Evaluation of the impacts of different treatments of spatio-temporal variation in catch-per-unit-effort standardization models Arnaud Grüss1, 2, a*, John F. Walter III3, b, Elizabeth A. Babcock1, c , Francesca C. Forrestal4, d, James T. Thorson5, e, Matthew V. Lauretta3, f, Michael J. Schirripa3, g ¹ Department of Marine Biology and Ecology, Rosenstiel School of Marine and Atmospheric Science, University of Miami, 4600 Rickenbacker Causeway, Miami, FL, 33149, USA ²School of Aquatic and Fishery Sciences, University of Washington, Box 355020, Seattle, WA, 98105-5020, USA ³ Southeast Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, 75 Virginia Beach Drive, Miami, FL, 33149-1099, USA 4 Cooperative Institute for Marine and Atmospheric Studies*,* Rosenstiel School of Marine and Atmospheric Science, University of Miami, 4600 Rickenbacker Causeway, Miami, FL, 33149, USA ⁵Habitat and Ecosystem Process Research program, Alaska Fisheries Science Center, National Marine Fisheries Service, NOAA, 7600 Sand Point Way N.E., Seattle, WA 98115, USA *Author email addresses* 25 agruss.arnaud@gmail.com 26 bjohn.f.walter@noaa.gov 27 ebabcock@rsmas.miami.edu 28 fforrestal@rsmas.miami.edu e James.Thorson@noaa.gov ^fmatthew.lauretta@noaa.gov 31 ^gmichael.schirripa@noaa.gov *Keywords:* Catch-per-unit-effort (CPUE); standardization methods; indices of relative abundance; simulation-testing; spatio-temporal models *Funding:* This work was supported in part by a NOAA grant through the Cooperative Institute for Marine and Atmospheric Studies at the University of Miami [grant number NA150AR4320064]. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript. **Corresponding author* Dr. Arnaud Grüss School of Aquatic and Fishery Sciences University of Washington Box 355020 Seattle, WA, 98105-5020 United States of America Telephone: (01) 305 606 5696 Email: gruss.arnaud@gmail.com

ABSTRACT

Many stock assessments heavily rely on indices of relative abundance derived from fisheries-dependent catch-per-unit-effort (CPUE) data. Therefore, it is critical to evaluate different CPUE standardization methods under varying scenarios of data generating processes. Here, we evaluated nine CPUE standardization methods offering contrasting treatments of spatio-temporal variation, ranging from the basic generalized linear model (GLM) method not integrating a year-area interaction term to a sophisticated method using the spatio-temporal modeling platform VAST. We compared the performance of these methods against simulated data constructed to mimic the processes generating fisheries-dependent information for Atlantic blue marlin (*Makaira nigricans*), a common bycatch population in pelagic longline fisheries. Data were generated using a longline data simulator for different population trajectories (increasing, decreasing, and static). These data were further subsampled to mimic an observer program where trips rather than sets form the sampling frame, with or without a bias towards trips with low catch rates, which might occur if the presence of an observer alters fishing behavior to avoid bycatch. The spatio-temporal modeling platform VAST achieved the best performance in simulation, namely generally had one of the lowest biases, one of the lowest mean absolute errors (MAEs), and 50% confidence interval coverage closest to 50%. Generalized additive models accounting for spatial autocorrelation at a broad spatial scale (one of the lowest MAEs and one of the lowest biases) and, to a lesser extent, non-spatial delta-lognormal GLMs including a year-area interaction as a random effect (one of the lowest MAEs and one of the best confidence interval coverages) also performed adequately. The VAST method provided the most comprehensive and consistent treatment of spatio-temporal variation, in contrast with methods that simply weight predictions by large spatial areas, where it is critical, but difficult, to get the *a priori* spatial stratification correct before weighting. Next, we applied the CPUE standardization methods to

real data collected by the National Marine Fisheries Service Pelagic Observer Program. The indices of relative abundance predicted from real observer data were relatively similar across CPUE standardization methods for the period 1998-2017 and suggested that the blue marlin population of the Atlantic declined over the period 1998-2004 and was relatively stable afterwards. As spatio-temporal variation related to environmental changes or depletion becomes increasingly necessary to consider, greater use of spatio-temporal models for standardizing fisheries-dependent CPUE data will likely be warranted.

1. Introduction

Stock assessments, and subsequent fisheries management advice, rely largely on fisheries-dependent data, i.e., data that are collected with the assistance of fishers (Maunder and Punt, 2004). Many stock assessment models use indices of relative abundance to fit predicted fish abundances or biomasses and to estimate stock parameters (Maunder and Starr, 2003; Lynch et al., 2012). Nearly all of the indices of relative abundance employed in the stock assessments of highly migratory populations and other fish populations lacking fisheries-independent surveys are derived from fisheries-dependent catch-per-unit-effort (CPUE) data (Bishop, 2006; Maunder et al., 2006; Walter et al., 2014a). However, as fisheries do not randomly sample fish stocks, it is necessary to "standardize" fisheries-dependent CPUE data to account for confounding factors that influence catchability which, if not accounted for, could result in a non-proportional relationship between fisheries-dependent CPUE and true stock abundance (Walters, 2003; Maunder and Punt, 2004; Ye and Dennis, 2009). Various methods have been developed to perform CPUE standardization (Maunder and Punt, 2004). To improve confidence in stock assessment outcomes and the fisheries management decisions based on these outcomes, it is critical to evaluate and compare CPUE standardization methods under different scenarios about fish abundance trends and the distribution of fish and fishing effort across time and space (Bigelow and Maunder, 2007; Goodyear, 2003; Lynch et al., 2012; Campbell, 2015).

Conventional methods for standardizing CPUE data consist of fitting generalized linear models (GLMs; McCullagh and Nelder, 1989), generalized additive models (GAMs; Wood, 2006) or generalized linear mixed models (GLMMs; Breslow and Clayton, 1993) integrating covariates influencing catchability to CPUE data. Often, the GLMs used for CPUE standardization simply include fixed year and area effects (e.g., the GLMs employed for standardizing the CPUE data of highly migratory species such as blue marlin (*Makaira*

nigricans); Forrestal et al., 2017). Hereafter, this basic CPUE standardization method is referred to as the "GLM" method (Table 1). The GLMs and GLMMs used for CPUE standardization sometimes also include a year-area interaction term when it is thought that annual trends in abundance may differ among areas of the study region (e.g., Nakano, 1989; Chang, 2003; Miyabe and Takeuchi, 2003; Forrestal et al., 2017). In their seminal paper, Maunder and Punt (2004) emphasized that the appropriate way to deal with year-area interactions is either to employ GLMMs integrating the year-area interaction term as a random effect (henceforth the "GLMMint" method), or to use GLMs integrating the year-area interaction term as a fixed effect and then weight GLM predictions for the individual area strata by the surface area of these area strata (see below). Employing GLMs integrating a year-area interaction term as a fixed effect and not weighting GLM predictions for the individual area strata by the surface area of these area strata (henceforth the "GLMint" method) negates the interest of the year-area interaction term, as the index of relative abundance will then be dependent and vary upon the specific area stratum chosen (Maunder and Punt, 2004; Lynch et al., 2012; Campbell, 2015).

The CPUE standardization methods that take into account the surface area of the areas making up the study region to weight CPUE observations have been studied in detail in Campbell (2004, 2015). Hereafter, we refer to these methods as the "GLMwt" and "GLMwt.int" methods, depending on whether they integrate a fixed year-area interaction term or not. With the GLMwt and GLMwt.int methods, first, CPUE data are standardized for individual areas and years, then they are multiplied by the surface areas of their respective areas and, finally, an index of relative abundance is computed as the sum of the products of standardized CPUE data and surface areas (Campbell, 2004, 2015; Maunder and Punt, 2004). In addition to promoting the weighting of the year-area interactions by the surface area of each area of the study region, Campbell (2004, 2015) argued that weights should be assigned

to raw CPUE data based on the year-area stratum to which they belong when the number of observations in each year-area stratum varies substantially. Assigning prior weights to raw CPUE data allows for a balanced dataset for GLM-parameter estimation (Campbell, 2015). Hereafter, we refer to the CPUE standardizing methods assigning prior weights to raw CPUE data as the "GLMprwt" and "GLMprwt.int" methods, depending on whether they integrate a fixed year-area interaction term or not.

Some CPUE standardization methods offer a more sophisticated treatment of spatio-temporal variation by accounting for spatial and/or spatio-temporal autocorrelation. GAMs can account for spatial autocorrelation at a broad spatial scale through the integration of an interaction term between eastings and northings (i.e., longitude and latitude expressed in UTM coordinates), and for spatio-temporal autocorrelation at a broad spatial scale by nesting 143 the year effect within the interaction term between eastings and northings (Su et al., 2011; Grüss et al., 2016, 2019). Hereafter, we refer to the CPUE standardizing methods using GAMs accounting for spatial and/or spatio-temporal autocorrelation as the "GAM" and "GAMint" methods, depending on whether they account for spatio-temporal autocorrelation at a broad spatial scale or not. Spatio-temporal models take a step further and exploit the property of spatial and spatio-temporal structure at a fine spatial scale to then predict variables of interest (Thorson et al., 2015; Grüss et al., 2017). Recent years have seen the emergence of spatio-temporal modeling methods for standardizing CPUE data (e.g., Pereira et al., 2012; Berg et al., 2014; Walter et al., 2014b; Thorson et al., 2015; Cao et al., 2017). Due to their properties, spatio-temporal models are particularly compelling for standardizing the CPUE data obtained from observers, i.e., the trained personnel placed on fishing boats to collect data. In fact, the data collected by observers are often clustered since they tend to be repeated samples from the same fishing boats at similar sites, and they cover only a limited spatial and temporal extent of the fishery of interest (Beerkircher et al., 2002; Walter et al., 2014b).

Furthermore, observer data could have sampling bias, as fishing boats with observers on board may try to avoid locations where bycatch is high (Benoît and Allard, 2009; Walter et al., 2014b), above and beyond the inherent potential biases of fisheries-dependent data.

