(Revised title)

Stock and risk assessments on bigeye tuna (*Thunnus obesus*) in the Indian Ocean based on AD Model Builder implemented Age-Structured Production Model (ASPM)

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Abstract

We applied an Age-Structured Production Model (ASPM) to assess the status of the bigeye tuna stock (*Thunnus obesus*) in the Indian Ocean using 61 years of data (1950-2010). In addition, risk assessments, based on the ASPM results, were conducted to evaluate the probablities of the Spawning Stock Biomass (SSB) falling below MSY level and Fishing mortality (F) exceeding this level in next 10 years (2011-2020) under five constant catch scenarios. The AD Model Builder (Otter Research) code for this ASPM is based on the (previouly used) Fortran-implemeted ASPM software (Restrepo, 1997). The ADMB implemented ASPM software is detailed in the users' manual in another document submitted to this meeting (IOTC-2011-WPTT13-46). An initial run was conducted before the meeting and the final one during the meeting. The final assessment results suggested that the bigeye stock ………………….

[to be completed after the final ASPM run is completed during the meeting]

Contents

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1. Introduction

In this paper, we attempted to assess the bigeye tuna (*Thunnus obesus*) (BET) stock in the Indian Ocean using the ADMB implemented Age-Structured Production Model (ASPM) software. We assume that BET in the Indian Ocean is a single stock. In addition we also conducted a risk assessement based on the ASPM results to investigate the probablities for SSB of falling below the estimated MSY level and F exceeding this level in next 10 years (2011-2020) under five constant catch scenarios. The (previouly used) Fortran-implemeted ASPM software (Restrepo, 1997) has been recoded using AD Model Builder (Otter Research) and used here. The ADMB implemented ASPM software is detailed in the users' manual in another document submitted to this meeting (IOTC-2011-WPTT13-46). An initial run was conducted before the meeting with a final run conducted during the meeting to take account of updated information. We cover both results in this document.

2. Input data

To implement ASPM, we used BET annual nominal catch, standardized (STD) CPUE, CAA (catch-at-age) data by gear and also biological information for the period 1950 to 2010 (61 years). Below are descriptions of the data used in the ASPM runs.

2.1 Nominal catch and type of fleets

IOTC Secretariat provided nominal catch by gear type, longline, purse seines (log school and free school) and others (mainly artisanal surface fisheries) (Figs. 1 and 2). In the ASPM analyses, three fleets were used i.e., LL, PS (free) and PS (log). Others (artisanal surface fisheries such as pole & line, gillnet and troll) have been included with the PS (log) catches as they have similar selectivity patterns to those of PS (log).

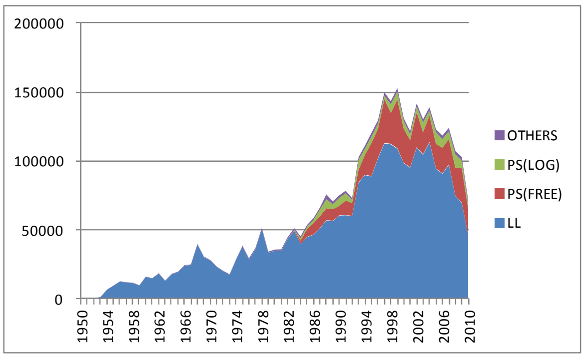


Fig.1 Annual trends of bigeye tuna catch by gear (tons)

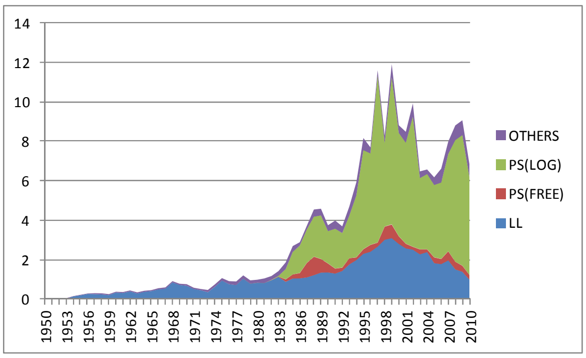


Fig.2 Annual trends of bigeye tuna catch by gear (million fish)

2.2 Standardized (STD) CPUE

Standardized (STD) CPUE series are available from Japan (personal communication with Dr Okamoto) and Taiwan (Yeh and Chang, 2011; IOTC-2011-WPTT13-35). We also expect to obtain the Korean STD CPUE later. There are two types of STD CPUE in each country, STD CPUE for the whole Indian Ocean (all sub areas in Fig. 3) and for the tropical area (sub areas 3+4+5 in Fig. 3). Figs. 4-5 show comparisons of two STD CPUEs in two areas.

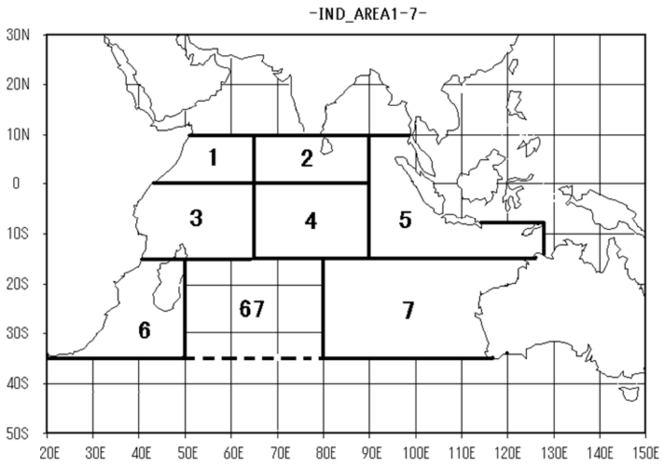


Fig. 3 Sub-areas used for the BET CPUE standardization.

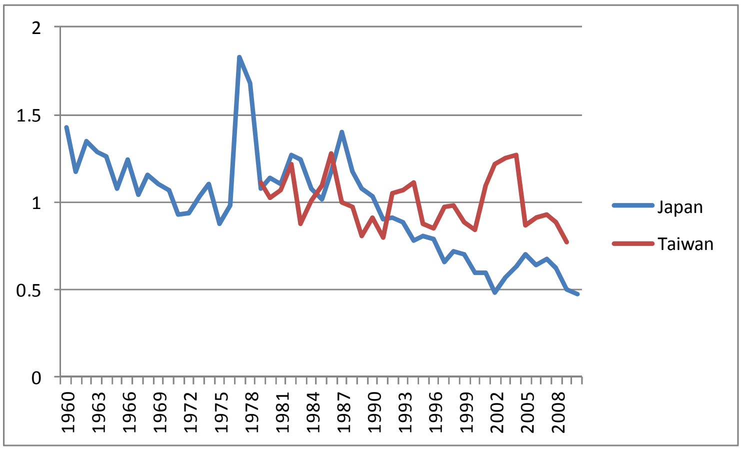


Fig. 4 Comparisons of STD CPUE between Japan and Taiwan **(Tropical IO)** (scaled as mean STD CPUE=1).

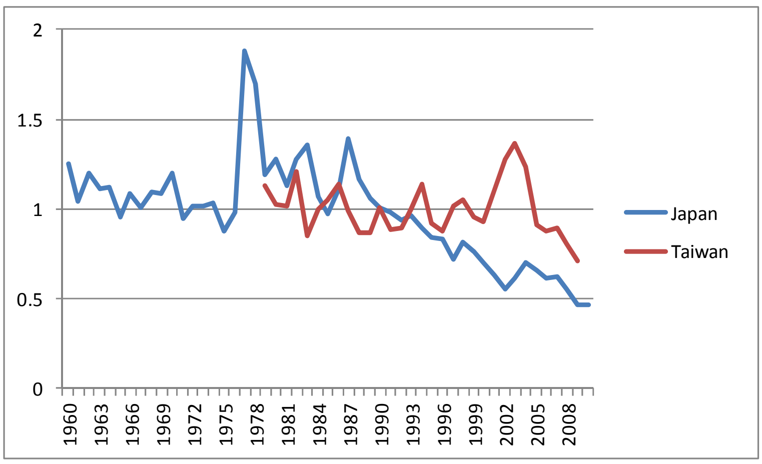


Fig. 5 Comparisons of STD CPUE between Japan and Taiwan **(whole IO)** (scaled as mean STD CPUE=1).

