SCIENTIFIC COMMITTEE
FIFTH REGULAR SESSION

10-21 August 2009
Port Vila, Vanuatu

Generalized Linear Bayesian Models for Standardization of CPUE with Incorporation of Spatial-Temporal Variations

WCPFC-SC5-2009/SA-WP-07

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Introduction

Catch and effort data from longline fleets are a key input in the assessment of yellowfin, bigeye, skipjack, and albacore tuna stocks in the WCPFC convention area (Hampton et al. 2006a, 2006b; Hoyle 2008). These data are used to derive standardised CPUE indices whose temporal trends are assumed to be proportional to the longline exploitable biomass. Improving existing catch effort standardization models for construction of stock assessment indices for key tuna species in the WCPO has been the focus of much research (e.g., Langley 2007). In this paper, we explore and develop alternative standardization models based on the Bayesian estimator and apply these models to albacore catch-effort data from the Japanese distant-water longline fleet. Bayesian models are appealing because they can easily incorporate heterogrenous data and they are flexible in allowing the use of new data (Zhang and Perry 2005, Zhang et al. 2008, Zhang et al. 2009).

Material and Methods

We developed three kinds of generalized linear Bayesian models for standardizing CPUE: lognormal, Delta (binomial + lognormal), and zero-inflated lognormal models. The lognormal model has both hierarchical and non-hierarchical forms, whereas the Delta and zero-inflated models were constructed only in a hierarchical format. Hierarchical generalized linear models are also known as Generalized Linear Mixed Models (GLMM).

The developed models are capable of estimating the effects of multiple explanatory variables: fishing year, fishing season, fishing area, fishing depth, and interaction of fishing year and area on catch rates (CPUEs). The entire fishing ground is divided into same-sized relatively small spatial blocks. The models have the capability to predict CPUEs for un-fished blocks based on the estimated effects of the explanatory variables as long as these blocks are fished in some of the years. We aim to mitigate the problems of estimating abundance index due to spatial contraction in fishing patterns.

1. Lognormal Model

CPUEs are modeled using the Log-normal distribution:

$$U_{i,j,k,l} \sim Lognormal(\overline{U}_{i,j,k,l}, \quad \sigma^2) \qquad (1)$$

where $U_{i,j,k,l}$ is the observed CPUE at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, $\overline{U}_{i,j,k,l}$ is the mean of the distribution on the log scale for CPUEs at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, and σ is the standard deviation of the distribution on the log scale. When zero catch rates are encountered, Eq. 1 is adjusted by adding a small constant (Δ) equivalent to 10% of the overall CPUE (total catch divided by total effort over all the years) to each observed CPUE values:

$$U_{i,j,k,l} + \Delta \sim Lognormal(\overline{U}_{i,j,k,l}, \quad \sigma^2) \qquad (2)$$

The expected CPUE, $\hat{U}_{i,j,k,l}$, is estimated as:

$$\hat{U}_{i,j,k,l} = \exp\left(\overline{U}_{i,j,k,l} + \frac{\sigma^2}{2}\right) - \Delta \qquad (3)$$

The mean, $\overline{U}_{i,j,k,l}$, is estimated based on the effects of explanatory variables:

$$\overline{U}_{i,j,k,l} = c0 + cy_i + cs_j + ca_k + cd_l + cya_{i,k} \qquad (4)$$

where c0 is the intercept, cy_i, cs_j, ca_k, and cd_l are the effects of *Year* i, *Season* j, *Area* k, and *Depth* l, respectively, and $cya_{i,k}$ is the interaction effect between *Year* i

and *Area* k. Corner constraints are applied to all these variables. Namely, the effects of *Year* 1, *Season* 1, *Area* 1, and *Depth* 1 are all assigned a value of 0, and the effects of remaining years, seasons, areas, and depths are estimated. The interaction effects between *Year* 1 and all areas, and between *Area* 1 and all years were also assigned a value of 0, and effects of the other year and area interactions are estimated.

For a non-hierarchical model, interaction between individual year and individual area has a fixed effect. Therefore, each interaction effect to be estimated is assigned an independent prior probability distribution. For a hierarchical model, interaction between individual year and individual area is assumed to have a random effect, which is exchangeable and comes from a normal distribution, $cya_{i,k} \sim N(U_c, \sigma_c^2)$, where the hyperparameters U_c and σ_c^2 denote the mean interaction effect and the variance of interaction effects over different years and areas, respectively. One of the advantages of using hierarchical models is that the interaction effect, $cya_{i,k}$, could be estimated more reliably, when no catch information was available from Area k in Year i, by borrowing information from observations in other years and areas. In contrast, non-hierarchical models could only estimate this interaction effect directly from the assigned prior probability distribution.

The abundance index for *Area* k in *Season* j of *Year* i, $YSA_{i,j,k}$, was estimated according to Campbell (2004):

$$YSA_{i,j,k} = \exp\left(c0 + cy_i + cs_j + ca_k + cya_{i,k} + \sigma^2/2\right) - \Delta \qquad (5)$$

Abundance index for year i, Y_i, was estimated in two different ways depending on whether predicted catch rates in the un-fished areas were used in the calculation of abundance index. If predicted catch rates were used, Y_i is simply the summation of $YSA_{i,j,k}$ over the entire area and seasons:

$$Y_i = \frac{1}{4 \times NA} \sum_{j=1}^{NS} \sum_{k=1}^{NA} \left(YSA_{i,j,k} \right) \tag{6}$$

where NS and NA are the total number of seasons and areas fished in the time series. If predicted catch rates were not used, Y_i is calculated as follows:

$$Y_i = \frac{1}{TFA_i} \sum_{j=1}^{NS} \sum_{A_{i,j}} YSA_{i,j,k} \tag{7}$$

where $A_{i,j}$ refers to the areas fished in *Season* j of *Year* i, and TFA_i is the total number of fished areas in *Year* i:

$$TFA_i = \sum_{j=1}^{NS} N_{i,j} \tag{8}$$

where $N_{i,j}$ is the number of areas fished in *Season* j of *Year* i.

