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AD MODEL BUILDER IMPLEMENTED AGE-STRUCTURED PRODUCTION MODEL (ASPM) SOFTWARE (VERSION 3, 2014)

User's manual

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Abstract and Release of the software

This user's manual describes how to run the 3rd version of the AD Model Builder implemented Age-Structured Production Model (ASPM) software. In the 3rd version, we added the batch job option to conduct the grid search to find most optimum parameters effectively. In the previous versions, users can make only one ASPM run at once. In this way, searching optimum parameters normally is laborious and takes a very long time by trials and errors. Even an optimum parameter set were found, they might be local minima which will provide biased results**.** This batch option improves such situation. In the next version 4, we will develop the ASPM with size data option as CAA often include biases when size data are converted to age and such biases will become higher especially when number of size data are very limited.

This software is free of charge. If some wants to obtain this software, please download from http://ocean-info.ddo.jp/kobeaspm/aspm/ASPM.zip (available from Nov. 18, 2014). After using this software and if any improvements are needed, please let us know. We will revise and release the better version in the future. This software development project has been funded by Fisheries Agency of Japan (2008 and 2011-2014) for Tuna and Skipjack Resources Division, National Research Institute of Far Seas Fisheries (NRIFSF), Fisheries Research Agency of Japan (FRA). We sincerely acknowledge their continuous financial supports for this project.

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Contents

ACRONYMS

ASPIC	A Stock-Production Model Incorporating Covariates
ASPM	Age-Structured Production Model
B	Biomass (total)
BMSY	Biomass which produces MSY
CE	Catch and effort
CI	Confidence interval
CPUE	catch per unit effort
current	Current period/time, i.e. $F_{current}$ means fishing mortality for the current assessment year
F	Fishing mortality; F2010 is the fishing mortality estimated in the year 2010
FL	Fork length
FMSY	Fishing mortality at MSY
GLM	Generalized Liner Model
IATTC	Inter-American Tropical Tuna Commission
ICCAT	International Commission for the Conservation of Atlantic Tunas
IO	Indian Ocean
IOTC	Indian Ocean Tuna Commission
LRP	Limit Reference Point
LL	Longline
M	Natural mortality
MFCL	Multifan-CL
MSY	Maximum Sustainable Yield
q	Catchability
SB	Spawning biomass (sometimes expressed as SSB)
SBMSY	Spawning stock biomass which produces MSY
SS3	Stock Synthesis III

1. INTRODUCTION

This project to develop the AD Model Builder implemented ASPM software initiated in 2008. Backgrounds on this project are described in Appendix A. To now, a number of stock assessments were conducted using this software (see References). A brief history of the development is as follows:

1st version (2010) (IOTC-2010-WPTT13-46 REV 1)

- Release of the initial ASPM software containing basic functions **(Sections 2-3 and 6.1)**

2nd version (2012) (IOTC-2012-WPM04-06)

- Graphic functions to present results of a single ASPM run were added, in order to users to look at results and diagnostics instantaneously, so that users can go to the next step (changing parameters values, seeding values etc.) effectively and efficiently to search optimum parameters in a very short time **(Section 5).**

3rd version (2014) (IOTC-2014-WPTT16-54)

- Grid search (batch job) option was added. In the previous versions, users can make only a single ASPM run. In this way, searching optimum parameters normally takes a very long time. Even optimum parameters set can be found, they might be local minima which will provide biased results. To improve this situation, the grid search (batch job) option was developed and added **(Section 4).**

4th version (2017) (IOTC-2017-WPTT19-   )

- ASPM with size data option will be developed and added by 2017. CAA has uncertainty when size data are converted to age and such uncertainty are much higher especially if size data are limited. To overcome these problems, ASPM with size data option will be developed within the current ADMB_ASPM framework.

- Such option will become similar to the integrated models such as SS3, Multifan-CL etc. However, one different point is the simplicity, i.e., ASPM has much less parameters (20-40), while the integrated models, hundreds of parameters. The critical point to develop this option is for anyone to be able to conduct ASPM with size data (quasi SS3) in much simpler way than the integrated ones.

2. INPUT FILES

To run ASPM, six input files are required as listed in Table 1. Their names cannot be changed. In all these files, "#" precedes a comment line. In all the input files, extra comment lines can be added without affecting the run, as long as these line starts with "#". The example files available in the ASPM software package contain annotations for input help. Contents of 6 input files are explained in 2.1-2.6.

Table 1 Six ASPM input files

Section	Type of input file	Contents	File names
2.1	Control	Basic settings to control ASPM run	control.inp
2.2	Parameter guesses	Initial guess values for biomass, steepness, and selectivities	aspm.pin
2.3	Biological data	Natural mortality, age-at-weights, maturity-at-age and fecundity at-age	biological.inp
2.4	Index	CPUE data (by fleet)	index.inp
2.5	Fishery	Catch data (by fleet)	fishery.inp
2.6	Projection	Parameters for projections	projection.inp

2.1 Control File (control.inp)

Line	Entry
1-3	Comments
4	First year of catch data
5	Last year of catch data
6	Comment
7	Number of fisheries or gear types for which yield data are available
8	Comment
9	Maximum age considered (taken to be a plus group) (for example, if users have 7 age classes from age 0 to age 6+, then the maximum age is 6 (not 7).
10	Comment
11	Stock-recruitment curve (1= Beverton-Holt, other = Ricker).
12	Comment
13	First year with recruitment fluctuations *(see equation (21), p.38)*
14	Last year with recruitment fluctuations
15	Comment
16	Standard deviation (σ_R) for the stock recruitment fluctuations *[see eq. (4), p34 and (21), p.38]*
17	Comment
18	Deterministic (=-1) or stochastic recruitment (>0)
19	Comment
20	Phase for dummy parameter. Always -1 except if running with ALL the parameters fixed, in that case it needs to be >0.
21	Comment
22	Phase for estimation of virgin spawning biomass (K^{sp}), i.e. whether virgin biomass is estimated (>0) or fixed (to value read in aspm.pin) (-1)
23	Comment
24	Phase for estimation of steepness (h), i.e. whether steepness is estimated (>0) or fixed (to value read in aspm.pin) (-1)
25	Comment
26	Phase for estimation of initial biomass as a fraction of virgin biomass *[(θ, see equation (8), p.34]*, i.e. whether θ, is estimated (>0) or fixed (to value read in aspm.pin) (-1)
27	Comment
28	Phase for estimation of deviation from equilibrium age-structure in the first year *[ϕ, see equation (11), p.35]*, i.e. whether ϕ is estimated (>0) or fixed (to value read in aspm.pin) (-1). ϕ, characterizes the average fishing proportion over the years immediately preceding y_0... If there is no fishing before the start year, phi[ϕ] =0
29	Comment
30	Phase for estimation of selectivity, i.e. whether selectivity is estimated (>0) or fixed (to value read in aspm.pin) (-1)
31	Comment
32	Type of weighting for the CPUE indices: 1 = maximum likelihood, 2 = equal weights, -1 = inverse-variance weighting for each point.

<u>Note</u>

The inputs corresponding to “phases” (lines 22, 24, 28 and 30) allow the minimization to be carried out over a subset of the parameters, while the others are fixed. In a non-linear model it can be useful to estimate the different parameters during different phase.

2.2 Parameter guesses File (aspm.pin)

Line	Entry
1	Comment
2	Guess for ln (natural log) of virgin spawning biomass ($\ln(SSB_0)$)
3	Comment
4	Guess for steepness
5	Comment
6	Guess for θ
7	Comment
8	Guess for ϕ
9	Comment
10	Comment
11-i	Guesses for recruitment deviations
i+1	Comment
i+2-ii	Guess for commercial selectivities

Notes:

If users want the biomass at the beginning of the first year to be the virgin biomass, line 6 must be 1 and line 8 must be zero, with the phase parameters for θ and ϕ (lines 26 and 28 of the control.inp file must be negative).

Guesses for the commercial selectivities go in the order: fleet, periods, ages (minus to plus). For example, two fleets, the first fleet has two selectivity periods and age minus=0, age plus=5, second fleet has only one period and goes from age minus=2 to age plus=7 (see below):

In the Fishery.inp file, there is a row after the plus group; it is the age for which the selectivity is "anchored", i.e., the selectivities for the other ages is estimated relative to the selectivity for that fixed age. The easiest way is to choose it about in the middle of the minus and plus group, which in this case corresponds nearly all the time to the maximum selectivity. In the example below, selectivity 1.0, highlighted by yellow markers are the "anchored" ones which should be in blank in aspm.pin file *(please note this example is not relevant to the example in fishery.inp file).*

# 0	1	2	3	4	5	6	7	
0.1	0.2	0.3	(1.0)	0.6	0.3			# fleet1, period 1
0.15	0.3	0.4	(1.0)	0.5	0.2			# fleet1, period 2
		0.6	0.8	0.9	(1.0)	0.8	0.6	# fleet2, period 1

Guesses for recruitment deviations are not really necessary.