Data simulators are valuable tools for evaluating CPUE standardization methods as they allow for a known true annual trend in fish abundance (Lynch et al., 2012; Forrestal et al., 2019b). Over recent years, several simulation analyses have been carried out for evaluating and comparing CPUE standardization methods (e.g., Carruthers et al., 2010, 2011; Lynch et al., 2012; Pereira et al., 2012; Ono et al., 2015; Thorson et al., 2016; Forrestal et al., 2017, 2019b). For example, Carruthers et al. (2011) employed spatial production models to simulate theoretical commercial fisheries, and then compared the performance of variants of the GLM method applied to CPUE data from the theoretical commercial fisheries. Another example is that of Lynch et al. (2012), who developed a data simulator for running a comparison of the accuracy of the GLM method and an habitat-based standardization method applied to CPUE data from the Atlantic Japanese longline fishery. No published study has utilized simulation analysis to compare the performance of CPUE standardization methods offering contrasting treatments of spatio-temporal variation (e.g., GLM vs. GLMMint vs. GAM vs. spatio-temporal method).

In this study, we evaluated and compared nine CPUE standardization methods offering contrasting treatments of spatio-temporal variation (Table 1), ranging from the basic GLM method to a sophisticated method using the Vector Autoregressive Spatio-temporal Model (henceforth the "VAST" method; Thorson, 2019). We applied these nine CPUE standardization methods to Atlantic blue marlin CPUE data collected by fisheries observers. Blue marlin is a large, highly migratory species of substantial importance to recreational and artisanal fisheries and primarily a bycatch species of open-ocean longline fleets (Sharma et al., 2017). Firstly, we evaluated the nine CPUE standardization methods utilizing simulated

data from the U.S. pelagic longline fishery developed with the LLSIM data simulator (Forrestal et al., 2017; Goodyear et al., 2017). Next, the CPUE data from the simulated pelagic longline fishery were subsampled to mimic sampling by an observer program. We either randomly subsampled 10% of the trips, or we selected 10% of the trips such that trips with lower than average catch rate were selected in a higher proportion, resulting in a biased sample that might reflect the process of an observer bias, where fishing trips with observers tend to avoid locations with high bycatch rates. We then applied the CPUE standardization methods to the subsampled CPUE data in a design where the model developer (Arnaud Grüss) did not know any details regarding the LLSIM simulations and the environmental conditions in the system simulated in LLSIM. Secondly, we applied the contrasting CPUE standardization methods to CPUE data collected by the National Marine Fisheries Service (NMFS) Pelagic Observer Program (Beerkircher et al., 2002) over the period 1992-2017.

2. Material and methods

2.1. Study region

Our study region is the portion of the North Atlantic shown in Fig. 1. This region encompasses the ten NMFS areas defined for stock assessments of the International Commission for the Conservation of Atlantic Tunas (ICCAT) (Fig. 1): (1) the Gulf of Mexico (GOM); (2) the Mid Atlantic Bight (MAB); (3) the South Atlantic Bight (SAB); (4) Florida East Coast (FEC); (5) the Caribbean (CAR); (6) the Northeast Coastal area (NEC); (7) the Sargasso area (SAR); (8) the Northeast Distant area (NED); (9) the North Central Atlantic (NCA); and (10) the Offshore South area (OFS). To be able to utilize the GAM and VAST 204 methods, we produced a 1° x 1° spatial grid covering the entire study region, and we

estimated the surface area of the cells of that spatial grid. The spatial grid for the North Atlantic includes 3,079 cells.

2.2. LLSIM data

In the present study, we employed the longline CPUE data simulator LLSIM (Forrestal et al., 2017, 2019a; Goodyear, 2017; Goodyear et al., 2017). In brief, the core of LLSIM is the computation of the catch of the U.S. pelagic longline fishery on a single hook of a longline set (Forrestal et al., 2017). Each hook is characterized by a depth distribution and a geographical position (latitude, and longitude) and is associated with a specific year, month, fraction of daylight and position along the longline. All the characteristics of the hook are associated with the individual longline set. LLSIM simulates the catch of the pelagic longline fishery as a stochastic process for each of the hooks of each longline set. The region covered 217 by LLSIM extends from -35 \degree latitude to 55 \degree and from -95 \degree longitude to 20 \degree ; however, only LLSIM data for the portion of that region shown in Fig. 1 were considered in this study. The 219 region covered by LLSIM is broken down into 1° x 1° cells, which each includes 46 depth data. To make computations, LLSIM integrates fish population size, a gear coefficient and a 221 habitat coefficient for each longline set. In each of the 1° x 1° cells, the habitat coefficient integrates the hook-depth probabilities with fish relative density in each of the 46 depth strata apportioned by the fraction of the longline sets that operate in hours of daylight and darkness. The hook-depth probabilities are derived from the measurements made by time-depth recorders attached to longlines of the U.S. pelagic longline fleet (Goodyear, 2017). The three-dimensional patterns of fish density considered by LLSIM come from a volume weighted habitat suitability model developed in Goodyear (2016). Goodyear (2016)'s habitat suitability model uses information on blue marlin oxygen tolerance from Brill (1994)'s study, as well as

temperature utilization and diel ΔT patterns from tagged blue marlins, to determine the three-dimensional patterns of blue marlin density from environmental data from a coupled ocean-biogeochemical model.

The LLSIM data employed in the present study were for three virtual blue marlin populations that had the exact same characteristics except that one maintained a constant abundance over time (Population 1), one was generally declining (Population 2) and the third one was generally increasing (Population 3) (Figs. 2a-c). LLSIM provided us with data for 294,305 longline sets for the U.S. pelagic longline fishery for each of the three populations, which covered the period 1987-2015. Catch was expressed as the number of blue marlins caught during the longline set, and fishing effort was expressed as the number of hooks in the 239 set. CPUE was then the number of blue marlins caught per 1,000 hooks. In addition to catch and fishing effort data, LLSIM provided values for a number of parameters, including year, season, the type of hook used, the number of light sticks used, the type of bait used, and the number of hooks between floats (Table 2). NMFS areas were assigned based on the latitude and longitude associated with each simulated longline set.

LLSIM offers some advantages over data simulators employed in previous CPUE standardization studies. Previous CPUE standardization studies generally used simplified data simulators that closely resembled the mechanics of the CPUE standardization models (e.g., Lynch et al., 2012; Carruthers et al., 2010). By contrast, LLSIM is based on conditioning of observed catch rates to complex layers of oceanographic data, real-world fleet dynamics and fisheries-dependent variables. Thus, the underlying dynamics of LLSIM are governed by "unobservable", non-linear environmental processes that are far more complex than the subset of information that is communicated to CPUE standardization models, making the simulation-evaluation process with LLSIM less idealized. Furthermore, the common challenges, such as violation of independence between fishing sets, are captured (at least spatially) by LLSIM.

The evaluation component of the simulation-evaluation process conducted in this study was such that the model developer (Arnaud Grüss) did not know any details regarding the LLSIM simulations and the environmental conditions in the system simulated in LLSIM.

2.3. CPUE standardization methods considered in this study

In this study, we considered nine CPUE standardization methods (Table 1), which we describe below. The raw CPUE data from LLSIM included many zeros. In this context, it was appropriate to fit delta GLMs, GAMs and GLMMs (Lo et al., 1992; Stefánsson, 1996; Barry and Welsh, 2002). The delta approach involves modeling the probability of encounter of a fish population assuming a binomial distribution, and the mean CPUE when fish are encountered assuming a lognormal distribution, and then multiplying the results together to obtain an overall standardized CPUE (Lo et al., 1992; Grüss et al., 2014). Future studies could explore other variants of the delta approach (e.g., Thorson, 2017), though we hypothesize that any improvements in statistical efficiency will affect CPUE standardization methods similarly and will not affect relative performance among the nine standardization methods explored in this study. Moreover, for all CPUE standardization methods, no model selection was conducted as all the covariates influencing catchability (henceforth "catchability covariates") were deemed likely to influence CPUE.

2.3.1. The GLM, GLMint and GLMMint methods

The delta GLMs we developed for the GLM method estimated terms for year and area as fixed effects and integrated the fixed effects of catchability covariates and no year-area

interaction term. We fitted both the binomial GLMs and the lognormal GLMs making up these delta GLMs in the R environment, following the equation:

developed for the GLM method, except that they also included a year-area interaction term 287 (*year* $*$ *area*) as a fixed effect. We fitted both the binomial GLMs and the lognormal GLMs making up these delta GLMs in the R environment, following the equation:

 $g(\eta) = year + season + area + hook + bait + light + hbf + year * area$ (2) The delta GLMMs we developed for the GLMMint method were similar to the delta 291 GLMs developed for the GLMint method, except that the $year * area$ term was included in the binomial and lognormal GLMMs as a random rather than as a fixed effect. The binomial and lognormal GLMMs developed for the GLMint method were fitted using the "glmer" function in the "lme4" library for R (Bates et al., 2015).

For the GLM, GLMint and GLMMint methods, following Punt et al. (2000) and Ono et al. (2015), we predicted mean annual probability of fish encounter and mean annual CPUE when fish are encountered with the fitted binomial and lognormal GLMs or GLMMs, using the levels of the season, area, hook, bait, light and hbf factors with the largest sample size

(Table 2). Then, the predicted mean probability of fish encounter was multiplied by the predicted mean annual CPUE when fish are encountered to generate the predicted total CPUE in each year. The standard errors of the predictions of the delta GLMs or GLMMs were computed from the standard errors of the predictions of the binomial and lognormal GLMs or GLMMs using the formula presented in Lo et al. (1992).

It is worth reiterating that employing the GLMint method negates the interest of the year-area interaction term, as a specific area stratum then needs to be chosen to construct an index of relative abundance (Maunder and Punt, 2004; Lynch et al., 2012; Campbell, 2015). Therefore, it would not be relevant to use the GLMint method evaluated here in the real world; we considered the GLMint method here solely to explore the consequences of integrating the year-area interaction effect in a GLM as a fixed vs. as a random effect.

