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Close-Kin Mark-Recapture in Atlantic Halibut

Atlantic Halibut are the target of an important fishery in the Northwest Atlantic; knowledge of their abundance is crucial for proper management and conservation. However, estimating the population size of a widely distributed and abundant marine fish is notoriously difficult. We plan to estimate the population abundance of Atlantic halibut on the Scotian Shelf using the Close Kin Mark Recapture (CKMR) approach. The method is based on the genotypic identification of kin (parent-offspring pairs, half-sib pairs, etc.), which are used as a substitute for physical recaptures in a traditional mark-recapture framework. We genotyped 10,303 samples collected between 2017 and 2024 at 4,000 single nucleotide polymorphic (SNP) markers. Pairwise pseudo-likelihood odds ratios were calculated across all individuals to identify 29 parent-offspring pairs and 571 half-sibling pairs in the sample. The CKMR likelihoods for Atlantic Halibut were constructed for parent-offspring pairs, cross-cohort half-siblings and grandparent-grandchild pairs. Likelihoods were adjusted according to the sex of parent in the kin pair and to include uncertainty from incomplete age information. The ultimate goal of the project is to provide the modeling framework for the estimation of population abundance, survivorship rates and connectivity for Atlantic Halibut that can be used to assess the state of the population on the Scotian Shelf and set sustainable fishing targets.