

# Applying Bayesian spatiotemporal models to fisheries bycatch in the Canadian Arctic

Aurelie Cosandey-Godin, Elias Teixeira Krainski, Boris Worm, and Joanna Mills Flemming

**Abstract:** Understanding and reducing the incidence of accidental bycatch, particularly for vulnerable species such as sharks, is a major challenge for contemporary fisheries management. Here we establish integrated nested Laplace approximations (INLA) and stochastic partial differential equations (SPDE) as two powerful tools for modelling patterns of bycatch through time and space. These novel, computationally fast approaches are applied to fit zero-inflated hierarchical spatiotemporal models to Greenland shark (*Somniosus microcephalus*) bycatch data from the Baffin Bay Greenland halibut (*Reinhardtius hippoglossoides*) gillnet fishery. Results indicate that Greenland shark bycatch is clustered in space and time, varies significantly from year to year, and there are both tractable factors (number of gillnet panels, total Greenland halibut catch) and physical features (bathymetry) leading to the high incidence of Greenland shark bycatch. Bycatch risk could be reduced by limiting access to spatiotemporal hotspots or by establishing a maximum number of panels per haul. Our method explicitly models the spatiotemporal correlation structure inherent in bycatch data at a very reasonable computational cost, such that the forecasting of bycatch patterns and simulating conservation strategies becomes more accessible.

**Résumé :** Comprendre et minimiser les répercussions relatives aux prises accessoires accidentelles, et plus particulièrement celles touchant les espèces vulnérables, tel le requin, constituent de nos jours un défi de taille en gestion halieutique. Par la présente recherche, nous soumettons que les approximations intégrées et agglomérées de Laplace (INLA) ainsi que les équations différentielles partielles stochastiques (EDPS), représentent de puissants outils de modélisation de la répartition des prises accessoires dans l'espace et le temps. Ces nouvelles approches informatiques, efficaces et innovantes sont ici utilisées afin de reproduire des modèles spatiotemporels hiérarchiques à inflation zéro en les appliquant aux données relatives aux prises accessoires du requin du Groenland (*Somniosus microcephalus*) dans la pêche au filet maillant du flétan noir (*Reinhardtius hippoglossoides*) de la baie de Baffin. Les résultats obtenus démontrent que les prises accessoires du requin du Groenland sont dispersées dans l'espace et le temps et varie de manière considérable selon les années. Certains facteurs quantifiables, tels le nombre de panneaux de filet par trait et la quantité de prises totale de flétans noirs, ainsi que certaines caractéristiques physiques, telle la bathymétrie, influent sur la fréquence des prises accessoires du requin du Groenland. Conséquemment, les probabilités de prises accessoires pourraient être réduites en limitant l'accès de pêche dans les endroits spatiotemporels à haut risque ou encore, en établissant une quantité maximum de panneaux de filet par trait. Ces méthodes modélisent d'une façon nette et précise la structure des corrélations spatiotemporelles inhérentes aux données sur les prises accessoires, et ce, à un coût informatique des plus raisonnables, rendant désormais possible et accessible le calcul des prévisions quant au nombre de prises accessoires ainsi que la planification de stratégies efficaces en conservation des espèces.

## Introduction

High levels of bycatch are a predominant problem in many fisheries around the world and contribute greatly to broader concern about overfishing (Kelleher 2005; Davies et al. 2009). Bycatch commonly refers to the part of the catch that is not a legal target of the fishery; it may be retained and landed but is often discarded (dead or alive) (FAO 2011). It tends to be particularly problematic for long-lived marine megafauna such as sharks, marine turtles, seabirds, and marine mammals (Lewison et al. 2004; Hall et al. 2000). Under the ecosystem approach to fisheries management, a core objective is to reduce and eliminate bycatch (Pikitch et al. 2004; Garcia et al. 2003). One of the first steps in addressing bycatch issues is to identify and prioritize key conservation and management areas (Kirby and Ward 2014). These priority areas are often referred to as “hotspots” and are locations where bycatch patterns indicate abnormally high risk (e.g., Huang and Yeh 2011; Cambiè et al. 2012; Roe et al. 2014). Detailed information on by-

catch patterns and their drivers can help establish effective spatial management, such as time-area closures and spatially explicit gear restrictions and catch quotas. These tools are increasingly used in marine resource management to better integrate multiple and often divergent economical and environmental objectives (Dunn et al. 2011; Douvère 2008). However, such regulations require some understanding of the spatiotemporal dynamics of the system.

Bycatch data are most often collected by at-sea observer programs and composed of the presence and absence (either count or mass) of nontarget species georeferenced by fishing location. They typically also contain information concerning the target species, vessel and gear specification, fishing effort, and environmental information like depth and sea surface temperature. Like many fishery datasets, bycatch data are characterized by complicated statistical features, such as excess of zeros, nonlinearity and nonconstant variance structure, and spatiotemporal correlation

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(Ciannelli et al. 2008). These characteristics violate the assumptions underlying basic statistical techniques such that more sophisticated models are required. Statistical tools that explicitly model the sources of zero observations (Martin et al. 2005) are commonly used in fisheries science and custom practice in bycatch studies (e.g., Minami et al. 2007; Barlow and Berkson 2012; Murray and Orphanides 2013).

To deal with nonlinearity and nonconstant variance, bycatch data are often modelled with well-established techniques used in catch-per-unit-effort (CPUE) standardization and stock assessments. These methods include generalized linear models (GLMs) (e.g., Megalofonou et al. 2009; Jannot and Holland 2013), generalized additive models (GAMs) (e.g., Minami et al. 2007; Murray and Orphanides 2013), and, to a lesser extent, generalized linear mixed models (GLMMs) (e.g., Trebilco et al. 2010) and generalized additive mixed models (GAMMs) (Bjorge et al. 2013). For a detailed discussion of these models in fisheries research, see Venables and Dichmont (2004).

Other techniques rely on matching animal telemetry and fleet distribution data to infer spatial overlap and derive bycatch predictions (e.g., Harden and Willard 2012; Roe et al. 2014; McClellan et al. 2009). These techniques offer advantages over fishery-dependent data but are limited to species with available tracking information. Bayesian hierarchical models have also been proposed for estimating bycatch probabilities (Gardner et al. 2008; Sims et al. 2008; Moore and Read 2008), but have not been widely adopted, likely because of high computational costs and complex estimation routines. However, these methods do represent very powerful approaches for dealing with complex ecological datasets with multiple sources of uncertainty (Cressie et al. 2009) and are readily used in other areas of fisheries science (e.g., Rivot et al. 2008; Yu and Leung 2010; Harley and Myers 2001).

Hierarchical models can simplify complex interactions by allowing parameters to vary at more than one level via the introduction of random effects. The expected value of the response is then expressed conditional on these random effects. Mixed models, such as GLMMs and GAMMs, are examples, the first being a fairly straightforward extension of linear regression (Venables and Dichmont 2004). Trebilco et al. (2010) modelled seabird bycatch in the eastern Australian tuna and billfish pelagic longline fishery using GLMMs with a random effect for each fishing vessel. Ortiz and Arocha (2004) standardized CPUE indices of billfish bycatch in the Venezuelan tuna longline fishery with all year interactions treated as random effects. Hierarchical approaches are very well-suited to nested data, such as bycatch data, where, for example, fishing sets are sampled from a trip, sampled from a vessel, which is part of a larger fleet. In this setting, errors associated with both the data and uncertainties about the ecological process are included, which results in more robust statistical inference (Cressie et al. 2009; Wikle 2003). The advantages of using hierarchical Bayesian models emerge more so as complexity increases, when, for example, spatiotemporal variability needs to be modelled explicitly (Cressie et al. 2009). The Bayesian framework also offers the advantage of providing full inference, such that model parameters and uncertainty can be quantified, which has great utility in applied conservation (Wade 2000; Wintle et al. 2003).

