Fish in Space:
Estimating groundfish population distribution in the Gulf of Alaska for management apportionment by subregion

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Abstract

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Management of fisheries relies on information about biomass of stocks in order to determine how many fish can be sustainably harvested in a given year. In addition to predicting total biomass, it is frequently important to accurately predict the distribution of stock biomass through space in order to avoid local depletions of stock and to more evenly distribute harvest among many stakeholders. Towards that end, this study compares the current modeling approach to predict the geographic apportionment of stock biomass for groundfish in the Gulf of Alaska (GOA), a random walk model, with a delta-GLMM spatiotemporal model implemented using the VAST package in R. These stocks are managed using subregional catch allocation, whereby the GOA is divided into 3 management areas: western, central, and eastern GOA. This analysis uses bottom trawl survey data collected by the Alaska Fisheries Science Center (AFSC) of the National Oceanic Atmospheric Administration National Marine Fisheries Service (NOAA

NMFS) for two species of groundfish, Pacific Ocean Perch (*Sebastes alutus*) and Northern Rockfish (*Sebastes polyspinis*).

Model performance was evaluated using the accuracy of the model estimate from jackknife resampled results for population proportion by subregion compared to survey design-based proportions, and on the precision of the model jackknife estimates. In terms of accuracy, the models performed similarly well, with the mean absolute difference between the model jackknife estimates and the design-based estimates for the random walk results being smaller by 0.086 or less than the delta-GLMM results, with significant overlap in the jackknife absolute difference values. Precision was measured by the CV calculated with the model jackknife results, and the delta-GLMM results had smaller mean CV values by at least 0.105, and very little overlap in the jackknife CV values. However, the precision of the delta-GLMM is small enough that it may lead to significant over- or underestimation compared to the survey design-based proportions and therefore may be a riskier option than the random walk model for estimating subregional catch apportionment for these stocks in the GOA.

Introduction

Fisheries management is a complex process regulating how much of a stock commercial, recreational, and subsistence fishers can harvest. Management strategies take many forms, but the basic goals of most modern fisheries management are to preserve healthy and self-sustaining fish populations, while simultaneously maximizing harvest for the benefit of the fishers and consumers (Costello et al. 2016). These goals can be difficult to balance, particularly when fish population characteristics are unknown, and in the past this has led to overfishing and endangering the health of some fish stocks.

To determine what a healthy and self-sustaining population for a given stock is, fisheries scientists use statistical modeling to estimate current and past stock biomasses, and project future stock biomasses. There are many statistical models that are used to both meet the needs of management and represent the stock biology and population dynamics as accurately and precisely as possible (Methot 2009). Some examples include abundance-focused models such as age- or size-structured models, or spatial distribution models, which predict where species will occur geographically (Levin and Goodyear 1980, Schnute 1987, Ciannelli et al. 2008). Fisheries scientists are continually looking for ways to improve our statistical models to provide more accurate and precise estimates of biomass for use in management decisions. More accurate and precise estimates on the status of the fish stocks will lead to more confident decision-making to fulfill both management goals of preserving self-sustaining populations and maximizing harvest.

This study focuses on the Gulf of Alaska (GOA) groundfish fishery, an economically important fishery both to local Alaskan fishers throughout the GOA and to other US West Coast commercial fishers (Williams et al. 2020, Hulson et al. 2020). In 2020, 178,000 tons of groundfish was harvested in the GOA, valued at $92.9 million (Fissel 2020).

The groundfish management category includes fish species that are generally found on or near the seabed of continental shelves, areas of the ocean that are less than 1000 meters deep and generally occur just offshore of coastlines. In the commercial fishery, groundfish are harvested primarily with bottom trawls (Williams et al. 2020, Hulson et al. 2020). It is fairly typical for groundfish stock trawl hauls to produce a few very large catches while the majority of hauls catch very few or none of a given stock, which may signify that these populations have a clustered spatial distribution. As a result, their populations' abundance and distribution is particularly difficult to model.

A lot is still unknown about the biology and ecology of most groundfish species, which also contributes to the challenge of modeling groundfish population dynamics. In the GOA, commercial groundfish fishing exploded in the 1960s and 70s, and some stocks subsequently experienced significant decreases in population (Williams et al. 2020, Hulson et al. 2020). While declines appear to be correlated with increased fishing pressure and therefore could be caused by overfishing, it is not usually possible to say definitively that a stock's decline is due directly to overfishing because there may be coinciding environmental variables that contribute to a decline. Regardless of the reason, once a population is clearly in decline, fisheries managers become concerned that the reduced population may be vulnerable to overfishing at that point and the stock will be driven into even further decline. Consequently, commercial fishing of groundfish in the GOA was regulated much more strictly starting in the 1980s, and many of the stocks have experienced increases in population since then (Williams et al. 2020, Hulson et al. 2020). Because of the declines and subsequent recoveries, these stocks are managed carefully and improving modeling methods is a priority for management (Williams et al. 2020, Hulson et al. 2020). Two groundfish stocks that experienced this decline and have subsequently recovered are Pacific Ocean Perch (*Sebastes alutus*) and Northern Rockfish (*Sebastes polyspinis*).

Pacific Ocean Perch and Northern Rockfish, like many groundfish species, are long lived and slow to mature, therefore it is reasonable to assume that the population biomass in a healthy population would not fluctuate an enormous amount from year to year (Davison et al. 2019). However, the data collected every 2 or 3 years in the bottom trawl survey conducted by the National Oceanic & Atmospheric Administration (NOAA) National Marine Fisheries Service's (NMFS) Alaska Fisheries Science Center (AFSC) shows a fairly large amount of interannual variation. This is likely less to do with true interannual changes in stock biomass and much more likely the result of low survey sample sizes (particularly for Northern Rockfish) applied to what appears to be clustered population distributions. In addition, there are logistical or data collection issues, particularly the inability to trawl in many areas of the GOA due to rocky bottom habitat, that contribute to this variability. Ideally, a statistical model that uses this survey data to predict stock biomass would seek to minimize the impact of this artificial variability.

Many groundfish stocks in the GOA are managed by allocating harvest rules across three designated subregions: western, central, and eastern GOA. Each subregion is allocated a proportion of the stock's harvest limit in the GOA management decisions according to the proportion of the stock's biomass that is estimated to occur in that subregion (Williams et al. 2020, Hulson et al. 2020).

The designation of these subregions is primarily used to ensure that local fishing communities across the GOA have access to a sustainable population of fish. In this management approach, there are two models used to estimate groundfish biomass: (1) an age-structured population model that generates biomass estimates across the entire GOA and (2) a state-space random walk model (hereafter referred to as random walk) that estimates the proportion of that biomass that occurs in each subregion of the GOA (Williams et al. 2020, Hulson et al. 2020).

The random walk model that is currently used to estimate the proportion of stock biomass across subregions for these stocks is a flexible model that has many advantages. However, a disadvantage of the model is that it is quite sensitive to variability in the input data. As a result, the high variability in the survey data causes high uncertainty in the model results and the biomass predictions are therefore not very precise, particularly in years without survey data. This high interannual variability makes it difficult for fishers to plan for each fishing season and requires managers to revisit harvest rules each year. Additionally, harvest rules may need to be set lower than is likely needed to reduce risk of overfishing. If the model produced more precise estimates, managers could potentially raise catch limits with confidence in maintaining sustainable populations. Precision must be balanced with accuracy, however, as estimates that are very precise but inaccurate may lead to either over-fishing or under-harvesting.

As currently implemented, the random walk model does not use spatial information as a variable and only the data from hauls caught in each subregion are used to fit the model to estimate the biomass in that subregion. This means that a lot of data is being excluded that could potentially be used to improve the precision or accuracy of the model. A spatiotemporal model that uses both temporal and spatial variables has the potential to produce biomass proportion estimates with increased precision or accuracy compared to the random walk.

In this study, I compare the ability of a spatiotemporal model to produce biomass proportion estimates with more precision compared to the random walk model proportion estimates for Pacific Ocean Perch and Northern Rockfish. In particular, an objective of this study is to determine if the spatiotemporal model produces estimates with less interannual variability. In addition to improving on precision, the spatiotemporal model needs to match or improve on the random walk model biomass proportion estimates in terms of accuracy when compared to the survey data in order to be considered a viable alternative.

Methods

Species & study area

This project focuses on two species, Pacific Ocean Perch (*Sebastes alutus*) and Northern Rockfish (*Sebastes polyspinis*). These are two of the most economically important stocks in the GOA commercial groundfish fishery, and they are managed as single species stocks with harvest allocated by subregion. Pacific Ocean Perch alone has accounted for more than 60% of the catch in the GOA groundfish fishery since 2015 (Williams et al. 2020, Hulson et al. 2020). In 2019 the catch for Pacific Ocean Perch was worth $23.9 million while Northern Rockfish catch was worth $2.4 million (Williams et al. 2020, Hulson et al. 2020).

