

New Approaches to Estimating Population Size for Marine Species

A major component of fisheries science is stock assessment, the process of collecting and analyzing data to determine changes in the abundance of fishery stocks and predict future trends. Here I discuss new approaches we are developing to address this challenge.

We introduce a new R package `staRve` for analyzing spatio-temporal point-referenced data in a hierarchical generalized linear mixed model framework. It is designed to be easy-to-use and computationally efficient for inference and prediction. `staRve` was motivated by the need to extract as much information on abundance as possible from fisheries research vessel survey data.

Approach to Estimating

By taking advantage of modern genetics, a new way to estimate abundance, the close-kin mark-recapture (CKMR) method, has recently been proposed. It only requires small pieces of tissue, taken from either live or dead animals, and generalizes the standard mark-recapture (MR) approach to use the resulting DNA marks to obtain information about relatedness among individuals in the sample. Here we demonstrate the potential for CKMR to estimate other key population parameters.