The ad hoc approach often taken in bycatch studies is to model space using a nonrandom factor variable, like a  $5^\circ \times 5^\circ$  grid cell (e.g., Brodziak and Walsh 2013) or geographical fishing boundaries (e.g., Bjorge et al. 2013; Barlow and Berkson 2012). Others commonly include one or two geographic coordinates (latitude and (or) longitude) in their models (e.g., Yeh et al. 2013; Jiménez et al. 2009; Orphanides 2010). Representing latitude and longitude as continuous variables offers the advantage that the data are not isolated in separate units, but these variables are still only incorporated into models as fixed effects and, as such, do not include spatial dependency. When fishing locations are georeferenced in

space and the main research questions revolve around spatial predictions, the most appropriate statistical approaches are geostatistics-based models, which intrinsically incorporate the first law of geography: “Everything is related to everything else, but near things are more related than distant things” (Tobler 1970). Hierarchical Bayesian models extend the concept of multilevel structure to include a spatial random effect (Gaussian random field, GRF). This random field is a stochastic process indexed in space that essentially represents all spatially explicit processes that may have an effect on the bycatch pattern. This is the real advantage of these models; they are built to approximate and include uncertainties with the entire bycatch phenomena as opposed to only uncertainty associated with discretely observed data. In so doing, bycatch hotspots cannot only be rigorously identified, they can also be better forecasted for management planning (Clark et al. 2001).

Hierarchical Bayesian models have traditionally relied on Markov chain Monte Carlo (MCMC) simulation techniques, which are computationally expensive and technically challenging, consequently limiting their use. However, a new statistical approach is now readily available, namely integrated nested Laplace approximations (INLA) via the R-INLA package (<http://www.r-inla.org>). INLA methodology and its powerful application to modelling complex datasets has recently been introduced to a wider nontechnical audience (Illian et al. 2013). As opposed to MCMC simulations, INLA uses an approximation for inference and hence avoids the intense computational demands, convergence, and mixing problems sometimes encountered by MCMC algorithms (Rue and Martino 2007). Moreover, included in R-INLA, the stochastic partial differential equations (SPDE) approach (Lindgren et al. 2011) is another statistical development that models GRFs much faster (similar to kriging) as well as constructs flexible fields that are better adept to handle datasets with complex spatial structure (Lindgren 2013). This is often the case with fisheries data, since fishermen tend to target particular fishing grounds, resulting in clustered spatial patterns and large regions without any values. Together, these new statistical methods and their implementation in R allows scientists to fit considerably faster and more reliably complex spatiotemporal models (Rue et al. 2009).

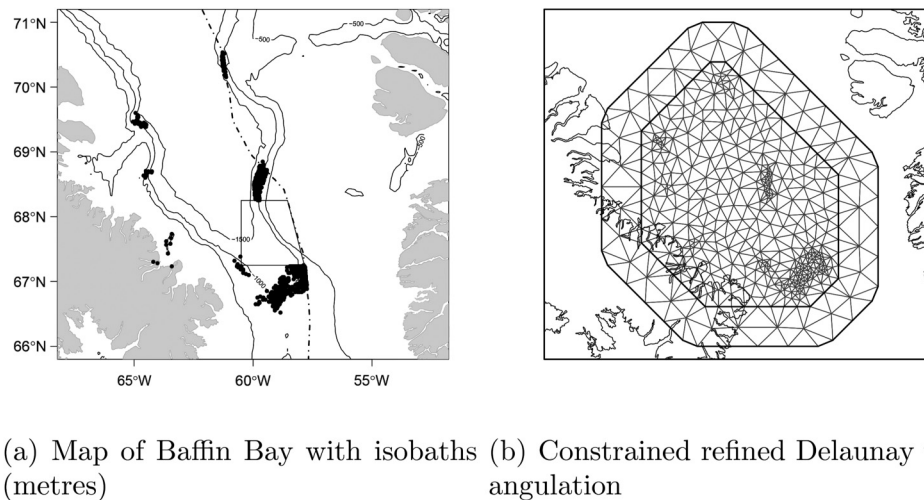
The aim of this paper is to analyze bycatch data using hierarchical Bayesian spatiotemporal models fitted using these two novel techniques. We present an analysis of Greenland shark (*Somniosus microcephalus*) bycatch in the Canadian gillnet fishery in Baffin Bay. We demonstrate how our approach can yield answers to the ubiquitous questions behind bycatch studies, that is, to (i) identify times and areas of higher bycatch risk (which may give insight into the species biology, i.e., suitable habitat); (ii) identify environmental and fisheries drivers affecting bycatch rates; and (iii) identify plausible mitigation measures. In this paper, we first fully describe the Greenland shark bycatch data, briefly discuss relevant aspects of INLA and SPDE, and specify all models that were investigated. We then address model selection, inference, and goodness of fit. Details on the final model are provided in Appendix A, and all R codes and datasets are available on the R-INLA website. In closing, we discuss future opportunities for the INLA framework in relation to bycatch studies.

## Materials and methods

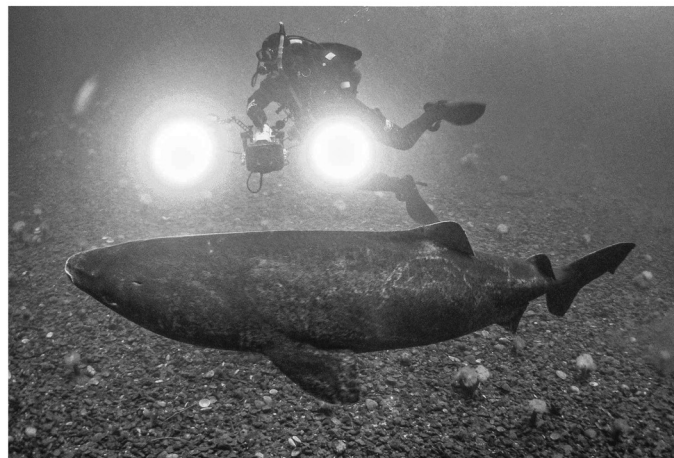
### Greenland shark bycatch dataset

Baffin Bay and Davis Strait are two large basins between Nunavut's Baffin Island and Greenland that connect the Arctic and Atlantic oceans. These regions sustain the only large-scale commercial fisheries in Canada's Arctic. A Greenland halibut (*Reinhardtius hippoglossoides*) fishery in Baffin Bay began in 1996 as a small exploratory fishery but has been expanding greatly since 2001 (DFO 2014). Greenland sharks are commonly caught as bycatch and

**Fig. 1.** (a) Spatial distribution of the observed Greenland halibut gillnet fishing hauls, location of the fishing closure (solid line), and Canadian Exclusive Economic Zone (dashed line); (b) mesh used to calculate the Gaussian (Markov) random field in the SPDE approach; and (c) image of a free-swimming Greenland shark.



(a) Map of Baffin Bay with isobaths (metres) (b) Constrained refined Delaunay triangulation



(c) *Somniosus microcephalus* ©Jeffrey Gallant

discarded (MacNeil et al. 2012). Currently, estimates of their biomass, productivity, and fishing mortality are unknown, which limits the ability to predict fishing impact on the Greenland shark population. As a result, there is concern that the species could become overexploited because of presumed low productivity; hence, a precautionary approach to their management is advocated (Davis et al. 2013). Investigating bycatch data, one of the only available sources of information for the species, can provide insights into the shark's biology and help establish appropriate management efforts.

At-sea observers are assigned to monitor the Greenland halibut fishery (DFO 2014). Observers record location of the net (at the start of the haul), target species (*R. hippoglossoides*) and mass captured, number of gillnet panels, mesh size, soak duration, depth at which the net was set, and bycatch mass and count per haul. Count information has only recently (since 2008) been recorded for pelagic species, including Greenland sharks.

