

SIMULTANEOUS ESTIMATION OF MIXING PROPORTIONS OF RELEASED POPULATIONS AND GENETIC DRIFT BASED ON INDIVIDUAL GENOTYPES

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Assessing the effectiveness of stock enhancement programs through the estimation of mixing proportions of released juveniles in the natural population is of great interest. To estimate such proportions, successive sampling of genetic tags from the fishing grounds, where wild and hatchery-reared populations are mixed, is sometime used. In this case, temporal changes in allele frequencies of the mixed population provide information on the mixing proportions. However, such changes in allele frequencies can also occur due to genetic drift, and the usual procedures for estimating mixing proportions can not be used.

The authors propose a statistical model and method for simultaneously estimating the yearly mixing proportions and genetic drift based on the data of multi-locus genotypes of individuals successively sampled from the mixed population across the years (Figure 1). Our statistical model includes unobservable latent variables to account for genetic drift. Unfortunately, no explicit expressions of likelihood function are available in our model. To handle this complicated model and achieve faster computation, we developed a Laplace approximation of the likelihood function.

Our simulation studies demonstrated that the estimation of both the mixing proportions and genetic drift performed well, especially for the cases where the effective population size was not particularly large or the number of loci used was large. Our method can be applied to monitor the mixing not only of released hatchery-reared juveniles but also of the invasion of outside populations.

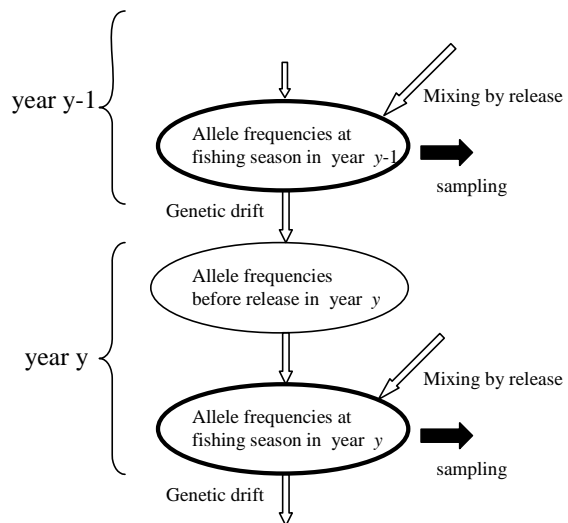


Figure 1. Temporal changes in allele frequencies in the mixed population and sampling stages supposed in the model.