

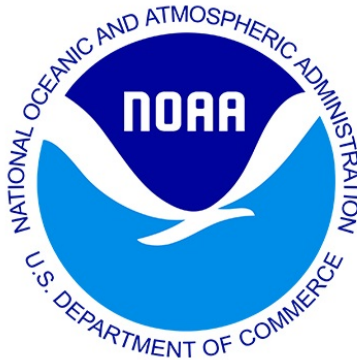
# **Stock Synthesis User Manual**

## **Version 3.30.14**

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# Contents

<b>Introduction</b>	<b>1</b>
<b>New Features Available in SS Version 3.30</b>	<b>2</b>
SS v.3.24 Issues Detected . . . . .	6
<b>File Organization</b>	<b>7</b>
Input Files . . . . .	7
Output Files . . . . .	7
Auxiliary Files . . . . .	8
<b>Starting SS</b>	<b>9</b>
<b>Converting Files from SS v.3.24</b>	<b>9</b>
<b>Starter File</b>	<b>10</b>
Jitter . . . . .	18
<b>Forecast File</b>	<b>19</b>
Benchmark Calculations . . . . .	27
Forecast Recruitment Adjustment . . . . .	29
<b>Data File</b>	<b>30</b>
Overview of Data File . . . . .	30
Units of Measure . . . . .	31
Time Units . . . . .	31
Seasons . . . . .	32
Subseasons and Timing of Events . . . . .	33
Terminology . . . . .	34
Model Dimensions . . . . .	34
Fleet Definitions . . . . .	35
Optional Bycatch Fleets . . . . .	37
Catch . . . . .	38
Bycatch . . . . .	39
Indices . . . . .	40
Discard . . . . .	43
Mean Body Weight or Length . . . . .	45
Population Length Bins . . . . .	47
Dirichlet Parameter Number and Effective Sample Sizes . . . . .	50
Length Composition Data . . . . .	51
Age Composition Option . . . . .	53
Age Composition Bins . . . . .	53
Ageing Error . . . . .	53

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Age Composition Specification . . . . .	55
Conditional Age-at-Length . . . . .	56
Mean Length or Body Weight-at-Age . . . . .	57
Environmental Data . . . . .	58
Generalized Size Composition Data . . . . .	59
Tag-Recapture Data . . . . .	61
Stock Composition Data . . . . .	63
Selectivity Empirical Data (future feature) . . . . .	64
Excluding Data . . . . .	64
Data Super-Periods . . . . .	64
<b>Control File . . . . .</b>	<b>66</b>
Overview of Control File . . . . .	66
Parameter Line Elements . . . . .	68
Terminology . . . . .	70
Beginning of Control File Inputs . . . . .	70
Empirical Weight-at-Age . . . . .	72
Recruitment Timing and Distribution . . . . .	72
Movement . . . . .	75
Time Blocks and Time-varying Parameter Controls . . . . .	77
Auto-generation . . . . .	78
Biology . . . . .	79
Natural Mortality . . . . .	79
Growth . . . . .	80
Maturity-Fecundity . . . . .	83
Hermaphroditism . . . . .	84
Parameter offset method . . . . .	85
Catch Multiplier . . . . .	86
Ageing Error Parameters . . . . .	86
Sex ratio . . . . .	87
Read Biology Parameters . . . . .	87
Time-Varying Biology Parameters . . . . .	91
Seasonal Biology Parameters . . . . .	92
Spawner-Recruitment . . . . .	93
Spawner-Recruitment Function . . . . .	100
Recruitment Eras . . . . .	104
Recruitment Likelihood with Bias Adjustment . . . . .	104
Recruitment Autocorrelation . . . . .	106
Recruitment Cycle . . . . .	106
Initial Age Composition . . . . .	106
Fishing Mortality Method . . . . .	107
Initial Fishing Mortality . . . . .	108
Catchability . . . . .	109

Mirrored Q with offset . . . . .	111
Float Q . . . . .	111
Q Conversion Issues Between SS v.3.24 and v.3.30 . . . . .	112
Selectivity and Discard . . . . .	113
Reading the Selectivity and Retention Parameters . . . . .	114
Selectivity Patterns . . . . .	116
Selectivity Pattern Details . . . . .	118
Retention . . . . .	130
Discard Mortality . . . . .	131
Sex-Specific Selectivity . . . . .	131
Dirichlet Multinomial Error for Data Weighting . . . . .	133
Time-varying Options . . . . .	133
Two-Dimensional Auto-Regressive Selectivity . . . . .	134
Tag Recapture Parameters . . . . .	136
Variance Adjustment Factors . . . . .	138
Lambdas (Emphasis Factors) . . . . .	140
Controls for Variance of Derived Quantities . . . . .	141
Using Time-Varying Parameters . . . . .	143
Parameter Priors . . . . .	147
<b>Optional Inputs</b>	<b>151</b>
Empirical Weight-at-Age (wtatage.ss) . . . . .	151
runnumber.ss . . . . .	153
profilevalues.ss . . . . .	153
<b>Likelihood components</b>	<b>154</b>
<b>Running SS</b>	<b>155</b>
Command Line Interface . . . . .	155
Example of DOS batch input file . . . . .	156
Simple Batch . . . . .	157
Complicated Batch . . . . .	157
Running Parameter Profiles . . . . .	158
Re-Starting a Run . . . . .	159
Debugging Tips . . . . .	159
Keyboard Tips . . . . .	160
Running MCMC . . . . .	160
<b>Output Files</b>	<b>161</b>
Standard ADMB output files . . . . .	161
SS Summary . . . . .	162
SIS table . . . . .	162
Derived Quantities . . . . .	162

Virgin Spawning Biomass (B0) vs Unfished Spawning Biomass . . . . .	162
Metric for Fishing Mortality . . . . .	163
Equilibrium SPR . . . . .	163
F std . . . . .	164
F-at-Age . . . . .	164
MSY and other Benchmark Items . . . . .	165
Brief cumulative output . . . . .	166
Bootstrap Data Files . . . . .	166
Forecast and Reference Points . . . . .	166
Main Output File, Report.sso . . . . .	167
<b>Using R To View Model Output (r4ss)</b>	<b>173</b>
<b>Special Set-ups</b>	<b>177</b>
Continuous seasonal recruitment . . . . .	177
<b>Change Log</b>	<b>178</b>
<b>Bibliography</b>	<b>179</b>
<b>Appendix A: Recruitment Variability and Bias Correction</b>	<b>180</b>
Issues with Including Environmental Effects . . . . .	185
Initial Age Composition . . . . .	186
<b>Appendix B: Data Weighting</b>	<b>186</b>
Applying the methods . . . . .	187
McAllister-Ianelli . . . . .	187
Francis . . . . .	188
Dirichlet-Multinomial . . . . .	189
<b>Appendix C: Forecast Module</b>	<b>191</b>
Introduction . . . . .	191
Multiple Pass Forecast . . . . .	192
Example Effects on Correlations . . . . .	194
Future Work . . . . .	195
<b>Appendix D: Code Examples</b>	<b>196</b>
Ageing Error Estimation . . . . .	196
Survival Based SRR Code . . . . .	197
Random Walk Selectivity: Pattern 17 . . . . .	198
Cubic Spline Selectivity . . . . .	200
Deviation Link . . . . .	201

# Introduction

Fish population (aka "stock") assessment models determine the impact of past fishing on the historical and current abundance of the population, evaluate sustainable rates of removals (catch), and project future levels of catch reflecting one or more risk-averse catch rules. These catch rules are codified in regional Fishery Management Plans according to requirements of the Sustainable Fisheries Act. In the U.S., approximately 500 federally managed fish and shellfish populations are managed under approximately 50 Fishery Management Plans. About 200 of these populations are assessed each year, based on a prioritized schedule for their current status. Despite this, many minor species have never been quantitatively assessed. Although the pace is slower than that for weather forecasting, fish stock assessments are operational models for fisheries management.

Assessment models typically assimilate annual catches, data on fish abundance from diverse surveys and fishery sources, and biological information regarding fish body size and proportions at age. A suite of models is available depending on the degree of data availability and unique characteristics of the fish population or its fishery. Where feasible, environmental time series are used as indicators of changes in population or observation processes, especially to improve the accuracy of the projections of abundance and sustainable catch into the future. Such linkages are based principally on correlations given the challenge of conducting field observations on an appropriate scale. The frontier of model development is in the rapid estimation of parameters to include random temporal effects, in the simultaneous modeling of a suite of interacting species, and in the explicit treatment of the spatial distribution of the population.

Assessment models are loosely coupled to other models. For example, an ocean-temperature or circulation model or benthic-habitat map may be directly included in the pre-processing of the fish abundance survey. A time series of a derived ocean factor, like the North Atlantic Oscillation, can be included as an indicator of a change in a population process. Output of a multi-decadal time series of derived fish abundance can be an input to ecosystem and economic models to better understand cumulative impacts and benefits.

Stock Synthesis (SS) is an age- and size-structured assessment model in the class of models termed integrated analysis models. SS has a population sub-model that simulates a stock's growth, maturity, fecundity, recruitment, movement, and mortality processes, an observation sub-model estimates expected values for various types of data, a statistical sub-model characterizes the data's goodness of fit and obtains best-fitting parameters with associated variance, and a forecast sub-model projects needed management quantities. SS outputs the quantities, with confidence intervals, needed to implement risk-averse fishery control rules. The model is coded in C++ with parameter estimation enabled by automatic differentiation ([www.admb-project.org](http://www.admb-project.org)). Windows, Linux, and iOS versions are available. Output processing and associated tools are in R, and a graphical interface is in QT. SS is available from NOAA's VLAB. The rich feature set in SS allows it to be configured for a wide range of situations. SS has become the basis for a large fraction of U.S. assessments and many other assessments around the world.

This manual provides a guide for using SS. The guide contains a description of the input and output files and usage instructions. An overview and technical description of the model itself is in Methot and Wetzel (2013). However, SS has continued to evolve and grow since the publication in 2013, with this manual reflecting the most up to date information regarding SS. The model and a graphical user interface are available from the NOAA VLAB at [vlab.ncep.noaa.gov/group/stock-synthesis/home](http://vlab.ncep.noaa.gov/group/stock-synthesis/home). The VLAB site also provides a user forum for posting questions and for accessing various additional materials. An output processor package, `r4ss`, in R is available for download from CRAN or GitHub. Additional information about the package can be located at [github.com/r4ss/r4ss](https://github.com/r4ss/r4ss).

Additional guidance for new users is available from the NOAA VLAB at [vlab.ncep.noaa.gov/group/stock-synthesis/document-library](http://vlab.ncep.noaa.gov/group/stock-synthesis/document-library). The "Begin Here - Introduction to Stock Synthesis" folder located in the Document Library contains step-by-step guidance for running Stock Synthesis.

## New Features Available in SS Version 3.30

Stock Synthesis version v.3.30 was designed specifically to provide more precise control in modeling temporal changes in biology, expected values for data, and for recruitment. In addition, a large number of new features that make substantial changes to the input formats have been introduced. Two executables of SS are provided. One, `ss_trans.exe`, will read SS v.3.24 input files and produce SS v.3.30 formatted versions of those input files. Nearly every feature in SS v.3.24 can be converted by this program. The other executable, `ss.exe`, is the primary new assessment tool. Additional information on each new feature is available by clicking on the item.

Category	Item	Description
General	<a href="#">Generic Fleets</a>	Fleet specification section of data file has substantially changed and now includes specific fleet type; fishery fleets, bycatch fleets, and surveys which can be specified in any order.
	<a href="#">List-oriented inputs</a>	Older versions of SS (3.24 and earlier) required users to specify the number of items to be read, now SS can determine the number of lines to read through the application of a terminator line using -9999 in first field of the read vector.
	<a href="#">Internal sub-seasons</a>	SS v.3.24 inherently has 2 subseasons within each season (begin and middle) at which the age-length-key is calculated; now user specifies an even number of sub-seasons to use (2 to many).

Category	Item	Description
	<a href="#">Observation Timing</a>	Timing of observations now is input as year and month (e.g., April 15 is 4.5). The age-length-key used for each observation is calculated to the nearest sub-season month. Old "survey_timing" replaced by the month specific inputs. Season is calculated at runtime from the input month and the input season durations.
	<a href="#">Speed</a>	Smarter at when to re-calculate the age-length-key; trims tails of size-at-age so calculations avoid many inconsequential cells of the age-length matrix. Age-length-key tail compression is specified in the starter file.
	<a href="#">Converter</a>	Special version of SS, ss_trans.exe, will read files in SS v.3.24 format and write *.ss_new files in SS v.3.30 format. This is the advised method for converting previous version files, but always do a side-by-side comparison.
	<a href="#">Empirical Weight-at-Age</a>	Implementing empirical weight-at-age is now specified separately in the control file rather than under the maturity options.
	<a href="#">Prior Type</a>	Change in the prior numbering for parameters. Now, 0 indicates no prior, and 6 indicates a normal distribution prior.
Fishery and Catch	<a href="#">Catch multiplier</a>	Each fishing fleet's catch can now have a catchability (Q) that is a parameter in the mortality-growth parameter section.
	<a href="#">Catch input</a>	Catch input now as list: year, season, fleet, amount, standard error.
	<a href="#">Observations</a>	Fishery composition observations can be related to season long catch-at-age, or to a month-specific timing.
	<a href="#">Retention</a>	Option for dome-shaped retention function and for age-based retention.
Selectivity	<a href="#">Scaling Options</a>	New non-parametric selectivity types that are scaled by the raw values at particular ages, rather than the max age.
	<a href="#">Two-Dimensional Autoregressive Selectivity</a>	Implementation of two-dimensional autoregressive selectivity implemented in SS v.3.30.10.



Category	Item	Description
Survey	Special Survey Types	Special selectivity options (type 30 or >) are no longer specified within the control file. Specifying the use of one of these selectivity types is now done within the data file by selecting the survey "units".
	Link functions	Q <sub>power</sub> is now one of several, and growing, set of link functions for catchability.
	Catchability setup reorganization	Major reorganization of catchability (Q) setup, including the link specification.
	Q as a parameter	Each survey now must have a Q parameter and its value still can float (as old option 5).
Recruitment	Shepherd SRR	The traditional 3-parameter Shepherd stock-recruitment curve is now an option.
	Shepherd SRR re-parameterization	A re-parameterized 3-parameter Shepherd stock-recruitment curve, distinct from the traditional parameterization, is now an option in SS v.3.30.11 and higher.
	Ricker SRR re-parameterization	A 3-parameter Ricker stock-recruitment curve is now an option in SS v.3.30.11 and higher.
	Recruitment timing	Replace "birthseason" with "settlement event" that has explicit timing offset from spawning. Month of spawning and each settlement event must be specified and need not be at beginning of a season.
Benchmark	Global MSY	Global MSY based on knife-edged age selection; also do calculation with single age selection. The global MSY value will automatically be included in the report file.
	Mean recruitment distribution	In multi-area model, can now specify range of years to use for the average recruitment distribution for forecasting. This feature is not yet implemented.
Forecast	Process error	Propagate random walk in mortality growth parameters, catchability, and selectivity into forecast. Specifying the end year for process error in the forecast period will implement this option. This option has only been partial implemented at this junction and will be completed in later versions.

Category	Item	Description
Biology	<a href="#">Parameter order</a>	Mortality growth parameters now have maturity, fecundity, sex ratio, and weight-length by growth pattern.
	<a href="#">Sex ratio</a>	Change sex ratio at birth from a constant to a morph-specific mortality growth parameter. This feature was not correctly implemented in SS v.3.30 earlier than v.3.30.12.
	<a href="#">Growth cessation</a>	New growth option which allows for growth cessation, implemented in SS v.3.30.13.
Statistical	<a href="#">Input variance adjuster</a>	Added variance adjustment factor for generalized size comp.
	Deviation vectors	Variance of deviation vectors is now specified with 2 parameters for standard error and auto-correlation (rho), so can be estimated.
	<a href="#">Dirichlet multinomial</a>	Dirichlet multinomial now a fleet-specific option; takes one parameter per fleet.
Parameters	<a href="#">Parameter order</a>	The prior standard deviation column for all parameter lines has been moved before the prior type column. This modification improves formatting output between integer and decimal inputs.
	Density dependence	Beginning of year summary biomass and the recruitment deviation parameters are mapped to the "environmental" matrix so that parameters can be density-dependent based on environmental factors.
	<a href="#">Re-order</a>	Pay attention to the new order of the time-varying adjustments to parameters (block/trend, then environmental, then deviations).
	<a href="#">Time-varying parameters</a>	Long parameter lines for spawner-recruit relationship (SRR), catchability (Q), and tag parameters and complete re-vamp of the way that time-varying parameters are implemented for SRR and Q. Now shares same internal code as mortality-growth and selectivity parameters for time-varying capabilities.