The observer dataset used for this case study represents 79.2% of the total fishing effort (number of hauls) of the Baffin Bay gillnet fleet over the 4-year period (2008–2011). Data were collected by a Newfoundland and Labrador-based observer company and obtained from Fisheries and Oceans Canada (DFO).

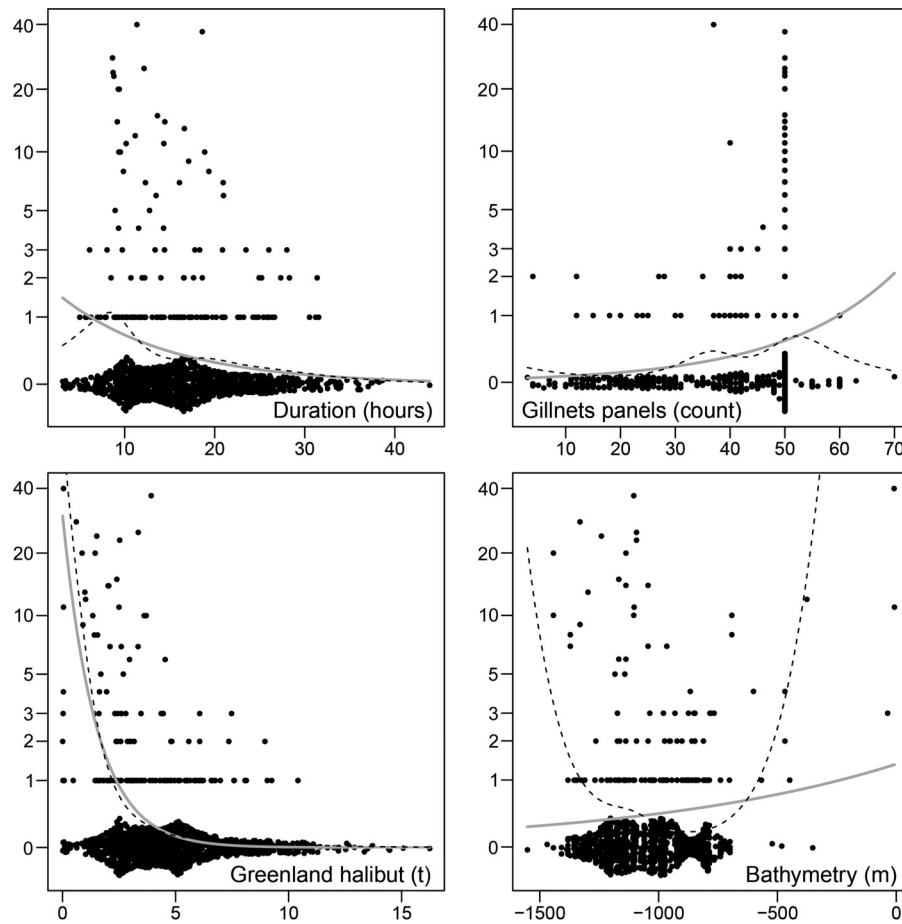
Gillnet vessels tend to be relatively small in size (65 feet; 1 foot = 0.304 m) and are allowed to carry a maximum of 500 nets per trip (DFO 2014). Fishermen usually set several gillnets a day with on

average about 40–50 panels in each gillnet (DFO 2005). Since 2007, a large portion of the Greenland shelf 11 750 km in the southeast was closed to fishing for the protection of narwhal (*Monodon monoceros*) and deepsea corals (DFO 2007). Gillnet effort is concentrated in areas to the north and south of the closure (Fig. 1). The fishery has expanded over the years, for example, the northeast of Baffin Bay (71°N) is a new fishing ground where the Greenland shelf projects into Canadian waters and provides suitable depths for halibut fishing.

There were 1647 hauls from 26 trips, spanning 2008 to 2011, with all observations occurring between the months of July and November. Three hauls were discarded because there was no information on the mass of Greenland halibut captured; none of these hauls had shark bycatch. Another three hauls were inside the closure or outside the 200 nautical mile (1 n.mi. = 1.852 km) Canadian Exclusive Economic Zone (EEZ) and hence were also disregarded. In addition, 25 hauls had recorded mass of Greenland sharks but no associated counts. The majority of these (21 records) were less than 300 kg. For each of these entries, we assumed a count of one, which makes sense given the average mass of a shark in the others hauls (127 kg). Hereinafter, a total of 1641 hauls were included in the analysis (Table 1). We refer to each haul as a fishing geolocation, 147 (9%) of which recorded bycatch of Greenland shark; counts varied from 1 to 40 sharks per haul.



**Fig. 2.** Relationship between Greenland shark bycatch counts and covariates of interest. Results of fitting both a Poisson regression (solid line) and a generalized additive model (broken line) are shown.



**Table 1.** Summary of the dataset showing the total number of hauls with bycatch (>0), number of observed hauls, mass (kg), and counts of Greenland shark bycatch per year.

Year	Hauls with bycatch	Hauls	Mass (kg)	Counts
2008	46	411	5 027	66
2009	34	378	8 765	83
2010	20	374	4 435	21
2011	47	478	92 425	400

In addition to the observed data, ocean depth was extracted from the National Oceanic and Atmospheric Administration (NOAA) global relief model ETOPO1 (Amante and Eakins 2014). Spatial data were projected from latitude–longitude locations on the surface of a sphere into locations on a plane using NAD83 (CSRS) – UTM zone 19N, a coordinate reference system suitable for use in Canada between 66°W and 72°W. The relationship between shark bycatch and four variables of potential interest (duration (soak time in hours and decimal minute), number of gillnet panels, total catch of Greenland halibut (in metric tonnes, t), and the bathymetry (metres, m)) were included in the models. Exploratory analysis revealed no clear relationships between Greenland shark bycatch and these covariates, with the exception of some evidence of a nonlinear relationship with bathymetry (Fig. 2).

### Hierarchical spatiotemporal model structure

Similar to a GLM framework, the response, in our case the observed Greenland shark bycatch (count) at a particular fishing

geolocation and time, is assumed to have a distribution that belongs to the exponential family, and the parameters of the family ( $\phi$ ) are linked to a structured additive predictor  $\eta$  through a link function  $g(\cdot)$  such that  $g(\phi) = \eta$ , where the linear predictor  $\eta$  is defined, in our case, as follows:

$$(1) \quad \eta = \beta_0 + \beta_1 \text{Duration} + \beta_2 \text{Panels} + \beta_3 \text{TC.tspp} + \sum_{k=1}^K f_k(\text{Bathymetry}) \mathbf{w}_k + f(\cdot)$$

where  $\beta_0$  is the intercept, and  $\beta_1$ ,  $\beta_2$ , and  $\beta_3$  are the (linear) regression coefficients for our covariates: duration or soak time in hours and decimal minutes (Duration), number of gillnet panels (Panels), and catch (t) of Greenland halibut (TC.tspp), respectively. The function  $f_k$  is the sum of smooth functions defining the random effect of bathymetry (m), where regression coefficients vary with bathymetry values ( $K$  values), and  $\mathbf{w}_k$  is a vector of known bathymetry values defined for each of the fishing geolocations. This is equivalent to a smooth function used in GAMs.  $f(\cdot)$  is a semiparametric function defining the spatiotemporal random effect included in the model (Table 2). All of these components form the (nonobservable) latent field defined as  $\theta = \{\beta_0, \beta, f\}$ , where  $\beta$  and  $f$  are the covariates and smooth functions, respectively, included in the linear predictor with their appropriate priors ( $\psi$ ).