The yearly abundance index relative to the abundance index for the reference year (1^{st} year) is calculated as:

$$I_i = \frac{Y_i}{Y_1} \tag{9}$$

2. Delta Model

Two probability models were used in the Delta approach, binomial and lognormal. The former is used to model, the number of non-zero catches, given the total number of catches, and the latter is used to model the non-zero catch rates:

$$\begin{cases} N_{i,j,k,l} & \sim \quad Binomial(p_{i,j,k,l}, \quad TN_{i,j,k,l}) \\ U_{i,j,k,l} & \sim \quad Lognormal(\hat{U}_{i,j,k,l}, \quad \sigma^2) \end{cases} \tag{10}$$

where $N_{i,j,k,l}$ and $TN_{i,j,k,l}$ are the number of non-zero catches and total number of fishing events, respectively, at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, and $p_{i,j,k,l}$ is the probability of obtaining a non-zero catch in a single fishing event at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i. $U_{i,j,k,l}$ is the observed non-zero CPUE at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, $\overline{U}_{i,j,k,l}$ is the mean of the distribution on the log scale for non-zero CPUEs at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, and σ is the standard deviation of the distribution on the log scale.

The expected CPUE (including zero catches) is estimated as:

$$\hat{U}_{i,j,k,l} = p_{i,j,k,l} \times \exp\left(\overline{U}_{i,j,k,l} + \frac{\sigma^2}{2}\right) \qquad (11)$$

The binomial probability, $p_{i,j,k,l}$, is associated with explanatory variables through the Logit link function, $Logit(p) = \log\left(p/(1-p)\right)$:

$$Logit(p_{i,j,k,l}) = p0 + py_i + ps_j + pa_k + pd_l + pya_{i,k} \qquad (12)$$

where $p0$ is the intercept, py_i, ps_j, pa_k, and pd_l are the effects of *Year* i, *Season* j, *Area* k, and *Depth* l, respectively, on the probability, and $pya_{i,k}$ is the effect of interaction between *Year* i and *Area* k on the probability. Corner constraints are applied to all the explanatory variables. The effects of *Year* 1, *Season* 1, *Area* 1, and *Depth* 1 are assigned a value of 0, and the effects of remaining years, seasons, areas, and depths are estimated. The effects of interaction between *Year* 1 and all areas, and between *Area* 1 and all years were also assigned a value of 0, and effects of the other year and area interactions are estimated. $\overline{U}_{i,j,k,l}$ is estimated in the same way as in the lognormal model (see Eq. 4).

The interaction variable, $pya_{i,k}$, is assumed to have a random effect. We also assume that individual interaction effects are exchangeable and are from a normal distribution, $pya_{i,k} \sim N(U_p, \sigma_p^2)$, where the hyperparameters U_p and σ_p^2 denote the mean interaction effect and the variance of interaction effects over different years and areas, respectively. The interaction variable, $cya_{i,k}$, is treated in the same way as described for the lognormal model.

The abundance index for *Area* k in *Season* j of *Year* i, $YSA_{i,j,k}$, is estimated as:

$$YSA_{i,j,k} = \begin{cases} 0 & (if\ all\ zero\, catches) \\ q_{i,j,k} \times \exp\left(c0 + cy_i + cs_j + ca_k + cya_{i,k} + \sigma^2/2\right) & (Otherwise) \end{cases}$$

(13)

where $q_{i,j,k}$ is the expected probability of obtaining a non-zero catch in a single fishing event in *Area* k in Fishing *Season* j of Fishing *Year* i, and is calculated as follows:

$$q_{i,j,k} = \frac{\exp\left(p0 + py_i + ps_j + pa_k + pya_{i,k}\right)}{1 + \exp\left(p0 + py_i + ps_j + pa_k + pya_{i,k}\right)} \quad (14)$$

The abundance index for a year, Y_i, is estimated in the same way as described for the lognormal model (see Eqs. 5 and 6). The yearly relative abundance index, I_i, is calculated using Eq. 8.

3. Zero-inflated Lognormal Model

A zero-inflated lognormal model differs from a lognormal model in that it introduces an extra probability parameter to capture non-zero or zero values that cannot be directly modeled by the lognormal distribution. It also differs from the Delta model, which consists of lognormal and binomial distributions. The Zero-inflated model is composed of one single model component. Specifically, CPUEs are modeled as follows:

$$\Pr(U_{i,j,k,l}) = \begin{cases} 1 - p_{i,j,k,l} & (if\ U_{i,j,k,l} = 0) \\ p_{i,j,k,l} \times f_{Ui,j,k,l} & (Otherwise) \end{cases} \qquad (15)$$

where $p_{i,j,k,l}$ is the probability of obtaining a non-zero catch in a single fishing event at *Depth* l in *Area* k in Fishing *Season* j of Fishing *Year* i, and $f_{Ui,j,k,l}$ is the probability function for the lognormal distribution:

$$f_{Ui,j,k,l} = \frac{1}{U_{i,j,k,l}\sigma\sqrt{2\pi}} \exp\left(\frac{-\left(\log(U_{i,j,k,l}) - \overline{U}_{i,j,k,l}\right)^2}{2\sigma^2} \right) \qquad (16)$$

The expected CPUE is calculated in the same way as Eq 11. The probability for non-zero catches, $p_{i,j,k,l}$, is also associated with explanatory variables through the Logit link function as described for the Delta model (see Eq. 12). The interaction variables, $cya_{i,k}$ and $pya_{i,k}$, are treated in the same way as described for the lognormal model and Delta model. The abundance index for *Area* k in *Season* j of *Year* i, $YSA_{i,j,k}$, is calculated using Eq. 13. Abundance index for a year, Y_i, is estimated in the same way as described for the lognormal model (see Eqs. 5 and 6). Yearly relative abundance index, I_i, is calculated using Eq. 8.

4. Application of the Models to Albacore Fisheries

The models were applied to CPUE data from Japanese longline fisheries on albacore tuna (*Thunnus alalunga*) in the south Pacific (south of the equator) for the years 1975-2006. The dataset consists of the month of fishing, number of hooks per basket, and catch and effort aggregated by $5° \times 5°$ spatial blocks within the WCPFC Convention Area. Explanatory variables considered in the models are Year, Season, Area, and Depth. The monthly catch data were aggregated across the four seasons. Each of such $5° \times 5°$ spatial blocks is considered to be an Area. Blocks in which the total number of longline sets was less than 50 over the 1975-2006 period, i.e., areas rarely fished, were removed from our analysis (Fig. 1). Altogether, 95 blocks were removed, leaving 91 blocks which experienced fishing more than 49 times for the modeling analysis. The hooks per basket (HPB) variable was categorized into 5 classes: <4, 5-6, 7-9, 10-14, and >14 HPB. Fishing data with no HPB information were removed from the analysis. Catch rate (CPUE) was expressed as number of albacore caught per thousand hooks.

