



## Original Article

# Explicit incorporation of spatial variability in a biomass dynamics assessment model

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The sustainable management of fisheries has largely relied on stock assessment models that assume stocks are homogeneous throughout their domain. However, ignoring complex underlying spatial patterns can lead to increased risk of failures in management. Utilizing geostatistical approaches in conjunction with a traditional fishery biomass dynamics model, we develop a spatially-explicit modelling framework that treats the underlying population dynamics as spatial processes. Simulation experiments demonstrate that this approach reliably estimates variance parameters and accurately captures true patterns of population change. We further demonstrate the utility of our modelling framework in a real setting using data from the Canadian Maritimes Inshore Scallop Fishery. The model captures time-varying spatial patterns in both population characteristics and fishing pressure without explicit knowledge of the underlying mechanisms and retains the ability to scale up to the whole spatial domain with less associated uncertainty than for temporal models. These results lead to improved scientific advice for management, future-proofing of the assessment to shifts in stock productivity and fishing effort, and provide information that can be used to develop more effective management approaches.

**Keywords:** biomass dynamics model, delay-difference model, *Placopecten magellanicus*, spatial structure, spatio-temporal model, stock assessment.

## Introduction

Stock assessment models (SAMs) that often guide the sustainable management of fisheries have traditionally relied on either regression frameworks (Venables and Dichmont, 2004) or fisheries-specific approaches (Hilborn, 1992) to predict changes in fish populations. These methods tend to be strictly temporal in nature and assume that the structure of both the underlying population and the exploitation is homogeneous across space. However, it has long been known that many fisheries exhibit strong spatial patterns in bi-

ological characteristics and fishing pressure (Baranov, 1918; Beverton and Holt, 1957; Caddy, 1975; Hutchings, 1996; Smith and Rago, 2004; Smith *et al.*, 2017) that can bias the estimates of population size (Reuchlin-Hugenholtz *et al.*, 2015; Berger *et al.*, 2017; Cadrin, 2020) used to provide advice to fisheries managers (Caddy and Mahon, 1995; Shertzer *et al.*, 2010; Nasmith *et al.*, 2016).

The exclusion of spatial structure in the calculations of population size estimates can result in management failures, which can have serious socioeconomic consequences and long lasting impacts on the conservation of a species. A clear illustration of these

ramifications is evident in the collapse of Atlantic cod (*Gadus morhua*) in Atlantic Canada (Hutchings and Myers, 1994; Myers et al., 1996). The survey indices used at the time did not reflect the ongoing collapse (Hutchings, 1996), whereas recent approaches using spatial methods would have been able to capture the changes in the spatial distribution that heralded the collapse (Reuchlin-Hughenoltz et al., 2016; Carson et al., 2017). More recently, evidence of serial depletion in other fisheries, such as sea cucumbers (Eriksson and Byrne, 2015; Rawson and Hoagland, 2019), indicates that such issues are not relegated to the past. Fortunately, in recent years, various advances have led to the development of statistical methods that can better account for the impact of spatial processes on stock dynamics [e.g. integrated nested Laplace approximation (Illian et al., 2012) and TMB (Kristensen et al., 2016)].

The implementation of more advanced spatial statistic techniques into fisheries research has tended to focus on either generalizations of common regression techniques or geostatistical approaches (Ciannelli et al., 2008). Spatial regression methods focus on modelling the mean, often through generalized additive frameworks (Ciannelli et al., 2008; Pedersen and Berg, 2017). Unfortunately, these methods typically require high-quality information on both environmental variables (temperature, nutrient availability, etc.) and the fish population (scientific surveys, high-quality fisheries data) that are not available for many fisheries (Costello et al., 2012). Alternatively, geostatistical approaches model spatial structure by incorporating spatial autocorrelation into the residual structure of the model (Ciannelli et al., 2008). This has the advantage of capturing the latent spatial variability in the data (Cadigan et al., 2017; Stock et al., 2020) without explicitly modelling the underlying mechanisms. These techniques have been used successfully to improve indices of abundance used for stock assessments (Thorson et al., 2015b; Thorson and Barnett, 2017; Thorson et al., 2019). Focusing on the residual structure allows the mean to be specified using traditional SAMs.

Traditional SAMs, such as biomass dynamics models, often require only an index of population abundance and landings (Hilborn, 1992). They have been extensively used in state-space frameworks (Kinas, 1996; Smith and Hubley, 2014; Best and Punt, 2020) and can be modified to incorporate spatial structure. A significant amount of effort has gone into modelling the spatial autocorrelation in fisheries data to obtain better indices (Thorson et al., 2015b), but comparatively little effort has gone into incorporating the spatial structure in the latent processes of interest such as recruitment (Thorson et al., 2015a). While spatial autocorrelation can be caused by a myriad of factors (Legendre, 1993), unquantified demographic and life-history variability within a stock are likely responsible for a substantial portion of the observed spatial patterns.

Incorporating spatial statistics may benefit many stocks (Berger et al., 2017), particularly sedentary benthic species that have demographic and life-history characteristics that lend themselves more intuitively to spatial modelling. Sea scallops (*Placopecten magellanicus*) are a shellfish species that inhabit the Western North Atlantic from Cape Hatteras to Labrador (Smith and Rago, 2004). These animals exhibit a strong spatial structure in growth rates and reproductive potential, minimal dispersal as adults, and recurring aggregation in scallop beds (Smith and Rago, 2004). Furthermore, the exploitation of these animals tends to focus on areas of high productivity, with fishing effort in these areas being higher than would be expected even if one allocated effort proportionally to the distribution of biomass (Caddy, 1975; Brown et al., 2012; Smith et al., 2017). Explicitly modelling this spatial variability should help im-

prove model predictions and in turn the science advice provided to fisheries managers.

Here we use recently developed statistical advances to incorporate spatial structure into a traditional biomass dynamics model. We modify the strictly temporal state-space model (SSM) described in McDonald et al. (2021), referred to as the Tow-Level Model (TLM), to explicitly account for spatial structure; we hereafter refer to this as the Spatially Explicit Biomass Dynamics Assessment Model (SEBDAM). We perform a series of simulations to explore the estimability and identifiability of SEBDAM. We then fit both models (SEBDAM and TLM) to Scallop Production Area 3 (SPA 3) of the Canadian Maritimes Inshore sea scallop fishery as a comparative study.

## Methods

### Sea scallop data

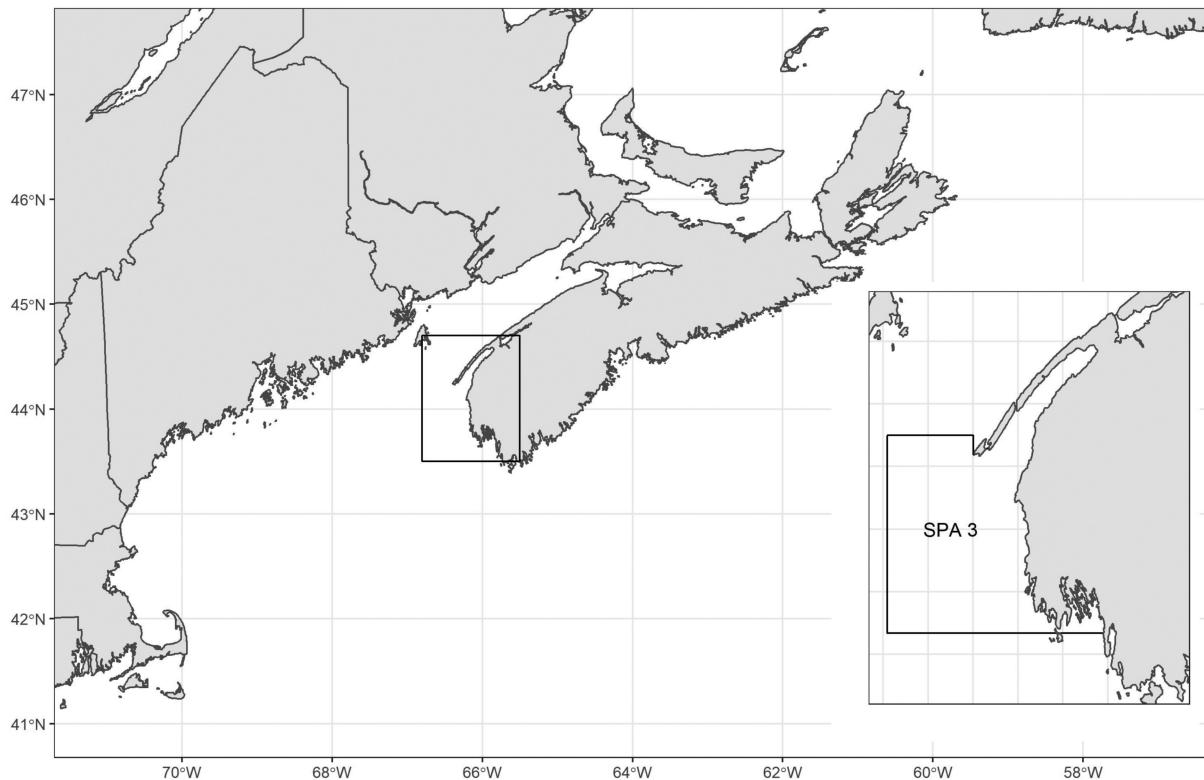
SPA 3 is a scallop management area in the Bay of Fundy, Canada (Figure 1) managed by Fisheries and Oceans Canada (DFO). This area is managed using total allowable catches in biomass of meat weight (scallop adductor meat). Fisheries assessment advice is derived using a modified version of a delay difference biomass dynamics model (Deriso, 1980; Schnute, 1985; Smith and Lundy, 2002; Smith and Hubley, 2014; Nasmith et al., 2016). The area is surveyed annually using a stratified random sampling design; however, due to the strong spatial structure in the productivity of this stock and spatially aggregated exploitation, the survey design was restratified in 2011 based on the distribution of fishing effort (Smith et al., 2012).

