

User Manual Stock Synthesis

Version 3.30 beta

August 15, 2015

Richard D. Methot Jr.
NOAA Fisheries
Seattle, WA USA

Contents

List of Figures	i
1 Introduction	1
2 New Features 3.30	1
3 File Organization	1
3.1 Input Files	1
3.2 Output Files	2
3.3 Auxiliary Files	3
4 Starting SS	4
5 Computer Requirements and Recommendations	4
6 Starter	4
6.1 Jitter	12
7 Forecast	12
8 Optional Inputs	18
8.1 Empirical Weight-at-Age (wtatage.ss)	18
8.2 runnumbers.ss	19
8.3 profilevalues.ss	20
9 Data File	20
9.1 Overview of Data File	20
9.2 Units of Measure	21
9.3 Time Units	21
9.4 Data File Syntax	22
9.4.1 Model Dimensions	22
9.4.2 Fleet Definitions	22
9.4.3 Catch	24
9.4.4 Abundance Indices	25
9.4.5 Discard	27
9.4.6 Mean Body Weight	28
9.4.7 Population Length Bins	29
9.4.8 Length Composition Data	32
9.4.9 Age Composition Bin Setup	33
9.4.10 Ageing Error	34
9.4.11 Conditional Age'-at-Length	36
9.4.12 Sex Ratio-at-Length	36

9.4.13	Mean Length or Body Weight-at-Age	37
9.4.14	Environmental Data	38
9.4.15	Generalized Size Composition Data	38
9.4.16	Tag-Recapture Data	40
9.4.17	Stock Composition Data	41
9.4.18	Excluding Data	42
9.4.19	Data Super Periods	43
10	Control File	44
10.1	Overview of Control File	44
10.2	Parameter Line Elements	46
10.3	Control File Syntax	47
10.3.1	Biology	48
10.3.2	Read Mortality-Growth Parameters	52
10.3.3	Natural Mortality Notes	56
10.3.4	Growth Notes	56
10.3.5	Growth Patterns (morphs) and Sub-Morphs	57
10.3.6	Recruitment, Age, and Growth	57
10.3.7	Cohort Growth Deviation	58
10.3.8	Movement Parameters	58
10.3.9	Recruitment Allocation and Movement Parameters	59
10.3.10	Catch Multiplier	61
10.3.11	Ageing Error Parameters	61
10.3.12	Time-Varying Biology Parameters	62
10.3.13	Notes on Seasonal Biology Parameters	64
10.3.14	Empirical Weight-at-Age (wtatage.ss)	64
10.3.15	Spawner-Recruitment	64
10.3.16	Spawner-Recruitment Function	69

List of Figures

1 Introduction

This manual provides a guide for using the stock assessment program, Stock Synthesis (SS). The guide contains a description of the input and output files and usage instructions. A technical description of the model itself is in Methot and Wetzel (2013). SS is programmed using Auto Differentiation Model Builder (ADMB; Fournier 2001. ADMB is now available at admb-project.org). SS currently is compiled using ADMB version 11.1 using the Microsoft C++ Optimizing Compiler Version 16.0. The model and a graphical user interface are available from the NOAA Fisheries Stock Assessment Toolbox website: <http://nft.nfsc.noaa.gov/>. An output processor package, r4ss, in R is available for download from CRAN or GitHub. Additional information about the package can be located at <https://github.com/r4ss/r4ss>.

2 New Features 3.30

Stock Synthesis version 3.30 has a number of new features:

1. Version conditional read
2. Forecast allocation group by year
3. Subseasons
4. Fleets - flexible ordering
5. Catch - revised input format
6. Catch multiplier
7. Catch - bycatch fleets

3 File Organization

3.1 Input Files

1. starter.ss: required file containing filenames of the data file and the control file plus other run controls (required).
2. datafile: file containing model dimensions and the data with file extension .dat (required)
3. control file: file containing set-up for the parameters with file extension .ctl (required)
4. forecast.ss: file containing specifications for forecasts (required)
5. ss3.par: previously created parameter file that can be read to overwrite the initial parameter values in the control file (optional)

6. runnumber.ss: file containing a single number used as runnumber in output to CumReport.sso and in the processing of profilevalues.ss (optional)
7. profilevalues.ss: file contain special conditions for batch file processing (optional)

3.2 Output Files

1. ss3.par, ss3.std, ss33.rep, ss3.cor etc. standard ADMB output files
2. echoinput.sso: This file is produced while reading the input files and includes an annotated echo of the input. The sole purpose of this output file is debugging input errors.
3. warning.sso: This file contains a list of warnings generated during program execution.
4. checkup.sso: Contains details of selectivity parameters and resulting vectors. This is written during the first call of the objective function.
5. Report.sso: This file is the primary report file.
6. CompReport.sso: Beginning with version 3.03, the composition data has been separated into a dedicated report
7. Forecast-report.sso: Output of management quantities and for forecasts
8. CumReport.sso: This file contains a brief version of the run output, output is appended to current content of file so results of several runs can be collected together. This is useful when a batch of runs is being processed.
9. Covar.sso: This file replaces the standard ADMB ss3.cor with an output of the parameter and derived quantity correlations in database format
10. data.ss_new: contains a user-specified number of datafiles, generated through a parametric bootstrap procedure, and written sequentially to this file
11. control.ss_new: Updated version of the control file with final parameter values replacing the Init parameter values.
12. starter.ss_new: New version of the starter file with annotations
13. Forecast.ss_new: New version of the forecast file with annotations.
14. rebuild.dat: Output formatted for direct input to Andre Punt's rebuilding analysis package. Cumulative output is output to REBUILD.SS (useful when doing MCMC or profiles).

3.3 Auxiliary Files

1. SS3-OUTPUT.XLS: Excel file with macros to read report.sso and display results
2. SELEX24_dbl_normal.XLS:
 - (a) This excel file is used to show the shape of a double normal selectivity (option number 20 for age-based and 24 for length-based selectivity) given user-selected parameter values.
 - (b) Instructions are noted in the XLS file but, to summarize
 - i. Users should only change entries in a yellow box.
 - ii. Parameter values are changed manually or using sliders, depending on the value of cell I5.
 - (c) It is recommend that users select plausible starting values for double-normal selectivity options, especially when estimating all 6 parameters
 - (d) Please note that the XLS does NOT show the impact of setting parameters 5 or 6 to "-999". In SS3, this allows the the value of selectivity at the initial and final age or length to be determined by the shape of the double-normal arising from parameters 1-4, rather than forcing the selectivity at the intial and final age or length to be estimated separately using the value of parameters 5 and 6.
3. SELEX17_age_randwalk.XLS:
 - (a) This excel file is used to show the shape of age-based selectivity arising from option 17 given user-selected parameter values
 - (b) Users should only change entries in the yellow box.
 - (c) The red box is the maximum cumulative value, which is subtracted from all cumulative values. This is then exponentiated to yield the estimated selectivity curve. Positive values yield increasing selectivity and negative values yield decreasing selectivity.
4. PRIOR-TESTER.XLS:
 - (a) The 'compare' tab of this spreadsheet shows how the various options for defining parameter priors work
5. SS-Control_Setup.XLS:
 - (a) Shows how to setup an example control file for SS
6. SS-Data_Input.XLS:
 - (a) Shows how to setup an example data input for SS
7. Growth.XLS:

- (a) Excel file to test parameterization between the growth curve options within SS.
 - (b) Instructions are noted in the XLS file but, to summarize
 - i. Users should only change entries in a yellow box.
 - ii. Entries in a red box are used internally, and can be compared with other parameterizations, but should not be changed.
 - (c) The SS-VB is identical to the standard VB, but uses a parameterization where length is estimated at pre-defined ages, rather than $A=0$ and $A=Inf$. The Schnute-Richards is identical to the Richards-Maunder, but similarly uses the parameterization with length at pre-defined ages. The Richards coefficient controls curvature, and if the curvature coefficient = 1, it reverts to the standard VB curve.
8. Movement.XLS:
- (a) Excel file to explore SS movement parameterization

4 Starting SS

SS runs as a DOS program with text-based input. The executable is named ss3.exe. It can be run at the command prompt in a DOS window, or called from another program, such as R or the SS-GUI or a DOS batch file. See the section in this manual on use of batch file which can allow ss3.exe to reside in a separate directory. Sometimes you may receive a version of SS with array checking turned on (SS-safe.exe) or without array checking SS_opt.exe. In this case, it is recommended to rename the one you are planning to use to SS3.exe before running it. Communication with the program is through text files. When the program first starts, it reads the file STARTER.SS, which must be located in the same directory from which SS is being run. The file STARTER.SS contains required input information plus references to other required input files, as described in the File Organization section. Output from SS is as text files containing specific keywords. Output processing programs, such as the SS GUI, Excel, or R can search for these keywords and parse the specific information located below that keyword in the text file.

5 Computer Requirements and Recommendations

SS is compiled to run under DOS with a 32-bit or 64-bit Windows operating system. It is recommended that the computer have at least a 2.0 Ghz processor and 2 GB of RAM. In addition SS has now been successfully compiled in Linux.

6 Starter

SS begins by reading the file starter.ss. Its format and content is as follows. Note that the term COND in the Typical Value column means that the existence of input shown there is

conditional on a value specified earlier in the file. Omit or comment out these entries if the appropriate condition has not been selected.

STARTER.SS

Typical Value	Options	Description
#C this is a starter comment	Must begin with #C then rest of the line is free form	All lines in this file beginning with #C will be retained and written to the top of several output files
data_file.dat	data_file.dat	File name of the data file
control_file.ctl	control_file.ctl	File name of the control file
0	Initial Parameter Values: 0=use values in control file; 1=use ss3.par after reading setup in the control file	Don't use this if there have been any changes to the control file that would alter the number or order of parameters stored in the SS3.par file. Values in SS3.par can be edited, carefully.
1	Run display detail: 0=none other than ADMB outputs; 1=one brief line of display for each iteration; 2=fuller display per iteration	With option 2, the display shows value of each logL component for each iteration and it displays where crash penalties are created
1	Detailed age-structure report 0 = omit catch-at-age for each fleet and cohort 1 = include all output	Detailed age-structured report in REPORT.SSO.
0	Check-up 0 = omit 1 = write detailed intermediate calculations to ECHOINPUT.SSO during first call	This output is largely unformatted and undocumented and is mostly used by the developer.

Typical Value	Options	Description
0	Parameter Trace 0 = omit 1 = write good iteration and active parms 2 = write good iterations and all parms 3 = write every iteration and all parms 4 = write every iteration and active parms	This controls the output to PARMTRACE.SSO. The contents of this output can be used to determine which values are changing when a model approaches a crash condition. It also can be used to investigate patterns of parameter changes as model convergence slowly moves along a ridge.
1	Cumulative Report 0 = omit 1 = brief 2 = full	Controls reporting to the file CUMREPORT.SSO. This cumulative report is most useful when accumulating summary information from likelihood profiles or when simply accumulating a record of all model runs within the current subdirectory
1	Full Priors 0 = only calculate priors for active parameters 1 = calculate priors for all parameters that have a defined prior	Turning on this option causes all prior values to be calculated. With this option off, the total logL, which includes the logL for priors, would change between model phases as more parameters became active.
1	Soft Bounds 0 = omit 1 = use	This option creates a weak symmetric beta penalty for the selectivity parameters. This becomes important when estimating selectivity functions in which the values of some parameters cause other parameters to have negligible gradients, or when bounds have been set too widely such that a parameter drifts into a region in which it has negligible gradient. The soft bound creates a weak penalty to move parameters away from the bounds.

Typical Value	Options	Description
1	Data File Output 0 = none 1 = output an annotated replicate of the input data file 2 = add a second data file containing the model's expected values with no added error 3+ = add N-2 parametric bootstrap data files	All output files are sequentially output to DATA.SS_new and will need to be parsed by the user into separate data files. The output of the input data file makes no changes, so retains the order of the original file. Output files 2-N contain only observations that have not been excluded through use of the negative year denotation, and the order of these output observations is as processed by the model. The N obs values are adjusted accordingly. At this time, the tag recapture data is not output to DATA.SS_new.
8	Turn off estimation -1 = exit after reading input files 0 = exit after one call to the calculation routines and production of SSO and SS_New files <positive value> = exit after completing this phase	The 0 option is useful for (1) quickly reading in a messy set of input files and producing the annotated CONTROL.SS_new and DATA.SS_new files, or (2) examining model output based solely on input parameter values. Similarly, the value option allows examination of model output after completing a specified phase. Also see usage note for restarting from a specified phase.
10	MCMC burn interval	Need to document this and set good default
2	MCMC thin interval	Need to document this and set good default
0.0	Jitter A positive value here will add a small random jitter to the initial parameter values	The jitter factor is multiplied by a random normal deviation $rdev = N(0,1)$ to a transformed parameter value based upon the predefined parameter bounds. <i>click here for more information</i>
-1	SD Report Start -1 = begin annual SD report in start year <year> = begin SD report this year	

Typical Value	Options	Description
-1	SD Report End -1 = end annual SD report in end year -2 = end annual SD report in last forecast year <value> = end SD report in this year	
2	Extra SD Report Years 0 = none <value> = number of years to read	In a long time series application, the model variance calculations will be smaller and faster if not all years are included in the SD reporting. For example, the annual SD reporting could start in 1960 and the extra option could select reporting in each decade before then.
COND: If Extra SD report years > 0		
1940 1950	Vector of years for additional SD reporting	
0.0001	Final convergence	This is a reasonable default value for the change in logL denoting convergence. For applications with much data and thus a large total logL value, a larger convergence criterion may still provide acceptable convergence
0	Retrospective year 0 = none -x = retrospective year relative to end year	Adjusts the model end year and disregards data after this year. May not handle time varying parameters completely.
0	Summary biomass min age	Minimum integer age for inclusion in the summary biomass used for reporting and for calculation of total exploitation rate
1	Depletion basis 0 = skip 1 = $X*B_0$ 2 = $X*B_{MSY}$ 3 = $X*B_{styr}$	Selects the basis for the denominator when calculating degree of depletion in SSB. The calculated values are reported to the SD report.
0.40	Fraction (X) for depletion denominator	So would calculate the ratio of $SSBy/(0.40*SSB_0)$

Typical Value	Options	Description
1	SPR report basis 0 = skip 1 = use $1 - \text{SPR}_{\text{TARGET}}$ 2 = use $1 - \text{SPR}$ at MSY 3 = use $1 - \text{SPR}$ at B_{TARGET} 4 = no denominator, so report actual $1 - \text{SPR}$ values	SPR is the equilibrium SSB per recruit that would result from the current year's pattern and intensity of F's. The SPR approach to measuring fishing intensity was implemented because the concept of a single annual F does not exist in SS. The quantities identified by 1, 2, and 3 here are all calculated in the benchmarks section. Then the one specified here is used as the selected denominator in a ratio with the annual value of $(1.0 - \text{SPR})$. This ratio (and its variance) is reported to the SD report output for the years selected above in the SD report year selection.
4	F std report value 0 = skip 1 = exploitation rate in biomass 2 = exploitation rate in numbers 3 = sum(full F's by fleet) 4 = population F for range of ages	In addition to SPR, an additional proxy for annual F can be specified here. As with SPR, the selected quantity will be calculated annually and in the benchmarks section. The ratio of the annual value to the selected (see F report basis below) benchmark value is reported to the SD report vector. Options 1 and 2 use total catch for the year and summary abundance at the beginning of the year, so combines seasons and areas. But if most catch occurs in one area and there is little movement between areas, this ratio is not informative about the F in the area where the catch is occurring. Option 3 is a simple sum of the full F's by fleet, so may provide non-intuitive results when there are multi areas or seasons or when the selectivities by fleet do not have good overlap in age. Option 4 is a real annual F calculated as a numbers weighted F for a specified range of ages (read below). The F is calculated as $Z - M$ where Z and M are each calculated as $\ln(N(t+1)/N(t))$ with and without F active, respectively. The numbers are summed over all biology morphs and all areas for the beginning of the year, so subsumes any seasonal pattern.

