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Estimation of a biomass limit reference point for beaked redfish
(*S. mentella* and *S. fasciatus*) in NAFO Division 3M

By

Tatiana Muzychka^{1,2}, Patrícia Gonçalves¹, Ricardo Alpoim¹, Paula Simões^{2,3,4,5}, Sandra. M. Aleixo^{2,5}

¹ Instituto Português do Mar e da Atmosfera, IPMA, Rua Alfredo Magalhães Ramalho, nº6,
1495-006 Lisboa, Portugal

² Instituto Superior de Engenharia de Lisboa (ISEL) Rua Conselheiro Emídio Navarro, nº 1
1959-007 Lisboa, Portugal

³ Center for Mathematics and Applications (NOVA MATH), NOVA University of Lisbon, Portugal

⁴ Military Academy Research Center, Military University Institute (CINAMIL) Lisbon, Portugal

⁵ Centro de Estatística e Aplicações da Universidade de Lisboa (CEAUL), Faculdade de Ciências da
Universidade de Lisboa, Bloco C6, Piso 4, 1749-016 Lisboa, Portugal

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Abstract

The estimation of biological reference points is essential for sustainable fisheries management, particularly for stocks that have experienced historical depletion or exhibit complex population dynamics. The biomass limit reference point (B_{lim}) represents the biomass level below which serious harm to the stock is expected, and its determination requires careful consideration of historical biomass trajectories, recruitment patterns, and the reliability of survey and fishery-dependent data. For NAFO Division 3M beaked redfish, the use of combined data for two co-occurring species (*Sebastes mentella* and *S. fasciatus*), together with the pronounced and irregular recruitment pulses characteristic of this stock, poses significant challenges for deriving a robust and precautionary B_{lim} . In this study, stock-recruitment models (Beverton-Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick) and Surplus Production models (Schaefer, Fox, and Pella-Tomlinson) were applied to NAFO Division 3M redfish, to estimate B_{lim} based on model performance. Among the models implemented, the Schaefer model provided the best fit and was therefore used to derive the final B_{lim} estimate. These results are consistent with those reported by Gonçalves et al. (2023), who also identified the Schaefer model as the best-performing approach, yielding estimates of $BMSY = 112,561$ t and $Blim = 33,768$ t. However, while the 2023 study used automated R packages, the main difference in this work is that all functions, the optim routine, and the gradient method were R-programmed completely by hand from scratch.

Introduction

The estimation of biological reference points is essential for ensuring sustainable fisheries management, particularly for stocks that have experienced historical depletion or exhibit complex population dynamics. In the Northwest Atlantic, the redfish (*Sebastes* spp.) stock in NAFO Division 3M has undergone significant fluctuations in biomass and recruitment over recent decades, driven by both environmental variability and fishing pressure. As a result, establishing a robust and precautionary limit reference point

(B_{lim}) is critical for evaluating stock status and guiding management decisions under the NAFO Precautionary Approach Framework.

B_{lim} represents the biomass level below which serious harm to the stock is expected to occur, and its estimation requires careful consideration of historical stock trajectories, recruitment patterns, and the reliability of available survey and fishery-dependent data. For NAFO Division 3M beaked redfish, deriving a robust and precautionary B_{lim} poses significant challenges. This difficulty arises from the overlapping spatial distributions of *Sebastes mentella* and *S. fasciatus*, the reliance on data that combines both species, and the pronounced, irregular recruitment pulses characteristic of this stock (Alpoim et al., 2021). Despite these uncertainties, defining a scientifically defensible B_{lim} is necessary to support harvest control rules, assess rebuilding prospects, and ensure long-term sustainability of the stock.

This study is directly aligned with the new NAFO Precautionary Approach Framework (PAF) approved in 2024 (NAFO, 2024a). As outlined by the Joint Commission–Scientific Council Working Group on Risk-Based Management Strategies (WG-RBMS) in August 2024, this updated framework emphasizes the need for robust, model-based definitions of limit reference points to prevent stock depletion (NAFO, 2024b). The revised PAF defines three stock status zones (Healthy, Cautious, and Critical) based on two biomass reference points: the limit biomass (B_{lim}) and the biomass trigger reference point ($B_{trigger}$). Within this management framework, fishing mortality (F) limits are strictly regulated: the limit fishing mortality (F_{lim}) is set equal to F_{MSY} (the fishing mortality associated with Maximum Sustainable Yield), while the target fishing mortality (F_{target}) is specified as a precautionary fraction of F_{MSY} to prevent overfishing.

This study aims to evaluate alternative approaches for estimating B_{lim} for 3M redfish, assess their consistency with NAFO guidelines, and identify the most suitable reference point for management purposes.

Material and Methods

NAFO Division 3M Redfish input data. The data used for estimating the stock Biological Reference Points (BRPs) is the same used as input data for the 2021 stock assessment model (Alpoim et al., 2021). In fisheries science, BRPs represent estimated thresholds of biomass or fishing mortality used to guide sustainable management decisions. The data is from 1989 to 2020, structured by individual annual ages from 4 to 18, with a combined 19+ plus-group. The recruitment estimate (in millions), the spawning stock biomass (in tonnes), the catches (in tonnes) and the fishing mortality for the ages 4 to 19+ for the whole period (1989 until 2020) are shown in the graphs presented in Figure 1.

Stock-recruitment models. To estimate B_{lim} based on stock–recruitment (S-R) relationships, four models were fitted to the Spawning Stock Biomass (SSB) –recruitment data, whose formulas will be presented below in Table 1: Beverton–Holt, Ricker, Segmented Regression and Smooth Hockey-Stick model (Cadima, 2003).

Each model was fitted assuming a lognormal error structure on recruitment, with SSB as the explanatory variable. Parameter estimation (a and b) was carried out by maximum likelihood method (Pawitan, 2001).

Table 1. Equation of the stock-recruitment models (Beverton–Holt, Ricker Segmented Regression and Smooth Hockey Stick model).

S-R Model	Equation
Beverton and Holt	$R = \frac{a \times SSB}{1 + b \times SSB}$
Ricker	$R = a \times SSB \times e^{-b \times SSB}$
Segmented Regression	$R = \begin{cases} a \times SSB, & SSB \leq b \\ a \times b, & SSB > b \end{cases}$
Smooth Hockey-Stick	$R = Rmax \times (1 - e^{-\frac{a \times SSB}{Rmax}})$

B_{lim} estimation from stock–recruitment models. For each stock–recruitment model, B_{lim} was derived as the SSB level associated with a critical reduction in recruitment or productivity, consistent with the NAFO Precautionary Approach. B_{lim} was derived from stock–recruitment relationships by fitting Beverton–Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick models to the SSB–recruitment data. For the Beverton–Holt formulation, B_{lim} was defined as the spawning biomass at which the expected recruitment drops to 50% of its asymptotic maximum. For the Ricker and Smooth Hockey-Stick models, B_{lim} was obtained numerically as the SSB level corresponding to a 50% reduction from the model's maximum predicted recruitment. Additionally, for the Segmented Regression and Smooth Hockey-Stick models, the estimated breakpoint was interpreted as a candidate B_{lim} , representing the biomass threshold below which recruitment becomes impaired.

