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# Estimating humpback whale abundance using hierarchical distance sampling



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#### ARTICLE INFO

Article history: Received 25 January 2013 Received in revised form 2 May 2017 Accepted 8 May 2017 Available online 22 May 2017

MSC: 13-52R1

Keywords: Megaptera novaeangliae Population size Hierarchical line transect sampling Bayesian inference Atlantic Ocean

#### ABSTRACT

We developed a Bayesian distance sampling analysis using a hierarchically structured model parameterization to estimate humpback whale abundance in the Southwest Atlantic Ocean (Breeding Stock A). We included covariates that affect detection (altitude and sighting cue) and occurrence probability (year and distance from shore). Population sizes for 2008, 2011 and 2015 were estimated to be 7,689 (P.I.95% = 6,585–8,931), 8652 (P.I.95% = 7,696–9,682), and 12,123 (P.I.95% = 10,811–13,531), respectively. The results indicate an aggregation of humpback whales in an intermediate distance from shoreline, an increasing in density from 2008 to 2001 and a substantial overlap between posterior distributions of density for 2011 and 2015, which suggests a stabilization of population growth over the last year. Our parameterization provided a clear view of observational and ecological processes and illustrates that the Bayesian hierarchical line transect approach provides a flexible tool to account for and evaluate various sources of uncertainty.

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#### 1. Introduction

Abundance and density are the most important demographic measures of a population (Liebhold and Gurevitch, 2002; MacKenzie et al., 2006) and are essential information for population assessments, viability analyses, and evaluations of management procedures (Barlow et al., 1995; Carretta et al., 2009; Wade, 1998). Although important, one common difficulty in abundance studies is accounting for negative bias due to undetected individuals because sampling procedures do not guarantee a perfect detection in most cases (Dorazio et al., 2006; Royle and Dorazio, 2008).

In some cases, it can be reasonable to consider sampling variability and imperfect detection to be constant across spatial or temporal units. However, this option is rarely feasible. Sampling protocols and statistical inference should allow an explicit and formal representation of data using constituent models of observations and underlying ecological or state processes (e.g. Moore and Barlow, 2011; Royle et al., 2004; Royle and Dorazio, 2008; Thomson et al., 2008; Link and Barker, 2010). The state process models vary in

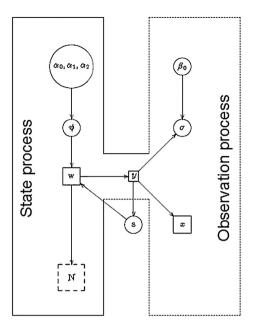
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http://dx.doi.org/10.1016/j.ecolmodel.2017.05.003 0304-3800/© 2017 Elsevier B.V. All rights reserved. underlying ecological phenomena, which are the primary object of inference. This process is manifest in a state variable, which is typically unobservable. In contrast, the observation process contains a probabilistic description of mechanisms that produce data. This structure is described as a hierarchical or state-space model (Royle and Dorazio, 2008).

The humpback whale (*Megaptera novaeangliae*) is a migratory species, moving seasonally between summer feeding grounds at high latitudes and winter breeding grounds at low latitudes (Dawbin, 1956; Mackintosh, 1965). The International Whaling Commission (IWC) recognizes seven humpback whale migratory breeding grounds in the Southern Hemisphere (IWC, 1998). The population of interest in this study is Breeding Stock A, which feeds east of the Scotia Sea, around South Georgia and the South Sandwich Islands, and breeds in the Southwest Atlantic Ocean along the coast of Brazil (Engel et al., 2008; Engel and Martin, 2009; Stevick et al., 2006; Zerbini et al., 2006).

The earliest quantitative studies of humpback whale populations used data from commercial catches, where it was possible to obtain relative measures of abundance (Clapham, 2000). The development of individual identification techniques based on the recognition of ventral fluke patterns (Katona and Whitehead, 1981) or, more recently, genotyping (Palsbøll et al., 1997) have enabled the application of mark-capture methods to this species (Hammond

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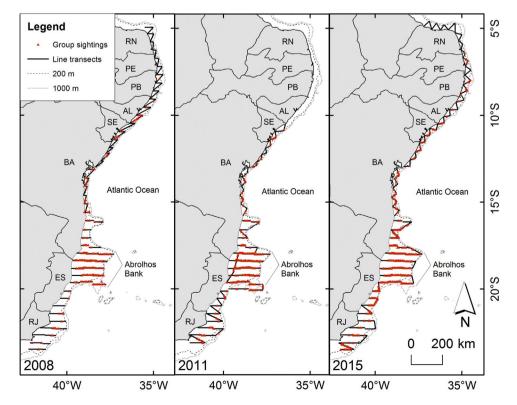
**Fig. 1.** Conceptual diagram of the hierarchical line transect sampling model highlighting the state and observation process.

et al., 1990). These methods are extremely useful if individual recapture probabilities are high. However, they do not perform as well if the rates of recapture are low, which can be a consequence of animals occupying relatively large areas, as is presently the case with some humpback whale populations. One of the most widely used techniques for quantifying cetacean abundance is line transect sampling. This method is suggested for widely distributed populations because it is less susceptible to failures of assumptions than are mark-recapture methods (Buckland et al., 2001, 2004).

A long period of exploitation by whaling (which ended in 1972) caused large population declines in the Southern Hemisphere humpback whale populations (Berzin, 2008; Clapham et al., 2005; Walsh, 1999; Yablokov, 1994). The majority of these populations have exhibited signs of recovery over the past decades (Bannister and Hedley, 2001; Clapham et al., 1999; Findlay et al., 1994, 2011; Flórez-González, 1991; Paterson et al., 1994; Paterson and Paterson, 1989), including Breeding Stock A (Ward et al., 2011).

The first abundance estimation for Breeding Stock A was conducted in 1995 using mark-recapture methods (Kinas et al., 1998). Since then, estimates of abundance from empirical data and assessment modelling have suggested that this population has been increasing (Andriolo et al., 2010; Freitas et al., 2004; Ward et al., 2011; Zerbini et al., 2011). Some of these estimates (e.g. Ward et al., 2011) are similar to those obtained through modelling of known life-history parameters from populations in various ocean basins (e.g. mean rate of increase of 7.3% year<sup>-1</sup> for one of the approaches used by Zerbini et al., 2010). Even if Breeding Stock A is growing at a rate that is approaching its maximum, some concerns remain because of the high uncertainty (evidenced through wide Bayesian probability intervals and frequentist confidence intervals) associated with the abundance estimates, which preclude precise estimates of some demographic parameters, such as the population growth rate.

Given the importance of current abundance estimates and the development of techniques that include habitat-specific explanatory variables over density (e.g. Hedley and Buckland, 2004), the goal of this study was to estimate the size of Breeding Stock A off the Brazilian coast using line transect sampling within a Bayesian statistical framework. A hierarchical modelling approach (Royle and Dorazio, 2008) was developed that incorporates covariates that have the potential to affect detection probability (altitude and sighting cue) and humpback whale occurrence (year and distance from shore) (Fig. 1). The detection probability and abundance of



**Fig. 2.** Locations of sightings of humpback whale groups (red) and transect lines (black) along the Brazilian breeding ground for 2008, 2011 and 2015. The isobaths of 200 m and 1,000 m are shown. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

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