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Biological Reference Points of 3M cod

by

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Abstract

In 2012, Fisheries Commission requested to Scientific Council: *to provide B_{msy} and F_{msy} for cod in Div. 3M*. The aim of this work is try to provide an estimative of these Reference Points. Results show that no stock recruitment relationship fits appropriately the 3M cod data. The level of B_{msy} estimated from YPR and SPR depends on assumptions about the level of recruitment. So, more research about the possibility of changes in productivity and the level of recruitment that should be used to estimate the MSY is needed.

Introduction

The NAFO Fisheries Commission formally adopted a Precautionary Approach (PA) framework in 2004 (NAFO/FC Doc. 04/17) as proposed by NAFO Scientific Council (NAFO SCS Doc. 03/23). The SC framework provides a structure that included limits, buffers, targets and management strategies that would adjust fishing mortality to keep stocks in the Safe Zone.

The 3M Atlantic cod (*Gadus morhua*) is managed by NAFO. This stock was under a fishing moratorium from 1999 to 2009 following its collapse. The assessments performed since the collapse of the stock confirmed the poor situation, with SSB at very low levels, well below B_{lim} (14 000 tons) (Vázquez and Cerviño, 2005). Above average recruitment levels were estimated for 2005 and 2006 and therefore a large increase in SSB in 2007-2009, reaching in 2010 the highest value of the studied series. The results of the 2009 assessment, with the SSB well above B_{lim} , led to the reopening of the fishery with 5 500 tons of catch in 2010. With the results of the 2010-2012 assessments TACs of 10 000 tons, 9 280 tons and 14 113 tons, respectively, were established. (González-Troncoso *et al.*, 2013).

A VPA based assessment of the cod stock in Flemish Cap was approved by NAFO Scientific Council (SC) in 1999 for the first time and was annually updated until 2002. However, most recent catches were very small undermining the VPA based assessment, as its results are quite sensitive to assumed natural mortality when catches are at low levels. Cerviño and Vázquez (2003) developed a method which combines survey abundance indices at age with catchability at age, the latter estimated from the last reliable accepted XSA. The method estimates abundances at age with their associated uncertainty and allows calculating the SSB distribution and, hence, the probability that SSB is above or below any reference value. The method has been used to assess the stock since 2003. In 2007 results from an alternative Bayesian model were also presented and in 2008 this Bayesian model was further developed and approved by the NAFO SC (Fernández *et al.*, 2008). This method allows to have years with no catch at age data, which happened to the 3M cod between the years 2002-2005 due to very few catches.

The assessment of this stock has been performed every year since 2008 using the Bayesian model. A B_{lim} of 14 000 tons was proposed by the NAFO Scientific Council in 2000. The appropriateness of this value given the results from the new method used to assess the stock was examined in 2008, concluding that it is still an appropriate reference.

In 2012, Fisheries Commission requested to Scientific Council: *to provide B_{msy} and F_{msy} for cod in Div. 3M.*

The aim of this document is to try to calculate the B_{msy} references points of the 3M cod.

Material and Methods

The 3M cod assessment performed since its reopening in 2009 uses a Bayesian XSA model. In 2013 this assessment was approved during the Scientific Council meeting of June using commercial data from 1972 to 2012 and the Canadian survey (1978-1985) and the EU survey (1988-2012) as tuning. Ages used were 1-8+. The number of iterations made for the Bayesian assessment was 5000, so we have 5000 iterations of all the parameters of the assessment. To see the details about this assessment, see González-Troncoso *et al.* (2013).

In this study and in all cases, the PR, the weight-at-age (both in catch and in stock) and the maturity ogive were taken as the mean of the values of the entire period studied (1972-2012), having 5000 iterations of each. Mean-weight-at-age in the catch and mean-weight-at-age in the stock are assumed with no uncertainty, so the value of these parameters for the 5000 iterations is the same.

Normally, when an age structured assessment provides a plausible set of stock and recruit pairs, the process of calculating the appropriate Maximum Sustainable Yield (MSY) reference points estimates should be based on combining the yield per recruit analysis and the stock recruit relationship. The two methods used in this study to estimate MSY reference points from the age structured assessment results was that proposed by Sissenwine and Shepherd (1987).

The first step to try to calculate the MSY of the 3M cod was to fit a good stock recruitment relationship. Three different relationships were used: Ricker, Beverton&Holt and Segmented Regression. All of them were fit with the results of the assessment for SSB and Recruitment, having a series of 40 pairs (SSB,R) as the recruitment of the 3M cod is estimated at age 1. We used two different points of view for fitting the data just to compare results. One of this was to fit the SRR in a way that can be named deterministic, taking as inputs of the fit the median of the SSB and the R from the 5000 draws of the assessment, as well as the median of PR and the maturity ogive. Another one was to estimate the Stock-Recruitment Relationship from each of the 5000 time series that we have for SSB and for R, getting 5000 different SR Relationships and presenting the median of them. The SSB/R fits were performed with FLR.

Additionally, the YPR reference points (F_{max} and $F_{0.1}$) were estimated as well as the Spawning per Recruit (SPR) reference points for $F_{30\%}$, $F_{35\%}$ and $F_{40\%}$ of the SSB unfished level.

Results

In table 1 we present the long term means (1972-2012) of mean-weight-at-age in catch, mean-weight-at-age in stock, maturity (median of the 5000 runs) and PR (median of the 5000 runs) by age for 3M Cod.

Table 2 presents the models used and the deterministic fit parameter values for each model. Figure 1 (A and B) presents the deterministic fit of the three models. Note that the maximum in all the cases is outside of the observed levels of SSB. As Beverton&Holt and Segmented Regression are almost identical for the estimated SSBs, a second graph is presented with a wider range in the x-axis to see where they differ (Figure 1B). In this case the maximum of Ricker is inside the range, but this is just because for this model the maximum Yield is the one corresponding to the maximum F (1 in this case). We tried with a larger F (just up to 3), and the results were always the Yield of the maximum F. Ricker model has negative β parameter value that does not make sense biologically. In the case of Beverton&Holt the β parameter has a very big value with a very difficult biological explanation. The change point of the Segmented Regression model is outside the observed range of SSB.