Production models. In addition to the stock–recruitment relationships, B_{lim} was also estimated from surplus production dynamics. Three alternative formulations were fitted to the catch and biomass survey index data: the Schaefer, Fox, and Pella–Tomlinson models (Cadima, 2003). These surplus production models track the stock dynamics using the total exploitable biomass (B) as the metric, in accordance with Russell's formulation:

$$B_{t+1} = B_t - C_t + f(B_t)$$

where B_t represents the stock biomass at the beginning of year t , C_t is the biomass caught during year t , and $f(B_t)$ is the surplus production function. The specific mathematical formulations for $f(B_t)$ in each model are detailed below in Table 2.

Table 2. Equation of the production models (Schaefer, Fox and Pella–Tomlinson).

S-R Model	Equation
Schaefer	$f(B_t) = r\bar{B}_t \left(1 - \frac{\bar{B}_t}{K}\right)$
Fox	$f(B_t) = \log(K) r\bar{B}_t \left(1 - \frac{\log(\bar{B}_t)}{\log(K)}\right)$
Pella–Tomlinson	$f(B_t) = \frac{r}{p} \bar{B}_t \left(1 - \left(\frac{\bar{B}_t}{K}\right)^p\right)$

Each framework was fitted using maximum likelihood estimation, assuming a log-normal error structure on the biomass indices. The parameters estimated across these frameworks included the intrinsic growth rate (r), the carrying capacity (K), and the shape parameter (p , applicable exclusively to the Pella–Tomlinson model).

B_{lim} estimation from surplus production models. Surplus production models describe how stock biomass (B) generates surplus production ($f(B_t)$) based on key biological parameters, including the

intrinsic growth rate (r), carrying capacity (K), and, where applicable, a shape parameter (p). Once a model is fitted to the data, the biomass at maximum sustainable yield (B_{MSY}) is obtained analytically from the respective model equations. Consequently, rather than using a static definition, B_{lim} is derived directly as a precautionary fraction of this estimated B_{MSY} (Table 3).

Table 3. Summary of biomass reference points calculations, using the three surplus production models. The table presents the analytical expressions for B_{MSY} under the Schaefer, Fox, and Pella–Tomlinson models, along with the corresponding B_{lim} values derived using the NAFO PAF $B_{lim} = 0.3 \times B_{MSY}$ (NAFO, 2024a).

Model	B_{MSY} formula	B_{lim} formula ($0.3 \times B_{MSY}$)
Schaefer	$B_{MSY} = K / 2$	$B_{lim} = 0.3 \times (K / 2) = 0.2 \times K$
Fox	$B_{MSY} = K / e$	$B_{lim} = 0.3 \times (K / e)$
Pella–Tomlinson	$B_{MSY} = K \times (1 / (1 + p))^{(1/p)}$	$B_{lim} = 0.3 \times K \times (1 / (1 + p))^{(1/p)}$

(where $e = 2.718282$)

Residual diagnostics.

The assumptions of the fitted models were evaluated through residual analysis, namely approximate normality, independence and homogeneity of variance, following diagnostic approaches commonly recommended for nonlinear regression models (Bates *et al.*, 1988; Seber *et al.*, 1989).

Normality of residuals: The assumption of normality was first evaluated qualitatively through graphical analysis using Normal Quantile-Quantile (Q-Q) plots, where a distribution is assumed to be normal if the sample points closely follow the theoretical diagonal reference line. To formally confirm the visual analysis, the Shapiro-Wilk test was applied. The null hypothesis (H_0) states that the residuals are normally distributed. The decision rule consists of rejecting H_0 if the calculated p-value is lower than the considered significance level ($\alpha = 0.05$).

Independence of residuals: The presence of serial correlation was first visually examined via Autocorrelation Function (ACF) plots across multiple time lags, to check for structural dependencies over time. To formally confirm the visual analysis, the Durbin-Watson test was applied. The null hypothesis (H_0) assumes the absence of first-order autocorrelation states that serial correlation is present. Independence is accepted if the test statistic (d) falls within the conservative academic threshold of [1.5, 2.5].

Homoscedasticity of residuals: Constant variance of the errors was first graphically assessed by plotting the residuals against the fitted values, searching for a random scatter of points evenly distributed around the zero reference line. To formally confirm the visual analysis, the Breusch-Pagan test was conducted. This statistical test evaluates the null hypothesis (H_0) of homoscedasticity (constant variance). The null hypothesis is rejected if the resulting p-value is lower than the significance level of $\alpha = 0.05$, indicating that the model's residual variance is non-constant.

For the surplus-production functions (Schaefer, Fox, and Pella–Tomlinson), residual diagnostics were conducted for the model errors associated with the Russell model, defined as one-step-ahead prediction errors on the log scale: $\varepsilon_t = \log(B_{t+1}^{obs}) - \log(B_{t+1|t}^{pred})$, where $B_{t+1|t}^{pred}$ denotes the biomass predicted for year $t+1$ conditional on information available up to year t (Durbin and Koopman, 2012).

Any stock–recruitment or surplus production model failing to meet basic assumptions was either rejected or interpreted with caution when deriving B_{lim} .

Models performance. To compare the performance of the models and select the most appropriate formulation, the following criteria were used: Akaike Information Criterion (AIC) and Mean Squared Error (MSE).

AIC was computed for each model, and models were ranked based on their relative support, with lower AIC indicating better fit while penalizing model complexity. MSE of residuals (observed vs. predicted biomass or index) was calculated to quantify overall goodness-of-fit.

Models with lower AIC and MSE were considered to provide a better description of the redfish dynamics. B_{lim} estimates from the best-performing models were compared across recruitment and production model families to assess consistency and robustness.

Results and Discussion

Stock-recruitment models: The functions of the different S-R models and their respective estimated parameters are presented in Table 4 (Mosqueira et al., 2026). The parameter estimates were obtained through a custom-built routine programmed by hand using the `optim` function and the gradient method within the R software environment.