Pacific Ocean Perch adults undergo a seasonal migration, where they move from deeper parts of the continental shelf (300 - 420 meters) in the winter to shallower parts (150 - 300 m) in the summer. They also move up higher in the water column during the day, likely to feed, and this may inflate the variance associated with bottom trawl sampling if a substantial portion of the population is absent from the bottom during trawling. Both Pacific Ocean Perch and Northern Rockfish are slow maturing and long-lived, like most rockfish species; the oldest Pacific Ocean Perch and Northern Rockfish individuals captured in the GOA were estimated to be 84 and 67 years old, respectively (Williams et al. 2020, Hulson et al. 2020). Very little is known about the larval or juvenile stages of either species, and even less is known about Northern Rockfish adult behavior than about Pacific Ocean Perch adult behavior, other than the fact that they live up to their name and appear to prefer rocky bottom habitat that is difficult to trawl (Williams et al. 2020, Hulson et al. 2020). This lack of life history information contributes to the difficulty of modeling their population dynamics.

The study area in this analysis includes the continental shelf of the Gulf of Alaska, which is separated into 3 management subregions: western, central, and eastern (Figure 1). The western and central subregions are separated by -157^o longitude and the central and eastern subregions are separated by -147^o longitude. The central subregion includes Kodiak Island, which is a significant source of local Alaskan fishing activity.

Bottom-trawl survey design

The data for this study come from a bottom trawl survey carried out by AFSC that has been operating in the GOA every 2 or 3 years since the 1980s. This is a multi-species survey that uses a

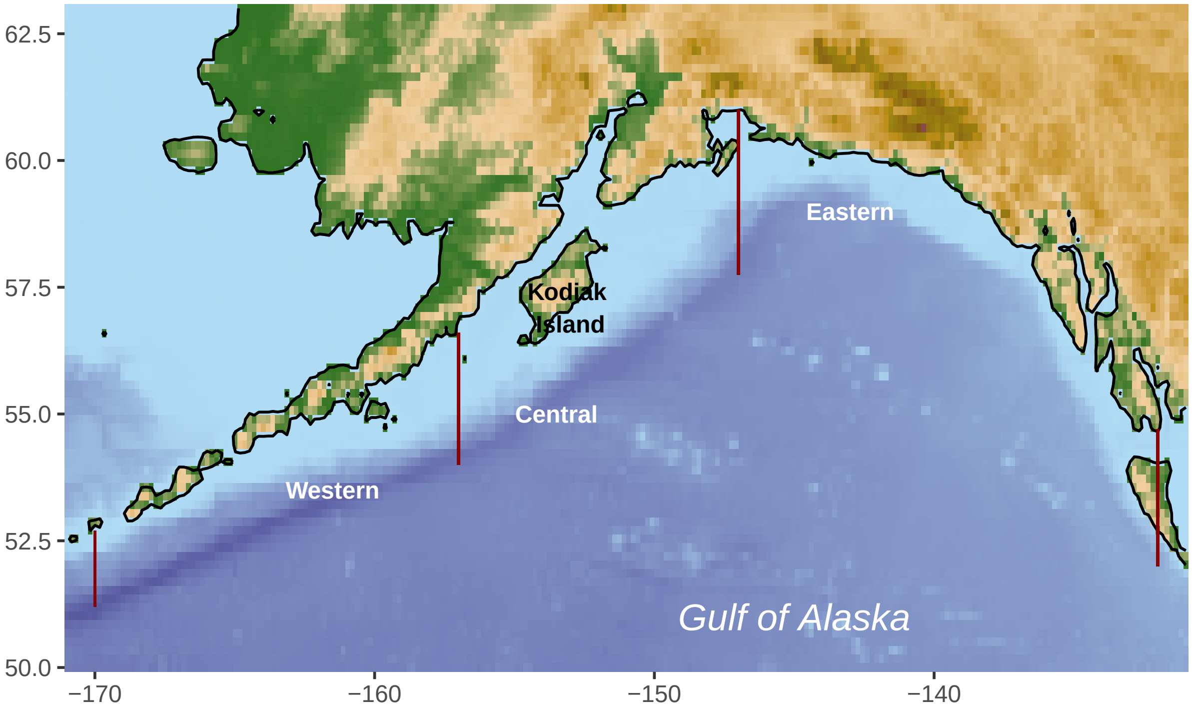


Figure 1: Map of the study area, the continental shelf of the Gulf of Alaska, shown in light blue. The three management subregions are delineated by red lines. The western edge of the western subregion is at -170^o longitude and the furthest east edge of the eastern subregion is at -132.6^o longitude.

spatially stratified random sampling method. The stratification used for this survey is primarily depth (with a maximum depth of 1000 m) with some influence from practicalities around logistical and economic considerations, and environmental features. A minimum of 2 primary sample locations is randomly selected for each depth strata each survey year (Stauffer 2004). When the primary sampling location is deemed untrawlable, a secondary location is randomized and sampling is attempted there. A significant challenge that this particular survey encounters is that large amounts of the bottom of the continental shelf are very rocky, making it difficult or impossible to trawl with the gear used by the survey (Stauffer 2004). The data for Pacific Ocean Perch used in this project start in 1990 and end in 2019 (14 years of survey data). The survey data for Northern Rockfish used in this project start in 1984 and end in 2019 (16 years of survey data).

Model Descriptions

Random walk model

In the implementation of the random walk model, the survey data are separated by subregion based on trawl haul location. The hauls in each subregion are then used to calculate a biomass per unit area surveyed, which is multiplied by the area of the subregion to produce a single value called the design-based estimate for each subregion in each year (y_t). A coefficient of variation for each subregion in each year is also calculated, using this design-based estimate and the variance of the catches in that subregion and year. The following steps are then performed for the data in each subregion separately.

The random walk model assumes that true biomass in year t (x_t) equals the true biomass in the year previous (x_{t-1}) plus process error (θ_p) from the previous year ($\theta_{p,t-1}$). The process error in a given year ($\theta_{p,t}$) is randomly drawn from a normal distribution with a mean of 0 and standard deviation, σ_p. The true biomass in the year before the first survey year, x_0, and σ_p are estimated from the survey data. The model assumes stationarity in the process error, meaning that birth rates and death rates are expected to be fairly consistent through time for these species. Specifically, biomass is estimated by

$$x_t = x_{t-1} + \theta_{p,t-1} \qquad \theta_{p,t} \sim \mathsf{N}(0, \sigma_p^2) \tag{1.1}$$

The model further assumes that the design-based estimate in a given year (y_t) equals the true biomass for that year plus observation error in that year ($\theta_{o,t}$). Unlike process error, we assume that the amount of observation error may change from year to year, based on individual conditions in each year. A new observation error distribution is calculated for each year, with a mean of 0 and a new variance ($\sigma^2_{o,t}$), taken from the coefficient of variation calculated with for survey data in each subregion in each year. In the case of these data, some likely contributors to observation error include the uncertainty associated with extrapolating sampled locations to unsampled locations given the likely clustered nature of the stocks' spatial distribution, and the fact that large portions of the bottom of the GOA are too rocky to trawl for this survey and may be preferred habitat for some or all of the species of interest. The observation model is

$$y_t = x_t + \theta_{o,t} \qquad \theta_{o,t} \sim \mathsf{N}(0, \sigma^2_{o,t}) \tag{1.2}$$

Spatio-temporal model

The spatio-temporal model I used is a hurdle model, specifically a delta-Generalized Linear Mixed Model (delta-GLMM) as described by Thorson (2017). The model uses a two-step process to predict stock biomass for each subregion. The first step is to determine whether the fish are in a particular area at a particular time (presence/absence). If no fish are present, the model estimates no biomass, regardless of the reason for absence (e.g., they are not present due to unsuitable habitat or seasonal/ontogenetic migration, they were present but the trawl did not capture them, or they were present and were captured but misidentified, etc). If the fish are present, then the second step is to estimate non-zero biomass at that place and time, also known as positive catch. The product of these two steps constitutes the delta-GLMM model.

The first equation represents encounter probability, the probability that the fish are present and at least 1 is sampled in a particular area at a particular time. The second equation predicts positive catch, the positive number of fish that can be caught in that area and time. Both equations use time, space and the interaction between time and space as variables. Positive catch is used to construct a gamma distribution representing observation error (as described for the Compound Poisson-Gamma model in Thorson 2017 (Thorson 2017)) and this is multiplied with encounter probability to produce an estimated biomass at time t and location s.