Evaluation of catch vs.STD CPUE relations

Catch and STD CPUE are expected to have a negative proportional relationship. We examined this relationship. Fig. 6-7 show results in the tropical and whole Indian Ocean respectively. Taiwan STD CPUE shows no relationship with catch, whereas Catch and STD CPUE for Japan are fairly well correlated. Within Japan, the one for the tropical IO shows the better situation in terms of R2. Fig. 8 compares the Japanese STD CPUE for the tropical and whole IO. From this analysis we suggest using the JPN STD CPUE as the base case in the ASPM analyses.

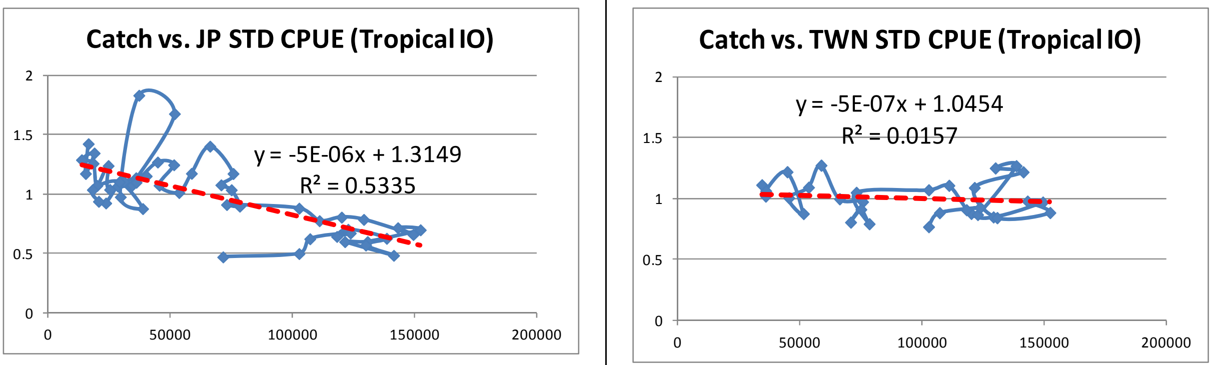


Fig. 6 Relation between Catch vs. STD CPUE (left: Japan, right Taiwan) **(Tropical IO)**

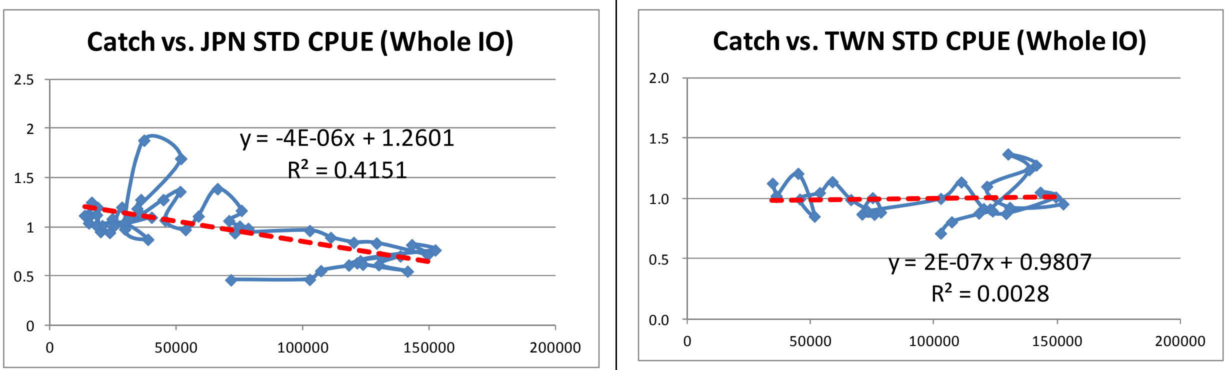


Fig. 7 Relation between Catch vs. STD CPUE (left: Japan, right Taiwan) **(Whole IO)**

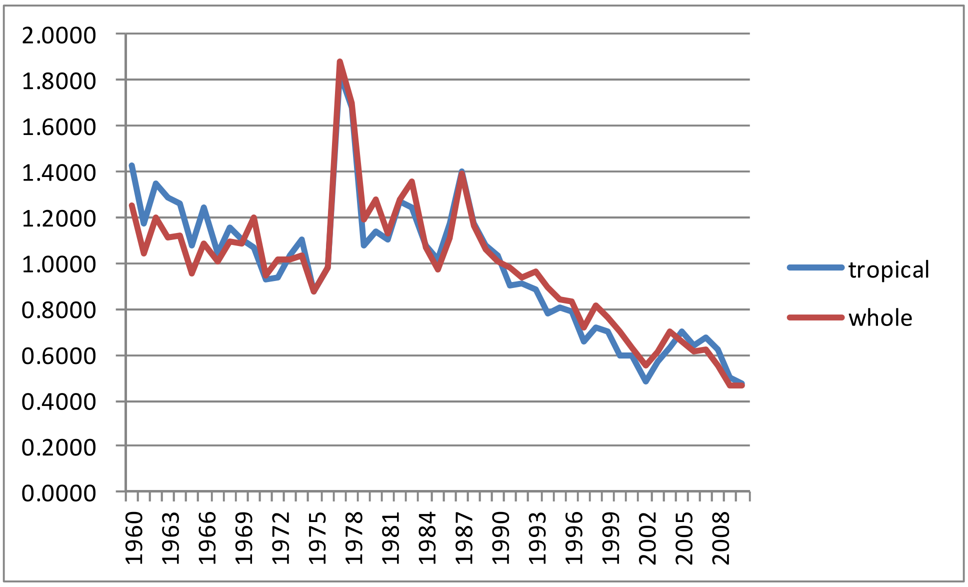


Fig 8 Comparison of Japanese STD CPUE between tropical and whole IO. (scaled as mean STD CPUE=1).

2.3 Catch-At-Age (CAA)

The IOTC Secretariat provided the CAA matrix data by gear. Fig. 9 shows annual trends of CAA by gear. For LL, the major age groups exploited are ages 3-6 (matures), while for PS (free) and PS (log), ages 0-2 (immature). PS (log) catches much more for of mature fish (ages 3-9) than PS (log).

Fig. 10 comprises catch (CAA) levels among three types of fleets (gears). PS (log) and LL catch the majority in term of numbers. Although catches PS (free) in term of numbers is very minor, it biomass (tons) are the second largest (Fig. 1). Thus all three fleets play important role in the ASPM.

2.4 Biological information

In the ASPM analyses, three types of age-specific biological inputs are needed, i.e., natural mortality-at-age (*M*), weights-at-age (beginning and mid-year) and proportion maturity-at-age.

(1) Natural mortality vector (*M*)

We applied *M* vectors used in ICCAT as shown in Box 1.

Box 1 *M* vectors

Natural mortality by age

#age	0	1	2	3	4	5	6	7	8	9
	0.8	0.8	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4