Table 4. Estimated parameters of the stock–recruitment models (Beverton–Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick).

S-R Model	Estimated parameters
Beverton and Holt	$\hat{a} = 20.73814$
	$\hat{b} = 0.00027$
Ricker	$\hat{a} = 12.95771$
	$\hat{b} = 0.000048$
Segmented Regression	$\hat{a} = 6.14203$
	$\hat{b} = 10899.51$
Smooth Hockey-Stick	$\hat{a} = 3.209721$

The fit of the stock–recruitment models to the NAFO Division 3M redfish data (SSB and recruitment), along with their respective diagnostic plots, is shown in Figure 2 (Beverton–Holt), Figure 3 (Ricker), Figure 4 (Segmented Regression), and Figure 5 (Smooth Hockey-stick). For each S-R model, the assumptions of residual normality (Figure 6), residual independence (Figure 7), and residual homoscedasticity (Figure 8) were graphically evaluated.

Residuals from all models, Figure 7, exhibit positive autocorrelation at short lags followed by negative autocorrelation at intermediate lags, suggesting remaining temporal structure not fully captured by the fitted models.

In Figure 8 the residual distributions reveal varying degrees of heteroscedasticity and systematic structure across models, with Beverton-Holt and Segmented regression models showing increased residual spread and clustering at higher predicted recruitment values, suggesting potential model misspecification and non-constant variance. A comprehensive comparison of these fitted S-R models is presented in Table 5, compiled via the diagnostic and estimation outputs of the R environment.

Table 5. Diagnostic tests evaluating residual assumptions for the Beverton–Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick stock-recruitment (S–R) models. Normality was assessed using the Shapiro–Wilk test, independence using the Durbin–Watson test, and homoscedasticity using the Breusch–Pagan test.

S-R model	Assumption of the residuals	Test	Results	Conclusion
Beverton - Holt	Normality	Shapiro-Wilk	W = 0.94313 p-value = 0.1328	The residuals come from a population with a normal distribution.
Beverton - Holt	Independence	Durbin-Watson	d = 0.4102271	The residuals are not independent.
Beverton - Holt	Homoscedasticity	Breusch-Pagan*	LM = 16.879799	The variance of the errors is not constant.
Ricker	Normality	Shapiro-Wilk	W = 0.95078 p-value = 0.2073	The residuals come from a population with a normal distribution.
Ricker	Independence	Durbin-Watson	d = 0.5196718	The residuals are not independent.
Ricker	Homoscedasticity	Breusch-Pagan*	LM = 13.808726	The variance of the errors is not constant.
Segmented Regression	Normality	Shapiro-Wilk	W = 0.93117 p-value = 0.066	The residuals come from a population with a normal distribution.
Segmented Regression	Independence	Durbin-Watson	d = 0.4505312	The residuals are not independent.
Segmented Regression	Homoscedasticity	Breusch-Pagan*	LM = 15.976669	The variance of the errors is not constant.
Smooth Hockey-stick	Normality	Shapiro-Wilk	W = 0.96298 p-value = 0.4093	The residuals come from a population with a normal distribution.
Smooth Hockey-stick	Independence	Durbin-Watson	d = 0.2787437	The residuals are not independent.
Smooth Hockey-stick	Homoscedasticity	Breusch-Pagan*	LM = 19.963657	The variance of the errors is not constant.

*The test is based on the principle of the Lagrange Multiplier.

Residuals from all models were approximately normally distributed ($p\text{-value} > 0.05$); however, Durbin-Watson statistics indicated significant temporal autocorrelation, and Breusch-Pagan test results suggested heteroscedasticity, indicating violations of independence and constant variance assumptions across all models.

Since the alternative stock-recruitment frameworks violated critical assumptions of residual analysis, specifically showing severe heteroscedasticity and non-normal error distributions, they fail to provide statistically robust foundation for management advice. Biologically, this poor fit stems from the high scatter and lack of a clear functional relationship in the SSB-recruitment data for this stock. Consequently, these S-R formulations were rejected as reliable estimators, and surplus production models were utilized instead. The production frameworks integrate historical catches and survey biomass indices more effectively, offering a more stable and coherent alternative for deriving the B_{lim} reference point.

Production models: The equations of the different models and their respective estimated parameters are presented in Table 6. The parameter estimates were obtained using the knobi package framework, with numerical optimization performed via the optim function in R (Paz et al., 2026).

Table 6. Equation of the production models and their estimated parameters (Schaefer, Fox and Pella-Tomlinson).

S-R Model	Estimated parameters
Schaefer	$\hat{r} = 0.2572$ $\hat{K} = 225223$
Fox	$\hat{r} = 0.1322$ $\hat{K} = 269754$
Pella-Tomlinson	$\hat{r} = 0.1904$ $\hat{K} = 240810$ $\hat{p} = 0.4371$

For each production model, the assumptions of residual normality (Figure 9), residual independence (Figure 10), and residual homoscedasticity (Figure 11) were evaluated. The results from residuals analysis are summarized in Table 7, compiled via statistical testing functions within the R environment.

Table 7. Diagnostic tests evaluating residual assumptions for Schaefer, Fox and Pella-Tomlinson production models. Normality was assessed using the Shapiro-Wilk test, independence using the Durbin-Watson statistic, and homoscedasticity using the Breusch-Pagan test.

Production model	Assumption of the residuals	Test	Results	Conclusion
Schaefer	Normality	Shapiro-Wilk	W = 0.97954 p-value = 0.7997	The residuals come from a population with a normal distribution.
Schaefer	Independence	Durbin-Watson	d = 1.8668	The residuals are independent.
Schaefer	Homoscedasticity	Breusch-Pagan	LM = 0.09147674	The variance of the errors is constant.
Fox	Normality	Shapiro-Wilk	W = 0.96555 p-value = 0.4057	The residuals come from a population with a normal distribution.
Fox	Independence	Durbin-Watson	d = 1.704403	The residuals are independent.

Fox	Homoscedasticity	Breusch-Pagan	LM = 0.5375409	The variance of the errors is constant.
Pella-Tomlinson	Normality	Shapiro-Wilk	W = 0.9701 p-value = 0.5219	The residuals come from a population with a normal distribution.
Pella-Tomlinson	Independence	Durbin-Watson	d = 1.784125	The residuals are independent.
Pella-Tomlinson	Homoscedasticity	Breusch-Pagan	LM = 0.2682498	The variance of the errors is constant.