The encounter probability of observation i at location s and time t ($p_{i,s,t}$) is based on a function with both random and fixed effects ($n_{i,s,t}$), with an offset for area ($a_{i,s,t}$).

$$p_{i,s,t} = 1 - \exp(-a_{i,s,t} \times n_{i,s,t}) \tag{2}$$

$n_{i,s,t}$ is subject to a log-link and is made up of an autocorrelated temporal random or fixed effect (depending on species), $\beta_{1,t}$, a spatial random effect, $\nu_{1,s}$, and a spatio-temporal random effect, $\epsilon_{1,s,t}$, as shown below.

$$\log[n_{i,s,t}] = \boldsymbol{\beta}_{1,t} + \nu_{1,s} + \epsilon_{1,s,t} \tag{3.1}$$

Both the spatial and spatio-temporal variables are drawn from multivariate normal distributions with means of 0 and variance-covariance matrices made up of two parts:

$$\begin{aligned} \nu_1 &\sim \mathsf{MVN}(0, \sigma^2_{1\nu}\mathbf{R}) \\ \epsilon_1 &\sim \mathsf{MVN}(0, \sigma^2_{1\epsilon}\mathbf{R}) \end{aligned} \tag{3.2}$$

The $\mathbf{R}$ term in the variance-covariance matrices is a matrix of the spatial correlations for the entire area given an estimated distance κ. The other part of the variance-covariance matrices, $\sigma^2_{1\nu}$ and $\sigma^2_{1\epsilon}$, are the estimated pointwise variances of spatial variation in the observations for $\nu_{1,s}$ and $\epsilon_{1,s,t}$, respectively (see Thorson and Barnett 2017 for a full description of the spatial method).

Initially both species were fit with $\beta_{1,t}$ set as a random walk. However, for Northern Rockfish the resulting parameter estimates were extremely small. Consequently, the temporal random effect is configured differently for each species. For Pacific Ocean Perch, $\beta_{1,t}$ is a random walk, with t_{min} as the first survey year:

$$\beta_{1,t} \sim \begin{cases} \mathsf{N}(0,1) & \text{if } t = t_{min} \\ \mathsf{N}(\beta_{1,t-1},1) & \text{if } t > t_{min} \end{cases} \tag{3.3}$$

For Northern Rockfish, $\beta_{1,t}$ is a fixed intercept and constant among years.

The second equation of the model represents positive catch ($w_{i,s,t}$), subject to a log-link and made up of a temporal random effect ($\beta_{2,t}$), a spatial random effect ($\nu_{2,s}$) and a spatio-temporal random effect ($\epsilon_{2,s,t}$). The spatial and spatio-temporal random effects are calculated in the same way as the corresponding encounter probability equations and with similar variable definitions. The temporal random effect, $\beta_{2,t}$ is a random walk for both species, specified in the same way as the $\beta_{1,t}$ for Pacific Ocean Perch.

$$\log[w_{i,s,t}] = \boldsymbol{\beta}_{2,t} + \nu_{2,s} + \epsilon_{2,s,t} \tag{4.1}$$

$$\begin{aligned} \nu_2 &\sim \mathsf{MVN}(0, \sigma^2_{2\nu}\mathbf{R}) \\ \epsilon_2 &\sim \mathsf{MVN}(0, \sigma^2_{2\epsilon}\mathbf{R}) \end{aligned} \tag{4.2}$$

Model evaluation

I created replicate data sets from the source data using jackknife resampling to produce multiple model results for a more robust comparison of model performance. For each replicate created through resampling, one year was excluded from the data. In 2001, the survey wasn't conducted in the eastern subregion, and the proportion calculation for the three subregions with the survey data was impossible for that year. I therefore omitted 2001 from both the survey data and model results, leaving 13 sets of model results for Pacific Ocean Perch (for 1990, 1993, 1996 and odd years from 1999 - 2019) and 15 for Northern Rockfish (for 1984, 1987, 1990, 1993, 1996 and odd years from 1999 - 2019) available to calculate the model evaluation metrics.

The delta-GLMM and random walk models were fit with each replicate dataset for each species. The estimated biomasses in subregion c in year t ($b_{c,t}$) were then used to calculate the proportion of estimated biomass from each model in subregion c in year t ($P_{c,t}$), with C indicating the number of subregions.

$$P_{c,t} = \frac{b_{c,t}}{\sum_{c=1}^{C} b_{c,t}} \tag{5}$$

The proportion of biomass in each subregion in each year from the survey data ($P_{d,c,t}$) was calculated in the same way, and will be referred to hereafter as the design-based proportion.

For the metrics described below, the calculations are all done with the model estimates for the jackknifed year in each dataset, hereafter referred to as the jackknife estimate or jackknife proportion estimate, with subscript e for year equations. This allows a comparison to be made both between how precise a model estimate is when data are excluded compared to when they are included (a year t subscript refers to the model estimate from the version that included all data). Additionally, it shows the maximum amount of difference in accuracy and precision that the model introduces when data don't exist when compared to the design-based proportion.

Accuracy was measured using an absolute difference ($D_{c,e}$) between the jackknife proportion estimate in subregion c and excluded year e ($P_{r,c,e}$) and the design-based proportion estimate for that year. For example, the jackknife proportion estimate for 1990 from the replicate that excluded the data for 1990 is compared to the design-based proportion for 1990. The closer $D_{c,e}$ is to 0, the more accurate the model results are compared to the design-based proportion.

$$D_{c,e} = |P_{r,c,e} - P_{d,c,e}| \tag{6}$$

I also compared the jackknife estimates to the design-based estimates directly through plotting to look for indications of consistent bias in the model proportion estimates. This comparison was done with a simple regression of $P_{r,c,e} = m * P_{d,c,e} + b$, using a reference line of y = x, to see if the models were consistently over- or underestimating compared to the survey proportion. Overestimates occur above the reference line and underestimates occur below the line. In a management context, overestimating stock biomass could lead to overfishing by failing to detect when a stock has reached an unsustainable population level while underestimating stock would result in lost income for fishers and fishing communities.

To measure precision, I calculated a coefficient of variation ($CV_{c,e}$) for subregion c and excluded year e using the jackknife proportion estimate described above ($P_{r,c,e}$) and the standard error of that proportion ($SE[P_{r,c,e}]$).

$$CV_{c,e} = \frac{SE[P_{r,c,e}]}{P_{r,c,e}} \tag{7}$$

The standard error of the model estimated proportion ($SE[P_{r,c,e}]$) was approximated using a method from Thorson and Haltuch (2018) that uses the estimated biomass in subregion c in year e ($b_{c,e}$), the sum of all subregional estimated biomasses for each year (B_e), and the estimated standard error of the biomass in subregion c in year e ($SE[b_{c,e}]$).

$$SE[P_{r,c,e}]^2 \approx \frac{b_{c,e}^2}{B_e^2}\left[\frac{SE[b_{c,e}]^2}{b_{c,e}^2} - 2\frac{SE[b_{c,e}]^2}{b_{c,e}B_e} + \frac{\sum_{c=1}^{C} SE[b_{c,e}]^2}{B_e^2}\right] \tag{8}$$

The mean jackknife CV value and the distribution of jackknife CVs was examined for each subregion, with more precision indicated by CV values being closer to zero. In addition, I calculated the ratio between the CV value calculated for jackknife CVs ($CV_{c,e}$) with the CV value calculated for that year t for subregion c in the model results version that included all of the data ($CV_{c,t}$). This comparison showed how much relative uncertainty estimating a year without data introduces for each model.

$$\frac{CV_{c,e}}{CV_{c,t}} \tag{9}$$

In order to quantify how well the standard errors of the proportion provided coverage for the difference between the jackknife estimates and the design-based estimates, I calculated that difference divided by the jackknife standard error.

$$\frac{P_{r,c,e} - P_{d,c,e}}{SE(P_{r,c,e})} \tag{10}$$

I then used the pnorm function in R to determine what the probability of these values occurring would be if they came from a normal distribution, with the expectation that good coverage would be approximately characterized by a normal distribution. I visually compared the histogram of the pnorm values with a normal curve (with mean = 0.5 and standard deviation = 0.16 to approximate a normal distribution on a 0 to 1 scale) to evaluate whether the models produced roughly normal-looking coverage. If the pnorm coverage values occur more frequently outside the bounds of the normal curve, then this would indicate that the jackknife standard errors are frequently very small compared to the difference between the jackknife estimate and the design-based estimate, and precision may be too high to compensate for the model's level of accuracy.

Finally, the delta-GLMM model was used to predict the proportion of biomass in each subregion for each species in 2020, 2021 and 2022. These predictions were then used to compare how different proportions estimated from the delta-GLMM model would be compared to the random walk for how total allowable catch (TAC) would be allocated by subregion for 2020 - 2022. This was done using the total biomass estimated for 2020, 2021 and 2022 by the age-structured model in the stock assessments.

Results

The majority of Northern Rockfish biomass is found in the western and central subregions, with less than one percent occurring in the eastern subregion, according to both the design-based proportion and both models' estimates. Due to this very minimal presence, the NOAA AFSC stock assessment only allocates catch to the western and central subregions. Accordingly, in this analysis the eastern subregion was excluded from the model comparison metrics for Northern Rockfish, while results for Pacific Ocean Perch were evaluated for all three subregions.