To fit to the lognormal models, a small constant has to be added to each CPUE due to a large number of zero CPUEs. To reduce the number of zero catch rates, CPUEs were combined for the same cells (based on depth, area, season and year), and the combined CPUEs were fitted to the lognormal models. To measure the fit of the data to the models, the coefficient of determination (R2) and deviance information criterion (DIC) were calculated

Bayesian analyses require that all model parameters have prior probability distributions. We assigned uninformative priors to all the parameters and hyperparameters. Specifically, $c0$, cy, cs, ca, cd were assigned a normal distribution with mean = 0, and variance = 100000 (~ $N(0,316^2)$); for Delta and Zero-inflated models, $p0$, py, ps, pa, pd were also assigned a normal distribution ~ $N(0,316^2)$; for the non-hierarchical lognormal model, each cya was independently assigned a normal distribution, $\sim N(0,316^2)$; $1/\sigma \sim Gamma(0.001,0.0001)$ where 0.001 and 0.0001 represent the parameters of shape and rate of the gamma distribution; for the hierarchical models, the hyperparameters, U_c and U_p, were assigned a normal distribution ~ $N(0,316^2)$; $1/\sigma_c$ and $1/\sigma_p$ were assigned a gamma distribution ~ $Gamma(0.001,0.0001)$.

The WinBUGS software program (Spiegelhalter et al. 2003) was used for the Bayesian analyses. The first 5000 samples from the posterior distribution were treated as a burn-in period. The next 5000 samples from the posterior distribution were saved. Two chains were used with different initial values for the convergence test by the Gelman-Rubin diagnostics (Gelman and Rubin, 1992). Evidence of convergence was warranted by this test.

Results

The lognormal model appears to fit the data better than the Delta or Zero-inflated model based on the values of R^2 (Table 1). For both the hierarchical and non-hierarchical lognormal models R^2 is greater than 0.4 when the data were not combined for the same cells (same depth, area, season and year). When the data were combined, only the hierarchical model exhibited an R^2 greater than 0.4, and the non-hierarchical model had an R^2 (0.23) which was between the R^2 values for Delta and Zero-inflated models. R^2 is 0.30 for the Delta model, only 0.19 for the Zero-inflated lognormal model (Table 1).

The estimated abundance index appeared to be similar to the nominal catch rates in the early years, but was, mostly, significantly less than the nominal catch rates in the later years (Figs. 2-5). The abundance index estimated with the incorporation of predicted catch rates for un-fished areas was consistently lower than those without such incorporation for the later years, regardless of the model used, whereas both abundance indices appear to be similar in the early years (Figs. 2-5). Variations for the estimated abundance index appear to be smaller, when predictions of catch rates are used for the lognormal models (Figs. 2-3). Variations appear to be similar whether or not predictions are used for the Delta or Zero-inflated lognormal models (Figs. 4-5).

Mean abundance indices estimated from all the models appear to be similar for the early years, but differ considerably in the later years (Figs. 6-7). Mean abundance indices estimated from the lognormal models are, in general, lower than those estimated from the Delta or zero-inflated lognormal models in the later years (Figs. 6-7).

The deviance information criterion (DIC) was introduced by Spiegelhalter et al. (2002) as a measure of model comparison and adequacy. Lower DIC values indicate a better model fit. Based on DICs, the Season variable is of more importance than the Depth variable to model performance as DIC increases were greater without incorporation of Season than Depth (Tables 2-3). The interaction between year and area is also a significant variable for the standardization model (Tables 2-3). For the lognormal models, the interaction variable appears to be of more importance than either the Season or Depth variables, as greater DIC increases were observed without incorporation of the interaction variable than without incorporation of Season or Depth, or both Season and Depth (Tables 2-3). The interaction between year and area on CPUE, cya, is of more importance than that on the probability of obtaining non-zero catches, pya, as DIC increases more without incorporation of the latter than the former (Tables 4-5).

For the hierarchical models, the hyperparameters U_c and U_p denote the overall mean interaction effect over different years and areas on CPUE and the probability of obtaining non-zero catches, respectively. The adequacy of model fitting appears to be similar whether U_c and U_p are fixed at zero or are estimated (Tables 3-5).

Discussion

We developed four Bayesian CPUE standardization models, non-hierarchical lognormal, hierarchical lognormal, Delta lognormal, and zero-inflated lognormal models. Based on R^2 when fitted to the data (Table 1) and DIC values (Tables 2-3), the hierarchical lognormal model outperformed the other three models.

Compared with nominal CPUEs for the albacore stock, standardized CPUEs in the later years are significantly lower, indicating that the impact of Area, Season, Depth, and interaction of Year and Area on catch rates was largely removed through the standardization process. Therefore, standardized CPUEs should more accurately reflect the relative changes in the albacore stock abundance. Standardized CPUEs with the incorporation of predicted catch rates for un-fished areas are largely lower than the corresponding predictions without these predictions for the later years, which we interpret as an indication that there may have been some spatial contraction in the albacore fishing patterns.

All explanatory variables used in the models are of significance for explaining variations in catch rates. In particular, the Season variable is of more importance for the model fitting than the Depth variable. However, in our analysis depth was approximated by hooks-per-basket, which may not be the most appropriate measure, but was the only one available. The interaction between year and area on catch rates was more important than either Season or Depth in explaining variations in catch rates. It is reasonable, at least for the albacore stock, to assume that the mean interaction over all years and areas on the catch rates is zero, as this assumption may lead to slightly reduced DIC than when the overall mean interaction to be estimated.

We provided some new tools for CPUE standardization. These models, especially the hierarchical lognormal model, produce promising outcomes on the albacore catch data. These models need to be further tested on other tuna species.

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Table 1. Coefficient of Determination (R^2) for the Models.