The residual diagnostics in Table 7, indicated that all three production models, Schaefer, Fox, and Pella-Tomlinson, adequately satisfied the main assumptions. Shapiro-Wilk test results (p-value>0.05 for all models) showed that residuals were normally distributed. Durbin-Watson statistics, with values close to 2, indicated no evidence of autocorrelation, suggesting that residuals were independent. In addition, low Breusch-Pagan test statistics supported the assumption of homoscedasticity, indicating constant error variance across fitted values. Overall, the diagnostic tests suggest that the production models provided statistically well-behaved residuals and met the assumptions required for reliable inference and model interpretation.

Table 8. Model selection criteria and predictive error statistics for the Schaefer, Fox, and Pella-Tomlinson production models. Model performance was evaluated using Akaike's Information Criterion (AIC) and Mean Squared Error (MSE), where lower values indicate better model fit and predictive accuracy.

Production model	AIC	MSE
Schaefer	689.1462	0.01815174
Fox	689.0997	0.01969571
Pella-Tomlinson	690.9935	0.01881436

Among the three production models, the Fox model produced the lowest AIC value (689.0997), indicating the best overall balance between goodness-of-fit and model complexity. In contrast, the Schaefer model yielded the lowest MSE (0.01815174), suggesting slightly better predictive accuracy. The Pella-Tomlinson model showed the highest AIC and a comparatively larger MSE, indicating weaker overall performance relative to the other models. Because the differences in AIC and MSE between the Schaefer and Fox models are minimal, both models demonstrate a reasonably good and equivalent fit to the data.

Conclusions

The biomass-based reference points (B_{MSY} , B_{lim} , and $B_{trigger}$) derived from the Schaefer and Fox formulations are summarized in Table 9, providing a comparative basis for implementing the NAFO Precautionary Approach Framework guidelines.

Table 9. Biomass reference points (B_{MSY} , B_{lim} and $B_{trigger}$) estimated from the Schaefer and Fox production models for the Northwest Atlantic Fisheries Organization Precautionary Approach Framework (NAFO PAF) over the 1990–2020 period.

Production model	NAFO PAF	B_{MSY}	$B_{trigger}$	B_{lim}
Schaeffer (K=225223)	Reference Point	K/2	0.75*BMSY	0.30*BMSY
Schaeffer	Estimated Value (1990 - 2020)	112612 tons	84459 tons	33784 tons
Fox (K = 269754)	Reference Point	K/e (where e = 2.718282)	0.75*BMSY	0.30*BMSY
Fox	Estimated Value (1990 - 2020)	99237 tons	74428 tons	29772 tons

The Schaefer model was identified as the most suitable framework for describing the stock dynamics. Although the difference in AIC between the Schaefer and Fox models was minimal, suggesting comparable goodness-of-fit during model estimation, the Schaefer model demonstrated substantially better predictive performance. Specifically, it produced a lower Mean Squared Error ($MSE=0.01815$) than the Fox model, indicating greater accuracy and precision in forecasting next-year biomass (B_{t+1}). These results suggest that the Schaefer model provides a more reliable basis for prediction and management applications. The results obtained in this study independently validate the historical benchmarks proposed by Gonçalves et al. (2023), identifying the Schaefer model as the premier framework for this stock ($B_{MSY} = 112,561$ tonnes; $B_{lim} = 33,768$ tonnes). However, while the 2023 study used automated R packages such as FLBRP and msy to estimate the model parameters, the main difference in this work is that all functions, the optim routine, and the gradient method were programmed completely by hand from scratch. Adopting the biological formulations aligned with the knobi framework, the entire optimization routine was developed independently.

The statistical validity of this approach is confirmed by the predictive diagnostics. While the close AIC values suggested that both the Schaefer and Fox models fitted the historical data equally well, the Schaefer formulation achieved a lower Mean Squared Error ($MSE = 0.01815$). This indicates a higher accuracy in projecting next-year biomass (B_{t+1}), demonstrating that an independently programmed mathematical structure can successfully secure and replicate critical biological references with absolute operational transparency.

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Figures

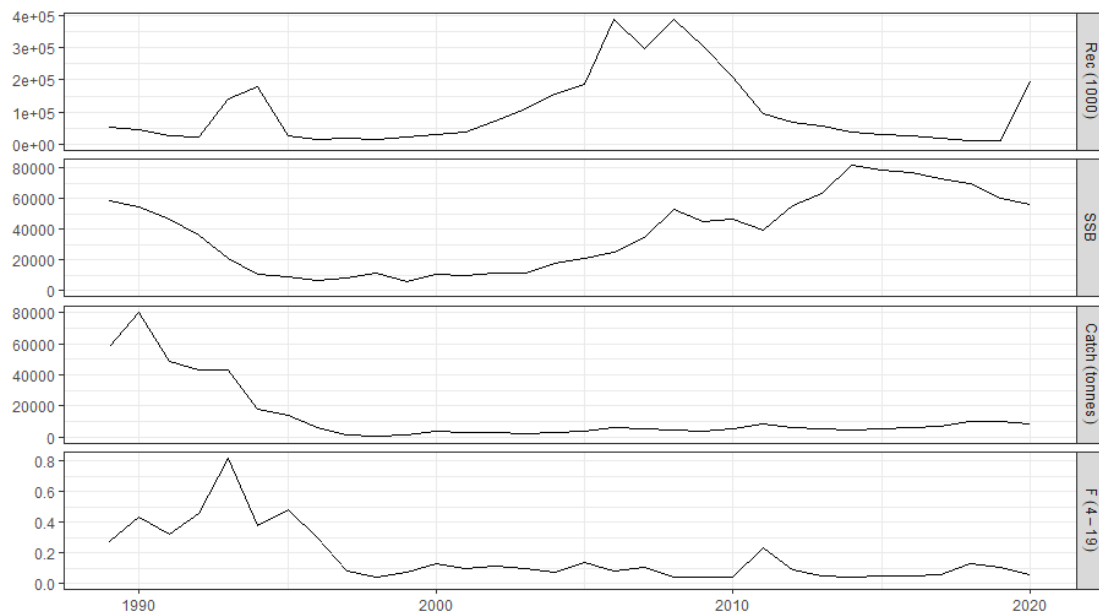


Figure 1. Redfish in Div. 3M: recruitment (millions), SSB, catch (tonnes) and $F(4-19)$ from 1989 until 2020.

