JABBA: Just Another Bayesian Biomass Assessment

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ARTICLE INFO

ABSTRACT

This study presents a new, open-source modelling software entitled 'Just Another Bayesian Biomass Assessment' (JABBA). JABBA can be used for biomass dynamic stock assessment applications, and has emerged from the development of a Bayesian State-Space Surplus Production Model framework, already applied in stock assessments of sharks, tuna, and billfishes around the world. JABBA presents a unifying, flexible framework for biomass dynamic modelling, runs quickly, and generates reproducible stock status estimates and diagnostic tools. Specific emphasis has been placed on flexibility for specifying alternative scenarios, achieving high stability and improved convergence rates. Default JABBA features include: 1) an integrated state-space tool for averaging and automatically fitting multiple catch per unit effort (CPUE) time series; 2) data-weighting through estimation of additional observation variance for individual or grouped CPUE; 3) selection of Fox, Schaefer, or Pella-Tomlinson production functions; 4) options to fix or estimate process and observation variance components; 5) model diagnostic tools; 6) future projections for alternative catch regimes; and 7) a suite of inbuilt graphics illustrating model fit diagnostics and stock status results. As a case study, JABBA is applied to the 2017 assessment input data for South Atlantic swordfish (*Xiphias gladius*). We envision that JABBA will become a widely used, open-source stock assessment tool, readily improved and modified by the global scientific community.

1. Introduction

Surplus Production Models (SPMs) are among the least parameter and data demanding population models that can produce estimates of Maximum Sustainable Yield (MSY) and associated fisheries reference points. Despite a number of limitations (Maunder, 2003; Punt and Szuwalski, 2012; Wang et al., 2014), SPMs remain an integral tool for data-limited to –moderate stock assessments (Dichmont et al., 2016; Punt et al., 2015) and meta-analyses of global fisheries (Froese et al., 2016; Rosenberg et al., 2017; Worm et al., 2009). SPMs approximate changes in biomass as a function of the biomass of the preceding year, the surplus production of biomass, and the removal by the fishery in the form of catch and are not differentiated by age and/or size. In SPMs, somatic growth, reproduction, natural mortality, and associated density-dependent processes are inseparably captured in the interplay of the two major parameters: the intrinsic rate of population increase r and carrying capacity K. The model requires an index of abundance, catch records, and an estimate of initial biomass (Prager, 1994).

A major criticism of SPMs is that they ignore the stock's size/age structure and therefore fail to account for dynamics in gear selectivity

(Wang et al., 2014) and lagged effects of recruitment and mortality (Aalto et al., 2015; Punt and Szuwalski, 2012), which can both lead to biased assessment results. Although these issues remain a limitation of SPMs, there has been considerable progress in optimizing the fitting procedures of SPMs, in consideration that they are continuously implemented by Regional Fishery Management Organizations (RFMOs) around the world. Such improvements include: Bayesian methods with improved prior formulations (McAllister et al., 2001); the development of estimation frameworks that allow incorporating both observation and process errors using mixed-effects (Punt, 2003; Thorson and Minto, 2015); and Bayesian state-space modelling approaches (Meyer and Millar, 1999; Millar and Meyer, 2000; Thorson et al., 2014). The Bayesian framework can reduce uncertainties about estimates of stock size, productivity, and biomass to carrying capacity ratios by using reasonably informative priors that incorporate information available from meta-analyses and published literature on historical stock levels and population demographics (McAllister et al., 2001; Punt and Hilborn, 1997). State-space models are regarded as powerful tools for modelling time-varying abundance indices because they simultaneously account for both process and observation errors (Buckland et al., 2004;

de Valpine, 2002; Meyer and Millar, 1999). Process error can account for model structural uncertainty as well as natural variability of stock biomass due to stochasticity in recruitment, natural mortality, growth, and maturation, whereas observation error determines the uncertainty in the observed abundance index due to measurement error, reporting error and other unaccounted variations in catchability (Francis et al., 2003; Meyer and Millar, 1999; Ono et al., 2012). More recently, Carvalho et al. (2014) investigated incorporating time blocks in SPMs to allow substantial variability in catchability over time caused by dominant changes in fishery strategies.

Due to their low data requirements, SPMs persist as a predominant assessment tool for large pelagic tuna, shark, and billfish assessments (Dichmont et al., 2016; Punt et al., 2015). The majority of SPMs implemented in RFMO stock assessments are based on third-party software, and among the most commonly used are 'A Stock Production Model Incorporating Covariates' (ASPIC; Prager, 2002, 1994) and 'Bayesian Surplus Production 2' (BSP2; McAllister, 2014).

ASPIC fits a generalized Pella and Tomlinson (1969) production function using several indices of abundance and conditions the stock population dynamics on either catch or effort. Uncertainty in ASPIC is evaluated with sensitivity tests, and a separate projections module is available in R. The greatest shortcoming of ASPIC is its inability to estimate process error, thus providing reference point estimates wholly reliant on the trends in data inputs alone. Regardless, ASPIC has been developed for and applied to several stock assessments that have been conducted by the International Commission for the Conservation of Atlantic Tunas (ICCAT). These include yellowfin tuna (*Thunnus albacares*), bigeye tuna (*Thunnus obesus*), skipjack tuna (*Katsuwonus pelamis*), albacore (*Thunnus alalunga*), swordfish (*Xiphias gladius*), and billfishes (Dichmont et al., 2016; Neilson et al., 2013; Punt et al., 2015). The software is provided on the National Oceanic and Atmospheric Administration's web-based toolbox as a standalone download (http://nft.nefsc.noaa.gov/ASPIC.html). Similarly, integrated statistical catch-at-age frameworks, such as Stock Synthesis (Methot and Wetzel, 2013), are capable of executing SPMs in a sophisticated modelling environment, though state-space formulation is not a possibility therein.