Category	Item	Description
Software version control	Version numbering	The implementation of as new version control has changed how executable versions will be specified. The executable releases are now named SS3.3x.xx.xx representing, in order; major features, minor features, and code fixes.

## SS v.3.24 Issues Detected

The process of updating and adding new features within SS v.3.30 exposed several issues with the previous version that have been corrected:

1. Recruitment timing in multi-season models: When spawning occurred in a late season one year and recruits occurred at beginning of a season the next year, the recruits were starting at age-0, which was illogical. SS v.3.30 corrects this so that recruits are age-0 only if recruiting at or between the time of spawning and the end of the year, and recruits after January 1st start at age-0. A manual option in the control file allows users to attempt to replicate the SS v.3.24 protocol.
2. Lorenzen  $M$  and time-varying growth interaction: There needs to be a revision to SS v.3.30 so that growth can be updated each season prior to calculating Lorenzen  $M$ .
3. Length at maximum age: SS v.3.24 intended to decay numbers at the maximum length over-time at  $M + F$  decreasing the abundance of fish implicitly older than the maximum age (agemax). However, this decay was only implemented in years for which time-varying growth was updated.
4. SS v.3.24 had a lower bound of 1 when adjusting annual sample size (Nsamp) downward for composition data (length and age). The variance adjustment factors specified in the control file are multiplied across all annual sample size values for each data source (fleet and composition type). The issue with the lower bound of 1 resulted in sample size adjustment not being constant across small and large sample size years, possibly resulting in smaller samples have higher impact than may be desired. SS v3.30 has reduced this lower bound to a value of 0.001 but has retained user control over this value within the data file ("minsamplesize" column in the Composition Data Structure matrix at the top of the length and age data sections) to allow comparison with older model versions.

# File Organization

## 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 (required)
3. control file: file containing set-up for the parameters (required)
4. forecast.ss: file containing specifications for reference points and forecasts (required)
5. ss.par: previously created parameter file that can be read to overwrite the initial parameter values in the control file (optional)
6. wtatage.ss: file containing empirical input of body weight by fleet and population and empirical fecundity-at-age (optional)
7. runnumber.ss: file containing a single number used as run number in output to CumReport.sso and in the processing of profilevalues.ss (optional)
8. profilevalues.ss: file contain special conditions for batch file processing (optional)

## Output Files

1. data.ss\_new: Contains a user-specified number of datafiles, generated through a parametric bootstrap procedure, and written sequentially to this file.
2. control.ss\_new: Updated version of the control file with final parameter values replacing the initial parameter values.
3. starter.ss\_new: New version of the starter file with annotations.
4. Forecast.ss\_new: New version of the forecast file with annotations.
5. warning.sso: This file contains a list of warnings generated during program execution.
6. 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.

7. Report.sso: This file is the primary report file.
8. ss\_summary.sso: Output file that contains all the likelihood components, parameters, derived quantities, total biomass, summary biomass, and catch. This file offers an abridged version of the report file that is useful for quick model evaluation. This file is only available in SS v.3.30.08.03 and greater.
9. CompReport.sso: Observed and expected composition data in a list-based format.
10. Forecast-report.sso: Output of management quantities and for forecasts.
11. 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.
12. Covar.sso: This file replaces the standard ADMB ss.cor with an output of the parameter and derived quantity correlations in database format.
13. ss.par: This file contains all estimated and fixed parameters from the model run.
14. ss.std, ss.rep, ss.cor etc.: Standard ADMB output files.
15. checkup.sso: Contains details of selectivity parameters and resulting vectors. This is written during the first call of the objective function.
16. Gradient.dat: New for SS v.3.30, this file shows parameter gradients at the end of the run.
17. 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).
18. SIS\_table.sso: Output formatted for reading into the NMFS Species Information System.
19. Parmtrace.sso: Parameter values at each iteration.
20. posteriors.sso, derived\_posteriors.sso, posterior\_vectors.sso: Files associated with MCMC.

## Auxiliary Files

These files are additional files (e.g. excel files) which allow for exploration or understanding of specific parameterization which can assist in selecting appropriate starting values. These files are available for download from the Vlab website.

1. SS3-OUTPUT.xls: Excel file with macros to read report.sso and display results.

2. SS\_330\_Control\_Setup.xls:
  - (a) Shows how to setup an example control file for SS.
3. SS\_330\_Data\_Input.xls:
  - (a) Shows how to setup an example data input file for SS.
4. SS\_330\_Starter&Forecast.xls:
  - (a) Shows how to setup an example starter and forecast input files for SS.

## Starting SS

SS is typically run through the command line interface, although it can also be called from another program, R, the SS-GUI or a script file (such as a DOS batch file). SS is compiled for Windows, Mac, and Linux operating systems. The memory requirements depend on the complexity of the model you run, but in general, SS will run much slower on computers with inadequate memory. See the Running SS section on page 155 for additional notes on methods of running SS.

Communication with the program is through text files. When the program first starts, it reads the file starter.ss, which typically 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 on page 7. The names of the control and data files must match the names specified in the starter.ss file. File names, including starter.ss, are case-sensitive on Linux and Mac systems but not on Windows. The echoinput.sso file outputs how the executable read each input file and can be used for troubleshooting when trying to setup a model correctly. Output from SS consists of 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.

## Converting Files from SS v.3.24

Converting files from SS v.3.24 to SS v.3.30 can be easily performed by using the program ss\_trans.exe. The following file structure and steps are recommended for converting model files:

1. Create "transition" folder. Place the 4 main model files (control, data, starter, and forecast) from version SS v.3.24 within the transition folder along with the SS transition executable

(ss\_trans.exe). One tip is to use the control.ss\_new from the SS v.3.24 estimated model rather than the control.ss file which will set all parameter values at the previous estimated maximum likelihood estimated (MLE) parameters. Run the transition executable with phase = 0 within the starter file with the read par file turned off (option 0).

2. Create "converted" folder. Place the ss\_new (data.ss\_new, control.ss\_new, starter.ss\_new, forecast.ss\_new) files created by the transition executable contained within the "transition" folder into this new folder. Rename the ss\_new files to the appropriate suffixes and change the names in the starter.ss file accordingly.
3. Review the control (control.ss\_new) file to determine that all model functions converted correctly. The structural changes and assumptions for a couple of the advanced model features are too complicated to convert automatically. See below for some known features that may not convert. When needed, it is recommended to modify the control.ss\_new file, the converted control file, for only the features that failed to convert properly.
4. Change the max phase to a value greater than the last phase in which the a parameter is set to estimated within the control file. Run the new SS v.3.30 executable (ss.exe) within the "converted" folder using the renamed ss\_new files created from the transition executable.
5. Compare likelihood and model estimates between the SS v.3.24 and SS v.3.30 model versions.

There are some options that have been substantially changed in SS v.3.30 which impedes the automatic converting of SS v.3.24 model files. Known examples of SS v.3.24 options that cannot be converted, but for which better alternatives are available in SS v.3.30 are:

1. The use of Q deviations,
2. Complex birth seasons,
3. Environmental effects on spawner-recruitment parameters,
4. Setup of time-varying quantities for models that used the no-longer-available features (e.g., logistic bound constraint).

## Starter File

SS begins by reading the file starter.ss. The term COND appears in the "Typical Value" column of this documentation (it does not actually appear in the model files), 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 ss\_new files.

## STARTER.SS

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		File name of the data file
control_file.ctl		File name of the control file
0	Initial Parameter Values: 0 = use values in control file; and 1 = use ss.par after reading setup in the control file.	Do not set equal to 1 if there have been any changes to the control file that would alter the number or order of parameters stored in the ss.par file. Values in ss.par can be edited, carefully. Do not run ss_trans.exe from a ss.par from SS v.3.24.
1	Run display detail: 0 = none other than ADMB outputs; 1 = one brief line of display for each iteration; and 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 = minimal (no Report file); 1 = include all output; and 2 = brief output.	Option 0 will forgo the writing of the Report file, but the ss_summary file will be written that has minimal derived and estimated quantities. This is a useful option for some data-limited assessment approaches (e.g., XSSS or SSS). Option 1 will write out the full Report file. Option 2 will write out select items in the Report file and will omit some more detailed sections (e.g., numbers-at-age).



Value	Options	Description
0	Write 1st iteration details: 0 = omit; and 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.
0	Parameter Trace: 0 = omit; 1 = write good iteration and active parameters; 2 = write good iterations and all parameters; 3 = write every iteration and all parameters; and 4 = write every iteration and active parameters.	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; and 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; and 1 = calculate priors for all parameters that have a defined prior.	Turning this option on (1) adds the log likelihood contribution from all prior values for fixed and estimated parameters to the total negative log likelihood. With this option off (0), the total negative log likelihood will include the log likelihood for priors for only estimated parameters.

Value	Options	Description
1	Soft Bounds: 0 = omit; and 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.
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; and 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; and <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.
1000	MCMC burn interval	Number of iterations to discard at the start of an MCMC run.
200	MCMC thin interval	Number of iterations to remove between the main period of the MCMC run.

Value	Options	Description
0.0	<b>Jitter:</b> 0 = no jitter done to starting values; and >0 starting values will vary with larger jitter values resulting in larger changes from the parameter values in the control or par file.	The jitter function has been revised with SS v.3.30. Starting values are now jittered based on a normal distribution with the $\text{pr}(P_{\text{MIN}}) = 0.1\%$ and the $\text{pr}(P_{\text{MAX}}) = 99.9\%$ . A positive value here will add a small random jitter to the initial parameter values. When using the jitter option, care should be given when defining the low and high bounds for parameter values and particularly -999 or 999 should not be used to define bounds for estimated parameters.
-1	SD Report Start: -1 = begin annual SD report in start year; and <year> = begin SD report this year.	
-1	SD Report End: -1 = end annual SD report in end year; -2 = end annual SD report in last forecast year; and <value> = end SD report in this year.	
2	Extra SD Report Years: 0 = none; and <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. The number of years need to equal the value specified in the above line (Extra SD Reporting).	

Value	Options	Description
0.0001	Final convergence	This is a reasonable default value for the change in log likelihood denoting convergence. For applications with much data and thus a large total log likelihood value, a larger convergence criterion may still provide acceptable convergence
0	Retrospective year: 0 = none; and -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 = $X \cdot SB_0$ ; 2 = $X \cdot SB_{MSY}$ ; 3 = $X \cdot SB_{styr}$ ; and 4 = $X \cdot SB_{endyr}$ .	Selects the basis for the denominator when calculating degree of depletion in SB. The calculated values are reported to the SD report.  Relative to virgin spawning biomass.  Relative to spawning biomass that achieves MSY.  Relative to model start year spawning biomass.  Relative to spawning biomass in the model end year.
1	Fraction (X) for depletion denominator	Value for use in the calculation of the ratio for $SSB_y / (X \cdot SB_0)$ .
1	SPR report basis: 0 = skip; 1 = use $1 - SPR_{target}$ ; 2 = use $1 - SPR$ at MSY;	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

Value	Options	Description
	3 = use 1-SPR at $B_{\text{target}}$ ; and 4 = no denominator, so report actual 1-SPR values.	denominator in a ratio with the annual value of $(1 - \text{SPR})$ . 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; and 5 = unweighted average 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.
COND: If F std reporting $\geq 4$		Specify range of ages. Upper age must be less than max age because of incomplete handling of the accumulator age for this calculation.
13 17	Age range if F std reporting = 4.	
1	F report basis: 0 = not relative, report raw values; 1 = use F std value corresponding to $\text{SPR}_{\text{target}}$ ; 2 = use F std value corresponding to $F_{\text{MSY}}$ ; and	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.

Value	Options	Description
	3 = use F std value corresponding to $F_{Btarget}$ .	
0.01	MCMC output detail: 0 = default; 1 = output likelihood components and associated lambda values; 2 = expanded output; and 3 = make output subdirectory for each MCMC vector.	Specify format of MCMC output. This input requires the specification of two items; the output detail and a bump value to be added to the $\ln(R0)$ in the first call to MCMC. A bias adjustment of 1.0 is applied to recruitment deviations in the MCMC phase, which could result in reduced recruitment estimates relative to the MLE when a lower bias adjustment value is applied. A small value, called the "bump", is added to the $\ln(R0)$ for the first call to MCMC in order to prevent the stock from hitting the lower bounds when switching from MLE to MCMC. If you wanted to select the default output option and apply a bump value of 0.01 this is specified by 0.01 where the integer value represents the output detail and the decimal is the bump value.
0	Age-length-key (ALK) tolerance level, 0 >= values required	Value of 0 will not apply any compression. Values > 0 (e.g. 0.0001) will apply compression to the ALK which will increase the speed of calculations. The size of this value will impact the run time of your model, but one should be careful to ensure that the value used does not appreciably impact the estimated quantities relative to no compression of the ALK. The suggested value if applied is 0.0001.
3.30	3.30: Indicates that the control and data files are currently in SS v3.30 format. 999: Indicates that the control and data file are in a previous SS v.3.24 version. The ss_trans.exe executable should be used which will convert the files to the new format in the control.ss_new and data.ss_new files.	The transition executable for SS v.3.30 will create converted files in the new format from previous versions (must be SS v.3.24) when 999 is given. All ss_new files are in the SS v.3.30 format, so starter.ss_new has SS v.3.30 on the last line. The mortality-growth parameter section has a new sequence, so SS v.3.30 cannot read a ss.par file produced by SS v.3.24 and earlier, so please ensure that read par file option at the top of the starter file is set to 0. The Converting Files from SS v.3.24 section has additional information on model features that may impede file conversion.
<b>End of Starter File</b>		

# Jitter

The jitter function has been updated with SS v.3.30. The following steps are now performed to determine the jittered starting parameter values (illustrated in the figure below):

1. A normal distribution is calculated such that the  $\text{pr}(P_{\text{MIN}}) = 0.1\%$  and the  $\text{pr}(P_{\text{MAX}}) = 99.9\%$ .
2. A jitter shift value, termed " $K$ ", is calculated from the distribution equal to  $\text{pr}(P_{\text{CURRENT}})$ .
3. A random value is drawn, " $J$ ", from the range of  $K$ -jitter to  $K$ +jitter.
4. Any value which falls outside the 0-1 range (in the cumulative normal space) is mapped back from the bound to a point one-tenth of the way from the bound to the initial value.
5.  $J$  is a new cumulative normal probability value.
6. Calculate a new parameter value,  $P_{\text{JITTERED}}$ , such that  $\text{pr}(P_{\text{JITTERED}}) = J$ .

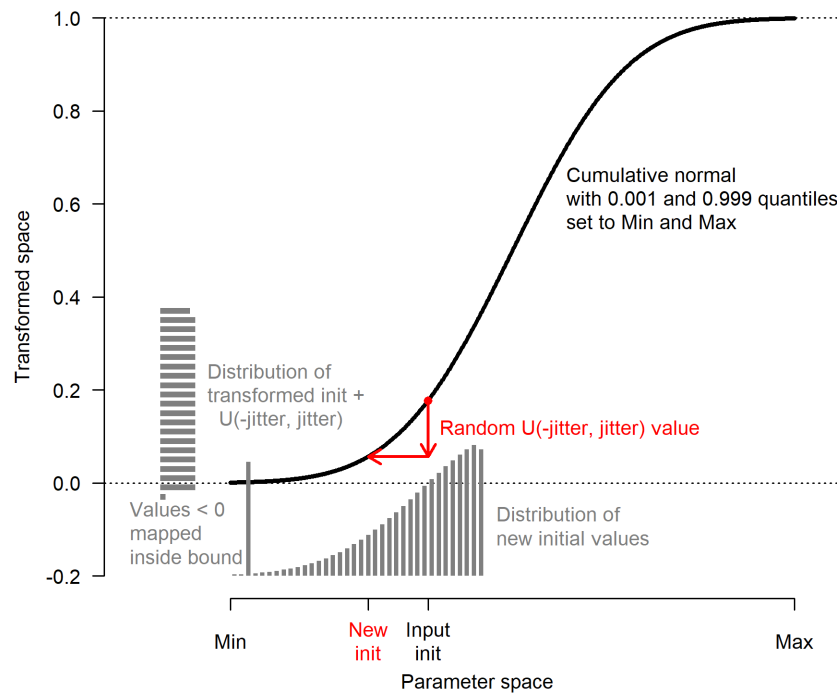


Illustration of the jitter algorithm

In SS, the jitter fraction defines a uniform distribution in cumulative normal space  $\pm$  the jitter fraction from the initial value (in cumulative normal space). The normal distribution for each parameter, for this purpose, is defined such that the minimum bound is at 0.001, and the maximum at 0.999 of the cumulative distribution. If the jitter fraction and original initial value are such that a

portion of the uniform distribution goes beyond 0.001 or 0.999 of the cumulative normal, the new value is set to one-tenth of the way from the bound to the original initial value.