At sea, all live and dead scallops (clappers: dead scallops whose shells are still hinged) are counted and sorted into 5 mm bins. Clappers are used to obtain an estimate of natural mortality. A subset of live scallops (3 per 5 mm bins that are 50 mm and larger) is dissected in order to record individual shell height and meat weight [weight of the adductor muscle (Glass, 2017)]. A length-weight relationship is modelled based on a cube law (Froese, 2006) with depth as a covariate in order to convert all numbers at height to meat weight. Commercial size scallops are defined as having shell heights greater than or equal to 80 mm, and recruits are those between 65 mm and 79 mm, which are expected to grow to be commercial size the following year. We refer to the biomass of recruits as recruitment and to the biomass of commercial size scallops as commercial biomass. The start and end position of each tow are recorded at sea using the commercial vessel navigational system Olex AS (Olex marine survey and navigation, www.olex.no); survey catches are standardized to 800 m length x 5.334 m width.

### Model description

SSMs are hierarchical models defined by two stochastic processes:  $\mathbf{X}_{s,t}$ ,  $t = 1, \dots, T$  and  $s = 1, \dots, S$ , representing the unobserved dynamic state process describing the real population dynamics between discrete time-steps  $t$  and knot locations  $s$ , and the observation process  $\mathbf{Y}_{s,t}$ , which links the observations to the true underlying dynamical processes of interest (Aeberhard et al., 2018). The model parameters are combined in a  $p$ -vector  $\boldsymbol{\theta} \in \Theta \subseteq \mathbb{R}^p$ , and fixed covariates are indicated by  $\mathbf{z}_{s,t}$ .

$\boldsymbol{\theta}$  is considered a vector of fixed effects and  $\mathbf{X}_{1:S,1:T}$  a vector of random effects predicted from estimates of  $\boldsymbol{\theta}$ . Due to this, the underlying processes (commercial biomass, recruitment, and natural mortality) are considered to be predicted in years with data, with future predictions in years without data referred to as projections. These projections are obtained by moving the process equations



**Figure 1.** Newfoundland to Cape Cod with inset map of SPA 3 off South West Nova Scotia, Canada.

forward 1 year and therefore represent the predicted mean and uncertainty. This is meant as an illustration of potential uncertainties when predicting in years without data. These variables can be combined into the following joint likelihood  $L(\cdot)$  and marginal log-likelihood  $\mathcal{L}(\cdot)$ :

$$L(\theta, \mathbf{Y}_{1:T}, \mathbf{X}_{1:T}) = \prod_{s=1}^S p(\mathbf{Y}_{s,1} | \mathbf{X}_{s,1}, \theta) \prod_{t=2}^T p(\mathbf{Y}_{s,t} | \mathbf{X}_{s,t}, \theta) \times p(\mathbf{X}_{s,t} | \mathbf{X}_{s,t-1}, \theta), \quad (1)$$

$$\mathcal{L}(\theta, \mathbf{Y}_{1:S,1:T}) = \log \int L(\theta, \mathbf{Y}_{1:S,1:T}, \mathbf{X}_{1:S,1:T}) d\mathbf{X}_{1:S,1:T}. \quad (2)$$

Approximations for these high-dimensional integrals are obtained using the Laplace method as implemented in the TMB package in R (Kristensen *et al.*, 2016). TMB’s use of automatic differentiation has been shown to be computationally more efficient than most other packages without loss of accuracy (Kristensen *et al.*, 2016; Auger-Méthé *et al.*, 2017).

### Spatial approach

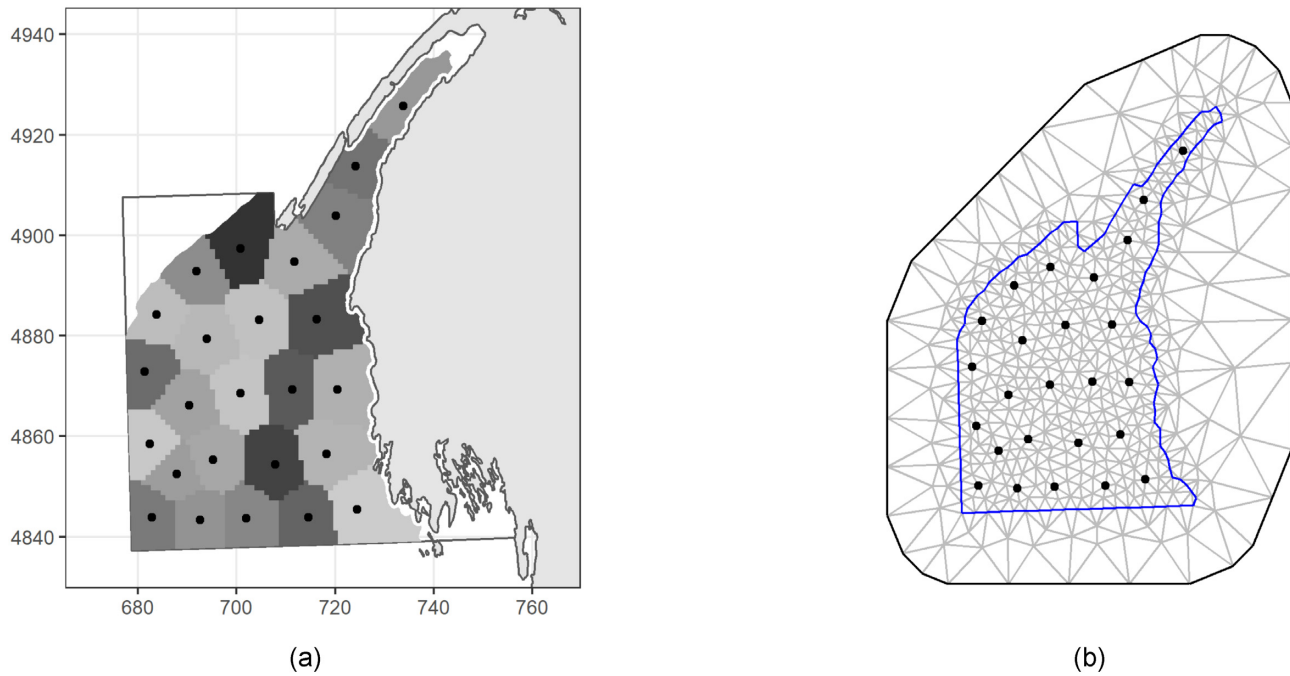
The predictive framework described in Thorson *et al.* (2015b) is adopted here. Instead of modelling a given random field over every possible location, its value is approximated as being piece-wise constant. The user must specify the number of locations, called “knots”, at which the model will track the value of the random field. This choice drives both the resolution of the model predictions and the computational load, since more knots leads to higher resolution but the fitting process will be slower. The decision concerning the number of knots used should be based on the spatial coverage of the data to control the accuracy of the piece-wise approximation. The loca-

tions of these knots are obtained by applying a  $k$ -means clustering algorithm on the location of all the survey tows. The number and location of knots is held constant for model fitting and all observations (both survey tows and landings) are attributed to the closest knot. In summary, the locations of the tows are used to obtain the knots, which are then used to create the mesh and are the only vertices inside that mesh that have data, as each tow is attributed to its closest knot. This allows the knots to have multiple replicate observations of the underlying processes in any given year.

Preliminary tests were undertaken with different numbers of knots to determine the optimal resolution. We chose to use 25 knots to strike a balance between computational demand and performance. The north-west section of SPA 3 is known to contain very few scallops due to the benthic substrate being primarily glaciomarine mud (Shaw *et al.*, 2012, 2014) and it is therefore not regularly included in the DFO survey domain; as such it was removed from the modelled area. The resulting grid is shown in Figure 2 alongside the triangulation used for model predictions.

### Spatially explicit biomass dynamics assessment model

A previous model, the TLM, tested the impact of directly incorporating tow level data into a SAM without first aggregating them into indices (McDonald *et al.*, 2021). This TLM is highly similar to SEBDAM, except that the spatial components are absent. Spatial information is incorporated into SEBDAM through the use of Gaussian Markov Random Fields (GMRFs), using the Stochastic Partial Differential Equation (SPDE) approach with a Matérn covariance structure (Lindgren and Rue, 2011). Only two parameters are required for this approach:  $\kappa$ , which is related to range  $\rho$  ( $\rho = \sqrt{8/\kappa}$ ) and controls the distance at which two points become uncorrelated,



**Figure 2.** a: Grid used to analyze SPA 3 with knots shown as black points and black lines indicating the management boundary for the area (greyscale used for visualization purposes). Nearshore knots are the nine easternmost knots, with the other knots considered offshore knots. b: Delaunay triangulation used for the model with black points indicating location of each knot.

and  $\tau$ , which controls the spatial variance [for details see Lindgren and Rue (2011) and Lindgren (2012)].

