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Comparison of individual-based model output to data using a model of walleye pollock early life history in the Gulf of Alaska[☆]

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ABSTRACT

Biophysical individual-based models (IBMs) have been used to study aspects of early life history of marine fishes such as recruitment, connectivity of spawning and nursery areas, and marine reserve design. However, there is no consistent approach to validating the spatial outputs of these models. In this study, we hope to rectify this gap. We document additions to an existing individual-based biophysical model for Alaska walleye pollock (*Gadus chalcogrammus*), some simulations made with this model and methods that were used to describe and compare spatial output of the model versus field data derived from ichthyoplankton surveys in the Gulf of Alaska. We used visual methods (e.g. distributional centroids with directional ellipses), several indices (such as a Normalized Difference Index (NDI), and an Overlap Coefficient (OC), and several statistical methods: the Syrjala method, the Getis-Ord Gi* statistic, and a geostatistical method for comparing spatial indices. We assess the utility of these different methods in analyzing spatial output and comparing model output to data, and give recommendations for their appropriate use. Visual methods are useful for initial comparisons of model and data distributions. Metrics such as the NDI and OC give useful measures of co-location and overlap, but care must be taken in discretizing the fields into bins. The Getis-Ord Gi* statistic is useful to determine the patchiness of the fields. The Syrjala method is an easily implemented statistical measure of the difference between the fields, but does not give information on the details of the distributions. Finally, the geostatistical comparison of spatial indices gives good information of details of the distributions and whether they differ significantly between the model and the data. We conclude that each technique gives quite different information about the model-data distribution comparison, and that some are easy to apply and some more complex. We also give recommendations for a multistep process to validate spatial output from IBMs.

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1. Introduction

Model validation (i.e. the comparison of model output to external, independently derived data) is a necessary part of the development and use of ecological models. Individual-based biophysical models (IBMs) of larval fish dispersal and early life history have been used in fisheries for several decades, but are often not well validated; there is much room for improvement (North et al., 2009). Depending on the purpose of the model, the type of validation will differ. In drift and connectivity studies, the emphasis is on validating spatial distributions and trajectories of larvae. Investigations examining growth, mortality and recruitment will need different types of validation; these are not discussed here. Spatial outputs of biophysical individual-based models are often compared to data by placing maps side-by-side for the reader, which is a good first step, but it is not quantitative. Several measures or indices have been used to compare individual-based model spatial outputs to empirical data, however there has been no consistent approach using multiple methods.

There are limited methods that can be used validate model predictions of larval dispersal and transport of individuals. One method

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compares trajectories from model predictions to those from satellite-tracked drifters (North et al., 2009). This comparative method is usually based on a relatively limited numbers of drifters that were depl`oyed at fixed depths, incorporate wind effects, and adds cost to the model validation. Characteristics of drifters predispose satellite-tracked drifter tracks to diverge from larval fish trajectories, such as the effect of wind on the drifter, or use of a constant depth of the drogue when individual fish often move vertically in the water column.

An alternative approach could be to use uniquely marked individual animals. Chemical marking has been attempted (North et al., 2009), and might be a useful validation technique but is only applicable when populations are small, mortality is low, and the likelihood of recapture is reasonable. Elemental fingerprinting has been used to infer natal origin of animals captured during distribution and abundance surveys (Thorrold et al., 2001; DiBacco and Levin, 2000; Zacherl et al., 2003; Becker et al., 2007), and might be used to validate individual-based model (IBM) connectivity between spawning and nursery grounds, but detectable differences in seawater trace elemental composition between sites is required, and still, actual trajectories remain unknown. The required gradient and resolution to detect change among sites may vary with factors other than seawater composition (e.g. temperature, salinity), and it adds cost to the validation. The use of otolith microchemistry enables assessment of larval fish natal origin (Campana, 1999; Thorrold et al., 2001), and seascape genetics or genetic fingerprinting may be used in some situations (Coscia et al., 2013; Selkoe et al., 2008; Galindo et al. 2010; Palumbi, 2003), but source populations must be known and characterized by detectable genetic differences (Hedgecock et al., 2007). Model error quantification techniques used for hydrodynamic models include cost functions (Delhez et al., 2004; Radach and Moll, 2006), root-mean-square error of modeled vs. observed values, model skill scores (Warner et al., 2005), and Taylor diagrams (Taylor, 2001).