Therefore  $\sigma = (\max - \min) / 6.18$ . For parameters that are on the log-scale,  $\sigma$  may be the correct measure of variation for jitters, for real-space parameters, CV (=  $\sigma / \text{original initial value}$ ) may be a better measure.

If the original initial value is at or near the middle of the min-max range, then for each 0.1 of jitter, the range of jitters extends about 0.25  $\sigma$ s to either side of the original value (though as the total jitter increases the relationship varies more than this), and the average absolute jitter is about half of that. For values far from the middle of the min-max range, the resulting jitter is skewed in parameter space, and may hit the bound, invoking the resetting mentioned above.

To evaluate the jittering, the bounds, and the original initial values, a jitter\_info table is available from r4ss, including  $\sigma$ , CV and InitLocation columns (the latter referring to location within the cumulative normal – too close to 0 or 1 indicates a potential issue).

Note: parameters with  $\min \leq -99$  or  $\max \geq 999$  are not jittered to avoid unreasonable values (a warning is produced to indicate this).

## Forecast File

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 C on page [191](#).

The term COND appears in the "Typical Value" column of this documentation (it does not actually appear in the model files), 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 ss\_new files.



## FORECAST.SS

Value	Options	Description
1	<b>Benchmarks/Reference Points:</b> 0 = omit; 1 = calculate $F_{SPR}$ , $F_{Btarget}$ , and $F_{MSY}$ ; and 2 = calculate $F_{SPR}$ , $F_{MSY}$ , $F_{0.10}$ .	SS checks for consistency of the Forecast specification and the benchmark specification. It will turn benchmarks on if necessary and report a warning.
1	<b>MSY Method:</b> 1 = $F_{SPR}$ as proxy; 2 = calculate $F_{MSY}$ ; 3 = $F_{Btarget}$ as proxy or $F_{0.10}$ ; and 4 = $F_{end\ year}$ as proxy.	Specifies basis for calculating a single population level $F_{MSY}$ value.
0.45	$SPR_{target}$	SS searches for F multiplier that will produce this level of spawning biomass per recruit (reproductive output) relative to unfished value.
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 0 0 0 0	<b>Benchmark Years:</b> -999: start year; >0: absolute year; and <= 0: year relative to end year.	Requires 10 values, beginning and ending years for (1,2) biology (e.g., growth, natural mortality, maturity, fecundity), (3,4) selectivity, (5,6) relative Fs, (7,8) movement and recruitment distribution; (9,10) stock-recruitment parameters for averaging years in calculating benchmark quantities.

Value	Options	Description
1	Benchmark Relative F Basis: 1 = use year range; and 2 = set range for relF same as forecast below.	The specification does not affect year range for selectivity and biology.
2	Forecast: 0 = none (no forecast years); 1 = use $F_{SPR}$ ; 2 = use $F_{MSY}$ ; 3 = use $F_{Btarget}$ or $F_{0.10}$ ; 4 = set to average F scalar for the forecast relative F years below; and 5 = input annual F scalar.	This input is required but is ignored if benchmarks are turned off. This determines how forecast catches are calculated and removed from the population which is separate from the "MSY Method" above. If $F_{MSY}$ is selected, it uses whatever proxy (e.g., $F_{SPR}$ or $F_{BTGT}$ ) is selected in the "MSY Method" row.
10	N forecast years (must be $\geq 1$ )	At least one forecast year now required which differs from SS v.3.24 that allowed zero forecast years.
1	F scalar	Only used if Forecast option = 5 (input annual F scalar), but is a required line in the forecast file.
0 0 0 0 0 0	Forecast Years: >0 = absolute year; and <= 0 = year relative to end year.	Requires 6 values: beginning and ending years for selectivity, relative Fs, and recruitment distribution that will be used to create averages to use in forecasts. In future, hope to allow random effects to propagate into forecast. Please note, relative F for bycatch only fleets is scaled just like other fleets. More options for this in future.

Value	Options	Description
0	Forecast Selectivity Option: 0 = forecast selectivity is mean from year range; and 1 = forecast selectivity from annual time-varying parameters.	Determines the selectivity used in the forecast years. Selecting 1 will allow for application of time-varying selectivity parameters (e.g., random walk) to continue into the forecast period.
1	Control Rule: 1 = catch as function of SSB, buffer on F; 2 = F as function of SSB, buffer on F; 3 = catch as function of SSB, buffer on catch; and 4 = F is a function of SSB, buffer on catch.	Used to apply reductions ("buffer") to either the catch or F based on the control rule during the forecast period.
0.40	Control Rule Upper Limit	Relative biomass level to unfished biomass above which F is constant at control rule $F_{\text{target}}$ .
0.10	Control Rule Lower Limit	Relative biomass level to unfished biomass below which F is set to 0 (management threshold).
0.75	Control Rule Buffer (multiplier or -1)	Control rule catch or $F_{\text{target}}$ as a fraction of selected catch or $F_{\text{MSY}}$ proxy. A value of -1 will allow the user to input a forecast year specific control rule fraction (added in v. 3.30.13).

Value	Options	Description
COND -1: Conditional input for annual control rule buffer	2019 0.8 2020 0.6 2021 0.5 -9999 0	Year and control rule buffer value. Can enter a value for each year, or starting sequence of years. The final control rule buffer value will apply to all sequent forecast years.
3	Number of forecast loops (1,2,3)	SS sequentially goes through the forecast up to three times. Maximum number of forecast loops: 1=OFL only, 2=ABC control rule and buffers, 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 calculated as if there was perfect knowledge about recruitment deviations in the future.
0	Forecast recruitment: 0 = spawner recruit curve; 1 = value*(spawner recruit curve); 2 = value*(virgin recruitment); and 3 = recent mean from year range above.	Option 0, ignore input and do forecast recruitment as before SS v.3.30.10, if 1, then use next value as a multiplier applied after env/block/regime is applied, if 2, then use value as multiplier times adjusted virgin recruitment (after time-varying adjustments to R0), and if 3, then use value as the number of years from end of main recruitment deviations to average (mean is the recruitments, not the deviations). Need to set phase to -1 in control to get constant recruitment in MCMC.
1	Scalar or number of years of recent main recruitments to average.	This input depends upon option selected directly above. If option 1 or 2 selected this value should be a scalar value to be applied to recruitment. If option 3 is selected above this should be input as the number of years to average recruitment.

Value	Options	Description
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 >0.0 to cause implementation error deviations to be an estimated parameter that will add variance to forecast).
0	Rebuilder: 0 = omit U.S. West Coast rebuilder output; and 1 = do U.S. West Coast rebuilder output.	Creates a rebuild.dat file to be used for U.S. West Coast groundfish rebuilder program.
2004	Rebuilder catch (Year Declared): >0 = year first catch should be set to zero; and -1 = set to 1999.	Input line is required even if Rebuilder = 0, specified in the line above.
2004	Rebuilder start year (Year Initial): >0 = year for current age structure; and -1 = set to end year +1.	Input line is required even if Rebuilder = 0, specified two line above.
1	Fleet Relative F: 1 = use first-last allocation year; and 2 = read season(row) x fleet (column) set below.	

Value	Options	Description
2	Basis for maximum forecast catch: 2 = total catch biomass; 3 = retained catch biomass; 5 = total catch numbers; and 6 = retained total numbers.	The maximum basis for forecasted catch will be implemented for the for the "First year for caps and allocations" selected above. The maximum catch (biomass or numbers) by fleet is specified below on the "Maximum total forecast catch by fleet" line.
COND 2: Conditional input for fleet relative F (Enter: Season, Fleet, Relative F)		
1 1 0.6	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.
1 2 0.4		
-9999 0 0	Terminator line	
1 50	Maximum total forecast catch by fleet (in units specified above total catch/numbers, retained catch/numbers)	Enter fleet number and its maximum value. Last line of the entry must have fleet number = -9999.
-9999 -1		
-9999 -1	Maximum total catch by area -1 = no maximum	Enter area number and its max. Last line of the entry must have area number = -9999.
1 1	Fleet assignment to allocation group	Enter list of fleet number and its allocation group number if it is in a group. Last line of the entry must have fleet number = -9999.
-9999 -1		

Value	Options	Description
COND: if N allocation groups is >0		Enter a year and the allocation fraction to each group for that year. SS will fill those values to the end of the forecast, then read another year from this list. Terminate with -9999 in year field. Annual values are rescaled to sum to 1.0.
2002 1	Allocation to each group for each year of the forecast	
-9999 1		
-1	<p>Basis for forecast catch:</p> <p>-1 = Read basis with each observation, allows for a mixture of dead, retained, or F basis by different fleets for the fixed catches below;</p> <p>2 = Dead catch (retained + discarded);</p> <p>3 = Retained catch; and</p> <p>99 = Input harvest rate (F).</p>	The dead or retained value in the forecast catch inputs will be interpreted in terms of numbers or biomass based on the units of the input catch for each fleet.
COND: == -1	Forecasted catches - enter one line per number of fixed forecast year catch	
2012 1 1 1200 2	Year & Season & Fleet & Catch or F value & Basis	
2013 1 1 1400 3	Year & Season & Fleet & Catch or F value & Basis	
-9999 0 0 0 0	Indicates end of inputted catches to read	
COND: > 0	Forecasted catches - enter one line per number of fixed forecast year catch	
2012 1 1 1200	Year & Season & Fleet & Catch or F value	
2013 1 1 1200	Year & Season & Fleet & Catch or F value	
-9999 0 0 0	Indicates end of inputted catches to read	
999	End of Input	
<b>End of Forecast File</b>		

## Benchmark Calculations

This feature of SS is designed to calculate an equilibrium fishing rate intended to serve as a proxy for the fishing rate that would provide maximum sustainable yield (MSY). Then in the forecast module these fishing rates can be used in the projections.

Four reference points can be calculated by SS. The first of which is the estimate of  $F_{MSY}$  within the model, while the others use proxies or an alternative estimated point.

- $F_{MSY}$ : Search for the  $F$  that produces maximum equilibrium (e.g. dead catch).
- $F_{SPR}$ : Search for the  $F$  that produces spawning biomass per recruit this is a specific fraction, termed  $SPR_{target}$ , of spawning biomass per recruit under unfished conditions. Note that this is in relative terms so it does not take into account the spawner-recruit relationship.
- $F_{Btarget}$ : Search for the  $F$  that produces an absolute spawning biomass that is a specified fraction, termed relative biomass target, of the unfished spawning biomass. Note that this is in absolute terms so takes into account the spawner-recruit relationship.
- $F_{0.10}$ : Search for the  $F$  that produces a slope in yield per recruit,  $dY/dF$ , that is 10% of the slope at the origin. Note that with SS, this option is mutually exclusive with  $F_{Btarget}$ . Only one will be calculated and the one that is calculated can serve as the proxy for  $F_{MSY}$  and forecasting.

### Estimation

Each of the potential reference points is calculated by searching across a range of  $F$  multiplier levels, calculating equilibrium biomass and catch at that  $F$ , using Newton-Raphson method to calculate a better  $F$  multiplier value, and iterating a fixed number of times to achieve convergence on the desired level.

### Calculations

The calculation of equilibrium biomass and catch uses the same code that is used to calculate the virgin conditions and the initial equilibrium conditions. This equilibrium calculation code takes into account all morph, timing, biology, selectivity, and movement conditions as they apply while doing the time series calculations. You can verify this by running SS to calculate  $F_{MSY}$  then hardwire initial  $F$  to equal this value, use the  $F_{method}$  approach 2 so each annual  $F$  is equal to  $F_{MSY}$  and then set forecast  $F$  to be the same  $F_{MSY}$ . Then run SS without estimation and no recruitment deviations. You should see that the population has an initial equilibrium abundance equal to  $B_{MSY}$  and stays at this level during the time series and forecast.

### Catch Units



For each fleet, SS always calculates catch in terms of biomass (mt) and numbers (1000s) for encountered (selected) catch, dead catch, and retained catch. These three categories differ only when some fleets have discarding or are designated as a bycatch fleet. SS uses total dead catch biomass as the quantity that is principally reported and the quantity that is optimized when searching for  $F_{MSY}$ . The quantity "dead catch" may occasionally be referred to as "yield".

## Biomass Units

The principle measure of fish abundance, for the purpose of reference point calculation, is female reproductive output. This is referred to as SSB (spawning stock biomass) and sometimes just "B" because the typical user settings have one unit of reproductive output (fecundity) per kg of mature female biomass. So when the output label says  $B_{MSY}$ , this is actually the female reproductive output at the proxy for  $F_{MSY}$ .

## Fleet Allocation

An important concept for the reference point calculation is the allocation of fishing rate among fleets. Internally, this is  $Bmark\_relF(f, s)$  and it is the fraction of the F multiplier assigned to each fleet,  $f$  and season,  $s$ . The value,  $F\_multiplier * Bmark\_relF(f, s)$ , is the F level for a particular fleet in a particular season and for the age that has a selectivity of 1.0. Other ages will have different F values according to their selectivity.

- The  $Bmark\_relF$  values can be calculated by SS from a range of years specified in the input for Benchmark Years or it can be set to be the same as the  $Forecast\_RelF$ , which in turn can be based on a range of years or can be input as a set of fixed values.
- Note that for Bycatch Fleets, the F's calculated by application of  $Bmark\_relF$  for a bycatch fleet can be overridden by a F value calculated from a range of years or a fixed F value that is input by the user. If such an override is selected for a bycatch fleet, that F value is not adjusted by changes to the F multiplier. This allows the user to treat a bycatch fleet as a constant background F while the optimal F for other fleets is sought. Also for bycatch fleets, there is user control for whether or not the dead catch from the bycatch fleet is included in the total dead catch that is optimized when searching for  $F_{MSY}$ .

## Virgin vs. Unfished

The concept of unfished spawning biomass,  $SSB_{unf}$ , is important to the reference points calculations. Unfished spawning biomass can be potentially different than virgin spawning biomass,  $SSB_{virgin}$ .

- Virgin spawning biomass is calculated from the parameter values associated with the start year of the model configuration and it serves as the basis from which the population model starts and the basis for calculation of stock depletion.

- Unfished spawning biomass can be calculated for any year or range of years, so can change over time as  $R_0$ , steepness, or biological parameters change.
- In the reference points calculation, the Benchmark Years input specifies the range of time over which various quantities are averaged to calculate the reference points. For biology, selectivity,  $F$ 's, and movement the values being averaged are the year-specific derived quantities. But for the stock-recruitment parameters ( $R_0$  and steepness), the parameter values themselves are averaged over time.
- During the time series or forecast, the current year's unfished spawning output ( $SSB_{unf}$ ) is used as the basis for the spawner-recruitment curve against which deviations from the spawner-recruitment curve are applied. So, if  $R_0$  is made time-varying, then the spawner-recruit curve itself is changed. However, if the regime shift parameter is time-varying, then this is an offset from the spawner-recruitment curve and not a change in the curve itself. Changes in  $R_0$  will change year-specific reference points and change the expected value for annual recruitments, but changes in regime shift parameter only change the expected value for annual recruitments.
- In reporting the time series of depletion level, the denominator can be based on virgin spawning output ( $SSB_{virgin}$ ) or  $B_{MSY}$ . Note that  $B_{MSY}$  is based on unfished spawning output ( $SSB_{unf}$ ) for the specified range of Benchmark years, not on  $SSB_{virgin}$ .

## Forecast Recruitment Adjustment

Recruitment during the forecast years sometimes needs to be set at a level other than that determined by the spawner-recruitment curve. One way to do this is by an environmental or block effect on the regime shift parameter. A more straightforward approach is now provided by the special forecast recruitment feature described here. There are 4 options provided for this feature. These are:

- 0 = Do nothing: this is the default and will invoke no special treatment for the forecast recruitments.
- 1 = Multiplier on spawner-recruitment: the expected recruitment from the stock recruitment relationship is multiplied by this factor.
  - This is a multiplier, so null effect comes from a value of 1.0.
  - The order of operations is to apply the SRR, then the regime effect, then this special forecast effect, then bias adjustment, then the deviations.
  - In the spawner recruit output of the report.sso there are 4 recruitment values stored.

