Using gradients in productivity to inform stock structure: a case study in Alaskan waters.

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# Abstract

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# Keywords

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# Introduction

The first step in the management of natural resources is to determine the management unit, which will depend on the management objectives. Thus, management units should evolve in concert with changing management objectives (Begg and Waldman, 1999). Historically, management units for exploited marine fishes (i.e. stocks) lacked biological foundations and instead were politically based. Currently, stock boundaries for many fish stocks remain unchanged despite the plea for better aligning the spatial scale of management with the natural scale of targeted populations in the 10 commandments for ecosystem-based fisheries scientists (Francis *et al*., 2007). Furthermore, the predominance of political boundaries is reflected in the recent defintion of the management unit by the International Council for the Exploration of the Sea: “a geographically delinated fishery resource that is based on practical or jurisdictional boundaries for operational stock assessment and fishery management, which may or may not reflect biological population structure” (ICES, 2013). Thus, research and application of methods that define stock boundaries based on biology are becoming increasingly needed as managers shift from the World War II era focus on single species maximum sustainble yield to optimal yield, which can incorporate biological, economic, and social objectives (Rothschild, 1973; Sissenwine, 1978).

Few marine fish species lack evidence of complex spatial structure (Conover *et al*., 2006; Cope and Punt, 2009). Stephenson (1999) even goes so far to claim that all distinct spawning groups should be considered stocks until proven otherwise . Furthermore, stock structures should not be seen as static; species ranges are predicted to shift with respect to depth and latitude as oceans warm in response to climate change (Perry *et al*., 2005; Dulvy *et al*., 2008; Nye *et al*., 2009), potentially increasing the mismatch between political and biological stock boundaries. Thus, accounting for spatial structure by properly identifying stock boundaries is necessary for several reasons, including but not limited to the i) fair allocation of catch among competing fisheries and/or nations (Kutkuhn, 1981; ), ii) protection of nursing and spawning areas (Smith *et al*., 1990; Stephenson, 1999), iii) development of optimal harvest and monitoring strategies (Begg *et al*., 1999a; Frank and Brickman, 2000), iv) reduction of localized depletion (), v) proper identification of choke species (), and vi) sustainability of prey resources (Bertrand *et al*., 2012).

Currently, no one method properly identifies all stocks. Thus, integrating the results from a suite of techniques to address multiple aspects of the biology and life-history characteristics of marine fishes increases the likelihood of detecting relevant variation among stocks (Hohn, 1997; Waldman *et al*., 1997; Coyle, 1998; Begg *et al*., 1999b; Abaunza *et al*., 2004; Hatfield *et al*., 2005). Several available techniques require a substantive amount of costly data, necessitating a balance between accuracy and efficiency (Hilborn and Walters, 1992). Thus, techniques that use data routinely collected for assessment and management purposes (i.e. life-history parameters) are advantageous. As a bare minimum, catch data and distribution data from fishery-independent surveys, if available, can provide basic information on the areas used by a stock. Life-history data can provide inferences about genotypic variation resulting from environmental and anthropocentric influences by categorizing phenotypic expressions. In short, using life-history data to deliniate stock can provide a good starting point for more advanced stock identification techniques (e.g. biochemical, immunological, serological, behavioural, morphometric, meristic, mark-recapture, etc.), while being cost effective and efficient (Begg et al, 1999b). Unfortunately, fisheries data are subject to both observation and process error, which can complicate analyses. Observation error can originate from many sources, including: i) imperfect detection, ii) environmental conditions hindering the logistics and replicability of observational studies, iii) human error, iv) discarding, v) small sample sizes, and vi) non-independent sampling (Doubleday and Rivard, 1983; Alverson *et al*., 1994). In contrast, process error is the variation in true population size due to stochastic environmental conditions. Biologists are often primarily interested in quantifying process error, as opposed to observation error, which is often seen as a nuisance. Approaches to accommodate both process and observation error in a single framework are limited and few methods fully account for the probability structure created by their joint presence. Typically, one or the other is ignored, assuming either that the observations are made perfectly or the process is purely deterministic. Ignoring one or the other can lead to biased parameter estimation (), invalid hypothesis testing (), and biased predictions ().