2.3.2. The GLMwt, GLMwt.int, GLMMprwt and GLMprwt.int methods

The GLMwt and GLMwt.int methods consisted of fitting binomial and lognormal 313 GLMs with and without a fixed *year* $*$ *area* term following, respectively, Eqs. (1) and (2), and then making a series of calculations rather than solely multiplying the predictions of binomial and lognormal GLMs together (see below). The GLMprwt and GLMprwt.int methods were similar, except that they assigned prior weights to the data based on the year-area stratum to which the data belonged. Following Campbell (2015), when the GLMprwt and 318 GLMprwt.int methods were employed, a weight $weight_{v,a}$ was assigned to an observation for year *y* and area *a* as follows:

$$
weight_{y,a} = \frac{Nobs}{Nstrata} \cdot \frac{1}{n_{y,a}} \tag{3}
$$

320 where $n_{y,a}$ is the number of observations for year *y* and area *a*; *Nobs* is the total number of 321 observations; and *Nstrata* is the total number of strata considered, with *Nstrata* = $Ny \times$ Na , where Ny is the number of years considered (29 when working with LLSIM data; 26 323 when working with real observer data) and Na is the number of areas considered (10). When the GLMwt, GLMwt.int, GLMprwt and GLMprwt.int methods are utilized, the estimation of annual CPUEs takes place in three steps (Campbell, 2004, 2015). First, probabilities of encounter are predicted with fitted binomial GLMs and CPUEs when fish are encountered are predicted with fitted lognormal GLMs for each year, each season and each area, using the levels of the hook, bait, light and hbf factors with the largest sample size (Table 2; Punt et al., 2000; Ono et al., 2015). Second, CPUE for year *y* and season *s* is estimated as follows:

$$
CPUE_{y,s} = \sum_{a=1}^{Na} SA_a \, prob_{y,s,a} u_{y,s,a}
$$
\n⁽⁴⁾

332 where $prob_{v,s,a}$ is the probability of encounter in year *y*, season *s* and area *a* predicted by the 333 binomial GLM; $u_{v,s,a}$ is the CPUE when fish are encountered in year *y*, season *s* and area *a* 334 predicted by the lognormal GLM; and SA_a is the surface area (in km²) of area *a*. Third and 335 lastly, annual CPUEs are computed from CPUE estimates for each year and season as 336 follows:

331

$$
CPUE_y = \frac{1}{Ns} \sum_{s=1}^{Ns} CPUE_{y,s}
$$
\n⁽⁵⁾

337 where Ns is the number of seasons (4). We computed the standard errors of these annual CPUEs using the formula developed in Campbell (2015). Note that a geometric mean could be employed in lieu of the arithmetic mean in Eq. (5); the advantage of geometric mean is that it is scale invariant and less sensitive to outliers (Campbell, 2015).

2.3.3. The GAM method

Regarding the GAM method, we fitted both the binomial GAMs and the lognormal GAMs making up the delta GAMs using the R package "mgcv" (Wood and Augustin, 2002; Wood, 2006), following the equation:

$$
g(\eta) = year + s(X, Y) + season + hook + bait + light + hbf
$$
 (6)

346 where $s(X, Y)$ is product smooth fitted to eastings (X) and northings (Y) , which replaces the fixed effect of area and represents spatial autocorrelation at a broad spatial scale (Grüss et al., 2016, 2019).

As for the previous models, we predicted annual probability of fish encounter and annual CPUE when fish are encountered for the cells of the spatial grid for the North Atlantic with the fitted binomial and lognormal GAMs, using the levels of the season, hook, bait, light and hbf factors with the largest sample size (Table 2; Punt et al., 2000; Ono et al., 2015; Grüss et al., 2018b, 2018c). We then calculated mean annual probabilities of fish encounter over all cells of the spatial grid for the North Atlantic and mean annual CPUEs when fish are encountered over all cells of the spatial grid. Finally, these two results were multiplied together to predict total CPUEs in each year. We computed the standard errors of mean annual probabilities of fish encounter and mean annual CPUEs when fish are encountered using Marra and Wood (2012)'s method, which accounts for covariance between predictions for the individual cells of the spatial grid. We then employed the formula presented in Lo et al. (1992) to compute the standard errors of delta GAM predictions from the standard errors of mean annual probabilities of fish encounter and mean annual CPUEs when fish are encountered.

The VAST method consisted of developing spatio-temporal delta GLMMs implemented using the R package "VAST" (Thorson, 2019), which is publicly available online (https://github.com/James-Thorson/VAST). Below, we describe the estimation of probabilities of encounter and CPUEs when fish are encountered with VAST. Additional details can be found in Appendix A1. One detail to highlight here is that, for computational reasons, 250 knots were defined in VAST via the application of a *k*-means algorithm (Thorson et al., 2015) to the locations of raw (observed) CPUE data. These knots are allocated spatially with a density proportional to sampling intensity, and indices of relative abundance are obtained by summing over the annual standardized CPUEs estimated for each knot. Another detail to highlight is that VAST integrates across the coefficients of the catchability covariates by implementing restricted maximum likelihood (REML) estimation (Grüss et al., 2018a, 376 2018d).

With VAST, probability of encounter was approximated using a spatio-temporal binomial GLMM with a logit link function and linear predictors, including a Gaussian Markov random field representing spatio-temporal variation in probability of encounter and another Gaussian Markov random field representing spatial variation in probability of 381 encounter. The spatio-temporal binomial GLMM predicts probability of encounter p_i at site $s(i)$ as follows:

$$
p_{i} = logit^{-1}\left(\sum_{y=1}^{Ny} \beta_{y}^{(p)} YEAR_{i,y} + \sum_{season=1}^{Nseason} \gamma_{season}^{(p)} SEASON_{i,season}
$$

+
$$
\sum_{\substack{hook=1 \text{Nlooks} \\ hook=1}}^{Nhooks} \delta_{hook}^{(p)} HOOK_{i,hook} + \sum_{\substack{bait=1 \text{Nloits} \\ hnhbf s}}^{Nbaits} \zeta_{bait}^{(p)} BAIT_{i,bait}
$$

+
$$
\sum_{\substack{Nilghts \\ light=1}}^{Nfup} \eta_{light}^{(p)} LIGHT_{i,light} + \sum_{hbf=1}^{Nhbf s} \theta_{hbf}^{(p)} HBF_{i,hbf} + \varepsilon_{J(i),Y(i)}^{(p)} + \omega_{J(i)}^{(p)}\right)
$$
(7)

383 where $YEAR_{i,y}$ is a design matrix where $YEAR_{i,y}$ is one for the year y during which sample *i* 384 was collected and zero otherwise; $\beta_y^{(p)}$ is an intercept that varies among years; 385 SEASON_{i, season} is a design matrix where $SEASON_{i, season}$ is one for the season level 386 associated with sample *i* and zero otherwise; $\gamma_{season}^{(p)}$ is a season effect on probability of 387 encounter (where $\gamma_{season}^{(p)} = 0$ for the season level with the largest sample size for a 388 population, where this constraint is imposed for identifiability of all year effects $\beta_y^{(p)}$; 389 Nseasons is the number of season levels (4); $HOOK_{i,hook}$ is a design matrix where 390 *HOOK*_{*i,hook*} is one for the hook level associated with sample *i* and zero otherwise; $\delta_{hook}^{(p)}$ is a 391 hook effect on probability of encounter (where $\delta_{hook}^{(p)} = 0$ for the hook level with the largest 392 sample size for a population, where this constraint is imposed for identifiability of all year 393 effects $\beta_{y}^{(p)}$; *Nhooks* is the number of hook levels (3); *BAIT*_{*i,bait*} is a design matrix where 394 *BAIT*_{*i,bait*} is one for the bait level associated with sample *i* and zero otherwise; $\zeta_{bait}^{(p)}$ is a bait 395 effect on probability of encounter (where $\zeta_{bait}^{(p)} = 0$ for the bait level with the largest sample 396 size for a population, where this constraint is imposed for identifiability of all year effects 397 $\beta_y^{(p)}$; *Nbaits* is the number of bait levels (4 when working with LSSIM data); *LIGHT*_{*i,light*} is a design matrix where $LIGHT_{i,light}$ is one for the light level associated with sample *i* and zero 399 otherwise; $\eta_{light}^{(p)}$ is a light effect on probability of encounter (where $\eta_{light}^{(p)} = 0$ for the light 400 level with the largest sample size for a population, where this constraint is imposed for 401 identifiability of all year effects $\beta_y^{(p)}$; *Nlights* is the number of light levels (4); $HBF_{i,hbf}$ is a 402 design matrix where $HBF_{i,hbf}$ is one for the hbf level associated with sample *i* and zero 403 otherwise; $\theta_{hbf}^{(p)}$ is an hbf effect on probability of encounter (where $\theta_{hbf}^{(p)} = 0$ for the hbf level 404 with the largest sample size for a population, where this constraint is imposed for 405 identifiability of all year effects $\beta_{y}^{(p)}$; *Nhbfs* is the number of hbf levels (5 when working

with LSSIM data; 4 when working with real observer data); $\varepsilon_{J(i),Y(i)}^{(p)}$ 406 with LSSIM data; 4 when working with real observer data); $\varepsilon_{(i)}^{(p)}$ is the spatially correlated 407 variability in probability of encounter at the knot *J(i)*, which is the nearest knot to sample *i*, in year $Y(i)$ in which sample *i* was collected; and $\omega_{J(i)}^{(p)}$ 408 year $Y(i)$ in which sample *i* was collected; and $\omega_{I(i)}^{(p)}$ is the spatially correlated variability in probability of encounter at the knot $J(i)$ that is persistent among years. Both $\varepsilon_{J(i),Y(i)}^{(p)}$ $L_{(i),Y(i)}^{(p)}$ and $\omega_{J(i)}^{(p)}$ 409 – probability of encounter at the knot $J(i)$ that is persistent among years. Both $\varepsilon_{i}^{(p)}$ and $\omega_{i}^{(p)}$ 410 are random effects.