2.3 Biological Data File (biological.inp)

Line	Entry
1-5	Comments
6	Weights at age at the start of the year for all ages
7-9	Comments
10	Weights at age at the middle of the year
11-14	Comments
15	Natural mortality at age
16-18	Comments
19	Proportion maturity at age

2.4 Index File (index.inp)

Line	Entry
1-3	Comments
4	Number of indices
5	Comments
6	Index type for each index (1 = biomass, other = numbers).
7	Comments
8	Index timing: Month of the year or -1 for mid-year.
9	Comments
10	Fleet the index corresponds to
11-13	Comments
14..	Nyears: Year, index value (0 for missing), CV(index),
	… start again for next index

NOTE:

The CV (index) values will be ignored if ML or equal weighting options are selected in the control file. The indices must start from the first year of the assessment period, if index doesn't exist for a particular year, set to zero.

2.5 Fishery File (fishery.inp)

Examples are highlighted by yellow markers

Line	Entry		
#(1-4)	(Comments)		
#(5)	(Comment) Number of selectivity periods by fleet (for example: GILL and LONGLINE)		
	1	1	
#(6)	(Comment) First year and last year for each selectivity period		
#	(1) GILL		
	1950	2011	
#	(2) LONGLINE		
	1950	2011	
#	(Comment) Minus group for each fleet(*)		
	0	2	
#	(Comment) Plus group for each fleet(*)		
	4	6	
#	(Comment) Pinned age for each fleet's selectivity (refer to aspm.pin file)		
	2	4	
#	(comment) Weight given to each commercial catch-at-age data set in the likelihood by fleet		
	0.1	0.1	
#	Annual catch by fleet (tons)		
#	Year	(1) GILL	(2) LONGLINE
	1950	1552	22489
	1951	3564	15487
	2011	6789	24566
#	(Comment) Annual catch-at-age by age		
#	(1) GILL		

#	Year	Age 0	Age 1	Age 2	Age 3	Age 4	Age 5	Age 6+
	1950	154170	28720	50591	4455	871	292	126
	1951	184406	28347	51120	4498	971	492	222

\# (2) LONGLINE

#	Year	Age 0	Age 1	Age 2	Age 3	Age 4	Age 5	Age 6+
	1950	454170	88520	80591	1155	371	125	23
	1951	784406	48347	91120	2298	671	567	98

NOTE:

If the selectivities are fixed (line 30 in control.inp is set to -1), then have the minus groups for each fleet be 0 and the plus groups for each fleet be the maximum age.

If the model is not fitted to the catch-at-age information (CAA weight=0), the program will still compare the observed and predicted CAA (but it won't be included in the likelihood). So if users don't have CAA information, rather fill the matrix with zeros.

(*) To decide plus and minus group (ages), younger and/or older ages making cumulative CAA less than 2% of the total CAA are rough criteria.

2.6 Projections File (projection.inp)

Line	Entry
1-3	Comments
4	Number of years to project forward
5	Comments
6	Project with constant catch (=1) or constant F (=2)
7	Comments
8	Future catch by fleet if project with constant catch
9	Comments
10	Future F by fleet if project with constant F

Note

For each fleet, selectivity in the future is assumed to be the average of the last 5 years. In a maximum likelihood run, the projections are deterministic, i.e. the recruitment is exactly determined by the stock-recruitment curve. If MCMC are run however, variations around the stock-recruitment curves are generated for each year, i.e. stochastic projections.

3. A SINGLE ASPM RUN

To run a single ASPM run, type aspm (or ASPM) in the command DOS prompt where there are 6 inputs files and ASPM.exe file in the same folder (see below):

The major results will be sent to aspm.rep files (refer to Section 5.1).

Suggestions

- To run with starting values other than those in the *parameter guesses* file (aspm.pin), type otherInitial.par (for example) as below:

  aspm –ainp otherInitial.par

- Always try different starting guesses to see if the program converges on the same solution.

- If the model does not converge, users can try restarting it with the parameter that have just been estimated, to do this type:

  ASPM –ainp aspm.par

  i.e., it will use the values in aspm.par as initial guesses.

- Since the input and output file names are fixed, it's easier to keep each run in a separate folder.

4. MULTIPLE ASPM RUNS BY BATCH JOB (GRID SEARCH OPTION)

In the previous ASPM versions, users need to search optimum parameters by setting seeding guess values then users need to explore the best parameters by trials and errors. In such approach, users need to make hand-written memos (for example) for important parameters and goodness-of-fitness values such as R2 and total likelihood.

Important parameters affecting results (parameters) are *h (steepness)* in ASPM.inp file, *Sigma* values for the stock recruitment fluctuations in control.inp, *CV* values for CPUE in index.inp and *weighting* values for CAA. This pencil-and-paper approach is time consuming and laborious work, which furthermore often select apparent parameters at the local minima mistakenly as the most optimum values. Then biased results will be produced. To avoid such problems, the grid search (batch job) function is developed in this new Version 3 (2014).

4.1 Batch job (Grid search)

Before starting the batch job, users need to set up all 6 input files with some initial seeding values and users also need to have “BatchASPM.exe” in their ASPM folders. After setting up all, then double click this BatchASPM.exe file:

Then users will see the batch job menu (Fig. 1) and users need to set up ranges (minimum and maximum) and class intervals for *h (steepness), Sigma values for the SR relation,* common *CV* for (standardized) $CPUE_1$-$CPUE_n$ (max. n=3 fleets) and *weighting* values of CAA.

Although users set up initial seeding values for these 4 parameters, ASPM batch job will ignore them and make runs according to number of combinations among these 4 parameters

Please note that number of CPUE is corresponding to number of indices shown in Indiex.inp (maximum number=3 fleet). For example, if users have Japanese and Korean standardized CPUE, 2 CPUE entries will appear in the menu as shown in Fig. 2. Then users need to specify fleet ID such as JPN (Japan) and KOR (Korea) (for example). Fig. 2 shows an example of the batch job set up and Fig. 3 shows the process of the batch job.