The locations of the observations are projected onto the Universal Transverse Mercator (UTM) system so that the spatial parameters are more interpretable since UTM coordinates are in meters (rescaled into kilometers for numerical stability).

Using the SSM hierarchical framework, we model the underlying process dynamics with the following equations:

$$B_{s,t} = [\exp(-m_{s,t})g_{t-1}(B_{s,t-1} - C_{s,t-1}) + \exp(-m_{s,t})g_{t-1}^R R_{s,t-1}] \exp(\Omega_{s,t}^B), \quad (3)$$

$$R_{s,t} = R_{s,t-1} \exp(\Omega_{s,t}^R), \quad (4)$$

$$m_{s,t} = m_{s,t-1} \exp(\Omega_{s,t}^m). \quad (5)$$

Equation (3) is the simplified delay-difference equation where  $B_{s,t}$  are the commercial biomass densities,  $C_{s,t}$  are landings,  $R_{s,t}$  are the recruitment biomass densities,  $m_{s,t}$  are the instantaneous natural mortalities, and  $g_t$  and  $g_t^R$  are the commercial size and recruit growth rates, respectively, which are estimated separately (Smith and Hubley, 2014; Nasmith et al., 2016).  $\Omega_t^B$  is the GMRF for commercial biomass in year  $t$ , which, using the SPDE approach, is reduced to a mean zero multivariate normal where its covariance matrix is  $\Sigma(s, s') = \text{Matérn}(\|\mathbf{H}^B(s - s')\|)$ , indicating that the covariance between two knots  $s$  and  $s'$  where  $s \neq s'$  follows a Matérn covariance structure. This structure allows for geometric anisotropy through  $\mathbf{H}^B$ , which is defined to maintain volume and has two parameters [for more details see Thorson et al. (2015b)]. The value at each knot  $s$  for year  $t = 1$  is simply  $B_{s,1} = B_0 * \exp(\Omega_{s,1})$  where  $B_0$  is an estimated mean parameter.

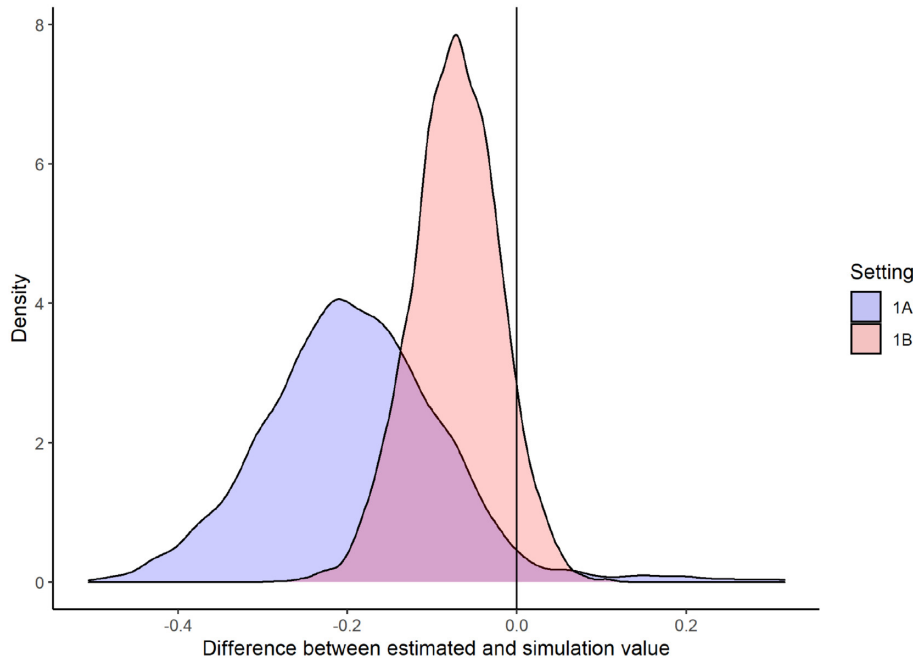
Equations (4) and (5) are lognormal random walks where the error terms  $\Omega_t^R$  (recruitment) and  $\Omega_t^m$  (natural mortality) are GM-

**Table 1.** Parameters used and their optimization starting values.

Parameter	Simulation value	Optimization starting value
$\kappa_B$	0.071	$\exp(-1)$
$\tau_B$	19.947	$\exp(1)$
$\kappa_R$	0.047	0
$\tau_R$	29.921	0
$\kappa_m$	0.141	0
$\tau_m$	19.947	0
$\sigma_\epsilon$	0.500	$\exp(-1)$
$\sigma_\nu$	0.500	$\exp(-1)$
$S$	0.600	$\exp(-1)$
$R_0$	100.000	150
$B_0$	600.000	3000
$m_0$	0.300	$\exp(-1)$
$q_R$	0.200	$\exp(-1)$
$p_I$	0.950	0.5
$p_I^R$	0.500	0.5
$H_{input}^{B1}$	-1.200	0
$H_{input}^{B2}$	-0.500	0
$H_{input}^{m1}$	-0.500	0
$H_{input}^{m2}$	0.400	0

RFs that are parameterized by the same methods as Equation (3). Recruitment is assumed to have the same anisotropy matrix as the commercial biomass, while natural mortality has a separate matrix. The value at each knot  $s$  for year  $t = 1$  are  $R_0 * \exp(\Omega_{s,1}^R)$  and  $m_0 * \exp(\Omega_{s,1}^m)$  where  $R_0$  and  $m_0$  are estimated mean parameters. The commercial biomass and recruitment for the whole area, hereafter referred to as the total biomass and recruitment, can be derived





**Figure 3.** Density plot of the differences between estimated  $q_{l(s)}$  and simulation value for settings 1A (blue) and 1B (red). Black vertical line indicates zero difference.

by multiplying  $B_{s,t}$  and  $R_{s,t}$  by the area covered by their respective knots, then summing up over all knots  $s$ .

The observations are linked to the underlying processes through the following equations:

$$I_{i,s,t} = \frac{q_{l(s)}B_{s,t}}{p_I} \epsilon_{i,s,t}, \quad \epsilon_{i,s,t} \stackrel{Ind}{\sim} u\ell N(\sigma_\epsilon^2), \quad (6)$$

$$I_{i,s,t}^R = \frac{q_R R_{s,t}}{p_I^R} \nu_{i,s,t}, \quad \nu_{i,s,t} \stackrel{Ind}{\sim} u\ell N(\sigma_\nu^2), \quad (7)$$

$$L_{i,s,t} \stackrel{Ind}{\sim} Bin(n_{i,s,t}, m_{s,t}S). \quad (8)$$

Equation (6) links the observed survey commercial biomass  $I_{i,s,t}$  in tow  $i$  at knot  $s$  and year  $t$  to the underlying biomass density  $B_{s,t}$  scaled by the commercial size catchabilities  $q_{l(s)}$  at each knot and adjusted by the probability of positive tows  $p_I$ . In comparison to usual approaches where there would be a unique catchability parameter for the whole area, it was decided to let the commercial size catchability vary through space. This is due to this area being known to have variable bottom types (Greenlaw *et al.*, 2010), which is known to impact gear efficiency (Miller *et al.*, 2019). Following the delta approach,  $p_I$  is estimated separately (with uncertainty propagated forward) through a binomial distribution based on the number of zeroes and non-zero survey tows.

Equation (7) is conceptually identical with the recruitment equivalent to Equation (6), with observed survey recruit biomass  $I_{i,s,t}^R$ , underlying recruitment density  $R_{s,t}$ , a single non-spatial recruit catchability  $q_R$ , and probability of positive recruit catches  $p_I^R$ , which is also estimated through a binomial distribution based on the number of survey tows with positive recruit catches.

Equation (8) links the number of clappers  $L_{i,s,t}$  to the natural mortality  $m_{s,t}$  scaled by clapper catchability  $S$  through a binomial distribution based on the number of commercial size paired shells (both clappers and live scallops)  $n_{i,s,t}$  caught in tow  $i$  at knot  $s$  in year  $t$ .