Typical Value	Options	Description
COND: If F std reporting = 4	13 17 Age range if F std reporting = 4	Specify range of ages. Upper age must be less than maxage because of incomplete handling of the accumulator age for this calculation.
1	F report basis 0 = not relative, report raw values 1 = use F std value corresponding to SPR_{TARGET} 2 = use F std value corresponding to F_{MSY} 3 = use F std value corresponding to $F_{BTARGET}$	Selects the denominator to use when reporting the F std report values. Note that order of these options differs from the biomass report basis options.
999	999: Indicates that the control and data file are in a previous SS 3.24 version and will be converted to the new formatting in the control.ss_new and data.ss_new files. 3.3: Indicates that the control and data files are currently in SS3.30 format.	SSv3.30 will create converted files in the new format from previous version when 999 is given. All ss_new files are in the 3.30 format, so starter.ss_new has 3.30 on the last line. Some Mgpargs are in new sequence, so 3.30 cannot read a ss3.par file produced by version 3.24 and earlier.
End of Starter File		

6.1 Jitter

The jitter factor is multiplied by a random normal deviation $rdev = N(0,1)$ to a transformed parameter value based upon the predefined parameter bounds:

$$temp = -\frac{1}{2}rdev \times jitter \times \ln\left(\frac{P_{MAX} - P_{MIN} + 0.0000002}{P_{VAL} - P_{MIN} + 0.0000001} - 1\right) \quad (1)$$

with the final jittered starting parameter value backtransformed as:

$$P_{NEW} = P_{MIN} + \frac{P_{MAX} - P_{MIN}}{1 + e^{-2 \times temp}} \quad (2)$$

7 Forecast

The specification of options for forecasts is contained in the mandatory input file named FORECAST.SS. For additional detail on the forecast file see Appendix B.

FORECAST.SS

Typical Value	Options	Description
1	Benchmarks/Reference Points 0 = omit 1 = calculate F_{spr} , F_{btgt} , and F_{msy}	SS checks for consistency of the Forecast specification and the benchmark specification. It will turn benchmarks on if necessary and report a warning.
1	Forecast Method 1 = F(SPR) 2 = F(MSY) 3 = F(Btarget) 4 = F(end year) 5 = Average recent F(enter years) - not yet implemented 6 = read Fmult - not yet implemented	Specifies whether or not to do a forecast and which F to use for that forecast.Basis for some additional conditional input.
COND: 0-4	No additional input for these options	
COND: 5	-4 First year for recent average F relative to the end year. 0 Last year for recent average F.	Read a range of years for calculation of recent average F (not yet implemented). Will be used to calculate an average F multiplier for each fleet over a range of years.
COND: 6	0.6 F multiplier for option 6 (not yet implemented).	
0.45	SPR_{TARGET}	SS searches for F multiplier that will produce this level of spawning biomass (Reproductive output) per recruit relative to unfished value.

Typical Value	Options	Description
0.40	Relative Biomass Target	SS searches for F multiplier that will produce this level of spawning biomass relative to unfished value. This is not “per recruit” and takes into account the Spawner-Recruitment relationship.
0 0 0 0 0 0	Benchmark Years beg. bio; end bio; beg. selex; end selex; beg relF; end relF; >0 = absolute year <= 0 = year relative to end year	Requires 6 values, beginning and ending years for biology, selectivity, and relative Fs, that will be used in to calculate benchmark quantities
1	Benchmark Relative F Basis 1 = use year range 2 = set range for relF same as forecast below	Does not affect year range for selectivity and biology.
2	Forecast 0 = none (no forecast years) 1 = set to F(SPR) 2 = search for F(MSY) 3 = set to F(BTGT) 4 = set to average F scalar for the forecast relative F years below 5 = input annual F scalar	This input is ignored in benchmarks are turned off, but its existence is not conditional on benchmark switch. If Benchmarks are on, then F_{SPR} and F_{BTGT} are calculated. This MSY switch determines whether F_{MSY} is also calculated or is set to one of these other quantities.
10	N forecast years (must be ≥ 1)	At least one forecast year now required which differs from version 3.24 that allowed zero forecast years.
1	F scalar	Only used if Forecast option = 5 (input annual F scalar).

Typical Value	Options	Description
0 0 0 0	Forecast Years Begin selex; end selex; begin relative F; end relative F >0 = absolute year <= 0 = year relative to end year	Requires 4 values: beginning and ending years for selectivity and relative Fs that will be used in population forecasts. Option to enter the actual year or values of 0 or negative integer values that will set the value to the model ending year.
1	Control Rule 1 = catch = F(SSB) U.S. West Coast 2 = F = F(SSB)	
0.40	Control Rule Upper Limit	Biomass level (as a fraction of SB0) above which F is constant.
0.10	Control Rule Lower Limit	Biomass level (as a fraction of SB0) above which F is set to 0.
0.75	Control Rule Buffer	Multiplier applied to forecast F before calculating catch.
3	Number of forecast loops (1,2,3)	Maximum number of forecast loops: 1=OFL only, 2=ABC control rule, 3=set catches equal to control rule or input catch and redo forecast implementation error.
3	First forecast loop with stochastic recruitment	If this is set to 1 or 2, then OFL and ABC will be as if there was perfect knowledge about recruitment deviations in the future.
0	Forecast loop control #3	Reserved for future model features.
0	Forecast loop control #4	Reserved for future model features.
0	Forecast loop control #5	Reserved for future model features.
2015	First year for caps and allocations	Should be after years with fixed inputs.
0	Implementation Error	The standard deviation of the log of the ratio between the realized catch and the target catch in the forecast. (set value
0	Rebuilder 0 = omit West Coast rebuilder output 1 = do rebuilder output	> 0.0 to cause active implementation error).

Typical Value	Options	Description
2004	Rebuilder catch (Year Declared) >0 = year first catch should be set to zero -1 = set to 1999	
2004	Rebuilder start year (Year Initial) >0 = year for current age structure -1 = set to end year +1	
1	Fleet Relative F 1 = use first-last allocation year 2 = read season(row) x fleet (column) set below	
2	Basis for maximum forecast catch 2 = cap in terms of total catch biomass 3 = cap in terms of retained catch biomass 5 = cap in terms of total catch numbers 6 = cap in terms of retained total numbers	
COND: 2 (Conditional input for fleet relative F)		
0.1 0.8 0.1	Fleet allocation by relative F fraction	The fraction of the forecast F value. For a multiple area model user must define a fraction for each fleet and each area. The total fractions must sum to one over all fleets and areas. Starting in version 3.3 this now also includes surveys which are treated similar to fleets. Ex: # Fleet 1 Fleet 2 Survey X 0.10 0.10 0.30 # Area1 0.10 0.10 0.30 # Area2

Typical Value	Options	Description
-1 -1 -1	Maximum total catch by fleet -1 = no maximum	Must enter value for each fleet. Starting in version 3.3 this now also includes surveys which are treated similar to fleets.
-1	Maximum total catch by area -1 = no maximum	Must enter value for each area. Starting in version 3.3 this now also includes surveys which are treated similar to fleets.
0 0 0	Fleet assignment to allocation group 0 = Fleet not included in allocation group	Enter group ID # for each fleet. Starting in version 3.3 this now also includes surveys which are treated similar to fleets.
COND: >0 0.2 0.3 0.5	Allocation to each group for each year of the forecast	For each year of the forecast, enter the allocation fraction to each group. Annual values are rescaled to sum to 1.0. Protocol for entering year-specific info will be changing
0	Forecast catch levels	Number of forecast catch levels to input, else calculated from the forecast F.
3	Basis for forecast catch 2 = Dead catch 3 = Retained catch 99 = Input harvest rate (F)	
COND: >0 2012 1 1 1200	Forecasted catches - enter one line per number of fixed forecast year catch Year Season Fleet Catch (of F value)	
999	End of Input	
End of Forecast File		

8 Optional Inputs

8.1 Empirical Weight-at-Age (wtatage.ss)

With version 3.04, SS adds the capability to read empirical body weight at age for the population and each fleet, in lieu of generating these weights internally from the growth parameters, weight-at-length, and size-selectivity. Selection of this option is done by setting Maturity_Option equal to 5. The values are read from a separate file named, wtatage.ss. This file is only required to exist if this option is selected.

The format of this input file is: # syntax for optional input file: wtatage.ss

10		# Number of rows							
40		# Number of ages (equal to Maximum Age)							
#Year	Season	Gender	GP	Birth Season	Fleet	Age-0	Age-1	...	
1971	1	1	1	1	1	0.0128586	0.13718	0.432243	
1971	1	1	1	1	2	
1971	1	1	1	1	0	

where:

- Fleet = -2 is age-specific fecundity*maturity, so time-varying fecundity is possible to implement
- Fleet = -1 is population wt-at-age at middle of the season
- Fleet = 0 is population wt-at-age at the beginning of the season
- There must be an entry for each fleet for fecundity*maturity, wt-at-age at the middle of the season, and wt-at-age at the beginning of the season.
- GP and birthseas probably will never be used, but are included for completeness
- A negative value for year will fill the table from that year through the ending year of the forecast, overwriting anything that has already been read for those years.
- Judicious use of negative years in the right order will allow user to enter blocks without having to enter a row of info for each year
- N ages here equal to maxage specified with the data file, , and N ages +1 columns are required because of age 0 fish.
- If N ages in this table is greater than Maxage in the model, the extra wt-at-age values are ignored.
- If N ages in this table is less than Maxage in the model, the wt-at-age for N ages is filled in for all unread ages out to Maxage.

- There is no internal error checking to verify that weight-at-age has been read for every fleet and every year.
- Fleets that do not use biomass do not need to have wt-at-age assigned
- The values entered for endyr+1 will be used for the benchmark calculations and for the forecast; this aspect needs a bit more checking

CAVEATS:

- SS will still calculate growth curves from the input parameters and can still calculate size-selectivity and can still examine size composition data.
- However, there is no calculation of wt-at-age from the growth input, so no way to compare the input wt-at-age from the wt-at-age derived from the growth parameters.
- If wt-at-age is read and size-selectivity is used, a warning is generated
- If wt-at-age is read and discard/retention is invoked, then a BEWARE warning is generated because of untested consequences for the body wt of discarded fish.
- Warning: age 0 fish seem to need to have weight=0 for spawning biomass calculation (code -2).

TESTING:

- A model was setup with age-maturity (option 2) and only age selectivity.
- The output calculation of wt-at-age and fecundity-at-age was taken from report.sso and put into wtatage.ss (as shown above).
- Re-running SS with this input wt-at-age (Maturity_Option 5) produced identical results to the run that had generated the weight-at-age from the growth parameters.

8.2 runnumbers.ss

This file contains a single integer value. It is read when the program starts, incremented by 1, used when processing the profile value inputs (see below), used as an identifier in the batch output, then saved with the incremented value. Note that this incrementation may not occur if a run crashes.

8.3 profilevalues.ss

This file contains information for changing the value of selected parameters for each run in a batch. In the ctl file, each parameter that will be subject to modification by profilevalues.ss is designated by setting its phase to -9999 .

The first value in profilevalues.ss is the number of parameters to be batched. This value MUST match the number of parameters with phase set equal to -9999 in the ctl file. The program performs no checks for this equality. If the value is zero in the first field, then nothing else will be read. Otherwise, the model will read runnumber * Nparameters values and use the last Nparameters of these to replace the initial values of parameters designated with phase = -9999 in the ctl file.

USAGE Note: If one of the batch runs crashes before saving the updated value of runnumber.ss, then the processing of the profilevalue.ss will not proceed as expected. Check the output carefully until a more robust procedure is developed.

9 Data File

9.1 Overview of Data File

1. Dimensions (years, ages, N fleets, N surveys, etc.)
2. Fleet and survey names, timing, etc.
3. Catch biomass
4. Discard
5. Mean body weight
6. Length composition set-up
7. Length composition
8. Age composition set-up
9. Age imprecision definitions
10. Age composition
11. Mean length of bodyweight-at-age
12. Generalized size composition (e.g. weight frequency)
13. Tag-recapture
14. Stock composition
15. Environmental data

9.2 Units of Measure

The normal units of measure are as follows:

- Catch biomass – metric tons
- Body weight – kilograms
- Body length – usually in cm, weight at length parameters must correspond to the units of body length and body weight.
- Survey abundance – any units if q is freely scaled; metric tons or thousands of fish if q has a quantitative interpretation
- Output biomass – metric tons
- Numbers – thousands of fish, because catch is in mtons and body weight is in kg
- Spawning biomass – metric tons of mature females if $\text{eggs/kg} = 1$ for all weights; otherwise has units that are proportional to egg production

9.3 Time Units

Year

- Spawning is restricted to happening once per year at a specified time of year (in real months).
- Time-varying parameters are allowed to change annually.
- Rates like growth and mortality are per year.
- All fish advance to the next older integer age on January 1, no matter when they were born during the year

Seasons

- Seasons are the time step during which constant rates apply
- Seasons are the time step for which catch and discard is input and for which F is calculated
- The year can have just 1 annual season, or be subdivided into seasons of unequal length.
- Season duration is input in real months and is converted into fractions of an annum. Annual rate values are multiplied by the per annum season duration.
- If the sum of the input season durations is not close to 12.0, then the input durations is divided by 12. This allows for a special situation in which the year could be only 0.25 in duration (e.g. seasons as years) so that spawning and time-varying parameters can occur more frequently.