Figure 2 presents the deterministic FLR fit plots for Ricker model. This figure has six plots. The upper left plot shows the stock-recruit pairs with the fitted stock recruitment relationship and a lowess smoother to suggest an appropriate functional form. It can be observed that the Ricker and lowess fit are very similar and that the Ricker function has a convex curvature, which means that it always increases. The upper right plot shows the residuals plotted against year, and a clear residual pattern can be observed in this case. This pattern in the residuals might indicate that average recruitment was either less or greater than expected, indicating either the wrong choice of model or a regime shift. The middle left plot presents the residuals with a lag of time 1, to identify autocorrelation, and it is clear in this case there is autocorrelation in the residuals. The middle right plot is of the residuals against SSB. It seems that the errors present a pattern, mainly in the lowest SSBs. Bottom left figure presents the observed residuals against their expected quantiles.

They seem to fit quite well, meaning a log-normal distribution of the errors. The bottom right plot presents the residuals against the fitted values as a check of the variance.

Figure 3 shows the likelihood profile of the deterministic Ricker's parameters. The likelihood profiles present for both parameters a clear maximum although the parameter values make no sense biologically.

Figure 4 presents the deterministic FLR fit plots for the Beverton-Holt model. We can observe the same fit problems as in the Ricker fit: clear residual pattern, big autocorrelation. And in this case, it seems that the errors don't follow a log normal distribution.

Figure 5 shows the likelihood profile of the deterministic Beverton-Holt parameters. The Likelihood for both parameters has a flat profile with a not well defined maximum. This is a clear sign of the difficulty to fit the data and to find a good value for the parameters, as many parameters values have a similar Likelihood.

Figure 6 presents the deterministic FLR fit plots for Segmented Regression model. We can observe the same fit problems as in the Ricker and Beverton-Holt fits: clear residuals pattern, big autocorrelation in the errors, not a log normal distribution of the errors.

Figure 7 shows the likelihood profile of the deterministic Segmented Regression parameters. The likelihood profile for α parameter presents a well defined maximum but for the β parameter the likelihood profile is quite flat. This is a clear sign of the difficulty to fit the data and to find a good value for this parameter, as many β parameter values have a similar Likelihood.

Table 3 presents the deterministic F_{msy} , SSB_{msy} and Y_{msy} estimations and the median, the 90 and 80 percentile values of the 5000 iterations for Ricker, Beverton&Holt and Segmented Regression Stock Recruitment relationships. The results for Ricker shows that it is no possible to achieve reasonable MSY indices in this case, as the F_{msy} is the largest value taken for F , as we said above. In Beverton-Holt, the values of SSB_{msy} and Y_{msy} do not make biological sense due to the lack of fit of the available data. For Segmented Regression, all the fits have a change point that is above the observed range of SSBs. In all cases, we can see that the deterministic values are almost the same as the median of the Bayesian values.

Table 4 presents the median, the 80 and the 90 percentile values for the different fishing mortality YPR and SPR reference points. F_{max} values are the highest of the F BPRs estimated and $F_{0.1}$ and $F_{40\%}$ have very similar levels.

Figure 8 shows the YPR and SPR median curves for different F values. It also showed the F_{max} , $F_{0.1}$, $F_{30\%}$, $F_{35\%}$ and $F_{40\%}$ median values. It can be observed that the YPR curve presents a maximum quite well defined and that the SPR reference points estimated (except $F_{40\%}$) are above the $F_{0.1}$ value.

The equilibrium yield and SSB for all F reference points were calculated with the mean recruitment of the period (1972-2012) applied to the YPR and SPR estimated for the different F reference points. Table 5 presents the median, 80% and the 90% percentile of the distribution for these values. In all cases, the SSB_{msy} and the F_{msy} are in the same range as the one calculated via a Segmented Regression.

Discussion

Figure 9 shows fishing mortality YPR (F_{max} and $F_{0.1}$), SPR ($F_{30\%}$, $F_{35\%}$ and $F_{40\%}$) reference points and Ricker, Beverton&Holt and Segmented Regression F_{msy} as well as their correspondent SSB and Yield assuming mean recruitment in the case of the YPR and SPR references points and functional recruitment in the other cases. For fishing mortality the F_{msy} of Ricker is always 1, so it is off the graph. The same occurs for the SSB_{msy} in the case of Beverton&Holt. The model that is more in agreement with the YPR and SPR values is the Segmented Regression, being the Reference Points calculated for the other two SSB/R relationship poor of biological meaning.

The lack of fit of the S/R relationships is one of the major problems in 3M cod. Figures 2 to 8 show these problems for all the functions analyzed: clear residuals pattern, big autocorrelation in the errors, not log normal distribution of the errors and problems in the fit parameters Likelihood profiles, and the fact that the maximums in the SSB/R models are defined above in the observed SSB range. This last problem is a *quid* point to estimate F_{msy} , B_{msy} and MSY as recognized the ICES Workshop on implementing the ICES F_{msy} framework (ICES, 2010): *F targets which imply equilibrium SSB's outside the 6 historic range should be looked at carefully, however it should be noted that where exploitation has historically been very high, this situation does not necessarily denote biological implausibility. The critical issue here is the fit to the S/R function. The fit to the Stock Recruit Relationship requires analysis (...). You could chose default function based on some statistical criteria for a measure of fit (e.g. AIC, BIC), but the fit needs to*

have biological plausibility. For example if the maximum in a dome shaped model is way out of the range of the observed biomass, there may be a problem.

In our opinion, when a stock recruitment function has a no well defined maximum of the recruitment in the observed SSB range, its use as the basis for defining Biological Reference Points should be treated with caution. In 3M cod all the functions analyzed have this problem. So, results of B_{msy} and F_{msy} estimated based on these methods are not plausible due to the high uncertainty in the stock-recruitment relationship for this stock.

The above cited workshop recommends that when the S/R relationship has these problems F_{msy} should be estimated using the segmented regression model, with constant recruitment above a threshold level. This results in F_{msy} being defined by the YPR estimate of F_{max} or if F_{max} is not well defined then $F_{0.1}$, $F_{35\%}$ or $F_{40\%}$ could be considered as a proxy for F_{msy} . In the 3M cod case, uncertainty is introduced in the SSB_{msy} via the Bayesian model used in the assessment. In this case the values found for F_{msy} of the segmented regression and for F_{max} are quite similar as it can see in Figure 9. Results show that the estimated values in all the cases of SSB_{msy} (from 116 102 for F_{max} , through 125 013 t for Segmented Regression to 189 998 t for $F_{40\%}$) are well above the approved value of B_{lim} for this stock, that is 14 000 t. F_{lim} is not defined for this stock.

