A censored likelihood approach for estimating hook-competition-adjusted relative abundance indices using longline fishing data

Monitoring and identifying changes in the population abundance of species is essential for the successful management of fisheries. Estimates of abundance trends of many demersal fish species are frequently made using data collected from fishery-independent longline surveys. These estimates are used as inputs for formal stock assessments to advise fisheries managers on harvest levels. It has long been known that catch-per-unit effort-based (CPUE-based) estimators of relative abundance applied to longline survey data can be severely biased due to numerous issues. These include inter- and intra-species hook-competition effects, gear-saturation effects, bait effects, and hook-type effects. Unfortunately, survey design cannot eliminate all these biases. Numerous instantaneous catch-rate-based (ICR-based) estimators of relative abundance have been put forward with the aim of better controlling for the biasing effects of gear saturation and hook competition. These estimators model the bait removal times from the actively fishing hooks as independent random variables with constant species-specific rates. However, in experimental settings, doubt has been cast on many of the strong assumptions that are required of these ICR-based methods to accurately infer relative abundance.

We present results from our comprehensive simulation study that confirms that both the CPUE-based and ICR-based estimators suffer from large biases and poor nominal coverage levels in many realistic settings. Then, we develop a new estimator of relative abundance, based on a statistical censored likelihood approach. Results from the simulation study confirm that the new censored likelihood estimator greatly outperforms both the CPUE-based and ICR-based estimators across all the simulation settings tested with respect to the measures of bias, root-mean-square error, and nominal coverage levels. The censored likelihood estimator is shown to be highly robust to model mis-specification, and easy to fit within popular and existing statistical packages. Finally, we apply our estimator to data on example species (Pacific Halibut and Yelloweye Rockfish) from longline surveys conducted by the International Pacific Halibut Commission and compare the results with existing estimators.