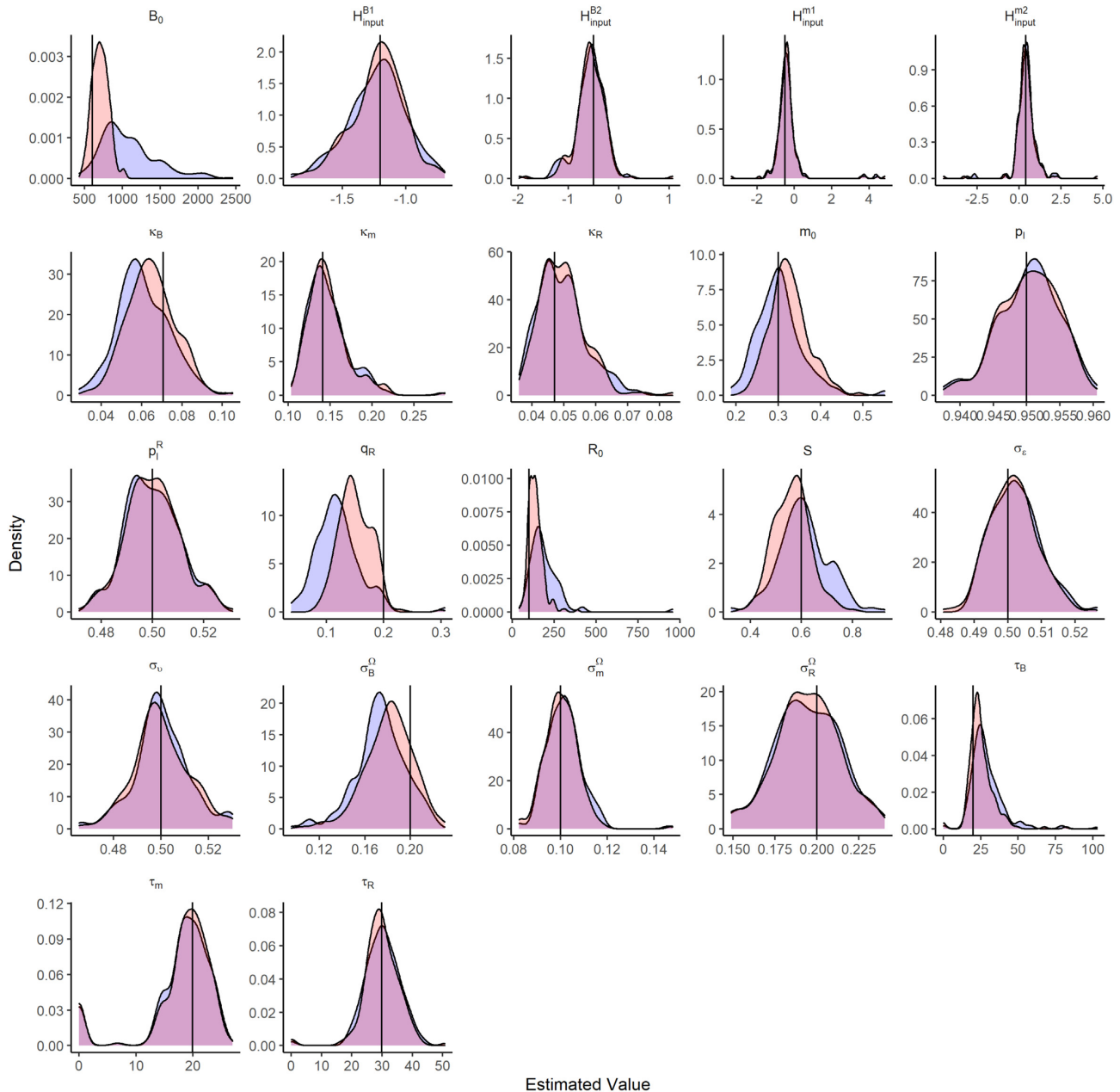
In summary, SEBDAM contains the observed states  $\mathbf{Y}_{s,t} = (I_{i,s,t}, I_{i,s,t}^R, L_{i,s,t})^T$ , the unobserved states  $\mathbf{X}_{s,t} = (B_{s,t}, R_{s,t}, m_{s,t})^T$ , the fixed covariates  $\mathbf{z}_{s,t} = (n_{i,s,t}, C_{s,t}, g_t, g_t^R)^T$ , and the parameters  $\boldsymbol{\theta} = (p_I, p_I^R, q_{l(s)}, q_R, S, \sigma_\epsilon^2, \sigma_\nu^2, B_0, R_0, m_0, \tau_B, \tau_R, \tau_m, \kappa_B, \kappa_R, \kappa_m, \mathbf{H}_{input}^B, \mathbf{H}_{input}^m)^T$ .

### Simulation study

This simulation study aims to assess the identifiability and estimability of SEBDAM and consists of two different settings both using the same simulation design. Setting 1A does not inform the estimation of  $q_{l(s)}$ , while 1B informs the estimation of  $q_{l(s)}$  using a beta distribution with shape parameters  $\alpha = 10$  and  $\beta = 12$  [slightly modified from the prior distribution used in DFO assessments; see Yin *et al.* (2019) for details]. A secondary study that examines the impact of fitting a strictly temporal model to data with spatial structure is described in Appendix A.

The simulation area is a 50 km by 50 km square. Data for 20 years with 125 tows each year are simulated to mimic a similar size to the SPA 3 dataset. The locations of these 2500 data points are randomly assigned across the simulation area from which knots are then obtained.  $g_t$  and  $g_t^R$  are assumed constant and set at 1.1 and 1.5, respectively, to reflect the average growth rates seen in the SPA 3 data. The total number of live and dead scallops caught ( $n_{i,s,t}$ ) is set to 120 in every tow.

The parameter values chosen for the simulations along with the starting values used during optimization are shown in Table 1 except for the 25  $q_{l(s)}$ , whose optimization starting values are all  $\exp(-1)$ . The parameters for  $\mathbf{H}_{input}^B$  are chosen to simulate strong anisotropy where the decorrelation range north-south is much larger than east-west, while those for  $\mathbf{H}_{input}^m$  are made to decorrelate rapidly in all directions. Range parameters  $\kappa_B, \kappa_R$ , and  $\kappa_m$  were obtained by setting mean decorrelation ranges of the GMRFs at 40 km for the commercial biomass, 60 km for recruitment, and 20



**Figure 4.** Density plots of parameter estimates from setting 1A (blue) and 1B (red). Black vertical line is simulation value.

km for mortality. Following the relationships between the marginal variance and parameters estimated through the SPDE approach (Lindgren, 2012), the spatial variability parameters  $\tau_B$ ,  $\tau_R$ , and  $\tau_m$  are obtained by setting the marginal variance of the random fields at 0.2 for  $\Omega_t^B$  and  $\Omega_t^R$  and 0.1 for  $\Omega_t^m$ .

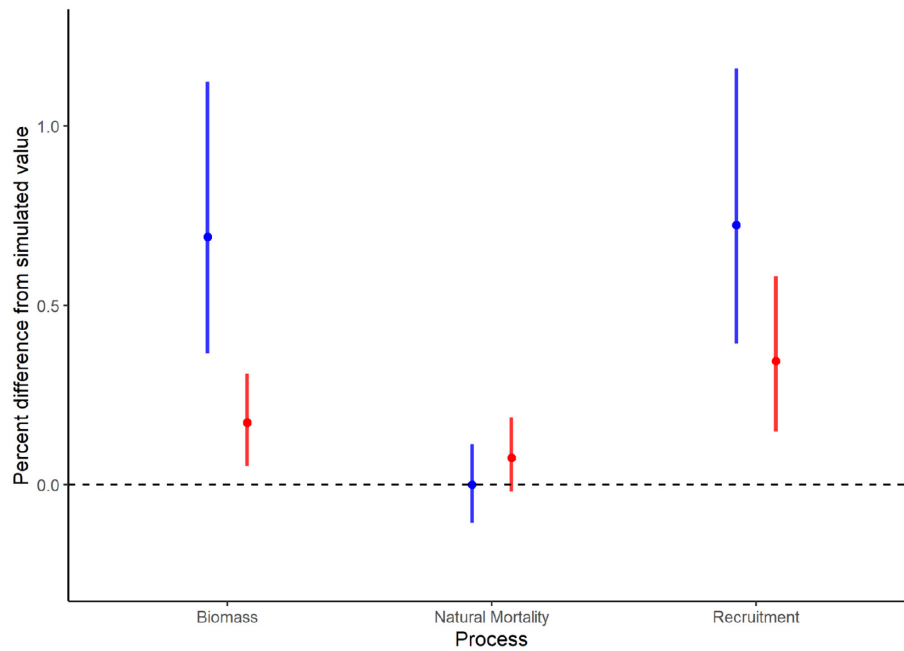
While the landings are not explicitly modelled by SEBDAM, we aim to mimic realistic settings where fisheries tend to exploit areas of higher biomass (Smith *et al.*, 2017). The total exploitation in each year is simulated from a lognormal distribution with a mean set to 10% of the simulated total biomass and a variance of 0.2 on the log scale. This total exploitation is then divided proportionally between knots with higher than average biomass following another lognormal distribution with a variance of 0.2 on the log scale. This results in approximately half the knots being

fished extensively, while knots with lower biomass densities are not fished at all. Scripts for running the simulations are available at <https://github.com/RaphMcDo/SPA3-Case-Study>.

#### Application to the Bay of Fundy sea scallop fishery

This application explores how SEBDAM performs when fit to real fishery data, using the SPA 3 scallop population. Its performance is compared to TLM. Our primary goal is to compare model performance to examine the effects of incorporating spatial structure. We also examine the effects of estimating multiple spatial catchabilities in SEBDAM (TLM assumes a single catchability parameter).

While survey data are available from 1996 to 2018, detailed log-books are only available from 1998 to 2018. The stock dynamics are



**Figure 5.** Median and interquartile range of the differences between predicted processes and their simulated value for settings 1A (blue) and 1B (red).

**Table 2.** Parameter estimates and standard errors for SEBDAM and TLM after being fitted to SPA 3 with  $q_I$  and  $q_{I(s)}$  informed with a beta distribution.