The level of B_{msy} estimated from YPR and SPR depends on assumptions about the level of recruitment. So, it is clear that more research about the possibility of changes in productivity and the level of recruitment that should be used to estimate the MSY is needed.

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Table 1.- Long term means (1972-2012) of weight-at-age in catch, in stock, maturity (median) and PR (median) by age for 3M Cod

Age	1	2	3	4	5	6	7	8
Cwt	0.023	0.256	0.779	1.304	2.177	2.939	4.232	5.949
Swt	0.054	0.298	0.769	1.352	2.202	3.265	4.361	6.869
mat	0.007	0.017	0.126	0.447	0.764	0.947	0.975	0.989
PR	0.003	0.201	0.609	1.008	1.380	1.442	1.635	1.635

Table 2.- Stock Recruitment models as well as their functions and the values of the parameters for the deterministic fit assuming log normal error distribution.

	Ricker		Beverton&Holt		SegReg	
Formula	$R=\alpha SSB \exp(-\beta SSB)$		$R=\alpha SSB / (\beta + SSB)$		$R=\{\beta \text{ if } SSB \leq \beta \text{ else } \alpha\beta\}$	
Parameters	alpha	beta	alpha	beta	alpha	beta
Deterministic	0.2526	-0.000053668	165447998743	302457367350	0.5471	37513
5%	0.2004	-0.000064158	19869359314	35077523440	0.4625	35862
10%	0.2136	-0.000060991	55259740843	103174202424	0.4762	37046
50%	0.2631	-0.000050443	144170370198	265587784669	0.5462	41324
90%	0.3243	-0.000040402	224854843659	396698499740	0.6357	49558
95%	0.3441	-0.000037538	254862847597	437747544833	0.6645	52945

Table 3.- Deterministic F_{MSY} , SSB_{MSY} and Y_{MSY} estimation and the median, the 90 and 80 percentile values of the Bootstrap distribution assuming Ricker (R), Beverton-Holt (BH) and Segmented Regression (SR) Stock Recruitment relationship.

	F_{MSY_R}	F_{MSY_BH}	F_{MSY_SR}
Deterministic	1.000	0.100	0.159
5%	1.000	0.090	0.128
10%	1.000	0.093	0.134
50%	1.000	0.100	0.159
90%	1.000	0.106	0.188
95%	1.000	0.108	0.198

	SSB_{MSY_R}	SSB_{MSY_BH}	SSB_{MSY_SR}
Deterministic	39657	1071032182344	114165
5%	35100	102134919226	83135
10%	36212	344847100069	92276
50%	41496	924927615184	125013
90%	49137	1519027121665	183631
95%	52013	1769843859085	206538

	Y_{MSY_R}	Y_{MSY_BH}	Y_{MSY_SR}
Deterministic	55586	143541974178	24018
5%	48864	14750531149	21338
10%	50730	47184253078	22401
50%	58224	123283445222	26481
90%	69233	196855363933	33262
95%	73055	223919893507	35903

Table 4.- YPR reference points (F_{max} and $F_{0.1}$) and SPR reference points ($F_{30\%}$, $F_{35\%}$ and $F_{40\%}$) estimated without uncertainty (via FLR) and the median, the 90 and 80 percentile values of the Bootstrap distribution.

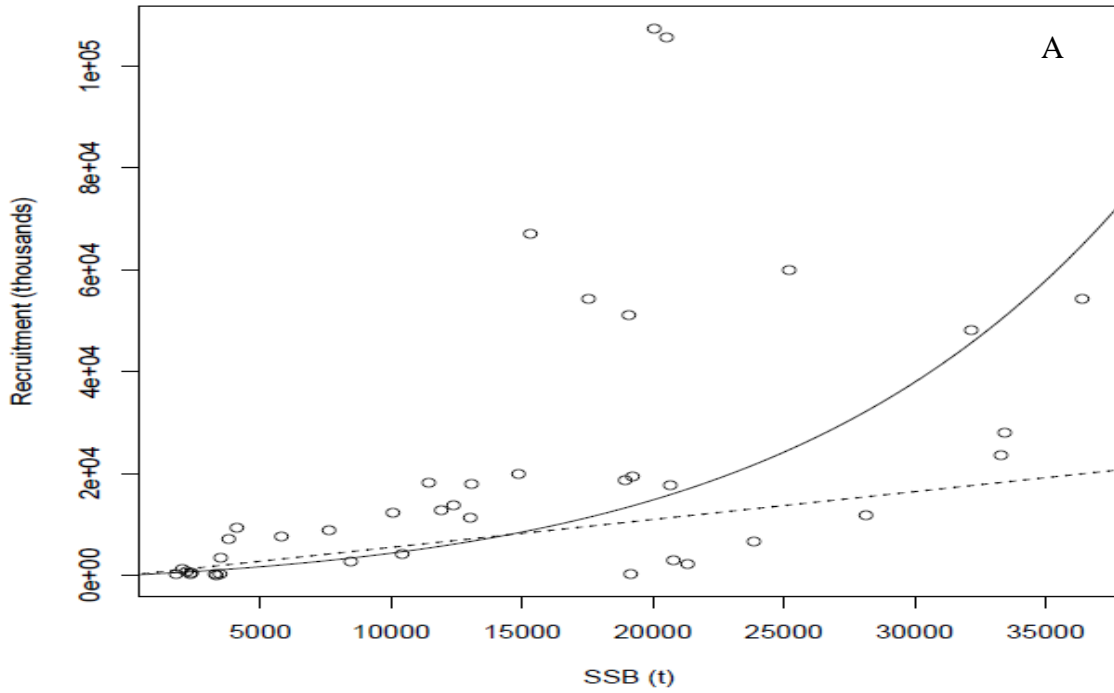
	F_{max}	$F_{0.1}$	$F_{30\%}$	$F_{35\%}$	$F_{40\%}$
5%	0.128	0.073	0.098	0.081	0.068
10%	0.134	0.076	0.104	0.086	0.071
20%	0.141	0.081	0.111	0.093	0.078
50%	0.159	0.091	0.128	0.106	0.089
80%	0.178	0.103	0.144	0.119	0.100
90%	0.188	0.108	0.153	0.126	0.106
95%	0.198	0.113	0.160	0.133	0.111

Table 5.- Equilibrium SSB and yield in tons for the YPR reference points (F_{\max} and $F_{0.1}$) and SPR reference points ($F_{30\%}$, $F_{35\%}$ and $F_{40\%}$) estimated without uncertainty (via FLR) and the median, the 90 and 80 percentile values of the Bootstrap distribution.