The random walk model results roughly follow the trajectory of the design-based proportion across all subregions in terms of the proportion of biomass across the timeseries for both Pacific Ocean Perch and Northern Rockfish (Figure 2). The delta-GLMM model shows less fluctuation between years than either the random walk model or the design-based proportions for both species, but consequently it deviates from the design-based estimates more than the random walk model does. There is a much more dramatic difference between the delta-GLMM estimates and the design-based estimates occurring for Northern Rockfish than for Pacific Ocean Perch.

According to both models and the design-based proportion, the proportion of total biomass for Pacific Ocean Perch has decreased in the western subregion, starting around 20% of biomass in 1990 and decreasing to less than 10% in 2019, with a brief spike in proportion up to as much as 25% between 2005 and 2007. In the central subregion, it has increased, from between 30-40% in 1990 (with delta-GLMM predicting the higher proportion), with more than 50% of biomass found in that subregion since 1993, and up to approximately 75% in 2019, according to both models and the design-based proportion. In 1990, more than 40% of the biomass was in the eastern subregion but that sharply decreased between 1990 and 2000 to less than 20% according to the random walk model and design-based proportion, although the delta-GLMM estimated approximately 25% between 1993 and 2000. Since 2000, the eastern subregion proportion has been maintained at approximately 20-25% of the total biomass according to both models and the design-based proportion. The largest difference between the delta-GLMM and the design-based and random walk estimates occurred between 1996 and 2003, when there was a relatively large fluctuation in the design-based proportion for all subregions (increasing in the central subregion and decreasing in the other two subregions, particularly in eastern) that the delta-GLMM did not follow.

For Northern Rockfish, the delta-GLMM model estimates follow the trajectory of the design-based proportion until 1996, when a large departure occurs for the delta-GLMM results (Figure 2). From 1999 to 2019, the delta-GLMM results estimate that consistently 50-70% of the Northern Rockfish biomass occurs in the western subregion while 30-50% occurs in the central subregion. In contrast, the design-based proportion and the random walk results fluctuate much more, with between 20 - 65% of the biomass in western and 35 - 80% in central.

Accuracy Metrics

When the design-based proportion estimate is directly compared to the jackknife proportion estimate for Pacific Ocean Perch, neither the random walk nor the delta-GLMM appear to consistently over- or underestimate for the western subregion (Figure 3). The delta-GLMM appears to slightly underestimate the proportion in the central subregion while more clearly overestimating in the eastern subregion. The random walk does not tend towards over- or underestimation for any of the subregions, but has a fairly even spread of values above and below the reference line. Both models produce estimates that are fairly tightly clustered around the reference line for all subregions, indicating that both models' estimates are fairly close to the design-based proportion in all subregions.

The direct comparison of the jackknife estimate with the design-based estimate for Northern Rockfish reveals that the delta-GLMM consistently overestimates in the western subregion and underestimates in the central subregion (Figure 3). The random walk estimates are more evenly spread, indicating no consistent over- or underestimation. However, both model estimates show a wide spread from the reference line, indicating that the estimates from both models diverge much more from the survey proportion than occurred with Pacific Ocean Perch.

The random walk model had lower mean absolute difference values for all three subregions than the delta-GLMM for Pacific Ocean Perch (Table 1). However, in all cases the difference between the means for the two models was quite small, and the distribution of the absolute difference values shows a lot of overlap between the two models (Figure 4). The two models appear to have a similar level of accuracy to the design-based proportion based on this metric. Similarly, for Northern Rockfish the random walk model has a lower mean absolute difference than the delta-GLMM for both subregions (Table 1) but the histograms of all of the absolute difference values show a lot of overlap (Figure 4). Based on these results, neither model has a clear advantage over the other in terms of accuracy for either species. The absolute difference values for both models are a greater magnitude for Northern Rockfish than for Pacific Ocean Perch, indicating that both models had more accurate estimates for Pacific Ocean Perch than for Northern Rockfish.

Precision Metrics

The delta-GLMM model had lower mean jackknife CV ($CV_{c,e}$) values than the random walk for both Pacific Ocean Perch and Northern Rockfish (Table 1). The distribution of jackknife CV values also shows that the delta-GLMM has lower values for almost all years in the western and eastern subregions for Pacific Ocean Perch and the western subregion for Northern Rockfish (Figure 5). The central subregion shows more overlap between models for both species, with a smaller difference between their mean CV values than the other subregions. The ratio of the jackknife CV with the CV calculated from the data set using all years revealed that the delta-GLMM model had more consistent and smaller CV ratios, indicating that excluding a year of data increase uncertainty more for the random walk model than the delta-GLMM (Figure 6). The exception to this trend is the CV ratios for 1990, 1993, 1996 and 1999 for Pacific Ocean Perch in the central and eastern subregions and 2005 for Northern Rockfish in both subregions, where the delta-GLMM had a greater increase in uncertainty when each of those years was excluded than the random walk model. Both species' results shows that the random walk model has a higher increase of uncertainty than the delta-GLMM when the most recent survey year (2019) is excluded.

A visual evaluation of the coverage of the jackknife standard errors relative to the difference between the jackknife estimates and the design-based estimates showed that the delta-GLMM results did not conform to a normal curve much more than the random walk results for both species (Figure 7). While the random walk results do not exactly look like a normal distribution either, there are far fewer coverage values that fall entirely outside of the normal curve, while the majority of the delta-GLMM values occurred outside the curve.

2020 - 2022 Total Allowable Catch

The delta-GLMM model produced TAC allocations for 2020 - 2022 that were somewhat different to the allocations generated by the random walk model for Pacific Ocean Perch (Table 2). The biggest difference was seen in the western subregion, where the delta-GLMM allocated higher biomass by between 850 - 950 mt, representing an approximately 60-64% increase because the allocation in that subregion is fairly small. In the eastern subregion, the delta-GLMM allocated between 50 and 275 mt more, representing only a 1-5% increase, and between 900 and 1,100 mt less to the central subregion (3-5% decrease) compared to the random walk model.

The difference between the delta-GLMM proportion predictions for 2020 - 2022, and how that would affect the TAC allocated to each subregion, is more dramatic for Northern Rockfish than for Pacific Ocean Perch (Table 2). The delta-GLMM estimates that a greater proportion of the population occurs in the western subregion while the random walk model and the design-based proportion estimates that the greater proportion occurs in the central subregion. In terms of metric tons, this means that between 1,300 and 1,600 mt would be shifted from the central subregion allocation to the western allocation in all 3 years. In 2020, this would shift 37.5% of the TAC from central to western, and in 2021 and 2022 it would shift approximately 26% of the TAC.

Discussion

The primary objective of this study was to use Pacific Ocean Perch and Northern Rockfish to explore whether the delta-GLMM model could be used instead of the random walk model to more precisely predict the proportion for groundfish species in each management subregion for the Gulf of Alaska, while matching or exceeding the accuracy of the random walk model estimates. Based on these results, the delta-GLMM has proved fairly equivalent in accuracy to the random walk model for Pacific Ocean Perch while the random walk is somewhat more accurate for Northern Rockfish, according to the proportion absolute difference metric ($D_{c,e}$). The metrics for precision, the jackknife CV ($CV_{c,e}$) and the ratio of those CVs with the CV for the model results using all data ($CV_{c,t}$), both indicate that the delta-GLMM is more precise than the random walk for both species, as expected.

However, the delta-GLMM showed some instances of possible bias in its estimates, particularly for Northern Rockfish. Additionally, it appears that the jackknife standard errors of the delta-GLMM are too small to cover the difference between the jackknife estimates and the design-based estimates much more frequently than would be expected if the coverage was normally distributed. The random walk model, however, does appear to approximately fit a normal distribution for its coverage. Consequently, although the delta-GLMM model technically meets the stated criteria to be considered as an alternative to the random walk model (increased precision and at least equal accuracy), it may not be a good alternative in this form, as there is a greater risk of of over- or under-estimating subregional population proportion compared to the random walk model.

Another objective of this study was to investigate if the delta-GLMM model produces results with a lower interannual variability than the random walk model. This does appear to be the case, as the delta-GLMM smooths estimates more than the random walk - this is particularly clear in the Northern Rockfish results in figure 2. This is an expected result, as the delta-GLMM is performing spatial smoothing while the random walk is not. However, the issue of overly small precision also affects this objective. While this objective is technically being met by the delta-GLMM model, particularly for Northern Rockfish, the greater difference between the model estimated proportions and the design-based proportion due to the smoothing is not covered enough of the time by the proportion standard errors, and over- or underestimation occurs too frequently.