9.4 Data File Syntax

9.4.1 Model Dimensions

Typical Value	Description
#C data using new survey	Data file comment. Must start with #C to be retained then written to top of various output files. These comments can occur anywhere in the data file, but must have #C in columns 1-2.
1971	Start year
2001	End year
1	Number of seasons per year
12	Vector with N months in each season. These do not need to be integers. Note: If the sum of this vector is close to 12.0, then it is rescaled to sum to 1.0 so that season duration is a fraction of a year. But if the sum is not close to 12.0, then the entered values are simply divided by 12. So with one season per year and 3 months per season, the calculated season duration will be 0.25, which allows a quarterly model to be run as if quarters are years. All rates in SS are now calculated in v3.3 by season (growth, mortality, etc.).
2	The number of subseasons. Entry must be even and the minimum value is 2. This is for the purpose of finer temporal granularity in calculating and using the length-at-age.
1	Spawning month; spawning biomass is calculated at this time of year and used as basis for the total recruitment of all settlement events resulting from this spawning.
2	Number of genders
20	Number of ages. The value here will be the plus-group age. SS start age 0.
1	Number of areas

9.4.2 Fleet Definitions

The catch data input has been modified to improve the user flexibility to add/subtract fishing and survey fleets to a model set-up. The fleet setup input is transposed so each fleet is now a row. Previous versions (3.24 and earlier) required that fishing fleets be listed first followed by survey only fleets. In version 3.30 all fleets now have the same status within the model structure and each has a specified fleet type. Available types are: catch fleet, bycatch only, or survey.

Inputs that define the fishing and survey fleets:

2	#Number of fleets which includes survey in any order						
#Fleet Type	Timing	Area	Catch Units	Eq. Catch SE	Catch SE	Catch Mult.	Fleet Name
1	-1	1	1	0.01	0.01	0	FISHERY1
1	-1	1	2	0.01	0.01	0	SURVEY1

Fleet Type

- 1 = fleet with input retained catch
- 2 = bycatch fleet
- 3 = survey
- 4 = ignored (not yet implemented)

Timing

Carryover from 3.24 approach, now superseded by real month input for data observations.

- 0.50 = now ignored in v3.30
- -1 = treat as catch from whole season

Area

An integer value indicating the area in which a fleet operates.

Catch Units

Ignored for survey fleets.

Equil. Catch SE

Standard error of the initial equilibrium catch.

Catch SE

Standard error of retained catch; ignored for survey fleets and bycatch fleets and with Pope's F method.

Catch Multiplier

Invokes use of a catch multiplier, which is then entered as a parameter in the MG parameter section. The estimated value or fixed value of the catch multiplier is multiplied by the estimated catch before being compared to the observed catch.

- 0 = no catch multiplier used
- 1 = Apply a catch multiplier which is defined as an estimatable parameter in the control file after the cohort growth deviation in the biology parameter section. The model's estimated retained catch will be multiplied by this factor before being compared to the observed retained catch.

After reading the fleet-specific indicators, a list of catch values by fleet and season are read in by the model. The format for the catches is year, season that the catch will be attributed to, fleet, a catch value, and a year specific catch standard error. To include an equilibrium catch value the year should be noted as -999 and be included as the first entry for the associated fleet. There is no longer a need to specify the number of catch records to be read; instead the list is terminated by entering a record with the value of -9999 in the year field. Additionally, initial equilibrium catch is now season specific and can be specified using -999 in the year column.

In addition, it is possible to collapse the number of seasons. So if a season value is greater than the N seasons for a particular model, that catch is added to the catch for N seasons. This is generally to collapse a seasonal model into an annual model. In a seasonal model, use of season=0 will cause SS to distribute the input value of catch equally among the N seasons.

If a bycatch fleet is included the continuous F method must be selected ($F_method = 2$) and are excluded from the catch log-likelihood. Bycatch fleets have selectivity and retention functions, so even though they are considered to have unknown catch levels, this does not mean that their calculated retained catch is zero. MSY and yield per recruit are calculated in terms of dead catch, and they currently include catch from bycatch fleets. The F for bycatch only fleets is kept constant in benchmark and forecast calculations, so it is not included in any forecast cap and allocation calculations. It is not part of the acceptable biological catch, but it is still calculated and reported.

9.4.3 Catch

The new format for version 3.30 for a 2 season model with 2 fisheries looks like the table below. The example is sorted by fleet, but the sort order does not matter. In data.ss_new, the sort order is fleet, year, season.

#Catches by year, season for every fleet:

# Year	Season	Fleet	Catches	Catch SE
-999	1	1	56	0.05
-999	2	1	62	0.05
1975	1	1	876	0.05
1975	2	1	343	0.05
...
-999	1	2	55	0.05
-999	2	2	22	0.05
1975	1	2	555	0.05
1975	2	2	873	0.05
...
-9999	0	0	0	0.05

- Catch can be in terms of biomass or numbers for each fleet.

- Catch is retained catch. If there is discard also, then it is handled in the discard section below.
- If there is reason to believe that the retained catch values underestimate the true catch, then it is possible in the retention parameter set up to create the ability for the model to estimate the degree of unrecorded catch. However, this is better handled with the new catch multiplier option.

If a bycatch fleet is used, continuous F (F_method 2) must be used and are excluded from the catch log likelihood. Bycatch fleets have selectivity and retention functions, so even though they are considered to have unknown catch levels, this does not mean that their retained catch is zero. SS v3.30 will later add the option for bycatch fleets to have retained and discarded catch calculated or have all their catch be assigned to discard. MSY and yield per recruit are calculated in terms of dead catch, and currently include catch from bycatch fleets. Future bycatch fleet options will address this.

9.4.4 Abundance Indices

For fishing fleets, catch-per-unit-effort (CPUE) is defined in terms of retained catch (biomass or numbers). For fishery independent surveys, retention/discard is not defined so CPUE is implicitly in terms of total CPUE. If a survey has its selectivity mirrored to that of a fishery, only the selectivity is mirrored so the expected CPUE for this mirrored survey is in terms of total catch. Also, fishing effort is related to F, which is the F for total catch.

If the statistical analysis used to create the CPUE index of a fishery has been conducted in such a way that its inherent size/age selectivity differs from the size/age selectivity estimated from the fishery's size and age composition, then you may want to enter the CPUE as if it was a separate survey and with a selectivity that differs from the fishery's estimated selectivity. The need for this split arises because the fishery size and age composition should be derived through a catch-weighted approach (to appropriately represent the removals by the fishery) and the CPUE should be derived through an area-weighted GLM (to appropriately serve as if it was a survey of stock abundance).

If the fishery or survey has time-varying selectivity, then this changing selectivity will be taken into account when calculating expected values for the CPUE or survey index.

#CPUE and Suvey Abundance Observations:				
#Fleet/Survey	Units	#Error Distribution		
1	1	0		
2	1	0		
...		
#Year	Month	Fleet/Survey	Observation	SE of log(value)
1991	7	3	80000	0.056
1995	7.2	3	65000	0.056
...
2000	7.1	3	42000	0.056

Units

NOTE: the “effort” option can only be used for a fishing fleet and not for a survey, even if the survey is mirrored to a fishing fleet. The values of these effort data are interpreted as proportional to the level of the fishery F values. No adjustment is made for differentiating between continuous F values versus exploitation rate values coming from Pope’s approximation. A normal error structure is recommended so that the input effort data are compared directly to the model’s calculated F , rather than to $\log_e(F)$. The resultant proportionality constant has units of $1/Q$.

Error Distribution

- -1 = normal error
- 0 = lognormal error
- >0 = Student’s t -distribution in log space with degrees of freedom equal to this value. For $DF > 30$, results will be nearly identical to that for lognormal distribution. A DF value of about 4 gives a fat-tail to the distribution (see Chen (2003)). The se values entered in the data file must be the standard error in \log_e space.

Abundance indices typically have a lognormal error structure with units of standard error of $\log_e(\text{index})$. If the variance of the observations is available only as a CV , then the value of se can be approximated as $\sqrt{\log_e(1 + (CV)^2)}$ where CV is the standard error of the observation divided by the mean value of the observation.

For the normal error structure, the entered values for se are interpreted directly as a se in arithmetic space and not as a CV . Thus switching from a lognormal to a normal error structure forces the user to provide different values for the se input in the data file.

If the data exist as a set of normalized Z -scores, you can either: assert a lognormal error structure after entering the data as $\exp(Z\text{-score})$ because it will be logged by SS. Preferably, the Z -scores would be entered directly and the normal error structure would be used.

Data Format

- Year values that are before start year or after end year are excluded from model, so the easiest way to include provisional data in a data file is to put a negative sign on its year value.
- Duplicate survey observations are not allowed.
- Observations can be entered in any order, except if the super-year feature is used.
- Observations that are to be included in the model but not included in the $-\log L$ need to have a negative sign on their fleet ID. Previously the code for not using observations was to enter the observation itself as a negative value. However, that old approach prevented use of a Z -score environmental index as a “survey”.

- Super-periods are turned on and then turned back off again by putting a negative sign on the season. Previously, super-periods were started and stopped by entering -9999 and the -9998 in the se field. See the “Data Super-Period” section of this manual for more information.

Special Surveys

Four special kinds of surveys are defined in SS. Here in the survey data section, there is no change in the way in which these survey data are entered. Then in the size-selectivity section of the control file, the selectivity pattern used to generate expected values for these surveys is specified by entering the selectivity pattern as 30, 31, 32, or 33. These four survey “selectivity” pattern options bypass the calculation of survey selectivity from explicit selectivity parameters.

- 30 = spawning biomass (e.g. for an egg and larvae survey)
- 31 = $\exp(\text{recruitment deviation})$, useful for environmental index affecting recruitment
- 32 = spawning biomass * $\exp(\text{recruitment deviation})$, for a pre-recruit survey occurring before density-dependence
- 33 = recruitment, age-0 recruits

9.4.5 Discard

If discard is not a feature of the model specification, then just a single input is needed:

#Input	Description
0	#Number of fleets with discard observations

If discard is being used, the input syntax is:

#Input	Description			
3	#Number of fleets with discard observations			
#Fleet	Units	Error		
1	2	-1		
3	2	-1		
#Year	Season	Fleet	Observation	Error
1980	1	1	0.05	0.25
1991	1	1	0.10	0.25
-9999	0	0	0	0

Discard Units

- 1 = values are amount of discard in either biomass or numbers according to the selection made for retained catch

- 2 = values are fraction (in biomass or numbers) of total catch discarded; bio/num selection matches that of retained catch
- 3 = values are in numbers (thousands) of fish discarded, even if retained catch has units of biomass

Discard Error Structure

The four options for discard error are:

- ≥ 1 = degrees of freedom for Student's t-distribution used to scale mean body weight deviations. Value of error in data file is interpreted as CV of the observation.
- 0 = normal distribution, value of error in data file is interpreted as CV of the observation
- -1 = normal distribution, value of error in data file is interpreted as standard error of the observation
- -2 = lognormal distribution, value of error in data file is interpreted as standard error of the observation in log space

Data Format

- Since discard refers to catch, its time units are in seasons, not months.
- Year values that are before start year or after end year are excluded from model, so the easiest way to include provisional data in a data file is to put a negative sign on its year value.
- Negative value for fleet causes it to be included in the calculation of expected values, but excluded from the log likelihood.
- Zero (0.0) is a legitimate discard observation, unless lognormal error structure is used.
- Duplicate survey observations are not allowed.
- Observations can be entered in any order, except if the super-period feature is used.

Cautionary Note

The use of CV as the measure of variance can cause a small discard value to appear to be overly precise, even with the minimum standard error (std. err.) of the discard observation set to 0.001. In the control file, there is an option to add an extra amount of variance. This amount is added to the standard error, not to the CV, to help correct this problem of underestimated variance.

9.4.6 Mean Body Weight

This is the overall mean body weight across all selected sizes and ages. This may be useful in situations where individual fish are not measured but mean weight is obtained by counting

the number of fish in a specified sample, e.g. a 25 kg basket. Version 3.24r added the capability to use mean length data by modifying the mean weight data approach. Now observations can be entered in terms of mean length by setting switching the partition code to 10=all, 11=discard, and 12=retained rather than the 0, 1, and 2 typically used with the mean body weight approach.

#Mean Body Weight Data Section					
#Degrees of freedom for Student's t-distribution used to evaluate mean body weight deviation. This is not a conditional input, must be here even if there are no mean body weight observations.					
30					
#Year	Month	Fleet	Partition	Value	CV
1990	1	1	0	4.0	0.95
1990	1	1	0	1.0	0.95
-9999	0	0	0	0	0

Partition

Mean weight data and composition data require specification of what group the sample originated from (e.g. discard, retained, discard + retained).

- 0 = whole catch in units of weight (discard + retained)
- 1 = discarded catch in units of weight
- 2 = retained catch in units of weight
- 10 = whole catch in units of length (discard + retained)
- 11 = discarded catch in units of weight
- 12 retained catch in units of length

Value - Units

Units must correspond to the units of body weight (or mean length in cm), normally in kilograms. The expected value of mean body weight (or mean length) is calculated in a way that incorporates effect of selectivity and retention.

Error

Error is entered as the CV of the observed mean body weight (or mean length)

9.4.7 Population Length Bins

The beginning of the length composition section sets up the bin structure for both the population and for the length composition data.

1	1 = use data bins 2 = generate from bin width min max below 3 = read vector	Length bin method - creates a conditional read situation below.
COND = 1	Selects option 1, no additional input necessary	
COND = 2	Selects option 2, read 3 additional input values.	
	2	Bin width
	10	Lower size of first bin
	82	Lower size of largest bin
The number of bins is then calculated from: $(\text{max Lread} - \text{min Lread})/(\text{bin width}) + 1$		
COND = 3	Selects option 3 - read 1 value and then read vector of bin boundaries	
	25	Number of population length bins to be read
	26 28 30 ...	Vector containing lower edge of each population size bin
End of conditional inputs for length bin method.		

