



# Length-based Brownie mark-recapture models: Derivation and application to Indian Ocean skipjack tuna



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## ABSTRACT

Standard Brownie mark-recapture models follow tagged cohorts of fish meaning an age-based setting is required, but there are many populations for which length-at-age cannot be characterised. This paper details the derivation of a length-based Brownie mark-recapture model, with specific application to Indian Ocean skipjack tuna. Instead of following cohorts (often tagged a number of times) the model follows the recapture history of animals tagged in a given length class and period. For Indian Ocean skipjack reporting rate uncertainty, related to mixing assumptions, is accounted for using two extreme options. Various mortality model structures were explored and length-specific natural mortality and a separable model for fishing mortality were ultimately selected. Absolute values of fishing and natural mortality depend strongly on the reporting rate assumptions, with total mortality being far more robust to assumptions about reporting rates. Estimates of fishing mortality were highest between mid 2006 and mid 2008, reducing thereafter to levels estimated in late 2005/early 2006.

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## 1. Introduction

The Brownie mark-recapture model (Brownie et al., 1985) has often been used when estimating both natural and fishing mortality rates from mark-recapture data (Brownie et al., 1985; Polacheck et al., 2006). The age-based population dynamic setting for the Brownie model has, to date, made it difficult to apply to populations that are either difficult or impossible to age, and length-based models have formed the core structure of stock assessments in such cases (Breen et al., 2003; Hillary et al., 2010; Punt et al., 1997). The assessment of tuna stocks is largely dependent on fishery-dependent data, such as catch composition and CPUE data. Often, the sampling properties of the catch composition are not well known, with the degree to which the CPUE reflects relative abundance also a major issue (Harley et al., 2001). This issue is even more pressing for skipjack tuna in the Indian ocean as there are no really reliable relative abundance series with which to conduct a formal stock assessment. Tagging data can be characterised as fishery semi-dependent and, where available and valid, they provide arguably the most informative observations relating to mortality rates and population abundance (Polacheck et al., 2006).

Hence, they can provide estimates of variables from which we can infer something about the status of the stock. In this paper we derive a length-based formulation of the Brownie mark-recapture model and apply it to Indian Ocean skipjack tuna mark-recapture data collected as part of the Regional Tuna Tagging Project of the Indian Ocean (RTTP-IO) (Hallier and Fonteneau, 2015). The example serves as both a proof of concept of the proposed model but also to estimate both fishing and natural mortality rates for Indian Ocean skipjack tuna over the years covered by the data (2006–2008).

The length-based Brownie formulation requires a transition matrix specifying the probability of an animal transiting from one length class to another in a single time step. The growth curve estimated for Indian Ocean skipjack from the RTTP-IO tagging data (Eveson, 2015) is used to estimate the growth transition matrix (Hillary, 2011; Punt et al., 2009), where both individual variation in growth and uncertainty in exact length structure are dealt with simultaneously. In the model a number of structural possibilities are explored for both fishing and natural mortality to investigate how time and/or fish length play a role in these key parameters. Although the base distributional assumption for the recapture model is multinomial, the presence of over-dispersion (variability beyond that assumed in the likelihood) is investigated using Bayesian bootstrap (Rubin, 1987) analyses on the standardised residuals.

In mark-recapture analyses time-specific relative changes in reporting rate are required to be able to estimate total mortality,

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but to estimate fishing and natural mortality separately absolute estimates of reporting rate are required. Reporting rate uncertainty is a key issue for Indian Ocean skipjack tuna tagging data, driven largely by a lack of clear information on how well mixed the tagged animals are in the wider fishing grounds beyond those of the purse seine fishery, where the overwhelming majority of recaptures come from, and for where we have actual reporting rate estimates. The complex interplay between the estimates of fishing, natural and total mortality – driven by absolute and relative differences in time-specific reporting rates – is explored using two “extreme” options. The first assumes the recaptures to be mixed only into the purse seine grounds, suggested by the very low return rates in other fisheries (Carruthers et al., 2015); and the second assumes them to be fully mixed into the whole fishery.

## 2. Materials and methods

### 2.1. Data

The general features of the skipjack tagging data can be found in Hallier and Fonteneau (2015). For the analyses undertaken in this paper, there were 74,301 tags released with 10,290 tags recovered – the overall recapture percentage being just under 14%. The majority of tags (over 85%) were released on animals between 45 and 60 cm, and around 80% of these were released in the years 2006 and 2007. The majority of recaptures (over 95%) are of animals between 45 and 65 cm, and around 80% of the recaptures are in the years 2006–2008. Over 95% of the recaptures (at least those reported) came from the purse-seine fishery, which is the only fishery for which direct reporting rate estimates are available. Thus, we omit any non-purse-seine recaptures in our analysis and assume that the reporting rate for these other fisheries is zero, which is not an unreasonable assumption (Carruthers et al., 2015).