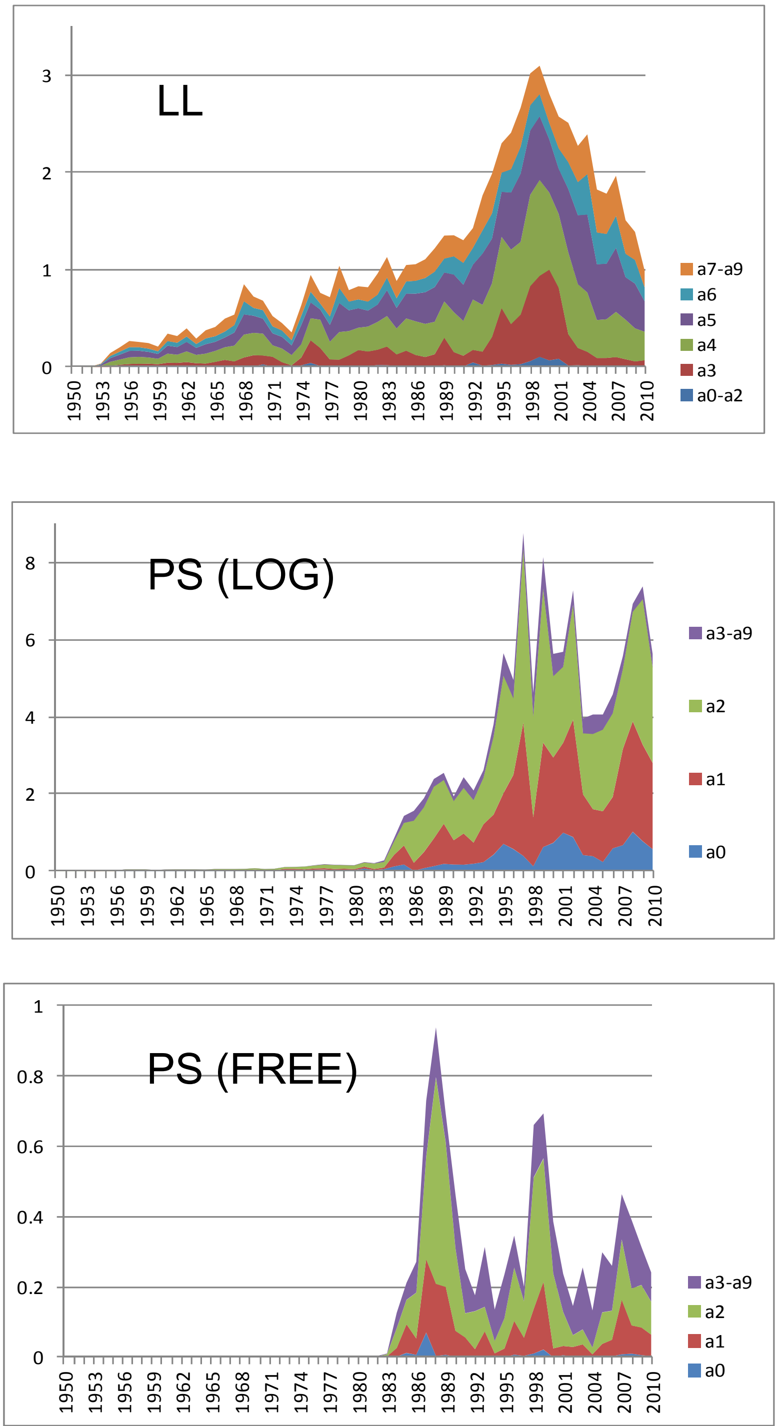


Fig. 9 Trends of CAA by gear type (Million numbers of fish)

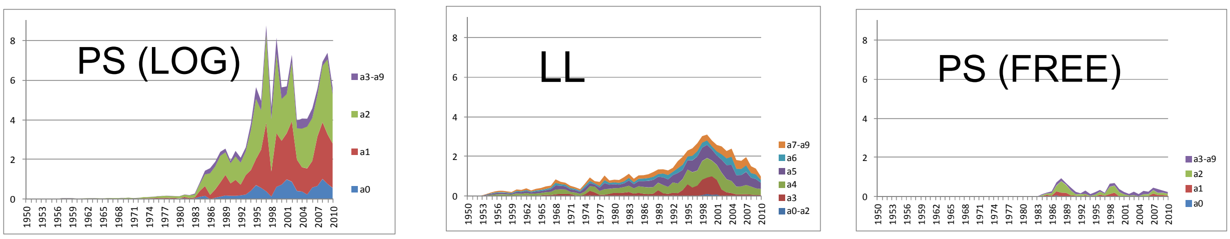


Fig. 10 Comparison of levels of catch (CAA) among three types of fleets (gears) using the same catch scale (million numbers of fish)

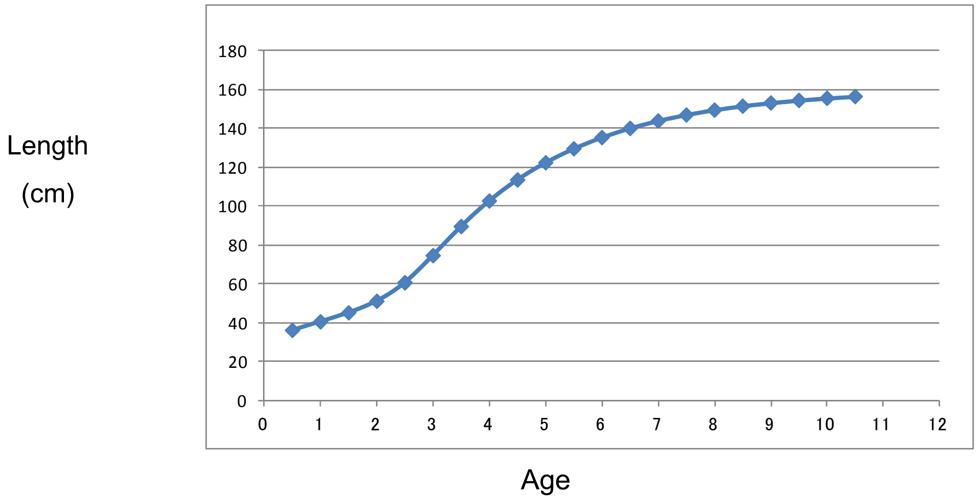
(2) Beginning- and mid-year weights-at-age

Using von Bertalanffy log k growth model by Laslett, Eveson and Polacheck method (IOTC-2008-WPTT-09) (Box 2) and the LW relationships (Box 3), we computed weight-at-age by 0.5 year (Box 4).

Box 2 Indian Ocean BET growth equation (Laslett et al, 2008)

$$L(t) = L_{\infty}\left(1 - e^{-k_2(t-t_0)}\left\{\frac{1+e^{-\beta(t-t_0-\alpha)}}{1+e^{\beta\alpha}}\right\}^{-(k_2-k_1)/\beta}\right)$$

Species	L_{∞}	k_1	k_2	α	β	t_0
BET	160	0.071	0.4207	5.6033	2.999	-3.09



Box 3 LW relation

For fork length < 80 cm: $W = (2.74 \times 10^{-5}) l^{2.908}$ Poreeyanond (1994) (Indian Ocean)

For 80cm <=fork length: $W = (3.661 \times 10^{-5}) l^{2.90182}$ Nakamura and Uchiyama (1966) (Pacific Ocean)

Box 4 BET Weights-at-age (tons) in the Indina Ocaen

Beginning of the year weights by age (tons)

# age	0	1	2	3	4	5	6	7	8	9
	0.00065	0.00149	0.00296	0.00891	0.02353	0.04013	0.05452	0.06565	0.07373	0.07938

#

Middle of the year weights by age (tons)

# age	0	1	2	3	4	5	6	7	8	9
	0.00106	0.00206	0.00473	0.01552	0.03195	0.04771	0.06050	0.07004	0.07682	0.08150

(3) Maturity-at-age

We assume that the proportion-at-maturity is 0% for age 0-2, 50% for age 3 and 100% for age 4-9+ (Box 5).

Box 5 Maturity and fecundity of YFT in the Indian Ocean

Proportion maturity by age

# age	0	1	2	3	4	5	6	7	8	9
	0	0	0	0.5	1	1	1	1	1	1

3. ASPM

3.1 AD Model Builder implemented ASPM

Conceptually ASPMs fall somewhere between simple biomass-based production models (e.g., Schaefer 1957; Prager 1994) and the more data-demanding sequential age-structured population analyses (Megrey, 1989) and integrated models such as SS3, CASAL and MULTIFAN-CL. Typically, simple production models estimate parameters related to carrying capacity, rate of productivity, biomass at the start of the time series, and coefficients that scale indices of abundance to the absolute magnitude of biomass. ASPMs estimate similar parameters but make use of age-structured computations internally, rather than lumped-biomass ones and directly estimate parameters of a stock-recruitment relationship. Their main advantage over simpler production models is that they can make use of age-specific indices of relative abundance and the spawner-recruitment relationship.

There are a number of applications of ASPM for various species in the past. As our experience is mainly on tuna stock assessments, here we introduce a few application of ASPM on tuna in the past. In the International Commission for the Conservation of Atlantic Tunas (ICCAT), ASPM were applied for albacore tuna (*Thunnus alalunga)* in the south Atlantic and bluefin tuna (*Thunnus thynnus*) in the western Atlantic. In the Indian Ocean Tuna Commission (IOTC), ASPM were applied for bigeye tuna (*Thunnus obesus*) and yellowfin tuna (*Thunnus albacares*) (IOTC, 2002-2008).

The above mentioned ASPM software was first coded in FORTRAN by Restrepo (ICCAT, 1997). However, this FORTAN implemented ASPM has the following limitations:

- Very slow operating speed especially to conduct the bootstrap to estimate variances;
- It can only handle a maximum of 4 fleets;
- Steepness of the stock-recruitment curve is estimated and cannot be fixed. This has caused problems in past assessment as steepness was estimated to be unrealistically high (0.999) or low (less than 0.4). The ability to fix the steepness in ASPM runs and evaluating sensitivities could provide more reliable results.

To improve these problems, we started to re-code the “FORTAN based ASPM” to “AD Model Builder implemented ASPM” in 2008 and this was completed in September 2011. It took 4 years as we temporarily stopped development and testing works for 2 years. This software development has been funded by the Fisheries Research Agency (FRA), Japan. Table 1 summarizes the differences between the FORTAN and AD Model Builder implementations.