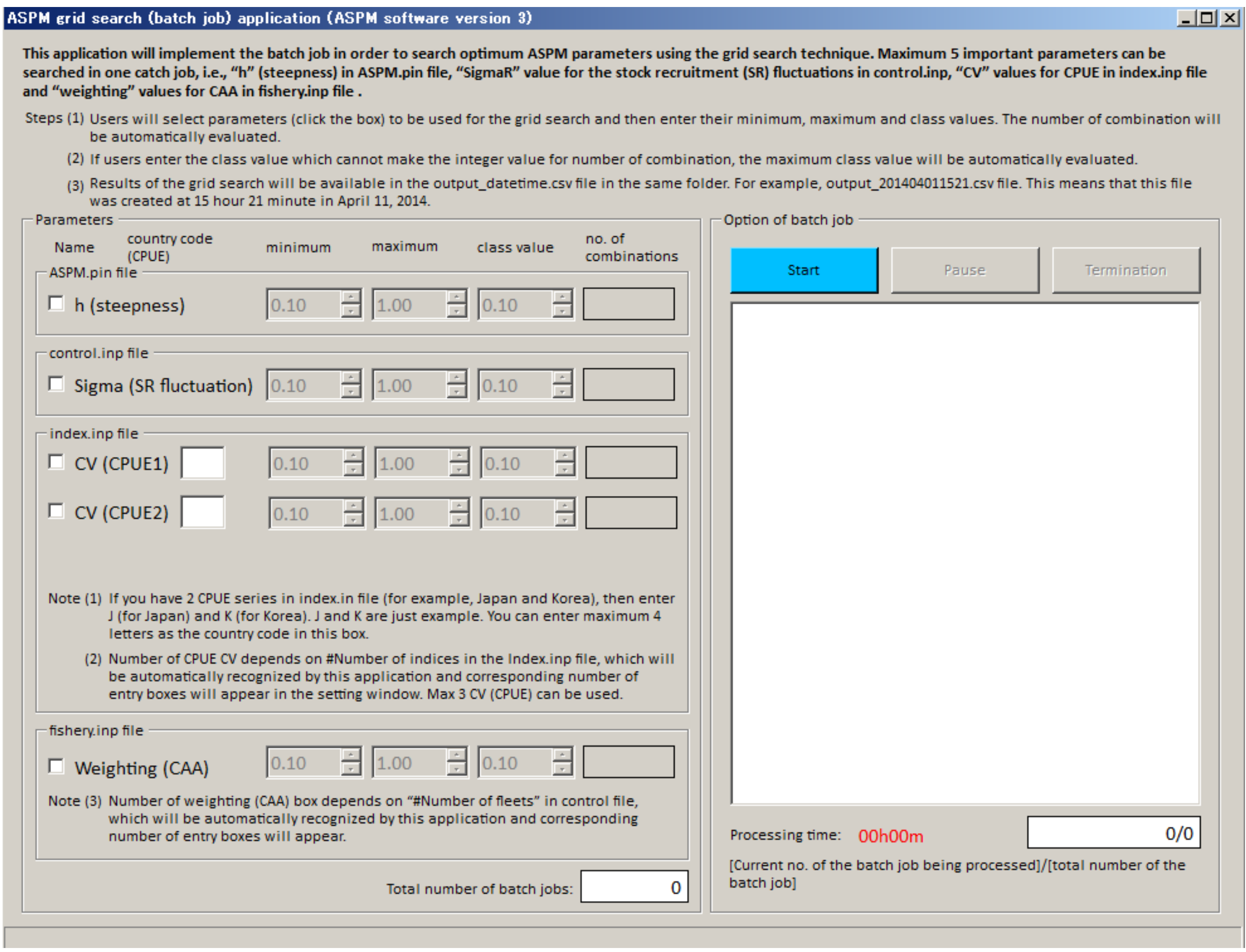


Fig. 1 Batch job menu window to enter ranges and grid intervals for *h (steepness), Sigma values for SR relation,* common *CV* for (standardized) $CPUE_1$-$CPUE_n$ and *weighting* values of CAA.

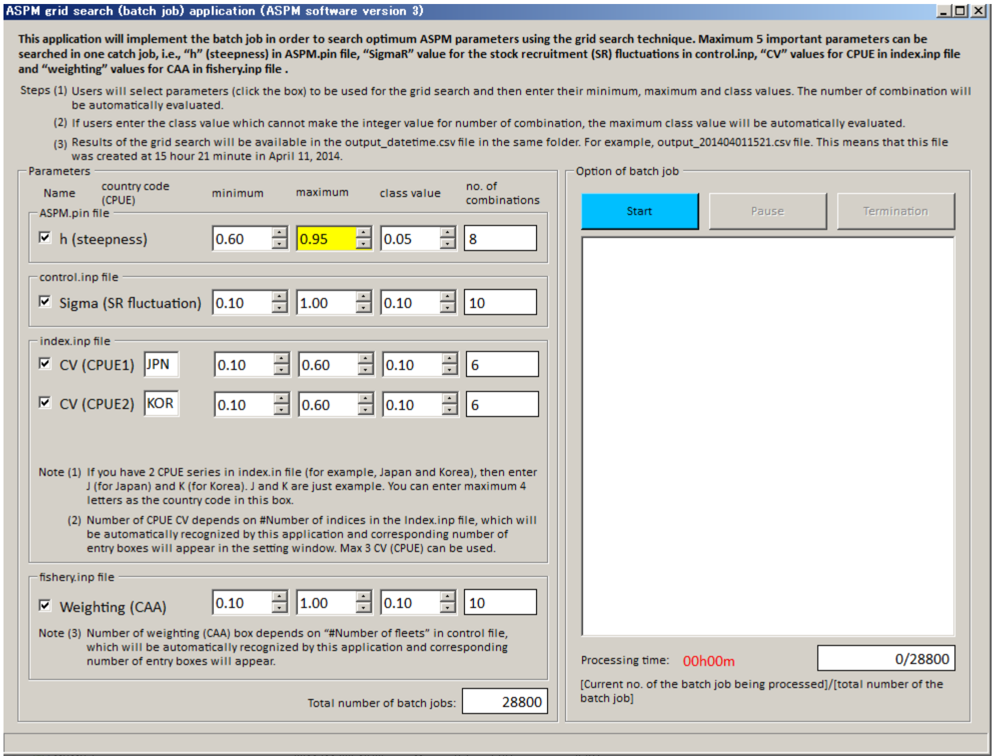


Fig.2 Example of set up in the batch job

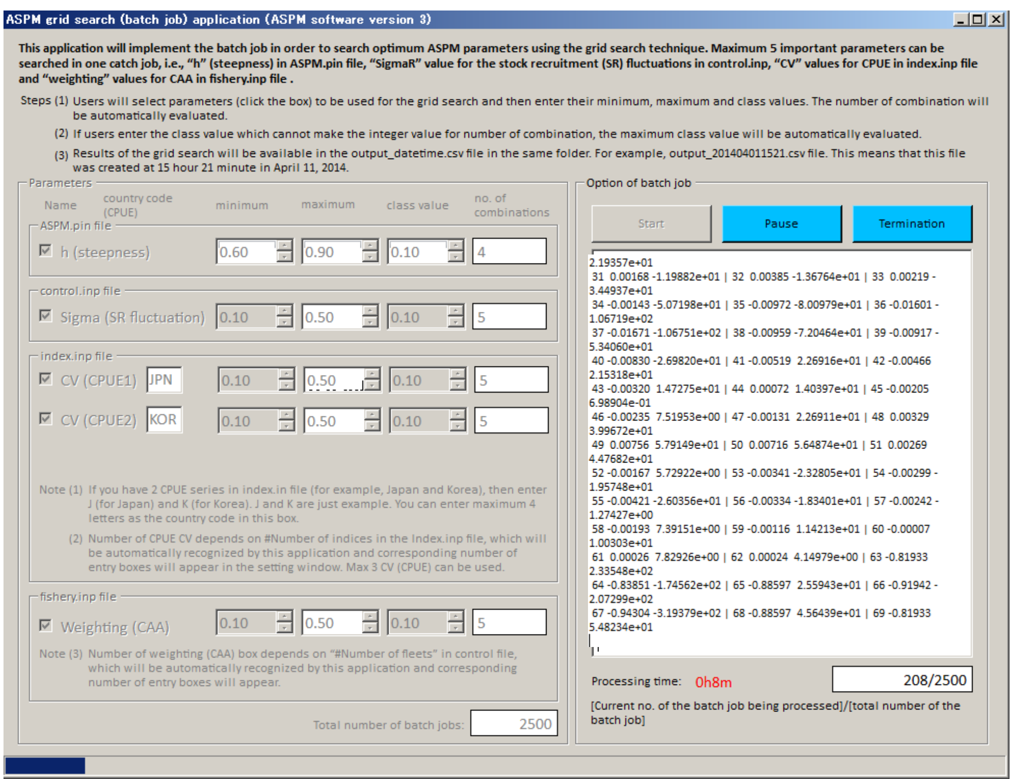


Fig. 3 Snapshot of the batch job during the process (at the 208th trial)
(different example from the one in Fig. 2)

4.2 Expected time (hours) to complete

Based on various tests, it was found that it will take 6 minutes to complete one job in average using the normal performance PC for the tests. But time might be shorter if higher-performance PC was used or vice versa.

Table 2 shows the expected time to complete ASPM batch job by number of runs using 6 minutes in average. To run the batch job effectively, it is suggested to conduct the plausible ranges with larger interval first, then narrow down ranges and intervals to find optimum parameters. In such way, optimum parameters can be found more efficiently in a shorter time.

Table 2 Expected time needed to conduct the batch job by number of ASPM runs
(6 minutes in average per one ASPM run is used)

Number of the batch job (ASPM runs)	100 times	200	500	1,000
Expected time to complete	10 hours	20 hours	2 days 2 hours	4 days 4 hours

4.3 Batch job output and selection of the optimum parameters

All the output will be save in the MS Excel .csv file automatically in the user's ASPM file folder. The file name of the CSV file will be as below (example):

Output_201411091411.csv - Microsoft Excel

This means that this ASPM batch job .csv file was created in 2014 (year) 11 (month) 09 (day) 1411(2PM 11 minutes in user's local time). Box 1 shows beginning and ending part of this file. From this output, users will select the most optimum result by sorting "total likelihood" (from lowest) and "R2" (from highest) values (Box 2). For this case users will select run numbers 20, 24, 28, 32 (same results). If users want to search finer scale optimum parameters values, users need to re-run ASPM batch job.