Notes:

- For option 2, bin width should be a factor of min size and max size. For options 2 and 3, the population length bins must not be wider than the length data bins, but the boundaries of the bins do not have to align. In SS_v3.02B and earlier, the data boundaries needed to align with the population boundaries but this requirement has been removed. The transition matrix is output to checkup.sso.
- The mean size at age 0.0 (virtual recruitment age) is set equal to the min size of the first population length bin.
- When using more population length bins than data bins, SS will run slower (more calculations to do), the calculated weights at age will be less aliased by the bin structure, and you may or may not get better fits to your data.
- While exploring the performance of models with finer bin structure, a potentially pathological situation has been identified. When the bin structure is coarse (note that some applications have used 10 cm bin widths for the largest fish), it is possible for a selectivity slope parameter or a retention parameter to become so steep that all of the action occurs within the range of a single size bin. In this case, the model will lose the gradient of the log likelihood with respect to that parameter and convergence will be hampered. A generic guidance to avoid this situation is not yet available.

Specify bin compression and error structure for length composition data:

#Min Compression	Tail added to proportions	Constant to males & females	Combine & Bins	Compress Error Distribution	Dirichlet Parameter Number	
0	0.0001	0	0	0	0	#Fleet 1
0	0.0001	0	0	0	0	#Fleet 2

Minimum Tail Compression

Compress tails of composition until observed proportion is greater than this value; negative value causes no compression; Advise using no compression if data are very sparse, and especially if the set-up is using agecomp within length bins because of the sparseness of these data.

Added Constant

Constant added to observed and expected proportions at length and age to make logL calculations more robust. Tail compression occurs before adding this constant. Proportions are renormalized to sum to 1.0 after constant is added.

Combine Males & Females

Combine males into females at or below this bin number. This is useful if the gender determination of very small fish is doubtful so allows the small fish to be treated as combined gender. If CombGender>0, then add males into females for bins 1 thru this number, zero out the males, set male data to start at the first bin above this bin. Note that CombGender is entered as a bin index, not as the size associated with that bin. Comparable option is available for age composition data.

Error Distribution

- 0 = Multinomial Error
- 1 = Dirichlet Error

Dirichlet Parameter Number

If the dirichlet error distribution is selected a number of parameters must be specified.

Notes:

- The tail compression and added constant are used in the processing of both the length composition and the age composition data. They do not apply to the generalized size composition data.
- If broad length bins are used, then beware of steep selectivity and retention parameters. An overly steep curve can disappear within the domain of a single length bin, thus causing ADMB to lose track of its gradient.

- The mean weight-at-length, maturity-at-length and size-selectivity are based on the mid-length of the population bins. So these quantities will be rougher approximations if broad bins are defined.
- Provide a wide enough range of population size bins so that the mean body weight-at-age will be calculated correctly for the youngest and oldest fish. If the growth curve extends beyond the largest size bin, then these fish will be assigned a length equal to the mid-bin size for the purpose of calculating their body weight.
- More bins create a bigger model internal structure and slower run times.
- When fish recruit at age 0.0, they are assigned a size equal to the lower edge of the smallest population size bin.
- Fish smaller than the first data bin are placed in the first bin.

9.4.8 Length Composition Data

30	#Number of length bins for data
26 28 30 ... 88 90	#Vector of length bins associated with the length data

Example of a single length composition observation:

#Year	Month	Fleet	Gender	Partition	Nsamp	data vector
1986	1	1	3	0	20	<female then male data>
...
-9999	0	0	0	0	0	0

Gender

If model has only one gender defined in the set-up, all observations must have gender set equal to 0 or 1. In a 2 gender model, the data vector always has female data followed by male data, even if only one of the two genders has data that will be used.

- Gender = 0 means combined male and female (must already be combined and information placed in the female portion of the data vector) (entries in male portion of vector must exist and will be ignored).
- Gender = 1 means female only (male entries must exist for correct data reading, then will be ignored).
- Gender = 2 means male only (female entries must exist and will be ignored after being read).
- Gender = 3 means both data from both genders will be used and they are scaled so that they together sum to 1.0

Partition

Partition indicates samples from either discards,retained, or combined.

- 0 = combined
- 1 = discard
- 3 = retained

Excluding Data

- If the value of year is negative, then that observation is not transferred into the working array. This feature is the easiest way to include observations in a data file but not to use them in a particular model scenario.
- If the value of fleet is negative, then the observation is processed and its logL is calculated, but this logL is not included in the total logL. This feature allows the user to see the fit to a provisional observation without having that observation affect the model.

Note:

- Version 3.30 no longer requires that the number of length composition lines to be read be specified. Entering -9999 at the end of the data matrix will indicate to the model the end of length composition lines to be read.
- Each observation can be stored as one row for ease of data management in a spreadsheet and for sorting of the observations. However, the 6 header values, the female vector and the male vector could each be on a separate line because ADMB reads values consecutively from the input file and will move to the next line as necessary to read additional values.
- The composition observations can be in any order. However, if the super-period approach is used, then each super-periods' observations must be contiguous in the data file.

9.4.9 Age Composition Bin Setup

The age composition section begins by reading a definition of the age bin structure, then the definition of ageing imprecision, then the age composition data itself. The bins are in terms of observed age (here age'). The ageing imprecision definitions are used to create one or more matrices to translate true age structure into expected age structure in terms of age'.

<hr/>																
17		#Number of age' bins; #can be equal to 0 if age data not used; #do not include a vector of agebins if Nage' bins is set equal to 0.														
<hr/>																
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	20	25

Above is the vector with lower age of age' bins. The first and last bins work as accumulators. So in this example any age 0 fish that are caught would be accumulated into the age'1 bin.

9.4.10 Ageing Error

Here, the capability to create a distribution of age' (e.g. age with possible bias and imprecision) from true age is created. One or many age error definitions can be created. For each, there is input of a vector of mean age' and stddev of age'. For one definition, the input vectors can be replaced by vectors created from estimable parameters. In the future, capability to read a full age' – age matrix could be created.

2	# Number of ageing error matrices to generate			
# Age-0	Age-1	Age-2	...	Max Age
-1	-1	-1	...	-1
0.001	0.001	0.001	...	0.001
0.5	1.5	2.3	...	Max Age + 0.5
0.5	0.65	0.67	...	4.3

The above table shows the values for the first 3 ages for each of two age transition definitions: the first defines a matrix with no bias and negligible imprecision and the second shows a small negative bias beginning at age 2.

Note:

- If no age data, there can be 0 vectors.
- In principle, one could have year or laboratory specific matrices.
- For each matrix, enter a vector with mean age' for each true age; if there is no ageing bias, then set age' equal to true age + 0.5. Alternatively, -1 value for mean age' means to set it equal to true age plus 0.5. The addition of +0.5 is needed so that fish will get assigned to the intended interger age'.
- The length of the input vector is Nage+1, with the first entry being for age 0 fish and the last for fish of age Nage. The following line is a a vector with the standard deviation (stddev) of age' for each true age.
- SS is able to create one ageing error matrix from parameters, rather than from an input vector. The range of conditions in which this new feature will perform well has not been evaluated, so it should be considered as a preliminary implementation and subject to modification.
 - To invoke this option, for the selected ageing error vector, set the stddev of ageing error to a negative value for age 0. This will cause creation of an ageing error matrix from parameters and any age or size-at-age data that specify use of this age error pattern will use this matrix. Then in the control file, add 7 parameters below the cohort growth dev parameter. These parameters are described in the control file section of this manual.

Specify bin compression and error structure for age composition data:

#Min Compression	Tail	Constant added to proportions	Combine males & females	Compress & Bins	Error Distribution	Dirichlet Parameter Number	
0		0.0001	1	0	0	0	#Fleet 1
0		0.0001	1	0	0	0	#Fleet 2
0		0.0001	1	0	0	0	#Survey 2
1		Bin method for age data 1 = value refers to population bin index 2 = value refers to data bin index 3 = value is actual length (which must correspond to population length bin boundary)					

An example age composition observation:

#Year	Month	Fleet	Gender	Partition	AgeErr	Lbin lo	Lbin hi	Nsamp	Data	Vector
1987	1	1	3	0	2	-1	-1	79	<enter	data
-9999	0	0	0	0	0	0	0	0	0	values>

Note:

- Syntax for Gender, Partition, and data vector are same as for length.
- Ageerr identifies which ageing error matrix to use to generate expected value for this observation.
- The data vector has female values then male values, just as for the length composition data.
- As with the length comp data, a negative value for year causes the observation to not be read into the working matrix, a negative value for fleet causes the observation to be included in expected values calculation, but not in contribution to total logL.
- Lbin lo, and Lbin hi are the range of length bins that this age composition observation refers to. Normally these are entered with a value of 1 and Maxbin. Whether these are entered as population bin number, length data bin number, or actual length is controlled by the value of the length bin range method above.
 - Entering value of 0 or -1 for Lbin lo converts Lbin lo to 1;
 - Entering value of 0 or -1 for Lbin hi converts Lbin hi to Maxbin;
 - It is strongly advised to use the “-1” codes to select the full size range. If you use explicit values, then the model could unintentionally exclude information from some size range if the population bin structure is changed.

- In reporting to the comp_report.sso, the reported Lbin_lo and Lbin_hi values are always converted to actual length.

9.4.11 Conditional Age'-at-Length

Use of conditional age'-at-length will greatly increase the total number of age' composition observations and associated model run time, but it is a superior approach for several reasons. First, it avoids double use of fish for both age' and size information because the age' information is considered conditional on the length information. Second, it contains more detailed information about the relationship between size and age so provides stronger ability to estimate growth parameters, especially the variance of size-at-age. Lastly, where age data are collected in a length-stratified program, the conditional age'-at-length approach can directly match the protocols of the sampling program.

In a two gender model, it is best to enter these conditional age'-at-length data as single gender observations (gender =1 for females and = 2 for males), rather than as joint gender observations (gender = 3). In this way, it isolates the age composition data from any gender selectivity as well.

When Lbin_lo and Lbin_hi are used to select a subset of the total size range, the expected value for these age' data is calculated within that specified size range, so is age' conditional on length.

9.4.12 Sex Ratio-at-Length

The conditional age'-at-length approach can be used to analyze sex ratio-at-length data. If you have no age data, then the following simple setup will allow entry of sex-ratio at length. Note that it must use the joint gender (code 3) approach.

#Example setup for sex ratio-at-length data:															
1	#N age bins so all fish are put into a single "age" bind regardless of their true age														
10	#Assigned "age" for this one bin														
1	#N of age error definitions														
10.5	10.5	10.5	10.5	...	repeat for each true age in model, beginning at age-0										
0.001	0.001	0.001	0.001	...	repeat for each true age in model, beginning at age-0										
1	# Lbin method: 1 = population length bins, 2 = data length bins, 3 = lengths														
0	#Combine males and females at or below this bin number														
#There are 4 females and 8 males in the 25th population length bin															
#Yr	Month	Fleet	Gender	Part	AgeErr	Lbinlo	Lbinhi	Nsamp							
1971	1	1	3	0	1	25	25	12	0	4	0	0	8	0	...
-9999															

If you have both real age data and sex ratio at length data, then you will need to set up the number of age bins to match the real age data, define an additional age error type to

use for the sex ratio data, put the sex ratio data into the correct bin. For example:

5	#N age bins so all fish are put into a single "age" bind regardless of their true age												
1 2 3	#Assigned "age" for this one bin												
4 5													
2	#N of age error definitions												
-1	1	1	1	...	repeat for each true age in model, beginning at age-0								
0.2	0.4	0.5	0.8	...	repeat for each true age in model, beginning at age-0								
3.5	3.5	3.5	3.5	...	repeat for each true age in model, beginning at age-0								
0.001	0.001	0.001	0.001	...	repeat for each true age in model, beginning at age-0								
1	# Lbin method: 1 = population length bins, 2 = data length bins, 3 = lengths												
0	#Combine males and females at or below this bin number												
#There are 4 females and 8 males in the 25th population length bin													
#Yr	Month	Fleet	Gender	Part	AgeErr	Lbinlo	Lbinhi	Nsamp					
1971	1	1	3	0	1	-1	-1	25	1	2	4	...	#real age data 5
1971	1	1	3	0	1	25	25	12	0	0	4	...	#sex ratio in bin 3
-9999													

9.4.13 Mean Length or Body Weight-at-Age

SS also accepts input of mean length-at-age' or mean bodywt-at-age'. This is done in terms of age', not true age, to take into account the effects of ageing imprecision on expected mean size-at-age'. If the value of "AgeErr" is positive, then the observation is interpreted as mean length-at-age'. If the value of "AgeErr" is negative, then the observation is interpreted as mean bodywt-at-age' and the abs(AgeErr) is used as AgeErr.

An example observation:

#Yr	Month	Fleet	Gender	Part	AgeErr	Nsamp	Female Data	Male Data	Female N	Male N
1989	1	1	3	0	2	999	<Mean size values>	<Mean size values>	<N fish>	<N fish>
-9999										

Note:

- Nsamp value is ignored if positive, but a negative value will cause the entire observation to be ignore.
- Negatively valued mean size entries with be ignored in fitting.

- Nfish value of 0 will cause mean size value to be ignored in fitting.
- Negative value for year causes observation to not be included in the working matrix.
- Each genders' data vector and N fish vector has length equal to the number of age' bins.
- Where age data are being entered as conditional age'-at-length and growth parameters are being estimated, it may be useful to include a mean length-at-age vector with nil emphasis to provide another view on the model's estimates.

9.4.14 Environmental Data

SS accepts input of time series of environmental data. Parameters can be made to be time-varying by making them a function of one of these environmental time series.

# Parameter values can be a function of an environmental data series:		
2	#Number of environmental variables	
10	#Number of environmental observations	
# Example of 2 environmental observations:		
#Year	Variable	Value
1990	1	0.10
1991	1	0.15

Note:

- Any years for which environmental data are not read are assigned a value of 0.0.
- It is permissible to include a year that is one year before the start year in order to assign environmental conditions for the initial equilibrium year. But this works only for recruitment parameters, not biology or selectivity parameters.
- Environmental data can be read for up to 100 years after the end year of the model. Then, if the recruitment-environment link has been activated, the future recruitments will be influenced by any future environmental data. This could be used to create a future "regime shift" by setting historical values of the relevant environmental variable equal to zero and future values equal to 1, in which case the magnitude of the regime shift would be dictated by the value of the environmental linkage parameter. Note that only future recruitment and growth can be modified by the environmental inputs; there are no options to allow environmentally-linked selectivity in the forecast years.