	SSB_{\max}	$SSB_{0.1}$	$SSB_{30\%}$	$SSB_{35\%}$	$SSB_{40\%}$
5%	78730	126282	95421	111366	127377
10%	86153	137824	104580	122087	139516
20%	95704	152524	116143	135468	154922
50%	116102	185374	142245	166181	189998
80%	142899	229305	178004	207527	237458
90%	158933	255971	200575	233864	267710
95%	173771	281720	221834	258652	296418

	Y_{\max}	$Y_{0.1}$	$Y_{30\%}$	$Y_{35\%}$	$Y_{40\%}$
5%	20767	19326	20571	20041	19257
10%	21550	20066	21332	20783	19967
20%	22458	20921	22220	21643	20790
50%	24420	22715	24146	23486	22517
80%	26764	24883	26397	25631	24530
90%	28118	26088	27684	26856	25670
95%	29335	27202	28872	27961	26740

SSB/R relationship of Cod 3M . Solid: Ricker; dashed: B&H; dotted=SegReg



SSB/R relationship of Cod 3M . Solid: Ricker; dashed: B&H; dotted=SegReg

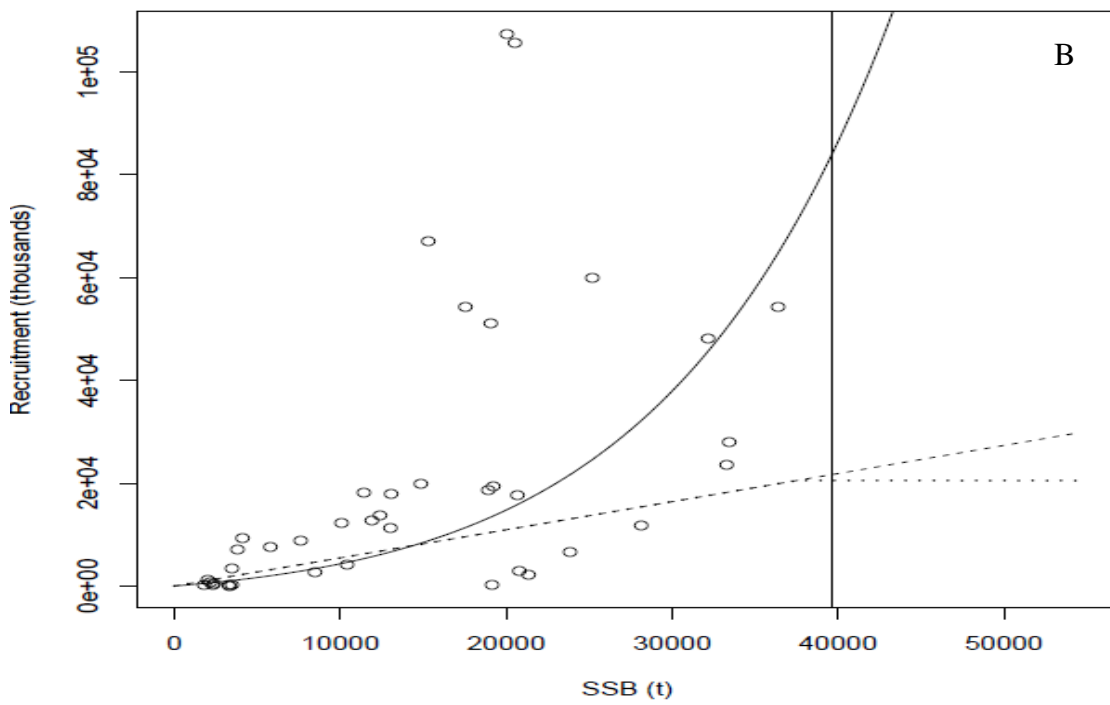


Figure 1.- Deterministic Ricker, Beverton-Holt and Segmented Regression stock recruitment models fit. The B graph is the same as the first one but with a different y-axis range.