- 2 = Multiplier on virgin recruitment: The virgin recruitment is multiplied by this factor.
  - This is a multiplier, so null effect comes from a value of 1.0.
  - The order of operations is to apply any environmental or block effects to  $R_0$ , then apply the special forecast effect, then bias adjustment, then the deviations.
  - Note that environmental or block effects on  $R_0$  are rare and are different than environment or block effects on the regime parameter.
- 3 = Mean recent recruitment: calculate the mean recruitment and use it during the forecast period.
  - Note that bias adjustment is not applied to this mean because the values going into the mean have already been bias adjusted.

This feature affects the expected recruitment in all years after the last year of the main recruitment deviations. This means that if the last year of main recruitment deviations is before end year, then the last few recruitments, termed "late", are also affected by this forecast option. For example, option 3 would allow you to set the last 2 years of the time series and all forecast years to have recruitment equal to the mean recruitment for the last 10 years of the main recruitment era.

## Data File

### Overview of Data File

1. Dimensions (years, ages, number of fleets, number of surveys, etc.)
2. Fleet and survey names, timing, etc.
3. Catch data (biomass or numbers)
4. Discard totals or rate data
5. Mean body weight or mean body length data
6. Length composition set-up
7. Length composition data
8. Age composition set-up

9. Age imprecision definitions
10. Age composition data
11. Mean length-at-age or mean bodyweight-at-age data
12. Generalized size composition (e.g., weight frequency) data
13. Environmental data
14. Tag-recapture data
15. Stock composition (e.g., morphs identified by otolith microchemistry) data
16. Selectivity observations (new placeholder, not yet implemented)

## Units of Measure

The normal units of measure are as follows:

- Catch biomass - metric tons
- Body weight - kilograms
- Body length - usually in centimeters, weight-at-length parameters must correspond to the units of body length and body weight
- Survey abundance - any units if catchability (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 metric tons and body weight is in kilograms
- Spawning biomass - metric tons of mature females if  $\text{eggs/kg} = 1$  for all weights; otherwise has units that are based on the user-specified fecundity

## Time Units

- Spawning:
  - Restricted to happening once per year at a specified date (in real months). To create

multiple spawning events per year, the way to do this is to change the definition of a year (e.g. call a 6 month period a "year" when there are two spawning events about 6 months apart) which you can do by having the total duration of the seasons be less than 1 year.

- Recruitment:
  - Occurs at specified recruitment events that occur at user-specified dates (in real months).
  - There can be one to many recruitment events across a year; each producing a platoon as a portion of the total recruitment.
  - A settlement platoon enters the model at age 0 if settlement is between the time of spawning and the end of the year; it enters at age 1 if settlement is after the first of the year; these ages at settlement can be overridden in the settlement setup.
- Timing
  - All fish advance to the next older integer age on January 1, no matter when they were born during the year. Consult with your ageing lab to assure consistent interpretation.
- Parameters:
  - Time-varying parameters are allowed to change annually, not seasonally.
  - Rates like growth and mortality are per year.

## Seasons

Seasonal quantities in the model are calculated and treated in the following methods:

- Seasons are the time step during which constant rates apply.
- Catch and discard amounts are per season and F is calculated per season.
- The year can have just one 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 do not equal 12.0, then the input durations are divided by the total duration input to rescale season duration to equal 1.0.
- 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.

## Subseasons and Timing of Events

The treatment of subseasons in SS v.3.30 provide more precision in the timing of events compared to earlier model versions. SS v.3.24 and all earlier versions effectively had two subseasons per season because the age-length-key (ALK) for each observation used the mid-season mean length-at-age and spawning occurred at the beginning of a specified season.

Time steps in SS v.3.30 now can be broken into subseason and the ALK can be calculated multiple times over the course of a year:

ALK	ALK*	ALK*	ALK	ALK*	ALK
Subseason 1	Subseason 2	Subseason 3	Subseason 4	Subseason 5	Subseason 6

ALK\* only re-calculated when there is a survey that subseason

- Even number (min = 2) of subseasons per season (regardless of season duration):
  - Two subseasons will mimic SS v.3.24
  - Specifying more subseasons will give finer temporal resolution, but will slow the model down, the effect of which is mitigated by only calculating growth as needed.
- Survey timing is now cruise-specific and specified in units of months (e.g., April 15 = 4.5).
  - sstrans.exe will convert year, season in SS v.3.24 format to year, real month in SS v.3.30 format.
- Survey integer season and spawn integer season assigned at run time based on real month and season duration(s).
- Growth and the age-length-key (ALK) is calculated at the beginning and mid-season or when there is a defined subseason with data observation.
- Fishery body weight uses mid-subseason growth.
- Survey body weight and size composition is calculated using the nearest subseason.
- Reproductive output now has specified spawn timing (in months fraction) and interpolates growth to that timing.
- Survey numbers calculated at cruise survey timing using  $e^{-z}$ .

- Continuous Z for entire season. Same as applied in version SS v.3.24.

## Terminology

The term COND appears in the "Typical Value" column of this documentation (it does not actually appear in the model files), 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 ss\_new files.

## Model Dimensions

Value	Description
#V3.30.XX.XX	Model version number. This is written by SS in the new files and a good idea to keep updated in the input files.
#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 the number of 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. If the sum is not equal to 12.0, then the entered values are summed and rescaled to 1. 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 calculated by season (growth, mortality, etc.) using annual rates and season duration.
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 growth and the associated age-length key.

1.5	Spawning month; spawning biomass is calculated at this time of year (1.5 means January 15) and used as basis for the total recruitment of all settlement events resulting from this spawning.
2	Number of sexes: 1 = current one gender, ignore fraction female input in the control file; 2 = current two gender, use fraction female in the control file; and -1 = one gender and multiply the spawning biomass by the fraction female in the control file.
20	Number of ages. The value here will be the plus-group age. SS starts at age 0.
1	Number of areas
2	Total number of fishing and survey fleets (which now can be in any order).

## 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 (SS v.3.24 and earlier) required that fishing fleets be listed first followed by survey only fleets. In version SS v.3.30 all fleets now have the same status within the model structure and each has a specified fleet type (except for models that use tag recapture data, this will be corrected in future versions). Available types are; catch fleet, bycatch only fleet, 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	Catch Mult.	Fleet Name
1	-1	1	1	0	FISHERY1
3	1	1	2	0	SURVEY1

### Fleet Type



Define the fleet type (e.g., fishery fleet, survey fleet):

- 1 = fleet with input catches;
- 2 = bycatch fleet (all catch discarded);
- 3 = survey: assumes no catch removals even if associated catches are specified below. If you would like to remove survey catch set fleet type to option = 1 with specific month timing for removals (defined below in Timing); and
- 4 = ignored (not yet implemented).

## Timing

Timing for data observations has been revised in SS v.3.30:

- Fishery = -1 catch is treated as if it occurred over the whole season. A user can override this assumption for specific data observations (e.g., length or age) by specifying a month.
- Survey = 1 The fleet timing here for surveys is not used and only the month value associated with each observation is relevant (e.g., month specification in the indices of abundance or the month for composition data).

## Area

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

## Catch Units

Ignored for survey fleets, their units are read later:

- 1 = biomass (in metric tons); and
- 2 = numbers (thousands of fish).

See [Units of Measure](#) for more information.

## Catch Multiplier

Invokes use of a catch multiplier, which is then entered as a parameter in the mortality-growth parameter section. The estimated value or fixed value of the catch multiplier is used to adjust the observed catch:

- 0 = No catch multiplier used; and

- 1 = Apply a catch multiplier which is defined as an estimable 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.

A catch multiplier can be useful when trying to explore historical unrecorded catches or ongoing illegal and unregulated catches. The catch multiplier is a full parameter line in the control file and has the ability to be time-varying.

## Optional Bycatch Fleets

The option to include bycatch fleets was introduced in SS v.3.30.10. This is an optional input and if no bycatch is to be included in to the catches this section can be ignored.

If a fleet above was set as a bycatch fleet (fleet type = 2), the following line is required:

Optional inputs that define bycatch fleet:

Fleet Index	Include in MSY	Fmult	F or First Year	F or Last Year	Not used
1	1	1	1982	2010	999

### Fleet Index

Fleet number for which to include bycatch catch. Fleet number is assigned within the model based on the order of listed fleets in the Fleet Definition section. If there are multiple bycatch fleets, then a line for each fleet is required in the bycatch section.

### Include in MSY

The options are:

- 1 = deadfish in MSY, ABC, and other benchmark and forecast output; and
- 2 = omit from MSY and ABC (but still include the mortality).

### Fmult

The options are:

- 1 = F multiplier scales with other fleets;
- 2 = bycatch F constant at input value; and

- 3 = bycatch F from range of years.

### F or First Year

The specified F or first year for the bycatch fleet.

### F or Last Year

The specified F or last year for the bycatch fleet.

### Not Used

This column is not yet used and is reserved for future features.

## 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 and season that the catch will be attributed to, fleet, a catch value, and a year specific catch standard error. Only positive catches need to be entered, so there is no need for records corresponding to all years and fleets. To include an equilibrium catch value the year should be noted as -999 and this is now fleet and season specific.

There is no longer a need to specify the number of records to be read; instead the list is terminated by entering a record with the value of -9999 in the year field. The updated list based approach extends throughout the data file (e.g., catch, length- and age-composition data), the control file (e.g., lambdas), and the forecast file (e.g., total catch by fleet, total catch by area, allocation groups, forecasted catch).

In addition, it is possible to collapse the number of seasons. So, if a season value is greater than the number of seasons for a particular model, that catch is added to the catch for the final season. This is one way to easily collapse a seasonal model into an annual model. The alternative option is to the use of season = 0. This will cause SS to distribute the input value of catch equally among the number of seasons. SS assumes that catch occurs continuously over seasons and hence is not specified as month in the catch data section. However, all other data types will need to be specified by month.

The new format for version SS v.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	Catch	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

- Catch can be in terms of biomass or numbers for each fleet, but cannot be mixed within a fleet.
- Catch is retained catch (aka landings). If there is discard also, then it is handled in the discard section below. This is the recommended setup which results in a model estimated retention curve based upon the discard data (specifically discard composition data). However, there may be instances where the data do not support estimation of retention curves. In these instances catches can be specified as all dead (retained + discard estimates).
- If there are challenges to estimating discards within the model, catches can be input as total dead without the use of discard data and retention curves.
- 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.

## Bycatch

Bycatch fleets have an F and hence impose mortality and catch fish. All this catch is discarded. There must be a value entered for retained catch so that SS knows to calculate an F for that season, but this catch amount is ignored in the log likelihood. The amount of discarded catch can be entered as a discard observation(s). Bycatch fleets have selectivity, which must be specified or estimated if observations of the size or age composition of the discards is entered.

- There is no retained catch amount to match and hence, the F for bycatch only fleets must be

implemented with the continuous F method ( $F_{\text{method}} = 2$ ).

- MSY and yield per recruit are calculated in terms of dead catch, and they currently include catch from bycatch fleets. The search for  $F_{\text{MSY}}$  scales the bycatch F along with the F for the fleets that retain catch.

## Indices

Indices are data that are compared to aggregate quantities in the model. Typically the index is a measure of selected fish abundance, but this data section also allows for the index to be related to a fishing fleet's F, or to another quantity estimated by the model. The first section of the "Indices" setup contains the fleet number, units, error distribution, and whether additional output (SD Report) will be written to the Report file for each fleet that has index data.

Catch-per-unit-effort (CPUE) and Survey Abundance Observations:

Fleet/ Survey	Units	Error Distribution	SD Report
1	1	0	0
2	1	0	0
...	...	...	...

## Units

The options for units for input data are:

- 0 = numbers;
- 1 = biomass;
- 2 = F; and
  - Note the F option can only be used for a fishing fleet and not for a survey, even if the survey selectivity 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  $\log(F)$ . The resultant proportionality constant has units of  $1/Q$  where Q is the catchability coefficient.
- $\geq 30$  special survey types. These options bypass the calculation of survey selectivity so no

selectivity parameters should be entered. The expected values for these types are:

- 30 = spawning biomass/output (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;
- 34 = depletion (spawning biomass/virgin spawning biomass);
- \* Special survey option 34 automatically adjusts phases of parameters. There are options for additional control over this in the control file Q setup section under the link information column where:
  - 0 = add 1 to phases of all parameters. Only R0 active in new phase 1. Mimics the default option of previous model versions;
  - 1 = only R0 active in phase 1. Then finish with no other parameters becoming active; useful for data-limited draws of other fixed parameters. Essentially, this option allows SS to mimic DB-SRA; and
  - 2 = no phase adjustments, can be used when profiling on fixed R0.
- 35 = survey of a deviation vector ( $e(\text{survey}(y)) = f(\text{parm\_dev}(k, y))$ ), can be used for an environmental time-series with soft linkage to the index. The selected deviation vector is specified in Q section of the control file. The index of the deviation vector to which the index is related is specified in the 2nd column of the Q setup table (see [Catchability](#)).

## Error Distribution

The options for error distribution form are:

- -1 = normal error;
- 0 = lognormal error; and
- >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. The standard error 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 coefficient of variation (CV), then the value of standard error can be approximated as  $\sqrt{(\log_e(1 + (CV)^2))}$  where the 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 standard error are interpreted directly as a standard error 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 standard error input in the data file.

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

## Enable SD Report

Indices with SD Report enabled will have the expected values for their historical values appear in the ss.std and ss.cor files. The default value is for this option is 0.

- 0 = SD Report not enabled for this index; and
- 1 = SD Report enabled for this index.

## Data Format

Year	Month	Fleet/Survey	Observation	SE
1991	7	3	80000	0.056
1995	7.2	3	65000	0.056
...	...	...	...	...
2000	7.1	3	42000	0.056
-9999	0	0	0	0

- For fishing fleets, 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 does not use the retention curve (if any) for the fishing fleet.
- 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.

- 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 for the same year are not allowed.
- Observations that are to be included in the model but not included in the negative log likelihood 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”. This approach is best for single or select years from an index rather than an approach to remove a whole index. Removing a whole index from the model should be done through the use of lambdas at the bottom of the control file which will eliminate the index from model fitting.
- Observations can be entered in any order, except if the super-year feature is used.
- 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.
- 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 approach to better serve as a survey of stock abundance.

## Discard

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

---

0	Number of fleets with discard observations
---	--

---

If discard is being used, the input syntax is:



1	Number of fleets with discard observations			
Fleet	Units	Error Distribution		
1	2	-1		
Year	Month	Fleet	Observation	Standard Error
1980	7	1	0.05	0.25
1991	7	1	0.10	0.25
-9999	0	0	0	0

## Discard Units

The options are:

- 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, biomass/number selection matches that of retained catch; and
- 3 = values are in numbers (thousands) of fish discarded, even if retained catch has units of biomass.

## Discard Error Distribution

The four options for discard error are:

- >0 = 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; and
- -3 = truncated normal distribution (new with SS v.3.30, needs further testing), value of error in data file is interpreted as standard error of the observation. This is a good option for low observed discard rates.

## Discard Notes

- 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 discard observations from a fleet for the same year are not allowed.
- Observations can be entered in any order, except if the super-period feature is used.
- Note that in the control file you will enter information for retention such that 1-retention is the amount discarded. All discard is assumed dead, unless you enter information for discard mortality. Retention and discard mortality can be either size-based or age-based (new with SS v.3.30).

## 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 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.

## Mean Body Weight or Length

This is the overall mean body weight or length 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.

#### Mean Body Weight Data Section:

1	Use mean body size data (0/1)					
COND > 0:						
30	Degrees of freedom for Student's t-distribution used to evaluate mean body weight deviation.					
Year	Month	Fleet	Partition	Type	Observation	CV
1990	7	1	0	1	4.0	0.95
1990	7	1	0	1	1.0	0.95
-9999	0	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; and
- 2 = retained catch in units of weight.

### Type

Specify the type of data:

- 1 = mean length; and
- 2 = mean body weight.

### Observation - Units

Units must correspond to the units of body weight, normally in kilograms, (or mean length in cm). 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)

## Population Length Bins

The first part of the length composition section sets up the bin structure for the population. These bins define the granularity of the age-length key and the coarseness of the length selectivity. Fine bins create smoother distributions, but a larger and slower running model. First read a single value to select one of three population length bin methods, then any conditional input for options 2 and 3:

1	Use data bins to be read later. No additional input here.	
2	generate from bin width min max, read next:	
	2	Bin width
	10	Lower size of first bin
	82	Lower size of largest bin
The number of bins is then calculated from: $(\text{max Lread} - \text{min Lread})/(\text{bin width}) + 1$		
3	Read 1 value for number of bins, and then read vector of bin boundaries	
	37	Number of population length bins to be read
	10 12 14 ... 82	Vector containing lower edge of each population size bin

### Notes

There are some items for users to consider when setting up population length bins:

- For option 2, bin width should be a factor of min size and max size. For options 2 and 3, the data length bins must not be wider than the population length bins and the boundaries of the bins do not have to align. The transition matrix between population and data length bins is output to echoinput.sso.
- The mean size at settlement (virtual recruitment age) is set equal to the min size of the first population length bin.
- When using more, finer population length bins, SS will create smoother length selectivity curves and smoother length distributions in the age-length key, but run more slowly (more calculations to do).
- 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.