Box 1 Example of the ASPM batch job .csv output (256 times)

Beginning part

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Processing time:	4h36m											
2		0.6-0.9 by 0.1	0.1-0.4 by 0.1	J0.1-J0.4 by 0.1	0.1-0.4 by 0.1								
3													
4	No	h (steepness)	Sigma (SR)	CPUE	Weighting (CAA)	SSB0	Total likelihood	R2	SSB	MSY	SSB/SSBmsy	F/Fmsy	Error Message
5	1	0.6	0.1	J0.1	0.1	394	-14.481	0.498	135	30	1.07	1.4	
6	2	0.6	0.1	J0.1	0.2	400	2.901	0.484	141	30	1.11	1.33	
7	3	0.6	0.1	J0.1	0.3	413	20.075	0.463	156	31	2.14	0.54	
8	4	0.6	0.1	J0.1	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite
9	5	0.6	0.1	J0.2	0.1	394	-14.481	0.498	135	30	1.07	1.4	
10	6	0.6	0.1	J0.2	0.2	400	2.901	0.484	141	30	1.11	1.33	
11	7	0.6	0.1	J0.2	0.3	413	20.075	0.463	156	31	2.14	0.54	
12	8	0.6	0.1	J0.2	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite
13	9	0.6	0.1	J0.3	0.1	394	-14.481	0.498	135	30	1.07	1.4	
14	10	0.6	0.1	J0.3	0.2	400	2.901	0.484	141	30	1.11	1.33	

Ending part

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Processing time:	4h36m											
2		0.6-0.9 by 0.1	0.1-0.4 by 0.1	J0.1-J0.4 by 0.1	0.1-0.4 by 0.1								
3	No	h (steepness)	Sigma (SR)	CPUE	Weighting (CAA)	SSB0	Total likelihood	R2	SSB	MSY	SSB/SSBmsy	F/Fmsy	Error Message
246	243	0.9	0.4	J0.1	0.3	567	14.91	0.646	263	66	2.45	0.27	
247	244	0.9	0.4	J0.1	0.4	658	30.857	0.602	333	77	2.68	0.22	
248	245	0.9	0.4	J0.2	0.1	460	-21.802	0.907	189	55	1.77	0.4	
249	246	0.9	0.4	J0.2	0.2	484	-1.691	0.69	200	57	2.18	0.35	
250	247	0.9	0.4	J0.2	0.3	567	14.91	0.646	263	66	2.45	0.27	
251	248	0.9	0.4	J0.2	0.4	658	30.857	0.602	333	77	2.68	0.22	
252	249	0.9	0.4	J0.3	0.1	460	-21.802	0.907	189	55	1.77	0.4	
253	250	0.9	0.4	J0.3	0.2	484	-1.691	0.69	200	57	2.18	0.35	
254	251	0.9	0.4	J0.3	0.3	567	14.91	0.646	263	66	2.45	0.27	
255	252	0.9	0.4	J0.3	0.4	658	30.857	0.602	333	77	2.68	0.22	
256	253	0.9	0.4	J0.4	0.1	460	-21.802	0.907	189	55	1.77	0.4	
257	254	0.9	0.4	J0.4	0.2	484	-1.691	0.69	200	57	2.18	0.35	
258	255	0.9	0.4	J0.4	0.3	567	14.91	0.646	263	66	2.45	0.27	
259	256	0.9	0.4	J0.4	0.4	658	30.857	0.602	333	77	2.68	0.22	

Box 2 Selection of the most optimum parameters by sorting Total likelihood and R2 values.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	Run No	h (steepness)	Sigma (SR)	CPUE	Weighting (CAA)	SSB0	Total likelihood	R2	SSBmsy	MSY (1000 tons)	SSB/SSB msy	F/Fmsy	Error Message					
2	162	0.8	0.3	J0.1	0.2	513	74.449	0.658	232	42	1.87	0.71	Warning -- Hessian does not appear to be positive definite					
3	166	0.8	0.3	J0.2	0.2	513	74.449	0.658	232	42	1.87	0.71	Warning -- Hessian does not appear to be positive definite					
4	170	0.8	0.3	J0.3	0.2	513	74.449	0.658	232	42	1.87	0.71	Warning -- Hessian does not appear to be positive definite					
5	174	0.8	0.3	J0.4	0.2	513	74.449	0.658	232	42	1.87	0.71	Warning -- Hessian does not appear to be positive definite					
6	98	0.7	0.3	J0.1	0.2	558	74.357	0.642	260	41	3.54	0	Warning -- Hessian does not appear to be positive definite					
7	102	0.7	0.3	J0.2	0.2	558	74.357	0.642	260	41	3.54	0	Warning -- Hessian does not appear to be positive definite					
8	106	0.7	0.3	J0.3	0.2	558	74.357	0.642	260	41	3.54	0	Warning -- Hessian does not appear to be positive definite					
9	110	0.7	0.3	J0.4	0.2	558	74.357	0.642	260	41	3.54	0	Warning -- Hessian does not appear to be positive definite					
10	226	0.9	0.3	J0.1	0.2	477	74.222	0.681	207	44	2.27	0.63	Warning -- Hessian does not appear to be positive definite					
11	230	0.9	0.3	J0.2	0.2	477	74.222	0.681	207	44	2.27	0.63	Warning -- Hessian does not appear to be positive definite					
12	234	0.9	0.3	J0.3	0.2	477	74.222	0.681	207	44	2.27	0.63	Warning -- Hessian does not appear to be positive definite					
13	238	0.9	0.3	J0.4	0.2	477	74.222	0.681	207	44	2.27	0.63	Warning -- Hessian does not appear to be positive definite					
14	114	0.7	0.4	J0.1	0.2	605	68.496	0.705	269	43	1.58	0.81	Warning -- Hessian does not appear to be positive definite					
15	118	0.7	0.4	J0.2	0.2	605	68.496	0.705	269	43	1.58	0.81	Warning -- Hessian does not appear to be positive definite					
16	122	0.7	0.4	J0.3	0.2	605	68.496	0.705	269	43	1.58	0.81	Warning -- Hessian does not appear to be positive definite					
17	126	0.7	0.4	J0.4	0.2	605	68.496	0.705	269	43	1.58	0.81	Warning -- Hessian does not appear to be positive definite					
18	4	0.6	0.1	J0.1	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite					
19	8	0.6	0.1	J0.2	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite					
20	12	0.6	0.1	J0.3	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite					
21	16	0.6	0.1	J0.4	0.4	785	63.918	0.233	539	61	2.11	0.33	Warning -- Hessian does not appear to be positive definite					
22	20	0.6	0.2	J0.1	0.4	564	59.368	0.446	279	42	1.58	0.71						
23	24	0.6	0.2	J0.2	0.4	564	59.368	0.446	279	42	1.58	0.71						
24	28	0.6	0.2	J0.3	0.4	564	59.368	0.446	279	42	1.58	0.71						
25	32	0.6	0.2	J0.4	0.4	564	59.368	0.446	279	42	1.58	0.71						
26	148	0.8	0.2	J0.1	0.4	535	59.152	0.549	268	56	2.13	0.36	Warning -- Hessian does not appear to be positive definite					
27	152	0.8	0.2	J0.2	0.4	535	59.152	0.549	268	56	2.13	0.36	Warning -- Hessian does not appear to be positive definite					
28	156	0.8	0.2	J0.3	0.4	535	59.152	0.549	268	56	2.13	0.36	Warning -- Hessian does not appear to be positive definite					
29	160	0.8	0.2	J0.4	0.4	535	59.152	0.549	268	56	2.13	0.36	Warning -- Hessian does not appear to be positive definite					
30	132	0.8	0.1	J0.1	0.4	439	52.453	0.427	218	45	2	0.47						
31	136	0.8	0.1	J0.2	0.4	439	52.453	0.427	218	45	2	0.47						
32	140	0.8	0.1	J0.3	0.4	439	52.453	0.427	218	45	2	0.47						
33	144	0.8	0.1	J0.4	0.4	439	52.453	0.427	218	45	2	0.47						
34	18	0.6	0.2	J0.1	0.2	641	51.814	0.441	366	50	1.73	0.46	Warning -- Hessian does not appear to be positive definite					
35	22	0.6	0.2	J0.2	0.2	641	51.814	0.441	366	50	1.73	0.46	Warning -- Hessian does not appear to be positive definite					
36	26	0.6	0.2	J0.3	0.2	641	51.814	0.441	366	50	1.73	0.46	Warning -- Hessian does not appear to be positive definite					
37	30	0.6	0.2	J0.4	0.2	641	51.814	0.441	366	50	1.73	0.46	Warning -- Hessian does not appear to be positive definite					
38	196	0.9	0.1	J0.1	0.4	380	38.368	0.406	170	45	2.32	0.4						

After users decide the most optimum ASPM run number from the batch job, then users need to make its final single run, in order to obtain the results in aspm.rep file.