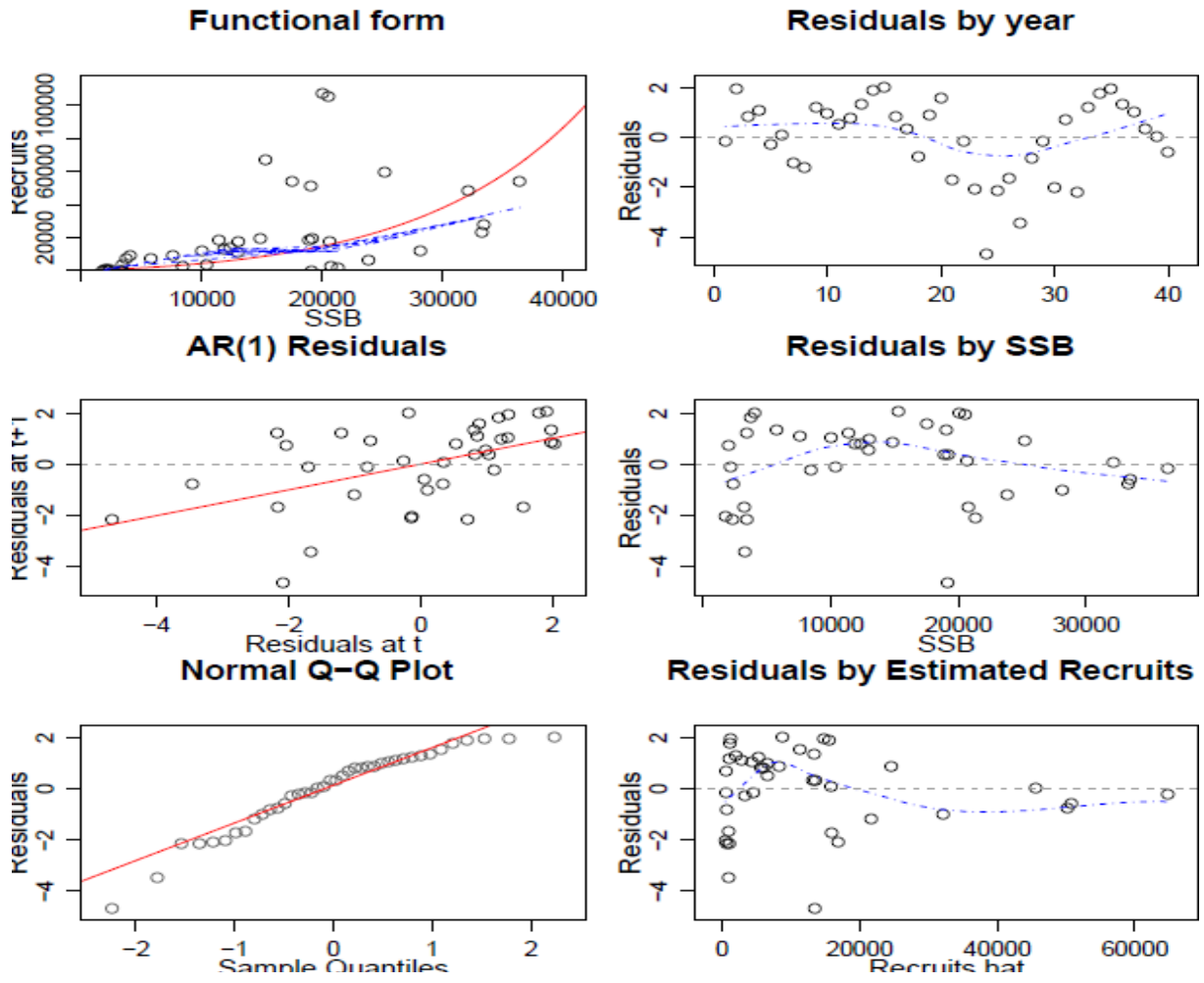


Figure 2.- Ricker fit (deterministic) FLR graphs

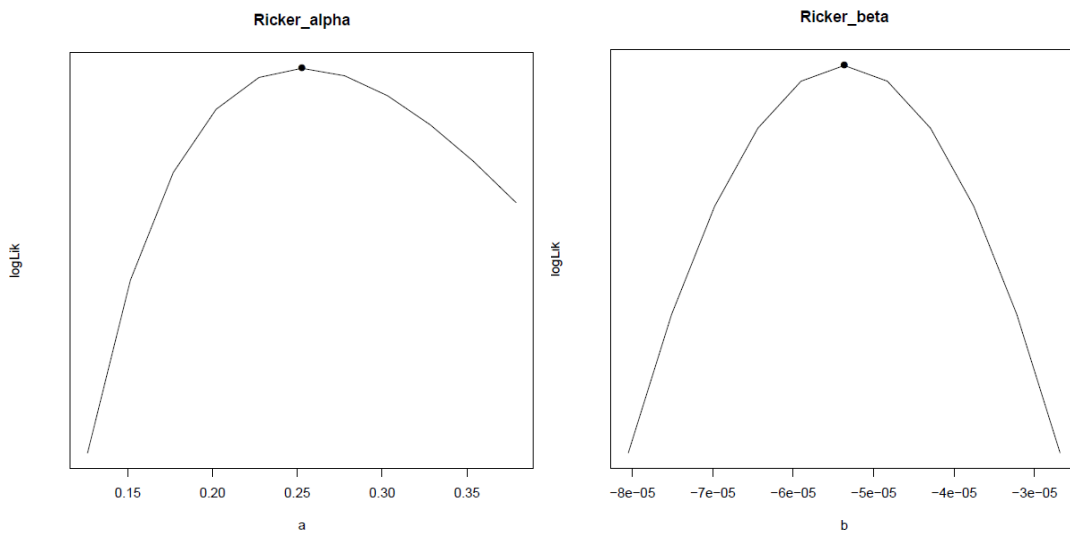


Figure 3.- Likelihood profiles of the Ricker's parameters deterministic fit.