Similarly, with VAST, positive catch rate was approximated using a spatio-temporal lognormal GLMM with a log link function and linear predictors, including a Gaussian Markov random field representing spatio-temporal variation in positive catch rate and another Gaussian Markov random field representing spatial variation in positive catch rate. The 415 spatio-temporal lognormal GLMM predicts positive catch rate λ_i at site $s(i)$ as follows:

$$
\lambda_{i} = exp \left(\sum_{y=1}^{Ny} \beta_{y}^{(\lambda)} Y E A R_{i,y} + \sum_{season=1}^{Nseason} \gamma_{season}^{(\lambda)} SEASON_{i,season} + \sum_{Nhooks}^{Nbaits} \delta_{hook}^{(\lambda)} HOOK_{i,hook} + \sum_{\substack{hook=1 \text{Nlights} \\ Nibpts}}^{Nbooks} \delta_{nook}^{(\lambda)} HOOK_{i,hook} + \sum_{\substack{hait=1 \text{Nhbfs} \\ Nhbfs}}^{Nbaits} \zeta_{bait}^{(\lambda)} B A I T_{i,bait}
$$
\n
$$
+ \sum_{light=1}^{Nlook=1} \eta_{light}^{(\lambda)} L I G H T_{i,light} + \sum_{hbf=1}^{Nhbfs} \theta_{hbf}^{(\lambda)} H B F_{i,hbf} + \varepsilon_{J(i),Y(i)}^{(\lambda)} + \omega_{J(i)}^{(\lambda)} \right)
$$
\n(8)

416 where the parameters on the right side of Eq. (8) have the same meaning and characteristics as 417 the parameters on the right side of Eq. (7), except that they apply to log-catch rate.

To make predictions with fitted spatio-temporal GLMMs, we assumed that the Gaussian Markov random field in each cell of the spatial grid for the North Atlantic was equal 420 to the value of the random field at the closest knot. Consequently, the surface area SA_i associated with knot *j* was calculated as the number of cells of the spatial grid for the North Atlantic associated with knot *j* times the surface areas of these cells. It was then possible to calculate total CPUE in year *y* across our entire study region as follows:

$$
\widehat{CPUE}_{y} = \sum_{j=1}^{n_j} SA_j \logit^{-1} \left(\widehat{\beta}_{y}^{(p)} YEAR_{j,y} + \widehat{\varepsilon}_{j,y}^{(p)} + \widehat{\omega}_{j}^{(p)} \right).
$$

\n
$$
\exp \left(\widehat{\beta}_{y}^{(\lambda)} YEAR_{j,y} + \widehat{\varepsilon}_{j,y}^{(\lambda)} + \widehat{\omega}_{j}^{(\lambda)} \right)
$$
\n(9)

where $\hat{\beta}_y^{\setminus}$ $\hat{\beta}_y^{(p)}$ and $\hat{\beta}_y^{(p)}$ 424 where $\hat{\beta}_{v}^{(p)}$ and $\hat{\beta}_{v}^{(\lambda)}$ are fixed effects of year estimated through maximum likelihood 425 estimation; and $\hat{\epsilon}_{j,y}^{(p)}$, $\hat{\omega}_j^{(p)}$, $\hat{\epsilon}_{j,y}^{(\lambda)}$ and $\hat{\omega}_j^{(\lambda)}$ are random effects set to the value that maximizes 426 the joint likelihood conditional on the estimated value of fixed effects of year (Thorson et al., 427 2015). The standard errors of the annual CPUEs predicted by the spatio-temporal GLMMs 428 were computed using a generalization of the delta method (Thorson et al., 2015; Thorson and 429 Barnett, 2017).

430

431 *2.4. Scenarios considered in this study*

Three scenarios were considered for each of the three virtual blue marlin populations: (1) the "ALL" scenario, where all LLSIM data (i.e., the 294,305 simulated longline sets) were employed to standardize CPUE data; (2) the "10%" scenario, where 10% of the fishing trips simulated by LLSIM were randomly selected, and (3) the "10%BIAS" scenario, which consisted of selecting 10% of the fishing trips simulated by LLSIM such that trips with lower than average catch rate were selected in a higher proportion, resulting in a biased sample that might reflect the process of an observer bias where fishing trips with observers operate differently than ones without observers to avoid bycatch species (e.g., sea turtles). In the real world, the percentage of trips of the U.S. pelagic longline fishery sampled by observers each year varies from one year to the next, but is around 10% on average (Beerkircher et al., 2002).

442 To build the 10% and 10%BIAS scenarios, we needed to work with fishing trips. 443 However, LLSIM provided us with simulated longline sets. Therefore, we needed to assign 444 each of the LLSIM longline sets to fishing trips, such that each fishing trip would have

longline sets around the same time and location. To generate fishing trips with these characteristics, we assigned fishing sets that were in the same year, month and NMFS area to the same fishing trip. This yielded a total of 18,870 fishing trips, with a median of 6 sets per trip and a maximum of 329. Since, in the real world, the number of longline sets per vessel month in the U.S. pelagic longline fishery has a median of 8 (range 1-40; Beerkircher et al., 2002), we broke up the fishing trips that had more than 40 longline sets into trips with 8 sets each, counting from the first longline set in the dataset, so as to maintain any structure in the data that might be incorporated in longline set order. The resulting dataset had a total of 37,327 fishing trips with a median of 8 longline sets each (range 1-40).

As mentioned above, the three virtual blue marlin populations had the exact same characteristics except that one maintained a constant abundance over time, one was generally 456 declining and the third one was generally increasing. Therefore, with respect to the 10% 457 scenario, it was possible to generate subsamples for the three virtual blue marlin populations together. Since the generation of subsamples for the 10% scenario is a stochastic process, we produced five subsamples for the 10% scenario so as to run five replicates of the scenario.

To obtain subsamples to explore the 10%BIAS scenarios, we randomly drew 10% of fishing trips with a probability of sampling a particular trip (*prob*) generated from the equation:

$$
logit(prob) = a + b \times C \tag{10}
$$

where *C* is here the total catch of blue marlin in the fishing trip under consideration. The parameters *a* and *b* were set so that the probability of sampling a given fishing trip was 0.1 at the mean catch level and decreased to 0.01 at the maximum catch level. This gave an overall sampling effort of around 10% of fishing trips, with a significantly lower probability of 467 sampling fishing trips that catch more blue marlins. Since the catches varied between the three virtual blue marlin populations, we generated different samples for each population.

Furthermore, since the generation of subsamples for the 10%BIAS scenario is a stochastic

process, for each virtual blue marlin population, we produced five subsamples for the

10%BIAS scenario so as to run five replicates of the scenario.

Following the best practices provided in Campbell (2015), for the ALL scenario and all replicates of the 10% and 10%BIAS scenarios, we constructed a "Walters' table" from the raw CPUE data with a row for each year and a column for each area (Table 3 and Table A2). The Walters' table for the ALL scenario showed that there were observations in all year-area strata (Table 3). By contrast, there were missing observations in many year-area strata for all 477 replicates of the 10% and 10%BIAS scenarios (Table A2). Therefore, under the 10% and 10%BIAS scenarios, it was necessary to impute CPUE values in unobserved year-area strata when working with the GLMwt.int and GLMprwt.int methods (Walters, 2003; Carruthers et al., 2010). There is no standard method for imputing CPUE values in unobserved year-area strata (Walters, 2003; Carruthers et al., 2010, 2011; Campbell, 2015). In this study, we used one of the imputation methods employed in Campbell (2015). This method consisted of imputing CPUE values in unobserved year-area strata by directly using the predictions made for those year-area strata by simpler GLMs not integrating a year-area interaction term. To illustrate the usefulness of spatio-temporal models beyond CPUE standardization, we estimated the eastward and northward centers of gravity (COGs) of the virtual blue marlin

populations and their effective area occupied with VAST when considering the ALL scenario (which uses all of the LLSIM data). The computation of COGs and effective areas occupied is described in Appendix A1.

2.5. Evaluation and comparison of the CPUE standardization methods

The first step in evaluating and comparing CPUE standardization methods was to plot the normalized estimated annual trend in CPUE for each method. Normalized CPUEs estimated for each standardization method were then compared amongst one another, as well as to the normalized virtual blue marlin population abundance (true abundance) (Figs. 2a-c) and to the normalized CPUEs calculated directly from the LLSIM data (nominal CPUEs) for each virtual blue marlin population. Normalization was carried out in all cases by dividing mean annual CPUEs or abundance by their mean value over the period from 1987-2015. Then, we assessed the performance of the CPUE standardization methods for each virtual blue marlin population and scenario based on three metrics: (1) a bias metric described below; (2) mean absolute error (MAE), which quantifies error in the estimated CPUEs; and (3) a confidence coverage metric described below.

503 The bias metric we considered was the coefficient \boldsymbol{d} of the following linear model (Thorson et al., 2015):

$$
\widehat{CPUE}_y = c + d \times I_y
$$

\n
$$
\varepsilon_y \sim Normal(0, \sigma_{\varepsilon}^2)
$$
\n(11)

505 where *c* is an intercept; \widehat{CPUE}_y is the normalized estimated CPUE in year *y*; I_y is the 506 normalized true abundance in year *y*; ε_v is the "estimation error" in the normalized estimated 507 CPUE; and σ_{ε}^2 is the variance of ε . A d of 1 is indicative that changes in true abundance are 508 reflected accurately by the estimated CPUE, while a d greater than 1 (lower than 1) indicates 509 that \widehat{CPU}_y underestimates (overestimates) changes in true abundance (Wilberg et al., 2010; Thorson et al., 2015). It was not possible to calculate bias for Population 1, whose true abundance is constant over time (Fig. 2a).

MAE was calculated for each virtual blue marlin population and scenario as (Willmott and Matsuura, 2005; Stow et al., 2009):

$$
MAE = \sum_{y=1}^{Ny} \frac{|C\widehat{PUE}_y - I_y|}{Ny}
$$
\n(12)

514 where Ny is the number of years considered (29). The higher the MAE, the greater the error in the estimated CPUEs (Stow et al., 2009).