	Data Un-Combined for the Same Cells	Data Combined for the Same Cells
Non-Hierarchical Lognormal	0.42	0.23
Hierarchical Lognormal	0.48	0.48
Delta	0.30	
Zero-inflated Lognormal	0.19	

Table 2. Coefficient of determination (R^2) and deviance information criterion (DIC) for the lognormal model with fixed effects for the year and area interaction (data un-combined).

Model Types	R^2	DIC
c0+cy+cs+ca+cd+cya	0.42	111163
c0+cy+cs+ca+cd	0.41	114834
c0+cy+ca+cd+cya	0.40	112602
c0+cy+cs+ca+cya	0.41	111681
c0+cy+ca+cya	0.39	113124

Table 3. Coefficient of determination (R^2) and deviance information criterion (DIC) for the lognormal model with random effects for the year and area interaction (data un-combined).

	R^2	DIC
c0+cy+cs+ca+cd+cya	0.48	110773
c0+cy+cs+ca+cd+cya^0	0.48	110774
c0+cy+cs+ca+cd	0.41	114835
c0+cy+ca+cd+cya^0	0.47	112210
c0+cy+cs+ca+cya^0	0.48	111304
c0+cy+ca+cya^0	0.47	112750

cya ~ $N(U,\sigma^2)$ The hyperparameters, U and σ are assigned a normal distribution and a gamma distribution, respectively.
cya^0 ~ $N(U,\sigma^2)$ The hyperparameter, U is fixed to be 0, and the hyperparameter, σ, is assigned a gamma distribution.

Table 4. Coefficient of determination (R^2) and deviance information criterion (DIC) for the Delta Model.

	R^2	DIC
c0+cy+cs+ca+cd+cya p0+py+ps+pa+pd+pya	0.30	111692
c0+cy+cs+ca+cd+cya p0+py+ps+pa+pd	0.29	113397
c0+cy+cs+ca+cd p0+py+ps+pa+pd+pya	0.28	113804
c0+cy+cs+ca+cd+cya^0 p0+py+ps+pa+pd+pya^0	0.30	111698
c0+cy+cs+ca+cd+cya^0 p0+py+ps+pa+pd	0.29	113395
c0+cy+cs+ca+cd p0+py+ps+pa+pd+pya^0	0.28	113800

cya ~ $N(U,\sigma^2)$ The hyperparameters, U and σ are assigned a normal distribution and a gamma distribution, respectively.
pya^0 ~ $N(U,\sigma^2)$ The hyperparameter, U is fixed to be 0, and the hyperparameter, σ, is assigned a gamma distribution

Table 5. Coefficient of determination (R^2) and deviance information criterion (DIC) for the Zero-inflated lognormal model.

	R^2	DIC
c0+cy+cs+ca+cd+cya p0+py+ps+pa+pd+pya	0.19	123593
c0+cy+cs+ca+cd+cya p0+py+ps+pa+pd	0.18	125064
c0+cy+cs+ca+cd p0+py+ps+pa+pd+pya	0.14	126642
c0+cy+cs+ca+cd+cya^0 p0+py+ps+pa+pd+pya^0	0.18	123419
c0+cy+cs+ca+cd+cya^0 p0+py+ps+pa+pd	0.18	125065
c0+cy+cs+ca+cd p0+py+ps+pa+pd+pya^0	0.14	125476

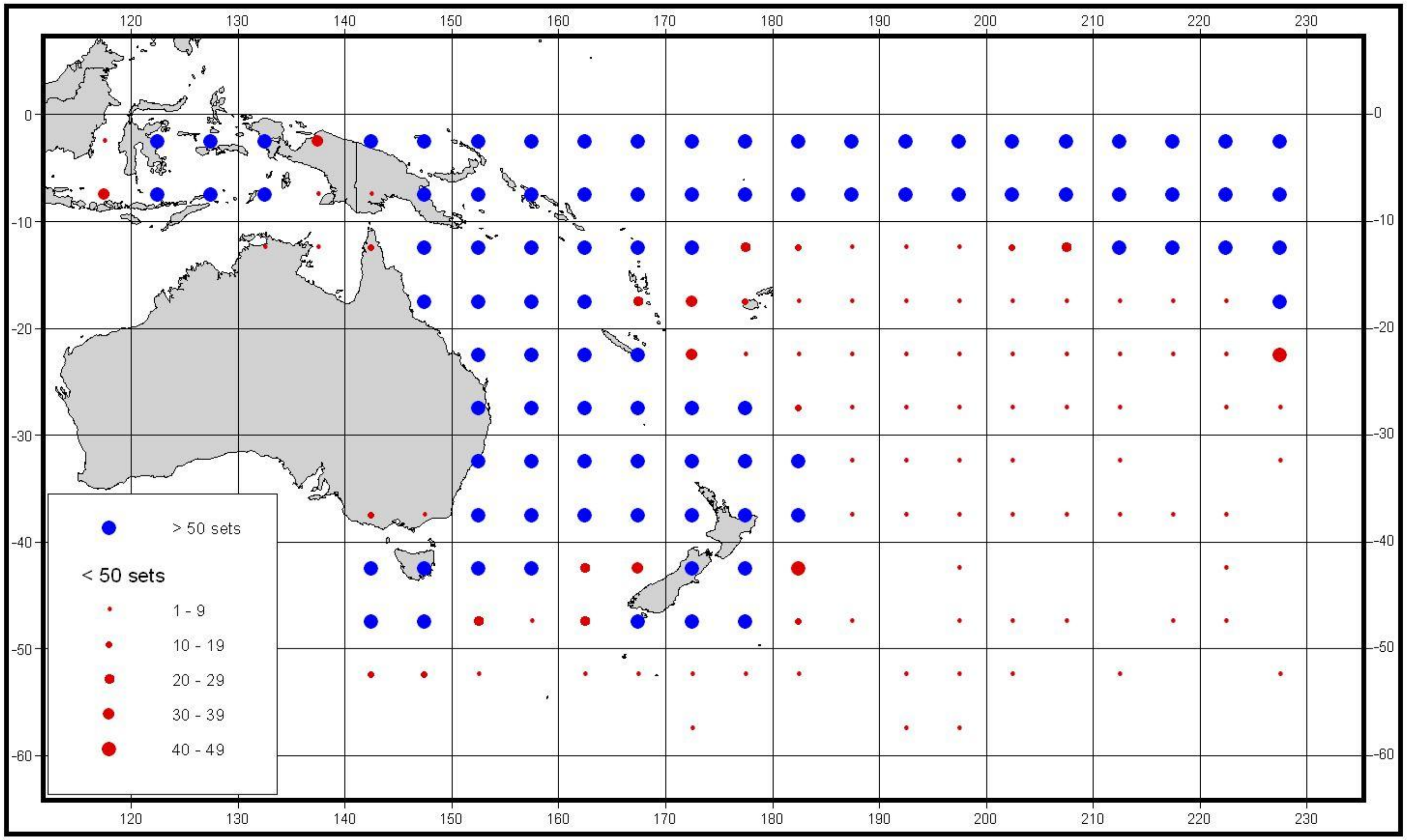

Fig. 1. Fishing distribution (longline sets less than 50 are not used in the analyses).