The latent field is characterized by a joint normal (Gaussian) multivariate distribution with mean  $\mathbf{0}$  and precision matrix  $\mathbf{Q}(\psi)$

**Table 2.** Spatiotemporal correlation structures considered.

Identifier	Spatiotemporal structure
m0	None
m1	Constant: $f(s, t) = f(s)$ is a Matérn correlation structure with $\nu = 1$ , where scale and variance need to be estimated
m2	Different each year: $f(s, t)$ is a Matérn correlation structure like model m1 but with a different realization every year
m3a	Correlated in consecutive years: $f(s, t)$ is a combination of model m1 with additional correlation structure between neighbouring years
m3b	Exchangeable correlation between years: $f(s, t)$ is similar to model m3a but correlation structure between years is repeated (i.e., the correlation between years 1 and 2 is the same as that between years 1 and 4)
m4	Different for each month: similar to model m2 but the time index is month rather than year
m5a	Correlated in consecutive months of the same year: same structure to model m3a for month
m5b	Exchangeable correlation between months of the same year (e.g., 2009–2007 has the same correlation with 2009–2008 as with 2009–2009)

(i.e.,  $\theta \sim N(\mathbf{0}, \mathbf{Q}^{-1}(\psi))$ ). Each observation  $y_i$  depends on a linear combination of a subset of the elements of  $\theta$  defined as follows:

$$(2) \quad y_i | \theta, \psi \sim p\left(y_i \middle| \sum_j A_{ij} \theta_j, \psi\right)$$

The term  $A_{ij}$  is the generic element of an observation matrix  $\mathbf{A}$  defined by the SPDE approach. Each  $y_i$  is independent and identically distributed given the latent field  $\theta$ . Simplistically, the SPDE method allows one to fully evaluate the continuous GRF as a **discretely** indexed random process (i.e., a Gaussian Markov Random Field; Lindgren and Rue 2013), and it does so by subdividing the domain  $D$  (the area of the ocean where the fishing fleet is active) into triangular tiles, creating an index mesh (Lindgren and Rue 2013). Further built-in R-INLA commands are then used to construct the observation matrix  $\mathbf{A}$  that extracts the values of the spatiotemporal random field at the measurement locations and time points used for the parameter estimation. The likelihood is linked to the latent field through  $\eta^*$  ( $\eta^* = \mathbf{A}\eta$ ) as

$$(3) \quad p(y | \theta, \psi) = \prod_{i=1}^n p(y_i | \eta^*, \psi)$$

Since the Greenland shark bycatch data are counts characterized by many zeros, we evaluated Poisson and negative binomial distributions, as well as their zero-inflated versions. R-INLA offers different forms of zero-inflation, namely Types 0, 1, and 2. In a nutshell, Type 0 is a hurdle model that treats the response variable as being in a “perfect state” where the probability of bycatch can only be positive (i.e., does not include zero), whereas Types 1 and 2 are mixture models (2 being an extension of 1, that allows for additional zero probability), which describe the probability of being in an “imperfect state” where positive events (e.g., bycatch) may occur but are not certain and, as such, include both zero and nonzero values. For more details refer to Martin et al. (2005) and the R-INLA website. Table 2 lists all spatiotemporal correlation structures evaluated in our models. Please see Cameletti et al. (2012) and the R-INLA website for further documentation on these latent random field models.

### Inference, goodness of fit, and prediction

All analyses were performed using R (R Development Core Team 2013), specifically the R-INLA package (Rue et al. 2009). The INLA procedure, in accordance with the Bayesian approach, calculates the marginal posterior distribution of all random effects and parameters involved in the model. There are different options offered in R-INLA with which to approximate the posterior marginal distributions; we used the most accurate one, the Laplace (Martins et al. 2013). We also used the default and recommended

settings for priors (Held et al. 2010). These priors are vague priors or approximations of “non-informative” priors, which have little influence on the posterior distributions; hence, results are mostly derived from the data (similar to a frequentist approach). Prior sensitivity tests were conducted on the final best model. Further information on priors is provided in Appendix A.

To use the SPDE approach, the first step is to create a mesh on which the GRF is to be built; this mesh defines the spatial domain of interest ( $\Omega$ ; Fig. 1b). This is straightforward in R-INLA, but still requires some tuning. The mesh function creates by default a constrained refined Delaunay triangulation (CRDT) for the set of spatial locations provided (i.e., uses the observed fishing locations as the triangle nodes). If desired, the mesh could be derived from another set of points, for example, a regular grid. However, using the discrete fishing locations offers precision and efficiency. With CRDT, smaller size triangles can be defined in areas that have been sampled (fished) and larger ones in areas with no information (no fishing). This saves computational costs and increases the accuracy of the spatial field where there is fishing. Best mesh designs have more regular-shaped triangles and include some outer extension to avoid the “boundary effect” (increased variance at borders; Lindgren and Rue 2013). Different mesh designs were evaluated to investigate their effects during model selection.

Best candidate models were selected based on deviance information criterion (DIC; Spiegelhalter et al. 2002). Further model selection was performed on the three best models using cross-validation; 10 samples, each with 1100 observations, were randomly drawn from the dataset (total of 1641 observations) and fitted with each model; the remaining 541 observations were used for validation. DIC values and the mean squared error (MSE) using the log of the positive observed values and the linear predictor were calculated for each cross-validation. Note that MSE was only computed for the positive counts (bycatch of shark), since it is bycatch events that we are interested in predicting accurately.

A final model was chosen for model inference and prediction of bycatch hotspots for 2008–2011. Estimated bycatch can be predicted over the whole spatial domain ( $\Omega$ ) determined by the mesh (Fig. 1b). However, in our case study, there are large areas of Baffin Bay that are not fished. To avoid predicting bycatch in areas where fishing is unlikely, we first created a lattice of 1 km  $\times$  1 km grid cells over  $\Omega$  and selected only the cells within a 5 km radius around our observed fishing locations. Note that these numbers (1 and 5 km) are arbitrary; we could choose a larger or smaller grid cell or radius, since we can predict bycatch everywhere in  $\Omega$ . However, predictions on finer grids and larger areas of  $\Omega$  will be more computationally intensive.

Bathymetry for each 1 km  $\times$  1 km grid cell was extracted from the NOAA TOPO1 raster. Since Greenland halibut catch also fluctuated in space and time, we interpolated catch for each grid cell using a weighted mean, where the weights are proportional to  $\exp(-\text{distance}/a)$ , where  $a$  is equal to 0.5 km, that is inversely proportional to the distance. Spatial predictions of the expected

**Table 3.** DIC values for all models tested.

	m0	m1	m2	m3a	m3b	m4	m5a	m5b
Poisson	2630.46	1400.51	1171.36	1176.61	1177.74	1144.19	1139.26	1143.51
zpoisson0	1678.52	1394.45	1375.65	1380.46	1376.68	1376.66	1370.33	1368.60
zpoisson1	1665.22	1321.45	1178.56	1180.23	1180.35	1151.52	1153.06	1137.73
zpoisson2	1859.05	1352.43	1186.43	1189.52	1187.79	1160.64	1165.65	NA
nbinom	1442.40	1297.25	1182.62	1183.76	1181.94	1149.13	1157.12	1163.13
znbinom0	1484.98	1415.29	1389.23	1391.14	1390.26	1385.27	1388.60	1400.54
znbinom1	1442.79	1298.10	1185.19	1186.59	1184.92	1154.65	1160.51	1168.08
znbinom2	1448.39	1292.72	1172.73	1174.23	1173.77	1153.38	1159.47	1168.11

**Note:** Poisson and negative binomial with 0, 1, 2 are referring to the zero-inflated types. Note that model m5b with zero-inflated Poisson 2 had a very large DIC suggesting that the model was inappropriate (NA).

bycatch for each year were then obtained by running the final model with the mean values of the other covariates (Duration = 15.94 and Panels = 43.33) and the grid values of the bathymetry and halibut catch. Results were then plotted on the 1 km × 1 km grid.

R scripts and datasets are available on the R-INLA website (<http://www.r-inla.org>).