- 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 see zero gradient of the log likelihood with respect to that parameter and convergence will be hampered.
- A value read near the end of the starter.ss file defines the degree of tail compression used for the age-length key, called ALK tolerance. If this is set to 0.0, then no compression is used and all cells of the age-length key are processed, even though they may contain trivial (e.g.,  $1 \times 10^{-13}$ ) fraction of the fish at a given age. With tail compression of, say 0.0001, SS will at the beginning of each phase calculate the min and max length bin to process for each age of each morphs ALK and compress accordingly. Depending on how many extra bins are outside this range, you may see speed increases near 10-20%. Large values of ALK tolerance, say 0.1, will create a sharp end to each distribution and likely will impede convergence. It is recommended to start with a value of 0 and if model speed is an issue, explore values greater than 0 and evaluate the trade-off between model estimates and run time. The user is encouraged to explore this feature.

## Length Composition Data Structure

Enter a code to indicate whether or not length composition data will be used:

---

1	Use length composition data (0/1)
---	-----------------------------------

---

If the value 0 is entered, then skip all length related inputs below and skip to the age data setup section. Otherwise continue:

Specify bin compression and error structure for length composition data for each fleet:

Min. Tail Compress.	Constant added to prop.	Combine males & females	Compress. Bins	Comp. Error Dist.	Dirichlet Param. Select	Min. Sample Size
0	0.0001	0	0	0	0	1
0	0.0001	0	0	0	0	1

---

## 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 age composition within length bins because of the sparseness of these data.

## Added Constant to Proportions

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

## Compress Bins

This option allows for the compression of length or age bins beyond a specific length or age by each data source. As an example, a value of 5 in the compress bins column would condense the final five length bins for the specified data source.

## Composition Error Distribution

The options are:

- 0 = Multinomial Error; and
- 1 = Dirichlet Multinomial Error.
  - The Dirichlet Multinomial Error distribution requires the addition of a parameter lines for the natural log of the effective sample size multiplier ( $\theta$ ) at the end of the selectivity parameter section in the control file. See the [Dirichlet parameter](#) in the control file for information regarding setup.
  - The Parameter Select option needs be used to specify which data sources should be weighted together or separate.

## Dirichlet Parameter Select

Value that indicates the groups of composition data for estimation of the Dirichlet parameter for weighting composition data.

- 0 = Default; and
- 1-N = Only used for the Dirichlet option. Set to a sequence of numbers from 1 to N where N is the total number of combinations of fleet and age/length. That is, if you have 3 fleets with length data, but only 2 also have age data, you would have values 1 to 3 in the length comp setup and 4 to 5 in the age comp setup. You can also have a data weight that is shared across fleets by repeating values in Parameter Select.

## Minimum Sample Size

The minimum value (floor) for all sample sizes. This value must be at least 0.001. Conditional age-at-length data may have observations with sample sizes less than 1. SS v.3.24 had an implicit minimum sample size value of 1.

## Dirichlet Parameter Number and Effective Sample Sizes

If the Dirichlet multinomial error distribution is selected, indicate here which of a list of Dirichlet multinomial parameters will be used for this fleet. So each fleet could use a unique Dirichlet multinomial parameter, or all could share the same, or any combination of unique and shared. The requested number of Dirichlet multinomial parameters are specified as parameter lines in the control file immediately after the selectivity parameter section. Please note that age-compositions Dirichlet multinomial parameters are continued after length-compositions, so a model with one fleet and both data types would presumably require two new Dirichlet multinomial parameters.

The Dirichlet estimates the effective sample size as  $N_{eff} = \frac{1}{1+\theta} + \frac{N\theta}{1+\theta}$  where  $\theta$  is the estimated parameter and  $N$  is the input sample size. Stock Synthesis estimates the log of the Dirichlet multinomial parameter such that  $\hat{\theta}_{fishery} = e^{-0.6072} = 0.54$  where assuming  $N = 100$  for the fishery would result in an effective sample size equal to 35.7.

This formula for effective sample size implies that, as the Stock Synthesis parameter log\_Theta goes to large values (i.e., 20), then  $N_{eff}$  will converge to the input sample size ( $N_{input}$ ). In this case, small changes in the value of the log\_Theta parameter has no action, and the derivative of the negative log-likelihood is zero with respect to the parameter, which means the Hessian will be singular and cannot be inverted. To avoid this non-invertible Hessian when the log\_Theta parameter becomes large, turn it off while fixing it at the high value. In summary, we recommend setting the upper bound for the Dirichlet multinomial parameter log\_Theta to a high value (i.e., 20-25), and then if any fleet has an estimate of log\_Theta > 15 then turn that Dirichlet multinomial parameter off while starting it at the estimated high value. This is equivalent to turning off down-weighting of fleets where evidence suggests that  $N_{eff} = N_{input}$ .

For additional information about the Dirichlet multinomial please see Thorson et al. (2017).

## Length Composition Data

Composition data within SS can be entered as proportions, numbers, or values of observations by length bin based on data expansions.

The data bins do not need to cover all observed lengths. The selection of data bin structure should be based on the observed distribution of lengths and the assumed growth curve. If growth asymptotes at larger lengths, having additional length bins across these sizes may not contribute information to the model and may slow model run time. Additionally, the lower length bin selection should be selected such that, depending on the size selection, to allow for information on smaller fish and possible patterns in recruitment. While set separately users should ensure that the length and age bins align. It is recommended to explore multiple configurations of length and age bins to determine the impact of this choice on model estimation.

Specify the length composition data as:

28	Number of length bins for data
26 28 30 ... 80	Vector of length bins associated with the length data.
The above data bins will combine 0-26 cm fish, >26 - 28 cm, ..., and 80+ cm fish.	

Example of a single length composition observation:

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

### Sex

If model has only one sex defined in the set-up, all observations must have sex set equal to 0 or 1 and the data vector by year will equal the number of the user defined data bins. This also applies to the age data.

In a 2 sex model, the data vector always has female data followed by male data, even if only one of the two sexes has data that will be used. The below description applies to a 2 sex model:

- Sex = 0 means combined male and female (must already be combined and information placed in the female portion of the data vector) (male entries must exist for correct data reading, then will be ignored).



- Sex = 1 means female only (male entries must exist for correct data reading, then will be ignored).
- Sex = 2 means male only (female entries must exist and will be ignored after being read).
- Sex = 3 means data from both sexes will be used and they are scaled so that they together sum to 1.0; i.e. sex ratio is preserved.

## Partition

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

- 0 = combined;
- 1 = discard; and
- 2 = 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 in the length or age composition observed data line is negative, then the observation is processed and its expected value and log likelihood are calculated, but this log likelihood is not included in the total log likelihood. This feature allows the user to see the fit to a provisional observation without having that observation affect the model.

## Note

When processing data to be input into SS, all observed fish of sizes smaller than the first bin should be added to the first bin and all observed fish larger than the last bin should be condensed into the last bin.

SS no longer requires that the number of length composition data lines 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 and replicate observations by a year for a fleet are allowed (unlike survey and discard data). However, if the super-period approach is used, then each super-periods' observations must be contiguous in the data file.

## Age Composition Option

The age composition section begins by reading the number of age bins. If the value 0 is entered for the number of age bins, then SS skips reading the bin structure and all reading of other age composition data inputs.

---

17	Number of age bins; can be equal to 0 if age data are not used; do not include a vector of agebins if the number of age bins is set equal to 0.
----	---

---

## Age Composition Bins

If a positive number of age bins is read, then SS reads the bin definition next.

---

1 2 3 ... 20 25	Vector of ages
-----------------	----------------

---

The bins are in terms of observed age (here age) and entered as the lower edge of each bin. Each ageing imprecision definition is used to create a matrix that translates true age structure into age structure. The first and last age' bins work as accumulators. So in the example any age 0 fish that are caught would be assigned to the age = 1 bin.

## 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 standard deviation 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. The dimension of the ageing error matrix requires the column length match the population maximum age specified at the top of the data file. However, the maximum age for binning of age data may be lower than the population maximum age.

2	Number of ageing error matrices to generate
---	---

Example with no bias and very little uncertainty at age:

Age-0	Age-1	Age-2	...	Max Age	
-1	-1	-1	...	-1	#Mean Age
0.001	0.001	0.001	...	0.001	#SD

Example with no bias and some uncertainty at age:

0.5	1.5	2.5	...	Max Age + 0.5	#Mean Age
0.5	0.65	0.67	...	4.3	#SD Age

Example with bias and uncertainty at age:

0.5	1.4	2.3	...	Max Age + Age Bias	#Mean Age
0.5	0.65	0.67	...	4.3	#SD Age

In principle, one could have year or laboratory specific matrices for ageing error. 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 integer age. The length of the input vector is equal to the population maximum age plus one (0-max age), with the first entry being for age 0 fish and the last for fish of population maximum age. The following line is a vector with the standard deviation of age for each true age with a normal distribution assumption.

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 standard deviation 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 a full parameter line below the cohort growth deviation parameter (or the movement parameter lines if used) in the mortality growth parameter section. These parameters are described in the control file section of this manual.

## Age Composition Specification

If age data are included in the model, the following set-up is required, similar to the length data section.

Specify bin compression and error structure for age composition data for each fleet:

Min. Tail Compress.	Constant added to prop.	Combine males & females	Compress. Bins	Comp. Error Dist.	Dirichlet Param. Select	Min. Sample Size
0	0.0001	1	0	0	0	1
0	0.0001	1	0	0	0	1

Specify method by which length bin range for age obs will be interpreted:

- 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	Sex	Partition	Age Err	Lbin lo	Lbin hi	Nsamp	Data Vector
1987	1	1	3	0	2	-1	-1	79	<enter data values>
-9999	0	0	0	0	0	0	0	0	0

Syntax for Sex, Partition, and data vector are same as for length. The data vector has female values then male values, just as for the length composition data.

### Age Error

Age error (Age Err) identifies which ageing error matrix to use to generate expected value for this observation.

### Lbin Low and Lbin High

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 -1 to select the full size range. 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.

## Excluding Data

As with the length composition data, a negative year value 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 log likelihood, a negative value for month causes start-stop of super-period.

## 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 sex model, it is best to enter these conditional age-at-length data as single sex observations (sex = 1 for females and = 2 for males), rather than as joint sex observations (sex = 3). Inputting joint sex observations comes with a more rigid assumption about sex ratios within each length bin. Using separate vectors for each sex allows 100% of the expected composition to be fit to 100% observations within each sex, whereas with the sex = 3 option, you would have a bad fit if the sex ratio were out of balance with the model expectation, even if the observed proportion at age within each sex exactly matched the model expectation for that age. Additionally, inputting the conditional age-at-length data as single sex observations isolates the age composition data from any sex 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 age is conditional on length.

## Mean Length or Body Weight-at-Age

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

---

1      Use mean size-at-age observation (0 = none, 1 = read data matrix)

An example observation:

---

Yr	Month	Fleet	Sex	Part.	Age Err.	Ignore	Data Vector (Female - Male)	Sample Size (Female - Male)
1989	7	1	3	0	1	999	<Mean Size values>	<Sample Sizes>
...								
-9999	0	0	0	0	0	0	0 0 0 0 0 0 0	0 0 0 0 0 0 0

---

### Note

- Negatively valued mean size entries will be ignored in fitting. This feature allows the user to see the fit to a provisional observation without having that observation affect the model.
- A number of fish value of 0 will cause mean size value to be ignored in fitting. This feature allows the user to see the fit to a provisional observation without having that observation affect the model.
- Negative value for year causes observation to not be included in the working matrix. This feature is the easiest way to include observations in a data file but not to use them in a particular model scenario.
- Each sexes' data vector and N fish vector has length equal to the number of age bins.
- The "Ignore" column is not used (set aside for future options) but still needs to have default values in that column (any value).
- 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.

- An experiment that may be of interest might be to take the body weight-at-age data and enter it to SS as empirical body weight-at-true age in the wtatage.ss file, and to contrast results to entering the same body weight-at-age data here and to attempt to estimate growth parameters, potentially time-varying, that match these body weight data.
- If using mean size-at-age data, please see the [lambda usage notes](#) regarding issues for model fitting depending upon other data within the model.

## 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:

---

1	Number of environmental variables
---	-----------------------------------

---

COND > 0 Example of 2 environmental observations:

Year	Variable	Value
1990	1	0.10
1991	1	0.15
-9999	0	0

---

### Note

- Any years for which environmental data are not read are assigned a value of 0.0. None of the current link functions in SS contain a link parameter that acts as an offset. Therefore, you should subtract the mean from your data before entering it into SS. This lessens the problem with missing observations, but does not eliminate it. A better approach for dealing with missing observations is to use a different approach for the environmental effect on the parameter. Set up the parameter to have random deviations for all years, then enter the zero-centered environmental information as a [special survey of type 35](#) and set up the catchability of that survey to be a link to the deviation vector. This is definitely a more complex approach and not much used, but it is superior in treatment of missing values and superior in allowing for error in the environmental relationship.
- 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.
- Some model derived quantities like summary biomass and recruitment deviation are assigned to some [negative valued environmental variables](#). This is a stepping stone towards creating ability for parameters to be density-dependent.

## Generalized Size Composition Data

A flexible feature with SS 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-sex model, the new composition data can be combined sex, single sex, or both sex.
- If a retention function has been defined, then the new composition data can be from the combined discard + retained, discard only or retained only.
- 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 as 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.



Example entry:

---

2	N of size frequency methods, if this value is 0, then omit all entries below.						
---	---	--	--	--	--	--	--

---

COND > 0

25	15	Nbins per method					
2	3	Units per each method (1 = biomass, 2 = numbers)					
3	3	Scale per each method (1 = kg, 2 = lbs, 3 = cm, 4 = inches)					
1e-9	1e-9	Min compression to add to each observation (entry for each method)					
2	2	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
-26	28	30	32	34	36	38	40	42	44	46	48	50	52	54			

---

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

---

Method	Year	Month	Fleet	Sex	Part	Sample Size	<composition females then males>
--------	------	-------	-------	-----	------	----------------	-------------------------------------

---

1	1975	1	1	3	0	43	<data>
1	1977	1	1	3	0	43	<data>
1	1979	1	1	3	0	43	<data>
1	1980	1	1	3	0	43	<data>

---

## Note

- There is no tail compression for generalized size frequency data.
- Super-period capability is enabled in same way as for length and age composition data.
- By choosing units=2 and scale=3, the size composition method can be nearly identical to the length composition 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 sex and for each season because weight-at-length can differ between sexes and can vary seasonally.

## Tag-Recapture Data

The ability to analyze tag-recapture data is available with SS. Each released tag group is characterized by an area, time, sex and age at release. Each recapture event is characterized by a time and fleet. SS fleets each operate in only one area, hence, it is not necessary to record the area of recapture. Inside the model, the tagged cohort is apportioned across all growth patterns in that area at that time (with options to apportion to only one sex or to both). The tag cohort combined with the 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 and recaptures follow the timing of the fleet that made the recapture.

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>	Sex	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 entered in tag group order.
- <tfill> values are place holders and are replaced by program generated values for model time.
- Analysis of the tag-recapture data has one negative log likelihood component for the distribution of recaptures across areas and another negative log likelihood component for the decay of tag recaptures from a group over time, hence informative about mortality. More on

this is in the control file.

## 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 morph composition, 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	Type	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 number of stocks entered with these data must match the number of growth patterns in the control file.
- The expected value is combined across sexes.
- 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. Currently, this value must be set to 0 (combined discard and retained fish).

- Note that there is a specific value of minimum compression to add to all values of observed and expected.

## Selectivity Empirical Data (future feature)

It is sometimes possible to conduct field experiments or other studies to provide direct information about the selectivity of a particular length or age relative to the length or age that has peak selectivity, or to have a prior for selectivity that is more easily stated than a prior on a highly transformed selectivity parameter. This section provides a way to input data that would be compared to the specified derived value for selectivity. This is a placeholder at this time, required to include in the data file and will be fully implemented soon.

Selectivity data feature is under development for a future option and is not yet implemented. The input line still must be specified in SS as follows:

---

0	Do data read for selectivity (future option)
---	--

---



---

End of Data File

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

---

## Excluding Data

Data that are before the model start year or greater than the retrospective year 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. 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.