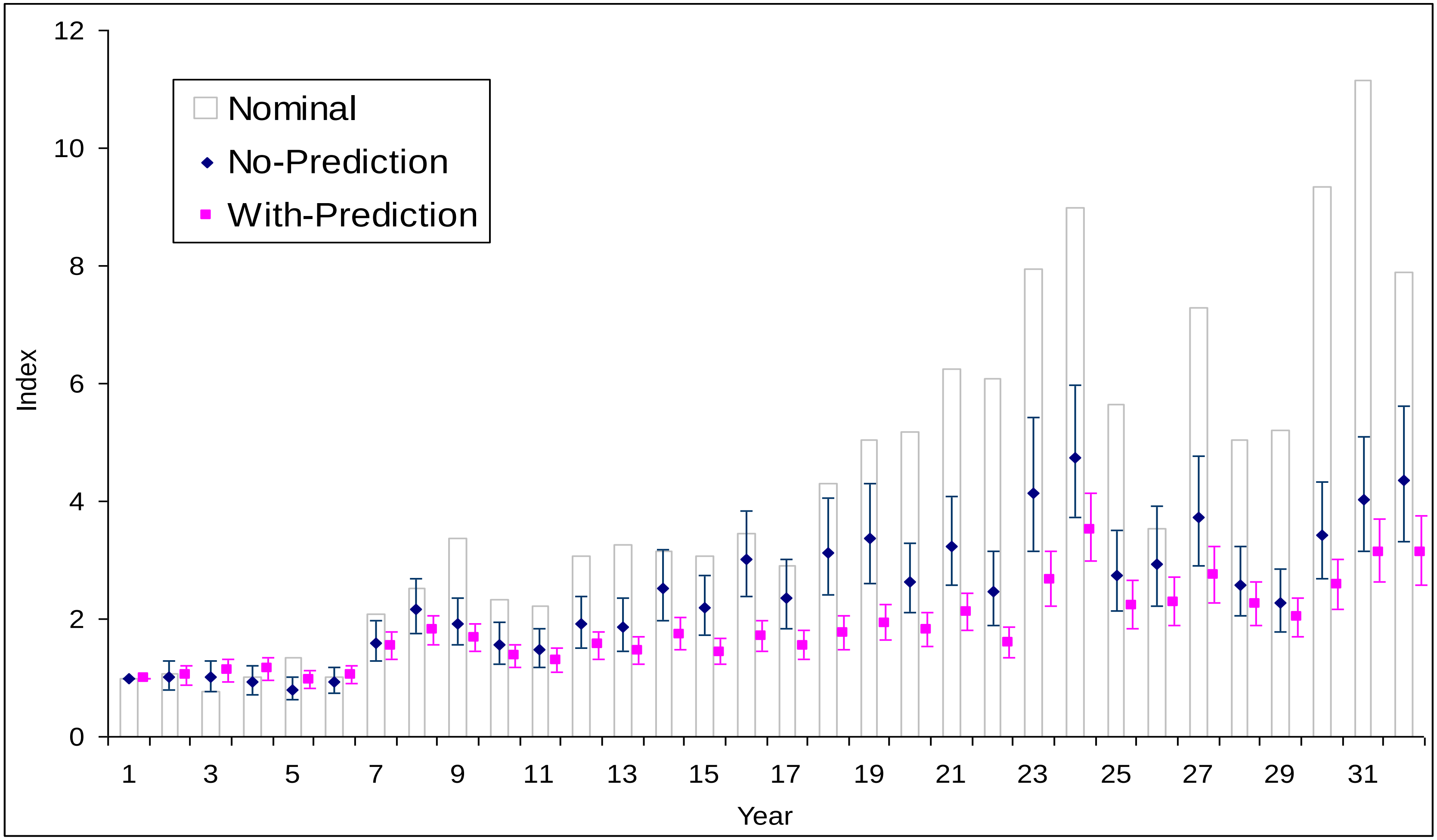

Fig. 2. Estimated annual abundance index relative to the first year with 95% credible intervals, using the Lognormal Model with catch data combined for each cell (same depth, area, season and year). Index was estimated either without (BLUE) or with (RED) incorporation of predictions of abundance index for the un-fished areas.

