Exploring an individual-based simulation model to investigate changes in life-history characteristics of a population under size-selective fishing

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Introduction

The efficacy of stock management and rebuilding may be limited by ecosystem changes, depensatory mechanisms, and heritable morphological changes. Williams and Shertzer (2005) demonstrated, through computer simulation, that the selection differential (the difference in the mean value of a phenotypic character of a population before and after fishing) can be substantial in some management scenarios. If morphological characteristics are influenced by genetics, then size-selective fishing pressure can, over generations, change the phenotypic characteristics of individuals in a population. Broad-sense heritability, h^2, is the proportion of phenotype variance in a population that is attributable to genetic variation among individuals, and is generally assumed to be 0.2. The magnitude of heritability varies for different phenotypic characteristics, populations, and species.

Objectives

In this study we examined the rate and extent at which phenotypic change may occur in a fished population as functions of fishing intensity (F year^{-1}) and the value of h^2 (a measure of the similarity of offspring to parents as a result of the importance of the genetic contribution) and analyze the fishing and population dynamics of a population using yield- and egg-per-recruit analysis under size-selective fishing using a value of heritability of 0.2.

Methods

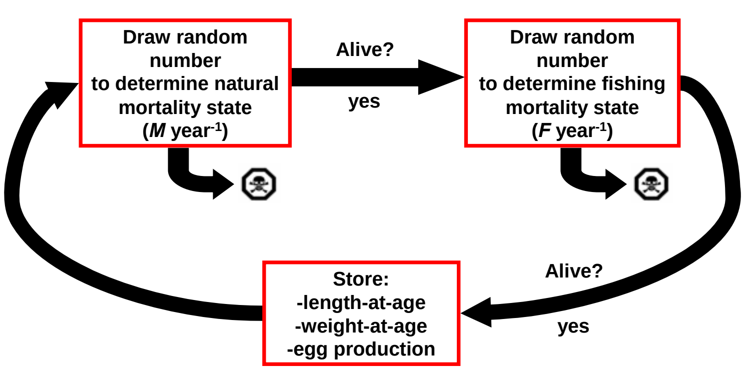
We constructed an individual-based simulation model following the method presented by Williams and Shertzer (2005). We simulated a population consisting of 100,000 individuals in 20 age classes using a stable age distribution with M equal to 0.2 y^{-1}. Unique biological parameters: length-at-age, weight-at-age, and size-specific annual egg production in the simulation were based on those of Atlantic cod (*Gadus morhua*), and were assigned to each individual.

Individuals were subject to a single natural mortality event (M = 0.2 y^{-1}) and a single fishing mortality event (F y^{-1}) annually. We assumed that fishing selectivity followed a logistic distribution. To determine that an individual has been subject to natural or fishing mortality a uniform random number was compared to the value of (e^{-M}) and (e^{-F}). If the random uniform random number was greater than (e^{-M}) and (e^{-F}) these individuals were removed from the population.

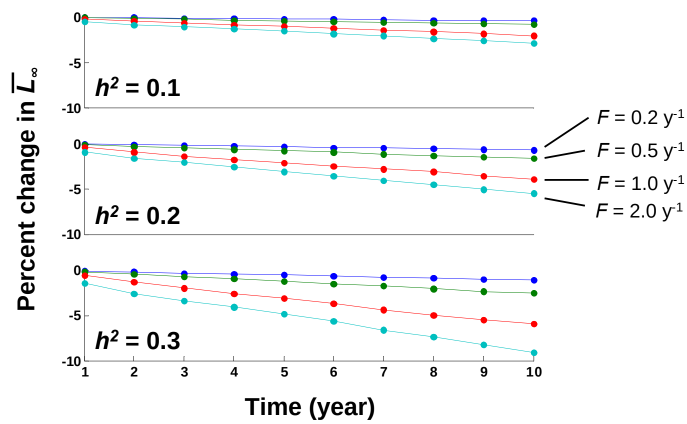
Following the annual mortality events, individuals not removed from the population that were old enough to reproduce were considered breeders and their biological characteristics were stored.

The mean L_∞ value of the recruits to the first age class was calculated as the difference in the mean L_∞ population prior to fishing and the mean value of the L_∞ of the breeding population. This value was multiplied by the value of h^2. We projected the population for ten years.

Flow chart of simulation model

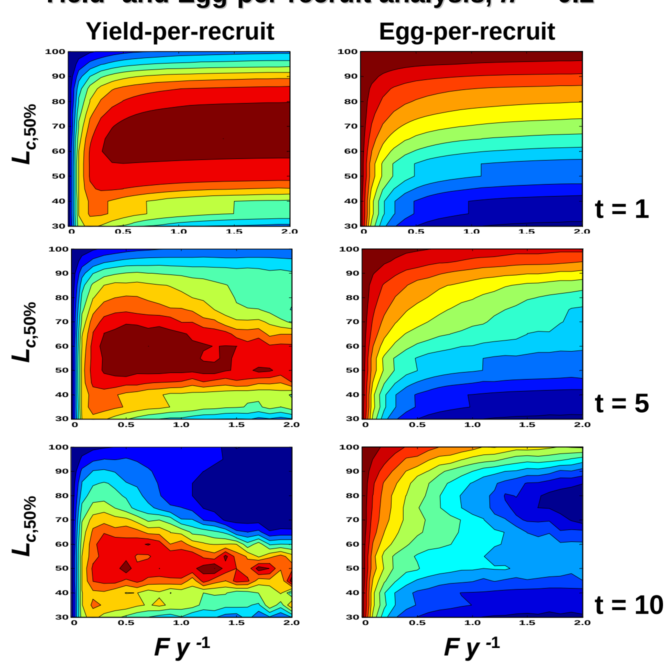


Results and Discussion



Population L_∞ values vary as a function of fishing intensity and the magnitude of heritability. At the smallest value of h^2 of F there is a relatively small change in the mean L_∞ of the population. Conversely, We observed a reduction of almost 10% in the mean value of L_∞ when the population was subjected to large fishing mortality and had large values of h^2.

Yield- and Egg-per-recruit analysis, h^2 = 0.2



We analyzed the population using yield-per-recruit and egg-per-recruit models and observed that over the ten year projection, the maximum yield per recruit decreased and was obtained at a smaller size-at-entry into the fishery and at lower fishing mortality rates. Similarly, the magnitude of egg-per-recruit declined over the projection. This preliminary work indicates that in some situations fishing mortality can cause substantial morphological changes in fished populations and that these changes can have considerable effects on the dynamics of the fishery.

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