)")), c("n=10", "n=100", "n=500", "n=1000"
#   lty = c(3,4,5,2,1), lwd = c(2,2,2,2,2), col = c("black", "red", "orange", "darkolivegreen", "royalblue"
# axis(1,lwd=2)
# axis(2,lwd=2)
# dev.off()
#
# png("Figure_3_NZSRW_calving_interval_2017_highres_col2.png", width = 14.8, height = 14.8, units = 'cm'
# plot(density(sample10$mean10,bw = .05),col = "black", main = "", lwd = 2,ylim = c(0,8),xlim = c(2.5,4.
# lines(density(sample100$mean100,bw = .05),col = "red", lwd = 2)
# lines(density(sample500$mean500,bw = .05),col = "orange", lwd = 2)
# lines(density(sample1000$mean1000,bw = .05),col = "darkolivegreen", lwd = 2)
# lines(density(sampleA$meanA,bw = .05),col = "royalblue", lwd = 2)
# legend(y = 8, x = 3.9,title = expression(bold("Sample size (n)")), c("n=10", "n=100", "n=500", "n=1000"
#   lwd = c(2,2,2,2,2), col = c("black", "red", "orange", "darkolivegreen", "royalblue"),cex=1)
# axis(1,lwd=2)
# axis(2,lwd=2)
# dev.off()

```