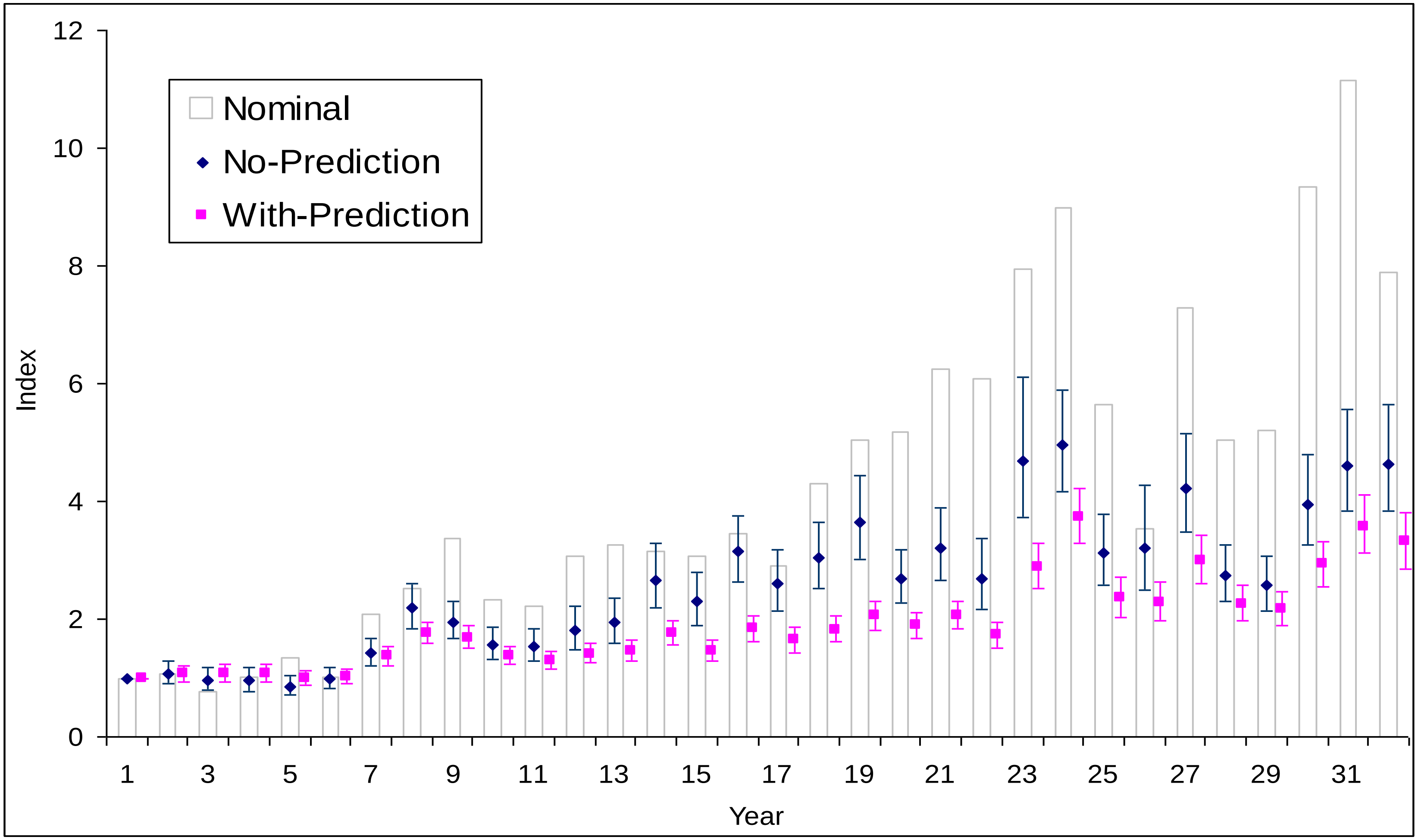

Fig. 3. Estimated annual abundance index relative to the first year with 95% credible intervals, using the Lognormal Model without (BLUE) or with (RED) incorporation of predictions of abundance index for the un-fished areas.

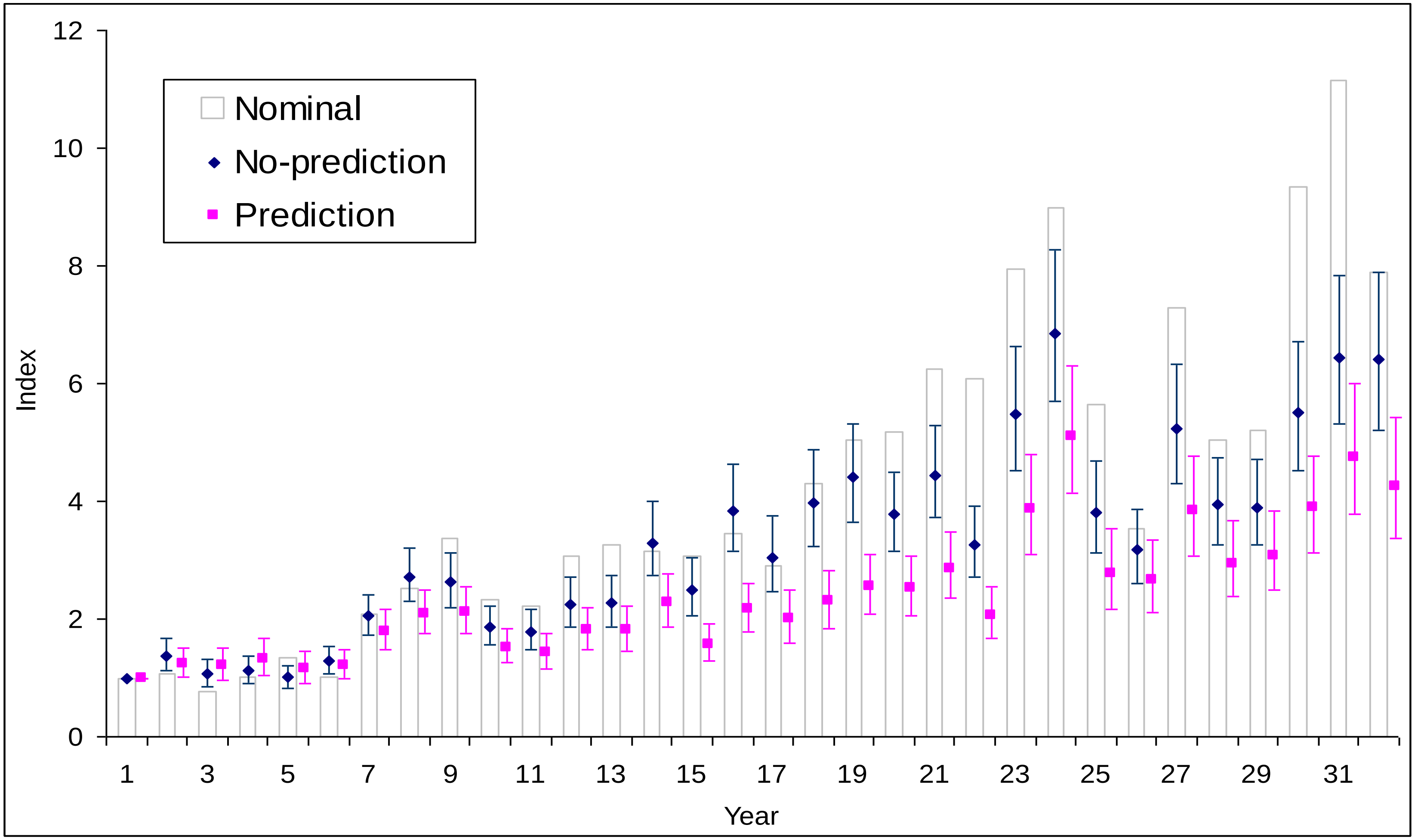

Fig. 4. Estimated annual abundance index relative to the first year with 95% credible intervals, using the Lognormal Model without (BLUE) or with (RED) incorporation of predictions of abundance index for the un-fished areas.