## Results

### Model selection

DIC results of all models tested are presented in Table 3. Models ran from less than 10 s to 45 min on an Apple Darwin 10.8.0 (64-bit) platform with 2.4 GHz Intel Core 2 Duo Processor. Models fitted with a more elaborate spatiotemporal random field performed better than those with no random field (m0) or one that is constant over time (m1), irrespective of the likelihood. Models with spatial correlation among years (m3a and m3b) did not perform as well as the others, which treated years as independent.

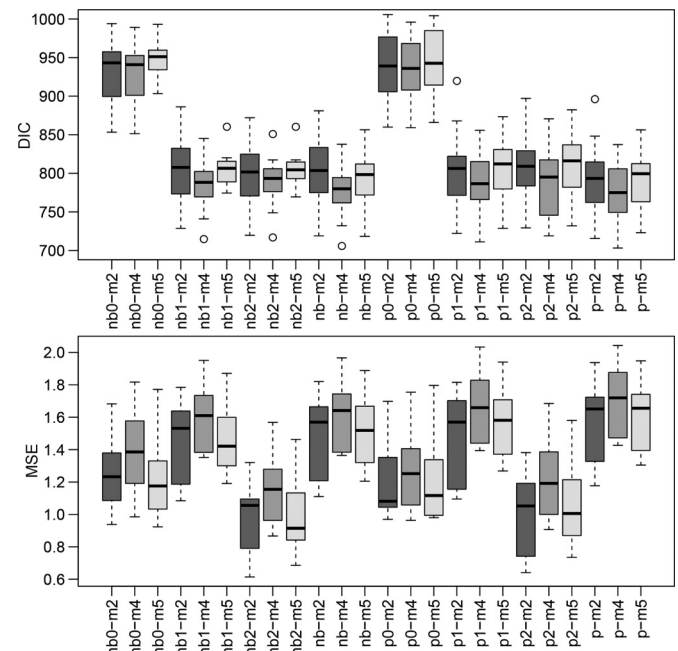
Correlation among months was very high (around 90%), such that m5 models were very similar. For further model selection, m2, m4, and m5a were investigated. DIC and MSE results from these models' validation simulations are shown in Fig. 3. All models with the exception of their Type 0 zero-inflated Poisson and negative binomial versions have similar DIC values (Fig. 3). However, MSE results show that the zero-inflated Type 2 Poisson and negative binomial likelihood performs better with all three models (i.e., MSE values are smaller). However, when these models were tested with different mesh designs with more triangulations and different boundaries, the Poisson likelihood's DIC values were very sensitive (large fluctuations with zero values), whereas the negative binomial likelihoods were stable irrespective of the mesh used. For this reason, the zero-inflated Type 2 negative binomial likelihood and the most parsimonious mesh (simplest boundary and lesser number of triangulations) were selected.

All three models provide similar prediction performance, as seen from the MSE boxplots in Fig. 3. Model m4 is not a practical model for predictions purpose, since each month is an independent realization of the random field. Under m2, we have a common spatial pattern for months within each year and no correlation between years. Under m5a, we have a high correlation between consecutive months, within each year. Note that this may have arisen because of observed hauls in consecutive months but very close in time. For this reason and because it is a simpler model, we selected m2 as our final model. This model includes a different realization of a spatial correlation structure every year. The model ran for less than 6 min on our platform. Inference, posterior means, and simulations of fitting model m2 with a zero-inflated negative binomial (Type 2) model are presented below. Additional details on the structure of this final model can be found in Appendix A.

### Inference and prediction

Results for all parameters are shown in Table 4 and Fig. 4. Duration of the hauls (soak time) had no significant effect. The number of gillnet panels was positively correlated with the amount of

**Fig. 3.** Model evaluation and selection. Shown are deviance information criterion (DIC) and mean squared error (MSE) boxplots under different likelihood families and spatiotemporal structures, considering different samples of the data. Grey shades refer to m2 (dark grey), m4 (medium grey), and m5 (light grey) models. Note that m5 refers to the m5a model.



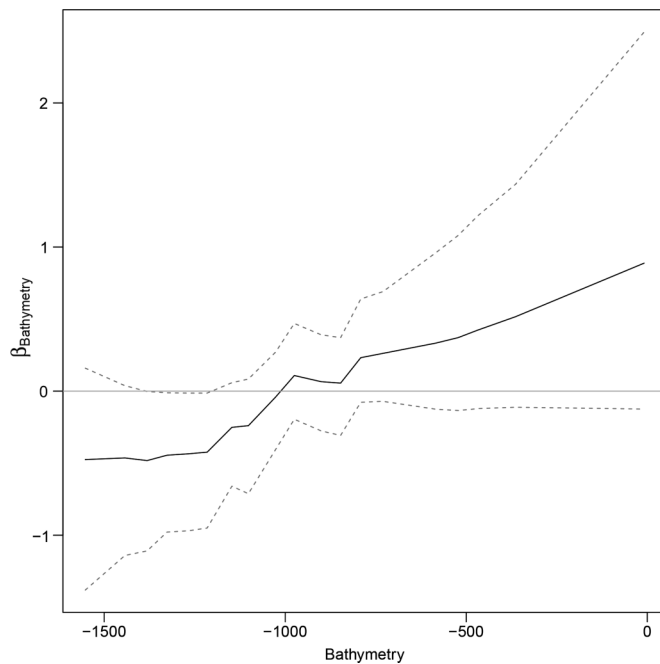
**Table 4.** Posterior estimates (mean and 95% credibility interval) of model parameters with negative binomial zero-inflated Type 2 likelihood and m2 spatiotemporal structure.

Parameters	Mean	$Q_{0.025}$	$Q_{0.975}$
Duration (hours and decimal minutes)	0.0053	-0.0170	0.0275
Number of gillnet panel	0.0271	0.0100	0.0446
Total halibut catch (t)	-0.1023	-0.1814	-0.0250
$n$	2.0316	0.9754	3.2489
$\alpha$	0.7557	0.3753	1.1876
Nominal range (km)	174.7362	75.2938	291.5277

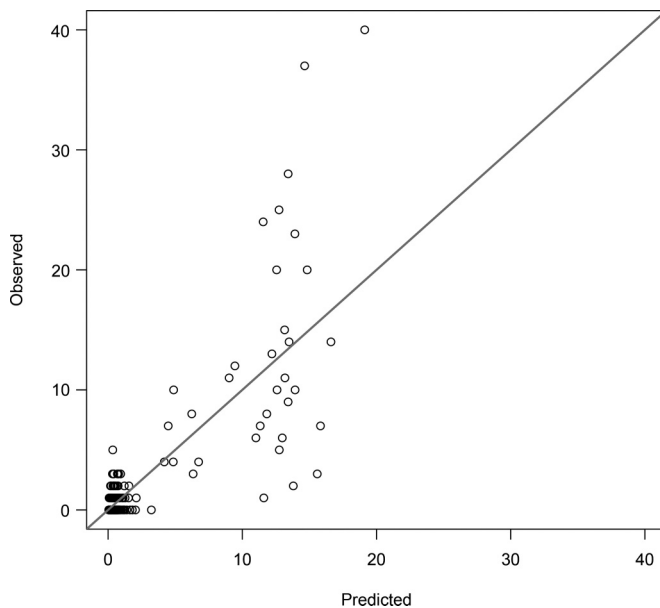
bycatch. For every 10 panels, the expected bycatch increased by approximately 30%. Total halibut catch was negatively correlated, such that higher expected bycatch was associated with hauls where less Greenland halibut was captured. Shallower waters (<1000 m) were associated with higher bycatch, whereas deeper waters (>1000 m) were associated with less bycatch; however, the credible intervals were large (Fig. 4). The spatial correlation range



**Fig. 4.** Mean and the 2.5% and 97.5% quantiles for the posterior distribution of the bathymetry smoothed regression effect.