5. PRESENTING A SINGLE ASPM RESULT BY GRAPHIC OPTION

5.1 Output files and preparing the plots

The output of a single ASPM run is available in aspm.rep file which includes annual spawning biomass, population size (in numbers and weight) by age, spawner-recruitment relation, fishing mortality, MSY, Fmsy, SSBmsy, goodness-of-fitness and many others. Users can visualize important results with the graphic option by following steps described as below (refer to Figs. 4-6):

- Prepare ASPM.xlsm (excel macro) file to implement the graphic function in the user's ASPM folder. This file is available in the ASPM software package.
- Open this file to see the opening window (menu) (Fig. 4).
- To activate (make the macro program gets started), click the "option" button (Fig. xx)
- Click the ASPM.rep button (Fig. 5).
- Select aspm.rep (ASPM output) file in the user's ASPM folder, which includes 7 different sheets (Fig. 6)

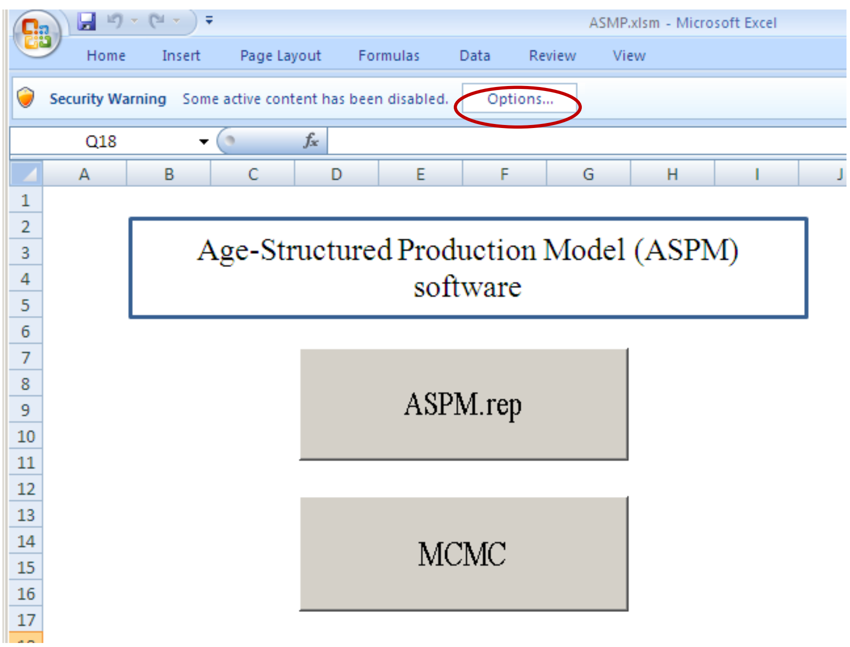


Fig. 4 ASPM.xlsm (excel macro) file to conduct the graphic function which is available in the ASPM software package.

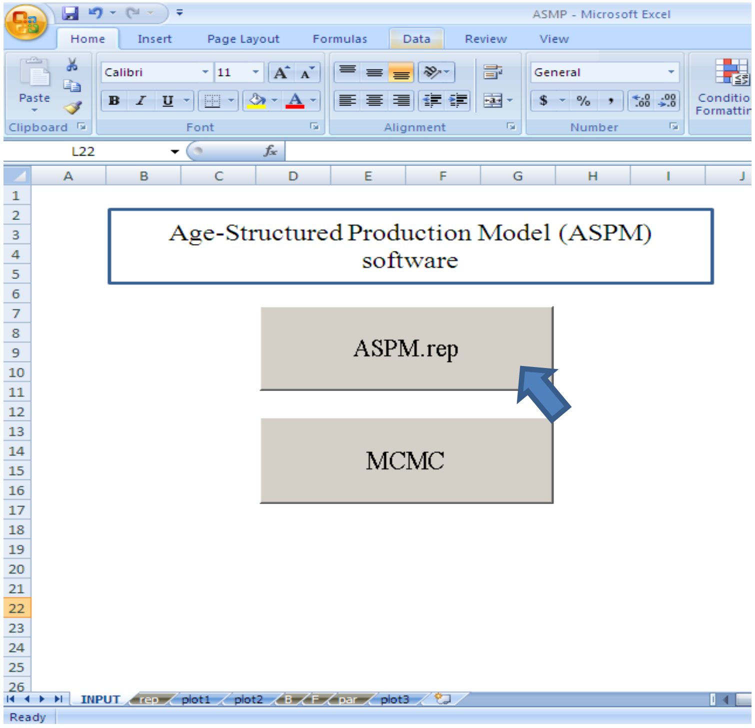
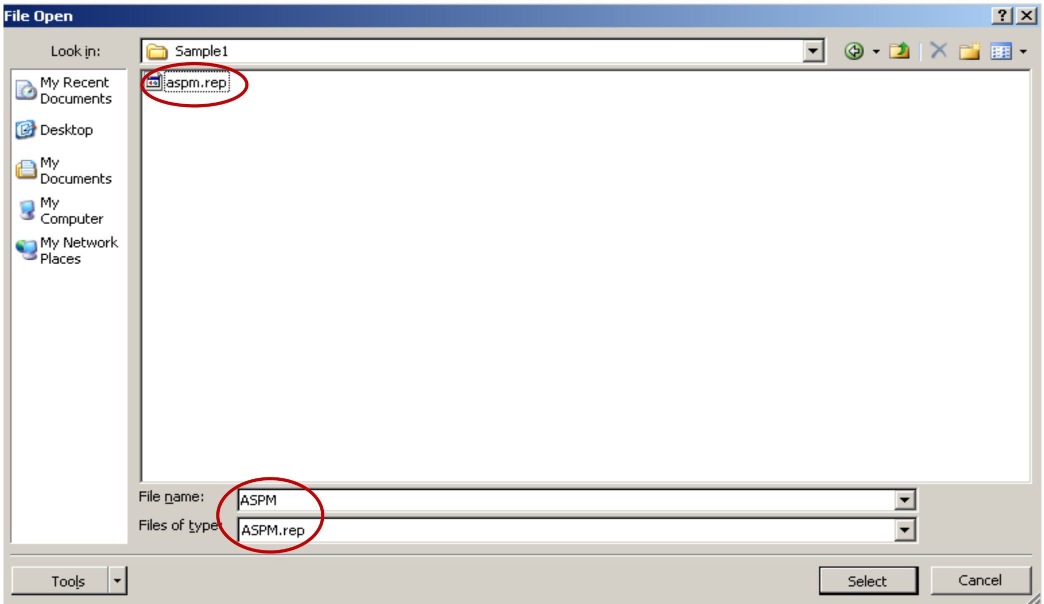


Fig. 5 Select ASPM.rep menu to get stared the ASPM graphic option



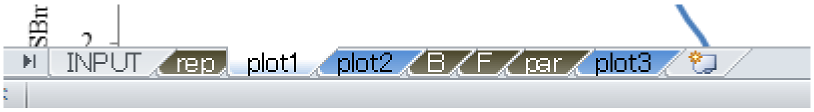


Fig 6 Select aspm.rep (excel file) (above) including 9 sheets

containing 3 plots and other 6 output sheets (below)

5.2 Plot 1: basic results (Fig. 7)

Plot 1 includes 7 graphs (Fig. 7), i.e., (1) estimated annual SSB, (2) catch vs. MSY, (3) annual trend of B ratio (SSB/SSBmsy), (4) annual trend of F ratio (F/Fmsy), (5) estimated SR relation vs. observed SR plot, (6) residuals of SR relations, (7) annual predicted vs. observed STD CPUE, (8) estimated selectivity-at-age and (9) simple Kobe plot 1 (stock trajectory).