SEBDAM			TLM		
Parameter	Estimate	SE	Parameter	Estimate	SE
$\kappa_B$	0.047	0.013	$\sigma_\tau$	0.168	0.041
$\tau_B$	24.347	7.639	$\sigma_\phi$	0.278	0.070
$\kappa_R$	0.060	0.011	$\sigma_\eta$	0.533	0.078
$\tau_R$	15.434	3.451	$\sigma_\epsilon$	1.165	0.016
$\kappa_m$	0.181	0.021	$\sigma_\nu$	1.071	0.024
$\tau_m$	1.541	0.165	$q_I$	0.422	0.109
$\sigma_\epsilon$	1.017	0.014	$q_R$	0.071	0.054
$\sigma_\nu$	0.919	0.021	$S$	0.277	0.143
$S$	0.572	0.080	$p_I$	0.917	0.005
$R_0$	93.108	35.266	$p_I^R$	0.350	0.009
$B_0$	467.500	112.113			
$m_0$	0.059	0.022			
$q_R$	0.052	0.016			
$p_I$	0.918	0.005			
$p_I^R$	0.350	0.009			
$H_{input}^{B1}$	-1.056	0.324			
$H_{input}^{B2}$	-0.856	0.445			
$H_{input}^{n1}$	0.031	0.321			
$H_{input}^{n2}$	-0.161	0.259			

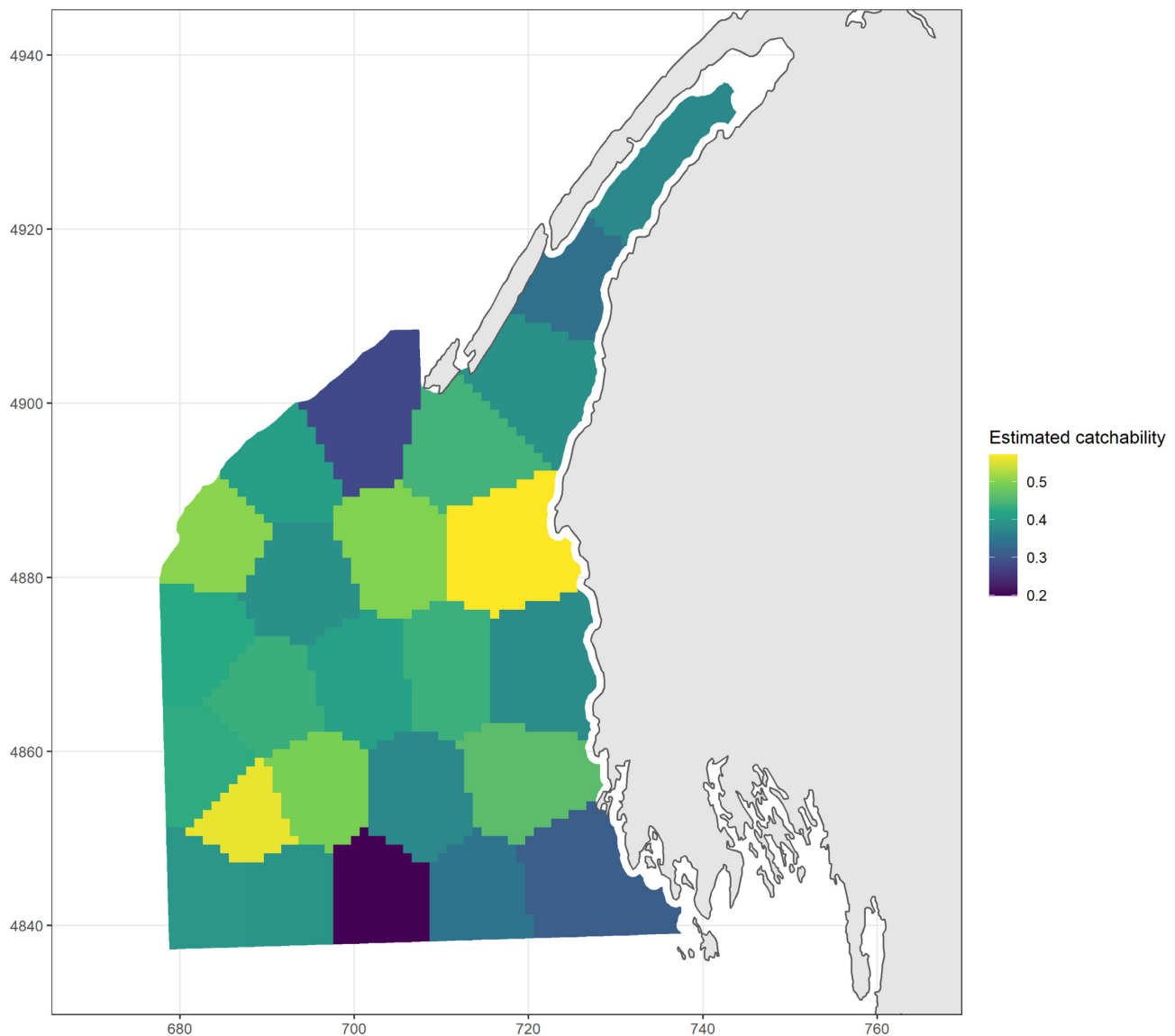
therefore modeled from 1997 to 2018 utilizing a total of 3035 survey tows, with a 1-year ahead projection for 2019. This one-year projection utilizes the same model and calculates the projection based on the estimated parameters and predicted random effects while propagating errors forward. Both models are fitted using the TMB pack-

age in R and the *nlm* optimizer. Optimization starting values are in Table 1. Preliminary analyses indicate that the model is somewhat sensitive to the values of  $\kappa_B$  and  $\tau_B$ , which is why their optimization starting values are different than the spatial parameters for the other processes. Random effects starting values are set to 0 for all random fields. Previous work has shown clear improvements in biomass predictions when informing  $q_I$  for TLM (McDonald *et al.*, 2021) and preliminary analyses indicates similar improvements for SEBDAM. Therefore, both SEBDAM and TLM are fitted to SPA 3 data twice, once without informing  $q_I$  and  $q_{I(s)}$  and once informing them using a beta distribution. While both models utilize different statistical methodologies, which can be difficult to compare (Aubry and Debozie, 2000), both models try to predict the true realization of the stochastic process for biomass. As there is only one dataset, and therefore one realization of this process, the main interest is to examine how both models treat the data to obtain an estimate of this actual realization. Survey data and R script are available at <https://github.com/RaphMcDo/SPA3-Case-Study>.

## Results

### Simulation results

For all simulation settings, the majority of simulations converged. For setting 1A, 191 simulations converged, two resulted in false convergence, six resulted in singular convergence, and one did not converge. For setting 1B, 197 simulations converged, two resulted in singular convergence and one did not converge. The catchabilities ( $q_{I(s)}$  in Figure 3,  $q_R$  and  $S$  in Figure 4) are underestimated for both settings but this bias is smaller when  $q_{I(s)}$  are informed (setting 1B). Informing  $q_{I(s)}$  reduces the consistent bias in commercial size catchabilities with the mean percent difference going from -48% to -18% (Figure 3). While the biomass and recruit processes are positively biased, the reduced estimation bias of  $q_{I(s)}$  further leads



**Figure 6.** Estimated commercial size catchabilities by SEBDAM at each knot in SPA 3 when informed with beta distribution.

to a comparable reduction of this bias in predicted biomass and recruitment (Figure 5). However, this does not impact the prediction of natural mortality substantively (Figure 5).

The distribution of estimated spatial parameters ( $\kappa$ ,  $\tau$ , and  $H_{input}$ ) are centered near the value used for simulations for both settings, e.g. 70% of estimates for  $\kappa_B$  are within 25% of simulation value in 1A (Figure 4). The GMRF marginal variances ( $\sigma_B^2$ ,  $\sigma_R^2$ , and  $\sigma_m^2$ ) are well captured, e.g. 83% of estimates are within 25% of simulation value for  $\sigma_B^2$  for 1A (Figure 4).