9.4.15 Generalized Size Composition Data

A new feature with SS_v3 is a generalized approach to size composition information. It was designed initially to provide a means to include weight frequency data, but was implemented

to provide a generalized capability. The user can define as many size frequency methods as necessary.

- Each method has a specified number of bins.
- Each method has "units" so the frequencies can be in units of biomass or numbers.
- Each method has "scale" so the bins can be in terms of weight or length (including ability to convert bin definitions in pounds or inches to kg or cm).
- The composition data is input as females then males, just like all other composition data in SS. So, in a two-gender model, the new composition data can be combined gender, single gender, or both gender.
- If a retention function has been defined, then the new composition data can be from the combined discard + retained, discard only or retained only.

Example entry:

2		#N of weight frequency methods
25	4	#Nbins per method
2	1	#Units per each method (1 = biomass, 2 = numbers)
3	2	#Scale per each method (1 = kg, 2 = lbs, 3 = cm, 4 = inches)
0.00001	-1	#Min compression to add to each observation (entry for each method)
40	5	#N observations per weight frequency method

Then enter the lower edge of the bins for each method. The two row vectors shown below contain the bin definitions for methods 1 and 2 respectively:

26	28	30	32	34	36	38	40	42	...	60	62	64	68	72	76	80	90
1	2.4	4	9	1

Note:

- There is no tail compression for generalized size frequency data.
- Super-period capability is enabled for generalized size comps beginning with V3.20.
- There are two options for treating fish that in population size bins that are smaller than the smallest size frequency bin.
 - Option 1: By default, these fish are excluded (unlike length composition data where the small fish are automatically accumulated up into the first bin.
 - Option 2: If the first size bin is given a negative value, then: accumulation is turned on and the negative of the entered value is used as the lower edge of the first size bin;

- By choosing units=2 and scale=3, the size comp method can be nearly identical to the length comp method if the bins are set identically;
- Bin boundaries can be real numbers so obviously do not have to align with population length bin boundaries, SS interpolates as necessary;
- Size bins cannot be defined to be narrower than the population binwidth; an untrapped error will occur;
- Because the transition matrix can depend upon weight-at-length, it is calculated internally for each gender and for each season because weight-at-length can differ between genders and can vary seasonally.

An example observation is below. Note that its format is identical to the length composition data, including gender and partition options, except for the addition of the first column to indicate the size frequency method.

#Method	Year	Month	Fleet	Gender	Part	Sample Size	<composition males>	females then
1	1975	1	1	3	0	43	<data>	

9.4.16 Tag-Recapture Data

The ability to analyze tag-recapture data has been introduced with SS_v3. Each released tag group is characterized by an area, time, gender and age at release. Each recapture event is characterized by a time and fleet. Because SS fleet's each operate in only one area, it is not necessary to record the area of recapture. Inside the model, the tag cohort is apportioned across all growth patterns in that area at that time (with options to apportion to only one gender or to both). The tag cohort x growth pattern then behaves according to the movement and mortality of that growth pattern. The number of tagged fish is modeled as a negligible fraction of the total population. This means that a tagging event does not move fish from an untagged group to a tagged group. Instead it acts as if the tags are seeded into the population with no impact at all on the total population abundance or mortality. The choice to require assignment of a predominant age at release for each tag group is a pragmatic coding and model efficiency choice. By assigning a tag group to a single age, rather than distributing it across all possible ages according to the size composition of the release group, it can be tracked as a single diagonal cohort through the age x time matrix with minimal overhead to the rest of the model. Tags are considered to be released at the beginning of a season (period).

Example set-up for tagging data:

1	#Do tags - if this value is 0, then omit all entries below							
COND = 1 All subsequent tag-recapture entries must be omitted if "Do Tags" = 0								
3	#Number of tag groups							
12	#Number of recapture events							
2	#Mixing latency period: N periods to delay before comparing observed to expected recoveries (0 = release period)							
10	#Max periods (months) to track recoveries, after which tags enter accumulator							
#Release Data								
#TG	Area	Year	Month	<tfill>	Gender	Age	N	Release
1	1	1980	1	999	0	24	2000	
2	1	1995	1	999	1	24	1000	
3	1	1985	1	999	2	24	10	
#Recapture Data								
#TG		Year		Month		Fleet		Number
1		1982		1		1		7
1		1982		1		2		5
1		1985		1		2		0
2		1997		1		1		6
2		1997		2		1		4
3		1986		1		1		7
3		1986		2		1		5

Note:

- The release data must be enter in TG order.
- <tfill> values are place holders and are replaced by program generated values for model time.

9.4.17 Stock Composition Data

It is sometimes possible to observe the fraction of a sample that is composed of fish from different stocks. These data could come from genetics, otolith microchemistry, tags or other means. The growth pattern feature in SS allows definition of cohorts of fish that have different biological characteristics and which are independently tracked as they move among areas. SS now incorporates the capability to calculate the expected proportion of a sample of fish that come from different growth patterns. In the inaugural application of this feature, there was a 3 area model with one stock spawning and recruiting in area 1, the other stock in area

3, then seasonally the stocks would move into area 2 where stock composition observations were collected, then they moved back to their natal area later in the year.

Stock composition data can be entered in SS as follows:

1	#Do morphcomp (if zero, then do not enter any further input below)							
COND = 1								
3	#Number of observations							
2	#Number of stocks							
0.0001	#Minimum Compression							
#Year	Month	Fleet	Part	Nsamp	Data	Vector		
1980	1	1	0	36	0.4	0.6	...	
1981	1	1	0	40	0.44	0.62	...	
1982	1	1	0	50	0.49	0.50	...	

Note:

- The N stocks entered with these data must match the N growth patterns in the control file.
- The expected value is combined across genders.
- The “partition” flag is included here in the data, but cannot be used because the expected value is calculated before the catch is partitioned into discard and retained components.
- Note that there is a specific value of mincomp to add to all values of observed and expected.

End of Data File

999	#End of data file marker
-----	--------------------------

9.4.18 Excluding Data

Data that are <styr or > retroyr are not moved into the internal working arrays at all. So if you have any alternative observations that are used in some model runs and not in others, you can simply give them a negative year value rather than having to comment them out and revise the observation read counter. The first output to data.ss_new has the unaltered and complete input data. Subsequent reports to data.ss_new produce expected values or bootstraps only for the data that are being used. Note that the Nobs values are adjusted accordingly.

Data that are to be included in the calculations of expected values, but excluded from the calculation of negative log likelihood, are flagged by use of a negative value for fleet ID.

9.4.19 Data Super Periods

The “Super-Period” capability allows the user to introduce data that represent a blend across a set of time steps and to cause the model to create an expected value for this observation that uses the specified set of time steps. The option is available for all types of data and a similar syntax is used. The syntax is revised for SS version 3.23 and higher. Previously, super-periods were started with a -9999 flag in a standard error (se) or Nsamp field and then stopped with a -9998 flag in that field. This was cumbersome and did not allow for super-periods with only 2 time periods. With model version 3.23 and higher, super-periods are started with a negative value for season, and then stopped with a negative value for season, placeholder observations within the super-period are designated with a negative fleet field. The standard error (se) or Nsamp field is now used for weighting of the expected values. An error message will be generated if the old syntax is used. Similarly, negative fleet is the sole allowable flag for omitting observations from the log likelihood calculation. An error message is generated if the super-period does not contain exactly one observation with a positive fleet field.

All super-period observations must be contiguous in the data file. All but one of the observations in the sequence will have a negative value for fleet ID so the data associated with these dummy observations will be ignored. The observed values must be combined outside of the model and then inserted into the data file for the one observation with a positive fleet ID. An expected value for the observation will be computed for each selected time period within in the super-period. Beginning with V3.23b, the expected values are weighted according to the values entered in the se (or Nsamp) field for all observations expect the single observation holding the combined data. The expected value for that year gets a relative weight of 1.0. So in the example below, the relative weights are: 1982, 1.0 (fixed); 1983, 0.85; 1985, 0.4; 1986, 0.4. These weights are summed and rescaled to sum to 1.0, and are output in the echoinput.sso file.

Not all time steps within the extent of a super-period need be included. For example, in a 3 season model a super-period could be set up to combine information from season 2 across 3 years, e.g. skip over the season 1 and season 2 for the purposes of calculating the expected value for the super-period. The key is to create a dummy observation (negative fleet value) for all time steps, except 1, that will be included in the super-period and to include one real observation (positive fleet value; which contains the real combined data from all the specified time steps).

Example:

#Year	Month	Fleet	Obs	SE	Comment
1982	-2	3	34.2	0.3	Start super-period. This observation has positive fleet value, so is expected to contain combined data from all identified periods of the super-period. The se entered here is use as the se of the combined observation. The expected value for the survey in 1982 will have a relative weight of 1.0 (default) in calculating the combined expected value.
1983	2	-3	55	0.3	In super-period; entered obs is ignored. The expected value for the survey in 1983 will have a relative weight equal to the value in the se field (0.85) in calculating the combined expected value.
1985	2	-3	88	0.40	Note that 1984 is not included in the supe-rperiod. Relative weight for 1985 is 0.4
1986	-2	-3	88	0.40	End super-period

A time step that is within the time extent of the super-period can still have its own separate observation. In the above example, the survey observation in 1984 could be entered as a separate observation, but it must not be entered inside of the contiguous block of super-period observations. For composition data (which allow for replicate observations), a particular time steps observations could be entered as a member of a super-period and as a separate observation.

The super-period concept can also be used to combine seasons within a year with multiple seasons. This usage could be preferred if fish are growing rapidly within the year so their effective age selectivity is changing within year as they grow; fish are growing within the year so fishery data collected year round have a broader size-at-age modes than a mid-year model approximation can produce; and it could be useful in situations with very high fishing mortality.

10 Control File

10.1 Overview of Control File

These listed model features are denoted in the control file in the following order:

1. Number of growth patterns and sub-morphs
2. Design matrix for assignment of recruitment to area/season/growth pattern
3. Design matrix for movement between areas

4. Definition of time blocks that can be used for time-varying parameters
5. Specification for growth and fecundity
6. Natural mortality and growth parameters for each gender x growth pattern
7. Maturity, fecundity and weight-length for each gender
8. Recruitment distribution parameters for each area, season, growth pattern
9. Cohort growth deviation
10. Catch Multiplier
11. Environmental link parameters for any mortality-growth (MG) parameters that use a link
12. Time-varying setup for any MG parameters that use blocks
13. Seasonal effects on biology parameters
14. Phase for any MG parameters that use annual deviations
15. Spawner-recruitment parameters
16. Recruitment deviations
17. Method for calculating fishing mortality (F)
18. Initial equilibrium F for each fleet
19. Catchability (Q) setup for each fleet and survey
20. Catchability parameters
21. Length selectivity, retention, discard mortality setup for each fleet and survey
22. Age selectivity setup for each fleet and survey
23. Parameters for length selectivity, retention, discard mortality for each fleet and survey
24. Parameters for age selectivity for each fleet and survey
25. Environmental link parameters for any selectivity/retention parameters that use a link
26. Time-varying setup for any selectivity/retention parameters that use blocks
27. Phase for any selectivity/retention parameters that use random annual deviation
28. Tag-recapture parameters
29. Variance adjustments
30. Lambdas for likelihood components

10.2 Parameter Line Elements

A primary role of the SS control file is to define the parameters to be used by the model. The general syntax of a parameter line is described here. Parameter lines will be used in three sections of the control file: (1) natural mortality and growth; (2) spawner-recruitment, initial F and catchability; and (3) selectivity. The first seven elements of a parameter line are used in every section and will be referred to as a short parameter line. The remaining elements are used just in sections (1) and (3). Each parameter line contains:

Column	Element	Description
1	LO	Minimum value for the parameter
2	HI	Maximum value for the parameter
3	INIT	Initial value for the parameter. If the SS3 PAR file is read, it overwrites these INIT values.
4	Prior Value	Expected value for the parameter. This value is ignored if the prior type is -1 or 1.
5	Prior Type	-1 = none, 0 = normal, 1 = symmetric beta, 2 = full beta, 3 = lognormal with bias adjustment, 5 = gamma
5	Prior StDev	Standard deviation for the prior, used to calculate likelihood of the current parameter value. This value is ignored if prior type is -1.
6	PHASE	Phase in which parameter begins to be estimated. A negative value causes the parameter to retain its INIT value (or value read from the PAR file).

Short parameter lines have only the above 7 elements. The full parameter line syntax for the Mortality-Growth and Selectivity sections provides additional controls to give the parameter time-varying properties. These are listed briefly below and described in more detail in the section Time Varying Parameter Options found at the end of the control file syntax section.

8	ENV	Create a linkage to an input environmental time-series
9	Use Dev	Invokes use of the deviation vector
10	Dev min yr	Beginning year for the deviation vector
11	Dev max yr	Ending year for the deviation vector
12	Dev StDev	Standard deviation for elements in the deviation vector
13	USE-BLOCK	Set up blocks or parameter trends
14	BLOCK-TYPE	Function form for the block offset

10.3 Control File Syntax

The control file is described here using a rather complex set-up with 2 seasons, 2 areas, 2 growth morphs, 2 genders, and 3 sub-morphs in order to demonstrate the order and interdependence of various factors.

Terminology:

- Where the term “COND” appears in the value column of this documentation (it does not actually appear in the control file), it indicates that the following section is omitted except under certain conditions, or that the factors included in the following section depend upon certain conditions.
- In most cases, the description in the Definition column is the same as the label output to the control.ss_new file.