It is interesting to note that in Figure 6 the delta-GLMM model shows consistent decreased uncertainty for Pacific Ocean Perch when data are excluded when surveys occur every other year as opposed to every 3 years (as was the case up until 1999), while the random walk model appears to vary in increased uncertainty regardless of whether the survey occurs every 3 or every 2 years. Northern Rockfish, on the other hand, showed more variation in the amount of uncertainty introduced by excluding a year of data regardless of whether the survey occurred every 2 vs 3 years. However, there was a consistently higher level of uncertainty introduced into results for the random walk model excluding 2019, the most recent survey year, for both species while the delta-GLMM model had about the same change in uncertainty when excluding 2019 as any of the previous several years. This result may be significant because the purpose of these models is to predict biomass proportion by subregion up to 3 years into the future, so based on these results the delta-GLMM may introduce less uncertainty in predictions of at least 2 years into the future than the random walk model for Pacific Ocean Perch. The assumption that the delta-GLMM would provide projections into the future with lower uncertainty appears to be supported by these results, and may indicate that further experimentation with the delta-GLMM model as an alternative to the random walk model is worth pursuing.

Assumptions & limitations of the study

A key assumption of this study is that the bottom trawl survey data are representative of the realistic population distribution across subregions. While this assumption is useful for the purposes of this study because it allows the two models to be compared with an accuracy metric, the survey is likely to be an imprecise representation of the annual distribution and abundance of the populations. If the survey data were believed to be truly representative on its own, then the design-based proportion estimates could be used directly to set subregional TAC, rather than using a statistical model. In this case, based on what we know of the life history of long-lived species like Pacific Ocean Perch and Northern Rockfish, the high amount of interannual variation seen in the survey data is unlikely to be an accurate representation of the population. An underlying clustered spatial distribution that is being unevenly sampled may be part of the reason for this variability, combined with the issue of a portion of the bottom of the GOA being untrawlable with the survey nets due to rockiness. The assumption inherent in the design-based proportions is that the samples of catch from trawled habitat can be extrapolated into the untrawlable habitat, and if these rocky areas are preferred habitat for some rockfish, such as Northern Rockfish, this assumption may be inaccurate.

In addition to untrawlable bottom and clustered spatial distributions, Pacific Ocean Perch are known to spend some amount of time in the pelagic zone (likely feeding), and consequently a survey consisting only of bottom trawl gear may miss some percentage of the population depending on the timing of the trawl and the movements of the fish. Since 2006, an average of 31% of the commercial catch for Pacific Ocean Perch came from pelagic trawl rather than bottom trawl methods, up from an average of 7% from 1990 - 2005 (Hulson et al. 2020). This increase in percentage of catch in pelagic hauls in the commercial fishery seems more likely to be due to changes in practices or gear in the fishery rather than increasing numbers of Pacific Ocean Perch occurring in the pelagic zone, but the fact remains that some portion of the population may not be available to the bottom trawl survey and this may need to be accounted for.

Pacific Ocean Perch and Northern Rockfish were the stocks chosen for this study because of their high economic value in the GOA groundfish fishery. However, these stocks may be particularly difficult to fit with the delta-GLMM model due to the very large catches that can occur with these stocks, leading to significant changes in abundance estimates from year to year. Therefore the results of this study may not be applicable to other groundfish stocks in the GOA. Consequently, a similar comparison study pursued with other stocks may yield different results.

Future research opportunities

There are multiple directions for future study opportunities, including addressing the issue of how the accuracy of the design-based proportions relative to the true population distributions affects model performance, modifying the delta-GLMM model to improve accuracy, or modifying the random walk model to decrease uncertainty. The issue of how the accuracy of the design-based proportions relative to the true population distribution affects model performance could be addressed using a simulation experiment where simulated survey data are created from age-structure populations with a gradient of accuracy compared to the underlying population distribution. The models can then be fit to these simulated data sets to see how much the accuracy of the survey affects model performance and if one model performs better than the other as accuracy of the survey data decreases.

There are several avenues that could be explored to modify the delta-GLMM model. A strength of the delta-GLMM is that other variables can be added into either or both equations, so environmental factors like bottom type (rocky, sandy, etc.) and various types of temperature-related covariates could be included in future versions of the model. Incorporating environmental covariates into the model are likely to be particularly valuable in light of likely climate change-driven environmental changes in the GOA, and may assist with predicting distributional shifts that may occur with changing environmental conditions. The delta-GLMM model has been used to incorporate environmental covariates for estimating stock distributions in the Bering Sea, and this would be a valuable avenue to explore for future studies (Brodie et al. 2020, O'Leary et al. 2020) . The delta-GLMM model can also be used to incorporate multiple types of data sources, including eDNA, acoustic, underwater drop-camera data, and industry surveys. Future studies could use these alternate data sources to improve inference into untrawlable habitat and improve model performance.

Other options for modifying the delta-GLMM model in future studies could include experimenting with using a more flexible Tweedie distribution for the observation error in the delta-GLMM model rather than the gamma distribution. This was initially attempted in this study, but for Northern Rockfish in particular there were issues with finding appropriate starting values for the model, and convergence issues even if viable starting values were identified. The decision was therefore made to concentrate on the simpler gamma distribution for this study. A possible reason for this is that the Tweedie distribution requires more parameters, and for the Northern Rockfish in particular the data set may not be large enough to adequately estimate additional parameters.

Alternatively, future studies could explore how to improve the precision of the random walk model by adding an informed prior for the process error variance. Based on what is currently known about the life history of long-lived species, this variance is likely to be fairly low and would likely lead to decreased uncertainty of the model estimates.

Tables & Figures

Table 1. Summary of average absolute difference and jackknife CV values for estimated excluded years (n = 13 for Pacific Ocean Perch, n = 15 for Northern Rockfish).

Species	**Subregion**	**Model**	**Absolute Difference**	**CV**
Pacific Ocean Perch	WESTERN	Random Walk	0.0667	0.6468
		delta-GLMM	0.0757	0.2411
	CENTRAL	Random Walk	0.1085	0.2155
		delta-GLMM	0.1218	0.1108
	EASTERN	Random Walk	0.0700	0.3841
		delta-GLMM	0.0918	0.1814
Northern Rockfish	WESTERN	Random Walk	0.1497	0.9067
		delta-GLMM	0.2357	0.2153
	CENTRAL	Random Walk	0.1497	0.4173
		delta-GLMM	0.2357	0.2263

Table 2. Comparing estimated predictions for 2020, 2021 and 2022 from delta-GLMM and the random walk for each species and subregion in metric tons, using the estimated total biomass for each year in the 2020 stock assessment multiplied by the model predicted proportion. The estimated biomass per subregion for the random walk model was also taken from the stock assessment, since that is the method currently used. The single ton of Northern Rockfish catch allocated in the eastern subregion has historically been added into the multispecies "Other Rockfish" stock TAC (Hulson et al. 2020), and the delta-GLMM proportion estimates would not change this practice.

	Metric tons			
Year	**Western**	**Central**	**Eastern**	**Source**
Pacific Ocean perch				
2020	1437	23678	6123	Random Walk
2020	2285	22550	6403	delta-GLMM
2021	1643	27429	7105	Random Walk
2021	2609	26344	7224	delta-GLMM
2022	1572	26234	6796	Random Walk
2022	2465	25380	6756	delta-GLMM
Northern Rockfish				
2020	1133	3178	1	Random Walk
2020	2749	1561	1	delta-GLMM
2021	2023	3334	1	Random Walk
2021	3439	1919	1	delta-GLMM
2022	1926	3173	1	Random Walk
2022	3290	1809	1	delta-GLMM