### Application to scallop data

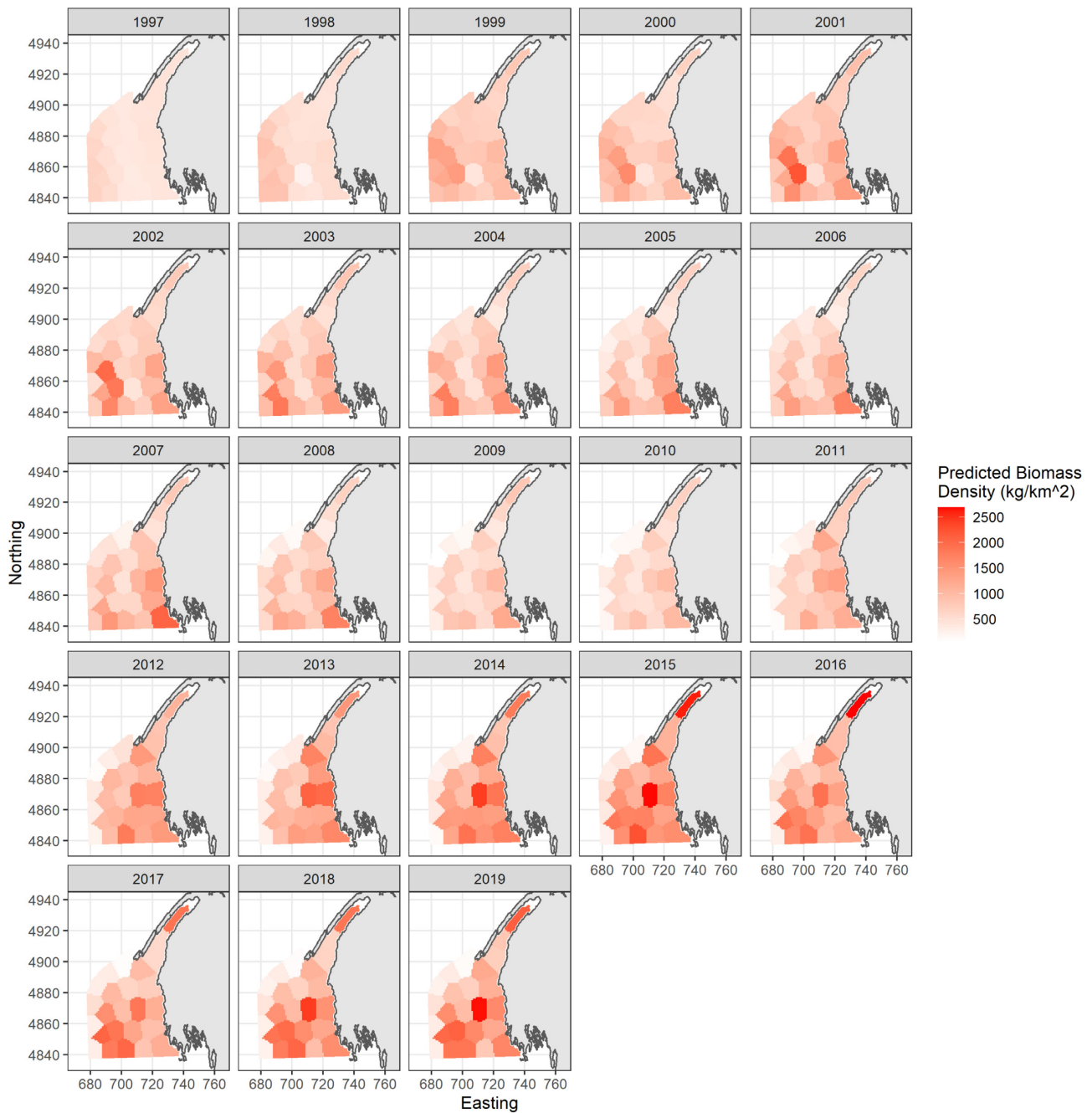
The simulations in 1A and 1B demonstrated that the outputs were more reliable when the  $q_{I(s)}$  were informed. Thus, we focus on the output from the model fits where the commercial size catchabilities are informed (see Supplementary Materials for output when uninformed). Both models converged successfully with parameter estimates shown in Table 2 and Figure 6. SEBDAM identifies fine-scale

time-varying spatial patterns of commercial biomass (Figure 7). Parameter estimates and standard errors for SEBDAM fit to the SPA 3 data with a single commercial size catchability parameter  $q_I$  are available in the Supplementary Materials.

The nearshore areas tend to have increased biomass in later years (e.g. 21.9% of total biomass between 2012 and 2018 in nine knots compared to 17% between 1997 and 2004 in the same knots). The knots with the highest predicted density are also the areas under higher fishing pressure (the nine nearshore knots contain 91.1% of the total effort between 2012 and 2018) and correspond to the majority of the area currently included in the stock assessment (Nasmith et al., 2016).

Time-varying spatial patterns of recruitment and natural mortality are also identified by the model (Figures 8 and 9). The outer areas tend to have consistently higher natural mortality rates than the rest of SPA 3 (average of 0.12 for the 16 outer knots). Recruitment is less spatially consistent, it tends to be higher in the nearshore areas in later years (e.g. 40.9% of recruitment between 1997 and





**Figure 7.** Predicted commercial biomass density  $B_{s,t}$  ( $\text{kg}/\text{km}^2$ ) at each knot between 1997 and 2018, with 1-year projections for 2019.

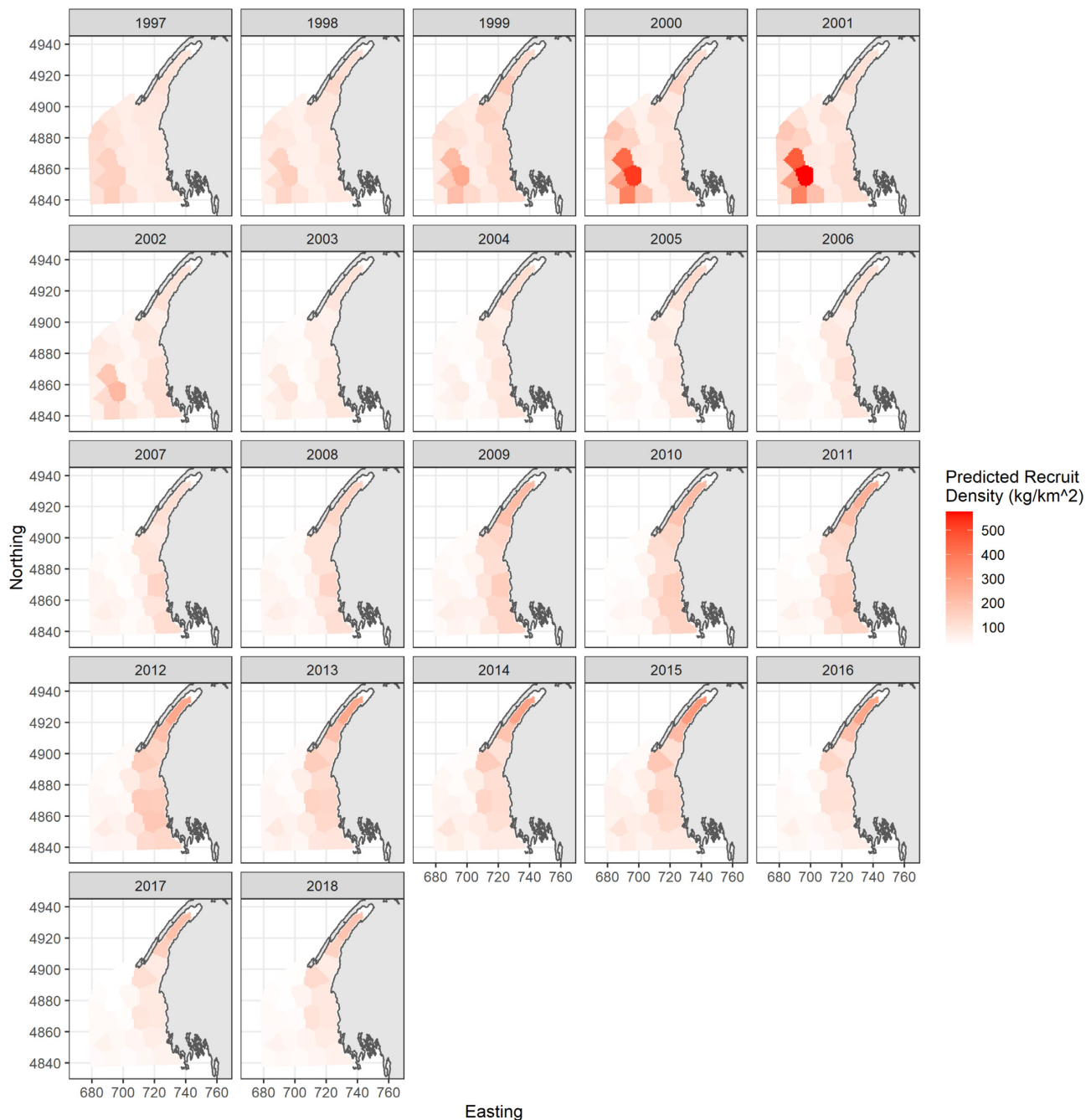
2006 in the nine nearshore knots and 64% between 2012 and 2018).

The marginal variances of the Matérn covariance structures [calculated following relation in Lindgren (2012)] are 0.29 for  $\Omega^B$ , 0.35 for  $\Omega^R$ , and 1.05 for  $\Omega^m$  when  $q_{l(s)}$  are uninformed. When they are informed the marginal variances are 0.21 for  $\Omega^B$ , 0.45 for  $\Omega^R$ , and 1.01 for  $\Omega^m$ .

The natural mortality, while it decorrelates relatively rapidly in all directions (mean decorrelation range of 14.8 km, Figure 10), is still highest in the areas closest to the glaciomarine mud bottom (Shaw *et al.*, 2014). Both commercial biomass and recruitment decorrelate rapidly on the east-west axis, but stay correlated at large

distances on the north-south axis (mean decorrelation ranges of 40.9 km and 39.1 km, respectively, Figure 10).