State-space models can simultaneously estimate process and observation error making them ideal for ecological data. Their use in ecology began with time-series data for single populations (Staples, Taper, and Dennis, 2004; Dennis *et al*., 2006) and later extended into two-dimensional space for movement data (Jonsen, Myers, and Flemming, 2003) and multiple subpopulations (Ward *et al*., 2009) and species (Mattsson *et al*., 2013). Multivariate time-series analysis is one way to detect spatial patterns of correlation and synchrony across multiple locations () and can provide inferences on stock structure based on ecological differences. More specifically, Bayesian multivariate state-space models provide posterior probabilities of growth rates, density dependence, process variability, and observation variability using time-series data from multiple sites (Hinrichsen and HoMEs, 2009; Ward *et al*., 2010 ). The method is extremely flexible and can accommodate several population growth models, unequal sampling effort, missing data, multiple stock structures, density dependence, and data from multiple species (). Here we present an ecological assessment of stock structures for three species, walleye pollock (*Theragra chalcogramma*; hereafter referred to as pollock), Pacific cod (*Gadus macrocephalus*; hereafter referred to as cod), and Atka mackerel (*Pleurogrammus monopterygius*; hereafter referred to as mackerel) in the north east Pacific Ocean using Bayesian multivariate autoregressive state-space models.

Pollock, cod, and mackerel are important both ecologically and commercially in the Bering Sea Aleutian Island (BSAI) and Gulf of Alaska (GOA) large marine ecosystems. Pollock and cod represent the two largest fisheries by weight in all of Alaska (1,310,330 and 329,040 (t), respectively; st.nmfs.noaa.gov ). Furthmore, pollock and mackerel are the main prey for cod, comprising approximately 19% and 27% of total cod stomach contents, respectively (Ortiz, 2007). As well, pollock and mackerel are the two most common prey species (frequency of occurrence (FO) 46.4% and 39.6%, respectively) of the federally endangered Steller sea lion (Eumetopias jubatus; SSL), with cod being the fourth most common (FO = 16.1%) (Sinclair and Zeppelin, 2002). Currently, pollock is managed as four stocks (BS, AI, GOA, and Bogoslof), cod is managed as three stocks (BS, Aleutian Island (AI), and GOA), and mackerel is managed as two stocks (BSAI and GOA), although there is no stock assessment for mackerel in the GOA region because there is no targeted fishery. Nevertheless, evidence for stock structures is cited as being equivocal and stock assessment documents suggest further research and analysis regarding stock structure as a research priorities ().

The AIs are complex and the least predictable of the three management areas. Thus, it may be most appropriate to delineate stocks based on current patterns, such as Samalga Pass (; Figure [AlaskaMap]) rather than politically established management boundaries (i.e. ; Pacific Fisheries Management Council, ). Furthermore, declines in pinnipeds and marine bird populations are often linked to decreases in prey availability, resulting from commercial exploitation or climate change (NRC, 1996; Loughlin and York, 2000; NRC, 2003; DeMaster *et al*., 2006; Hennen, 2006). Reductions in prey abundance and quality is one of the more supported hypotheses for the decline in SSL abundance in western and central Alaska since the 1960’s (). Studies revealed that diets were more similar between island rookeries in close proximity to one another (Sinclair and Zeppelin, 2002). Thus, decreasing the risk of localized prey extinction may be important for SSL recovery and understanding the stock structure of these three fish species is an important task, not to mention a federally mandated one according to the Endangered Species Act and the Sustainable Fisheries Act.

Bayesian state-space models were used here to determine localized growth rates and process variability for three species (pollock, cod, and mackerel) in the BS, AIs, and GOA regions, while testing various hypotheses regarding localized stock structure. The hypotheses are based on known current patterns. The best model was chosen using model-selection criteria. The method should be useful to researchers looking to esablish stock structures that will lead to robust ecosystem based fisheries management and minimize the chances of localized depletion for multiple species in a single analysis.

# Methods

## Study area

The study area included the Aleutian management area (170° E to 170° W), a portion of the Southern Bering Sea management area (165° W to 170° W along the north side of the Aleutian Islands), and the Gulf of Alaska management area (132°40’ W to 170° W) (Figure [AlaskaMap]). The AIs are an extensive archipelago comprised of 14 large and hundreds of small volcanic islands, characterised by a relatively narrow continental shelf, crossed by numerous deep passes. Conversely, the GOA is characterized by a semi-enclosed basin, with a relatively shallow shelf that varies in width from 5 km in the southeast to more than 200 km in the north.

## Data

Survey data were collected by the Alaska Fisheries Science Center of the National Marine Fisheries Service from 1982 to 2012 during the triennial GOA and AI bottom trawl surveys. Data serves to provide estimates of absolute or relative abundances (Aydin *et al*., 2013; A’mar *et al*., 2013), define distributions, and inform biological parameters of groundfish and crab to the the North Pacific Fishery Management Council (NPFMC).