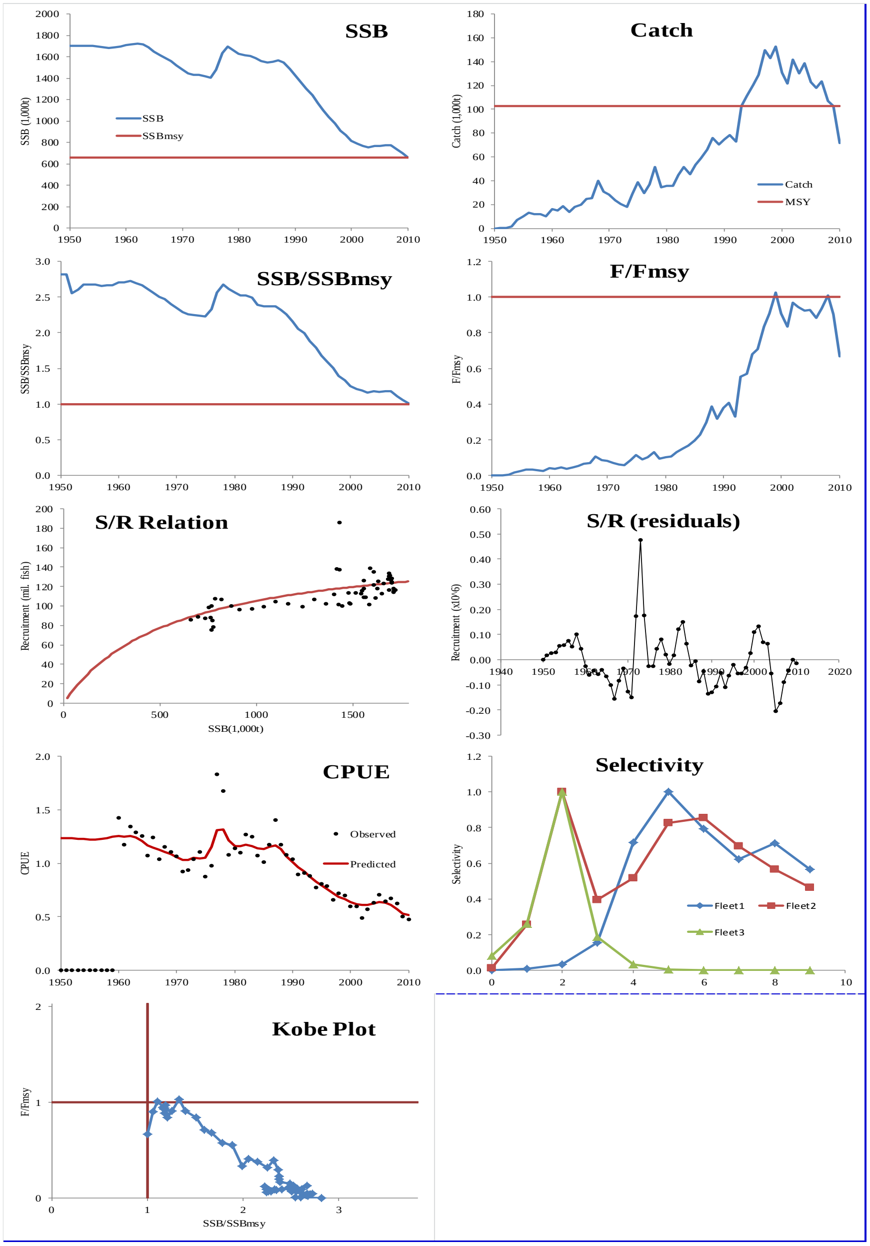


Fig. 7 Plot 1 to present the basic result of one ASPM run (sample)

5.3 Plot 2: Selectivity by fleet (Figs. 8-9)

Plot 2 (Fig. 8) depicts estimated selectivities and their residuals by fleet. Number of fleets can be displayed up to 9 automatically. If users have 10 or more fleets, users can present all using the combo box (indicated by the arrow below).

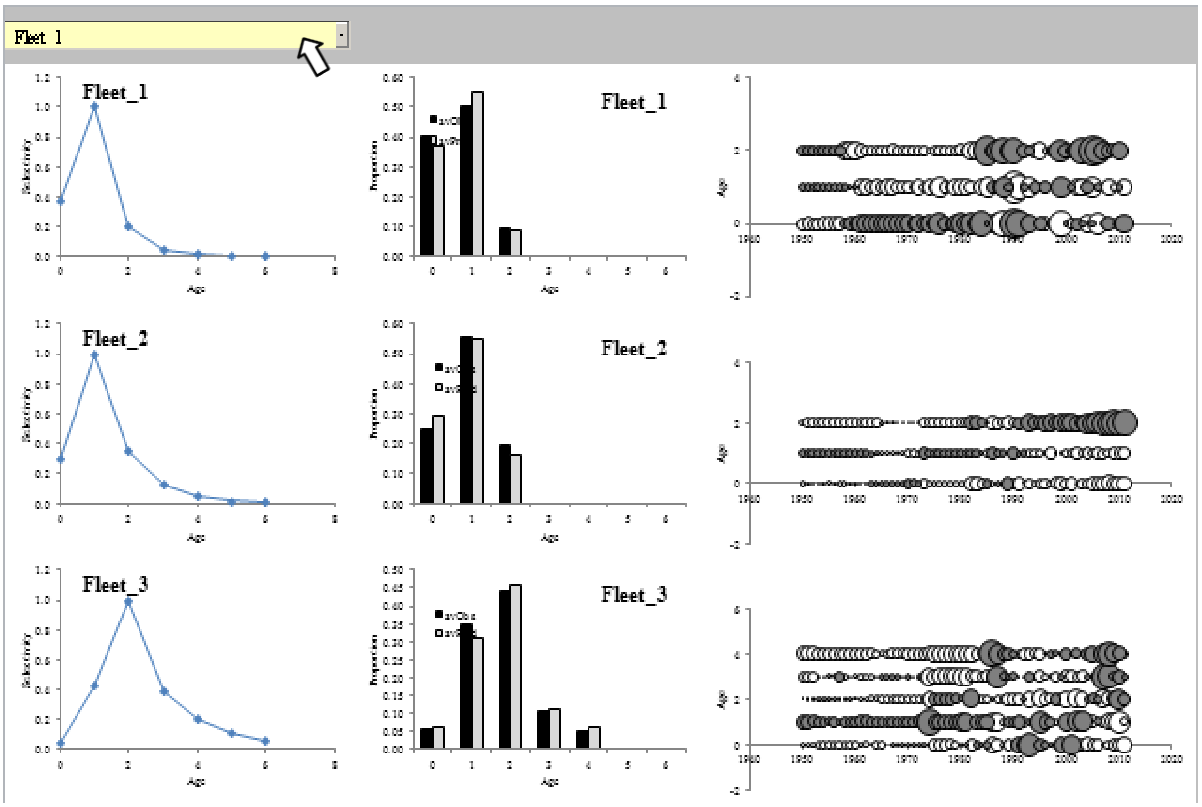


Fig. 8 Plot 2 (selectivity by fleet)

Users can change the fleet name (note: the default name is like “Fleet_1”, “Fleet_2” etc.) to the real names (such as “gillnet”, “longline” etc.) using the small sheet available in the bottom of Plot 2 (Fig. 9). After change, users should push the "Update of Graph Titles" button (indicated by arrow below).

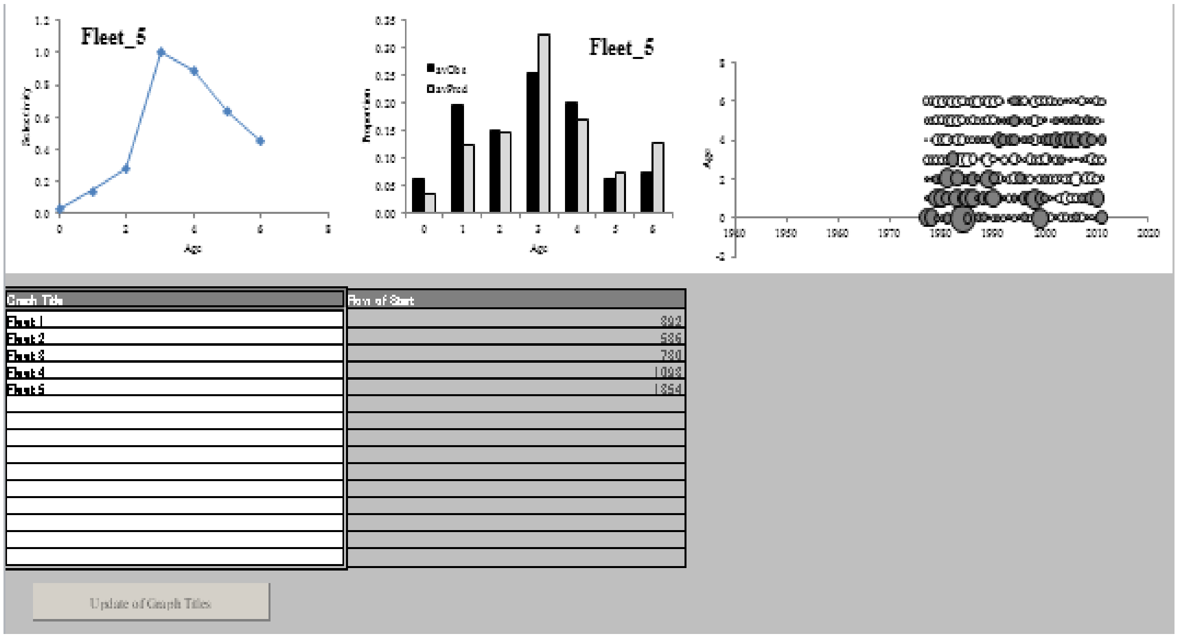


Fig. 9 changing the fleet name

6. PRESENTING UNCERTAINTIES

6.1 MCMC to present uncertainties within a single ASPM run

(1) Running MCMC

ADMB includes a Markov Chain Monte Carlo (MCMC) routine for Bayesian analysis. The objective is to represent the posterior distributions by means of a (large) number of vectors of parameters. The basic idea is to set up a (long) "chain" which starts at a pre-specified parameter vector and that then traverses the posterior distribution. The contribution from *Equation 21 (p.38)* correspond to a prior on the distribution of the recruitment residuals, while priors on the other estimable parameters (SSB_0 , θ, ϕ and the selectivity parameters) are taken to be uniform over wide and/or feasible ranges with the intent that they be uninformative.