Table 1 Comparison between the FORTAN and AD Model Builder ASPM implementations.

	FORATN ASPM	AD Model Builder ASPM (refer to Appendix A: Formation) (IOTC-2011-WPTT13-42)
Fleets	4	No limits
steepness	Estimated	Estimated or Fixed between 0 and 0.95
computing speed	1	10 times or more faster
catch equations	Pope’s approximation	
minimization routines	simplex algorithm	automatic differentiation
uncertainty (variances) estimation	bootstrap	delta method MCMC
Selectivity	Fixed	Fixed or Estimated (model free, ad hoc basis)
Others		Negative log likelihood is computed without the constants.

The users’ manual is available in another document of this meeting (IOTC-2011-WPTT13-46) and the ADMB ASPM software (free of charge) will be provided upon request by the first author of this paper.

3.2 Initial ASPM runs

(1) ASPM run

In the initial ASPM run before the WPTT13 meeting, we use the Japanese tropical STD CPUE and the biological information stated in the previous section. A first attempt at estimating h (steepness) lead to a very low value (h=0.39) which was deemed unrealistic. Thus we conducted further ASPM runs by fixing plausible h values [0.5, 0.6, 0.7 and 0.9] to see which h produced the best fit to the data.

Table 2 shows the results which indicate that h=0.5 produces the best fit. Then we decided h=0.5 as the best model in the initial ASPM run. Fig. 11 shows results of the initial ASPM run and Fig. 12 shows estimated selectivities and results of the residual analyses of selectivities. Fig 13 shows the Kobe plot (stock trajectory) with confidence surfaces in the initial ASPM run. This plot was made by the Kobe plot software. For details refer to IOTC-2011-WPTT13-45 submitted to the current meeting.

Table 2 Results of the initial ASPM attempts to investigate the best h (steepness)

h	0.39 estimated (too low)	0.5 (initial ASPM run)	0.6	0.7	0.8
Likelihood	'Total -116.119 Indices -91.036 CAA -33.685 SR_fits 8.602 R-square 0.834	'Total -115.249 Indices -91.949 CAA -31.731 SR_fits 8.431 R-square 0.839	'Total -114.295 Indices -91.962 CAA -30.831 SR_fits 8.498 R-square 0.839	'Total -113.287 Indices -91.967 CAA -30.071 SR_fits 8.751 R-square 0.839	'Total -112.312 Indices -91.966 CAA -29.441 SR_fits 9.095 R-square 0.839

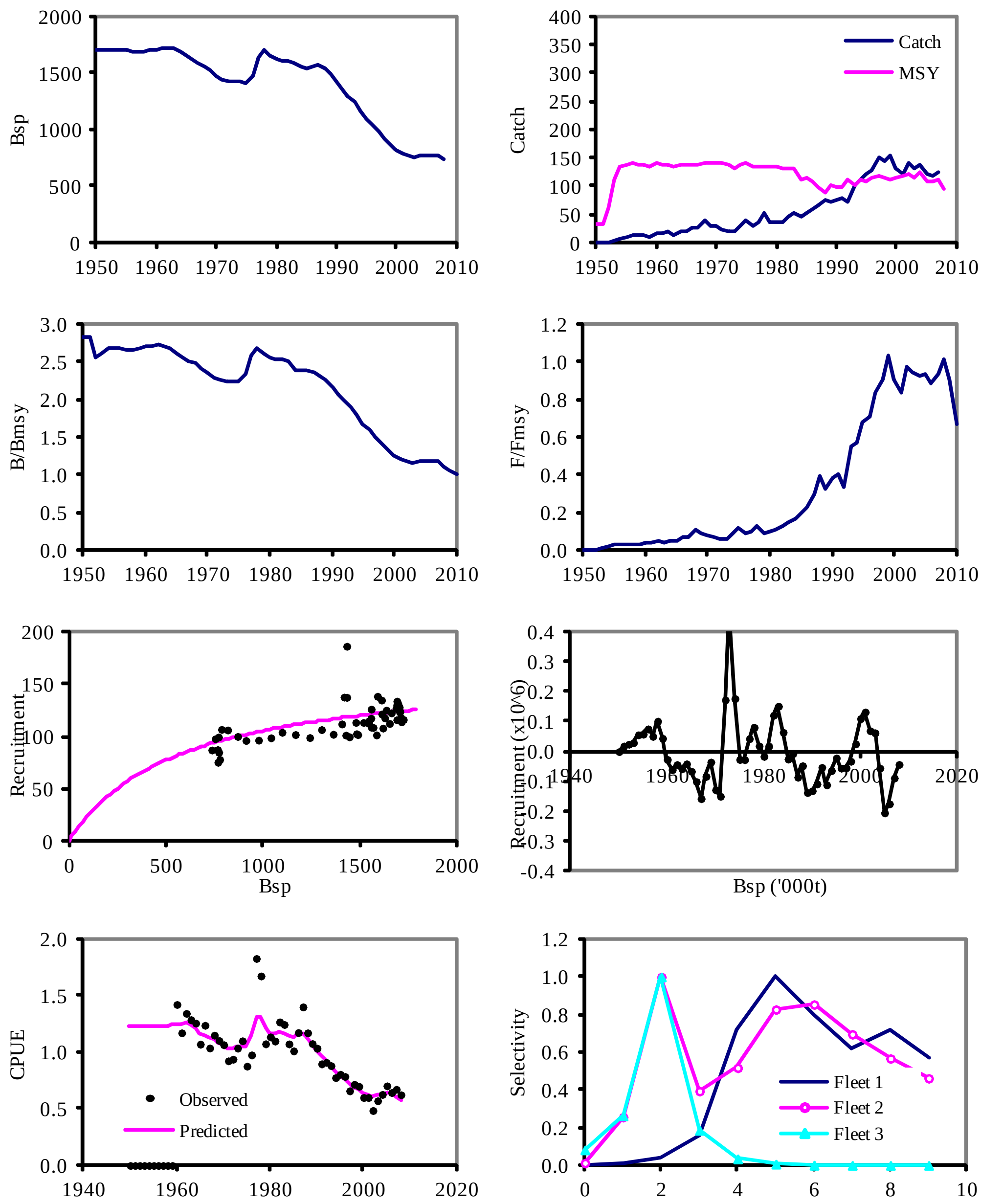


Fig. 11 Results of the initial ASPM run.

