**Population Estimation from Mark-Recapture Experiments**

The enclosed R code is for estimating population size from a single mark-recapture program (ie one marking even and one recapture, or one mark event and multiple recaptures).

There are three ways to calculated population size, the standard Peterson estimate, the Peterson-Chapman estimate for low sample size (recaptures <50), and a Bayesian maximum likelihood estimation. All three estimators use three parameters to calculate the sample size and associated 95%CI. The parameters necessary are:

n1=the original number of marked individuals released into the population

n2=the total size of the recapture sample (number marked + number unmarked)

Y=the number of marked individuals in recapture sample.

The file: FisheriesPopulationEstimates\_Analysis.R will run the analysis using all three estimators and relies on the file: functions\_PopulationEstimates\_Peterson\_and\_MaximumLikelihood.R to be in the same folder. The FisheriesPopulationEstimates\_Analysis.R file contains all the information necessary to run the analysis.

To run only the Peterson estimates, use the file Peterson\_Population\_Estimate.R. With large sample sizes the Peterson and Bayesian estimators are very similar, and the Peterson may only be run. Note also that the Bayesian estimator can take a few minutes to run, so be patient.

The R code will output tables to the R console. The text within these can be copied and pasted into whatever spreadsheet program you use.