Finally, for each virtual blue marlin population, scenario and standardization method, coverage was calculated as the percentage of years over the period 1987-2015 that the 50% confidence interval of the normalized estimated CPUE index contained the normalized true abundance (Agresti and Coull, 1998; Newcombe, 1998; Brown et al., 2001). We chose a nominal probability of 50% rather than 90 or 95% confidence intervals to provide greater contrast in performance. Well-performing confidence intervals are ones where the nominal (predetermined) probability equals the actual proportion of replicates where the confidence interval contains the true value. In our case, coverage values >50% indicate that the confidence intervals are too wide and coverage values <50% indicate that the confidence intervals are too narrow (Bolker, 2008; Johnson et al., 2016).

2.6. Application of the CPUE standardization methods to real observer data

All CPUE standardization methods with the exception of the GLMint method were also applied to real observer data collected by the NMFS Pelagic Observer Program (Beerkircher et al., 2002) over the period 1992-2017. We did not consider the GLMint method, since, as explained earlier, this method is not relevant for standardizing CPUE data in the real world (Maunder and Punt, 2004; Lynch et al., 2012; Campbell, 2015). As was the case for the analysis conducted with LLSIM data, we worked with CPUE per set expressed as the number of blue marlins caught per number of hooks set. The catchability covariates considered for the application to real observer data were identical to those considered when

working with LLSIM data, except bait, which was excluded as a factor as more than 99% of the observations were with dead bait (Table 4). The "Walters' table" we constructed from the raw NMFS Pelagic Observer Program CPUE data showed that were missing observations in 40 year-area strata (i.e., in around 15.4% of the year-area strata; Table 5). Therefore, when working with the GLMwt.int and GLMprwt.int methods, we used one of the imputation methods employed in Campbell (2015), which consisted of imputing CPUE values in the unobserved year-area strata by directly using the predictions made for those year-area strata by simpler GLMs not integrating a year-area interaction term. When working with VAST, we also estimated the eastward and northward COGs and the effective area occupied of the blue marlin population, following the methodology described in Appendix A1.

3. Results

3.1. COGs and effective area occupied of the virtual blue marlin populations

The eastward and northward COGs and the effective area occupied of virtual blue marlin populations 1, 2, and 3 were estimated under the ALL scenario via the spatio-temporal GLMMs computed using VAST (Figs. 2d-l). This analysis suggested that Population 1, which maintained a constant abundance over the period 1987-2015 (Fig. 2a), also had a constant effective area occupied between 1987 and 2015 (Fig. 2f) and that, between 1996 and 2015, the COG of Population 1 moved northward (Fig. 2e). The spatio-temporal GLMMs indicated that the COG of Population 2, whose abundance generally declined over the period 1987- 2015 (Fig. 2b), moved northward between 1996 and 2015 but also westward in 2006 (Figs. 2g-h). Moreover, the predicted effective area occupied of Population 2 decreased between 2000 and 2006 and then stabilized (Fig. 2i). Finally, the spatio-temporal GLMMs indicated that the COG of Population 3, whose abundance generally increased over the period 19872015 (Fig. 2c), moved northward between 1996 and 2015 (Fig. 2k). The predicted effective area occupied of Population 3 increased slightly between 1987 and 1995 and was stable afterwards (Fig. 2l).

3.2. Analyses conducted with LLSIM data

We considered three virtual blue marlin populations, three sampling scenarios (ALL, 10%, and 10%BIAS) and nine standardization methods (GLM, GLMint, GLMMint, GLMwt, GLMwt.int, GLMprwt, GLMprwt.int, GAM, and VAST). Moreover, for each virtual blue marlin population, we ran five replicates of the 10% scenario and five replicates of the 569 10%BIAS scenario. Therefore, we estimated a total of $3*(1+5+5)*9=297$ indices of relative abundance. Under the 10% and 10%BIAS scenarios, there were instances where inclusion of the fixed year-area interaction term led to convergence issues with the binomial GLMs; convergence issues arise when any year-area stratum has 0% or 100% encounter rates, as noted in previous studies (Lynch et al., 2012; Campbell, 2015). When binomial GLMs integrating a fixed year-area interaction effect did not converge, we combined the predictions of a binomial GLM without a year-area interaction effect with the predictions of a lognormal model integrating a fixed year-area interaction effect.

The relative sample size of the levels of the area factor and catchability covariates varied largely over the period 1987-2015 (Fig. 3 and Fig. A3), justifying the standardization of the LLSIM CPUE data. Notably: (1) the "unknown" hook type was dominant until 2004, after what virtually all the hooks used were circle hooks; and (2) the "unknown" bait type was employed in 1987 and 1988, while the "dead" bait type was dominant between 1989 and 2015 (Fig. 3 and Fig. A3).

Overall, the indices of relative abundance estimated by all CPUE standardization methods matched true abundances well (Fig. A4). However, under the 10% and 10%BIAS scenarios, there were several instances where the standardization methods relying on GLMs integrating a fixed year-interaction effect (i.e., the GLMint, GLMwt.int and GLMprwt.int methods) resulted in poorly estimated indices of relative abundance (Figs. 4-5 and Figs. A4). We examine some of these instances in detail below.

In general, CPUE standardization methods had relatively little bias (Fig. 6). An exception to this general pattern was Population 3 under the 10%BIAS scenario, for which two CPUE standardization methods (GLMprwt and GLMMint) noticeably underestimated the true changes in abundance. Under all scenarios and for all populations, generally, the GLMMint method had the strongest negative bias (representing hyperstability in the estimated index of abundance), while the GLMint method had the strongest positive bias. Under the ALL and 10% scenarios, the GLMprwt.int, VAST and GLMprwt methods had the lowest biases. Under the 10%BIAS scenario, the GLM and GAM methods had the lowest biases, the GLMprwt.int method had a relatively low negative bias similar to that of the VAST method for all populations combined and Population 2, and the GLMwt method had a relatively low negative bias similar to that of the VAST method for Population 3 (Fig. 6).

MAE showed great variation among CPUE standardization methods (Fig. 7). Under all scenarios and for all populations, the GAM method was usually the CPUE standardization methods with the lowest MAE, followed closely by the VAST, GLMwt and GLMMint methods, in this order. Under the ALL scenario, the GLMint method was the method with the largest MAE, usually followed by the GLMwt.int and GLMprwt.int methods. Under the 10% scenario, the GLMprwt and GLMprwt.int methods, which both assigned prior weights to data based on the year-area stratum to which the data belonged, had, in general, the largest MAEs, followed by the GLMint method. An exception to this general pattern was Population 2, for

To understand why, in some instances, the standardization methods relying on GLMs incorporating a fixed year-interaction effect (i.e., the GLMint, GLMwt.int, and GLMprwt.int methods) resulted in poorly estimated indices of relative abundance, we examined: (1) the results obtained for Population 1 under the 10%BIAS scenario with Replicate 2 (Fig. 4 and Figs. A6 and A7); and (2) the results obtained for Population 3 under the 10%BIAS scenario with Replicate 1 (Fig. 5 and Figs. A8 and A9). Note that, in addition to the poorly estimated indices of relative abundance obtained with the GLMint, GLMwt.int and GLMprwt.int methods, Figs. 4 and 5 illustrate the low coverage of the GLMprwt and GLMprwt.int methods. In the two cases examined here, the fixed year-area interaction term did not lead to convergence issues with the binomial GLMs. For the two cases, we: (1) plotted the year-area interaction coefficients of the binomial and lognormal GLMs developed for the GLMint

method (Figs. A6 and A8); and (2) produced maps showing the spatial distribution of observer data for each year of the period 1987-2015 (Figs. A7 and A9).

In the first case examined (Population 1, 10%BIAS scenario, Replicate 2), while the true abundance of the virtual blue marlin population was constant over the period 2000-2015, the GLMint method predicted the index of relative abundance to increase over that period (Fig. 4). This result is due to the fact that: (1) predictions were made with the GLMs developed for the GLMint method using the NEC factor level (binomial model) and the FEC factor level (lognormal model) (Table 2); and (2) the year-area interaction terms estimated for the FEC and NEC areas for the GLMs developed for the GLMint method tended to increase over the period 2000-2015 (Fig. A6). The GLMwt.int and GLMprwt.int methods, which weighted year-area interactions by the surface area of each NMFS area, downweighted the influence of the FEC and NEC areas and did not predict an increase in the index of relative abundance over the period 2000-2015; yet, the indices of relative abundance estimated by the GLMwt.int and GLMprwt.int methods fitted the true data more poorly than those estimated by some of the other CPUE standardization methods such as the VAST, GAM and GLMwt methods (Fig. 4). Almost all the year-area coefficients of the binomial and lognormal models fitted by the GLMwt.int method were non-significant at the 5% level. To further gauge the significance of the year-area interaction terms, for both the binomial and lognormal models fitted by the GLMwt.int method, we performed stepwise model selection by the Akaike Information Criterion (AIC), using the function "stepAIC" from the R package "MASS" (Venables and Ripley, 2002). The stepwise model selection procedure resulted in the year-area interaction term being dropped from both the binomial and lognormal models.

In the second case examined (Population 3, 10%BIAS scenario, Replicate 1), the GLMint method predicted erroneous spikes over the most recent years (e.g., in 2008; Fig. 5). These erroneous spikes were due to: (1) the fact that predictions were made with the GLMs

developed for the GLMint method using the NEC factor level (binomial model) and the FEC factor level (lognormal model) (Table 2); and (2) the year-area interaction coefficients estimated for the FEC and NEC areas for the GLMs developed for the GLMint method (e.g., which both peak in 2008; Fig. A8). Moreover, in the second case study examined, the GLMwt.int and GLMprwt.int methods estimated indices of relative abundance that fitted true abundances more poorly than those estimated by the GLMint method; the indices of relative abundance estimated by the GLMwt.int and GLMprwt.int methods exhibited additional erroneous spikes (e.g., in 2002 and 2006; Fig. 5). This result stems from the fact that the NED and NCA areas, which are located, respectively, in the northeast and the southeast of our study region, are associated with very large surface areas (Fig. A9) and high year-area interaction coefficients in some years (e.g., 2002 and 2006; Fig. A8). However, over the period 1996-2015, Population 3 was predicted to move northward (Fig. 2k). Consequently, the GLMwt.int and GLMprwt.int methods, which weight year-area interactions by the surface area of each NMFS area and give more weights to the NED and NCA areas than the GLMint method, overestimated relative abundance in some years (e.g., in 2002 and 2006; Fig. 5).