The initial parameter vector used to start the MCMC computational process is the mode of the posterior. A chain of N iterations is run and the chain is "thinned" by taking every mth value in the chain. The results of the first iterations (5-50% of the total chain length) should be discarded to allow for a "burn-in" period, i.e. reduce the impact of the initial parameter vector.

To run MCMCs, type

aspm –mcmc N –mcsave m

,where N is the number of simulations performed and every m'th simulations are saved.

To get the desired output, type

aspm –mceval

See the ADMB manual for further MCMC options.

The output file **ASPM.hst** contains the means, standard deviations and observed distributions for all parameters included in the aspm.std file (after the estimable parameters, i.e. starting from K downwards). Once MCMC for a particular model has been run, stochastic projections can be run for different future catches (or F) without rerunning the MCMC, just changing the future catches and rerun **‘aspm –mceval’.**

① **proj.out**: Projected spawning biomass and projected SSB_{msy}.

② **ASPM.par:** a standard ADMB output file, giving the objective function value, its gradient (this should be very small if the model has converged) and the parameters estimated/fixed for that run.

③ **ASPM.std** (Table 3): a standard ADMB output file, with the parameters estimated for that run and their estimated Hessian-based standard deviation (SD) included those for the projected years. Annual SSB, Btot, SSB/SSBmsy, F, F/Fmsy and MSY their estimated standard deviations are also included. Table 3 (sample) shows the list of output parameters in the case of fixed steepness. Parameters with (*) will provide annual figures. If users have 50 years data and 10 years projected years, users will get 60 data sets for the parameters with (*). Table 3 shows values and std dev (just examples). With this information users can compute the Confidence Intervals (CI), e.g. **95% CI** by 1.96± SD. Please note that lnK and K (carrying capacity) will produce just one figure each for value and std dev.

Table 3 Output of ASPM.std

	name	value	std dev
	lnK	1.42E+01	9.79E-02
*	Selpar	8.70E-04	1.01E-03
	K	1.47E+06	1.44E+05
*	Bsp	1.47E+06	1.44E+05
*	Btot	1.74E+06	1.71E+05
*	Fmort_overall	1.65E-04	1.98E-05
*	MSY	1.27E+05	1.16E+04
*	FoverFmsy	2.27E-04	2.73E-05
*	BoverBmsy	3.64E+00	1.70E-01

④ Another useful ADMB standard output files is **ASPM.cor** for the correlations of the parameter estimates.

⑤ **ASPM.hst:** a standard ADMB output file when MCMCs are run.

⑥ **MCMC_B.csv:** SSB, Btot and SSB/SSBmsy for each year. If MCMC has been run, one vector for each iteration. Probability intervals for these parameters can then be computed, taken the burn-in period into account.

⑦ **MCMC_F.csv**: F, F/Fmsy and MSY for each year. If MCMC has been run, one vector for each iteration. Probability intervals for these parameters can then be computed, taken the burn-in period into account.

(2) Plotting MCMC results (Figs. 10-13)

- Get the first window of the ASPM excel macro file and click MCMC button.

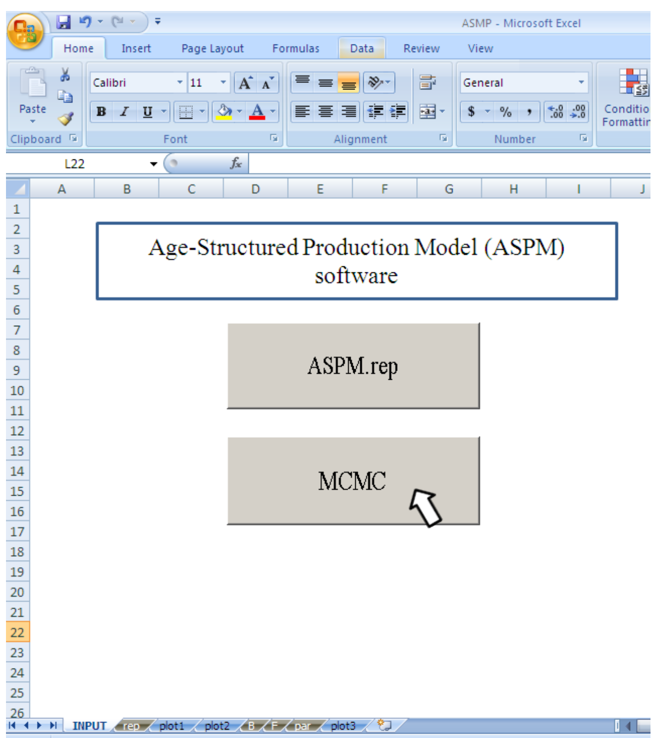


Fig. 10 Selecting MCMC option in the ASPM software

- Select one of "MCMC_B.csv", "MCMC_F.csv" and "MCMC_par.csv" files available in user's ASPM folder. Then ASPM excel file will read relevant data in these 3 files. Wait until users see the graphs appear. It will take some time depending of numbers of user's MCMC trials.

Fig. 11 shows 5 types of graphs in Plot 3 excel sheet, i.e., "estimated and future annual trends of SSB", "SSB/SSBmsy", "F" and "F/Fmsy" including medians by solid lines and 90 percentile intervals (PI) by broken lines, in addition to "K" generated by MCMC. To indicate the starting year of the future projections, enter the year then click the apply button so that the vertical red lines (except for K) will be inserted as the starting year (see below).

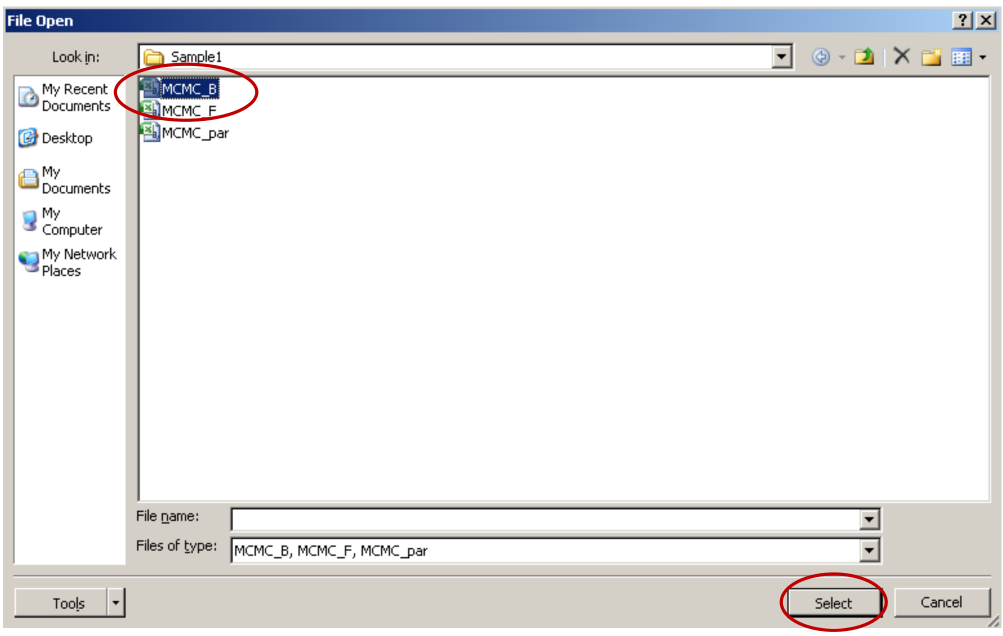


Fig. 11 Select one of three MCMC output files (above) then MCMC results will be depicted in Plot 3.