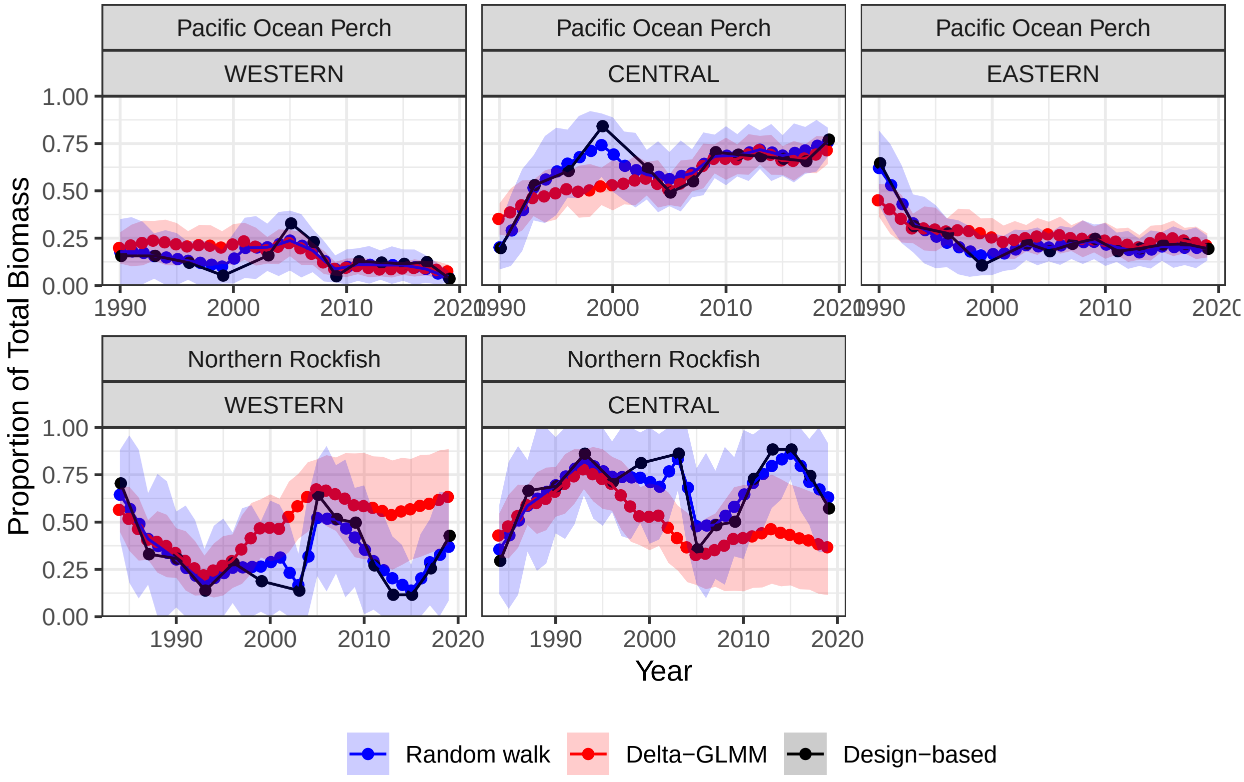


Figure 2: Estimate of proportion for each year using the random walk model (blue) and delta-GLMM model (red), showing both estimates (points) and +/- 2 estimated standard error (colored ribbons), along with the design-based proportions (black bullets) for each region and species. Model estimates shown are the results calculated with all years of data (no years excluded).

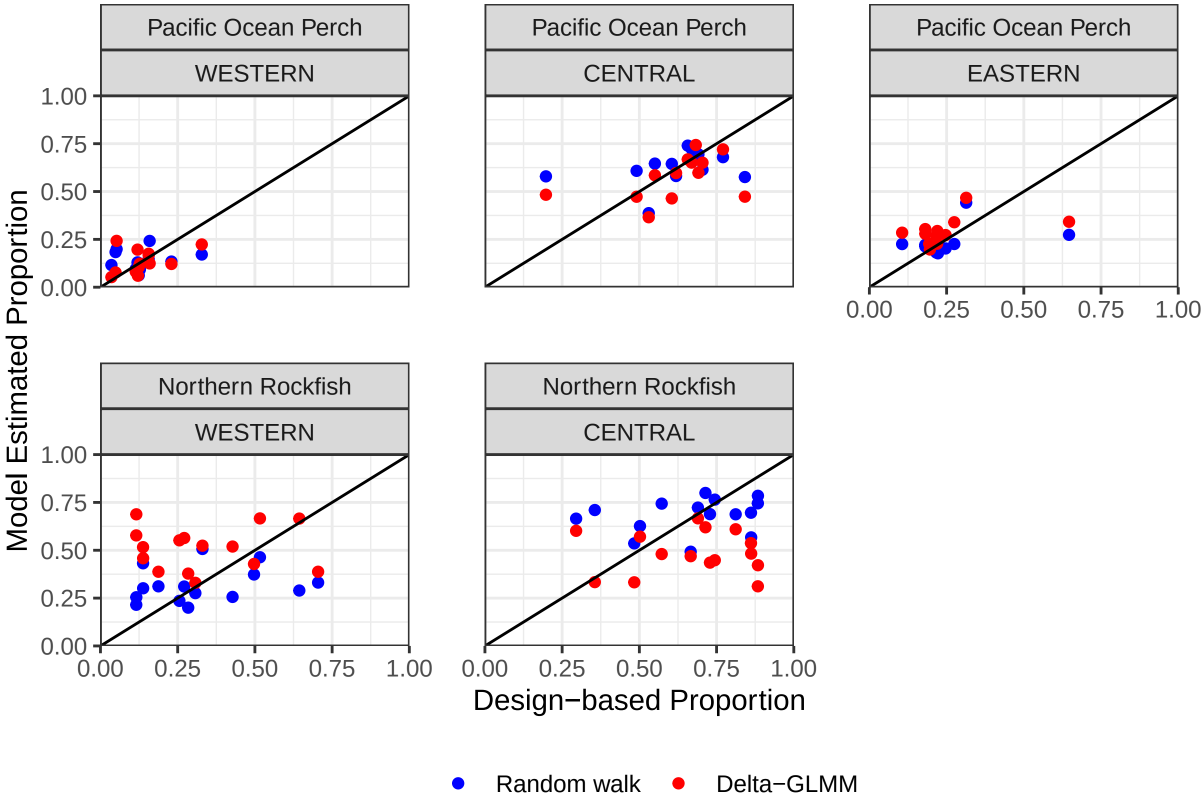


Figure 3: Design-based proportion estimate against jackknife proportion estimate for the random walk (blue plots) vs. delta-GLMM (red points) for each subregion and species. The black lines mark the reference line y = x, where the design-based estimate would be the same as the jackknife estimate.

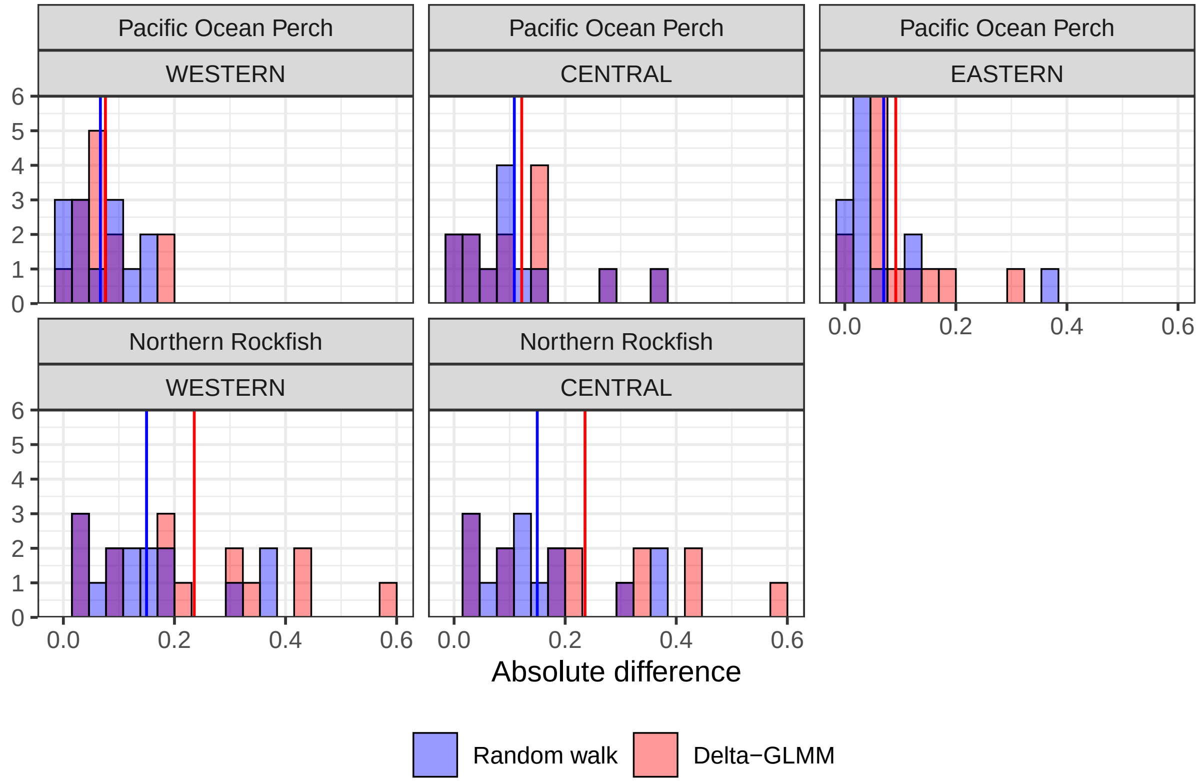


Figure 4: Histogram of absolute difference between the jackknife proportion estimates relative to the design-based proportion estimates, comparing the random walk (blue shading) vs. delta-GLMM (red shading) models. The mean absolute difference for the random walk model is shown with the blue line and the mean absolute difference for the delta-GLMM model is shown with the red line.