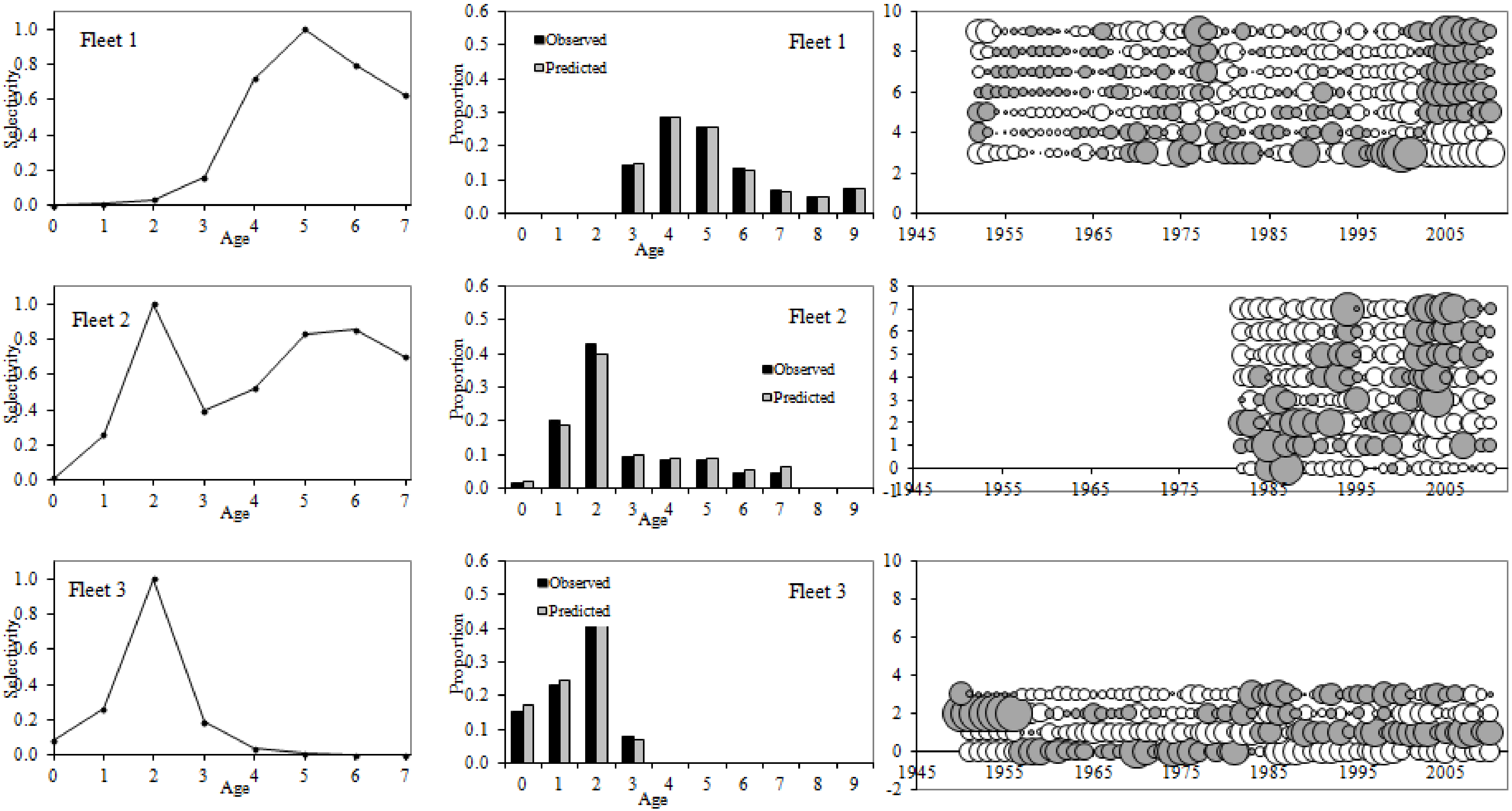


Fig. 12 Estimated selectivities and residual analyses [Fleet1=LL, Fleet 2=PS(Free) and Fleet 3=PS(log)]

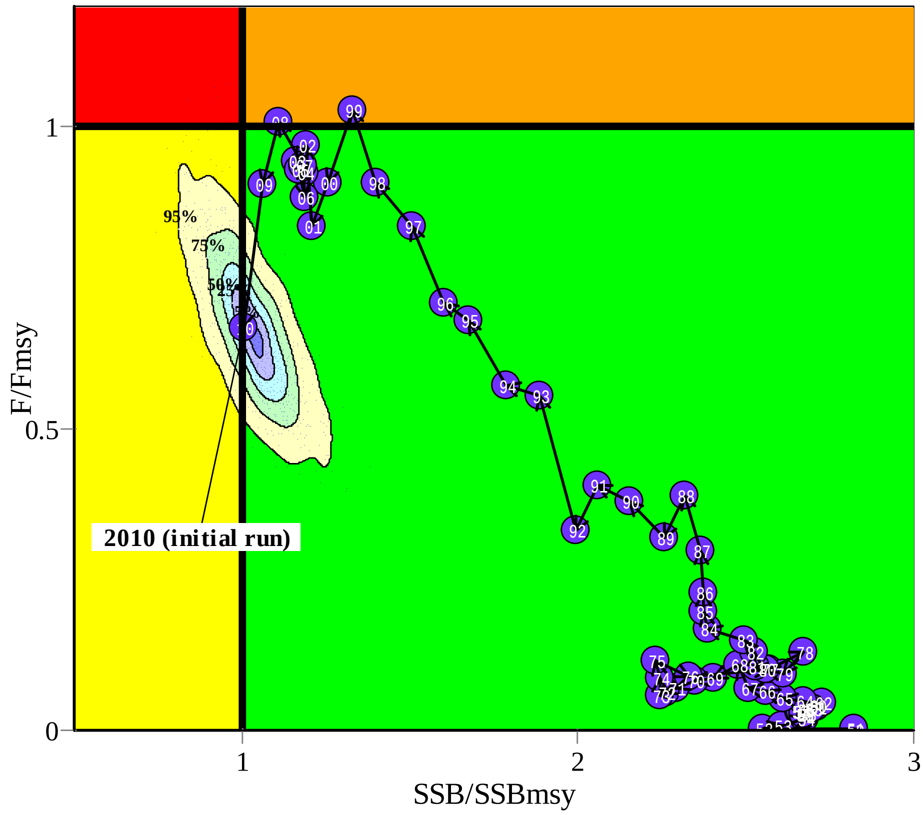


Fig 13 Kobe plot (stock trajectory) with confidence surfaces in the initial ASPM run
(This plot was made by the newly developed Kobe plot software. For details refer to IOTC-2011-WPTT13-45)

Summary of ADMB ASPM results (initial trial) (requested format by the IOTC)

Table 3 Indian Ocean bigeye stock status summary based on the ASPM analyses

Management Quantity	Indian Ocean
Most recent catch estimate (t) (2010)	71,490
Mean catch over last 5 years (t) (2006-2010)	104,673
MSY (t) (90%CI)	102,928 (86,574-119,286)
Current Data Period	1950-2010
F(Current)/F(MSY) (90% CI)	0.67 (0.48-0.86)
SSB(Current)/SSB(MSY) (90% CI)	1.00 (0.77-1.24)
TB(Current)/TB(MSY)	NA
TB(Current)/TB(0) (90% CI)	0.43 (NA)
SSB(Current)/SSB(0)	0.39
SSB(Current)/SSB(Current, F=0)	NA

(2) Projections and risk assessment (Kobe II)

Using the MCMC option available in the ADMB ASPM software, we conducted 0.5 million times of MCMC runs with sampling interval every 500th for 1950-2020 including the projected period (2011-2020). The projections include variability in future recruitments. Then we got 1,000 generated F ratios and SSB ratios in five scenarios (-40% of the current catch, -20%, 0%, +20% and +40%).

Projections and risk analyses for F ratio (F/Fmsy)

Using MCMC results we computed the medians of F ratios and produced the projections of five scenarios (Fig. 14). Then using MCMC results (1,000 generated data), we made the risk assessment matrix table (Table 4) and the diagram (Fig. 15) showing the probability in median term of exceeding the MSY level over the 2011-2020 period.

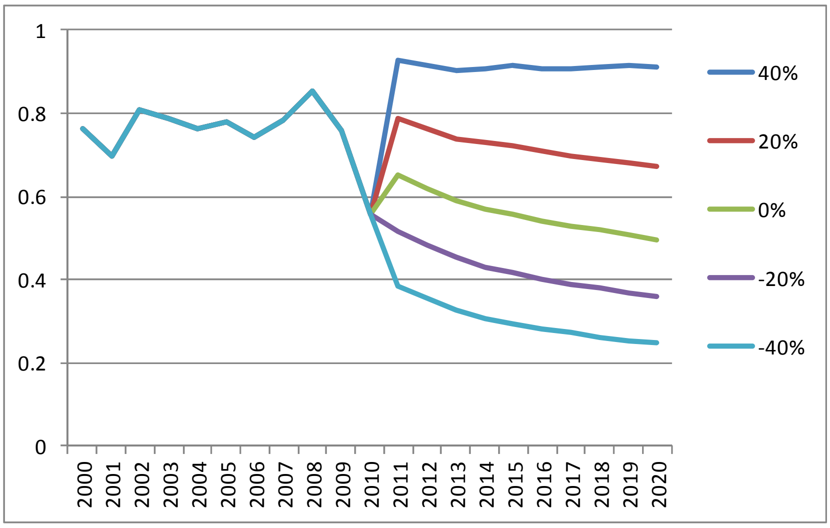


Fig. 14 Projection of median F ratio in 5 scenarios (0%: the current BET catch in 2010) based on 1000 generated data by MCMC.