Aggregating over the whole area, TLM predicts higher total commercial biomass than SEBDAM, with the difference narrowing over time (Figure 11). The difference was on average 15.5% from 1997 to 2003 and declined to an average difference of 9.1% between 2013 and 2018 (the average difference was 9.6%). The convergence in the biomass predictions between TLM and SEBDAM in more recent years mirrors the results from the secondary simulation experiment (see Appendix A). The 95% confidence interval of the SEBDAM biomass predictions are 65.7% smaller than for TLM. The uncertainty of the 1-year projection (2019) was more similar between



**Figure 8.** Predicted recruit biomass density  $R_{s,t}$  ( $\text{kg}/\text{km}^2$ ) at each knot between 1997 and 2018.

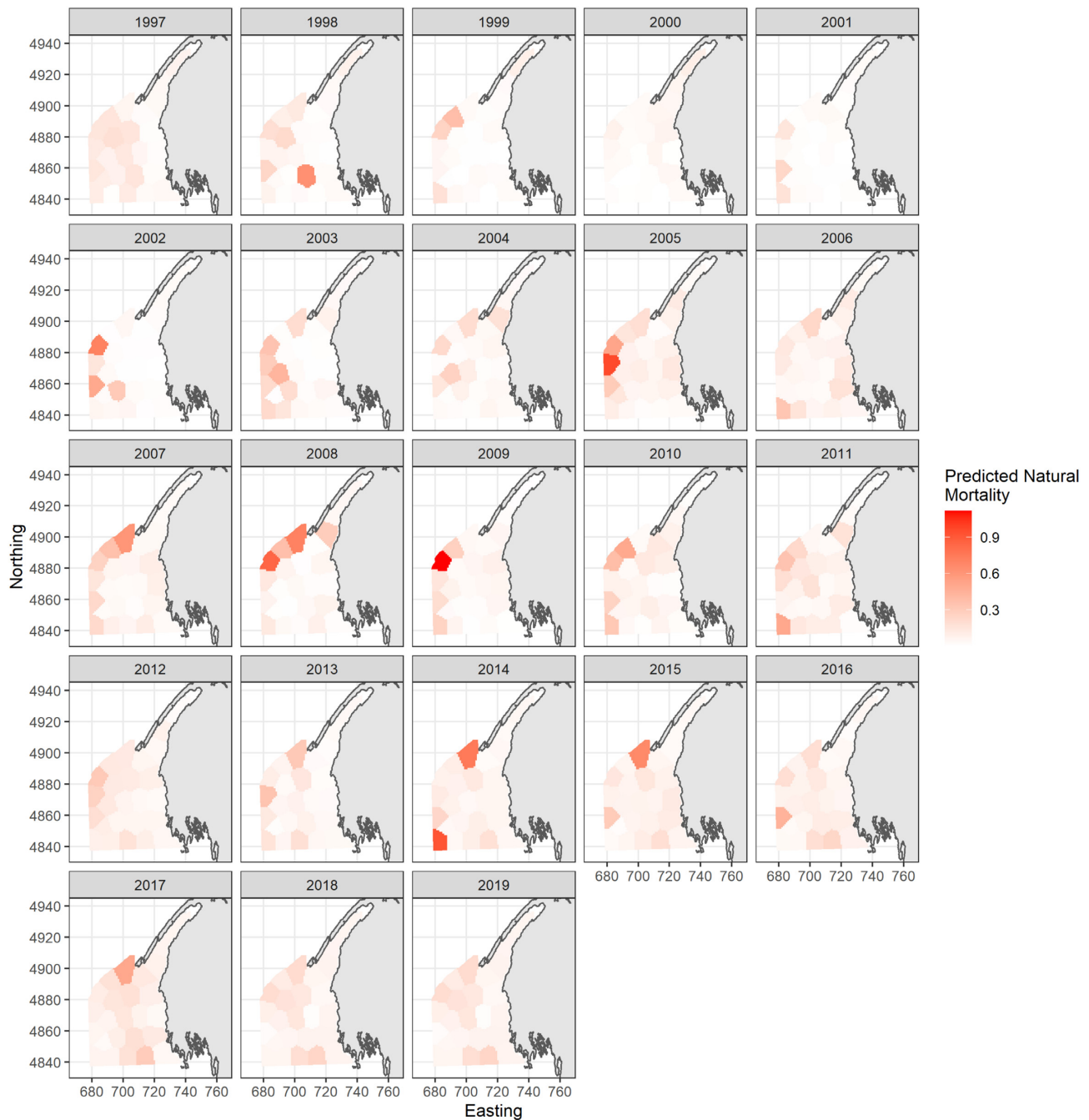
the two models as the 95% confidence interval from SEBDAM was 33.8% smaller than for TLM. The recruitment predictions of SEBDAM and TLM are very similar, but the 95% confidence interval for TLM are on average 126.3% larger than for SEBDAM.

The mean natural mortality predicted by SEBDAM is on average lower by 0.09 than the one predicted by TLM. The effects of particularly strong influential tows with a high proportion of clappers is greatly reduced for SEBDAM, which is clearly seen in 2003 (Figure 11). While these tows inform localized mortality patterns (e.g. the elevated mortality in the outside area; Figure 9), they are no longer extrapolated to the entire population in SEBDAM (Figure 11, see Figure 14 in Supplementary Materials for visualization of indi-

vidual tows in 2003). The reduced impact of strong influential tows is also present for biomass and recruitment, but is most evident for the natural mortality. This also results in substantially smaller 95% confidence intervals for natural mortality in SEBDAM, which are 136.5% smaller on average than for TLM.

## Discussion

SEBDAM reliably captures population changes across both space and time while simultaneously accounting for spatio-temporal patterns in productivity. Furthermore, it has the relatively uncommon ability to incorporate spatio-temporal patterns in exploitation (Cao



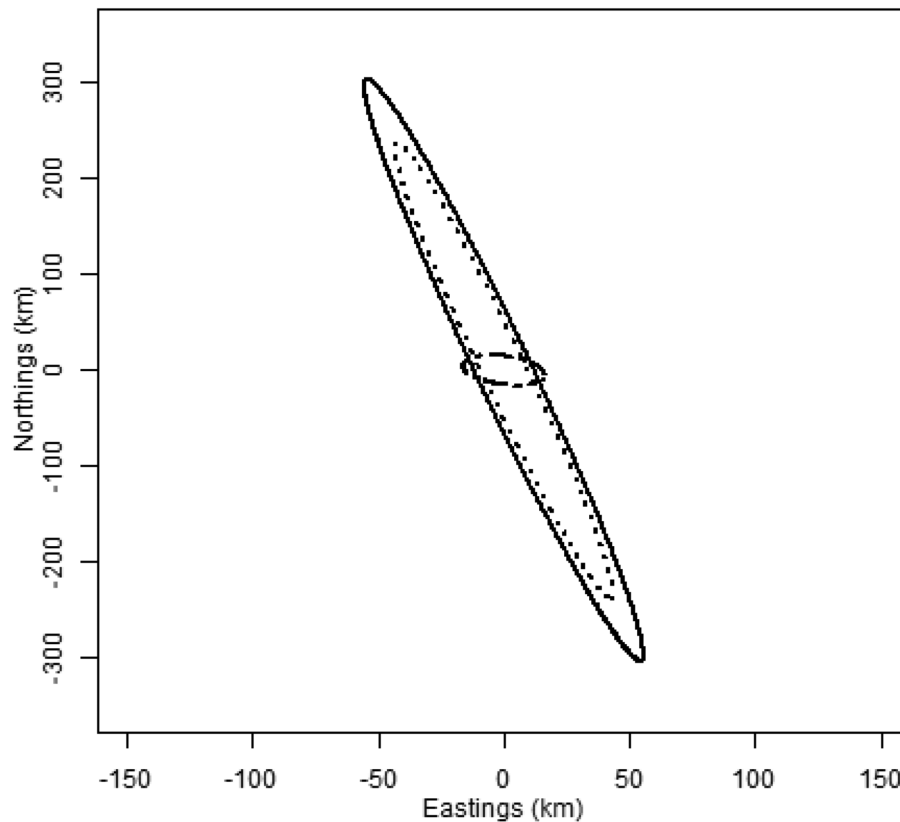
**Figure 9.** Predicted natural mortality  $m_{s,t}$  at each knot between 1997 and 2018, with 1-year projections for 2019.

*et al.*, 2019). SEDBAM is also able to provide a single synoptic biomass estimate for a region. All of the underlying processes are estimated with minimal bias, especially when a moderately informative prior is assumed for the catchability parameter. It is also able to project 1 year ahead with less associated uncertainty than its temporal predecessor (TLM) in a simplistic forecast setting.

Unusually large tows, characteristic of fisheries data, can unduly influence predicted population patterns and stock indices (Chen *et al.*, 2000; Hinrichsen, 2001). Although these tows contain real information, non-spatial methods tend to give them undue weight. In the SPA 3 time series, there are large spikes in biomass, recruitment and natural mortality. However, a closer inspection reveals

that these spikes are due to a few tows that are constrained to relatively isolated areas [see Supplementary Materials and Nasmith *et al.* (2016)]. Stratification approaches help reduce the impact of these tows on analyses (Smith, 1996; Kimura and Somerton, 2006), but the influence of such large rare events still persist. Desirably, this spatio-temporal approach accounts for both the local and overall impact of these tows by borrowing information from neighboring tows. That is, the impact of outlying tows is informed by their spatial extent rather than their magnitude (or that of a small cluster of outlying tows).