3.3. Application of the CPUE standardization methods to real observer data

The CPUE standardization methods applied to real observer data tended to predict similar patterns, particularly a decline in the blue marlin population over the period 1998- 2004 followed by a relative stabilization of the population (Figs. 9 and 10). However, while the GLM, GLMMint GLMwt and GAM methods predicted a slight increase in blue marlin abundance in 1997-1998, the GLMwt.int, GLMprwt, GLMprwt.int and VAST methods predicted a marked peak in abundance for the same time period (Fig. 10). Moreover, the indices of relative abundance estimated with the GLMwt.int and GLMprwt.int methods were

more variable than those estimated with the other CPUE standardization methods, and they exhibited lots of peaks and troughs (Figs. 9 and 10). VAST predicted that blue marlin COG moved both eastward and southward in 1996-1997 and then moved slightly westward between 1998 and 2014 (Figs. 11a-b). VAST also predicted that the effective area occupied by blue marlin remained relatively constant over the period 1992-2017 (Fig. 11c).

To understand the estimated peak in relative abundance predicted for 1996-1997, we generated maps showing: (1) the spatial distribution of observer data for each year of the period 1992-2017 (which cannot be provided here or in the Supplementary data due to the confidentiality of the observer data); and (2) the standard errors associated with the indices of relative abundance estimated by the VAST method for each year of the period 1992-2017 (Fig. A10). The first maps suggested that the predicted peak in relative abundance for 1996- 1997 may be in part due to a few fishing trips with high catch rates made off the northeast coast of Brazil, in an area where sets were not observed by the NMFS Pelagic Observer Program outside of 1996 and 1997. The second maps showed that: (1) the locations of the observer data collected in the area off the northeast coast of Brazil were used by VAST to define a relatively large knot in the southeasternmost corner of our study region; but that (2) despite the low number of samples and large surface area of that knot over which these samples were extrapolated, the standard errors associated with the indices of relative abundance predicted for that knot and adjacent knots were low, in 1996-1997, but also pre-701 1996 and post-1997 (Fig. A10).

4. Discussion

In general, fisheries-independent surveys use sampling designs which on average provide unbiased indices of relative abundance (Thompson, 2002). Unfortunately, because

fisheries-independent surveys are costly and time-consuming, they are generally conducted during specific months and rarely entirely cover large marine regions such as the North Atlantic (Lynch et al., 2012; Bourdaud et al., 2017). Consequently, many exploited fish populations such as Atlantic blue marlin are not monitored by fisheries-independent surveys (Lynch et al., 2012; Walter et al., 2014a). Instead, for these fish populations, indices of relative abundance are derived from fisheries-dependent CPUE data, which are collected with the assistance of fishers who adapt their fishing grounds and behavior based on prevailing environmental and socio-economic conditions and, perhaps, the presence of observers onboard (Walters, 2003; Maunder and Punt, 2004; Marchal et al., 2006; Walter et al., 2014a). Under these circumstances, it is critical to assess the performance of methods for standardizing fisheries-dependent CPUE data. In the present study, we evaluated and compared nine CPUE standardization methods, which offered contrasting treatments of spatio-temporal variation: (1) non-spatial methods that accounted or not for the interaction between the year and area effects (GLM, GLMint, and GLMMint); (2) methods that accounted or not for the interaction between the year and area effects, but also weighted or not model predictions for individual areas by the surface area of each these areas and/or assigned prior weights to raw CPUE data based on the year-area stratum to which the CPUE data belonged (GLMwt, GLMwt.int, GLMprwt, and GLMprwt.int); (3) a method that accounted for spatial autocorrelation at a broad spatial scale (GAM); and (4) a method that accounted for spatial and spatio-temporal autocorrelation at a fine spatial scale (VAST).

Despite the substantial degradation of the simulated datasets by subsetting 10% randomly and then 10% nonrandomly, across all of the virtual blue marlin populations, the great majority of the CPUE standardization methods considered in this study managed to extract a relatively unbiased trend in relative abundance. While we do not have unequivocal evidence of observer effect bias occurring in the U.S. pelagic longline fishery, the commonly

employed GLM and GLMMint methods, the GAM method and the VAST spatio-temporal method seem to be fairly robust to this potential problem. In this study, there were also virtual populations for which other CPUE standardization methods (the GLMwt and GLMprwt.int methods) had a relatively low negative bias similar to that of the VAST method when the simulated datasets were nonrandomly subsampled to mimic observer bias (Fig. 6). We caveat these ideas with the observation that simulated data rarely perform as poorly as true observations, as it is difficult to mimic the full data generating process. Even 10% observer coverage (as was assumed in this study) may not be possible in many fisheries (National Marine Fisheries Service, 2016), and it is quite possible that the bias between what is observed and what is caught in an overall fishery may change over time.

While the different CPUE standardization methods generally provided relatively unbiased trends in relative abundance, with exceptions noted below, we found that the VAST spatio-temporal method generally had one of the lowest biases, one of the lowest MAEs and coverage closest to 50%. The strong performance in simulations of the VAST method argues for greater consideration of spatio-temporal methods in standardization of fisheries-dependent CPUE data. Additionally, spatio-temporal methods are particularly suited for working with fisheries-dependent CPUE data, because they: (1) diminish the influence of repeated fishing operations in sites, thus decreasing the influence of selection bias by fishers; and (2) allow for imputation or extrapolation where CPUE is unknown (Walter et al., 2014a, 2014b). Moreover, VAST is useful not only for standardizing CPUEs and can also be used, among other things, for estimating COGs and effective areas occupied and conducting habitat and climate-vulnerability assessments (see Thorson (2019) for a review). The spatio-temporal modeling platform VAST has benefited from numerous recent developments, including a GitHub repository enabling issue tracking (https://github.com/James-Thorson/VAST) and well-documented example code accompanied by a detailed user guide (which can both be accessed

in GitHub). Also, VAST now has a fairly large and dynamic user community with numerous applications to fisheries-independent datasets, and the present study represents one of the very first applications of VAST to fisheries-dependent data (Thorson, 2019). However, when working with large datasets, VAST simulations can take a long computation time. For instance, it took us around four hours to run each of the VAST simulations under the ALL scenario with a laptop with a 2.6 GHz Intel Core i5-6440HQ processor, using single-thread.

Our results suggest that good alternatives to the VAST method are the GLMMint method, i.e., the variant of the basic GLM method incorporating a random year-area interaction effect, and the GAM method. The GLMMint method had one of the lowest MAEs and one of the best coverages, yet this method also had the strongest negative bias. The GLMMint method is practical in that it obviates the need for imputing CPUE values in unobserved year-area strata when working with unbalanced datasets (Campbell, 2015). The GLMMint method also performs reasonably well and is flexible in terms of fixed and random effects structure; for example, it would probably be feasible to extend the random effect term so that the season effect is nested within area and year. However, the GLMMint method should ideally be utilized only if year-area interactions can be fully explained as random effects (e.g., do not show a significant trend; Cooke, 1997; Maunder and Punt, 2004; Campbell, 2015). The GAM method, which accounts for spatial autocorrelation at a broad spatial scale, may also be a good alternative to the VAST method, because it had the lowest MAE among the nine CPUE standardization methods we tested, as well as the lowest bias under the observer bias scenario. On the other hand, we also found that the GAM method had confidence intervals that were often too wide. In this study, for computational reasons, we did not consider the GAMint method, which also accounts for spatial autocorrelation at a broad 779 spatial scale by integrating a $s(X, Y, by = year)$ term (Wood, 2006). Had we used the

GAMint method in this study, we suspect that the GAMint method would have had a lower MAE than the GAM method, at the expense of exceedingly wide confidence intervals.

It is important to note that the estimated coverages of the GLMMint and GAM methods are in large part due to the very large standard errors associated with their predictions (Fig. A5). As the CPUE standardization methods considered in this study rely on different procedures for computing standard errors from two independent models (a binomial and a lognormal models), some of the calculated standard errors may not be accurate. Therefore, to some extent, the utility of the coverage metric is dependent on the relative accuracy of the standard errors calculated by each CPUE standardization method. Thus, everything else equal, one may be more confident in using a CPUE standardization method with one of the lowest MAEs and one of the lowest biases (e.g., the GAM method) than a method with one of the lowest MAEs and one of the best coverages (e.g., the GLMMint method).

In most cases, the year-area interaction effects in the simulated datasets were not very strong, such that the CPUE standardization methods that either did not estimate them (GLM, GLMwt, and GLMprwt) or estimated them as random effects (GLMMint) performed better than the standardization methods that estimated them as fixed effects and did (GLMwt.int, and GLMprwt.int) or did not (GLMint) use them in predictions. The GAM and the VAST methods model the spatio-temporal effects as fixed and random, respectively, and uses them in the predictions. Hence, the lack of substantial performance differences between including or not including year-area interactions can likely be attributed to the simulated datasets having year-area interaction effects that are not very strong. As no year-area interactions were imposed on the simulated data and would only have been emergent properties of the abundance trends, oceanography and habitat preferences of blue marlin, it is likely that any induced year-area interactions were nor very strong or directional. In this study, our main goal was to compare the performance of CPUE standardization methods integrating or not year-

area interaction terms. For this reason, we did not conduct any model selection procedure (besides for understanding the results of one case study). Future studies interested in estimating indices of relative abundance based on the most parsimonious models should perform stepwise model selection by AIC (Venables and Ripley, 2002). This would allow dropping the year-area interaction term from the binomial and/or lognormal models if this interaction term is non-significant (along with non-significant catchability covariates), thereby improving the predictions of the CPUE standardization process.