Surveys employed a stratified random sampling design, with grids determined by NPFMC regulatory areas, which were further divided by depth stratas. The AI surveys covered depths up to 500 m along the north side of the AIs from Unimak Pass (165° W) westward to Samalga Pass (170° W) and on both sides of the AIs from Samalga Pass to Stalemate Bank (170° E) (von Szalay *et al*., 2011). The GOA survey covered depths up to 1000 *m* from Samalga Pass to Dixon Entrance (54°30’ N, 132°40’ W) (Raring *et al*., 2011). Surveys in the AIs were conducted in 1983, 1986, 1991, 1994, 1997, 2000, 2002, 2004, 2006, 2010, and 2012. Surveys in the GOA were conducted in 1984, 1987, 1990, 1993, 1996, 1999, 2001, 2003, 2005, 2007, 2009, 2011, and 2013. The analysis was restricted to data collected after 1989 and east of 140° W because of the lack of standardized gear and effort measurements prior to 1990 (Munro and Hoff, 1995) and because of the Southeast Alaska Trawl Closure (Figure [AlaskaMap]), respectively.

Tows of 15 min (estimated on bottom duration) at speeds of 3 knots were conducted at each sampled station. For each tow, species composition of the catch was determined and species specific catch per unit effort (*CPUE*) was calculated as the weight of the catch (kg) divided by the area swept (ha) for a given trawl. Global positioning (GPS) locations for each trawl were projected using the Albers equal-area conic projection, an equal area map projection.

## Spatial fields

Spatial data were defined as realizations of a stochastic process indexed by space

, Eq. 1

where the domain (Ɗ) is a fixed subset of ℝd (here d = 2). The point referenced data of nonzero *CPUE* measurements, , where is a set indicating the spatial units at which the measurements were taken, were modelled using a stochastic partial differential equation (SPDE) approach proposed by Lindgren *et al*. (2011). Continuous spatial processes were represented using discretely indexed latent stationary Gaussian Markov random fields (GMRFs), which is the same as saying the parameters of the process have a multivariate Normal distribution with mean **μ** = (μ­1, …, μn)′ and a spatially structured covariance matrix Σ, whose generic element Σi,j = Cov(θi, θj) = . GMRFs use sparse precision matrices rather than dense covariance matrices, making them computationally efficient compared to Gaussian fields (Jona-Lasinio *et al*., 2012; Banerjee *et al*., 2004). Triangulation of Ɗ facilitates the transformation of a continuous space () to a discretely indexed GMRF via a basis function

, Eq. 2

where *G* is the total number of vertices in the triangulation, { is the set of basis functions, and are the non-zero distributed weights. Basis functions were chosen such that was 1 at vertex *g* and 0 everywhere else (Lindgren *et al*., 2011). Here is the variance component for and is the (isotropic) Matérn spatial covariance function (Cressie, 1993), which depends on the Euclidean distance between the locations . It follows that,

, Eq. 3

where is the modified Bessel function of second kind and order , which measures the degree of smoothness. The range (), defined as the distance at which the spatial correlation becomes less than or equal to 0.1, was empirically derived using

, Eq. 4

where κ>0 is a scaling parameter and λ was set to 1.

## Gompertz model

Population dynamics for each species were modelled using a spatial equivalent of the log-linear stochastic Gompertz model,

, Eq. 5

where is the density at all spatial locations in year *t*, ρ is the strength of density dependence, Ω is a GMRF representing the spatial variation in productivity, and is a GMRF representing the spatial variation in process error in year *t*. It follows that, Ω ~ *MVN*(α**1**, ΣΩ) and Εt ~ *MVN*(0, ΣΕ), where α**1** is a vector and α is the mean productivity of the GMRF. ΣΩ and ΣΕ­ are defined as above (Eq. 3) with independent variance components and equal Matérn spatial covariance functions.

Initial conditions were specified using the following equation:

, Eq. 6

where ϕ**1** is the log-ratio of expected abundance in the initial year (*t*=1) and the median of the stationary distribution for abundance at equilibrium.

## Estimation procedure

Data were assumed to follow a lognormal distribution

, Eq. 7

where, is the predicted density at a given vertex, *i*, located at the points [*x*, y] on the triangulation network, is the standard deviation of the observation error, and are the observed *CPUE* observations located in the triangulation vertex *i* in year *t*. and are statistically independent of and conditional on a fixed value for and , implying partial separability.

GMRF matrices were computed using functions available in the INLA package (Rue *et al*., 2014; Illian *et al*., 2012) implemented in the R statistical software environment (R Core Team, 2014). A single triangulation network used to facilitate the comparison of productivity across species. Parameters of the models were then estimated using the Template Model Builder (TMB) software (Kristensen *et al*., 2013). TMB uses the integrated nested Laplace approximation (Skaug and Fournier, 2006) to calculate the marginal likelihood of the fixed-effect parameters integrated across all random fields, while also calculating the gradient of the marginal likelihood via automatic differentiation. Fixed effects are then subsequently optimized using traditional tools in R by maximizing the log-marginal likelihood. Confidence intervals are available using the hessian matrix and delta-method.

# Results

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# Discussion

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# Acknowledgements

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# References

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