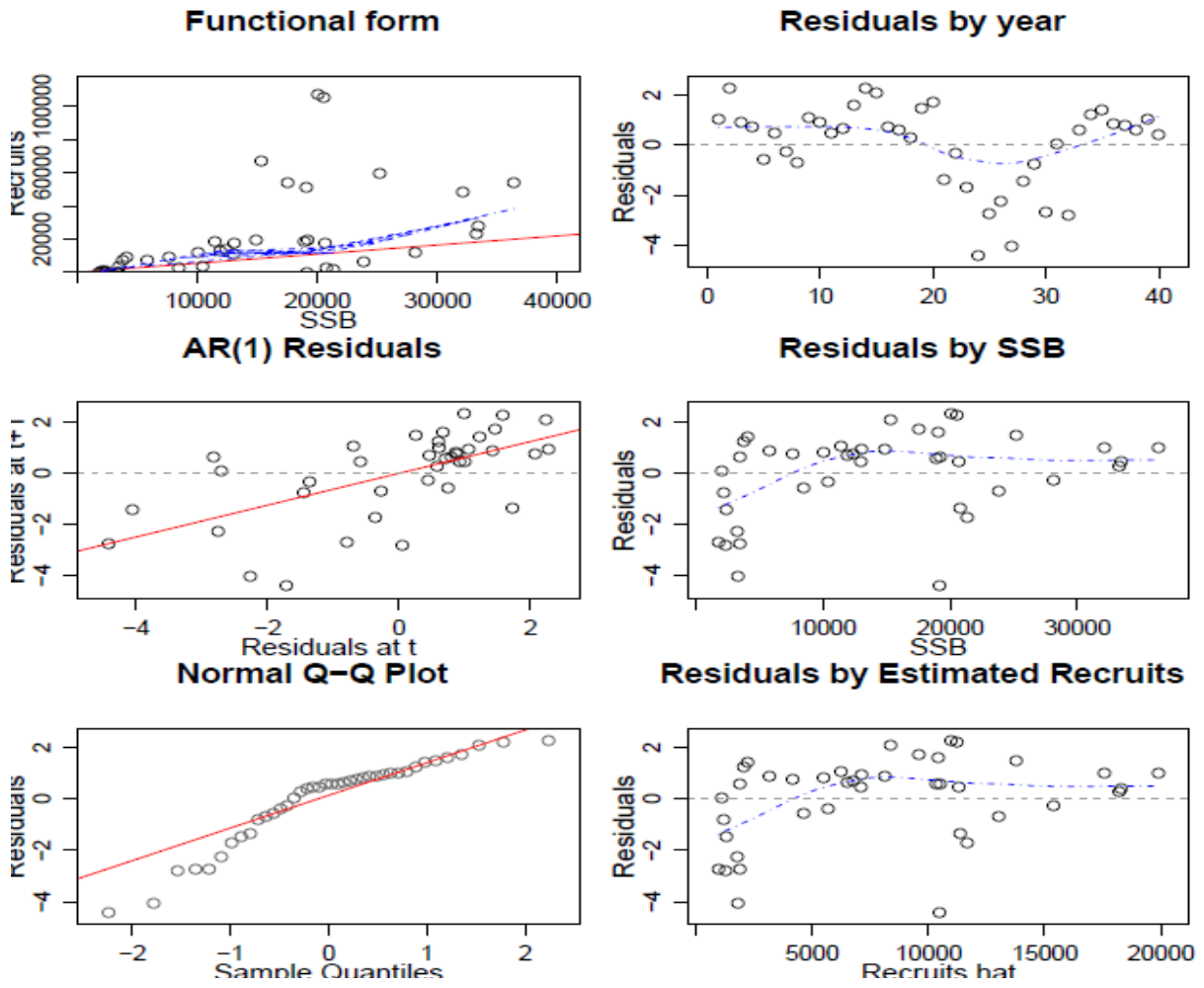


Figure 4.- Beverton and Holt fit (deterministic) FLR graphs

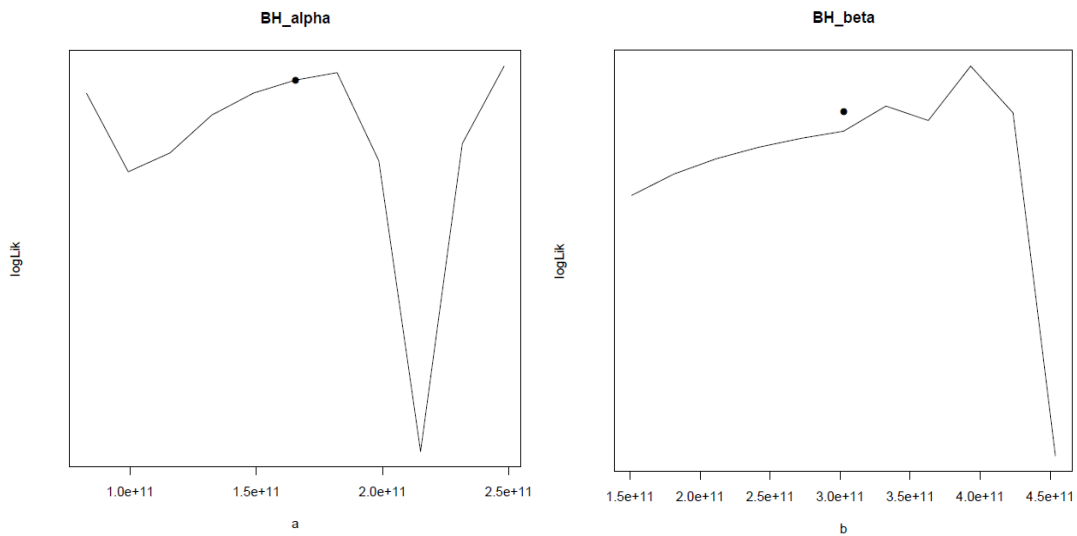


Figure 5.- Likelihood profiles of the Beverton and Holt's parameters deterministic fit.

