

Homework 1

Warming up to R Markdown and the Chapman's modification

YOUR NAME HERE

In this homework assignment, you will become more familiar with using **R** and R Markdown to analyze and visualize data and report your results. To accomplish these goals, we will continue our discussion of estimating abundance using mark-recapture data.

First, make sure you have:

- 1a) Changed the **author** field in the YAML header to your name;
- 1b) Clicked **Knit** to check that you can create a pdf document from the .Rmd file;
- 1c) Saved the .Rmd file as **LastnameFirstname-homework1.Rmd** in a directory named **LastNameFirstName-Homework1**

If you have any problems with these steps, be sure to get help from either the instructor or the TA

Lincoln-Peterson is unbiased when sample sizes are large

By unbiased, we mean that the Lincoln-Peterson estimator will *on average* match the true abundance of the population. It is important to note that bias applies to the average estimate - for any given sample, our estimate of \hat{N} may be a little bigger or a little smaller than N . But if we took a large number of samples, we would get about the same number of low estimates as we get high estimates, so the average of all the samples would be N .

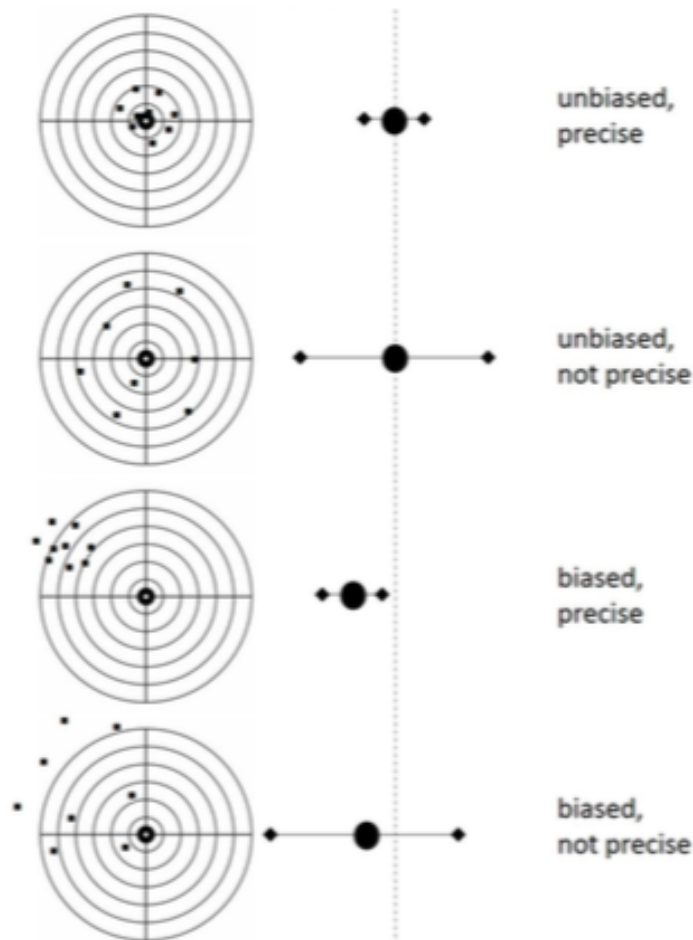


Figure 2.5: Illustrations of the concepts of bias and precision with shot patterns (left) (bull's-eye is truth; after White et al. 1982 and Williams et al. 2002) and 95% confidence intervals (right) (dotted line shows true parameter value, circle shows parameter estimate). The typical goal of an archer and an ecologist is shown at top as the combination of a lack of bias and high precision.

In most real-life scenarios, we only get to take a single sample of the target population so we never know if our estimate is a little bigger than N or a little smaller than N (that is why we estimate uncertainty - so we at least know the range of plausible values of N given our data). However, we can use R to prove that the L-P estimator is unbiased by *simulating* a large number of samples from an imaginary population.

Simulating mark-recapture samples in R

To start, we will add a code chunk

systematically *underestimate* abundance when sample sizes are small.