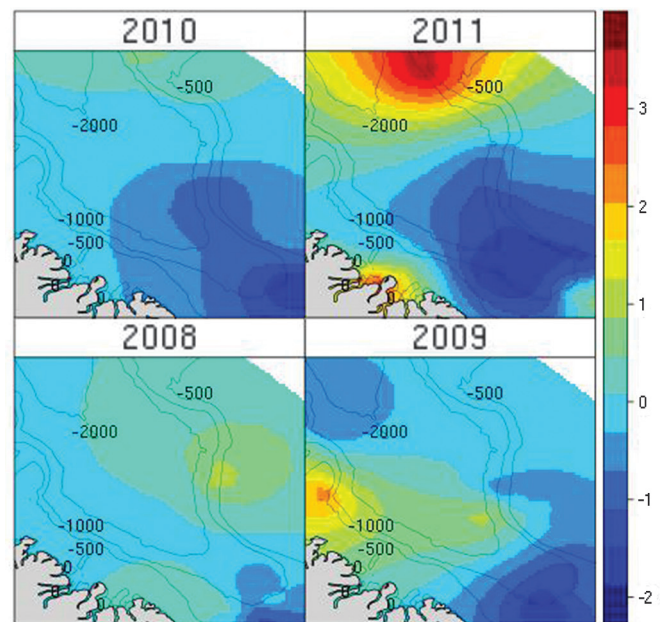
**Fig. 5.** Observed versus predicted Greenland shark bycatch (counts) of the final model, including a negative binomial zero-inflated Type 2 likelihood and m2 spatiotemporal structure.



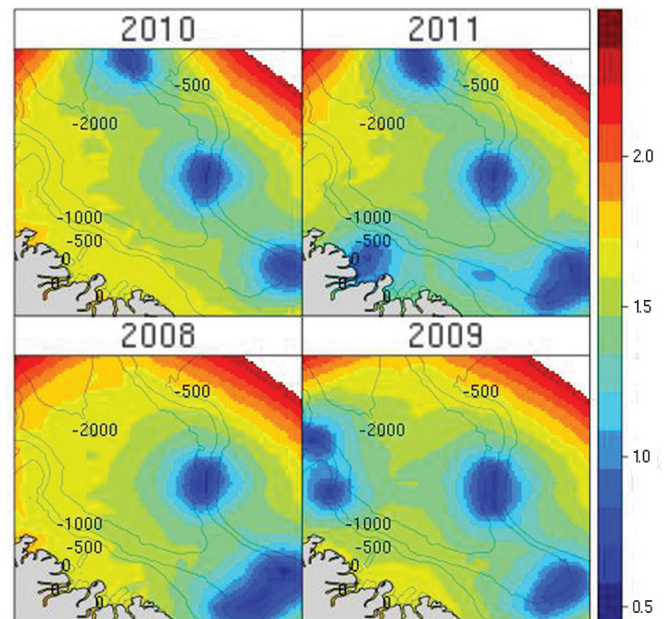
(nominal range) was 175 km with 95% credible interval (75, 292). The posterior mean of the overdispersion parameter ( $\eta$ ) was 2.03 and the 95% credible interval was (0.98, 3.25). Since this overdispersion parameter was significantly greater than zero, we can conclude that there was evidence that bycatch was clustered. The posterior mean of  $\alpha$  was 0.76 with 95% credible interval (0.4, 1.19). This indicated that the extra probability of zero was also significantly dependent on the linear predictor (i.e., greater values of the linear predictor resulted in less zeros).

Predicted versus observed bycatch of Greenland shark are shown in Fig. 5. The model was able to predict with more accuracy small to medium bycatch events (1–10 sharks per haul) but under-

**Fig. 6.** Summary of the spatial random effect (Gaussian random field) every year included in the final model with negative binomial zero-inflated Type 2 likelihood and m2 spatiotemporal structure. For the coloured version of this figure, refer to the Web site at <http://www.nrcresearchpress.com/doi/full/10.1139/cjfas-2014-0159>.



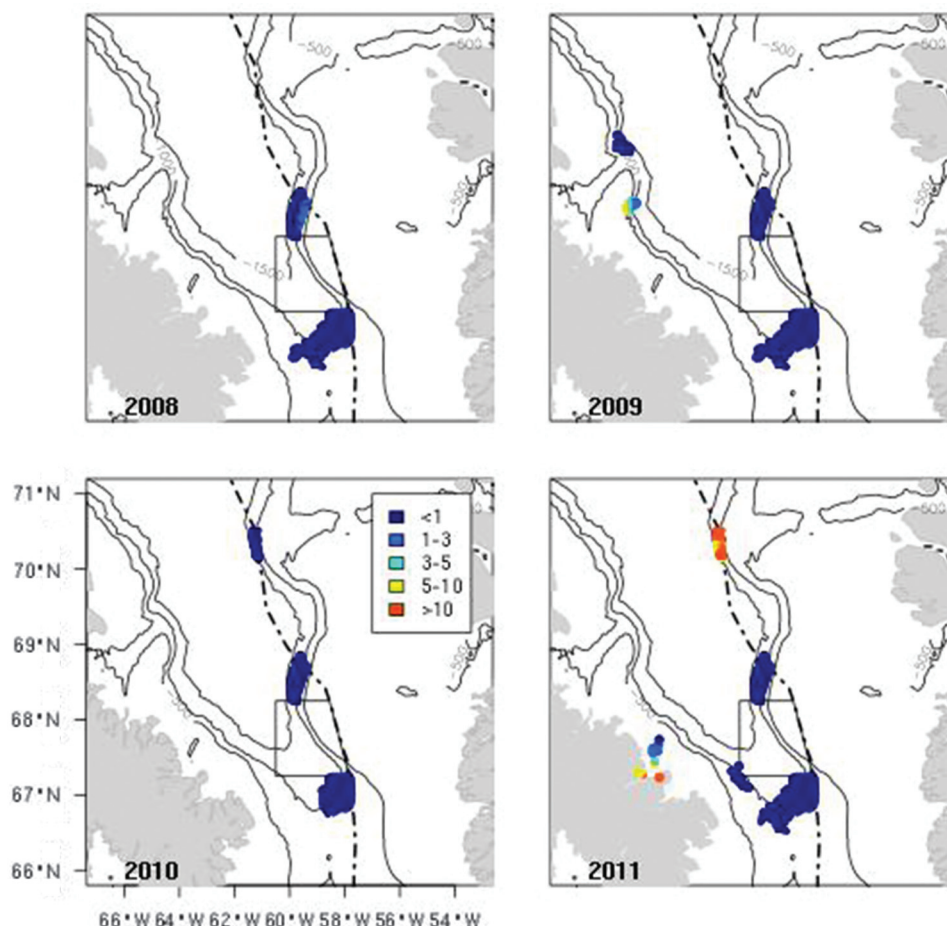
(a) Mean



(b) Standard deviation

estimated rare catch of large numbers of sharks (>20 sharks). This is expected since the zero-inflated negative binomial distribution is a generalization of the Poisson distribution, which assumes a variance equal to the mean, such that larger means are associated with larger errors. The mean and standard deviation of the yearly spatial random field are shown in Fig. 6. The final model included a different realization of the GRF every year, and accordingly, the

**Fig. 7.** Simulated posterior means of the relative risk of Greenland shark bycatch (counts) in the Baffin Bay Greenland halibut gillnet fishery for the years 2008–2011. For the coloured version of this figure, refer to the Web site at <http://www.nrcresearchpress.com/doi/full/10.1139/cjfas-2014-0159>.



spatial effects differ from year to year. The southeastern part of Baffin Bay has always been negatively correlated with Greenland shark bycatch, while the waters near the coast (fished in 2009, 2011) and the northeastern fishing ground (fished in 2010, 2011) were positively correlated with Greenland shark bycatch. Standard deviation patterns for the spatial random field are driven by the amount of information; there is reduced uncertainty where fishing occurred. Prediction of bycatch risk (expected mean counts) of Greenland shark is shown in Fig. 7. Each year is different, but high levels of bycatch remain the same throughout the year (i.e., no month effect). Shallower waters observed in 2011 and the northernmost area in 2011 were associated with nearly 100 times higher bycatch risk, calculated as the exponential differences between the mean linear predictor values of these regions:  $\exp[3.1 - (-1.5)]$ .