SEDBAM captures and predicts spatial population and productivity patterns without explicitly modelling the underlying causal



**Figure 10.** Decorrelation ranges in all directions for biomass (solid line), recruitment (dotted line), and natural mortality (dashed line).

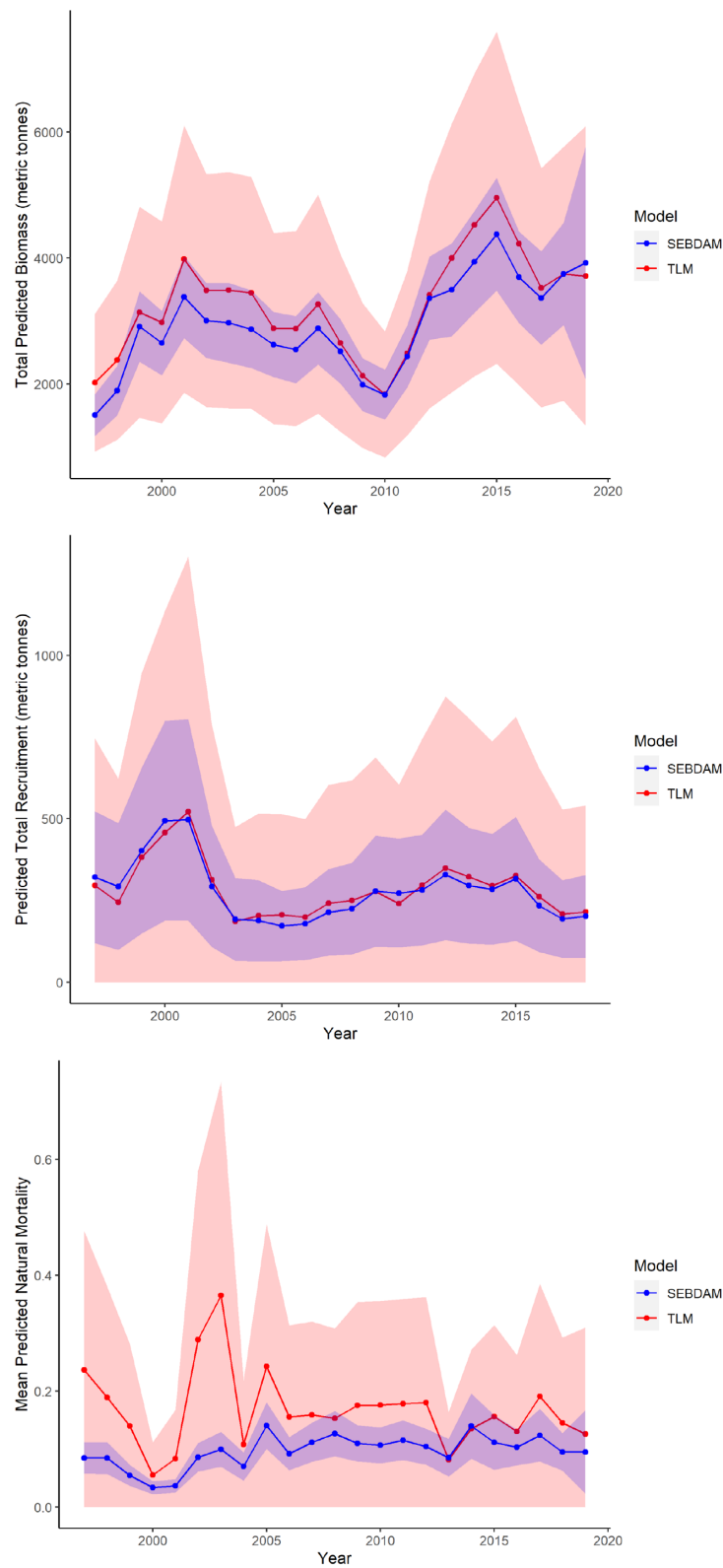
mechanisms. By capturing the spatial information contained in the data, the latent impact of the environment on the population is modelled without explicit knowledge of the environmental factors driving these patterns (Besag, 1974; Legendre, 1993). Given that relationships between easily measured proxies for environmental drivers and population dynamics are known to change over time (Myers, 1998), the development of models which can track spatio-temporal changes in productivity patterns can help to provide deeper insights into the factors driving changes in productivity (Guan *et al.*, 2019). This incorporation of the environment without modelling the underlying mechanisms can therefore be seen as embracing an ecosystem approach to fisheries management (EAFM; Colloca *et al.*, 2013; Laugen *et al.*, 2014; Gullestad *et al.*, 2017; Bastardie *et al.*, 2021) and is part of the necessary work required to build up next-generation SAMs (Cadrin, 2020; Punt *et al.*, 2020).

Explicitly modelling key characteristics of a given stock as spatial processes has been identified as an essential feature of next-generation assessment models (Berger *et al.*, 2017; Punt *et al.*, 2020). Our approach improves on many of the challenges that need to be addressed to move in this direction, from the incorporation of spatial structure to the inclusion of a simulation framework (Berger *et al.*, 2017; Punt *et al.*, 2020). SEBDAM can explicitly model the spatial structure inside of a stock by tracking the population density at a data-driven resolution, and is able to incorporate spatial random effects using computationally efficient methods through the use of TMB. Furthermore, SEBDAM has a built-in simulation framework that allows for “self-tests” (Punt *et al.*, 2020) under various settings and can be combined with other methods to show patterns of biases that come from ignoring spatial structure (see Ap-

pendix A). While SEBDAM does not explicitly model the impact of specific environmental factors, its ability to capture spatio-temporal patterns in productivity can help us formulate hypotheses to explain the drivers of these patterns.

By combining the predicted population patterns with the estimated decorrelation ranges, we can make inferences about the causal mechanisms driving observed environmental patterns. In the case of SPA 3, there is a clear productivity gradient from east (higher productivity) to west (lower productivity) where all three processes follow the bathymetry and/or tidal flow in some way. This aligns with the depth profiles, major currents and tidal flows of the Bay of Fundy (Hannah *et al.*, 2001; Aretxabaleta *et al.*, 2008) that likely impact the growth and survival of scallops that have settled into the benthic environment (Shumway *et al.*, 1987; Smith and Rago, 2004). The habitat suitability for benthic species such as scallops is often related to bathymetry (Brown *et al.*, 2012), and it has been linked to increased productivity, increased fishing pressure (Brown *et al.*, 2012; Smith *et al.*, 2017), and to settlement success for juvenile scallops (Hart and Chute, 2004). Work has already gone into identifying and creating habitat suitability maps for sea scallops (Brown *et al.*, 2012) and while they have been used to develop precautionary approach reference points for the purpose of stock assessment (Smith and Sameoto, 2016; Smith *et al.*, 2017), these maps have not yet been used as direct inputs into the SAMs themselves. Using habitat information to incorporate suitability patterns promises to further improve these types of spatially-explicit models.

Our approach provides science advice for the entire management area as well as any subset of interest. It can be used to provide the information necessary for traditional forms of science advice, such



**Figure 11.** Predicted total biomass, total recruitment and mean natural mortality for SPA 3 from TLM (red) and SEBDAM (blue). Envelopes represent interpolated point-wise 95% confidence intervals.



as biomass reference points and removal reference points while also facilitating the development of novel indices that can be used to develop new types of science advice (Caddy and Mahon, 1995; Nasmith *et al.*, 2016; Shertzer *et al.*, 2010; Smith *et al.*, 2017) such as dynamic reference points (Berger, 2019) by capturing shifts in productivity or simply guide the development of spatial reference points (Reuchlin-Hughenoltz *et al.*, 2016). Entirely new management tools could also be developed, for example “hierarchical” reference points in which typical synoptic reference points for an entire stock could be retained (Caddy and Mahon, 1995; Shertzer *et al.*, 2010). These could then be used alongside more targeted reference points, which focus on management measures to protect particular spatial regions within the stock [similar to managing on spawning stock biomass within more productive regions such as examples in Pikitch *et al.* (2012)] or focusing on regions in which exploitation tends to be elevated (Nasmith *et al.*, 2016). Incorporating spatial information into traditional SAMs opens up the possibilities of developing new types of science advice that can help facilitate sustainable fisheries management goals.

The ability of our spatio-temporal approach to capture population changes with minimal bias represents an improvement over more traditional temporal approaches and brings to light the importance of including spatial structure. Embracing a spatio-temporal approach implicitly embraces an EAFM by incorporating the impact of unmodelled environmental processes while simultaneously informing reasonable hypotheses of what these processes might be. Further, “going spatial” enables the assessment models to be future proofed against shifts in productivity or fishing effort without requiring extensive work modifying survey strata and subsequent indices. This approach increases the amount of information available to fisheries managers, reduces the uncertainty around the traditional estimates of population size, and should subsequently increase the confidence in the scientific advice provided to managers and stakeholders, thereby reducing the inherent risk in fisheries management decision-making.

## SUPPORTING INFORMATION

Supplementary material is available at the *ICES/JMS* online version of the manuscript.

## Data Availability Statement

The survey data underlying this article are available at <https://github.com/RaphMcDo/SPA3-Case-Study>. The landings data cannot be shared publicly as they are protected by privacy laws.

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