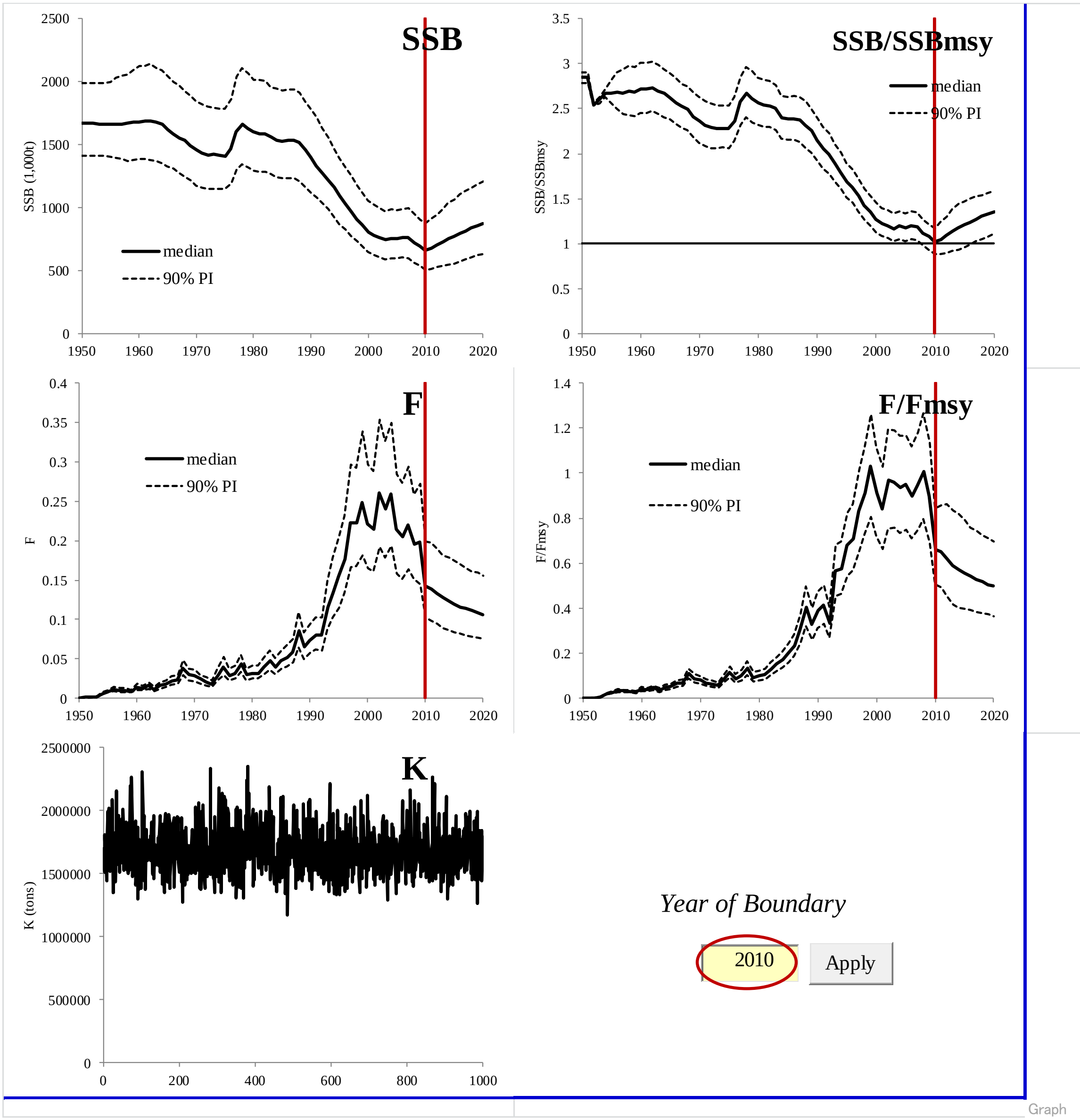


Fig. 12 Plots of MCMC results created by the ASPM graphic option

6.2 Kobe plots to present uncertainties among parameters

Users can create Kobe Plot showing uncertainties among different parameters, for example, different values (parameters) of h (steepness), M, growth equations etc. These can be plotted directory to Kobe Plot or weighed averaged can be plotted.

7. ASPM WITH SIZE DATA OPTION (FUTURE RELEASE)

ASPM with size data option will be developed and added by 2017 by the following reasons: CAA has uncertainty when size data are converted to age and such uncertainty are much higher especially in case size data are very limited. To overcome these problems, ASPM with size data option will be developed within the current ADMB_ASPM framework. In this way, ASPM runs based on 2 options (CAA vs. size based) can be compared

Such option will become similar to the integrated models such as SS3, Multifan-CL etc. However, one different point is the simplicity, i.e., ASPM has much less parameters (20-40), while the integrated models, hundreds of parameters. The critical point to develop this option is for anyone to be able to conduct ASPM with size data (quasi SS3) in much simpler way than the integrated ones.

ACKNOWLEDGEMENTS

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APPENDIX A: BACKGROUNDS OF THE ASPM SOFTWARE DEVELOPMENT PROJECT

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 has been applied for bigeye tuna (*Thunnus obesus*), yellowfin tuna (*Thunnus albacares*), albacore (*Thunnus alalunga*) and swordfish (*Xiphias gladius*) (IOTC, 2002-2014).

The above mentioned ASPM software was first coded in FORTRAN by Restrepo (ICCAT, 1997). However, this FORTRAN implemented ASPM have 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.

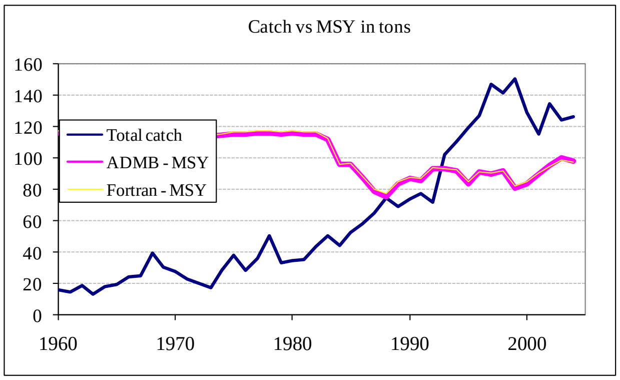
To improve these problems, we started to re-code the "FORTRAN based ASPM" to "AD Model Builder implemented ASPM" in 2008 and completed the 1st version in 2011. It took 4 years as we temporarily stopped development and testing works for 2 years. This software development has been funded by the Fisheries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

Table 4 Comparison between the FORTRAN and AD Model Builder ASPM implementations

	FORTRAN ASPM	**AD Model Builder ASPM** *(refer to Appendix B: Formation)*
Fleets	4	No limits
steepness	Estimated	Estimated or Fixed between 0.2 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
Others		Negative log likelihood is computed without the constants.

Performance tests

Runs with the FORTRAN and ADMB implementations for bigeye tuna in the IOTC were compared in WPTT08 in 2006. The three figures below show the results of the performance tests. The negligible discrepancies were caused by the different type of optimization methods used between two implementations. In addition CSIRO scientists in Australia evaluated the FORTAN ASPM and it was concluded that results by the FORTAN ASPM were robust (2004). This implies that ADMB ASPM is also robust as both are almost identical (Fig. 13).



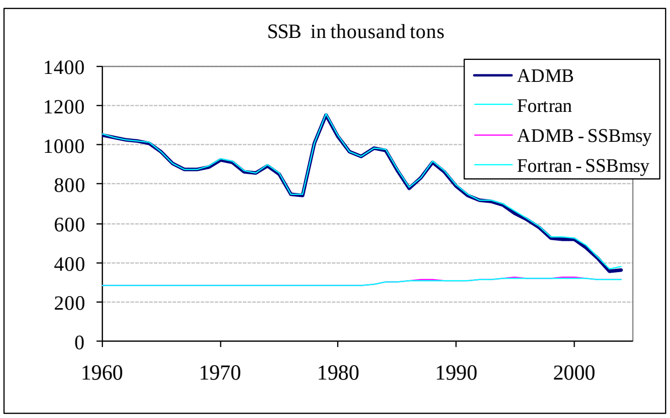


Fig. 13 Results of the performance tests

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,

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

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

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

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:

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

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

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

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

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,

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

where ί 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 $\sigma_{i,t}^2$ 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, $\sigma^2_{i,t}$. If all the values for all indices are given equal weight, they can be set to

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

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:

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

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 $\sigma^2_{i,t}$ 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 inequilibrium 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

$$N_{1,t} = R_0 e^{\nu} \tag{14}$$

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 $\nu_{t.}$. 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

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

with $\varepsilon_{t+1} = \rho \varepsilon_t + \eta_{t+1}, \quad |\rho| < 1,$ 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):

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

where the residuals would be computed as

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

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

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

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

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

$$\sum_{t=2}^{n_t-1}\left[\ln(N_{1,t+1}) - \ln\left(\frac{4R_0 S_t \tau}{\tau(5S_t - \gamma) - S_t + \gamma}\right) - \rho\ln(N_{1,t}) + \rho\ln\left(\frac{4R_0 S_{t-1}\tau}{\tau(5S_{t-1} - \gamma) - S_{t-1} + \gamma}\right)\right]^2 \tag{20}$$

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

$$N_{2,1} = R_0 e^{v_0} e^{-M_1} \quad (21a)$$

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

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:

$$-\ln(L_T) = -\ln(L_1) - \lambda_2 \ln(L_2) - \lambda_3 \ln(L_3) \quad (23)$$