Table 4 Kobe II risk assessment matrix showing risk probabilities exceeding MSY levels of F ratio in 2011-2020.
[NB: 5 tuna RFMO requests to show the situation in 2013 (3 years later) and 2020 (10) which specified in **bold]**

Kobe II Risk matrix for F ratio										
	Legend	Low risk Pr < 0.20		Low-Medium risk 0.20 <=Pr <40				Midium-High risk 0.4<=Pr <0.6		
catch level	2011	2012	**2013**	2014	2015	2016	2017	2018	2019	**2020**
-40%	0.00	0.00	**0.00**	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
-20%	0.00	0.00	**0.00**	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
0%	0.00	0.01	**0.01**	0.01	0.01	0.00	0.00	0.00	0.00	**0.00**
20%	0.08	0.08	**0.08**	0.08	0.07	0.07	0.06	0.06	0.05	**0.05**
40%	0.32	0.34	**0.33**	0.35	0.36	0.36	0.36	0.36	0.37	**0.38**

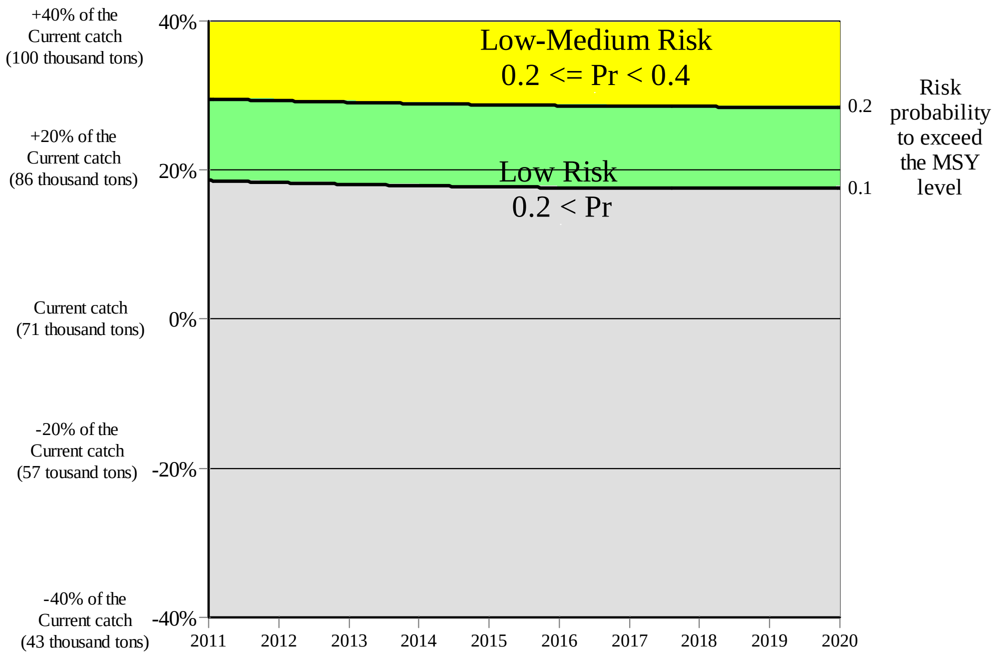


Fig.14 The diagram for the Kobe II risk assessment matrix showing risk probabilities of F ratios to exceed their MSY levels in 2011-2020.

Projections and risk analyses for SSB ratio (SSB/SSBmsy)

Using MCMC results we computed the medians of SSB ratios and produced the projections of five scenarios (Fig. 15). Then using MCMC results (1,000 generated data), we made the risk assessment matrix table (Table 5) and the diagram (Fig. 15) showing the probabilities in median terms of falling below the MSY level over the 2011-2020 period.

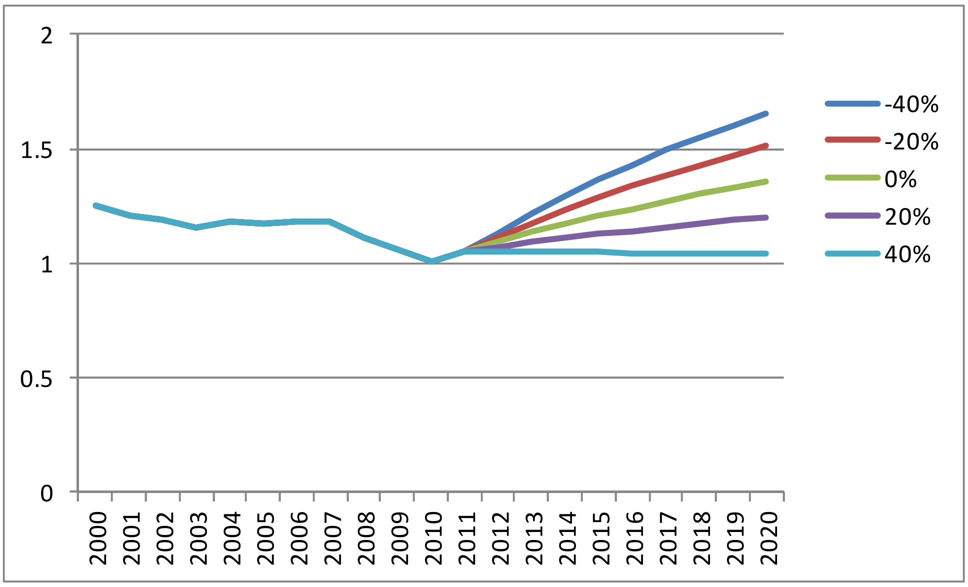


Fig. 15 Projection of median BET SSB ratio in 5 scenarios (0%: the current catch in 2010) based on 1,000 generated data by MCMC.

Table 5 Kobe II risk assessment matrix showing risk probabilities exceeding MSY levels of the BST SSB ratio in 2011-2020. [NB: 5 tuna RFMO requests to show the situation in 2013 (3 years later) and 2020 (10) which are specified in **bold]**

Kobe II Risk matrix for SSB										
	Legend	Low risk Pr < 0.20		Low-Medium risk 0.20 <=Pr <40				Midium-High risk 0.4<=Pr <0.6		
catch level	2011	2012	**2013**	2014	2015	2016	2017	2018	2019	**2020**
-40%	0.30	0.13	**0.04**	0.01	0.00	0.00	0.00	0.00	0.00	**0.00**
-20%	0.30	0.17	**0.08**	0.05	0.02	0.01	0.00	0.00	0.00	**0.00**
0%	0.30	0.21	**0.15**	0.11	0.09	0.06	0.04	0.02	0.02	**0.01**
20%	0.30	0.26	**0.24**	0.24	0.20	0.17	0.15	0.13	0.12	**0.11**
40%	0.30	0.32	**0.35**	0.38	0.39	0.39	0.40	0.40	0.40	**0.41**

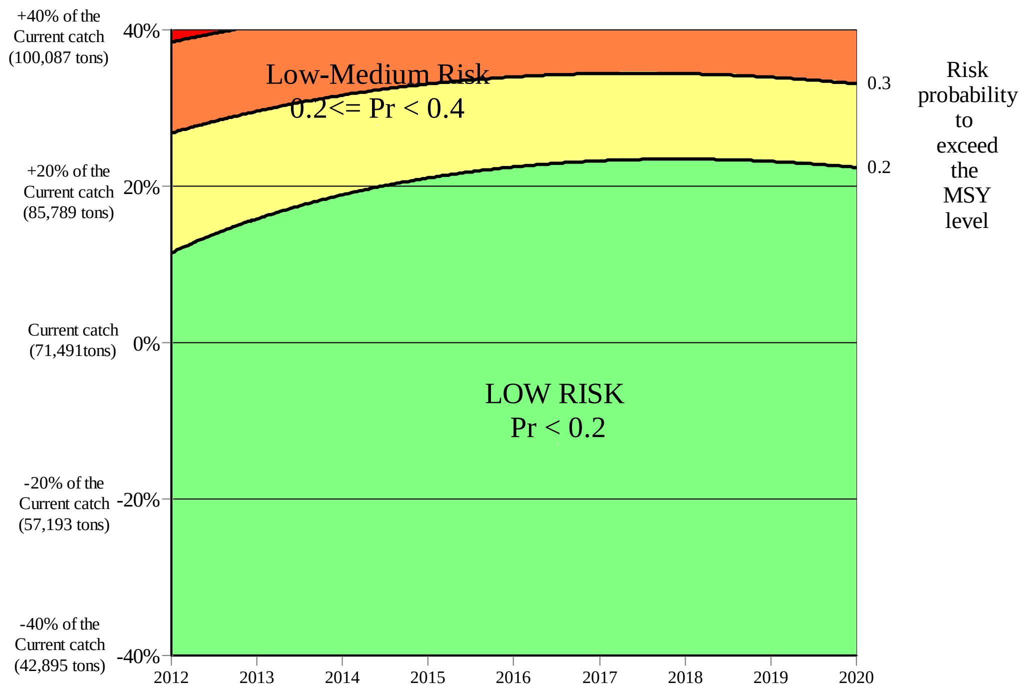


Fig.15 The diagram for the Kobe II risk assessment matrix showing risk probabilities of BET SSB ratios to exceed their MSY levels in 2011-2020.

3.2 Final ASPM runs

To be completed during the meeting

4. Discussion and Conclusion

To be completed during the meeting

Acknowledgements

We sincerely thank to Miguel Herrera, Data manager (IOTC) for providing the nominal catch and Catch-At-Age (CAA) data of bigeye tuna in the Indian Ocean.