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 number.

## 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 same

set of time steps. The option is available for all types of data and a similar syntax is used.

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 number.

Super-periods are started with a negative value for month, and then stopped with a negative value for month, observations within the super-period are designated with a negative fleet field. The standard error or input sample size field is now used for weighting of the expected values. An error message is generated if the super-period does not contain one observation with a positive fleet field.

An expected value for the observation will be computed for each selected time period within the super-period. The expected values are weighted according to the values entered in the standard error (or input sample size) field for all observations except 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 three 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 3 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).

Super-period 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 standard error (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 observation is ignored. The expected value for the survey in 1983 will have a relative weight equal to the value in the standard error field (0.85) in calculating the combined expected value.
1985	2	-3	88	0.40	Note that 1984 is not included in the super-period 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.

## Control File

### Overview of Control File

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

1. Number of growth patterns and platoons

2. Design matrix for assignment of recruitment to area/settlement event/growth pattern
3. Design matrix for movement between areas
4. Definition of time blocks that can be used for time-varying parameters
5. Controls for all time-varying parameters
6. Specification for growth and fecundity
7. Natural mortality growth parameters, weight-at-length, maturity, and fecundity, for each sex
8. Hermaphroditism parameter line (if used)
9. Recruitment distribution parameters for each area, settlement event, and growth pattern
10. Cohort growth deviation
11. Movement between areas (if used)
12. Age error parameter line (if used)
13. Catch multiplier (if used)
14. Fraction female
15. Setup for any mortality-growth parameters are time-varying
16. Seasonal effects on biology parameters
17. Spawner-recruitment parameters
18. Setup for any stock recruitment parameters are time-varying
19. Recruitment deviations
20. F ballpark value in specified year
21. Method for calculating fishing mortality (F)
22. Initial equilibrium F for each fleet
23. Catchability (Q) setup for each fleet and survey
24. Catchability parameters



25. Setup for any catchability parameters are time-varying
26. Length selectivity, retention, discard mortality setup for each fleet and survey
27. Age selectivity setup for each fleet and survey
28. Parameters for length selectivity, retention, discard mortality for each fleet and survey
29. Parameters for age selectivity, retention, discard mortality for each fleet and survey
30. Setup for any selectivity parameters that are time-varying
31. Tag-recapture parameters
32. Variance adjustments
33. Lambdas for likelihood components

The order in which they appear in the control file has grown over time rather opportunistically, so it may not appear particularly logical at this time, especially various aspects of recruitment distribution and growth. When the same information is entered via the SS GUI, it is organized more logically and then written in this form to the text control file.

## Parameter Line Elements

The primary role of the SS control file is to define the parameters to be used by the model. The general syntax of the 14 elements of a long parameter line is described here. If used, time-varying parameter lines use only the first seven elements of a parameter line and will be referred to as a short parameter line. Three types of time-varying properties can be applied to a base parameter: blocks or trend, environmental linkage, and random deviation. 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 phase (described below) for the parameter is negative the parameter is fixed at this value. If the ss.par file is read, it overwrites these INIT values.
4	PRIOR	Expected value for the parameter. This value is ignored if the prior type is 0 (no prior) or 1 (symmetric beta). If the selected prior type (described below) is lognormal, this value is entered in log space.
5	PRIOR SD	Standard deviation for the prior, used to calculate likelihood of the current parameter value. This value is ignored if prior type is 0.
6	PRIOR TYPE	0 = none, 1 = symmetric beta; 2 = full beta; 3 = lognormal without bias adjustment; 4 = lognormal with bias adjustment; 5 = gamma; and 6 = normal.
7	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 ss.par file).
8	Env var & Link	Create a linkage to an input environmental time-series
9	Dev link	Invokes use of the deviation vector in the linkage function
10	Dev min yr	Beginning year for the deviation vector
11	Dev max yr	Ending year for the deviation vector
12	Dev phase	Phase for estimation for elements in the deviation vector
13	Block	Time block or trend to be applied
14	Block function	Functional form for the block offset.

Note that relative to SS v.3.24, the order of PRIOR SD and PRIOR TYPE have been switched and the PRIOR TYPE options have been renumbered.

The full parameter line (14 in length) syntax for the mortality-growth, spawn-recruitment, catchability, and selectivity sections provides additional controls to give the parameter time-varying properties. If a parameter (a full parameter line of length 14) is set up to be time-varying (i.e., parameter time blocks, annual deviations), short parameter lines, the first 7 elements, are required to be specified immediately after the main parameter block (i.e., mortality-growth parameter section). Additional information regard time-varying parameters and how to implement them in SS is available in the [Using Time-Varying Parameters](#) section.

## Terminology

The term COND appears in the "Typical Value" column of this documentation (it does not actually appear in the model files), 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 ss\_new files.

## Beginning of Control File Inputs

Typical Value	Description and Options
#C comment	Comments beginning with #C at the top of the file will be retained and included in output.
0	<p>0 = Do not read the weight-at-age (wtatage.ss) file;</p> <p>1 = Read the weight-at-age (wtatage.ss) file, also read and use the growth parameters; and</p> <p>2 = Future option to read the weight-at-age (wtatage.ss) file, then omit reading and using growth parameters and all length-based data.</p> <p>Additional information on the weight-at-age file and the expected formatting can be found <a href="#">in the Empirical Weight-at-Age section</a>.</p>

Typical Value	Description and Options
1	<p>Number (N) of growth patterns (GP), also referred to as morphs:</p> <p>These are collections of fish with unique biological characteristics (growth, mortality, weight-length, reproduction). The GP x Sex x Settlement Events constitute unique growth patterns that are tracked in SS. They are assigned these characteristics at birth and retain them throughout their lifetime. At recruitment, growth pattern members are distributed across areas (if any) and they retain their biological characteristics even if they move to another area in which a different cohort with different biological characteristics might predominate. For example, one could assign a fast-growing growth pattern to recruit predominately in a southern areas and a slow-growing growth pattern to a northern area. The natural mortality and growth parameters are specified for each growth pattern in the mortality-growth parameter section in the order of females growth pattern 1 to growth pattern N followed by males growth pattern 1 to growth pattern N in a two sex model.</p>
1	<p>Number of platoons within a growth pattern/morph:</p> <p>This allows exploration of size-dependent survivorship. A value of 1 will not create additional platoons. Odd-numbered values (i.e., 3, 5) will break the overall morph into that number of platoons creating a smaller, larger, and mean growth platoon. The higher the number of platoons the slower SS will run, so values above 5 not advised. The fraction of each morph assigned to each platoon is custom-input or designated to be a normal approximation. When multiple platoons are designated, an additional input is the ratio of between platoon to within platoon variability in size-at-age. This is used to partition the total growth variability. For the platoons, 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 that Growth Pattern x Sex.</p>
COND > 1	Following 2 lines are conditional on N platoons > 1.
0.7	Platoon between/within standard deviation ratio. Ratio of the amount of variability in length-at-age between platoons to within platoons.
0.2 0.6 0.2	Distribution among platoons. Enter either a custom vector or enter a vector of length N with the first value of -1 to get a normal approximation: (0.15, 0.70, 0.15) for 3 platoons, or 5 platoons (0.031, 0.237, 0.464, 0.237, 0.031).

## Empirical Weight-at-Age

With version 3.04, SS added 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. The values are read from a separate file named, wtatage.ss. This file is only required to exist if this option is selected. See the section on [weight-at-age](#) for additional information on file formatting for empirical weight-at-age.

## Recruitment Timing and Distribution

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 produced one annual total recruitment value. The annual recruitment value was then distributed among seasons, areas, and growth types according to other model parameters.

In SS v.3.30, more control of the seasonal timing is provided and there now is an explicit elapsed time between spawning and recruitment. Spawning still occurs, just once per year, which defines a single spawning biomass for the stock-recruitment curve but its timing can be at any specified time, not just the beginning of a season. Recruitment of the progeny from an annual spawning can now enter the population in one or more settlement event, at some point after spawning as defined by the user.

Example set-up where there are multiple settlement events:

3	Number of recruitment settlement events		
0	Unused option		
Growth Pattern	Month	Area	Age (for each settlement assignment)
1	11.0	1	0
1	12.0	1	0
1	1.0	1	1

## Recruitment Timing and Settlement

Details regarding recruitment timing and settlement:

- Recruitment happens in specified settlement events (growth pattern, month, area).

- Number of unique settlement timings calculated at runtime.
- Now there is explicit elapsed time between spawning and recruitment.
- Growth and natural mortality of the platoon begins at time of settlement, which is its real age 0.0 for growth; but pre-settlement fish exist from the beginning of the season of settlement, so can be caught if selected.
- Age at recruitment now user-controlled (should be 0 if in year of spawning).
- All fish become integer age 1 (for age determination) on their first January 1st.
- Recruitment can occur >12 months after spawning which is achieved by setting the settlement age to a value greater than 1.0.

The distribution of recruitment among these settlement events is controlled by recruitment apportionment parameters. There must be a parameter line for each growth pattern, then for each area, then for each settlement. All of these are required, but only those growth pattern x area x settlements designated to receive recruits in the recruitment design matrix will have the parameter used in the recruitment distribution calculation. For the recruitment apportionment, the parameter values are the natural log of apportionment weight. The sum of all apportionment weights is calculated for each growth pattern x area x settlements that have been designated to receive recruits in the recruitment design matrix. Then the apportionment weights are scaled to sum to 1.0 so that the total recruitment from the spawning event is distributed among the cells designated to receive recruitment. These distribution parameters can be time-varying, so the fraction of the recruits that occur in a particular growth pattern, area, or settlement can change from year to year.

## Recruitment Distribution and Parameters

- SS processes the parameter values according to the following equation:

$$\text{apportionment}_i = \frac{e^{p_i}}{\sum_{j=1}^N e^{p_j}} \quad (1)$$

- Set the value for one of these parameters,  $p_i$ , to 0.0 and not estimate it so that other parameters will be estimated (if not fixed) relative to its fixed value.
- Give the estimated parameters a min-max of something like -5 and 5, so they have a good range relative to the base parameter.
- 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.
- 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 spawned in the late fall. In general, this means that SS operates under the assumption that all age data have been adjusted so that fish are age 0 at the time of spawning and all fish graduate to the next age on January 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 more ideally 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 maximum length (e.g., no seasonal effects on growth).
- At the time of settlement, fish 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 January 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 standard deviation (necessary for the growth model used in SS2 V1.x), but the option to add a constant has been retained in the model.

Typical Value	Description and Options
1	Recruitment distribution method. This section controls which combinations of growth pattern x area x settlement will get a portion of the total recruitment coming from each spawning. Options: 1 = no longer available (used the SS v.3.24 or earlier setup); 2 = main effects for growth pattern, settle timing, and area; 3 = each settle entity; and 4 = none, no parameters (only if growth pattern x settlement x area = 1).
1	Spawner-Recruitment (not implement yet, but required), options: 1 = global; and 2 = by area (by area is not yet implemented; there is a conceptual challenge to doing the equilibrium calculation when there is fishing).

Typical Value	Description and Options
1	Number of recruitment settlement assignments. Must be at least 1 even if only 1 settlement and 1 area because the timing of that settlement must be specified.
0	Future feature, not implement yet but required.
1 5.5 1 0	Recruitment assignment to growth pattern, month, area, and age (for each settlement event). Here settlement is set to mid-May (month 5.5). Note that normally the calendar age at settlement is 0 if settlement happens between the time of spawning and the end of that year, and at age 1 if settlement is in the year after spawning.

## Movement

Here the movement of fish between areas are defined. This is a box transfer with no explicit adjacency of areas, so fish can move from any area to any other area in each time step. While not incorporated yet, there is a desire for future versions of SS to have the capability to allow sex-specific movement, and also to allow some sort of mirroring so that sexes and growth patterns can share the same movement parameters if desired.

Typical Value	Description and Options
COND: only if areas > 1	
2	Enter Number of movement definitions.
1.0	First age that moves. This value is a real number, not an integer, to allow for an in-year start to movement in a multi-season model. It 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).



Typical Value	Description and Options
1 1 1 2 4 10 1 2 2 1 4 10	Movement definitions: season, growth pattern, source area, destination, age1, and age2. The example shown here has 1 growth patterns and 2 areas with fish moving between the two areas. The rate of movement will be controlled by the movement parameters later defined in the mortality-growth parameter section. Here the age1 and age2 specify the range over which the movement parameters are interpolated with movement constant below age1 and above age2.

Two parameters will be entered later for each growth pattern, area pair, and season.

- Movement is constant at the first parameter (P1) below the specified minimum age for movement change, constant at the second parameter (P2) above maximum age for movement change, and linearly interpolated for intermediate ages.
- A movement rate parameter can be set to use the same value as the corresponding parameter for the first defined movement pattern by entering a parameter value of -9999 and a negative phase value.
- For each source area, the implicit movement parameter value is 0.0 (movement within a single area). However, this default value can be replaced if the stay movement is selected to have an explicit pair of parameters (e.g., specify movement rate for area 1 to area 1) and will require additional parameter lines.
- A constant movement rate across all ages can be accomplished by either:
  - Setting both movement ages to 0, not estimating the first movement parameter, and using a second movement parameter to cover all ages from 0 to the maximum number of ages.
  - Setting movement ages to any value, estimating the first movement parameter, and setting the second movement parameter to have a value of -9998 with a negative phase.
- The parameter is exponentiated so that a movement parameter value of 0 becomes 1.0.
- 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.

$$\text{rate}_i = \frac{e^{p_i}}{\sum_{j=1}^N e^{p_j}} \quad (2)$$

- At least one movement parameter must be fixed so that all other movement parameters are estimated relative to it. This is achieved naturally by not specifying the stay rate parameter so it has a fixed value of 0.0.

- The resultant movement rates are multiplied by season duration in a seasonal model.

## Time Blocks and Time-varying Parameter Controls

Typical Value	Description and Options
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 > 0: 3 2 1	Following inputs are omitted if the number of block patterns equals 0. Blocks per pattern:
1975 1985 1986 1990 1995 2001	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.
1987 1990 1995 2001	Beginning and ending years for blocks in design 2.
1999 2002	Beginning and ending years for blocks in design 3.

When using time blocks, it is important to consider which parameters will affect which years of the time series. There are three main situations:

1. Offset approach: One or more time blocks are created and cover all or a subset of the years. Each block gets a parameter that is used as an offset from the base parameter. In this situation you typically will allow SS to estimate the base parameter and each of the offset parameters. In years not covered by blocks, the base parameter alone is used. However, if blocks cover all the years, then the value of the block parameter is completely correlated with the mean of the block offsets, so model convergence and variance estimation could be affected. The recommended approach when using offsets is to not have all the years be covered by blocks when doing offsets, or to fix the base parameter value at a reasonable level when doing offsets for all years.
2. Replacement approach: Option A: Here time blocks are created which cover a subset of the years. The base parameter is used in the non-block years and the value of that base parameter is replaced by the block parameter in each respective block. In this situation, you typically allow SS to estimate the base parameter and each of the block parameters.
3. Replacement-Option B: Here replacement time blocks are created for all the years. In this case

the base parameter is simply a placeholder that is always replaced by a block parameter. In this situation, do not allow SS to estimate the base parameter and only estimate the corresponding block replacement parameters, otherwise, the search algorithm will be attempting to estimate parameters that do not contribute to the log likelihood, so model convergence and variance estimation could be affected. Note however, that the minimum and maximum for the base parameter are used as checks on the minimum and maximum of the blocks.

Regardless of the block set-up approach, special consideration should be given regarding which parameter values are applied during forecast years. The model will default to use all base parameter values during the forecast period. However, there are controls in the forecast file which allow the user to specify specific parameter years to be applied during the forecast period for selectivity, relative F, and recruitment.