Typical Value	Description and Options
#C comment	Comments beginning with #C at the top of the file will be retained and included in output
2	N growth patterns (GP)
3	Number of sub-morphs within a growth pattern. Permissible values are 1, 3, 5 only. Typical value is 1. Values of 3 or 5 allow exploration of size-dependent survivorship.
COND > 1	Following 2 lines are conditional on N sub-morphs > 1
0.7	Morph between/within stdev ratio. Ratio of the amount of growth variability between sub-morphs to within sub-morphs.
0.2 0.6 0.2	Distribution among sub-morphs. Enter custom vector or enter -1 to first value of vector to get a normal approximation: (0.15, 0.70, 0.15) for 3 sub-morphs, (0.031, 0.237, 0.464, 0.237, 0.031) for 5 sub-morphs.
1	Recruitment distribution method. Options: 1 = use the 3.24 or earlier setup, 2 = main effects for GP, settle timing, and area, 3 = each settle entity, and 4 = none when N GP*Nsettle=1
1	Number of recruitment settlement assignments. Options: 1 = global, 2 = by area
COND = 1	Only read if recruitment distribution method is set to 1 (3.24 and earlier version)
0	Year x Area x Settlement Event Interaction Requested
1 1 1	Recruitment assignment to GP, season, area (for each settlement event).
COND:	If there are multiple GP, season, and areas, specify the additional lines:

Typical Value	Description and Options
1 1 1	Recruitment assignment to GP1, season 1, area 1
2 1 2	Recruitment assignment to GP1, season 1, area 2
2 1 1	Recruitment assignment to GP2, season 1, area 1
2 2 2	Recruitment assignment to GP2, season 2, area 2
COND:	If N areas > 1:
0	Movement: Only read following movement section if N areas > 1
COND > 0	Following lines are conditional if movement is selected:
4	N movement definitions
0.60	First age that moves. Real, not integer age at the beginning of season. This control primarily used to keep new recruits from moving until after their first year.
1 1 1 2 4 10	The four requested movement definitions appear here. Each definition specifies: season, GP source area, destination area, min age, max age. The rate of movement will be controlled by the movement parameters later. Here the minage and maxage controls specify the range over which the movement parameters are active.
1 1 2 1 4 10	
1 2 1 2 4 10	
1 2 2 1 4 10	
3	Number of block patterns. These patterns can be referred to in the parameter sections to create a separate parameter value for each block.
COND:	Following inputs are omitted if N Block patterns equals 0
3 2 1	Blocks per pattern
1975 1985	Beginning and ending years for blocks in design 1; years not assigned to a block period retain the baseline value for a parameter that uses this pattern.
1986 1990	
1995 2001	
1987 1990	Beginning and ending years for blocks in design 2.
1995 2001	
1999 2002	Beginning and ending years for blocks in design 3.

10.3.1 Biology

This section controls the biology parameters. These include: natural mortality, growth, maturity, fecundity, distribution of recruitment, and movement. Collectively, these are referred to as the MG parameters. The top of the biology section includes several factors

that control the number of parameters to be subsequently read and the method by which SS will use these parameters.

Typical Value	Description and Options
0.50	Fraction female - a constant that applies to all growth patterns
1	Natural Mortality Option: 0 = A single parameter 1 = N breakpoints 2 = Lorenzen 3 = Read age specific M and do not do seasonal interpolation 4 = Read age specific and do seasonal interpolation, if appropriate
COND = 0	No additional natural mortality controls
COND = 1	
4	Number of breakpoints. A value of 2 would correspond to the M pattern as defined in SS V2. Then read a vector of ages for these breakpoints (e.g. corresponding to natM_amin and natM_amax in SS V2). Later, per gender x GP, read N parameters for the natural mortality at each breakpoint.
2.0 4.5 9.0	Vector of age breakpoints
15.0	
COND = 2	
4	Lorenzen Natural Mortality: read one additional value that is the reference age (integer) (<i>click here for more information</i>). Later read one parameter for each gender x GP that will be the M at the reference age. Other ages will have an M scaled to its body size-at-age. However, if sub-morphs are used, all will have the same M a their growth pattern. Lorenzen M calculation will be updated if the starting year growth parameters are active, but if growth parameters vary during the time-series, the M is not further updated. So be careful in using Lorenzen when there is time-varying growth.
COND = 3 or 4	Do not read any natural mortality parameters. With option 2, these M values are held fixed for the integer age (no seasonality or birth season considerations). With option 4, there is seasonal interpolation based on real age, just as in options 1 and 2.
0.20 0.25 ...	Age-specific M values: row 1 is female GP1, row 2 is female 2
0.20 0.23 ...	GP2, row 3 is male GP1, etc.

Typical Value	Description and Options
1	<p>Growth Model:</p> <p>1 = von Bertalanffy (2 parameters)</p> <p>2 = Schnute's generalized growth curve (aka Richards curve) with 3 parameters</p> <p>3 = von Bertalanffy with age-specific k deviations for specified range of ages</p>
1.66	Growth Amin (A1): Reference age for first size-at-age parameter (<i>click here for more information</i>)
25	Growth Amax (A2): Reference age for second size-at-age parameter.
COND = 3	Growth option age-specific k
5	Minimum age for age-specific k
7	Maximum age for age-specific k
0	Standard deviation added to length-at-age: Enter 0.10 to mimic SS2 V1.xx. Recommend using a value of 0.0. (<i>click here for more information</i>)
1	<p>CV Pattern</p> <p>0: $CV=f(LAA)$, so the 2 parameters are in terms of CV of the distribution of length-at-age and the interpolation between these 2 parameters is a function of mean length-at-age.</p> <p>1: $CV=f(A)$, so interpolation is a function of age.</p> <p>2: $SD=f(LAA)$, so parameters define the standard deviations of length-at-age and interpolation is a function of mean length-at-age.</p> <p>3: $SD=f(A)$</p> <p>4: Lognormal distribution of size-at-age. Input parameters will specify the standard deviation of loge size at age. E.g. entered values will typically be between 0.05 and 0.15. A bias adjustment is applied so the lognormal distribution of size-at-age will have the same mean size as when a normal distribution is used.</p>
2	<p>Maturity Option:</p> <p>1 = length logistic,</p> <p>2 = age logistic,</p> <p>3 = read age-maturity for each female GP</p> <p>4 = read an empirical age-maturity vector for all ages</p> <p>5 = read empirical age-fecundity and body weight-at-age from separate file, wtatage.ss. Allows for reading time series of input. See section <i>Empirical Wt-at-Age</i> for details. NOTE: need to read 2 parameters even if option 3, 4, or 5 is selected.</p>

Typical Value	Description and Options
	6 = read an empirical length-maturity vector by population length bin (available in v3.24q)
COND = 3 or 4	Maturity Option
0 0.05 0.10	Vector of age-specific maturity or fecundity. One row of length Nages + 1 for each female GP
...	
COND = 6	Maturity Option
0 0.05 0.10	Vector of length-specific maturity or fecundity. One row of length of the population length bins for each female GP
...	
1	First Mature Age: Overridden if maturity option is 3, 4, or 5, but still must exist here. Otherwise, all ages below the first mature age will have maturity set to zero.
1	<p>Fecundity Option (irrelevant if maturity option is 4 or 5):</p> <p>1 = to interpret the 2 egg parameters as linear eggs/kg on body weight (current SS default), so fecundity = $wt * (a + b * wt)$, so value of a=1, b=0 causes eggs to be equivalent to spawning biomass.</p> <p>2 = to set fecundity = $a * L^b$</p> <p>3 = to set fecundity = $a * W^b$, so values of a=1, b=1 causes fecundity to be equiv to spawning biomass</p> <p>4 = fecundity = $a + b * L$</p> <p>5 = Eggs = $a + b * wt$</p>
0	Hermaphroditism Option: 0 = no, 1 = invoke female to male transition
COND = 1	Read 2 lines below if herma. is selected; also read 3 parameters after reading the male weight-length parameter
-1	<p>Hermaphroditism Season:</p> <p>-1 to do transition at the end of each season (after mortality and before movement)</p> <p><positive integer> to select just one season</p>
1	<p>Include males in spawning biomass</p> <p>0 = no males in spawning biomass</p> <p>1 = simple addition of males to females</p> <p>xx = more options to come later</p>
2	<p>Parameter Offset Method</p> <p>1 = direct assignment</p> <p>2 = for each GP x gender, parameter defines offset from gender 1, offsets are in exponential terms, so for example, old_male M = old_female M * exp(old_male parameter)</p>

Typical Value	Description and Options
	3 = for each GP x gender, parameter defines offset from GP 1 gender 1. For females, given that “natM option” is breakpoint and there are two breakpoints, parameter defines offset from early age (e.g., $\text{old_female_M} = \text{young_female_M} * \exp(\text{old_female_M_parameter})$). For males, given that “natM option” is breakpoint and there are two breakpoints, parameter is defined as offset from females AND from early age (e.g., $\text{old_male_M} = \text{young_female_M} * \exp(\text{young_male_M_parameter}) * \exp(\text{old_male_M_parameter})$).
1	Time-varying adjustment constraint: 1 = standard parameter adjustments for environmental, block, and deviations are not constrained by bounds 2 = logistic transform - parameter adjustments use a logistic transformation to assure that adjusted parameter value stays within bounds of base parameter 3: standard with no bound check

10.3.2 Read Mortality-Growth Parameters

Next, SS reads the MG parameters in generally the following order (may vary based on selected options):

Parameter	Description
Females	Female natural mortality and growth parameters in the following order by GP
natM	Natural mortality for female GP1, where the number of natural mortality parameters depends on the option selected.
Lmin	Length at Amin (units in cm) for female, GP1
Lmax	Length at Amax (units in cm) for female, GP1
VBK	Von Bertalanffy growth coefficient (units are per year) for females, GP1
COND if growth type =2	
Richards Coefficient	Only include this parameter if Richards growth function is used. If included, a parameter value of 1.0 will have a null effect and produce a growth curve identical to Bertalanffy.

Parameter	Description
COND if growth type =3	Age-Specific K
K deviations for first age in rage	
K deviations for next age in rage	
...	
K deviations for last age in rage	
CV young	Variability for size at age \leq AFIX (units are fraction) for females, GP1. Note that CV cannot vary over time, so do not set up env-link or a dev vector. Also, units are either as CV or as standard deviation, depending on assigned value of CV pattern.
CV old	Variability for size at age \geq AFIX (units are fraction) for females, GP1. For intermediate ages, do a linear interpolation of CV on means size-at-age. Note that the units for CV will depend on the CV pattern and the value of MGparm as offset.
COND: GP > 1	Repeat female parameters in the above order for GP2
Males	Male natural mortality and growth parameters in the following order by GP
natM	Natural mortality for male GP1, where the number of natural mortality parameters depends on the option selected.
Lmin	Length at Amin (units in cm) for male, GP1
Lmax	Length at Amax (units in cm) for male, GP1
VBK	Von Bertalanffy growth coefficient (units are per year) for males, GP1
COND if growth type =2	
Richards	
Coefficient	Only include this parameter if Richards growth function is used. If included, a parameter value of 1.0 will have a null effect and produce a growth curve identical to Bertalanffy.
COND if growth type =3	Age-Specific K
K deviations for first age in rage	
K deviations for next age in rage	
...	
K deviations for last age in rage	

Parameter	Description
CV young	Variability for size at age \leq AFIX (units are fraction) for males, GP1. Note that CV cannot vary over time, so do not set up env-link or a dev vector. Also, units are either as CV or as standard deviation, depending on assigned value of CV pattern.
CV old	Variability for size at age \geq AFIX (units are fraction) for males, GP1. For intermediate ages, do a linear interpolation of CV on means size-at-age. Note that the units for CV will depend on the CV pattern and the value of MGparm as offset.
COND: GP > 1	Repeat male parameters in the above order for GP2
Females	Weight length relationship parameters, maturity and fecundity
WtLen scale	Coefficient to convert length in cm to weight in kg for females
WtLen exp	Exponent in to convert length to weight for females
Mat-50	Maturity logistic inflection (in cm or years). Where female maturity-at-length (or age) is a logistic function: $maturity = 1/(1 + \exp(slope * (size - at - age - inflection)))$
Mat-slope	Logistic slope (must have negative value)
Eggs-alpha	Two fecundity parameters; usage depends on the selected fecundity option. Must be included here even if vector is read in the control section above.
Eggs-beta	
COND: GP > 1	Repeat female parameters in the above order for GP2
Males	Weight length relationship parameters
WtLen scale	Coefficient to convert length in cm to weight in kg for males
WtLen exp	Exponent in to convert length to weight for males
COND: GP > 1	Repeat male parameters in the above order for GP2
COND: Hermaphrodism	3 parameters define a normal distribution for the transition rate of females to males
Inflect Age	Hermaphrodite inflection age
StDev	Hermaphrodite standard deviation (in age)
Asmp Rate	Hermaphrodite asymptotic rate
Recr Dist GP	Recruitment apportionment by GP, if multiple GP, multiple entries required

Parameter	Description
Recr Dist Area	Recruitment apportionment by area, if multiple areas, multiple entries required
Recr Dist Seas	Recruitment apportionment by season, if multiple seasons, multiple entries required
COND:	If recruitment distribution interaction = 1 (on)
N patterns x N areas x N seasons	Note that the order of recruitment distribution parameters has areas then seasons for main effect, and seasons then areas for interactions.
Cohort growth deviation	If no deviations the INIT set equal to 1
2 x N selected movement pairs	Movement parameters
COND:	The following lines are only required when the associated features are turned on
Ageing Error	Turned on in the data file
Catch	Turned on in the data file
Multiplier	

Example format for MG parameter section:

LO	HI	INIT	Prior Value	<other entries>	Block Type	Parameter Label
0	0.50	0.15	0.1	...	0	#NatM_p_1_Fem_GP_1
0	45	21	36	...	0	#L_at_Amin_Fem_GP_1
40	90	70	70	...	0	#L_at_Amax_Fem_GP_1
0	0.25	0.15	0.10	...	0	#VonBert_K_Fem_GP_1
0.10	0.25	0.15	0.20	...	0	#CV_young_Fem_GP_1
0.10	0.25	0.15	0.20	...	0	#CV_old_Fem_GP_1
-3	3	2e-6	0	...	0	#Wtlen_1_Fem
-3	4	3	3	...	0	#Wtlen_2_Fem
50	60	55	55	...	0	#Mat50%_Fem
-3	3	-0.2	-0.2	...	0	#Mat_slope_Fem
-5	5	0	0	...	0	#Eggs/kg_inter_Fem
-50	5	0	0	...	0	#Eggs/kg_slope_wt_Fem
0	0.50	0.15	0.1	...	0	#NatM_p_1_Mal_GP_1
0	45	21	36	...	0	#L_at_Amin_Mal_GP_1
40	90	70	70	...	0	#L_at_Amax_Mal_GP_1
0	0.25	0.15	0.10	...	0	#VonBert_K_Mal_GP_1
0.10	0.25	0.15	0.20	...	0	#CV_young_Mal_GP_1

LO	HI	INIT	Prior Value	<other entries>	Block Type	Parameter Label
0.10	0.25	0.15	0.20	...	0	#CV_old_Mal_GP_1
-3	3	2e-6	0	...	0	#Wtlen_1_Mal
-3	4	3	3	...	0	#Wtlen_2_Mal

10.3.3 Natural Mortality Notes

The options for natural mortality have been expanded. In addition, M is now, in most options, calculated according to real age since the beginning of a cohort's birth season, rather than annual, integer age. So, if M varies by age, M will change by season and cohorts born in early seasons of the year will have different M than late born cohorts.

