



Estimating growth within size-structured fishery stock assessments: What is the state of the art and what does the future look like?



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ABSTRACT

Most growth studies have considered the relationship between age and growth. Such relationships are essential to age-structured fishery stock assessments. In contrast, assessments based on stage-structured population dynamics models require information on the probability of animals moving from one stage to each of the other stages at each time-step. Size-structured population dynamics models are a special case of stage-structured population dynamics models in which each class represents a unique set of sizes. These models form the basis of assessments for many valuable, hard to age, marine species, including crabs, abalone, lobsters and prawns. Growth within these models is governed by a size-transition matrix. The values for the parameters of a size-transition matrix can either be estimated externally to the assessment, generally utilizing data from tag-recapture experiments, or the estimation of growth can be integrated within the assessment model. This paper reviews the approaches used to construct size-transition matrices, including the underlying structural formulation, statistical estimation framework, and the consequences of error when specifying these matrices on the ability to estimate population size and manage populations sustainably.

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1. Introduction

Management advice for many of the world's fish and invertebrate stocks is based on quantitative stock assessments that provide estimates of productivity, and time-series of biomass and recruitment. These stock assessments often form the basis for forecasts and can serve as the basis for the application of harvest control rules. Single-species stock assessments can be classified into three broad classes: (a) surplus production (or biomass dynamic) models, (b) age-structured models, and (c) size- (or length-/stage-) structured models (hereafter referred to as size-structured models). The majority of contemporary stock assessments are based on age-structured models. However, such methods cannot easily be applied to species which are hard to age such as crustaceans and molluscs (in particular crabs, rock lobsters, prawns, abalone, and

oysters), but also some teleosts such as tunas and billfish, all of which form the basis for very valuable fisheries.

Stock assessments may be based on stage-structured models when (a) there are no data on the age-structure of the population or the removals from the population, (b) many of the key biological processes (such as growth, selectivity, natural mortality, and fecundity) are size- rather age-based, or (c) there is concern regarding the impact size-selective mortality on the distribution of length-at-age. Size-structured population dynamics models are a special case of stage-structured population dynamics models in which each stage represents a unique set of sizes. Assessments based on size-structured population dynamics models require information on the probability of animals growing from one size-class to each of the other size-classes at each time-step and staying in the same size class.

Punt et al. (2013a) provide a review of methods based on size-structured population dynamics models which can utilize size-composition data to estimate biomass, recruitment and fishing mortality. Most of the recent methods are based on 'integrated' (or 'statistical') approaches. These methods involve modelling the population dynamics and how the observations pertain to the model separately. The earliest such methods were developed by Fournier

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and Archibald (1982) in the context of age-structured dynamics, while the first integrated size-structured assessment method was developed by Sullivan et al. (1990). There are now many variants on the basic approach of Sullivan et al. (1990).

The basic dynamics of most integrated size-structured stock assessment methods are governed by the equation:

$$N_{t+1} = \mathbf{X}_t \mathbf{S}_t N_t + \phi R_{t+1} \quad (1)$$

where N_t is a column vector of length H (number of size-classes, which need not all be the same size) containing the numbers-at-size at the start of time-step t , \mathbf{X}_t is the transition matrix (dimension $H \times H$) for time-step t (where $X_{ij,t}$ is the probability of growing from size-class j to size-class i during time-step t), \mathbf{S}_t is a $H \times H$ diagonal matrix, with the diagonal terms equal to the proportion surviving (the complement of fishing and natural mortality) at size during time-step t , R_t is the recruitment in numbers during time-step t (assumed to occur at the end of the time-step after mortality and growth) and ϕ is a column vector of length H containing the proportions of recruitment to each size-class.

Growth appears in Eq. (1) through the matrix \mathbf{X} and the vector ϕ . The focus for this paper is on the matrix \mathbf{X} because there are seldom data to allow ϕ to be estimated (some assessments, e.g. Zheng and Siddeek (2013) do, however, estimate it). Consequently, the values for ϕ are usually pre-specified, and the smallest population size-class selected so that ϕ covers the full size distribution of cohorts entering the fished population in what are assumed to be the correct proportions by size-class. An alternative is to start the model at very small sizes in which case the values of ϕ will be inconsequential for the estimates of quantities of management interest. However, there is likely little benefit to starting a model at very small size unless there are data on growth of such animals, which is often not the case.