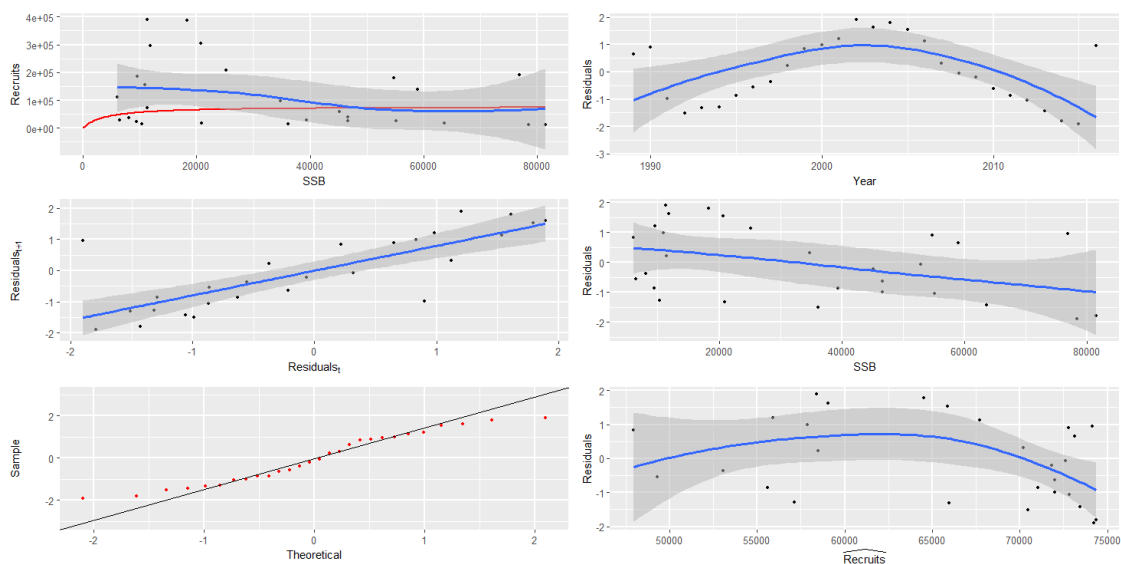


Figure 2. Redfish in Div. 3M: Diagnostic plots for the fitted Beverton-Holt stock-recruitment model for 3M redfish. Panels show: (a) recruitment as a function of SSB with fitted model curves; (b) residuals over time; (c) lag-1 residual autocorrelation (residuals_{t+1} vs. residuals_t); (d) residuals as a function of SSB; (e) Q-Q plot assessing residual normality; and (f) residuals as a function of predicted recruitment. These diagnostics evaluate model fit, residual structure, and adherence to assumptions of independence, normality, and homoscedasticity.

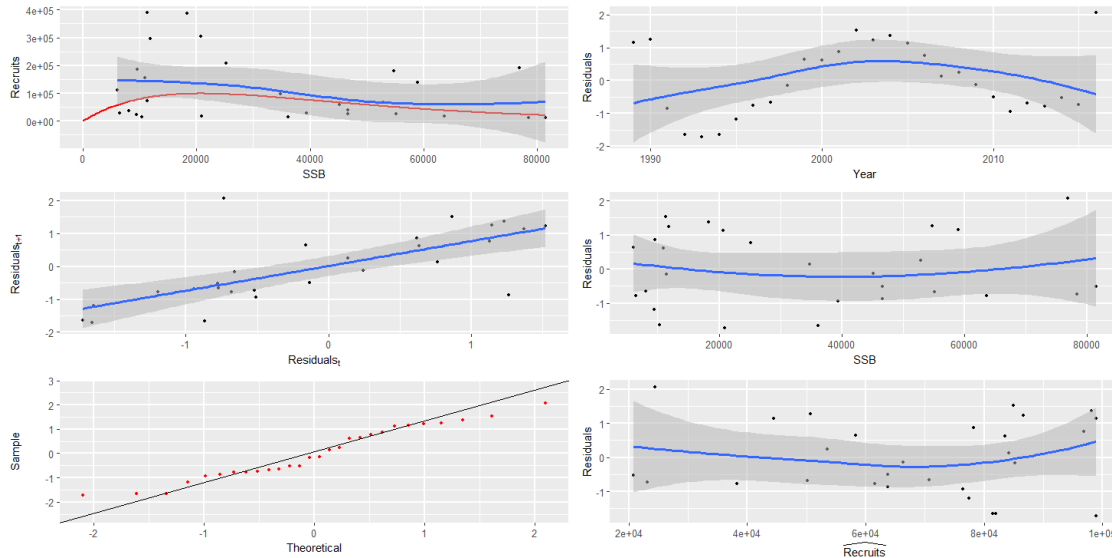


Figure 3. Redfish in Div. 3M: Diagnostic plots for the fitted Ricker stock-recruitment model for 3M redfish. Panels show: (a) recruitment as a function of SSB with fitted model curves; (b) residuals over time; (c) lag-1 residual autocorrelation (residuals_{t+1} vs. residuals_t); (d) residuals as a function of SSB; (e) Q-Q plot assessing residual normality; and (f) residuals as a function of predicted recruitment. These diagnostics evaluate model fit, residual structure, and adherence to assumptions of independence, normality, and homoscedasticity.

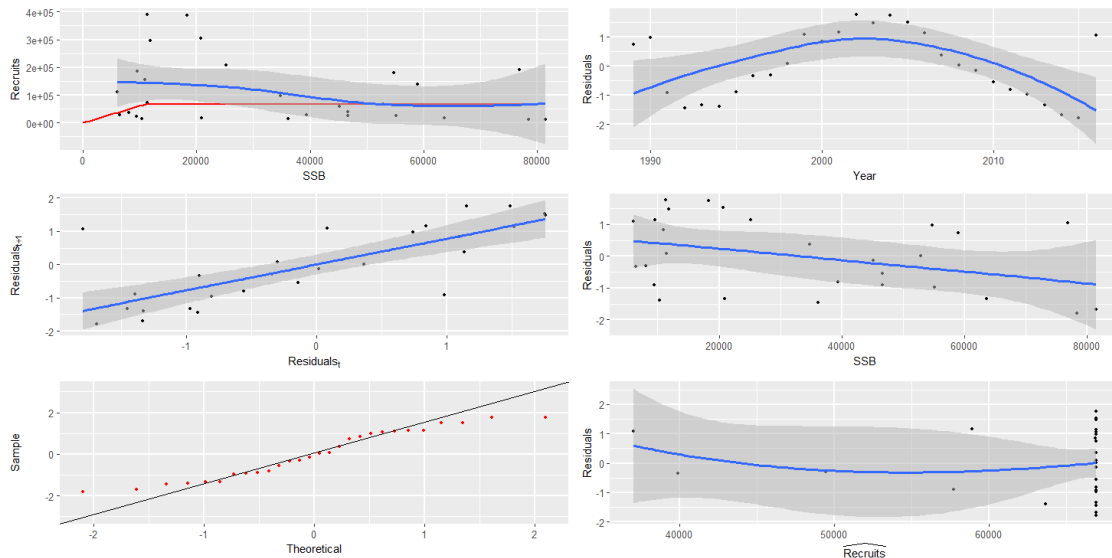


Figure 4. Redfish in Div. 3M: Diagnostic plots for the fitted Segmented regression stock-recruitment model for 3M redfish. Panels show: (a) recruitment as a function of SSB with fitted model curves; (b) residuals over time; (c) lag-1 residual autocorrelation (residuals_{t+1} vs. residuals_t); (d) residuals as a function of SSB; (e) Q-Q plot assessing residual normality; and (f) residuals as a function of predicted recruitment. These diagnostics evaluate model fit, residual structure, and adherence to assumptions of independence, normality, and homoscedasticity.