## Discussion

The objective of this study was to detail a computationally efficient and statistically powerful approach to analyze spatially explicit bycatch data and provide an example of its application using the case study of Greenland shark bycatch in Canadian gillnet fisheries in Baffin Bay. The first part of this discussion is concerned with the biological results and management applications, while the second part focuses on the model and modelling approach and future applications to bycatch studies.

Our results provide novel insight into the pattern of Greenland shark bycatch in gillnet fisheries. There is evidence that fishing locations less than 175 km apart are spatially correlated, hence

sharing similar underlying processes (e.g., oceanographical, biological, fisheries). In our case, most of the fishing clusters are spatially dependent, with the exception of the southernmost and northernmost fishing clusters. This suggests that spatially explicit bycatch management could potentially be considered for these two regions. Greenland shark bycatch patterns are distinct from year to year, but hotspots remain the same for the fishing season. Given that the fishing season is currently short, limited by the ice-free season during the summer months, it is sensible that bycatch hotspots remain constant throughout the year. Maps show clear evidence of bycatch hotspots (100 times higher risk), particularly in shallower areas in coastal fjords near Broughton Island as well as to the northeast of Baffin Bay. Some of these coastal areas (Scott Inlet and Sam Ford Trough) may be nursery grounds for the species (N. Hussey, unpublished data), which may explain the higher incidence of bycatch in these areas. The northeast hotspot, on the other end, appeared to be associated with larger (>200 kg) individuals (A.C. Godin, unpublished data), which were present across a broad geographic area in the region (Campana et al. 2013). The northeast hotspot was only present in 2011, although was fished as well in 2009. This area may be of some biological importance to the species, but future bycatch monitoring and tracking studies are required here. Greenland shark bycatch is clustered; where bycatch occurs, it is more likely to catch more than one shark in the same haul, which supports recent tracking data suggesting that Greenland sharks have schooling behavior (N. Hussey, unpublished data). Note that we assume the count of a single animal in hauls with observed



bycatch mass but missing count information, such that this “clustering” parameter is most likely larger than estimated.

Given the increasing commercial fishing interest in the region (Christiansen et al. 2014) and the recent expansion of gillnet fisheries, and high postrelease mortality associated with gillnets (usually >70%; e.g., Manire et al. 2001; Thorpe and Frierson 2009), precautionary management that aims at minimizing bycatch of Greenland shark is timely. Our modelling approach allows forecasting of bycatch patterns on a year-by-year basis at a high spatial resolution. In our case study, hauls set in shallower waters, with more gillnet panels, and less halibut yield resulted in more shark bycatch. Hence, sensible bycatch management options could be to limit fishing in hotspots (e.g., using time–area closure or spatially explicit discard quotas), set a maximum number of gillnet panels per haul, or limit fishing to deep waters (>1000 m). The relationship with low halibut yield associated with higher shark bycatch is less intuitive. Greenland halibut may display some avoidance behaviors when confronted with higher abundance of predators, but more likely, habitat conditions along the Baffin coast (e.g., temperature, salinity) are not as favourable for Greenland halibut as they are for Greenland sharks. The above is by no means an exhaustive list of mitigation options, but highlights those that can be directly inferred from our model results. We caution the readers that the analysis is based on a limited dataset with only 4 replicated years. The data were statistically challenging with overdispersion, zero-inflation, and discontinuous temporal and spatial domains (i.e., patchy fishing pattern), and not all fishing grounds were fished every year. Our case study was not attempting to describe the full cost–benefit of bycatch mitigations, but rather to present an effective modelling scheme for inference and predictions, which could eventually be used to quantitatively assess the effect of spatially explicit management scenarios.

Our analysis captures the variations in fishing effort as well as the correlation with bathymetry and fishery variables, in addition to the spatiotemporal random effect. This spatiotemporal random field was necessary to rigorously capture the heterogeneity of Greenland shark bycatch. In general, bycatch studies always find that spatial and temporal factors are very influential factors for bycatch distribution, while other factors are of lesser importance (e.g., Megalofonou et al. 2009; Winter et al. 2011). Hotspots are sensitive to the structure of the data; Viana et al. (2012) showed that omitting the hierarchical and spatial and temporal structure in the modelling pattern of discards in the Irish Sea greatly affects the ability to characterize hotspots. This strongly indicates that there is a need to better incorporate space (and time) within the modelling scheme when analyzing bycatch data. However, there has been a slow progress in this area, most likely due to the unique difficulties arising from the spatial structure of fisheries data and the large computational burden of fitting complex spatiotemporal models.

The proposed Bayesian hierarchical spatiotemporal models are extremely powerful and flexible, specifically when the focus of the study is to quantify the spatial magnitude and uncertainty of this process. This is because the latent field is explicitly specified in the hierarchical model, such that information can be directly extracted from the model. To our knowledge, no applied bycatch studies to date have included such random processes to better capture the spatial and temporal correlation in the data (but see Sims et al. 2008; Viana et al. 2012). This is somewhat surprising considering the fact that the use of GRFs is very popular in the field of epidemiology (Best et al. 2005), where the research interest is analogous to bycatch studies: describing the variation of a biological process over space and time.

However, it is our hope that INLA, SPDE, and their R interface will allow fisheries bycatch scientists to explore these sophisticated models, which can now be more easily fitted. INLA avoids the vast computational demands of MCMC methods, and SPDE directly models georeferenced data rather than gridding the data

first, which necessarily results in a substantial loss of information. Moreover, probability maps can easily be obtained from the posterior distribution, and results are more intuitive and interpretable (i.e., the probability is explicit) for nonstatisticians than *p* values (Wade 2000). Unfortunately, many fisheries receive very little observer coverage, mostly because of the expense associated with such programs. Hence, observer-based bycatch datasets are often of poor quality, and maps of raw bycatch rates can be misleading (Sims et al. 2008). In such cases, it is especially important to include the hierarchical structure and spatiotemporal heterogeneity to better estimate total bycatch and hotspot locations for the fleet of interest. The framework we developed here allows for this and can be extended to complex situation where multispecies bycatch occurrences are of interest (Sims et al. 2008). Moreover, since the computational cost is low and time constraints not an issue, scientists can now simulate a large number of cost–benefit scenarios with which to investigate best management options.

R-INLA is continuously evolving, greatly extending the scope of models available to applied scientists. These methods have now been applied in health sciences (Bessell et al. 2010; Li et al. 2012; Musenge et al. 2012; Wilking et al. 2012), climate research (Cameletti et al. 2012), ecology (Johnson et al. 2011; Haas et al. 2011; Holand et al. 2013; Illian et al. 2013), and recently in marine ecology research (Muñoz et al. 2012). The package interface resembles the *glm* function in R, such that scientists already familiar with these common tools should find it straightforward to use R-INLA. An advantage of the Bayesian approach is that prior knowledge can be incorporated into the model to get more precise posterior distributions. Instead of using noninformative priors (default priors in R-INLA), user-friendly commands for prior specificity are currently undergoing development (H. Rue, personal communication). Moreover, there is great interest in bycatch studies in combining datasets from different sources (e.g., oceanographic data) to better predict high incidental catch. Each subset of data may be described by a different family of distributions. Fitting models with different likelihoods is nearly impossible with most popular R packages, but is implemented in R-INLA. See Martins et al. (2013) for a complete overview of INLA’s new features.