BSP2 (McAllister, 2014) is an updated version of ICCAT's deterministic Bayesian surplus production model (BSP) software documented in McAllister and Babcock (2006). The essential improvement of BSP2 over BSP is the implementation of a state-space approach, so that the user may include process error. Like ASPIC, BSP2 uses a Pella-Tomlinson production function, but the shape parameter is constrained to low values when biomass is less than biomass at sustainable yield (B_{MSY}) to avoid unrealistically high estimates of population increase at low population size (McAllister et al., 2000). A projection function for BSP2 was developed in 2012. The most current version of BSP2 has been developed through implementations in assessments of numerous Canadian fish stocks, as well as pelagic fish stocks in the Atlantic and Pacific oceans including North Pacific blue shark, Atlantic yellowfin, bigeye, and bluefin tuna, and billfishes. Historically, BSP2 was available on the ICCAT Stock Assessment Software Catalog.

Third-party software presents advantages by allowing analysts to explore varied assessment configurations and facilitating the peer-review of assessments. However, changes to such programs may be slow as development relies on few developers, and the record of issues addressed may be unclear. Sometimes, for independent software, access and collaboration with the original developer may be limited by website issues and it may be unclear to whom problems should be directed. Some fisheries scientists construct their own models from scratch, typically vetted internally by those involved with the singular assessment at hand. Code written independently for standalone assessments carries the risk of version corruption and likely presents redundancies or crucial discrepancies between similar models. All such assessments would benefit greatly from sourcing a standardized, central protocol from which changes could be suggested, implemented, and archived for the fishery in question.

The ubiquity of SPM use across RFMOs presents a clear need for a unified approach that is reproducible, well-documented, and easily implemented for a variety of fisheries. The open-source platform GitHub provides a means for fisheries scientists to share, document, and improve assessment procedures in a standardized manner, greatly reducing time spent constructing redundant models, and democratizing modelling approaches across nations. Hosting such tools in a globally-accessible repository also increases transparency in the assessment workflow; enables rapid, continuous modification of the code not limited to a single developer (via "forks"), and acts as an archive of model improvements over time (via the "issues" tracker).

This study presents a new, open-source modelling framework called 'Just Another Bayesian Biomass Assessment' (JABBA). The name is a reference to JAGS (Just Another Gibbs Sampler, Plummer, 2003), which is the language in which the Bayesian algorithm is executed. JABBA is a generalized Bayesian State-Space Surplus Production Model and represents an innovative approach to biomass dynamic modelling. The motivation for developing JABBA was to provide a user-friendly R (R Development Core Team, 2013) to JAGS (Plummer, 2003) interface for fitting generalized Bayesian State-Space SPMs to generate reproducible stock status estimates and diagnostics for a wide variety of fisheries. Specific emphasis has been placed on flexibility for specifying alternative model scenarios and achieving high stability and convergence rates throughout the development process. The open source R/JAGS interface provides a means to rapidly modify and run standard assessment scenarios, while still enabling the experienced user to customize the easily accessible R/JAGS source code for specific purposes. In this manuscript, several core features of JABBA are illustrated using data from the 2017 South Atlantic swordfish stock assessment conducted through ICCAT.

2. Materials and methods

JABBA emerged from the development of improved optimization procedures in Bayesian state-space modelling approaches (Meyer and Millar, 1999; Millar and Meyer, 2000), which were subsequently applied and tested for assessments of South Atlantic blue shark (ICCAT, 2016), North Pacific blue shark (ISC, 2017), Mediterranean albacore (ICCAT, 2017a), North and South Atlantic shortfin mako shark (ICCAT, 2017b), and South Atlantic swordfish (ICCAT, 2017c). Features of JABBA include: 1) an integrated state-space tool for averaging and automatically fitting multiple catch-per-unit-effort (CPUE) time series; 2) data-weighting through an estimation of additional observation variance for individual or grouped CPUE; 3) selection between Fox, Schaefer, or Pella-Tomlinson production functions, with the option to estimate the function as B_{MSY}/K; 4) options to fix or estimate the process and observation variance components; 5) model diagnostics tools; 6) future projections for alternative catch regimes; and 7) a suite of inbuilt graphics illustrating model fits and diagnostics, surplus production estimates, historical stock status trajectories, Kobe plot, and future projections.

A JABBA assessment model is comprised of user-selected model processes, data, and statistical methods for comparing data to model predictions. A crucial development in the JABBA framework is the model diagnostic step, which aids in checking for parameter and model-structure misspecification and aims to avoid convergence errors. Systematic misfit to data or conflict between abundance indices within an assessment model should be considered a diagnostic of model misspecification. Unacceptable model fits (i.e., model estimates which do not match the data) can be detected by either the magnitude of the residuals being larger than implied by the observation error, or trends in residuals indicating systematic misfit (Carvalho et al., 2017). Data conflicts occur when different data series, given the model structure, provide conflicting information about important aspects of the dynamics. Unacceptable model misfit or data conflict can be dealt with by either data weighting or changing the model structure (Maunder and