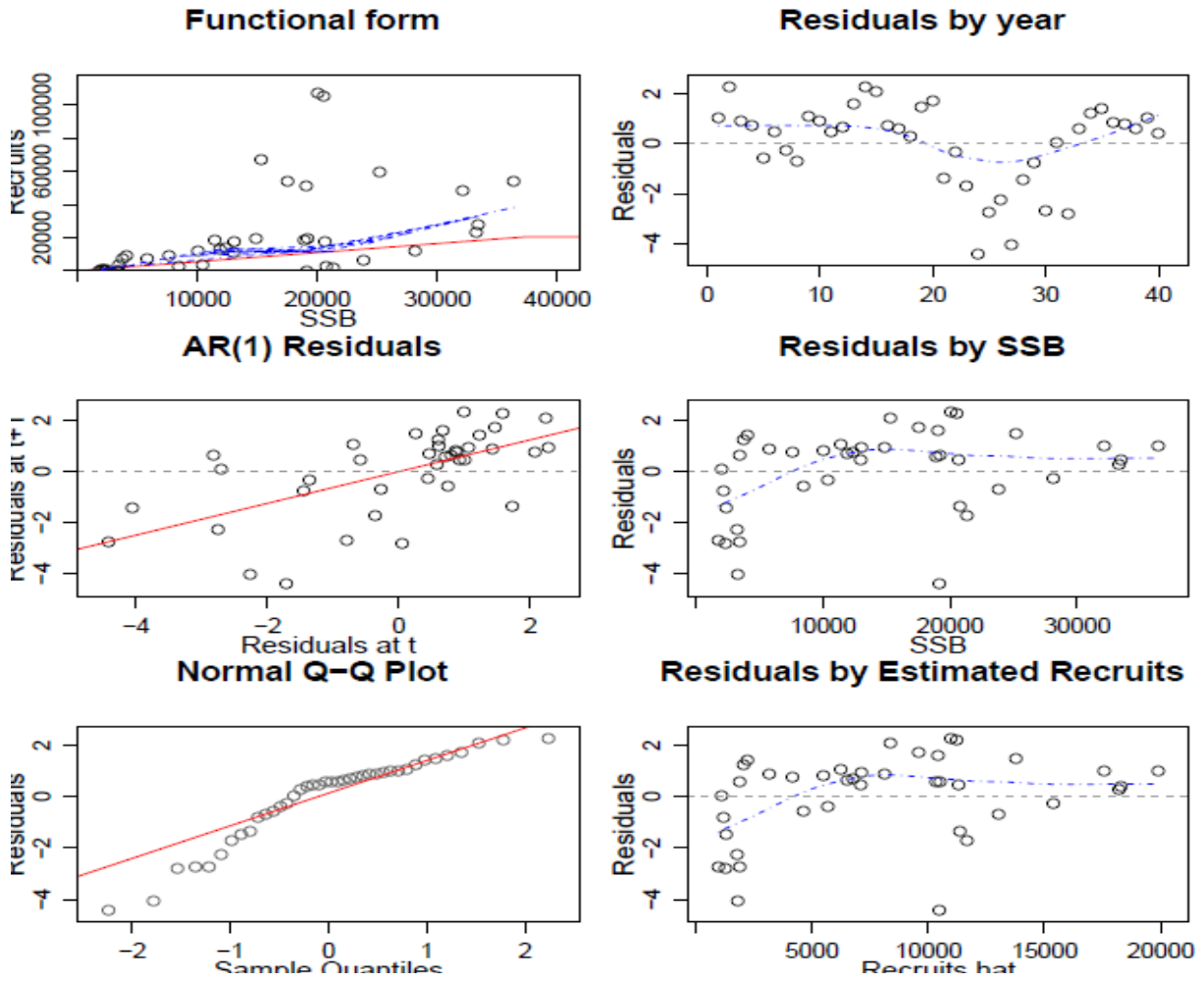


Figure 6.-Segmented regression fit (deterministic) FLR graphs

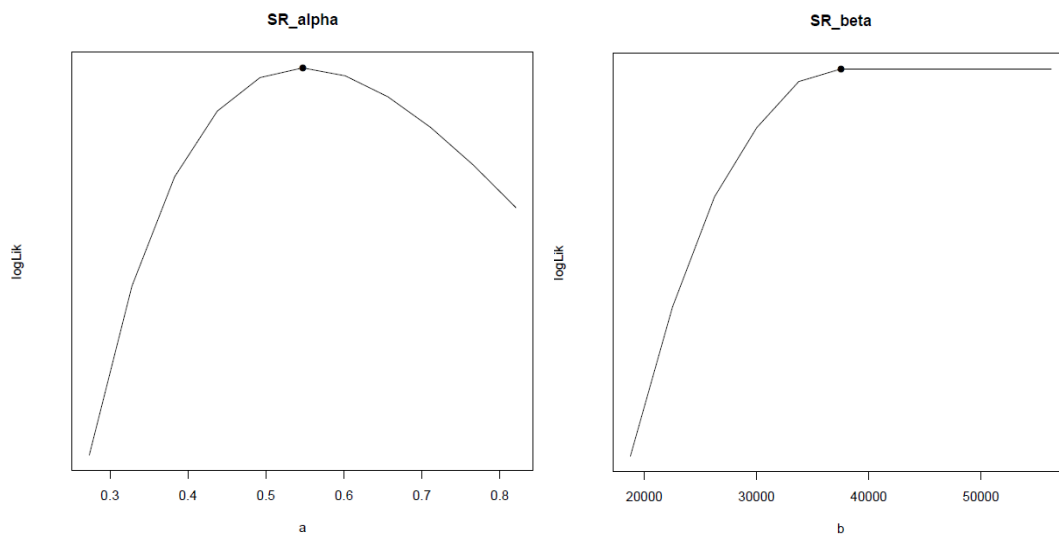


Figure 7.- Likelihood profiles of the Segmented Regression's parameters deterministic fit.