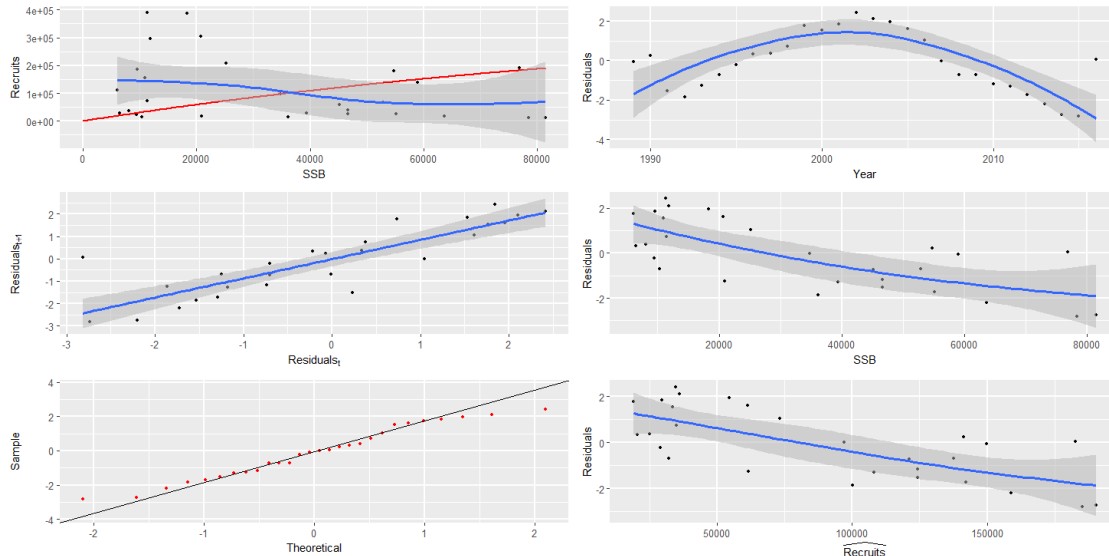


Figure 5. Redfish in Div. 3M: Diagnostic plots for the fitted Smooth Hockey-Stick regression stock-recruitment model for 3M redfish. Panels show: (a) recruitment as a function of SSB with fitted model curves; (b) residuals over time; (c) lag-1 residual autocorrelation (residuals_{t+1} vs. residuals_t); (d) residuals as a function of SSB; (e) Q-Q plot assessing residual normality; and (f) residuals as a function of predicted recruitment. These diagnostics evaluate model fit, residual structure, and adherence to assumptions of independence, normality, and homoscedasticity.

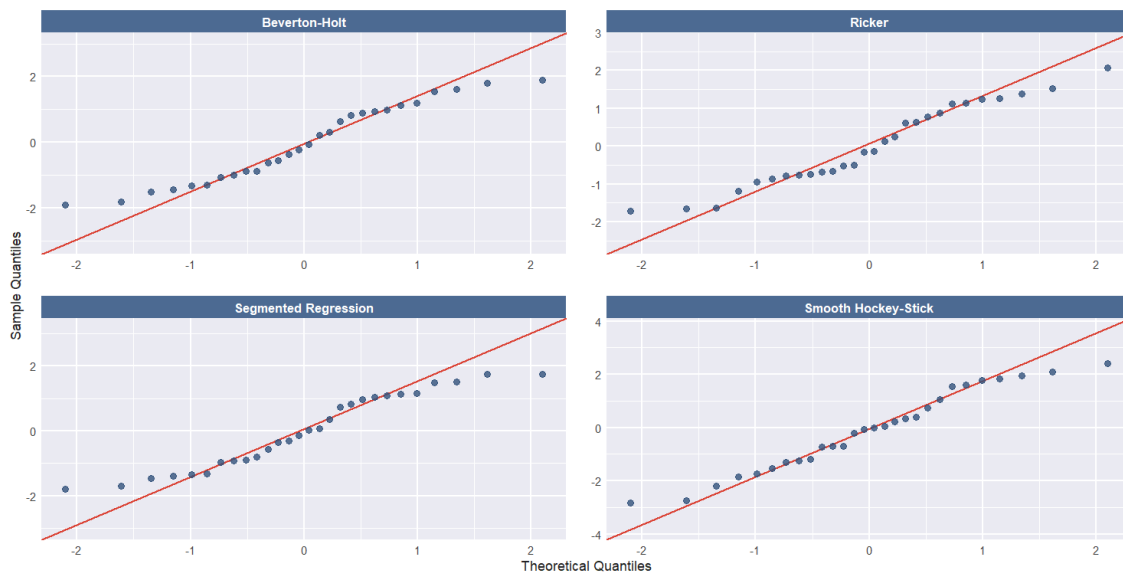


Figure 6. Redfish in Div. 3M: Quantile-quantile (Q-Q) plots of residuals for the four stock-recruitment models applied to 3M redfish: Beverton-Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick. Each panel compares sample residual quantiles with theoretical normal quantiles to assess the assumption of residual normality for the corresponding model.

