Northwest Atlantic   Fisheries Organization

SCIENTIFIC COUNCIL MEETING - JUNE 1998

Age Structured Model for the Cod Population in NAFO Divisions 3NO

by

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INTRODUCTION

This paper presents an age structured production model applied to the cod population in NAFO divisions 3NO. Age structured production models explicitly fit stock recruitment relationships and apply them along with yield per recruit and spawning stock biomass per recruit concepts (Sisenwine and Shepherd, 1987). An example of this approach can be found in Sinclair (1997). The paper illustrates for the 3NO cod data set the difficulties in fitting this set of data to parametric stock/recruitment relationships and the sensitivity of MSY-based biological reference points (BRP) to the fitted parameters, i.e. Fmsy and Bmsy. BRPs based on non parametric relationships were also estimated, i.e. Floss and Fmed.

DATA

Input data from the last SPA for the 3NO cod (Stansbury et al, 1995). All parameters entering in the calculations were estimated as the mean over the whole time series. The partial recruitment vector was scaled to the mean F for the age range 7-10 in 1992 (0.693). M was fixed at 0.2.

The parameters of the S-R relationship (Ricker curve) were fit to the data for 1959-1994 by nonlinear techniques assuming lognormal error distribution (Table 1).

BRPs were estimated using FISHLAB functions fed with the data detailed above. The variability of the BRP estimates was estimated by bootstrapping. Concerning the S-R relationship, the observed pairs were resampled with replacement from the observed set of data. 1000 bootstrap replicates were used. Montecarlo replicates were obtained for the remainder input parameters parallel to the S/R replicates. The following text table illustrates the kind and level of errors used, the latter being based on the observed variability:

Parameter	type of error	level
F (partial recruitment)	normal error	0.5 CV
M = 0.2	normal error	0.2 CV
Stock weights	lognormal error	log sd 0.1 for ages 3-5 0.3 for ages 5-12+
Catch weights	lognormal error	log sd 0.1 for ages 3-5 0.3 for ages 5-12+
Maturity ogive (SCR 1995)	normal error after logit transformation	sd = 1 on logit transformed values

RESULTS

Table 1 below shows the fittings of the Ricker S-R model. The statistical fitting appear in row 1, whereas rows 2 and 3 correspond to two different eye fittings (Figure 1). MSY-based BRPs as calculated by the Ricker S-R relationship appear in Table 2. The estimates of Fmsy substantially change among sets from 0.19 (statistical fit) to 0.34 (eye fit 1) and 0.2 (eye fit 2) whereas Bmsy and MSY range from 478 and 139 to 112 and 76 and to 176 and 67 respectively.

	Ricker fit	a	b
1	Statistical fit	**0.686**	**0.00198**
2	Eye fit 1	2.000	0.01000
3	Eye fit 2	1.000	0.00500

Table 1

Ricker curve fittings			
	1	2	3
Fmsy	0.19	0.34	0.24
Bmsy	478	112	176
MSY	139	76	67

Table 2

The family of curves describing yield (Y) per recruit (R), spawning biomass (SSB) per recruit and yield as a function of fishing mortality (F) and equilibrium spawning biomass (SSBe) are presented in Figures 2 to 4 (Sisenwine and Shepherd, 1987). Figure 2 corresponds to the statistical fit of the Ricker curve, and Figure 3 & 4 to the two eye fits respectively. The biological reference points derived in this analysis are shown in the first column ("observed") of Table 3. F0.1 and Fmax are 0.130 and .215 respectively. The estimate of Floss is 0.526 and Fmed reach 0.388.

Table 3 also shows the bootstrapping estimates of the BRPs. The average and median values are similar to the "observed" values except for Floss. Coefficients of variation (cv) are 31% for F01, 30% for Fmax, 34% for Floss and 29% for Fmed. The minimum values and the 5, 10 and 20 percentiles are also presented in Table 3. These percentiles give the probability level for a given F of being greater than the F of reference.

Table 3

	Observed	average	cv	Minimum value	5% percentile	10% percentile	20% percentile	median
F01	**0.130**	**0.135**	**0.31**	**0.032**	**0.077**	**0.088**	**0.100**	**0.129**
YPR	1.028	1.061	0.13	0.744	0.871	0.900	0.953	1.046
SPR	4.998	5.212	0.25	2.546	3.497	3.749	4.104	5.019
Fmax	**0.215**	**0.226**	**0.30**	**0.054**	**0.131**	**0.147**	**0.170**	**0.217**
YPR	1.095	1.131	0.13	0.797	0.929	0.956	1.012	1.117
SPR	2.793	2.912	0.31	0.709	1.696	1.880	2.147	2.813
Fmsy	**0.187**	**0.275**	**0.40**	**0.065**	**0.135**	**0.157**	**0.183**	**0.243**
Bmsy	478	488	0.07	407.881	439.404	447.675	458	486
MSY	139	146	0.13	97.878	116.314	121.728	130	144
Floss	**0.526**	**0.560**	**0.34**	**0.076**	**0.287**	**0.339**	**0.405**	**0.543**
Fmed	**0.388**	**0.398**	**0.29**	**0.108**	**0.232**	**0.264**	**0.300**	**0.388**