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APPENDIX A: SS3 IMPLEMENTED ASPM

Richard Methot (NOAA, USA) developed SS-3 software which core structure is similar to the one of the ASPM. He converted SS3 to make it possible to run ASPM (named as SS3 ASPM).

The input files in SS3 ASPM contain many comments to help users to interpret how to make changes. The input files show commented-out (with a #) place-holder values for many inputs that are not being used. Followings are steps how to use the SS3 ASPM.

(1) Translate the ASPM input into the SS3 format

In the spreadsheet ASPM_input.xls there is a page that finds the SS3 growth parameters that will match the ASPM wt-at-age. There also is a page that converts the ASPM selectivity into SS selectivity parameters.

(2) Prepare SS3 input files

4 files are needed, i.e., STARTER.SS, FORECAST.SS, likeASPM.ctl and likeASPM.dat.

(3) CPUE index

It is interpreted as one continuous time series because in the likeASPM.ctl file, the section on catchability instructs the model to use the catchability for fleet 1 as the catch-ability for fleets 2 and 3, so on. When SS3 estimates the value for this fleet 1 catchability coefficient, it gets a value that includes data from fleets 2 and 3 also.

(4) Run SS3 ASPM

Type SS3 at a DOS command prompt in the directory containing the model and the input files. Results will be saved in REPORT.SSO file.

Note:

If you are interested in this application, please contact the first author of this paper (IOTC-2011-WPTT13-42).

Appendix B: Formulation of the ASPM

The deterministic formulation, for ease of presentation, precedes the formulation for the stochastic model. A Beverton and Holt (1957) type of stock recruitment relationship (SRR) is assumed here. Note, however, that other forms could be implemented following the same basic procedure outlined here.

Deterministic formulation

The deterministic model is essentially like that of (Punt 1994), which was based on ideas presented by Hilborn (1990). It consists of a forward population projection,

$$N_{1,t+1} = f(S_t) \quad \text{for age 1} \quad (1a)$$

$$N_{a+1,t+1} = N_{a,t} e^{-z_{a,t}} \quad \text{for other ages except the "plus" group, and} \quad (1b)$$

$$N_{p,t+1} = N_{p-1,t} e^{-z_{p-1,t}} + N_{p,t} e^{-z_{p,t}} \quad \text{for the plus group, } p, \quad (1c)$$

where $f(S)$ *is* a stock-recruitment function (explained below), a and t index age and year, and age 1 is, for simplicity, assumed here as the age of recruitment. *Z* denotes the total age and year-specific mortality rate, which is the sum of natural mortality (M_a, an assumed input value) and fishing mortality, *F*. In the (Restrepo *in press*) implementation, *F* is calculated based on total yields, weights at age $(\overline{W}_{a,t})$, and age –specific selectivities that are input and assumed exact, for up to five fisheries. This is accomplished by solving for the fishery-specific multipliers $(F_{g,t})$ of the input selectivities ($s_{g,a,t}$) that result in the observed yields (*Y*), given the estimates of stock sizes:

$$Y_{g,t} = \sum_{a=1}^{p} F_{g,t} s_{g,a,t} \overline{w}_{a,t} N_{a,t} U_{a,t} \quad \text{with}$$

$$U_{a,t} = \frac{\left[1 - e^{-\sum_g F_{g,t} s_{g,a,t} - M_a}\right]}{\sum_g F_{g,t} s_{g,a,t} + M_a} \quad (2)$$

Thus, the population projection is conditioned on known yields. The Beverton and Holt SRR can be described by the equation

$$R_{t+1} = f(S_t) = \frac{\alpha S_t}{\beta + S_t}, \quad (3)$$

where *R* is the number of recruits $(N_{l,t+1}$ in eq.1a) and *S* is the reproductive output, namely the product of numbers times maturity times fecundity, summed over all ages. For simplicity, we hereafter refer to *S* as “spawning biomass”, which is often used as a proxy for reproductive output.

Formulation (3) is not very desirable for estimation because starting values of the parameters α and β are not easy to guess. For this reason, the ASPM uses a different parameterization, following (Francis 1992). It consists of defining a “steepness” parameter, τ, which is the fraction of the virgin recruitment (R_0) that is expected when *S* has been reduced to 20% of its maximum (i.e., $R = \tau R_0$ when $S = \gamma / 5$, where γ is the virgin biomass). The SRR can thus be defined in terms of steepness and virgin biomass, two parameters that are somewhat easier to guess initial values. For a Beverton-Holt relationship, virgin biomass should generally be of similar magnitude to the largest observed yields, while steepness should fall somewhere between0.2and1.0, with higher values indicating higher capacity for the population to compensate for losses in spawning biomass with increases in the survival of recruit.

Nothing that equilibrium recruitment at virgin biomass can be computed as the ratio of virgin spawning biomass to spawning biomass per recruit in the absence of fishing $(S/R)_{F=0}$,

$$R_0 = \frac{\gamma}{(S/R)_{F=0}} \tag{4}$$

α and β are given by

$$\alpha = \frac{4\tau\ R_0}{5\tau - 1} \tag{5}$$

and

$$\beta = \frac{\gamma(1-\tau)}{5\tau - 1} \tag{6}$$

The spawning potential ratio, *SPR,* is measured by the spawning biomass per recruit obtained under a given *F,* divided by that under *F*=0 (Goodyear 1993). A useful benchmark for management is the *SPR* corresponding to the slope of the *SRR* at the origin, i.e., at the point when the stock is expected to "crash". From equations (4) to (6) it follows that this SPR_{crash} is given by

$$SPR_{crash} = \frac{(S/R)_{crash}}{(S/R)_{F=0}} = \frac{\beta/\alpha}{\gamma/R_0} = \frac{1-\tau}{4\tau} \tag{7}$$

Hence, in a deterministic sense, any fishing mortality that results in an *SPR* lower than SPR_{crash} is not sustainable.

Fitting the model requires finding the values of the **SRR** parameters that best explain the trends in indices of abundance, given the observed yields and other inputs. For a set of initial conditions ($N_{a,t}$ for all ages in *t*=1), equations (1) and (3) are used to project the population forward, with the fishing mortalities being calculated conditional on observed yields, by equation (2). Values of the parameters γ and τ are chosen to minimize the negative log-likelihood,

$$-\ln(L_1) = \sum_i \left[\frac{n_i}{2} \sum \ln\left(\sigma^2_{i,t}\right) + \sum_t \frac{1}{2\sigma^2_{i,t}} \left(I_{i,t-} \hat{I}_{i,t}\right)^2 \right] \tag{8}$$

where í denotes each available index. The last term is for the squared differences between observed and predicted indices (these could be in logarithmic units if a lognormal error is assumed), and $\sigma^2_{i,t}$ are variances whose computation is explained below. The predicted indices are obtained as the summation of stock sizes, times an input index selectivity, *u*, over all ages:

$$\hat{I}_{i,t} = q_i \sum_a N_{a,t} u_{a,i} \omega_i \tag{9}$$

where ω indicates some input control as to whether the index is in numbers or biomass (in which case the product being summed include weight at age), and whether computations are for the start or middle of the year. The parameters q_i scale each index to absolute population numbers (or biomass) and their maximum likelihood values can be obtained analytically by setting the derivative of equation (8) with respect to q_i equal to zero, and solving for the q_i.

There are several options for handling the variances, $\sigma_{i,t}^2$. If all the values for all indices are given equal weight, they can be set to

$$\sigma_{i,t}^2 = \sum_i \left[\frac{1}{n_i} \sum_t \left(I_{i,t} - \hat{I}_{i,t} \right)^2 \right] \tag{10}$$

or, if all values within an index are to have equal weights but each index is weighted depending on how it is fitted by the model (maximum likelihood weighting)then:

$$\sigma_{i,t}^2 = \frac{l}{n_i} \sum_t (I_{i,t} - \hat{I}_{i,t})^2 \tag{11}$$

Alternatively, the variances could be input for each value, based on external information.

So far, the presentation of the method has indicated that parameters γ and τ (or, equivalently, α and β) are estimated directly in the search, and the parameters q_i and $\sigma_{i,t}^2$ are obtained indirectly or externally The remaining requirement to complete the estimation procedure has to do with the initial conditions. This can be handled in various ways and perhaps the easiest is to assume that the initial age composition corresponds to an equilibrium one in virgin state. For this to be approximately valid, the time series of yield data should be extended as far back in time as possible, preferably to the onset of fishing. In this case,

$$N_{1,1} = R_0 \tag{12a}$$

$$N_{a,1} = N_{a-1,1} e^{-M_{a-1}} \quad \text{for ages } a = 2 \text{ to } p-1, \text{and} \tag{12b}$$

$$N_{p,1} = \frac{N_{p-1,1} e^{-M_{p-1}}}{(1 - e^{-M_p})} \quad \text{for the plus group.} \tag{12c}$$

An alternative consists of estimating the equilibrium recruitment in year *t* =1 as an additional parameter and solving for the initial age composition that produces a spawning biomass that results in that recruitment given τ and γ. Several other options exist, but it appears that none will generally be superior unless there is adequate relative abundance information for the start of the time series. A useful option may be to “fix” the initial age composition at same scaled fraction of the virgin one, and to conduct sensitivity trials for that choice.