Size-transition matrices are used to model both crustacean growth and the continuous growth of molluscs and, less often, fish. The moulting growth of crustaceans (reviewed by Caddy, 1987) has been modelled by separately considering the discrete increase in body size, moult increment (Hiatt, 1948; McGarvey and Feenstra, 2001), and time period between moulting events, the intermoult period (Hoenig and Restrepo, 1989; Zheng et al., 1995; Millar and Hoenig, 1997). A focus of crustacean growth studies had been to quantify the slowing of growth following sexual maturity, particularly for females (Hiatt, 1948; Kurata, 1962; Mauchline, 1977; Somerton, 1980; Easton and Misra, 1988). The size-transition growth model formulation can describe both continuous and moulting growth because it applies to populations, not to individuals. The probabilities of transition are understood to predict the proportions of animals growing to larger size classes (or remaining in their size class) over time spanning one or several model time steps.

While it is theoretically possible to estimate the individual elements of size-transition matrices as independent parameters, in practice these are too numerous. Instead, size-transition probabilities are parameterized as functions of (pre-growth) body length, often with different growth matrices by season and sex. The growth increment is usually modelled using the von Bertalanffy equation, although dependence on other factors affecting growth, such as population density and state of sexual maturity are also possible, as described below.

For the purposes of this paper, the matrix \mathbf{X} is defined as the probability of, or proportion, of animals growing from one size-class to each of the other size-classes (usually constrained so that shrinkage is prohibited). Some assessments generalize the N vector to include maturity state and shell condition (e.g. Stockhausen et al., 2013; Turnock and Rugolo, 2013; Zheng and Siddeek, 2013) in which case \mathbf{X} , now a multi-dimensional array, represents movement among states as well as growth. In its simplest form, the

matrix \mathbf{X} assumes that all animals grow each time-step, i.e. there is no terminal moultⁱ for crabs and no intermoult intervals longer or shorter than the modelled time-step. Allowing for different states permits, for example, terminal moults to be represented in the model. Eq. (1) is written in terms of time-steps, which may be a year or a shorter time-period, and each time-step need not be of the same duration. For example, the assessment for rock lobsters, *Jasus edwardsii*, conducted by Punt and Kennedy (1997) was based on a monthly time-step and growth occurred at the end of March, June, September and December rather than during each month, primarily due to lack of tag-recovery data to estimate monthly size-transition matrices.

The parameter values for the size-transition matrix can either be estimated independently of the assessment or integrated within the assessment. The latter allows data other than the tag-recapture information to impact estimates of growth, including size frequencies sampled from the catch, and allows uncertainty in the estimation of the size-transition matrix to be accounted for more rigorously in final stock assessment outputs. However, integrating growth estimation into the assessment is more computationally intensive, and estimation outside of the assessments has been preferred by some authors (e.g. Chen et al., 2000). The main focus for this paper is on assessments for crustaceans and molluscs because these are the species groups to which size-structured assessment methods have been applied most frequently. The example applications are taken from Australia, New Zealand, South Africa and Alaska as these are the regions where size-structured ‘integrated’ methods of assessment have been applied most often. The methods of this paper are framed in the context of size-structured models. However, they can also be used in models in which the population is represented using an age- and size-structured model where each cohort is subdivided into pre-specified size classes (e.g. Frøysa et al., 2002; Gilbert et al., 2006; Gardner et al., 2007) or where length bins grow with the cohort length-at-age distribution (McGarvey et al., 2007). Section 2 of this paper identifies a set of models on which size-transition matrices can be based and how the values for their parameters can be estimated using tag-recapture data. Section 3 outlines how the values for size-transition matrices can be estimated when that estimation is fully integrated into the assessment. Section 4 describes how errors in the size-transition matrix can impact the quantities on which management advice are based. Section 5 summarises the current state of progress with the use of size-transition matrices. Finally, Section 6 outlines some general issues and provides recommendations and suggestions for future work.

2. Methods to estimate size-transition matrices

The growth process for crustaceans can be characterized by a combination of the distribution for the time between moults and the distribution for the growth increment given a moult (Caddy, 1987; Chang et al., 2012). For a discrete-time discrete-size-class model such as Eq. (1), this can be approximated by a combination of the probability of a growth transition (by size) multiplied by the distribution for the growth increment (by size) given a moult occurs. Many analyses have been based on explicitly modelling growth increment and the probability of moulting or equivalently the intermoult period (e.g. Chen and Kennedy, 1999; Ehrhardt, 2008; Zheng and Siddeek, 2013; Turnock and Rugolo, 2013).

ⁱ A terminal moult implies that at some stage (usually after reaching sexual maturity) the animals stops growing.

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