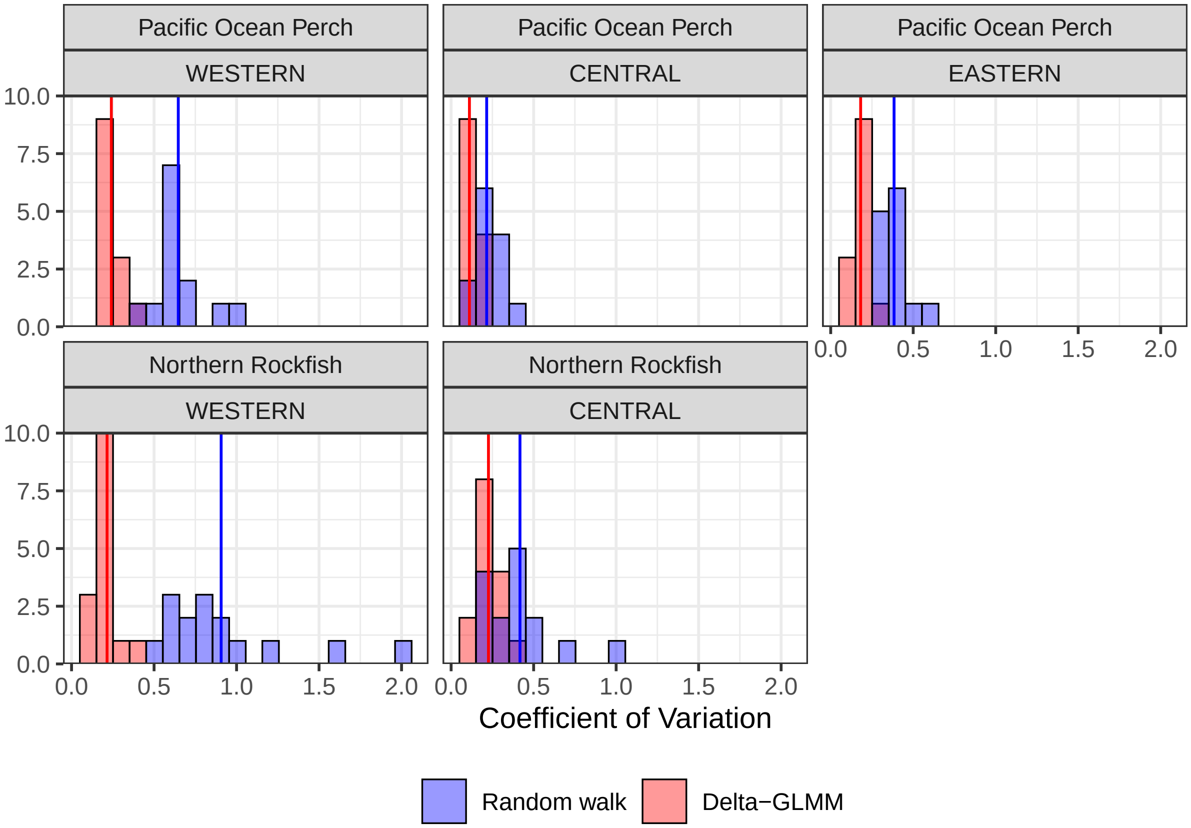


Figure 5: Histogram of CV values for random walk (blue shading) and delta-GLMM (red shading) results, calculated with the jackknife proportion estimates and jackknife standard errors (resulting in 13 values for Pacific Ocean Perch, 15 for Northern Rockfish). The mean CV for the random walk model is shown with the blue line and the mean CV for the delta-GLMM model is shown with the red line.

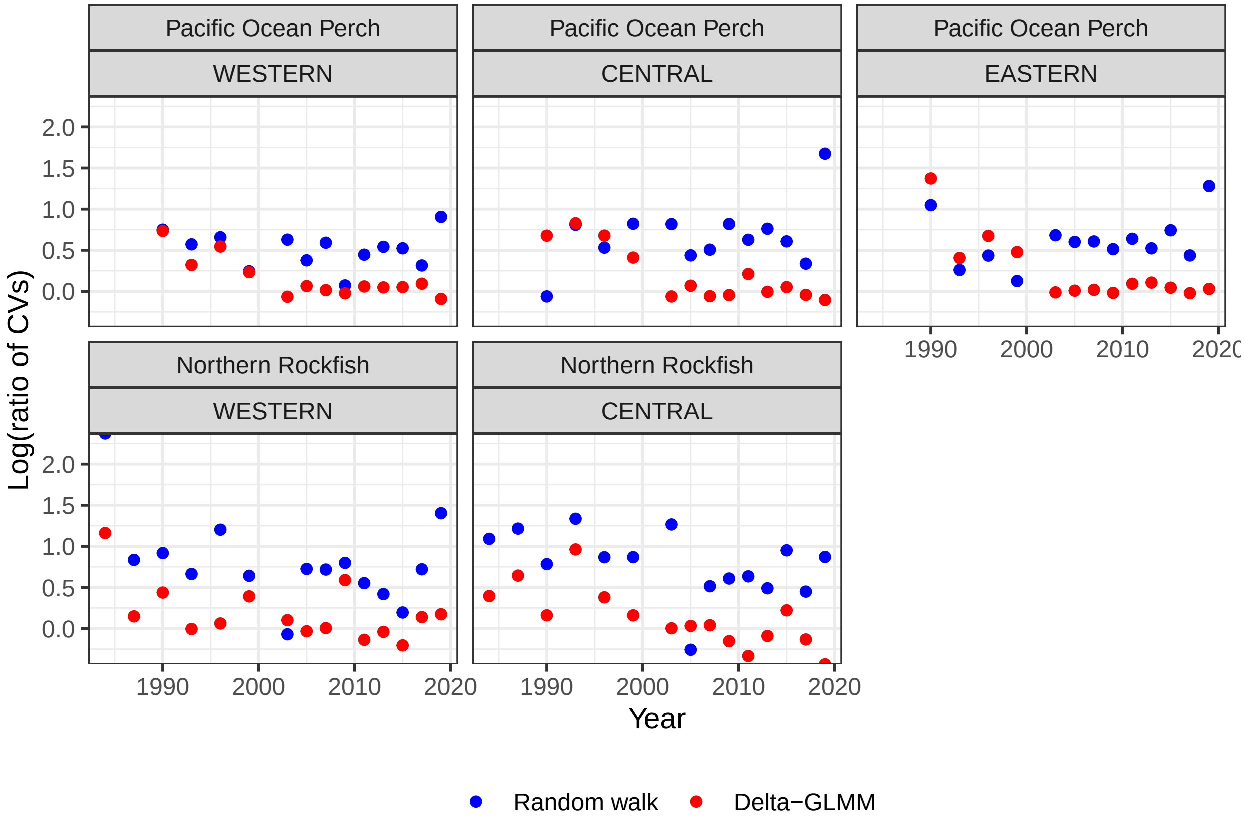


Figure 6: Histogram of the ratio of jackknife CVs ($CV_{c,e}$) to the CV calculated with all years' data included($CV_{c,t}$), on log scale. The random walk values are shown in blue and the delta-GLMM values are in red.