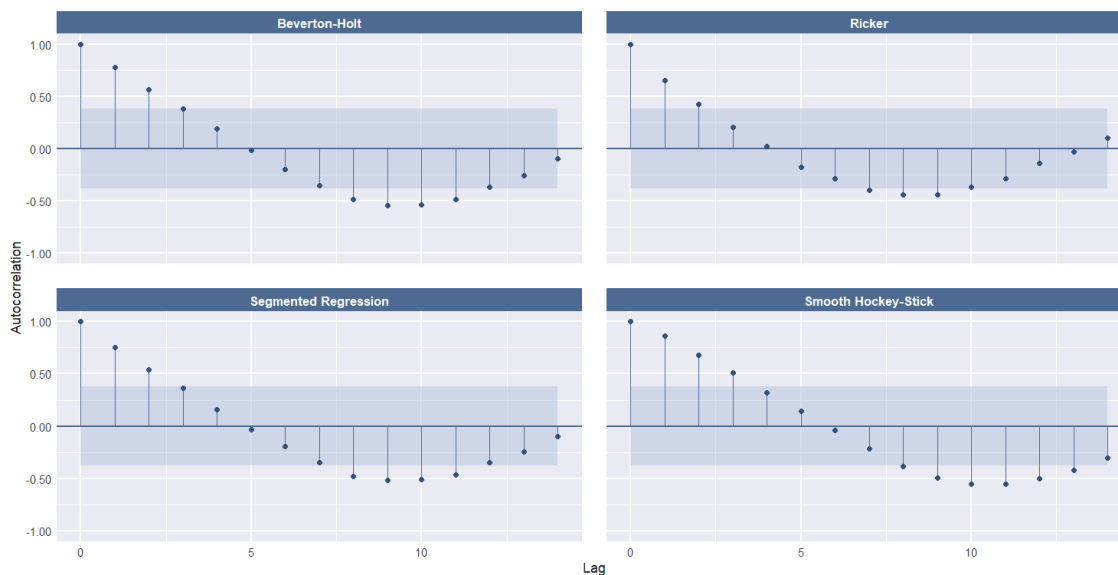


Figure 7. Redfish in Div. 3M: Autocorrelation function (ACF) plots of model residuals for the Beverton-Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick models. Vertical stems represent residual autocorrelation coefficients at successive lags, with the shaded regions indicating approximate 95% confidence intervals under the null hypothesis of no serial correlation.

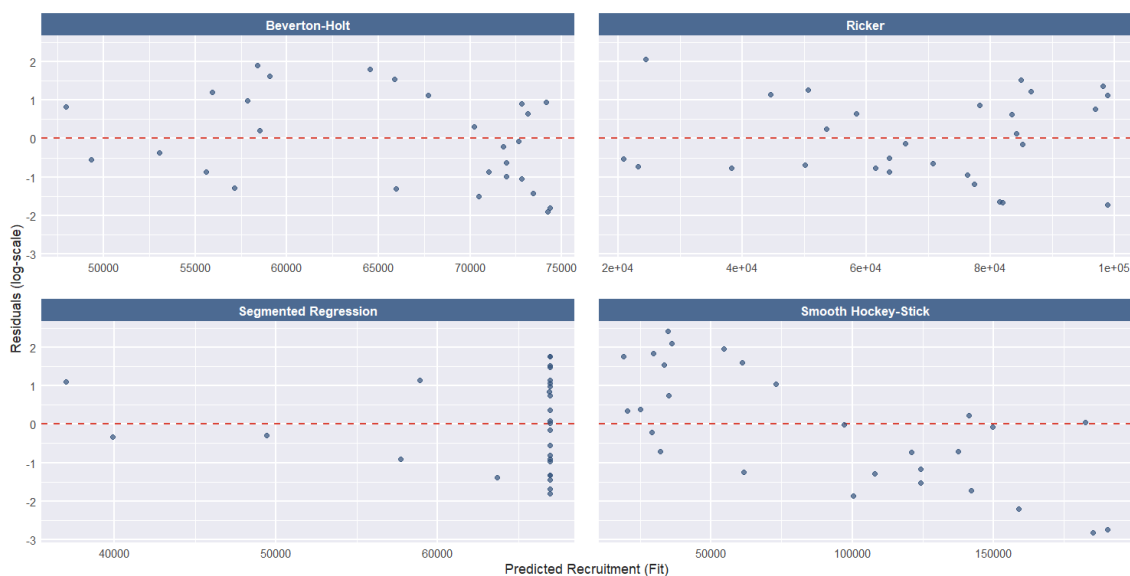


Figure 8. Redfish in Div. 3M: Residuals plotted against predicted recruitment values (Fit) for the Beverton-Holt, Ricker, Segmented Regression, and Smooth Hockey-Stick models. Points represent model residuals on the log-scale, with the dashed horizontal red line indicating zero residual error.

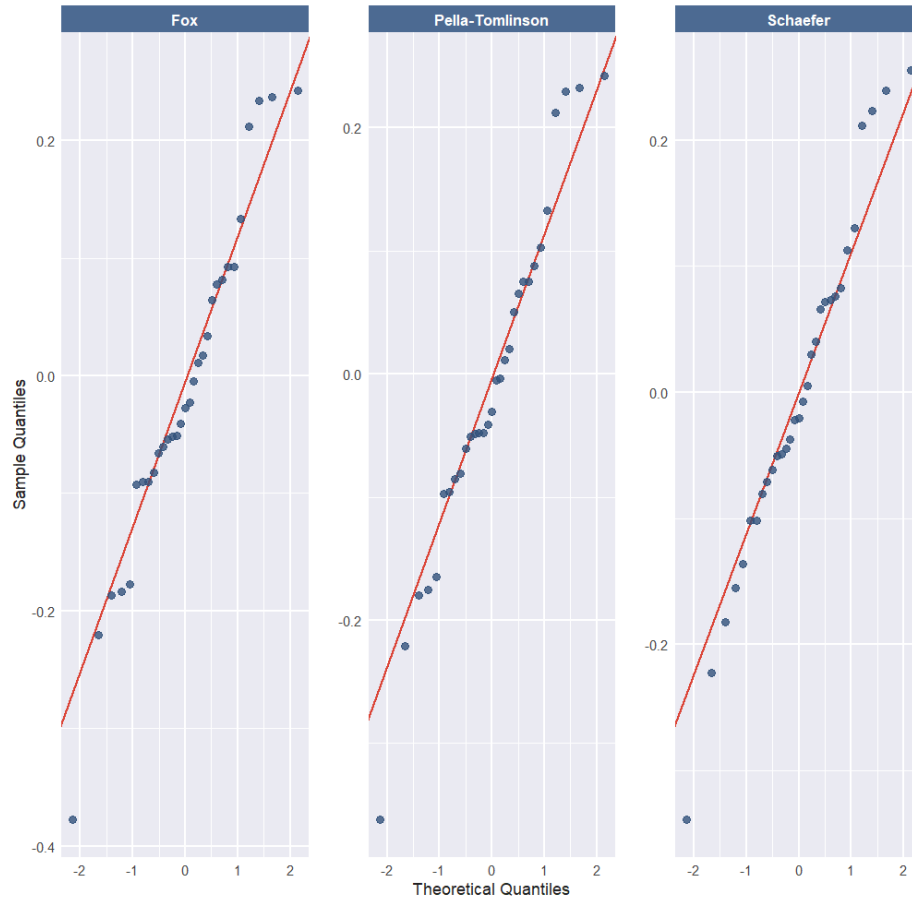


Figure 9. Redfish in Div. 3M: Quantile–quantile (Q–Q) plots of residuals for the four stock–recruitment models applied to 3M redfish: Schaefer, Fox, and Pella–Tomlinson. Each panel compares sample residual quantiles with theoretical normal quantiles to assess the assumption of residual normality for the corresponding model.