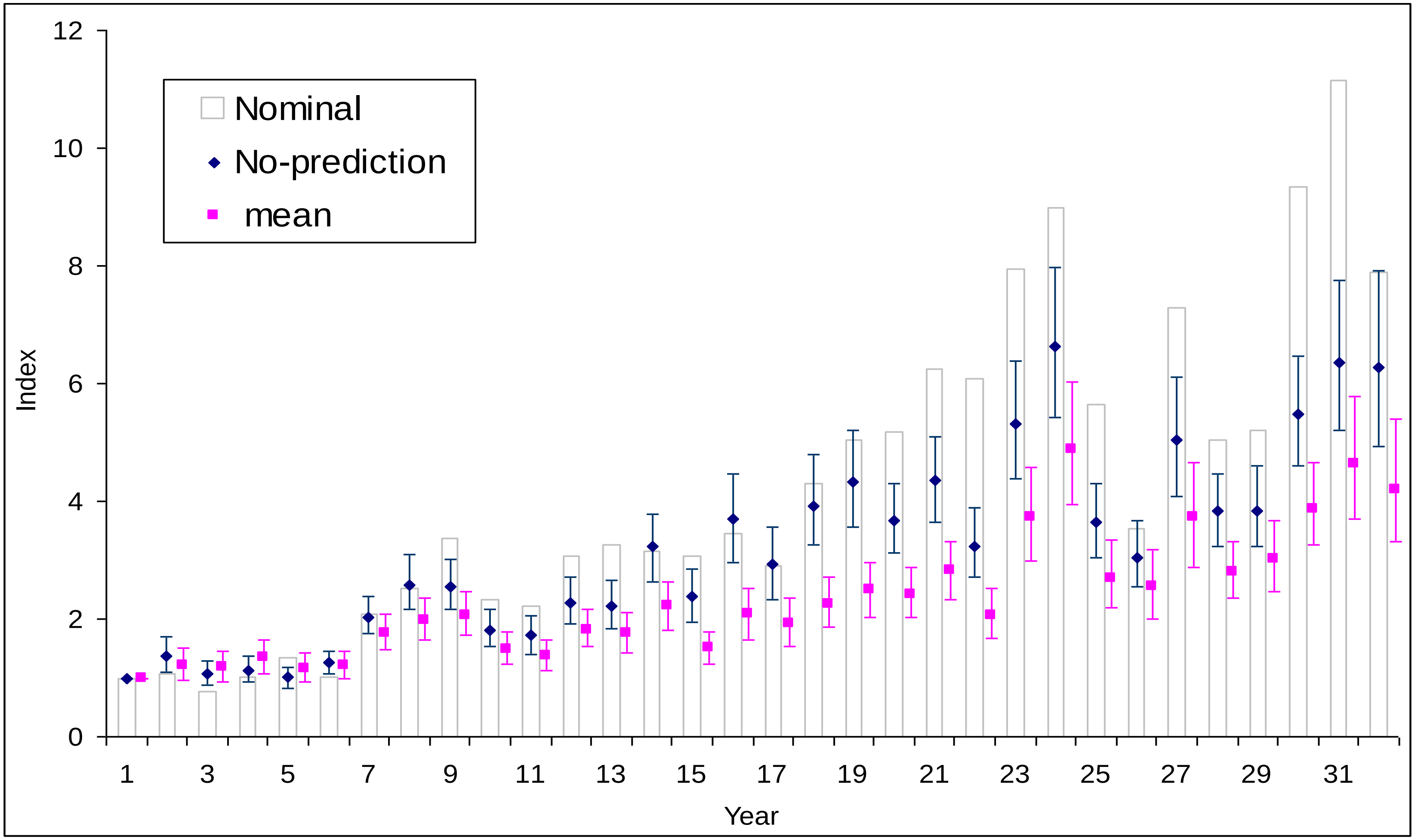

Fig. 5. Estimated annual abundance index relative to the first year with 95% credible intervals, using the Zero-inflated Lognormal Model without (BLUE) or with (RED) incorporation of predictions of abundance index for the un-fished areas.