Lorenzen Natural Mortality

Lorenzen natural mortality is based on the concept that natural mortality varies over the life cycle of a fish, which is driven by physiological and ecological processes.

10.3.4 Growth Notes

When fish recruit at the real age of 0.0 at the beginning of their birth season, they have body size equal to the lower edge of the first population size bin. Previously, they recruited at a size equal to the lower edge of the smallest data size bin. The fish then grow linearly until they reach a real age equal to the input value "growth_age_for_L1" and have a size equal to the parameter value for L1. As they age further, they grow according the Bertalanffy growth equation. The growth curve is calibrated to go through the size L2 when they reach the age "Growth_age_for_L2".

If "Growth_age_for_L2" is set equal to 999, then the size L2 is used as Linf. If MGparm_def option ==1 (direct estimate, not offsets), then setting a male growth or natural mortality parameter value to 0.0 and not estimating it will cause SS to use the corresponding female parameter value for the males. This check is done on a parameter, by parameter basis and is probably most useful for setting male L1 equal to female L1, then letting males and females have separate K and Linf parameters.

Schnute growth function

The Schnute implementation of a 3-parameter growth function is invoked by entering 2 in the grow_type field. Then a fourth parameter is read after reading the von Bertalanffy K parameter. When this fourth parameter has a value of 1.0, it is equivalent to the standard von Bertalanffy growth curve. When this function was first introduced in SS, it required that A0 be set to 0.0.

Age-specific K

A new growth option, #3, has been introduced in V3.23. This option creates age-specific

K deviations for each age of a user-specified age range, with independent additive deviations for each age in the range and for each growth pattern / gender. Each of these deviations is entered as a full parameter line, so inherits all time-varying capabilities of full parameters. The lower end of this age range cannot extend younger than the specified age for which the first growth parameter applies. This is a beta model feature, so examine output closely to assure you are getting the size-at-age pattern you expect. Beware of using this option in a model with seasons within year because the K deviations are indexed solely by integer age according to birth year. There is no offset for birth season timing effects, nor is there any seasonal interpolation of the age-varying K.

10.3.5 Growth Patterns (morphs) and Sub-Morphs

The user specifies a number of growth patterns (usually just 1), a number of genders (usually 2), and a number of birth seasons. The collection of Bio_pattern x Gender x BirthSeas constitute the “morphs”. The number of sub-morphs per morph can be 1, 3, or 5. The fraction of recruits that are female is specified as an input value (not a parameter), and the fraction of recruits assigned to each sub-morph is custom-input or designated to be a normal approximation. When multiple sub-morphs are designated, an additional input is the ratio of between sub-morph to within sub-morph variability in size-at-age. This is used to partition the total growth variability. Growth parameters are read for each growth pattern x gender combination. For the sub-morphs, their size-at-age is calculated as a factor (determined from the between-within variability calculation) times the size-at-age of the central morph which is determined from the growth parameters for the growth pattern x gender.

10.3.6 Recruitment, Age, and Growth

Recruitment can occur in any season. In older versions of SS one value of spawning biomass was calculated annually at the beginning of one specified spawning season and this spawning biomass produces one annual total recruitment value and this annual recruitment was distributed among seasons, areas, and growth types according to other model parameters. SSv3.3 allows for the spawning biomass in a season to produce recruitment that may vary over the year based on the spawning biomass which associated with the area and growth types according to the model parameterization. These distribution parameters can be time-varying, so the fraction of the recruits that occur in a particular season can change from year to year. For the recruitment apportionment, the parameter values are the $\ln(\text{apportionment weight})$, so should have values ranging from about -4 to $+4$. The product of all apportionment weights is calculated for each pattern x area x season cell that has been designated to receive recruits in the recruitment design matrix. Then the apportionment weights are scaled to sum to 1.0 (within year, not within season) so that the total annual recruitment is distributed among the cells designated to receive recruitment.

In a seasonal model, all cohorts graduate to the age of 1 when they first reach January 1, even if the seasonal structure of the model has them being born in the fall. In general,

this means that SS operates under the assumption that all age data have been adjusted so that fish graduate to the next age on Jan 1. This can be problematic if the ageing structures deposit a ring at another time of year. Consequently, you may need to add or subtract a year to some of your age data to make it conform to the SS structure, or you may need to define the SS calendar year to start at the beginning of the season at which ring deposition occurs. Talk with your ageing lab about their criteria for seasonal ring deposition!

Seasonal recruitment is coded to work smoothly with growth. If the recruitment occurring in each season is assigned the same growth pattern, then each seasonal cohort's growth trajectory is simply shifted along the age/time axis. At the end of the year, the early born cohorts will be larger, but all are growing with the same growth parameters so all will converge in size as they approach their common Lmax.

Age 0.0 fish (at beginning of their birth season) are assigned a size equal to the lower edge of the first population size bin and they grow linearly until they reach the age A1. SS generates a warning if the first population length bin is greater than 10 cm as this seems an unreasonably large value for a larval fish. A1 is in terms of real age elapsed since birth. All fish advance to the next integer age on Jan 1, regardless of birth season. For example, consider a 2 season model with some recruitment in each season and with each season's recruits coming from the same GP. At the end of the first year, the early born fish will be larger but both of the seasonal cohorts will advance to an integer age of 1 on Jan 1 of the next year. The full growth curve is still calculated below A1, but the size-at-age used by SS is the linear replacement. Because the linear growth trajectory can never go negative, there is no need for the additive constant to the stddev (necessary for the growth model used in SS2 V1.x), but the option to add a constant has been retained in the model.

10.3.7 Cohort Growth Deviation

This parameter must be given a value of 1.0 and be given a negative phase so it is not estimated. Its importance is in serving as a base for blocks or annual devs, which may be estimated, around this base value of 1.0.

10.3.8 Movement Parameters

There are 2 movement parameters per area pair flagged in the movement design matrix as needing estimable movement parameters. For each, the first parameter is for the movement coefficient for young fish and the second is for old fish (with intermediate ramp calculated using the designated start age and end age. Parameter values are the $\ln(\text{movement coefficient})$. For fish that stay in their source area (e.g. move from area 1 to area 1 in season 1), they are given a movement coefficient of $\ln(1)=0$, but this default value is replaced if the stay movement is selected as needed parameters. For each source area, each movement coefficient is exponentiated and then they are scaled to sum to 1.0. At least one needs to not be estimated so that all others are estimated relative to it.

The movement model has been augmented to define movement parameters for each growth pattern. With this capability, it will be possible to have homing of a growth pattern

back to its natal area.

An added feature is the reading of `migr_firstage` immediately after reading the `do_migration` flag if the `do_migration` flag is positive. This value is a real number, not an integer, to allow for an in-year start to movement in a multi-season model. The value is the real age at the beginning of a season, even though movement does not occur until the end of the season. For example, in a setup with two 6-month seasons: a value of 0.5 will cause the age 0 fish to not move when they complete their first 6 month season of life, and then to move at the end of their second season because they start movement capability when they reach the age of 0.5 years (6 months).

A new feature added in v3.3 allows for a multi-season setup to have a growth pattern (GP) to have some fish recruit in different “birthseasons”. The movement parameters are now specific to GP x birthseason x actual season.

Future Need: augment the capability further to allow sex-specific movement, and also to allow some sort of mirroring so that genders and growth patterns can share the same movement parameters if desired.

The model will allow movement only between source-destination pairs that have an explicit movement definition. For fish that stay in an area, there are two options:

1. define an explicit movement pattern where the destination area is the same as the source area. This will allow you to control its parameters explicitly;
2. allow the model to create an implicit stay rate definition equivalent to setting the movement strength parameter to 0 for all ages.

For all explicit definitions requested, there must be 2 parameters included with the MG parameter section. As before, the age-specific movement strength is:

1. constant at P1 below minage, constant at P2 above maxage, and linearly interpolated for intermediate ages;
2. exponentiated so that a movement strength parameter value of 0 becomes 1.0;
3. for movement out of an area, the exponentiated value is multiplied by season duration;
4. for each source area, all movement rates are then summed and divided by this sum so that 100% of the fish are accounted for in the movement calculations;
5. it is best if at least one of the destinations for each source area has a predefined movement strength so that other destinations are estimated relative to the fixed value.

10.3.9 Recruitment Allocation and Movement Parameters

In a 2 season, 2 area, 2 growth pattern set-up, the recruitment distribution, cohort growth deviation, and movement parameters could be:

LO	HI	INIT	Prior Value	<other entries>	Block Type	Parameter Label
-4	4	0	1	...	0	#RecrDist_GP_1
-4	4	0	1	...	0	#RecrDist_GP_2
-4	4	0	1	...	0	#RecrDist_Area_1
-4	4	-4	1	...	0	#RecrDist_Area_2
-4	4	0	1	...	0	#RecrDist_Seas_1
-4	4	-4	1	...	0	#RecrDist_Seas_2
-4	4	0	1	...	0	#CohortGrowthDev
COND: Only if movement is defined						
-5	5	-4	1	...	0	#MoveParm_A_seas_1_GP_1from_1to2
-5	5	-4	1	...	0	#MoveParm_B_seas_1_GP_1from_1to2
-5	5	-4	1	...	0	#MoveParm_A_seas_1_GP_1from_2to1
-5	5	-4	1	...	0	#MoveParm_B_seas_1_GP_1from_2to1
-5	5	-4	1	...	0	#MoveParm_A_seas_1_GP_2from_1to2
-5	5	-4	1	...	0	#MoveParm_B_seas_1_GP_2from_1to2
-5	5	-4	1	...	0	#MoveParm_A_seas_1_GP_2from_2to1
-5	5	-4	1	...	0	#MoveParm_B_seas_1_GP_2from_2to1

Note:

- For the recruitment parameters, there must be a line for each season, area and GP. But only those seasons, areas, and GPs designated to receive recruits in the recruitment design matrix will have the parameter used in the recruitment distribution calculation.
- For both recruitment allocations and movement rates, SS processes the parameter values according to the following equation:

$$rate_i = \frac{e^{p_i}}{\sum_{j=1}^N e^{p_i}} \quad (3)$$

- Set the value of one of these parameters to 0.0 and not estimate it so that other areas will be estimated relative to that base area.
- Be sure that estimated parameters are given a min-max of something like -5 and 5 so they have a good range relative to the base area.
- In order to get a different distribution of recruitments in different years, you will need to make at least one of the recruitment distribution parameters time-varying.

10.3.10 Catch Multiplier

This parameter line is only included in the control file if the catch multiplier field in the data file is set to 1. A single value may be fixed or estimated where:

$$C_{obs} = C_{exp} * c_{mult} \quad (4)$$

where C_{exp} is the expected catch and c_{mult} is the catch multiplier. It has year-specific, not season-specific, time-varying capabilities. In the catch likelihood calculation, expected catch is multiplied by the catch multiplier by year and fishery before being compared to the observed retained catch, so value of 1.1 means that the observed catch has overestimated actual catch by 10%.

10.3.11 Ageing Error Parameters

These 7 parameters are only included in the control file if one of the ageing error definitions in the data file has requested this feature (by putting a negative value for the ageing error of the age zero fish of one ageing error definition. Although these are input with full parameter lines (with inherent time-varying capability), the time-varying updating has not been implemented.

Until a more complete description and examples are developed, here is the code for creation of the vectors of mean age' and stddev of age':

INSERT CODE HERE

The 7 parameters are:

- age at which the estimated pattern begins (just linear below this age). This is “start age”
- bias at start age (as additive offset from unbiased age')
- bias at maxage (as additive offset from unbiased age')
- power fxn coefficient for interpolating between those 2 values (value of 0.0 produces linear interpolation in the bias)
- stdev at age
- stdev at max age
- power fxn coefficient for interpolating between those 2 values

10.3.12 Time-Varying Biology Parameters

Any of the parameters defined above can be made time-varying through linkage to an environmental data series, through time blocks, or by setting up annual deviations. The options for making biology and selectivity parameters change over time is detailed in the section labeled Time-Varying Parameters. After reading the biology parameters above, which will include possible instructions to create environmental link, blocks, or dev vectors, then read the following section. Note that all inputs in this section are conditional (COND) on entries in the biology parameter section. So if no biology parameters invoke any time-varying properties, this section is left blank (or completely commented out with #) except for the line with the input of seasonal factors.

When time-varying growth is used, there are some additional considerations to be aware of:

- Growth deviations propagate into the forecast. The user can select which growth parameters get used during the forecast by setting the end year of the last block. If the last block ends in the model's endyr, then the growth parameters in effect during the forecast will revert to the “no-block” baseline level. By setting the end year of the last block to end year (endyr) + 1, the model will continue the last block's growth parameter levels throughout the forecast.
- The equilibrium benchmark quantities (MSY, F40%, etc.) previously used end year (endyr) body size-at-age, which is a disequilibrium vector. There is a capability to specify a range of years over which to average the size-at-age used in the benchmark calculations.
- An addition issue occurred in versions prior to 3.20. Its description is retained here, but it was resolved with the growth code modification for version 3.20.
 - Issue for versions prior to 3.20: When the growth reference ages have $A1 > 0$ and $A2 < 999$, the effect of time-varying K has a non-intuitive aspect. This occurs because the virtual size at age 0.0 and the actual L_{inf} are calculated annually from the current $L1$, $L2$ and K parameters. Because these calculated quantities are outside the age range $A1$, $A2$, a reduction in K will cause an increase in the calculated size-at-age 0.0 that year. So there is a ripple effect as the block's growth parameters affect the young cohorts in existence at the time of the change. The workaround for this is to set $A1=0$ and $A2=999$. However, this may create another incompatibility because the size-at-age 0.0 cannot be allowed to be negative and should not be allowed to be less than the size of the first population length bin. Therefore, previous use of $A1=2$ might have implied a virtual size at age 0.0 that was negative (which is ok), but setting $A1=0$ does not allow the size at age= $A1$ to be negative.