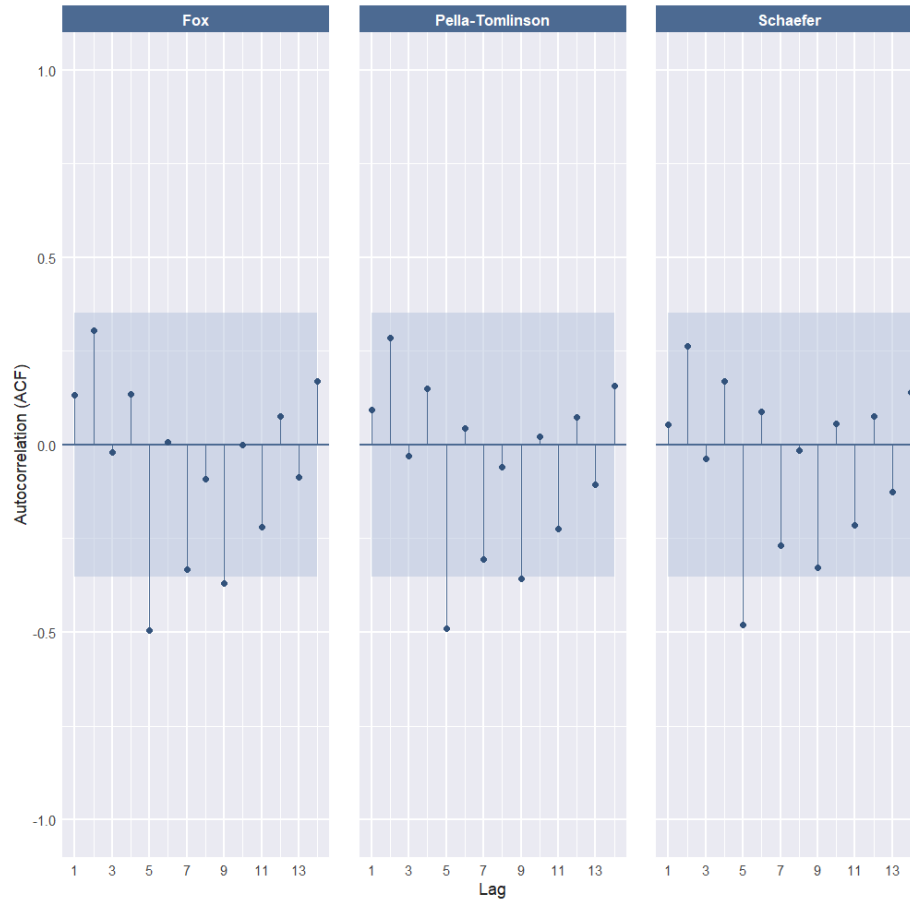


Figure 10. Redfish in Div. 3M: Autocorrelation function (ACF) plots of model residuals for the Schaefer, Fox, and Pella-Tomlinson models. Vertical stems represent residual autocorrelation coefficients at successive lags, with the shaded regions indicating approximate 95% confidence intervals under the null hypothesis of no serial correlation.

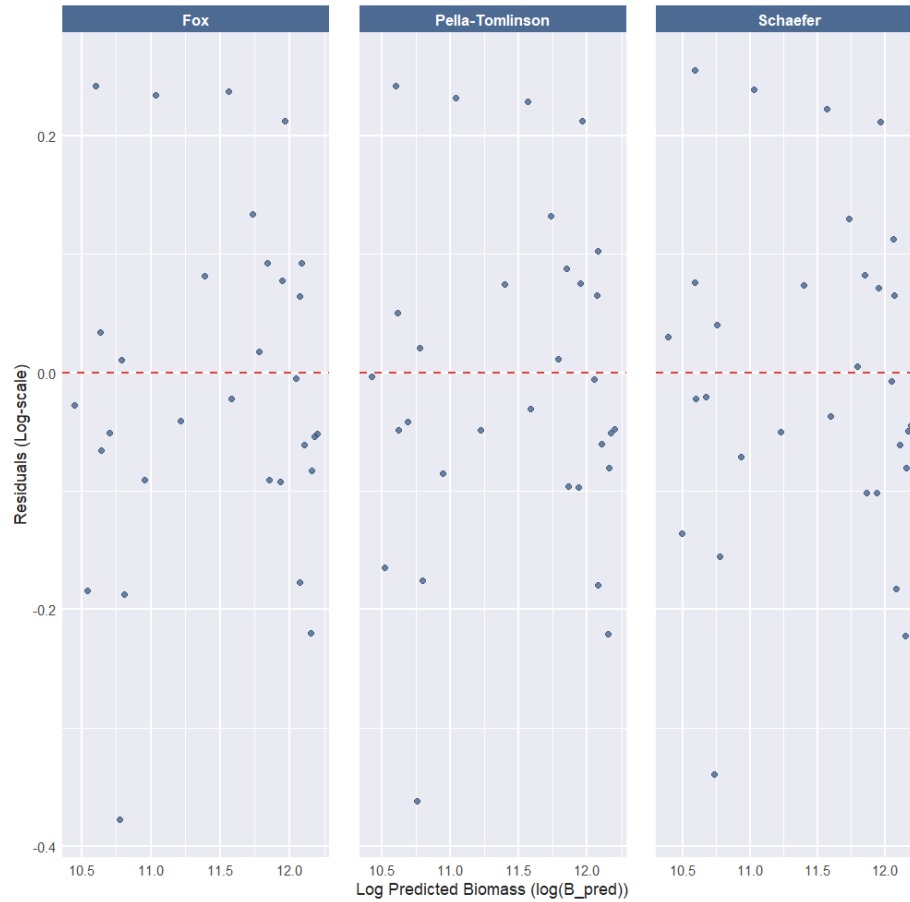


Figure 11. Redfish in Div. 3M:Residuals plotted against predicted recruitment values (Fit) for the Schaefer, Fox, and Pella–Tomlinson models. Points represent model residuals on the log-scale with the dashed horizontal red line indicating zero residual error.