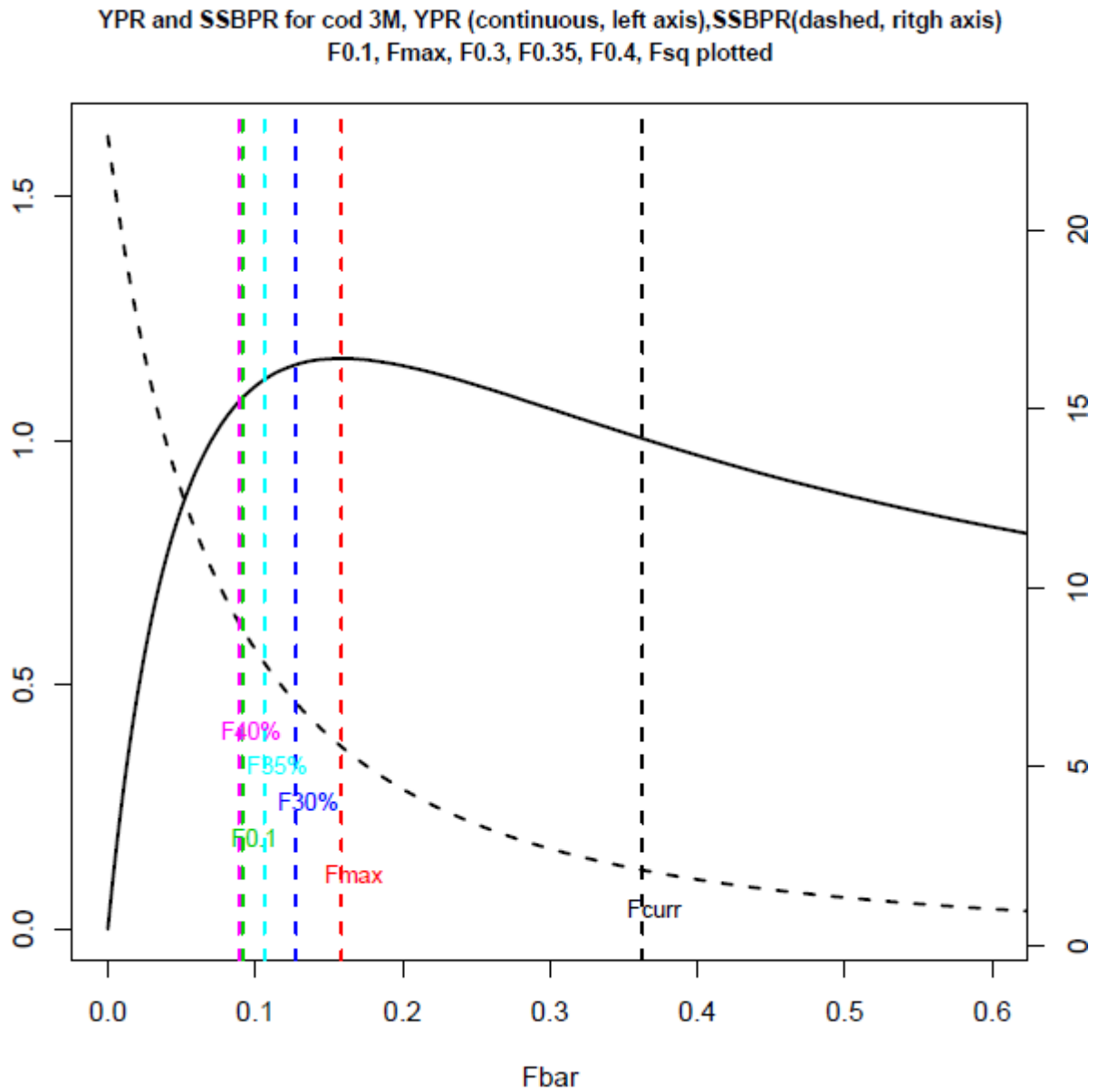


Figure 8.- Median Yield per Recruit (YPR) and SSB per Recruit (SPR) curve. The dash lines represent the median values of the Bootstrap distribution for the Biological references points (F_{max} , $F_{0.1}$, $F_{30\%}$, $F_{35\%}$ and $F_{40\%}$).

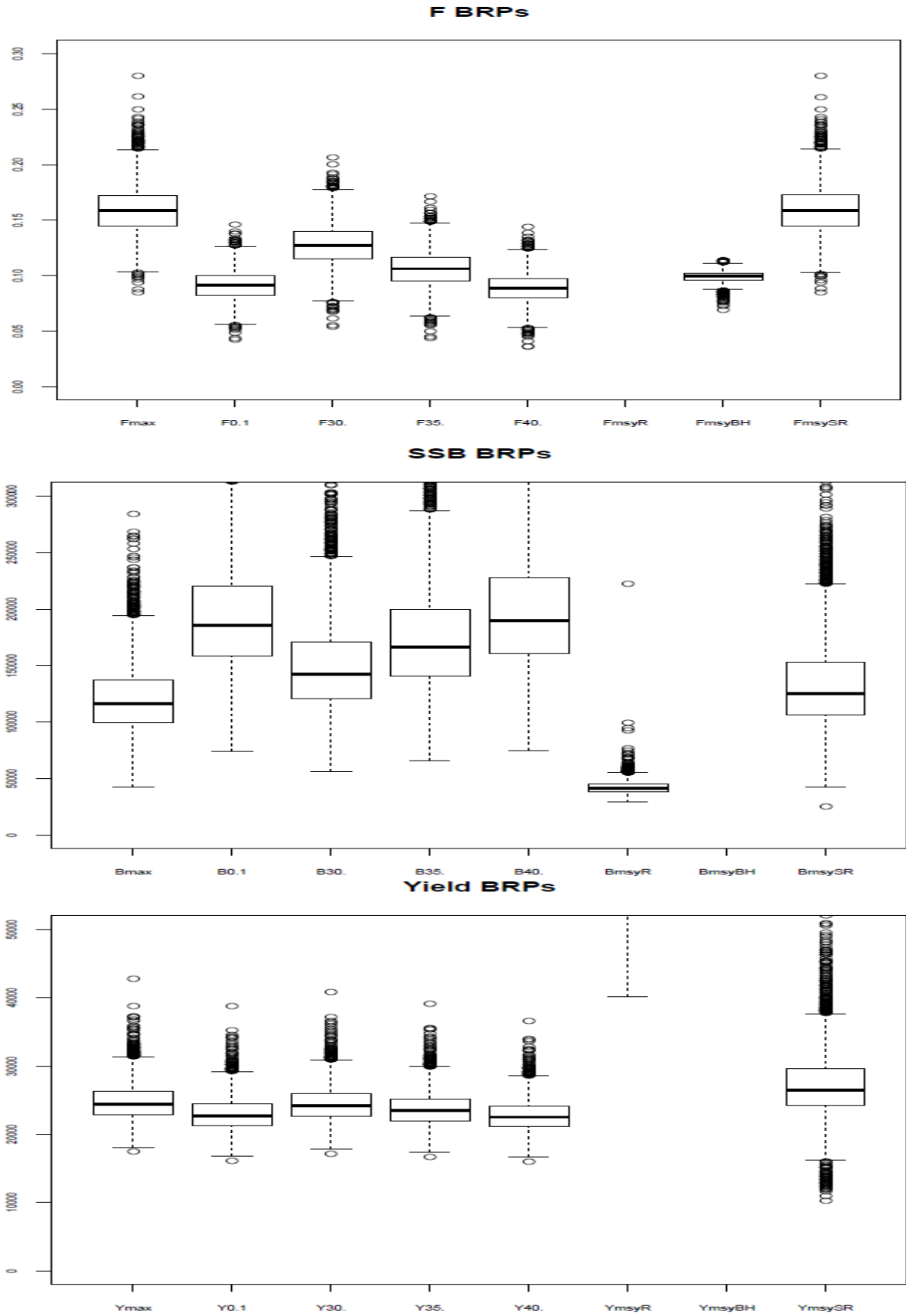


Figure 9.- Fishing mortality YPR (F_{max} and $F_{0.1}$), SPR ($F_{30\%}$, $F_{35\%}$ and $F_{40\%}$) reference points and Ricker, Beverton&Holt and Segmented Regression F_{msy} as well as their correspondent SSB and Yield assuming mean recruitment in the case of the YPR and SPR reference points and functional recruitment in the other cases.