### 2.2. Length-based dynamics

While not essential, it usually makes sense to discretise length into a set of length classes, so  $l \in \{\lambda_1, \dots, \lambda_M\}$ . For a given time interval,  $\tau$ , one is assumed to have already estimated a growth transition matrix  $\Gamma_{ij}$  (Punt et al., 1997; Hillary, 2011), where the  $i, j$ th entry is the probability of being in length class  $j$  if you were in length-class  $i$  in the previous period and we assume a “closed” system so that  $\sum_j \Gamma_{ij} = 1$ . In the simplest case the dynamics of a population  $N_{t,l}$  are as follows:

$$N_{t+\tau,l} = \sum_k N_{t,k} \Gamma_{k,l} e^{-M_{t,k} - F_{t,k}} \quad (1)$$

where  $M$  and  $F$  are the instantaneous rates of natural and fishing mortality, respectively. The dynamics are updated so that the numbers in each length class are the total numbers of animals predicted to grow into that length class and survive from the previous year, which is a slightly different to the age-based and simpler  $a \rightarrow a + 1$  structure. This is the part which causes the added complication for the application of a Brownie approach because a group of fish in a single length class do not progress from one length class to another over time; they spread over an (often increasing) variety of length classes.

### 2.3. Defining a growth transition matrix

There are a number of ways to obtain a growth transition matrix (there is no unique matrix as it depends on both method and length partition). Historically, this has been done by calculating the probability with which animals of a given length grow – a specified amount of time later – into the other length classes.

The uncertainty due to process error (often via proxies for individual growth variation) is usually assumed to be the main driver (Punt et al., 1997, 2009). These methods usually ignore parametric variation in the growth parameters and uncertainty in the initial length (the midpoint of the given interval is often assumed). A new measure-theoretic method was proposed in Hillary (2011) that can accommodate both parametric and individual variation in growth and deals with the implicit uncertainty related to the use of discrete length intervals, instead of length as a continuous variable. This method has associated complexities as one obtains a distribution of growth transition matrices, not a single matrix. This can be difficult to deal with in moderately complex statistical models such as the Brownie.

If the main sources of uncertainty are individual variation in growth and the nature of the length intervals themselves, and not parametric uncertainty, then a workable compromise would perhaps be to include the key features of both approaches. This is what was done for skipjack whereby a single transition matrix was constructed by integrating over both variation in asymptotic length  $\ell_\infty$  and the distribution of possible lengths in any given length class.

In a general setting, suppose we can define a probability distribution for the length,  $l$ , of a given animal at time  $t + \tau$ , given it was of length  $l$  at time  $t$ :  $p(l|l)$  (in principle this is defined through the distribution of the growth parameters and growth function but in this case just by the population-level distribution of  $\ell_\infty$ ). The definition of the  $\{i, j\}$ th entry of the transition matrix,  $\Gamma_{ij}$  is as follows (Hillary, 2011):

$$\Gamma_{ij} = \int_{k \in \lambda_j} p(k|l \in \lambda_i) dk, \quad (2)$$

which is the probability of finding an animal in length class  $\lambda_j$  at time  $t + \tau$  given it was in interval  $\lambda_i$  at time  $t$ . The added complication in defining the distribution in Eq. (2) is we must also account for the fact that the reference length  $\bar{l} \in \lambda_i$  will have its own distribution. Length intervals are not discrete points so selecting a single point in  $\lambda_i$  will bias the results. To account for this we must first define the distribution of lengths in a given length class and integrate over it, so that:

$$\Gamma_{ij} = \int_{k \in \lambda_j} \int_{l \in \lambda_i} p(k|l) p(l) dl dk. \quad (3)$$

The integral in Eq. (3) appears complex for a given growth function (the VB log  $k$  function from Eveson (2013) was used), with the distribution of  $\ell_\infty$  (again see Eveson (2013)). In this work a uniform distribution for length in all partition elements was assumed (although any suitable distribution is permitted) and Monte Carlo methods can be used to efficiently generate the transition matrix  $\Gamma$ .

Ten length bins (in cm) were defined: 20–30, 30–40, 40–45, 45–50, 50–55, 55–60, 60–65, 65–70, 70–75 and 75–85. This choice ensured that, for the assumed quarterly time-step (i.e.  $\tau = 0.25$  years), the equilibrium distribution of animals in a simple per-recruit system (and irrespective of the overall mortality rates) was reasonably smooth. This does not mean a strictly monotonically decreasing equilibrium abundance at length, as complex growth and mortality models cannot guarantee this outcome. As a general rule of thumb, while exploring *a priori* plausible mortality levels, ensure that the length bins do not result in obvious discontinuities or clear gaps in the length distribution, nor that length bins overlap any potential growth change points for example. Poor choices of length bins can have a serious effect on the resultant population dynamics as there can be length bins that in theory no animals will ever be found in, because the growth model predicts that within the time interval  $\tau$  all animals will have by-passed this bin and grown into the next ones. This causes serious conflict with animals

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