One of the most straightforward ways to validate dispersal and transport IBMs is by comparing modeled spatial distributions with empirical distributions of larvae and juveniles. Although it cannot be known if individuals from spawning sites are the same individuals that are caught during surveys, this comparative approach can be useful when the sources of individuals caught in the field are relatively well known. Several studies using IBMs have used several different measures to analyze spatial distributions (overlap index, (Hinrichsen et al., 2005), Morisita's simplified overlap index, (Utne and Huse, 2012), centroids (center of gravity), (Vikebø et al., 2005; Castaño-Primo et al., 2014), (defined as convex hull), (Petrik et al., 2014) and (Utne and Huse, 2012), Jaccard's Coefficient, (Wiedmann et al., 2012), a Correlation Index based on linear regression, (Pedersen et al., 2006), Root Mean Square Deviation (RMSD), (Utne and Huse, 2012), the local index of collocation (Petrik et al., 2014), but no comparison of methods has been published.

We use walleye pollock (*Gadus chalcogrammus*) in the Gulf of Alaska (GOA) as a case study to validate the spatial output from an individual-based dispersal model. Walleye pollock has been studied intensively for several decades, and many lab studies and field surveys have been done. We used 1987 as our test year in this study, as there were several sequential surveys of different early life stages done in that year. Walleye pollock in the Gulf of Alaska have a life history where spawning and nursery habitat appear to be spatially disaggregated, and most of the currents in the region where pollock spawn are highly advective. Historically, a large part of the egg production of pollock has been located at the southwestern entrance to Shelikof Strait, an area between Kodiak Island and the Alaska Peninsula (Fig. 1, Kendall et al., 1987; Schumacher and Kendall, 1991). Pollock eggs are spawned between mid-March and early May, with spawning peaking at the beginning of April (Doyle and Mier, 2016). By May, larvae are advected southwest by the Alaska Coastal Current (ACC) along the Alaska Peninsula. By summer and through early fall, juveniles arrive at their primary nursery area in the vicinity of the Shumagin Islands (Hinckley et al., 1991, 2001; Spring and Bailey, 1991; Wilson et al., 1996). Other potential spawning and nursery areas have been reported in the literature (Wilson, 2000; Bailey et al., 1999; Mazur et al., 2007), but their relative contribution to the recruitment of pollock in the GOA is not known, nor is how their contributions

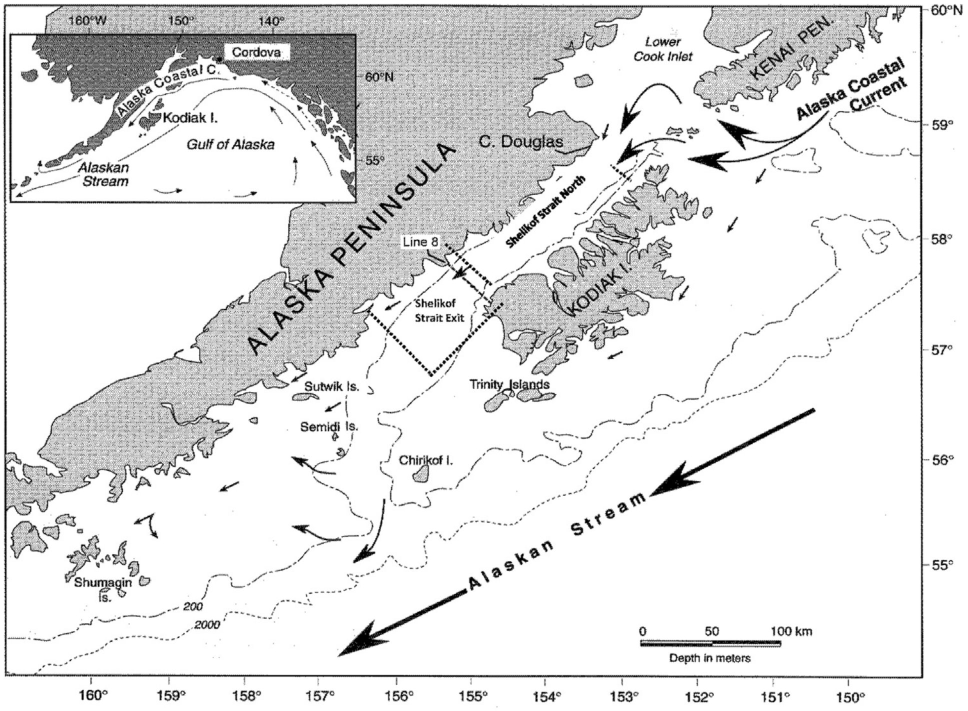

Fig. 1. The study area in the western Gulf of Alaska, where the surveys and model simulations took place.

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