In SS v.3.30, several changes are introduced to the implementation of time-varying parameters:

- Time-varying parameters for biology, spawner-recruitment, catchability, and selectivity are implemented using the same approach and share code.
- The block feature that allowed input of one block parameter line and replication of that line by SS as often as needed has been replaced. Now there is a complete time-varying parameter auto-generation capability.
- The logistic bound constraint is no longer implemented due to the challenges it created to interpreting parameter values. Instead, the auto-generate feature now creates bounds on time-varying parameters for blocks such that the combination of a bounded value of the time-varying parameter and the base parameter will not violate the base parameter bounds.
- For more information on the implementation of time-varying parameters, see the [Using Time-Varying Parameters](#) section

## Auto-generation

Auto-generation is a useful way to automatically have SS create the required short time-varying parameter lines which will be written in the control.ss\_new file. These parameter lines can then be copied into the control file and modified as needed. As example, if you want to add a block to natural mortality, modify the block and block function entry of the mortality parameter line, ensure that auto-generation is set to 0 (for the biology section at least) and run the model without estimation. The control.ss\_new file will now show the required block parameter line specification for natural mortality and this line can be copied into the main control file. Note, that if auto-generation is on (set to 0), the model will not expect to read the time-varying parameters in that section of the control file and will error out if they are present

Typical Value	Description and Options
1	Environmental/Block/Deviation adjust method for all time-varying parameters. 1 = warning relative to base parameter bounds; and 3 = no bound check. Logistic bound check form from previous SS versions (e.g., SS v.3.24) is no longer an option.
1 1 1 1 1	Auto-generation of time-varying parameter lines. Five values control auto-generation for parameter block sections: 1-biology, 2-spawn-recruitment, 3-catchability, 4-tag (future), and 5-selectivity. The accepted values are: 0 = auto-generate all time-varying parameters (no time-varying parameters are expected); 1 = read each time-varying parameter line as exists in the control file; and 2 = read each line and auto-generate if read if the time-varying parameter value for LO = -12345. Useful to generate reasonable starting values.

## Biology

### Natural Mortality

Natural mortality (M) has some options that are referenced to integer age, and some to real age since settlement. So, if M varies by age, M will change by season and cohorts born early in the year will have different M than late born cohorts.

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. So, natural mortality is scaled by the length of the fish.

Typical Value	Description and Options
1	Natural Mortality Options: 0 = A single parameter; 1 = N breakpoints; 2 = Lorenzen; 3 = Read age specific M and do not do seasonal interpolation; and 4 = Read age specific and do seasonal interpolation, if appropriate.

Typical Value	Description and Options
COND = 0	No additional natural mortality controls.
COND = 1	
4	Number of breakpoints. Then read a vector of ages for these breakpoints. Later, per sex x GP, read N parameters for the natural mortality at each breakpoint.
2.5 4.5 9.0 15.0	Vector of age breakpoints.
COND = 2	
4	Reference age for Lorenzen natural mortality: read one additional integer value that is the reference age. Later read one parameter for each sex x growth pattern that will be the M at the reference age. Other ages will have an M scaled to its body size-at-age. However, if platoons are used, all will have the same M as 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 in the mortality growth parameter section. With option 3, 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 where in a 2 sex model the first row is female and the
0.20 0.23 ...	second row is male. If there are multiple growth patterns female growth pattern 1-N is read first followed by males 1-N growth pattern.

## Growth

### Timing

When fish recruit at the real age of 0.0 at settlement, they have body size equal to the lower edge of the first population size bin. The fish then grow linearly until they reach a real age equal to the input value “growth-at-age for L1” and have a size equal to the parameter value for L1 (the minimum length parameter). As they age further, they grow according the selected growth equation. The growth curve is calibrated to go through the size L2 parameter when they reach the age of maximum length.

### Maximum Length (Linf)

If “Growth at age for L2” is set equal to 999, then the size at the L2 parameter is used as Linf.

## Schnute growth function

The Schnute implementation of a 3-parameter growth function is invoked by entering 2 in the growth type field. Then a fourth parameter is read after reading the von Bertalanffy growth coefficient parameter (K). 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.

## Mean size-at-maximum age

The mean size of fish in the max age age bin depends upon how close the growth curve is to Linf by the time it reaches max age and the mortality rate of fish after they reach max age. SS provides an option for the mortality rate to use in this calculation during the initial equilibrium year. This must be specified by the user and should be reasonably close to M plus initial F. In SS v.3.30, this uses the von Bertalanffy growth out to 3 times the maximum population age and decays the numbers at age by  $\exp(-\text{value set here})$ . For subsequent years of the time series, SS should update the size-at-maximum age according to the weighted average mean size of fish already at maximum age and the size of fish just graduating into maximum age. Unfortunately, this updating is only happening in years with time-varying growth. This will hopefully be fixed in a the future version.

## Age-specific K

This option creates age-specific K multipliers for each age of a user-specified age range, with independent multiplicative factors for each age in the range and for each growth pattern / sex. The null value is 1.0 and each age's K is set to the next earlier age's K times the value of the current age's multiplier. Each of these multipliers 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.

## Growth cessation

A growth cessation model was developed for the application to tropical tuna species (Maunder et al., 2018). Growth cessation allows for a linear relationship between length and age, followed by a marked reduction of growth after the onset of sexual maturity by assuming linear growth for the youngest individuals and then a logistic function to model the decreasing growth rate at older ages.

Example growth specifications:

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. Third parameter has null value of 1.0;</p> <p>3 = von Bertalanffy with age-specific K multipliers for specified range of ages,</p> <p>4 = age specific K. Set base K as K for age = nages and working backwards and the age-specific K = K for the next older age * multiplier;</p> <p>5 = age specific K. Set base K as K for nages and work backwards and the age-specific K = base K * multiplier;</p> <p>6 = not implemented;</p> <p>7 = not implemented; and</p> <p>8 = growth cessation. Decreases the K for older fish. If implemented, the Amin and Amax parameters, the next two lines, need to be set at 0 and 999 respectively. The mortality-growth parameter section requires the base K parameter line which is interpreted as the steepness of the logistic function that models the reduction in the growth increment by age followed by a second parameter line which is the parameter related to the maximum growth rate.</p>
1.66	Growth Amin (A1): Reference age for first size-at-age (post-settlement) parameter.
25	Growth Amax (A2): Reference age for second size-at-age parameter (999 to use as L infinity).
0.20	<p>Exponential decay for growth above maximum age (plus group: fixed at 0.20 in SS v.3.24; should approximate initial Z). Alternative Options:</p> <p>-998 = Disable growth above maximum age (plus group) similar to earlier versions of SS (prior to SS v.3.24); and</p> <p>-999 = Replicate the simpler calculation done in SS v.3.24.</p>
0	Placeholder for future growth feature.
COND >= 3	Growth option age-specific K
2	Number of K multipliers to read;
5	Minimum age for age-specific K; and

Typical Value	Description and Options
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.
1	<p>CV Pattern (cannot be time-varying)</p> <p>0: <math>CV=f(LAA)</math>, 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: <math>CV=f(A)</math>, so interpolation is a function of age;</p> <p>2: <math>SD=f(LAA)</math>, so parameters define the standard deviations of length-at-age and interpolation is a function of mean length-at-age;</p> <p>3: <math>SD=f(A)</math>; and</p> <p>4: Lognormal distribution of size-at-age. Input parameters will specify the standard deviation of natural log 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>

## Maturity-Fecundity

Typical Value	Description and Options
2	<p>Maturity Option:</p> <p>1 = length logistic;</p> <p>2 = age logistic;</p> <p>3 = read maturity-at-age for each female growth pattern;</p> <p>4 = read a fecundity x maturity-at-age vector for all ages;</p> <p>5 = disabled; and</p> <p>6 = read vector of length-based maturity values.</p> <p>Note: need to read 2 parameter lines (maturity at 50% and maturity slope) even if option 3 or 4 is selected.</p>
COND = 3 or 4 0 0.05 0.10 ...	<p>Maturity Option</p> <p>Vector of age-specific maturity or fecundity. One row of length Nages + 1 based on the maximum population age for each female growth pattern.</p>
COND = 6	Maturity Option



Typical Value	Description and Options
0 0.05 0.10 ...	Vector of length-specific maturity or fecundity, based on the population length bins. One row of length equal to the number of population length bins (defined in the data file) for each female growth pattern.
1	First Mature Age: all ages below the first mature age will have maturity set to zero. This value is overridden if maturity option is 3 or 4 or if empirical weight-at-age (wtatage.ss) is used, but still must exist here.
1	<p>Fecundity Option (irrelevant if maturity option is 4 or wtatage.ss is used):</p> <p>1 = to interpret the 2 egg parameters as linear eggs/kg on body weight (current SS default), so fecundity = <math>wt * (a + b * wt)</math>, so value of a=1, b=0 causes eggs to be equivalent to spawning biomass;</p> <p>2 = to set fecundity = <math>a * L^b</math>;</p> <p>3 = to set fecundity = <math>a * W^b</math>, so values of a=1, b=1 causes fecundity to be equivalent to spawning biomass;</p> <p>4 = fecundity = <math>a + b * L</math>; and</p> <p>5 = eggs = <math>a + b * wt</math>.</p>

## Hermaphroditism

Typical Value	Description and Options
0	<p>Hermaphroditism Option:</p> <p>0 = not used;</p> <p>1 = invoke female to male age-specific function; and</p> <p>-1 = invoke male to female age-specific function.</p> <p>Note: this creates the annual, age-specific fraction that change sex, it is not the fraction that is each sex.</p>
COND = 1 or COND = -1	Read 2 lines below if hermaphroditism is selected. Also read 3 parameters after reading the male (option 1) or female (option -1) weight-length parameter.
-1	<p>Hermaphroditism Season:</p> <p>-1 to do transition at the end of each season (after mortality and before movement); and</p> <p>&lt;positive integer&gt; to select just one season.</p>

Typical Value	Description and Options
1	<p>Include males or females, dependent upon sex change direction, in spawning biomass;</p> <p>0 = no males or females, dependent upon sex change direction, in spawning biomass; and</p> <p>1 = simple addition of males to females.</p>

The hermaphroditism option requires three full parameter lines in the mortality growth section:

1. A parameter line for inflection point (in age) at when fish may begin to change sex.
2. The standard deviation.
3. The asymptote of the maximum proportion that will transition to the other sex

These parameter lines are entered directly after the weight-at-length parameters for males.

## Parameter offset method

Typical Value	Description and Options
1	<p>Parameter Offset Method:</p> <p>1 = direct assignment;</p> <p>2 = for each growth pattern by sex, parameter defines offset from sex 1, offsets are in exponential terms, so for example: <math>M_{\text{old male}} = M_{\text{old female}} * \exp(M_{\text{old male}})</math>; and</p> <p>3 = for each growth pattern by sex, parameter defines offset from growth pattern 1 sex 1. For females, given that "natM option" is breakpoint and there are two breakpoints, parameter defines offset from early age (e.g., <math>M_{\text{old female}} = M_{\text{young female}} * \exp(M_{\text{old female}})</math>). 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., <math>M_{\text{old male}} = M_{\text{young female}} * \exp(M_{\text{young male}}) * \exp(M_{\text{old male}})</math>).</p>

## Catch Multiplier

These parameter lines are only included in the control file if the catch multiplier field in the data file is set to 1 for a fleet. The model expected catch  $C_{exp}$  by fleet is estimated by:

$$C_{exp} = \frac{C_{obs}}{c_{mult}} \quad (3)$$

where  $C_{obs}$  is the input catch by fleet (observed catch) within the data file and  $c_{mult}$  is the estimated (or fixed) 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 to get  $C_{obs}$  before being compared to the observed retained catch as modified by the  $c_{mult}$ .

## Ageing Error Parameters

These 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). As of version 3.30.12, these parameters now have time-varying capability. Seven additional full parameter lines are required. The parameter lines specify:

1. Age at which the estimated pattern begins (just linear below this age), this is the start age.
2. Bias at start age (as additive offset from unbiased age).
3. Bias at maximum (as additive offset from unbiased age).
4. Power function coefficient for interpolating between those 2 values (value of 0.0 produces linear interpolation in the bias).
5. Standard deviation at start age.
6. Standard deviation at max age.
7. Power function coefficient for interpolating between those 2 values.

Code for implementing vectors of mean age and standard deviation of age within SS can be located in [the appendix](#) on page 196.

## Sex ratio

The last line in the mortality-growth parameter section allows the user to fix or estimate the sex ratio between female and male fish at recruitment. The parameter is specified in the fraction of female fish. The default option is a sex ratio of 0.50 with this parameter not being estimated. Estimation of the sex ratio is a new feature within SS and should be done with care with the user checking that the answer is reflective of the data. As of v.3.30.12, this parameter now has time-varying capability similar to other parameters in the mortality-growth section.

## Read Biology Parameters

Next, SS reads the mortality-growth (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 growth pattern.
M	Natural mortality for female growth pattern 1, where the number of natural mortality parameters depends on the option selected.
COND if M option = 1	
N breakpoints	N-1 parameter lines as an exponential offsets from the previous reference age.
Lmin	Length at Amin (units in cm) for female, growth pattern 1.
Lmax	Length at Amax (units in cm) for female, growth pattern 1.
VBK	von Bertalanffy growth coefficient (units are per year) for females, growth pattern 1.
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 von Bertalanffy.
COND if growth type >=3	Age-Specific K
N parameter lines equal to the number K deviations for the ages specified above.	

Parameter	Description
CV young	Variability for size at age $\leq A_{min}$ for females, growth pattern 1. Note that CV cannot vary over time, so do not set up env-link or a deviation 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 $\geq A_{max}$ for females, growth pattern 1. 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 mortality-growth parameter as offset. The CV value cannot vary over time.
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: $M_l = 1/(1 + \exp(\alpha * (l_a - \beta)))$ . The $\alpha$ is the slope, $l_a$ is the size-at-age, and $\beta$ is the inflection of the maturity curve. Value ignored for maturity option 3, 4, and 6.
Mat-slope	Logistic slope (must have negative value). Value ignored for maturity option 3, 4, and 6.
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: growth pattern > 1	Repeat female parameters in the above order for growth pattern 2.
Males	Male natural mortality and growth parameters in the following order by growth pattern.
M	Natural mortality for male GP1, where the number of natural mortality parameters depends on the option selected.
COND if M option = 1	
N breakpoints	N-1 parameter lines as an exponential offsets from the previous reference age.
Lmin	Length at $A_{min}$ (units in cm) for male, growth pattern 1. In a two sex model, fixing the INIT value a 0 will assume the same Lmin as the female parameter value.

Parameter	Description
Lmax	Length at Amax (units in cm) for male, growth pattern 1. In a two sex model, fixing the INIT value a 0 will assume the same Lmax as the female parameter value.
VBK	von Bertalanffy growth coefficient (units are per year) for males, growth pattern 1. In a two sex model, fixing the INIT value a 0 will assume the same k as the female parameter value.
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 N parameter lines equal to the number K deviations for the ages specified above.	Age-Specific K
CV young	Variability for size at age $\leq$ Amin for males, GP1. Note that CV cannot vary over time, so do not set up env-link or a deviation 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 $\geq$ Amax for males, growth pattern 1. 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 mortality-growth parameters as offset.
WtLen scale WtLen exp	Coefficient to convert length in cm to weight in kg for males. Exponent to convert length to weight for males.
COND: growth pattern > 1	Repeat male parameters in the above order for growth pattern 2.
COND: Hermaphroditism  Inflect Age StDev Asmp Rate	3 parameters lines define a normal distribution for the transition rate of females to males (or vice versa). Hermaphrodite inflection age. Hermaphrodite standard deviation (in age) . Hermaphrodite asymptotic rate.
COND: Recruitment Distribution Method = 2 or 3	3 parameters lines defining recruitment distribution.

Parameter	Description
Recruitment Dist. GP	Recruitment apportionment by growth pattern, if multiple growth patterns, multiple entries required.
Recruitment Dist. Area	Recruitment apportionment by area, if multiple areas, multiple entries required.
Recruitment Dist. Month	Recruitment apportionment by month, if multiple months, multiple entries required.
Cohort growth deviation	Set equal to 1.0 and do not estimate; it is deviations from this base that matter.
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	For each fleet selected for this option in the data file.
Multiplier	
Fraction female	Fraction female at the time of recruitment by growth pattern, if multiple growth patterns, multiple entries required.

Example format for mortality-growth parameter section with 2 sexes, 2 areas. Parameters marked with COND are conditional on selecting that feature:

LO	HI	INIT	Prior Value	<other entries>	Block Fxn	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

LO	HI	INIT	Prior Value	<other entries>	Block Type	Parameter Label
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
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
0	0	0	0	...	0	#RecrDist_GP_1
0	0	0	0	...	0	#RecrDist_Area_1
0	0	0	0	...	0	#RecrDist_Area_2
0	0	0	0	...	0	#RecrDist_Settlement_1
0.2	5	1	1	...	0	#CohortGrowDev
-5	5	-4	1	...	0	#Move_A_seas1_GP1_from_1to2 (COND)
-5	5	-4	1	...	0	#Move_B_seas1_GP1_from_1to2 (COND)
-99	99	1	0	...	0	#AgeKeyParm1 (COND)
-99	99	0.288	0	...	0	#AgeKeyParms 2 to 5 (COND)
-99	99	0.715	0	...	0	#AgeKeyParm6 (COND)
0.2	3.0	1.0	0	...	0	#Catch_mult_fleet1 (COND)
0.001	0.999	0.5	0.5	...	0	#FracFemale_GP_1

## Setting Male Parameters Equal to Females

SS allows a short-cut for males to use the same parameter values as female fish for natural mortality, length minimum (Length at Amin), maximum length (Length at Amax), coefficient at younger ages (CV1), coefficient at older ages (CV2) and the growth coefficient (K). If the INIT parameter value for males is set equal to 0.0 and the phase set to negative, not estimated, each of these male parameters will use the corresponding female parameter value for the males.