Control file continued:

Value	Description
COND:	If any MG parameters use environmental linkage, then read next factor
0	0: Do not use custom environmental linkage setup, read just one parameter line 1: Use custom environmental linkage, so read one parameter line for each MG parameter that uses linkage
<short parameter line(s)>	Read 0, 1 or many short parameter lines as necessary
COND:	If any MG parameters use blocks then read next factor
0	0: Do not use custom block setup, read just one parameter line 1: Use custom block setup, so read one parameter line for each MG parameter that uses blocks
<short parameter line(s)>	Read 0, 1 or many short parameter lines as necessary
#Seasonality for selected biology parameters (not a conditional input)	
0 0 0 0 0 0 0 0 0 0	Read 10 integers to specify which biology parameters have seasonality: femwtlen1, femwtlen2, mat1, mat2, fec1, fec2, malewtlen1, malewtlen2, L1, K. Reading a positive value selects that factor for seasonality (<i>click here for more information</i>)
COND:	If any factors have seasonality, then read N seasons parameters that define the seasonal offsets from the base parameter value.
<short parameter line(s)>	Read N seasons short parameter lines for each factor selected for seasonality. The parameter values define an exponential offset from the base parameter value.
COND:	If any MG parameters use annual deviations, then read the phase next.
-1	All MG parameters using annual deviations will have the deviations begin estimation in this phase.

10.3.13 Notes on Seasonal Biology Parameters

SS_v3 begins to introduce seasonal effects on selected biology parameters. Currently, seasonal option is only available for the four wt-len parameters and for the growth K. Seasonality is not needed for the maturity and fecundity parameters because spawning is only defined to occur in one season. Seasonal L1 may be implemented at a later date. The seasonal parameter values adjust the base parameter value for that season.

$$P' = P * \exp(seas_value) \quad (5)$$

10.3.14 Empirical Weight-at-Age (wtatage.ss)

With version 3.04, SS adds the capability to read empirical body weight at age for the population and each fleet, in lieu of generating these weights internally from the growth parameters, weight-at-length, and size-selectivity. Selection of this option is done by setting Maturity_Option = 5. The values are read from a separate file named, wtatage.ss. This file is only required to exist if this option is selected. See section 8.1 for additional information on file formatting for empirical weight-at-age.

10.3.15 Spawner-Recruitment

The spawner-recruitment section starts by specification of the functional relationship. The number of parameters needed by each relationship is stored internally (same approach as is used for the number of parameters for each selectivity relationship).

Control file continued:

Value	Description
3	Spawner- Recruitment Relationship
	The options are: 1: null 2: Ricker (2 parameters) 3: standard Beverton-Holt (2 parameters) 4: ignore steepness and no bias adjustment. Use this in conjunction with very low emphasis on recruitment deviations to get CAGEAN-like unconstrained recruitment estimates. (2 parameters, but only uses the first one.) 5: Hockey stick (3 parameters) for $\ln(R_0)$, fraction of virgin SSB at which inflection occurs, and the R level at SSB=0.0. 6: Beverton-Holt with flat-top beyond Bzero (2 parameters) 7: Survivorship function (3 parameters). Suitable for sharks and low fecundity stocks to assure recruits are \leq pop production 8: Sheperd (3 parameters)

Value	Description
Read the required number of short parameter set-up lines (ex. LO HI INIT PRIOR PR_Type SD PHASE). These parameters are:	
log(R0)	Log of virgin recruitment level
steepness	Steepness of S-R, bound by 0.2 and 1.0 for the Beverton-Holt
COND:	If SRR = 5, 7, or 8
3rd Parameter	Optional depending on which SRR function is used
sigma-R	std.dev. of log recruitment; This parameter has two related roles. It penalizes deviations from the spawner-recruitment curve, and it defines the offset between the arithmetic mean spawner-recruitment curve (as calculated from log(R0) and steepness) and the expected geometric mean (which is the basis from which the deviations are calculated. Thus the value of sigmaR must be selected to approximate the true average recruitment deviation.
env-link	environmental linkage coefficient. The recruitment parameters are short parameters, so cannot have the generic block or environmental link options. Instead, this dedicated env-link is provided. It is used to create a multiplicative adjustment to the target parameter, so $P_{y'} = P * exp(env/link * env/ata_y)$. An alternative that provides an additive link is under development.
log(R1)	Offset for initial equilibrium recruitment to virgin recruitment.
AutoCorrelation	Autocorrelation in recruitment

Then read additional spawner-recruitment conditions:

0	SR_env_link	This is the index of the environmental variable that will be used as the basis for adjustment of SR expectations. This works for both the forecast period and for the initial equilibrium (by entering a value for the environmental variable one year before the start of the time series).
3	SR_env_target	This factor determines what aspect of spawner-recruitment is affected by the environmental variable. The options are: 1: annual deviations 2: R0 3: steepness

Value		Description
		<p>If the application needs to compare the environment to annual recruitment deviations, then the preferred option is to transform the environmental variable into an age 0 pre-recruit survey and enter these as a survey with expected value based on selectivity option #31. Use of SR_env_target=1 is discouraged because it interacts with the level of residual recruitment variability and there is no implementation of a bias correction for the variability in recruitment caused by the environmental variable. If the application is investigating regime shifts, then enter an environmental variable with a time series of zeros and ones to describe the regime periods, then use SR_env_target of 2 or 3 to adjust the expected level of recruitment according to the regime variable. Note that MSY related quantities will be calculated with the regime in the zero state only. However, the forecast can be responsive to designated regime levels.</p>
1	Do_Recr_Dev	<p>This selects the way in which recruitment deviations are coded:</p> <p>0: none (so all recruitments come from S-R curve)</p> <p>1: dev vector (previously the only option). Here the deviations are encoded as a dev_vector, so ADMB enforces a sum-to-zero constraint.</p> <p>2: simple deviations. Here the deviations do not have an explicit constraint to sum to zero, although they still should end up having close to a zero sum. The difference in model performance between options (1) and (2) has not been fully explored to date.</p>
1971	Main recr devs begin year	<p>If begin year is less than the model start year, then the early deviations are used to modify the initial age composition. However, if set to be more than Nages before start year, it is changed to equal Nages before start year.</p>
1999	Main recr devs end year	<p>If recr devs end year is later than retro year, it is reset to equal retro year.</p>
3	Main recr dev phase	
1	Advanced Options	<p>0: Use default values for advanced options</p> <p>1: Read values for the 11 advanced options</p>
COND = 1 Beginning of advanced options		
	1950	Early Recruitment Deviation Start Year:

Value	Description
	0: skip (default)
	+year: absolute year (must be less than begin year of main recr devs)
	-integer: set relative to main recr dev start year
	NOTE: because this is a dev vector, it should be long enough so that recr devs for individual years are not unduly constrained.
6	Early Recruitment Deviation Phase: Users may want to set to a late phase if there is not much early data; Default: -4
0	Forecast Recruitment Phase: Forecast recruitment deviations always begin in the first year after the end of the main recruitment deviations. Setting their phase to 0 causes their phase to be set to max lambda phase +1 (so that they become active after rest of parameters have converged.). However, it is possible here to set an earlier phase for their estimation, or to set a negative phase to keep the forecast recruitment devs at a constant level. Default: 0
1	Forecast Recruitment Deviations Lambda: This lambda is for the logL of the forecast recruitment devs that occur before endyr+1. Use a larger value here if solitary, noisy data at end of time series cause unruly recr dev estimation. Default: 1.0
1956	Last Year With No Bias Adjustment
1970	First Year With Full Bias Adjustment
2001	Last Year With Full Bias Adjustment
2002	First Recent Year With No Bias Adjustment

Value	Description
	These four entries control how the bias adjustment is phased in and then phased back out when the model is searching for the maximum logL. Bias adjustment is automatically turned off when in MCMC mode. For intervening years between the first and second years in this list, the amount of bias adjustment that will be applied is linearly phased in. The first year with full bias adjustment should be a few years into the data-rich period so that SS will apply the full bias-correction only to those recruitment deviations that have enough data to inform the model about the full range of recruitment variability. See the recruitment advisory for more information. Defaults for the four year values: Start year – 1000, Start year – Nages, Main recr dev final year, End year +1.
0.85	Max Bias Adjustment: Value for the maximum bias adjustment during the MLE mode. Use value of 1.0 for compatibility with previous versions of SS. All estimated recrdevs, even those within a ramped era, switch to maxbias=1.0 during MCMC.
0	Period For Recruitment Cycles: Use this when SS is configured to model seasons as years and there is a need to impose a periodicity to the expected recruitment level. If value is >0, then read that number of full parameter lines below define the recruitment cycle
-5	Minimum Recruitment Deviation: Min value for recruitment deviation. Default: -5
5	Maximum Recruitment Deviation: Max value for recruitment deviation. Default: 5
2	Number of Explicit Recruitment Deviations to Read: 0: Do not read any recruitment deviations; Integer: read this number of recruitment deviations; Default: 0
END OF ADVANCED OPTIONS	
COND = Enter N full parameter lines below if N recruitment cycles is > 0	
<parameter line>	Full parameter line for each of the N periods of recruitment cycle
COND = If N explicit recruitment deviations is > 0, then enter N lines below	
1977 3.0	Enter Year and Deviation

Value	Description
1984 3.0	Two example recruitment deviations being read. NOTE: SS will rescale the entire vector of recrdevs after reading these deviations, so by reading two positive values, all other recrdevs will be scaled to a small negative value to achieve a sum to zero condition before starting model estimation

10.3.16 Spawner-Recruitment Function

The number of age-0 fish is related to spawning biomass according to a stock-recruitment relationship. SS has the option of the Beverton-Holt, Ricker, Hockey-Stick, and a survival-based stock recruitment relationship.

Beverton-Holt

The Beverton-Holt Stock Recruitment curve is calculated as:

$$INSETEQUATIONHERE \quad (6)$$

where $R0$ is the unfished equilibrium recruitment, $SB0$ is the unfished equilibrium spawning biomass (corresponding to $R0$), SBy is the spawning biomass at the start of the spawning season during year y , h is the steepness parameter, by is the bias adjustment fraction applied during year y , σ is the standard deviation among recruitment deviations in log space, and ϵ_y is the lognormal recruitment deviation for year y . The bias-adjustment factor (Methot and Taylor 2011) ensures unbiased estimation of mean recruitment even during data-poor eras in which the maximum likelihood estimate of the is near 0.0.

Ricker

The Ricker Stock Recruitment curve is calculated as:

$$INSETEQUATIONHERE \quad (7)$$

Hockey-Stick

The hockey-stick recruitment curve is calculated as:

$$INSETEQUATIONHERE \quad (8)$$

where R_{min} is the minimum recruitment level predicted at a spawning size of zero and is set by the user in the control file, and h is defined as the fraction of $SB0$ below which recruitment declines linearly.

Survivorship

Survival-based recruitment (Taylor et al. 2012) is constrained so that the recruitment rate cannot exceed fecundity:

$$INSERTEQUATIONHERE \quad (9)$$

where z_0 (P) is the negative log of the pre-recruit mortality rate at unfished equilibrium, z_{min} is the limit of the pre-recruit mortality as relative spawning biomass approaches 0, parameterized as a function of z_{frac} (P) (which represents the reduction in mortality as a fraction of z_0), and ρ (P) is a parameter controlling the shape of density-dependent relationship between relative spawning biomass and pre-recruit survival. The steepness (h) of the spawner-recruit curve (defined as recruitment relative to R_0 at a spawning depletion level of 0.2) is:

INSERT EQUATION

This 3-parameter function was created for use with low fecundity species, but its use of 3-parameters provides a flexibility comparable to the 3-parameter Shepherd function. This survival based spawner-recruitment function defines survival from the egg (e.g. hatched pups) to the recruits stage to be a declining function of the initial number of pups produced (Taylor et al. 2012).

- Start with the parameter, $\ln(R_0)$, which is the \ln (mean number of recruits) that enter the population in unfished conditions.
- These recruits over their lifetime will produce some total number of eggs (pups), termed $Pups_0$, which can be calculated from natural mortality, which defines the numbers at age in the adult population, and fecundity at age.
- Because the unfished condition is considered to be a stable equilibrium, we can calculate $PPR_0 = Pups_0/R_0$ and its inverse which is survivorship, which we will define in logarithmic space. So, $Z_0 = \ln(R_0/Pups_0)$. Note that there is no explicit time over which this Z acts. Such an explicit time (e.g. the age at recruitment) may be implemented in the future. For now, this means that the Z is really a $Z \cdot \Delta t$.
- So, Z_0 is the survival when the population is at carrying capacity. On the other extreme, the maximum survival is 1.0, so the maximum Z is 0.0.
- The parameter, S_frac , defines the level of Z when the population approaches an abundance of 0.0. This has values bounded by 0.0 and 1.0 and creates a Z_max which is between Z_0 and 0.0. $Z_max = Z_0 + S_frac \cdot (0.0 - Z_0)$
- Then for the current level of pup production (e.g. total population fecundity, aka “spawning biomass”):
 - $Z_y = (1 - (Pupy/Pups_0)Beta) \cdot (Z_max - Z_0) + Z_0$
 - So $R_y = Pupy \cdot \exp(-Z_y)$

- Where beta is the third parameter and which logically has values between about 0.4 for a left-shifted spawner-recruitment curve, and 3.0 for a right-shifted curve.
- With the other spawner-recruitment relationships, the mean level of recruits, R_y , serves as the base against which environmental effects and annual lognormal deviations are applied. However, in a survival context, it is possible that a large positive deviation on recruitments could imply survival greater than 1.0, so an alternative approach is needed for this survival approach. Here, the lognormal deviations are applied to Z and the resultant S is constrained to not exceed 1.0.
- In SS, it is also necessary to be able to calculate the equilibrium level of spawning biomass (pup production) and recruitment for a given level of spawning biomass per recruit (pups per recruit), PPR.
 - $Pups_equil = Pups_0 * (1 - (LN(1/PPR) - Z_0) / (Z_max - Z_0))^{(1/Beta)}$
 - Then, $R_equil = Pups_equil * exp(-(1 - (Pups_equil/Pups_0)^{Beta}) * (Z_max - Z_0) + Z_0)$
- Some example plots for various levels of S_frac and beta are shown below:

INSERT IMAGE