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Effect of data weighting on the mature male biomass estimate for Alaskan golden king crab

M.S.M. Siddeek^{a,*}, J. Zheng^a, A.E. Punt^c, D. Pengilly^b

^a Alaska Department of Fish and Game, Division of Commercial Fisheries, P.O. Box 115526, Juneau, AK 99811, USA
 ^b Alaska Department of Fish and Game, Division of Commercial Fisheries, 351 Research Court, Kodiak, AK 99615, USA
 ^c School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA 98105-5020, USA

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ABSTRACT

Size-structured integrated population dynamics models are used to estimate the time-trajectories of mature male biomass (MMB) of Alaska crab stocks for stock status determination and harvest allocation. Lack of annual biomass surveys makes it difficult to assess the status and biomass of the Aleutian Islands golden king crab (Lithodes aequispinus). The assessment for this stock relies on commercial catch, sizecomposition, crab bycatch in groundfish (trawl and fish pot) fisheries, effort, catch-per-unit of effort, and tagging data to determine the biomass and other stock assessment parameters. The effect of data reweighting (i.e., stage-2 weighting) methods on MMB estimates was investigated for this stock in relation to the sensitivity of the trends in MMB to the data re-weighting method. The McAllister and Ianelli, and Francis methods were used to re-weight the size-composition data and Punt's method was applied to re-weight the tagging data. Model misspecification (e.g., natural mortality and growth) and the effect of omitting a potentially conflicting data source on estimates of MMB were also investigated. Re-weighting and model misspecification changed the magnitude of estimated values for MMB and their coefficients of variation, but not the MMB trends. The stage-2 weighting of tagging data led to slightly lower estimates of MMB. Under the robust multinomial likelihood for size-composition data, there was not much of a difference between the results of the McAllister and Ianelli method, which ignores correlations in residuals for size-compositions, and the Francis method, which explicitly accounts for these correlations. Specifically, both re-weighting methods led to similar trends, precision, and point estimates of MMB. The R_0 profiles indicated that there was information for abundance estimation when all the data were considered under base or variable growth increment scenarios. The CPUE indices were more informative about absolute abundance than the size-composition data. Hence the issue of data weighting should continue to be explored using case studies.

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1. Introduction

Due to the difficulties in ageing crustaceans, size-structured population dynamics models, which model cohorts moving through various size-classes over time, have been used for assessment of several crustacean stocks (e.g., Chen et al., 2005; Punt et al., 2016; Zheng et al., 1995). The size-transition matrix, which governs the probability of animals moving from one size-class to the others, plays an important role in size-structured models (Hillary, 2011; Siddeek et al., 2016). Tagging and size-composition data provide information to estimate the size-transition matrix (Punt et al., 1997, 2013). Those data have been used in combination with catch, bycatch, effort, and indices of abundance (e.g., catch-per-

* Corresponding author. E-mail address: shareef.siddeek@alaska.gov (M.S.M. Siddeek).

http://dx.doi.org/10.1016/j.fishres.2017.02.001 0165-7836/Published by Elsevier B.V. unit-effort) data within integrated models to estimate quantities of management importance, such as mature male biomass, fishing mortality, and recruitment (e.g., Zheng and Siddeek, 2015; Turnock and Rugolo, 2015). Tagging data are not available for many crustacean stocks. For those stocks, growth-increment estimates from related species can be used in addition to size-composition data to determine the size-transition matrix (e.g., eastern Bering Sea Tanner crab, Stockhausen, 2016).

Francis (2011) provides two main reasons why data weighting is important in stock assessment: (1) it can substantially change the results, and (2) it affects all the usual tools of statistical inference that are used in stock assessment such as hypothesis tests and calculation of confidence intervals. Francis (2011) argues that greater emphasis should be placed on mimicking abundance indices than size-composition data when assigning weights to data sets. He recommends that process error should be accounted for when setting the 'stage-2' effective samples sizes based on







the 'stage-1' sample sizes when fitting to size-composition data. He emphasizes that stage-1 fitting only accounts for observation errors resulting from data measurements and the sampling design. We follow his suggestion and estimate stage-2 effective sample sizes for size-composition data and extend his advice to re-weighting tagging data following Punt et al. (2017), while keeping the weights assigned to the abundance data fixed at values used in the stock assessment (Siddeek et al., 2015). The stage-2 fitting of size-composition and tagging data affects the estimation of the size-transition matrix. We apply re-weighting procedures to the specific case of the pot fishery for golden king crab (*Lithodes aequispinus*) in the Aleutian Islands region of Alaska (henceforth 'Al golden king crab').

Annual stock status determination and catch allocation for Al golden king crab rely on fishery-dependent data, such as catch, effort, catch-per-unit-effort, and catch size-composition given the absence of annual fishery-independent survey data (Pengilly, 2015). Crab fisheries in the Bering Sea and Aleutian Islands, Alaska, are male-only, with minimum size limits. Most stocks lack essential reproductive biological information to determine a spawning biomass index based on female reproductive potential. Hence, management advice is based on mature male biomass (MMB) as the measure of spawning potential (NPFMC, 2008).

This paper investigates the effects of stage-2 weighting of sizecomposition and tagging data on trends in MMB estimated using a size-structured model applied to data for the eastern sub-stock of Al golden king crab. The effects are investigated for model scenarios defined by a range of natural mortality values (low to high), halving and doubling mean growth increment from the best estimate, and including or not including highly uncertain groundfish bycatch (trawl and fish pot) size-composition data. *R*₀ profiles (e.g. Wang et al., 2014) were also constructed to investigate the information content of various data components for abundance estimation.