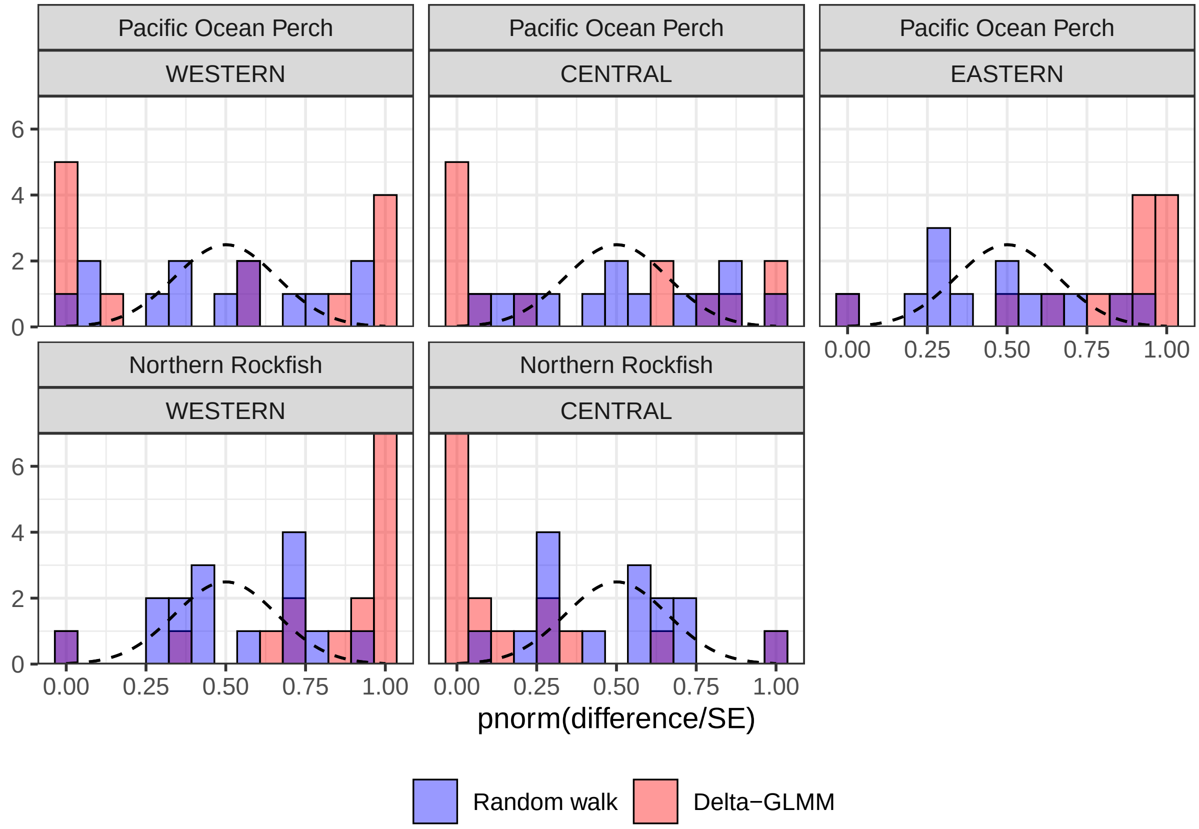


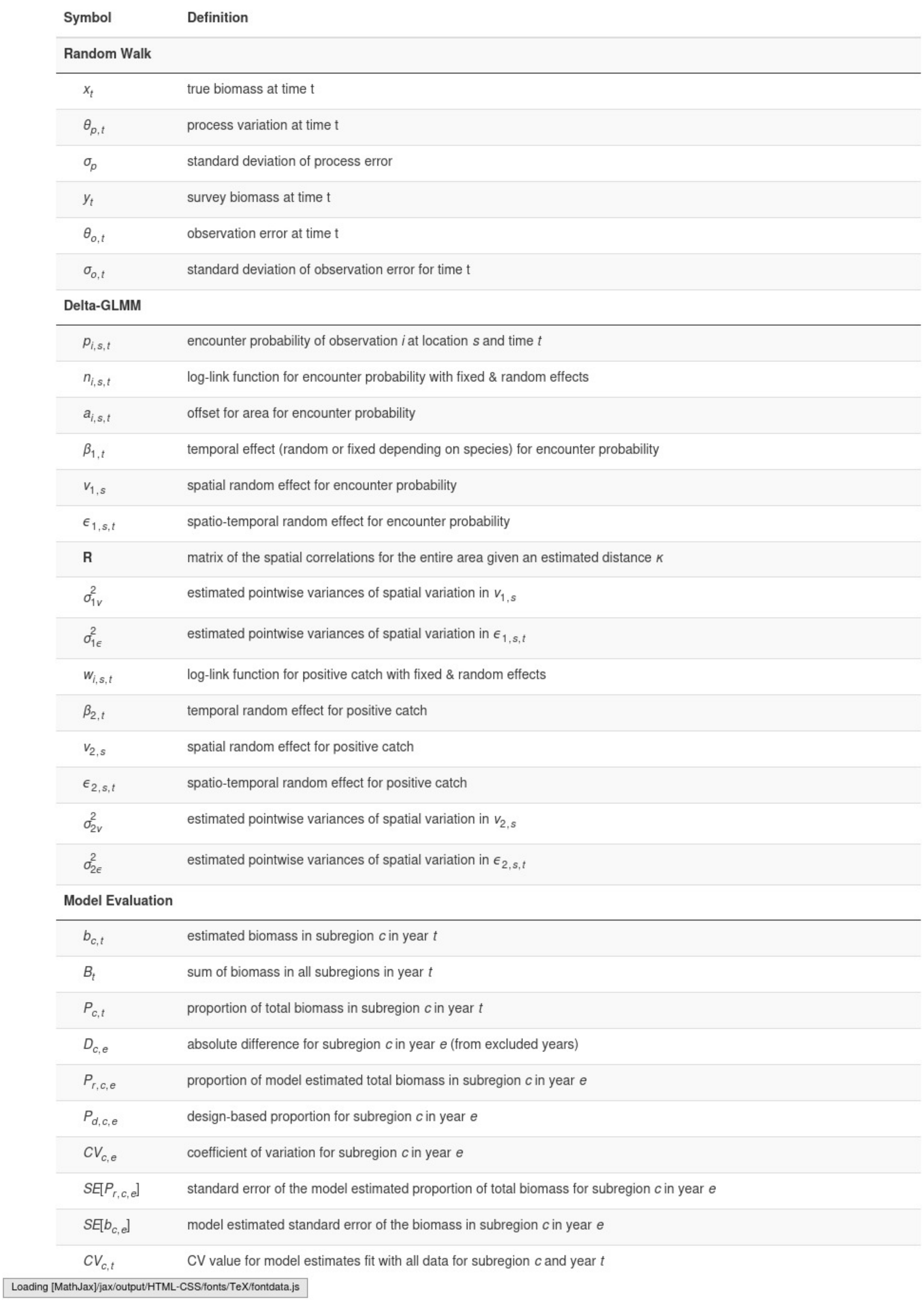
Figure 7: Histogram of the jackknife standard error coverage relative to the difference between the jackknife estimates if the values were normally distributed (using pnorm in R) for random walk (blue shading) and delta-GLMM (red shading) results. A normal curve with a mean of 0.5 and standard deviation of 0.16 is shown by the dashed line to approximate what a normally distributed histogram on a 0 to 1 scale would look like.

Appendix

Table S1. VAST software v3.9.0 and model version 12.0.0 were used to estimate numbers-density and biomass. See Thorson (2019) and https://github.com/James-Thorson-NOAA/VAST for details on model settings and inputs. Complete code and model information for this study can be found on the project repository: https://github.com/krmistry/fish_in_space

```
make_settings(Version = "VAST_v12_0_0", n_x = 500, Region = "User",
    purpose = "index2", ObsModel = c(2, 1), FieldConfig = matrix(c("IID",
        "IID", "IID", "IID", "IID", "IID"), ncol = 2, nrow = 3,
        dimnames = list(c("Omega", "Epsilon", "Beta"), c("Component_1",
            "Component_2"))), RhoConfig = c(Beta1 = 2, Beta2 = 2,
        Epsilon1 = 2, Epsilon2 = 2), strata.limits = data.frame(STRATA = as.factor(c("Western"
        "Central", "Eastern")), west_border = c(-Inf, -159, -147),
        east_border = c(-159, -147, Inf)), knot_method = "grid",
    fine_scale = TRUE, bias.correct = TRUE, use_anisotropy = TRUE)
```

Table S2. Definitions of all symbols used in the model and evaluation metrics equations, divided into three sections; parameter and data symbols used in the random walk model equations, parameter and data symbols used in the delta-GLMM model equations, and symbols used in the model evaluation equations.



Symbol	Definition
Random Walk	
x_t	true biomass at time t
$\theta_{p,t}$	process variation at time t
σ_p	standard deviation of process error
y_t	survey biomass at time t
$\theta_{o,t}$	observation error at time t
$\sigma_{o,t}$	standard deviation of observation error for time t
Delta-GLMM	
$p_{i,s,t}$	encounter probability of observation i at location s and time t
$n_{i,s,t}$	log-link function for encounter probability with fixed & random effects
$a_{i,s,t}$	offset for area for encounter probability
$\beta_{1,t}$	temporal effect (random or fixed depending on species) for encounter probability
$v_{1,s}$	spatial random effect for encounter probability
$\epsilon_{1,s,t}$	spatio-temporal random effect for encounter probability
$\mathbf{R}$	matrix of the spatial correlations for the entire area given an estimated distance κ
σ^2_{1v}	estimated pointwise variances of spatial variation in $v_{1,s}$
$\sigma^2_{1\epsilon}$	estimated pointwise variances of spatial variation in $\epsilon_{1,s,t}$
$w_{i,s,t}$	log-link function for positive catch with fixed & random effects
$\beta_{2,t}$	temporal random effect for positive catch
$v_{2,s}$	spatial random effect for positive catch
$\epsilon_{2,s,t}$	spatio-temporal random effect for positive catch
σ^2_{2v}	estimated pointwise variances of spatial variation in $v_{2,s}$
$\sigma^2_{2\epsilon}$	estimated pointwise variances of spatial variation in $\epsilon_{2,s,t}$
Model Evaluation	
$b_{c,t}$	estimated biomass in subregion c in year t
B_t	sum of biomass in all subregions in year t
$P_{c,t}$	proportion of total biomass in subregion c in year t
$D_{c,e}$	absolute difference for subregion c in year e (from excluded years)
$P_{r,c,e}$	proportion of model estimated total biomass in subregion c in year e
$P_{d,c,e}$	design-based proportion for subregion c in year e
$CV_{c,e}$	coefficient of variation for subregion c in year e
$SE[P_{r,c,e}]$	standard error of the model estimated proportion of total biomass for subregion c in year e
$SE[b_{c,e}]$	model estimated standard error of the biomass in subregion c in year e
$CV_{c,t}$	CV value for model estimates fit with all data for subregion c and year t

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