The lack of convergence in a high number of bootstrapped replicates impeded to get bootstrapping Ricker parameters and therefore no bootstrapping estimates were achieved for the MSY based reference points. However, the sensitivity of these reference points to the fitted parameters is illustrated when comparing the

values in Table 2. The estimates of reference Fs based on non parametric relationships, i.e. Floss and Fmed seems to be more stable than Fmsy.

REFERENCES

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Sisenwine, M.P. and J.G. Shepherd, 1987. An alternative perspective on recruitment overfishing and biological reference points. Can. J. Fish Aquat. Sci. 44: 913:918.

Stansbury, D. C.A. Bishop, E.F. Murphy and M.B. Davis, 1995. An Assessment of the Cod Stock in NAFO Div. NO. SCR 1995/70. Serial No. N2585.
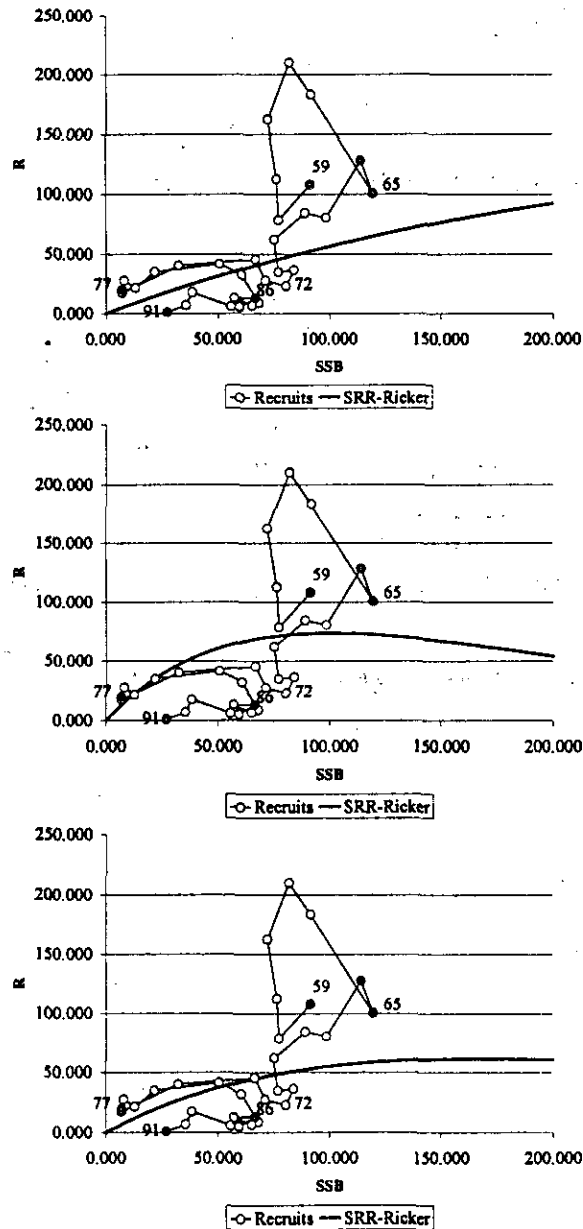
Figure 1: S-R relationship fits for the Ricker model. Top panel: statistical fit. Middle panel: eye fit 1. Bottom panel: eye fit 2.
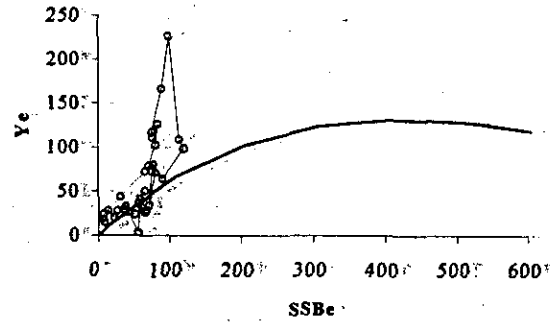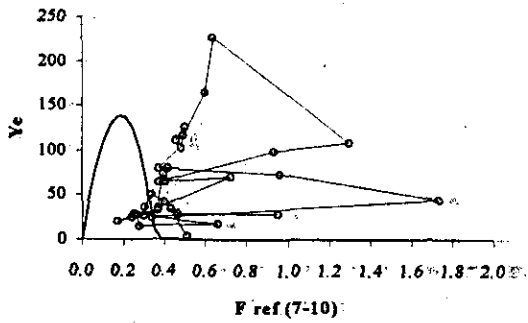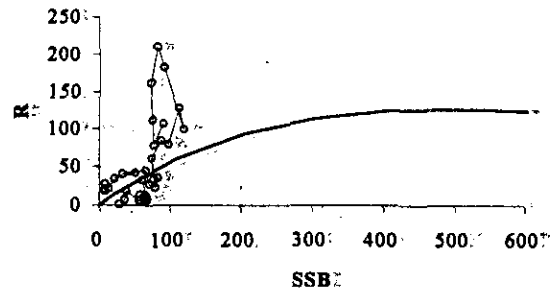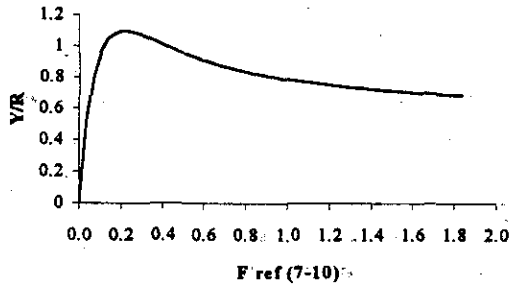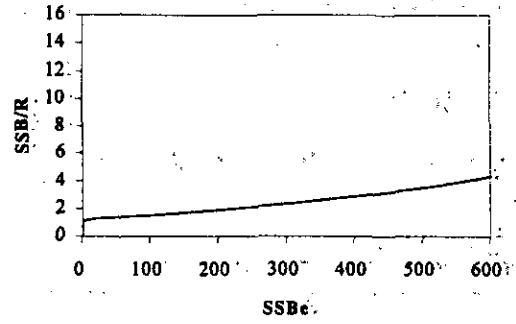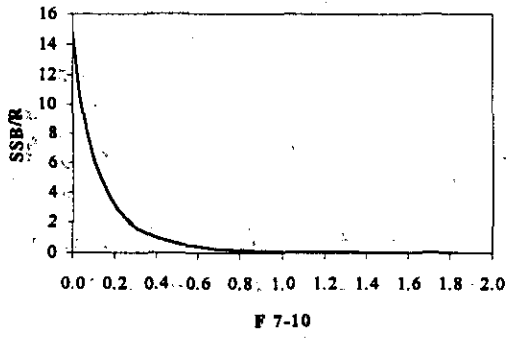
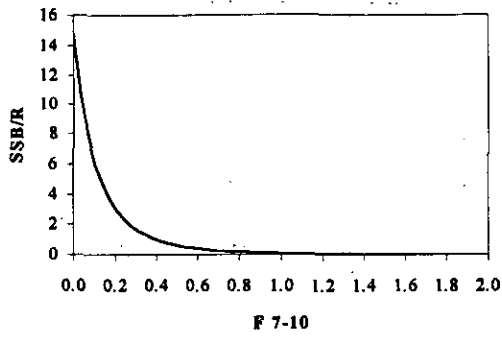Figure 2: Family of curves when using the statistical fitting for the Ricker model.
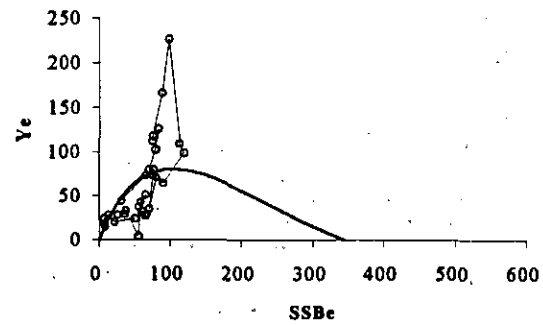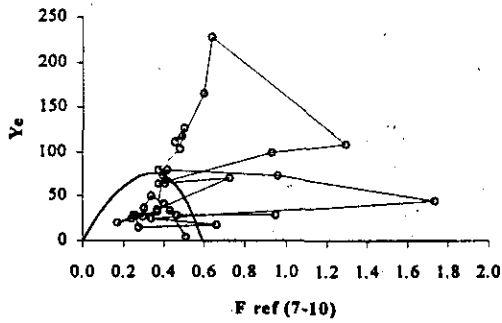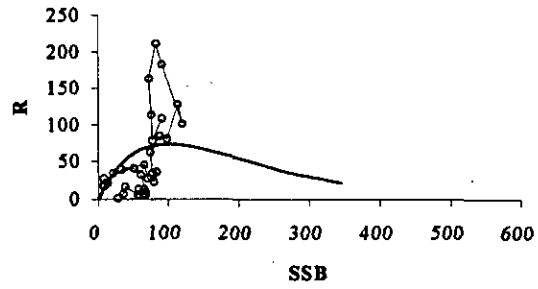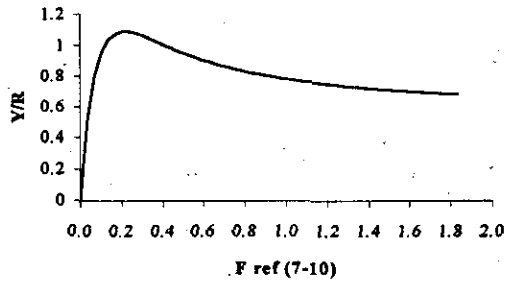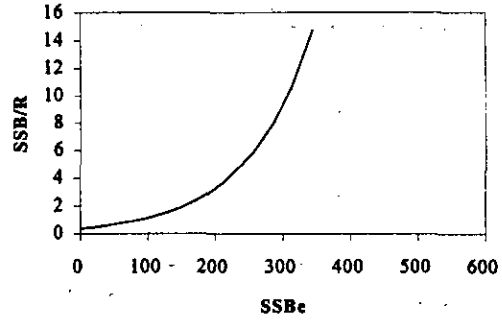
Figure 3: Family of curves when using eye fitting 1 (Table 1) for the Ricker model.