The greatest degradation in performance was with CPUE standardization methods relying on GLMs incorporating a fixed year-area interaction effect (i.e., the GLMint, GLMwt.int, and GLMprwt.int methods), which often resulted in poorly estimated indices of relative abundance, the largest MAEs and the lowest coverages (though not necessarily the largest biases). Similar results were obtained by Thorson and Ward (2013); using delta GLMMs, the authors found that a random year-area interaction often had better performance than a fixed year-area interaction when analyzing sparse fisheries-independent survey data. The literature generally recommends to include year-area interactions as random effects (e.g., Lynch et al., 2012) where the effects are often constrained by distributional assumptions such as to be normally distributed with a mean of zero. The main issue with the GLMint method is that it gives too much weight to areas whose year-area coefficients hit bounds, are highly erratic or have standard errors indicative of very poor estimation (Figs. A6 and A8). While the spatial weighting employed in the GLMwt.int and GLMprwt.int methods could potentially improve estimation by differentially weighting each year-area interaction coefficient, there is no guarantee that a poorly estimated coefficient will get a small weight. Quite the opposite happened in this study in some cases, where certain large spatial areas had very sparse sampling.

Another notable result of the present study was the poor performance of the methods assigning prior weights to data based on the year-area stratum to which the data belong (i.e., the GLMprwt and GLMprwt.int methods) under the 10% and 10%BIAS scenarios. When dealing with subsamples of the LLSIM data that mimic sampling by observers, the GLMprwt and GLMprwt.int methods often resulted in poorly estimated indices of relative abundance, and they had among the largest MAEs and among the lowest coverages. (Yet, the GLMprwt.int and GLMprwt methods had among the lowest biases; Fig. 6). This result was relatively surprising, given that one would *a priori* expect that assigning prior weights to data would compensate for a very unbalanced dataset by altering the relative influence of each data 838 point (Campbell, 2015). However, we observed virtually no differences between the indices of relative abundance produced by the methods assigning prior weights to data and those not assigning prior weights to data (Figs. 4-5). Using simulated CPUE data for Pacific broadbill swordfish (*Xiphias gladius*) and the Australian pelagic longline fishery, Campbell (2015) also found little differences between the predictions of the methods assigning vs. not assigning prior weights to data. Furthermore, the author observed that assigning prior weights to data resulted in slightly more biased predictions. Campbell (2015) discussed that the results he obtained with the methods assigning or not assigning prior weights to data were likely due to the fact that definition of areas in his study region appropriately stratified CPUE spatial distribution.

Thus, neither of the instances of poor performance reported in this study reflect upon the theory or merits of the GLMwt and GLMwt.int, GLMprwt and GLMprwt.int methods, but rather relate to the nature and representativeness of the data relative to the NMFS areas to which they are assigned. While the NMFS areas (Fig. 1) were chosen based on expert opinion and generally reflect homogenous fishing regions, they are of very different sizes and have very different sample coverage per unit area. This leads to correspondingly erratic estimates

of year-area interaction coefficients which may not be representative of the NMFS area to which they are assigned and, when weighted by the surface areas of the NMFS areas, can compound errors. For many fisheries, the area stratification chosen is not based on the biological characteristics of the fishery or the species of interest (such as homogeneity of fish density), but for other management-related reasons. Carruthers et al. (2011) found that GLMs with fixed year-area interaction terms performed better than GLMs without year-area interaction terms, which may have been because the authors employed a regular grid of cells to define areas, where each individual cell had a similar surface area such that no cells could dominate the predicted index of relative abundance. The fact that we relied on an irregular grid of cells to define areas where some cells had an extremely large surface area, combined 864 with the fact that the LLSIM datasets were unbalanced spatially (Figs. A7 and A9), likely degraded the performance of the GLMwt.int and GLMprwt.int methods. Naturally, this raises the question: should we have developed better spatial stratification either by adopting a regular grid or by applying one of several algorithms that search for optimal partitioning to create homogenous spatial regions and minimize the strength of year-area interactions (Ichinokawa and Brodziak, 2010; Ono et al., 2015)?

While a better spatial partitioning might have improved the performance of the GLMwt.int and GLMprwt.int methods, our results support using spatio-temporal modeling to obviate the need to specify *a priori* spatial partitioning entirely. A regular grid would likely exacerbate issues of missing data and would not achieve homogenous stratification or minimization of year-area interactions, whereas an optimal partitioning *sensu* Ichinokawa and Brodziak (2010) and Ono et al. (2015) would likely result in disparate area sizes and sample coverage. It may be possible to restrict the data to a limited spatial area of inference where sampling is more uniform, but this may greatly reduce the sample size and can lead to problems when fishing fleets shift spatial locations (Campbell, 2004). The essential problem

is one of confounding where all further results depend critically on the initial spatial partition. In situations where strong year-area interactions such as range contraction/range expansion/spatial depletion are likely to occur, spatio-temporal modeling approaches provide a consistent and compelling means of addressing them.

Overall, the application to real observer data collected by the NMFS Pelagic Observer Program suggested that the relative abundance of the blue marlin population of the Atlantic declined over the period 1998-2004 and was relatively stable afterwards. VAST also suggested that Atlantic blue marlin COG may have moved slightly westward between 1998 and 2014 (Fig. 11a). Such a trend could potentially be indicative of a small spatial overlap between the U.S. pelagic longline fishery and the expansion of the oxygen minimum zone in the Eastern Atlantic (Stramma et al., 2012).

An issue observed with real observer data was the peak in abundance predicted in 1996-1997 by the GLMwt.int, GLMprwt, GLMprwt.int and VAST methods (Figs. 9 and 10). An examination of the spatial distribution of observer data indicated that these peak CPUEs occurred off the northeast coast of Brazil and were the result of only three trips by two fishing vessels in 1996 and 1997 which had exceptionally high catch rates of blue marlin. Trips in these locations were rarely ever observed in the remaining time series and these three trips represent the only data for these southeasternmost spatial areas in 1996 and 1997, indicating that they have substantial leverage on the estimations. However, the standard errors associated with the predictions for the VAST knot defined from the observer data collected off northeast Brazil and adjacent knots were low (Fig. A10), which is indicative that the model prediction uncertainty was not increased by having very few samples to extrapolate over a large surface area. This is in contrast to traditional geostatistical theory where, assuming stationarity of spatial autocorrelation, having only a few samples to cover the entire southeastern prediction region would result in very large standard errors relative to prediction regions in other areas

which were much more comprehensively sampled. This indicates that, in application, care in developing the prediction knots is necessary to avoid overpredicting beyond the range of spatial autocorrelation. While methods such as VAST can avoid the *a priori* specification of spatial strata, they are not devoid of making some decisions regarding spatial structuring of the prediction area. Hence, some greater curation of the placement of knots when setting up VAST modeling approaches is recommended when working with spatially imbalanced fishery-dependent datasets. This was not done in the present study, because we worked in a design where the model developer was purposefully not provided with any details regarding the datasets being analyzed, though this is an important issue to consider in future studies. Contrary to the GLMwt.int, GLMprwt, GLMprwt.int and VAST methods, the GLMMint method did not predict a peak in abundance in 1996-1997. This is because the GLMMint method is a non-spatial method that models year-area interactions as random effects and that does not assign weights to year-area strata; thus, the few trips off the northeast coast of Brazil in 1996-1997 did not have a strong influence on the predictions made by the GLMMint method.

The main avenues for future research we envision are the following ones: (1) an analysis of the consequences of differential patterns of observer coverage, spatial sampling distribution or observer bias; (2) improved consideration of spatial knot selection for VAST; and (3) evaluating the performance of CPUE standardization methods under conditions of stronger year-area interactions designed to mimic environmental changes and when area-season and/or year-season interactions are considered. First, in the present study, we developed algorithms to mimic sampling by an observer program, which allocate longline sets to fishing trips so as to enable the application of CPUE standardization methods to 10% of the fishing trips; this percentage was chosen because this is the average percentage of trips sampled by the NMFS Pelagic Observer Program each year (Beerkircher et al., 2002).

However, future studies working with LLSIM data should take advantage of our algorithms to investigate whether sampling less or more than 10% of the fishing trips undertaken by the U.S. pelagic longline fishery would significantly alter the accuracy and precision of the indices of relative abundance estimated from CPUE data. Additionally, given the effect of a small number of spatial "outlier" trips in 1996 and 1997 on some indices using the real blue marlin data, it may be necessary to consider the potential influence of more isolated and sparse spatial samples which appear in the real data, as well as the impacts of variation in observer coverage across years. Second, given that sparse spatial samples can have undue influence on population trends and potentially, on COG inferences, it may be necessary to re-evaluate the methodology of knot allocation which allocates knots spatially with a density proportional to sampling intensity (Thorson et al., 2015). Hence there are few knots where sampling intensity is low so that these few knots represent a very large spatial area. Future studies could instead place knots with uniform spatial area (i.e., using a two-dimensional grid), and this would likely have better performance when applied to spatially unbalanced datasets like those explored in the present study. Finally, evaluating CPUE standardization methods under conditions of stronger year-area interactions would be valuable for informing climate-vulnerability assessments, and also for checking whether the GLMwt.int and GLMprwt.int methods would then perform better than the GLMwt and GLMprwt methods, as would be expected in theory (Campbell, 2015). We also recommend future studies to examine the performance of CPUE standardization methods when area-season and/or year-season interactions are considered. In the case of Atlantic blue marlin, these interactions terms should explain more variation in the CPUE standardization models and would likely provide more contrast in the performance evaluation, given that seasonal environmental changes are considered in LLSIM and also largely influence Atlantic blue marlin ecology in the real world (Goodyear, 2016). Future studies will also need to explore whether CPUE standardization

models which include year-area, area-season and/or year-season interactions as random effects terms are adequate when these interactions are strong.