The computation of statistics such as maximum sustainable yield (*MSY*) and related benchmarks (e.g. S_{MSY}, F_{MSY}) is straightforward once the parameters for the *SRR* have been obtained. Shepherd (1982) describes the procedure used to compute equilibrium yield curves from a *SRR*, together with yield-per-recruit and spawning biomass-per-recruit calculations. Conditional on a given *F* (including an overall selectivity pattern), equilibrium spawning biomass, recruitment and yield are computed as (for the Beverton and Holt SRR)

$$S_F = \alpha (S/R)_F - \beta \quad , \tag{13a}$$

$$R_F = \frac{S_F}{(S/R)_F} \quad , \text{ and} \tag{13b}$$

$$Y_F = R_F (Y/R)_F \tag{13c}$$

where $(S/R)_F$ and $(Y/R)_F$ are the spawning biomass and yield per recruit values resulting from exploitation at *F* . To search for *MSY* –related statistics, this procedure is built into an algorithm to obtain the desired target, e.g. to find the maximum Y_F as the estimates of *MSY.* Note that, if the selectivity pattern changes over time, then the computed MSY-related values will also change as a result of changes in the per-recruit computations.

Stochastic formulation

A stochastic ASPM requires that a recruitment value be estimated for every year. If this were attempted without constrains on the possible recruitment values, while simultaneously estimating the SRR, the application would be over-parameterized in most real situations. In this work, we have chosen to estimate the recruitments as lognormal deviations from the equilibrium SRR, assuming that these deviations follow a first-order autoregressive process.

The population projection equations are as in equation (1), except that recruitment is estimated as

$$N_{1,t} = R_0 e^{\nu} \qquad (14)$$

That is, recruitment is estimated as deviations from a virgin level. Instead of estimating γ and τ directly as parameters, the model estimates γ and all the ν_t. R_0 is computed from equation (4). These are essentially all parameters that would be needed to project the population forward and compute the log-likelihood in equation (8). The AR [1] process is incorporated by assuming that the recruitment estimates thus obtained vary around the expected stock recruitment relationship as

$$R_{t+1} = \frac{\alpha S_t}{\beta + S_t} e^{\varepsilon_{t+1}} \qquad (15)$$

with $\varepsilon_{t+1} = \rho\varepsilon_t + \eta_{t+1}$, $|\rho| < 1$, the η have zero expectation and variance equal to σ_η^2. In equations (14) and (15) we distinguish between recruitment values estimated as parameters ($N_{1,t}$) and those predicted from the estimated stock-recruitment relationship (R_t). The negative log-likelihood for these residuals would be (Seber and Wild 1989):

$$-\ln(L_2) = \frac{n_t}{2}\ln(\sigma_\eta^2) - \frac{1}{2}\ln(1-\rho^2) + \frac{1}{2\sigma_\eta^2}\left[(1-\rho^2)\varepsilon_1^2 + \sum_{t=2}^{n_t}(\varepsilon_t - \rho\varepsilon_{t-1})^2\right] \qquad (16)$$

Where the residuals would be computed as

$$\varepsilon_{t+1} = \ln(N_{1,t+1}) - \ln(R_{t+1}) = \ln(N_{1,t+1}) - \ln\left(\frac{\alpha S_t}{\beta + \mathrm{S}_t}\right) \qquad (17)$$

Computation of the first residual would depend on the initial conditions. For example, in a virgin state, it would be

$\varepsilon_1 = \ln(N_{1,1}) - \ln(R_0)$.

Note that α and β in equations (15) and (17) could be computed from knowledge of virgin biomass and steepness (see equations (5) and (6)). However, only the former is being estimated directly as a parameter. To include steepness as an additional parameter to be directly estimated by the search would confound the information contained in R_0 and γ (refer to equations. (4), (5), and (6)). Our approach is to replace α and β in the *SRR* of equation (17) by a function of those parameters being estimated in the search, and steepness. From equations (5) and (6) it follows that

$$R_{t+1} = \left(\frac{4R_0 S_t \tau}{\tau(5S_t - \gamma) - S_t + \gamma}\right), \text{ such that} \qquad (18)$$

$$\varepsilon_{t+1} = \ln(N_{1,t+1}) - \ln\left(\frac{4R_0 S_t \tau}{\tau(5S_t - \gamma) - S_t + \gamma}\right) \qquad (19)$$

We take advantage of this relationship in order to solve for τ, nothing that, for a given ρ and σ_η^2, equation (16) will be at a minimum when

$$\sum_{t=2}^{n_t-1}\left[\ln(N_{1,t+1})-\ln\left(\frac{4R_0S_t\tau}{\tau(5S_t-\gamma)-S_t+\gamma}\right)-\rho\ln(N_{1,t})+\rho\ln\left(\frac{4R_0S_{t-1}\tau}{\tau(5S_{t-1}-\gamma)-S_{t-1}+\gamma}\right)\right]^2 \quad (20)$$

is also at a minimum. Thus, in every iteration in the search, a subprocedure is invoked to minimize (20) with respect to τ. Having thus calculated the steepness (and, consequently, α and β), the log-likelihood of equation (16) is added to the overall objective function.

It remains to be mentioned what to do about the parameters ρ and σ_η^2. In theory, there is a potential for these to also be estimated. In practice, however, it is unlikely that data will contain so much information as to determine the relative contribution from recruitment variability with respect to the variability in the index values (see equations (8) and (16)). In our limited experience with this model, it appears that these values should be controlled by the analyst in much the same way as contributions to the likelihood from different data sources are weighted externally in other assessment methods (e.g., Deriso et al.1985). Lower σ_η^2 values will result in lower stochasticity in recruitment, while higher σ_η^2 values will allow recruitment to fluctuate more widely in order to better fit the index data. A value of ρ=0 would assume no autocorrelation between successive recruitment deviations. Empirical studies such as those of Beddington and Cooke (1983) and Myers et al. (1990) may yield information about likely ranges of values for ρ and σ_η^2 for species groups. Reported values for these parameters (Myers et al.1990) are quite variable across species.

Estimating the initial conditions for the stochastic model can be problematic, as with the deterministic model. Estimating the age structure in year 1 would not generally be an option as the model would easily become highly over-parameterized unless there were age-specific relative abundance data for the start of the series. Thus, using a long time series of data extending to the onset of fishing, and assuming an initial equilibrium state at γ, remains a useful option. Other alternatives are also possible. In this paper we examine one in which we calculate a stable age structure (with only natural mortality) resulting from a pre-series recruitment that is fixed. That is, we fix $v_{t=0}$ and set the starting population sizes as

$$N_{2,1}=R_0e^{v_0}e^{-M_1} \quad (21\text{a})$$

$$N_{a,1}=N_{a-1,1}e^{-M_{a-1}} \quad \text{for ages } a = 3 \text{ to } P\text{-}1, \text{and} \quad (21\text{b})$$

the plus group is calculated as in equation (12c). This alternative allows the initial age structure to be either higher or lower than that corresponding to an equilibrium virgin state. The parameter $v_{t=0}$ could potentially be estimated in the search procedure as well. If it is, it may be desirable to place a penalty on how much it can alter the initial biomass, say, away from γ. This could be accomplished with the term

$$-\ln(L_3)=\frac{\ln(\sigma_v^2)}{2}+\frac{(\ln(S_1)-\ln(\gamma))^2}{2\sigma_v^2} \quad (22)$$

where σ_v^2 is a variance value to be fixed by the analyst.

Estimation of the stochastic model parameters for any given data set then requires several choices associated with how much recruitment can fluctuate around its deterministic predictions and about the initial conditions. In addition to choices about variances ($\sigma_\eta^2, \sigma_v^2$ and possibly $\sigma_{i,l}^2$), the log-likelihood components could be given different emphases (λ) to obtain model estimates by minimizing:

$$-\ln(L_T)=-\ln(L_1)-\lambda_2\ln(\mathrm{L}_2)-\lambda_3\ln(L_3) \quad (23)$$