The models that we have proposed here are not yet widely used in fisheries and aquatic sciences. To this end, we have demonstrated the merits of using Bayesian hierarchical spatiotemporal models, for bycatch studies in particular, but have gone further to present an effective way of fully implementing these models (R-INLA). Bycatch studies tend to have a strong ecological focus, seeking insight into the causal drivers of bycatch frequency and spatial distribution. However, increasing demand for mapped products for fisheries spatial planning is requiring scientists to look into new statistical techniques that can explicitly include the inherent uncertainties associated with the observations, sampling, models, and parameters, such that accurate predictions of bycatch can be obtained and included in decision-making. Under a Bayesian hierarchical model, all uncertainties (e.g., resulting from sampling bias and uncertainty due to the variability across space (and time)) are incorporated, and as such it is straightforward to obtain posterior predictive probability distributions for nonsampled areas as demonstrated in our case study. By making available both the data and the code necessary to implement the models for our particular application, we hope to facilitate the uptake of these powerful approaches by marine scientists.

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## Appendix A

### Model

In the generalized linear model (GLM) framework, we define a link function that maps the mean of the response to the linear predictor. For example, under the assumption that the response variable has a negative binomial (NB) distribution and that the bycatch at location  $s$  at time  $t$  is equal to  $k$  with dispersion parameter  $n$ , then we can write  $P[Y(s, t) = k]$  as

$$NB[k, n, \theta(s, t)] = \frac{\Gamma(k + n)}{\Gamma(n)\Gamma(k + 1)} \theta(s, t)^n [1 - \theta(s, t)]$$

The mean of the above distribution,  $\mu(s, t) = n \frac{1 - \theta(s, t)}{\theta(s, t)}$ , is linked to the linear predictor  $\eta(s, t)$  by  $\mu(s, t) = \exp[\eta(s, t)]$ , where

$$\eta(s, t) = X(s, t)\beta + f(s, t)$$

Note that in the above expression,  $X(s, t)$  is the design matrix with  $p$  fixed covariates,  $\beta = (\beta_0, \dots, \beta_p)$  is the regression coefficients vector, and  $f(s, t)$  introduces the spatiotemporal structure via random effects by considering a Gaussian random field (that is spatially and temporally correlated) as per Cameletti et al. (2012). To proceed, we consider  $f(s, t)$  to be a realization of a continuously indexed spatial process (random field) changing in time denoted by

$$\{f(s, t) : (s, t) \in D \subseteq \mathbb{R}^2 \times \mathbb{R}\}$$

These realizations are used to make inference about the process and to predict it at desired locations. Usually, we deal with a Gaussian field (GF) that is completely specified by its mean and spatiotemporal covariance function  $\text{cov}[f(s, t), f(s', t')] = \sigma^2 \text{cov}(s, t, (s', t'))$ , defined for each  $(s, t)$  and  $(s', t')$  in  $\mathbb{R}^2 \times \mathbb{R}$ . Unfortunately, implementation of a GF suffers from the so-called “big  $n$  problem” because it requires the factorization of the covariance matrix to compute the likelihood (see Diggle and Ribeiro 2007); this arises particularly with large datasets in space and time. One solution is to represent a GF as a **discretely** indexed random process (i.e., a Gaussian Markov random field, GMRF; see Rue and Held 2005). This proposal is based on the work of Lindgren et al. (2011), where an explicit link between GFs and GMRFs is proven through the use of stochastic partial differential equations (SPDE). This is the approach taken here.

By assuming a zero-inflated negative binomial distribution rather than a standard negative binomial distribution, we are allowing for additional probability of  $Y(s, t) = 0$ . For example, under the Type 2 formulation, we have

$$P[Y(s, t) = k] = p(s, t)I_{k=0} + [1 - p(s, t)] \times NB[k, n, \theta(s, t)]$$

where  $p(s, t)$  is the extra probability added to the negative binomial for  $k = 0$  (a similar relationship exists between the Poisson and zero-inflated Poisson distribution). The extra probability of zero,  $p(s, t)$ , depends on the linear predictor  $\eta(s, t)$  (i.e., the extra



probability depends on the covariates and on the spatiotemporal random effect). That is

$$p(\mathbf{s}, t) = 1 - (\exp[\eta(\mathbf{s}, t)] / \{1 + \exp[\eta(\mathbf{s}, t)]\})^\alpha$$

This means that the probability of zero bycatch at location  $\mathbf{s}$  at time  $t$  is inversely proportional to the linear predictor  $\eta(\mathbf{s}, t)$ , which makes sense because under the negative binomial distribution, for example, we have  $\mu(\mathbf{s}, t) = \exp[\eta(\mathbf{s}, t)]$  (i.e.,  $\eta(\mathbf{s}, t)$  is proportional to the expected number of sharks that were recorded as bycatch). We also have  $\pi(\mathbf{s}, t) = \exp[\eta(\mathbf{s}, t)] / \{1 + \exp[\eta(\mathbf{s}, t)]\}$  proportional to  $\eta(\mathbf{s}, t)$ , and writing this in one equation, we arrive at

$$P[Y(\mathbf{s}, t) = k] = [1 - \pi(\mathbf{s}, t)^\alpha]_{k=0} + [\pi(\mathbf{s}, t)^\alpha] \times \text{NB}[k, n, \theta(\mathbf{s}, t)]$$

The parameter  $\alpha$  can be thought of as a hyperparameter that controls both the impact of the linear predictor on the extra probability at zero as well as that for the positive counts. When  $\alpha = 0$  we have  $\pi(\mathbf{s}, t)^\alpha = 1$  and simply  $P[Y(\mathbf{s}, t) = k] = \text{NB}[k, n, \theta(\mathbf{s}, t)]$ , namely, no extra probability at zero. Because  $\pi(\mathbf{s}, t)^\alpha \in (0, 1)$  and  $\alpha > 0$  if  $\alpha$  increases,  $\pi(\mathbf{s}, t)$  also increases and the extra probability of zero decreases.

### Priors

We used the default priors and hyperparameters currently implemented in R-INLA. For further information, refer to the R-INLA documentation available on the website (<http://www.r-inla.org>). Note that this is an active area of research for the R-INLA team.

**Table A1.** Summary of the default priors used in the model tested.

$\log(n)$	$\text{loggamma}(1, 1)$
$\log(\alpha)$	$N(0.693, 1)$
$\beta_0$	$N(0, \infty)$
$\beta_j, j = 1, 2, 3$	$N(0, 1/0.001)$
$\tau_1$	$\text{Gamma}(1, 0.00005)$
$\theta_1$	$N(0, 10)$
$\theta_2$	$N(0, 1)$
$\log\left(\frac{1+\rho}{1-\rho}\right)$	$N(0, 0.15)$

For the overdispersion parameter  $n$  (size), represented as  $\log(n)$ , the prior is a  $\text{loggamma}(1, 1)$ . For the  $\alpha$  parameter on the Type 2 zero-inflated model, we assume  $N(0.693, 1)$  for  $\log(\alpha)$ .

Every components of the latent field  $\boldsymbol{\theta} = \{\beta_0, \boldsymbol{\beta}, \mathbf{f}\}$  have priors. For the smooth function of bathymetry, we assumed a random walk of order one, which is defined in terms of a Gaussian distribution  $N(0, \tau_1 \mathbf{R}_1)$ , where  $\mathbf{R}_1$  is the (fixed and known) structure matrix, and  $\tau_1$  is the precision parameter. To model the spatial correlation, we assume a spatial Matérn correlation using the SPDE approach, with parameters  $\theta_1 = \log(\tau)$  and  $\theta_2 = \log(\kappa)$  and priors defined in Lindgren and Rue (2013).

The SPDE framework allows the easy linkage of different GRFs in time and in this way develop a dynamic model where the spatial field evolves according to time-varying processes, for example, an autoregressive process. For these dynamic models (i.e., m3a, m3b, m5a, and m5b), we also had an additional correlation parameter  $\rho$  for time,  $\log\left(\frac{1+\rho}{1-\rho}\right)$ , with a Gaussian prior.