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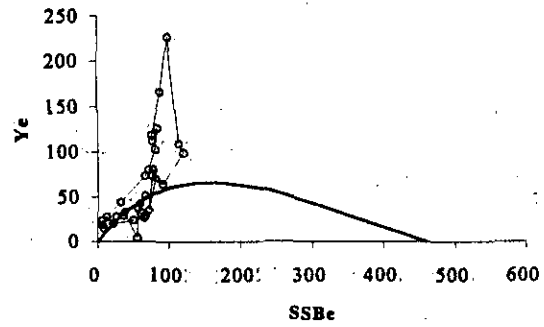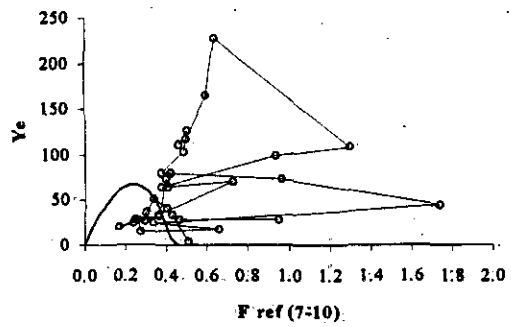
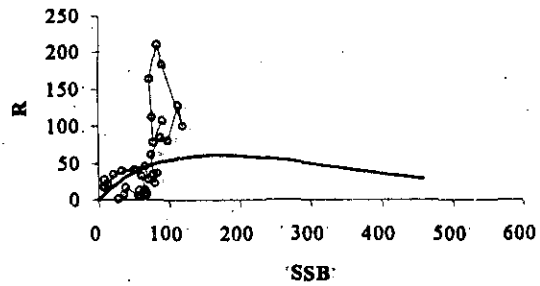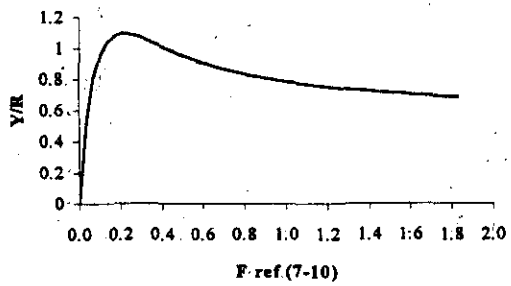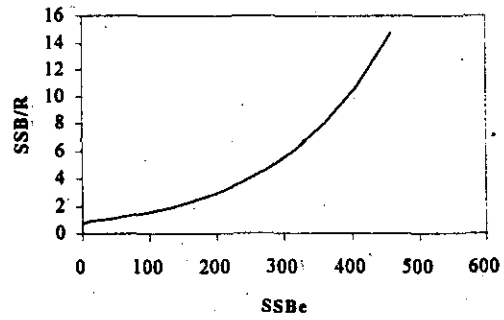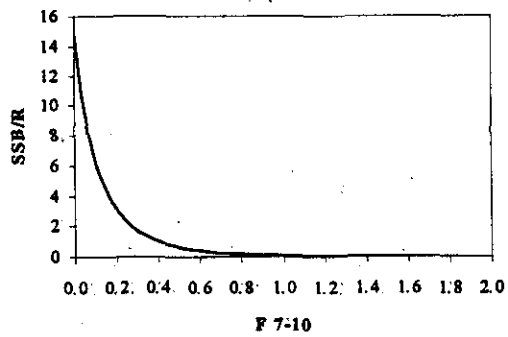Figure 4: Family of curves when using eye fitting 2 for the Ricker model.