2. Materials and methods

2.1. Model and data sources

The size-structured model is outlined in Appendix A while the estimated parameters are listed in Appendix B Siddeek et al. (2015) provide full details of the model. The assessment was implemented using AD Model Builder (Fournier et al., 2012). The data sets included in the assessment are summarized in Table 1. Each data set was weighted, with arbitrarily large weights assigned to catch biomass (to ensure the model mimics the observed removals closely), and sample variance-based weights for standardized observer catch-per-unit-effort (CPUE) indices (Table 1).

2.2. Effective sample size for length composition

The annual number of length measurements in each category of catch (retained, total, and groundfish crab bycatch) is extremely large (thousands) and heterogeneous among years. It is a common practice to use the number of sets/pot lifts or another measure of sampling effort as a starting point for sample sizes instead of the number of length measurements when applying integrated stock assessment methods (Thorson, 2014). Consequently, the initial (stage-1) effective sample sizes were set to the number of days fished by the sampled vessels for the retained and total catch size-composition data, but number of sampled trips for the groundfish crab bycatch. The groundfish fishery uses a variety of gears and hence it is difficult to use 'day' as the initial effective sample size unit. We refer to the stage-1 effective samples sizes for the size-composition of the retained catch, total catch, and the groundfish crab bycatch for year t as $\tau_{1,t}^r$, $\tau_{1,t}^T$, and $\tau_{1,t}^{Tr}$ respectively.

Based on the assumption that the size-composition data are a multinomial sample, McAllister and Ianelli (1997) provided an estimator for the stage-2 effective sample sizes (referred to as stage2a weights) based on the ratio of the theoretical variance of expected proportions to the actual variance of proportions,

$$\tau_{2,t} = \frac{\sum_{l} \hat{P}_{t,l} \left(1 - \hat{P}_{t,l} \right)}{\sum_{l} \left(P_{t,l} - \hat{P}_{t,l} \right)^2} \tag{1}$$

where $\hat{P}_{t,l}$ and $P_{t,l}$ are the estimated and observed proportions of the catch during year *t* in size-class *l*, and $\tau_{2,t}$ is the stage-2 effective sample size for year *t*.

McAllister and Ianelli (1997) set the effective sample size for each size-composition data set for eastern Bering Sea yellowfin sole (*Limanda aspera*) as the arithmetic mean of $\tau_{2,t}$ over years t (i.e., a year-invariant effective sample size) and iterated the model fitting, updating the effective sample sizes, until convergence occurred. Eq. (1) ignores correlation among the residuals for the catch proportions so likely overestimates effective sample sizes (Francis, 2011). Punt (2017) suggests using the harmonic mean of $\tau_{2,t}$ if the McAllister and Ianelli formula is used. A harmonic mean (constant) multiplier was consequently used to update the effective sample sizes at each iteration of model fitting until convergence occurred; i.e.

$$\tau_{2,t,i} = \left\{ \frac{1}{n_t} \sum_{t} \left[\frac{\hat{\tau}_{2,t,i-1}}{\tau_{2,t,i-1}} \right]^{-1} \right\}^{-1} \tau_{2,t,i-1}.$$
 (2)

where $\tau_{2,t,i}$ is the stage-2 effective sample size for year *t* in iteration $i(\tau_{2,t,0} = \tau_{1,t})$ and $\dot{\tau}_{2,t,i}$ is the result of applying Eq. (1). Convergence of the process of setting the stage-2 effective sample sizes using Eq. (2) was visually assessed by plotting $\tau_{2,t,i-1}$ vs. $\tau_{2,t,i}$ at the final iteration.

Francis' (2011) mean-length based re-weighting method (i.e., Francis formula TA1.8, Punt, 2017) was considered as another way to re-weight the size-composition data (stage-2b) for iteratively re-weighting the initial (stage-1) effective sample sizes. Francis (2011)'s procedure accounts for correlation among catch length proportion residuals using the formula:

$$W^{-1} = var\left\{\frac{\bar{l}_t - \hat{l}_t}{\sqrt{var(\hat{l}_t)}}\right\}$$
(3)

where \bar{l}_t and \bar{l}_t are respectively the observed and model-predicted mean lengths for year *t*:

$$\overline{l_t} = \sum_{i=1}^n l_i \times P_{t,i} \quad \hat{\overline{l}}_t = \sum_{i=1}^n l_i \times \hat{P}_{t,i}$$
(4)

 l_i is the mid-point of length-class *i*, $var(\hat{l}_t)$ is the variance of the predicted mean length for year *t*:

$$\operatorname{var}\left(\widehat{\mathbf{l}}_{t}\right) = \frac{\Sigma_{i=1}^{n}\widehat{p}_{t,i}\left(\mathbf{l}_{t,i} - \widehat{\mathbf{l}}_{t}\right)^{2}}{S_{t}}$$
(5)

and S_t is the effective sample size in year *t*. Francis (2017) suggested that a good stopping criterion for the iteration process is when there is no appreciable change in the key outputs. Hence, we considered a stopping criterion of no appreciable change in *W*, terminal year MMB (Eq. (A10)), and retained catch overfishing level (OFL, Eqs. (A11a)–(A11c)). S_t is related to the initial (stage-1) effective sample size according to:

$$S_{t,i} = W_i \tau_{1,t} \tag{6}$$

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