In conclusion, the varying performance of the different CPUE standardization methods reflect their different treatments of spatio-temporal variation with the spatio-temporal method providing a more comprehensive and consistent treatment of this variation. This is in contrast with methods that simply weight predictions by large spatial areas, where it is critically important but particularly difficult to get the *a priori* spatial stratification correct before weighting. If year-area interactions are truly small in magnitude, random, spurious or ignorable, then the GLMMint method provides fairly good performance in CPUE standardization. The GAM method is another valuable alternative to spatio-temporal CPUE standardization methods. Moreover, some CPUE standardization methods not considered in this study, such as random forests (Li et al., 2015) or variants of the GLMwt.int and GLMprwt.int methods modeling year-area interactions as random effects (Campbell, 2015), could be employed in future studies. However, as issues of range contraction/expansion and shifts increase in frequency with environmental changes, evaluating them through the lens of arbitrary spatial strata will likely impede both detection and quantification of these phenomena. Hence, we encourage future studies to consider spatio-temporal modeling platforms such as VAST for standardizing fisheries-dependent CPUEs in different marine regions, so as to enable a generalization of the performance of spatio-temporal methods for standardizing fisheries-dependent CPUE data.

Authorship statement

- AG, JFW, EAB and JTT designed and analyzed the models; AG, JFW, EAB, FCF, JTT, MVL
- and MJS conceived the models; AG, JFW, EAB, FCF, JTT and MVL wrote the paper; all
- authors have approved the final article.
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Appendix A. Supplementary data

- Supplementary data associated with this article can be found in the online version of
- the manuscript.
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- https://github.com/James-Thorson/VAST

Figure captions

Fig. 1. Study region, located in the North Atlantic, which encompasses the ten National

- Marine Fisheries Service (NMFS) areas defined for the stock assessments of the International
- Commission for the Conservation of Atlantic Tunas (ICCAT): (1) the Gulf of Mexico
- (GOM); (2) the Mid Atlantic Bight (MAB); (3) the South Atlantic Bight (SAB); (4) Florida
- East Coast (FEC); (5) the Caribbean (CAR); (6) the Northeast Coastal area (NEC); (7) the
- Sargasso area (SAR); (8) the Northeast Distant area (NED); (9) the North Central Atlantic
- (NCA); and (10) the Offshore South area (OFS).

Fig. 2. (a-c) Relative abundance, **(d, g, j)** eastward center of gravity (COG; in km), **(e, h, k)** northward COG (in km) and **(f, i, l)** effective area occupied (in ln(km²)) of the three virtual populations of blue marlin (*Makaira nigricans*) over the period 1987-2015. **(a, d-f)** are for Population 1, **(b, g-i)** are for Population 2, and **(c, j-l)** are for Population 3. **(a-c)** show the true annual abundances of the virtual populations of blue marlin relative to their mean over the period 1987-2015, while **(d-l)** were estimated by the spatio-temporal modeling platform VAST from all the blue marlin catch-per-unit-effort data provided by the longline catch-per-unit-effort data simulator LLSIM. For **(d-l)**, the shaded area represents 95% confidence intervals.

Fig. 3. Evolution over the period 1987-2015 of the sample size of the levels of the factors considered in the analyses conducted with data from the longline catch-per-unit-effort (CPUE) data simulator LLSIM. Here, all the data provided by LLSIM are considered.

Fig. 4. Annual time series of nominal and estimated catch-per-unit-effort (CPUE) relative to mean CPUE for the virtual population of blue marlin (*Makaira nigricans*) #1, under the

10%BIAS scenario (see legend for color code). Replicate #2 is considered here. Nine methods were employed to estimate CPUEs (Table 1). The annual time series of the true simulated abundance of the virtual population of blue marlin #1 divided by its mean simulated abundance is also given here. The dashed lines represent the 95% confidence intervals of estimated CPUEs.

Fig. 5. Annual time series of nominal and estimated catch-per-unit-effort (CPUE) relative to mean CPUE for the virtual population of blue marlin (*Makaira nigricans*) #3, under the 10%BIAS scenario (see legend for color code). Replicate #1 is considered here. Nine methods were employed to estimate CPUEs (Table 1). The annual time series of the true simulated abundance of the virtual population of blue marlin #3 divided by its mean simulated abundance is also given here. The dashed lines represent the 95% confidence intervals of estimated CPUEs.

Fig. 6. Bias of estimated annual catches-per-unit-effort (CPUEs) for the simulated populations of blue marlin (*Makaira nigricans*), under three scenarios (ALL, 10%, and 10%BIAS). For the 10% and 10%BIAS scenarios, barplots represent mean biases over five replicates, while the black bars overlaid on barplots represent minimum and maximum biases over the five replicates. See the main text for details on the scenarios. Nine methods were employed to estimate CPUEs (Table 1).

Fig. 7. Mean absolute error (MAE) of estimated annual catches-per-unit-effort (CPUEs) for the simulated populations of blue marlin (*Makaira nigricans*), under three scenarios (ALL, 10%, and 10%BIAS). For the 10% and 10%BIAS scenarios, barplots represent mean MAEs over five replicates, while the black bars overlaid on barplots represent minimum and

maximum MAEs over the five replicates. See the main text for details on the scenarios. Nine methods were employed to estimate CPUEs (Table 1).

Fig. 8. Coverage (in %) for the simulated populations of blue marlin (*Makaira nigricans*), under three scenarios (ALL, 10%, and 10%BIAS). Coverage is the percentage of years over the period 1987-2015 the 50% confidence interval for a normalized estimated catch-per-unit-effort (CPUE) contains the normalized true abundance. For the 10% and 10%BIAS scenarios, barplots represent mean coverages over five replicates, while the black bars overlaid on barplots represent minimum and maximum coverages over the five replicates. See the main text for details on the scenarios. Nine methods were employed to estimate CPUEs (Table 1). **Fig. 9.** Annual time series of nominal and estimated catch-per-unit-effort (CPUE) relative to

mean CPUE for the Atlantic blue marlin (*Makaira nigricans*) population, computed from the data collected within the National Marine Fisheries Service Pelagic Observer Program over the period 1992-2017. All the methods listed in Table 1 except the GLMint method were employed to estimate CPUEs.

Fig. 10. Annual time series of estimated catch-per-unit-effort (CPUE) relative to mean CPUE for the Atlantic blue marlin (*Makaira nigricans*) population, computed from the data collected within the National Marine Fisheries Service Pelagic Observer Program over the period 1992- 2017. All the methods listed in Table 1 except the GLMint method were employed to estimate CPUEs.

Fig. 11. (a) Eastward center of gravity (COG; in km), **(b)** northward COG (in km) and **(c)**

effective area occupied (in ln(km²)) of the Atlantic blue marlin (*Makaira nigricans*)

- population, estimated by the spatio-temporal modeling platform VAST from the data
- collected within the National Marine Fisheries Service Pelagic Observer Program over the
- period 1992-2017. For all panels, the shaded areas represent 95% confidence intervals.

1268 **Tables**

1269 Table 1. Overview of the nine catch-per-unit-effort (CPUE) standardization methods used in

1270 this study.

1271 **Table 2.** Factors considered in the analyses conducted with data from the longline catch-per-

Year\NMFS area Caribbean (CAR) Florida East Coast (FEC) Gulf of Mexico (GOM) Mid Atlantic Bight (MAB) North Central Atlantic (NCA) Northeast Coastal (NEC) Northeast Distant (NED) Offshore South (OFS) South Atlantic Bight (SAB) Sargasso (SAR) 1987 568 2619 3208 9 2169 436 942 43 258 252 **1988** 700 3247 2720 37 478 2339 1510 204 760 275 **1989** 556 3795 2286 33 493 3454 1822 131 883 331 **1990** 610 3003 1780 29 534 3921 1210 273 1350 246 **1991** 552 2777 2055 23 408 4172 1198 78 1078 261 **1992** 431 2718 2113 17 448 3792 1251 151 1051 313 **1993** 644 2439 1677 67 459 3767 1167 65 1361 392 **1994** 715 2310 1595 72 945 3908 984 81 1619 578 **1995** 507 2340 2070 83 1426 4478 916 280 1341 280 **1996** 589 2510 2422 105 891 3125 766 645 2261 468 **1997** 527 2764 2534 57 379 3228 793 678 1689 265

1273 **Table 3.** "Walters' table" (Campbell, 2015) constructed from the raw data from the longline catch-per-unit-effort (CPUE) data simulator LLSIM,

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1276 **Table 4.** Factors considered in the analyses conducted with data collected within the National

1277 Marine Fisheries Service (NMFS) Pelagic Observer Program.

Table 5. "Walters' table" (Campbell, 2015) constructed from the raw data collected within the National Marine Fisheries Service (NMFS)

Pelagic Observer Program, showing the number of data points in each year-area stratum.

National Marine Fisheries Service

area

Type of bait used ("bait")

Number of light sticks used ("light")

Number of hooks between floats $("hbf")$

Type of hook used ("hook")

Season

Population 1 - Scenario 10%BIAS - Replicate 2

GLM

 2.5

 2.0

 1.5

 $\frac{0}{1}$

 0.5

 0.0

1990

1995 2000 2005

CPUE / (mean CPUE)

GLMint

2.5

 2.0

 1.5

 1.0

 0.5

 0.0

1990

1995 2000 2005 2010

Year **GLMwt.int**

CPUE / (mean CPUE)

GLMMint

GLMwt

Year

2010 2015

1990 1995 2000 2005 2010 2015

CPUE / (mean CPUE)

 0.5

 $\overline{0}$.0

2015

Year

VAST

Population 3 - Scenario 10%BIAS - Replicate 1

GLM

2.5

 2.0

 1.5

 $\frac{1}{2}$

 0.5

 0.0

1990 1995 2000 2005 2010

CPUE / (mean CPUE)

GLMint

CPUE / (mean CPUE)

2015

2.5

 2.0

 1.5

 1.0

 0.5

 0.0

1990 1995

GLMMint

GLMwt

Year

GLMwt.int

2000

Year

2005 2010 2015

GLMprwt

VAST

Population 3

 $\frac{1}{2}$

 $Bias_{0.8}$

 \overline{a}

 $\overline{0}$

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 $\frac{1}{2}$

 $\frac{2}{3}$

 \overline{a}

 $\overline{0}$

 $\frac{1}{2}$

 $Bias_{0.8}$

 \tilde{a}

 $\overline{0}$

GLM

GLMMint

GLMwt