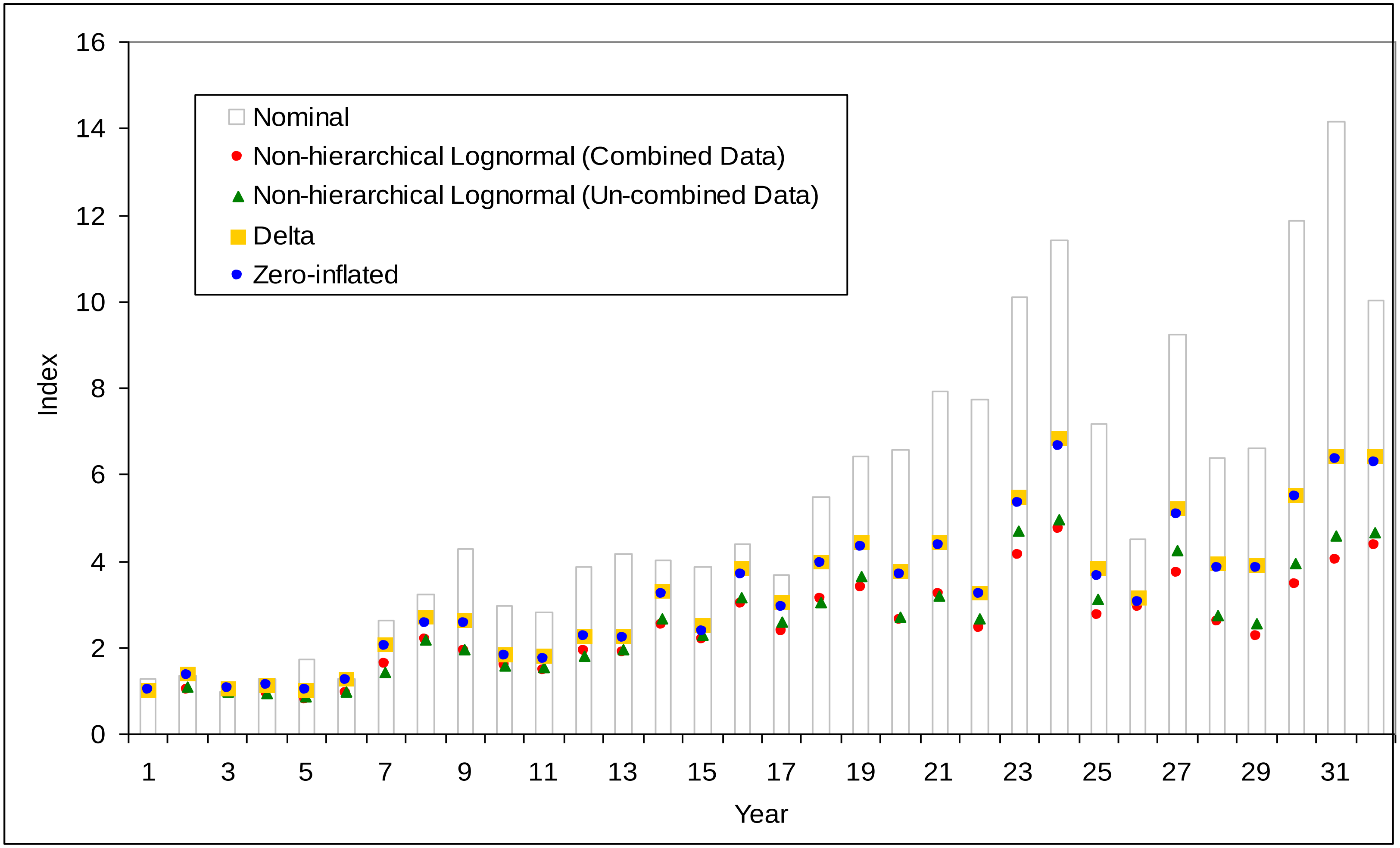

Fig. 6. Estimated annual mean abundance index relative to the first year, using non-hierarchical lognormal(with combined and un-combined data), Delta, and Zero-inflated lognormal models without incorporation of predictions of abundance index for the un-fished areas.

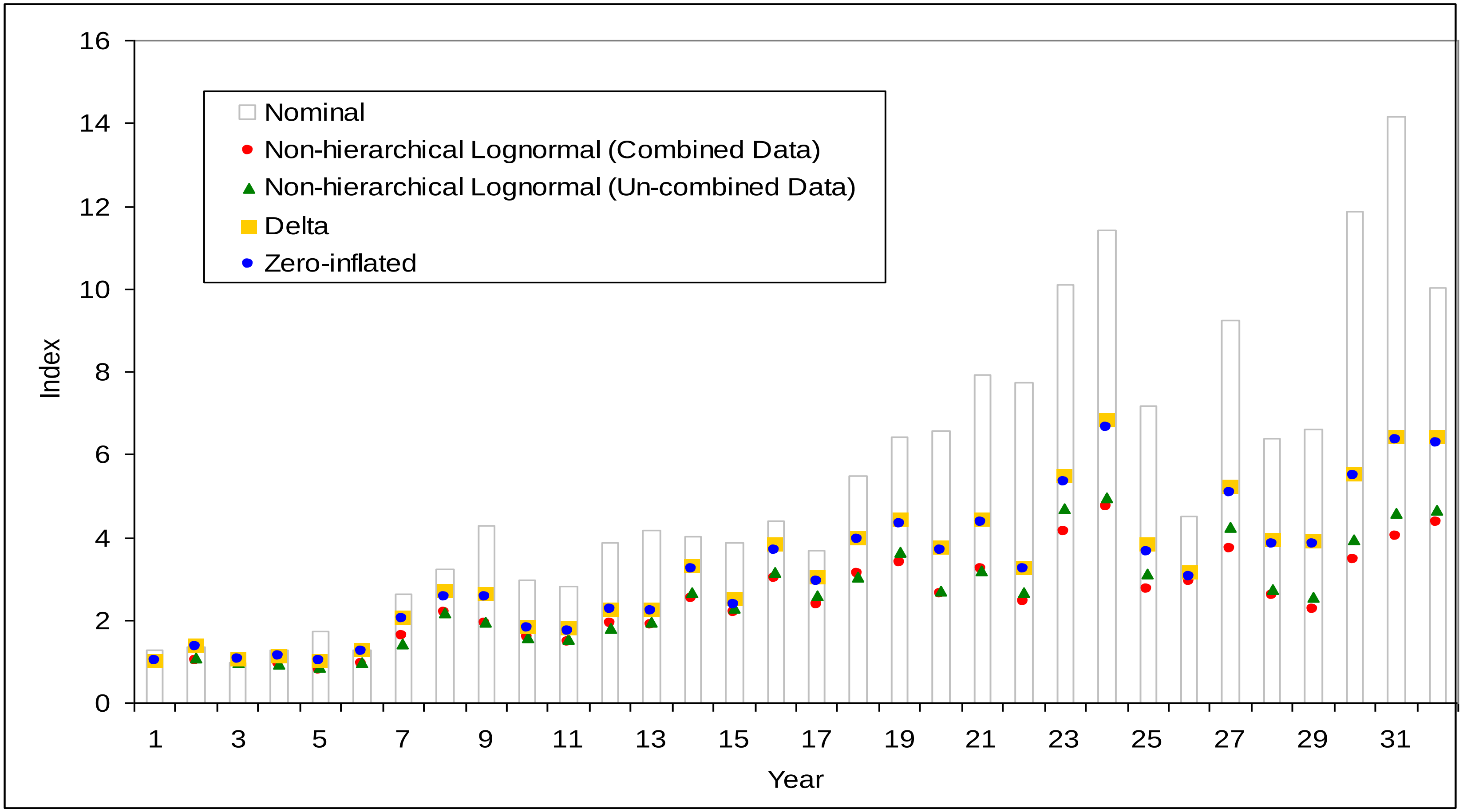

Fig. 7. Estimated annual mean abundance index relative to the first year, using hierarchical lognormal (with combined and un-combined data), Delta, and Zero-inflated lognormal models with incorporation of predictions of abundance index for the un-fished areas.