## 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 trend, or by setting up annual deviations. The options for making biology, spawner-recruitment, catchability and selectivity parameters change over time is detailed in the [Using Time-Varying Parameters](#) section. After reading the biology parameters above, which will



include possible instructions to create environmental link, blocks, or deviation 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 #).

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 end year, 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.

Time-varying parameter specification:

LO	HI	INIT	Prior Value	Prior SD	Prior Type	Phase	Parameter Label
COND: Only if MG parameters are time-varying							
-99	99	1	0	0.01	0	-1	#Wtlen_1_Fem_ENV_add
-99	99	1	0	0.01	0	-1	#Wtlen_2_Fem_ENV_add

## Seasonal Biology Parameters

Seasonal effects are available for weight-length parameters, maturity, fecundity, and for the growth parameter K. The seasonal parameter values adjust the base parameter value for that season.

$$P' = P * \exp(\text{seas\_value}) \quad (4)$$

Control file continued:

Value	Description
0 0 0 0 0 0 0 0 0 0	Seasonality for selected biology parameters (not a conditional input). Read 10 integers to specify which biology parameters have seasonality: female-wtlen1, female-wtlen2, maturity1, maturity2, fecundity1, fecundity2, male-wtlen1, male-wtlen2, L1, K. Reading a positive value selects that factor for seasonality.
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.

## Spawner-Recruitment

The spawner-recruitment section starts by specification of the functional relationship that will be used.

Control file continued:

Value	Label	Description
3	Spawner- Recruitment Relationship	The options are: 1: Null; 2: Ricker: 2 parameters: $\ln(R_0)$ and steepness ( $h$ ); 3: Standard Beverton-Holt, 2 parameters: $\ln(R_0)$ and steepness; 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: <a href="#">Hockey stick</a> : 3 parameters: $\ln(R_0)$ , steepness, and $R_{\min}$ 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: $\ln(R_0)$ and steepness;

Value	Label	Description
		7: <a href="#">Survivorship function</a> : 3 parameters: $\ln(R0)$ , $z_{frac}$ , and $\beta$ , suitable for sharks and low fecundity stocks to assure recruits are $\leq$ population production; 8: <a href="#">Shepherd</a> : 3 parameters: $\ln(R0)$ , steepness, and shape parameter, $c$ ; 9: <a href="#">Shepherd re-parameterization</a> : 3 parameters: $\ln(R0)$ , steepness, and shape parameter, $c$ (added to version 3.30.11 and is in beta mode); and 10: <a href="#">Ricker re-parameterization</a> : 3 parameters: $\ln(R0)$ , steepness, and Ricker power, $\gamma$ (added to version 3.30.11 and is in beta mode).
1	Equilibrium recruitment	Use steepness in initial equilibrium recruitment calculation  0 = none; and 1 = use steepness (h).
0	Future Feature	Reserved for the future option to make realized $\sigma_R$ a function of the stock-recruitment curve.

The number of parameters needed by each relationship is stored internally. In SS v.3.24 and before, only a short parameter line was used for the spawner-recruitment section. SS v.3.30 now requires long parameter lines in the spawner-recruitment section because it now uses the same time-varying parameter approach as the biology and selectivity parameters. This generic time-varying approach replaces the spawner recruit envlink concept in SS v.3.24. Also, the R1 offset was effectively a block to implement a regime shift for the initial equilibrium year. Now in v.3.30, the R1 offset parameter is replaced by a parameter termed "regime shift". The spawner recruit regime parameter is intended to have a base value of 0.0 and not be estimated. Similar to the cohort-growth deviation, it serves simply as a base for adding time-varying adjustments. This regime shift parameter can have blocks, environmental links or random deviations.

If a SS v.3.24 model implemented the R1 offset approach this can be mimicked in v.3.30 by the stock recruit regime parameter. For any given year, including startyr - 1, the  $R0$  is replaced by  $R0 * \exp(SR\_Regime_y)$ . So to mimic the R1\_offset, you need to put a block on SR\_regime for  $y = \text{startyr} - 1$ . But if SR\_regime has some change during your main time series, that change will be filtered through the stock-recruit relationship into an impact on the numbers at age for whatever years are impacted. This can also apply to the forecast. A block on SR\_regime is also easier than some of the old dummy environmental variables that were created in the past to adjust recruitment up and down for long periods.

If the  $R0$  or steepness parameters are time-varying, then SS will use the current year's parameters to calculate recruits as a function of the spawning biomass. If the spawner recruit regime parameter is

time-varying, then SS applies this offset after calculating recruits as function of spawning biomass. The expected deviations can no longer be linked to "env": instead the environmental effect will be on the "regime".

Read the required number of long parameter set-up lines (e.g. LO, HI, INIT, PRIOR, PRIOR TYPE, SD, PHASE, ..., and BLOCK TYPE). These parameters are:

Value	Label	Description
8.5	ln(R0)	Log of virgin recruitment level.
0.60	Steepness	Steepness of spawner recruitment relationship, bound by 0.2 and 1.0 for the Beverton-Holt.
COND:	3rd Parameter	If SRR = 5, 7, or 8 Optional depending on which spawner-recruitment relationship function is used.
0.60	$\sigma_R$	Standard deviation of natural 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 ln(R0) and steepness) and the expected geometric mean (which is the basis from which the deviations are calculated. Thus the value of $\sigma_R$ must be selected to approximate the true average recruitment deviation.
0	Regime Parameter	This replaces the R1 offset parameter. It can have a block for the initial equilibrium year, so can fully replicate the functionality of the previous R1 offset approach. The SR regime parameter is intended to have a base value of 0.0 and not be estimated. Similar to cohort-growth deviation, it serves simply as a base for adding time-varying adjustments. This concept is similar to the old environment effect on deviates feature in SS v.3.24 and earlier.
0	Autocorrelation	Autocorrelation in recruitment.

Example set-up of the spawner-recruitment section:

LO	HI	INIT	PRIOR	<other entries>	Block Fxn	Parameter Label
3	31	8.81	10.3	...	0	#SR_LN(R0)

0.2	1	0.61	0.70	...	0	#SR_BH_steep
0	2	0.60	0.80	...	0	#SR_sigmaR
-5	5	0	0	...	0	#SR_regime
-99	99	0	0	...	0	#SR_autocorr

---

- The  $R_0$ , steepness, and regime shift parameters can be time-varying by blocks, trends, environmental linkages, or random deviation. However, not all of these options make sense for all parameters. Before discussing these, another important change must be noted.
- The  $\sigma_R$  and autocorrelation parameters can not be time-varying.
- In SS v.3.24, the  $R_0$  and steepness parameters were used for both the virgin calculation and for the MSY (benchmark) calculations. In SS v.3.30, these usages are more explicitly defined. The value of  $R_0$  and steepness in the initial year are used for virgin and for calculation the denominator in depletion estimates. The average value of  $R_0$  and steepness in the range of years specified as the benchmark years 9 and 10 (see forecast.ss) is used for MSY type calculations. So, for example, a long-term climate effect could cause  $R_0$  to change over time and  $B_{MSY}$  could now be calculated for some future range of years.
- Since  $R_0$  can be time-varying, what is regime shift for? Regime shift is for multi-year or environmentally driven deviations from  $R_0$  without changing  $R_0$  itself. Then the recruitment deviations are annual deviations from the current regime and these recruitment deviations can have autocorrelation.
  - Use these options judiciously because the same algebraic effect on the calculated recruitment can be achieved by different combinations of these options.
- Preliminary recommendation: Use block, trend or environmental effects on  $R_0$  only for very long-term and highly persistent effects; use time-vary effects on regime shift for transitory, but multi-year deviations from  $R_0$ .
- The time-vary parameter lines are short lines because they themselves cannot be time-varying.
- The order of time-vary parameters are;  $R_0$ , steepness, then regime shift. The number of time-varying parameters from each of these can range from zero to many.
- Note that setting a block for just the initial equilibrium year is equivalent to  $R1\_offset$ . If  $R1\_offset$  is being used in SS v.3.24, then sstrans.exe will automatically add a new block for the initial equilibrium year so that you can easily re-implement a  $R1\_offset$  effect.

Control file continued:

Value	Label	Description
1	Do Recruitment Deviations	<p>This selects the way in which recruitment deviations are coded:</p> <p>0: None (so all recruitments come from spawner recruitment curve).</p> <p>1: Deviation vector (previously the only option): the deviations are encoded as a deviation vector, so ADMB enforces a sum-to-zero constraint.</p> <p>2: Simple deviations: 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> <p>3: Deviation vector (added in v.3.30.13) where the estimated recruitment is equal to the R0 adjusted for blocks multiplied by a simple deviation vector of unconstrained deviations. The negative log likelihood from the deviation vector is equal to the natural log of the estimated recruitment divided by the expected recruitment by year adjusted for the spawner-recruit curve, regimes, environmental parameters, and bias-adjustment. The negative log likelihood between option 2 and 3 is approximately equal.</p> <p>4: Similar to option 3 but includes a penalty based on the sum of the deviations (added in v.3.30.13).</p>
1971	Main recruitment deviations begin year	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 the population maximum age before start year, it is changed to equal to the maximum age before start year.
1999	Main recruitment deviations end year	If recruitment deviations end year is later than retro year, it is reset to equal retro year.
3	Main recruitment deviations 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	<p>Early Recruitment Deviation Start Year:</p> <p>0: skip (default);</p>

Value	Label	Description
		<p>+year: absolute year (must be less than begin year of main recruitment deviations); and</p> <p>-integer: set relative to main recruitment deviations start year.</p> <p>Note: because this is a deviation vector, it should be long enough so that recruitment deviations for individual years are not unduly constrained.</p>
6		<p>Early Recruitment Deviation Phase:</p> <p>Negative value: default value to not estimate early deviations.</p> <p>Users may want to set to a late phase if there is not much early data.</p>
0		<p>Forecast Recruitment Phase:</p> <p>0 = Default value.</p> <p>Forecast recruitment deviations always begin in the first year after the end of the main recruitment deviations. Recruitment in the forecast period is deterministic derived from the specified stock-recruitment relationship. 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 deviations at a constant level.</p>
1		<p>Forecast Recruitment Deviations Lambda:</p> <p>1 = Default value.</p> <p>This lambda is for the log likelihood of the forecast recruitment deviations that occur before endyr + 1. Use a larger value here if solitary, noisy data at end of time series cause unruly recruitment deviation estimation.</p>
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	Label	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 log likelihood. 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. Defaults for the four year values: start year – 1000, start year – Nages, main recruitment deviation final year, end year + 1. See <a href="#">Recruitment Likelihood with Bias Adjustment</a> for more information.
0.85		Max Bias Adjustment: Value for the maximum bias adjustment during the MLE mode. A value of -1 will set the bias adjustment to 1.0 for all years with estimated recruitment deviations. Likewise, all estimated recruitment deviations, 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. Negative phase = Default value.
5		Maximum Recruitment Deviation: Max value for recruitment deviation. Late Phase = Default value (e.g., 5)
2		Number of Explicit Recruitment Deviations to Read: 0: Default, do not read any recruitment deviations; Integer: read this number of recruitment deviations.
End of advanced options		
COND = If N recruitment cycle is > 0, enter N full parameter lines below.		



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

## 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:

$$R_y = \frac{4hR_0SB_y}{SB_0(1-h) + SB_y(5h-1)} e^{-0.5b_y\sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim N(0; \sigma_R^2) \quad (5)$$

where  $R_0$  is the unfished equilibrium recruitment,  $SB_0$  is the unfished equilibrium spawning biomass (corresponding to  $R_0$ ),  $SB_y$  is the spawning biomass at the start of the spawning season during year  $y$ ,  $h$  is the steepness parameter,  $b_y$  is the bias adjustment fraction applied during year  $y$ , is the standard deviation among recruitment deviations in natural log space, and is the lognormal recruitment deviation for year  $y$ . The bias-adjustment factor (Methot et al., 2011) ensures unbiased estimation of mean recruitment even during data-poor eras in which the maximum likelihood estimate of the recruitment deviation is near 0.0.

### Ricker

The Ricker Stock Recruitment curve is calculated as:

$$R_y = \frac{R_0SB_y}{SB_0} e^{h(1-SB_y/SB_0)} e^{-0.5b_y\sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim N(0; \sigma_R^2) \quad (6)$$

where the stock recruitment parameters have the same meaning as described above for the Beverton-Holt.

## Hockey-Stick

The hockey-stick recruitment curve is calculated as:

$$R_y = \text{join}(R_{\min}R_0 + R_0 \frac{SB_y}{hSB_0}(1 - R_{\min})) + R_0(1 - \text{join})e^{-0.5b_y\sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim N(0; \sigma_R^2) \quad (7)$$

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,  $h$  is defined as the fraction of  $SB_0$  below which recruitment declines linearly, and  $\text{join}$  is defined as:

$$\text{join} = \left[ 1 + e^{1000 * \frac{(SB_0 - hSB_0)}{SB_0}} \right]^{-1} \quad (8)$$

## Survivorship

The survivorship stock recruitment relationship based on Taylor et al. (2013) is a stock-recruitment model that enables explicit modeling of survival between embryos and age 0 recruits, and allows the description of a wide range of pre-recruit survival curves. The model is especially useful for low fecundity species that produce relatively few offspring per litter and exhibit a more direct connection between spawning output and recruitment than species generating millions of eggs.

Survival-based recruitment is constrained so that the recruitment rate cannot exceed fecundity. The relationship between survival and spawning output is based on parameters which are on a natural log scale. These are:

$$z_0 = -\ln(S_0) \quad (9)$$

which is the negative of the natural log of the equilibrium survival  $S_0$ , and can be thought of as a pre-recruit instantaneous mortality rate at equilibrium, and

$$z_{\min} = -\ln(S_{\max}) = z_0(1 - z_{\text{frac}}) \quad (10)$$

which is the negative of the natural log of the maximum pre-recruit survival rate ( $S_{\max}$ , the limit as spawning output approaches 0), and is parameterized as a function of  $z_{\text{frac}}$  (which represents the reduction in mortality as a fraction of  $z_0$ ) so the expression is well defined over the parameter range  $0 < z_{\text{frac}} < 1$ .

Recruitment at age 0 for each year in the time series is calculated as:

$$R_y = SB_y e^{\left( -z_0 + (z_0 - z_{\min}) \left( 1 - (SB_y/SB_0)^\beta \right) \right)} e^{\tilde{R}_y} \quad \tilde{R}_y \sim N(0; \sigma_R^2) \quad (11)$$

where  $SB_y$  is the spawning output in year  $y$ ,  $\beta$  is a parameter controlling the shape of density-dependent relationship between relative spawning depletion  $SB_y/SB_0$  and pre-recruit survival (with limit  $\beta < 1$ ),  $\tilde{R}_y$  is the recruitment in year  $y$ , and  $\sigma_R$  is the standard deviation of recruitment in natural log space.

As implemented in Stock Synthesis, the parameters needed to apply the stock-recruitment relationship based on the pre-recruit survival are  $\ln(R_0)$ ,  $z_{\text{frac}}$ , and  $\beta$ . The value of  $\ln(R_0)$  defines the equilibrium quantities of  $SB_0$ ,  $S_0$ , and  $z_0$  for a given set of biological inputs (either estimated or fixed), regardless of the values of  $z_{\text{frac}}$  and  $\beta$ .

The interpretation of the quantity  $z_0 = -\ln(S_0)$  as pre-recruit instantaneous mortality rate at unfished equilibrium is imperfect because the recruitment in a given year is calculated as a product of the survival fraction  $S_y$  and the spawning output  $SB_y$  for that same time period so that there is not a 1-year lag between quantification of eggs or pups and recruitment at age 0, which is when recruits are calculated within Stock Synthesis. However, if age 0 or some set of youngest ages is not selected by any fishery or survey, then density dependent survival may be assumed to occur anywhere before the first appearance of any cohort in the data or model expectations. In such cases, the upper limit on survival up to age  $a$  is given by  $S_{\text{max}}e^{-aM}$ .

Nevertheless, interpreting  $z_0$  as an instantaneous mortality helps with the understanding of  $z_{\text{frac}}$ . This parameter controls the magnitude of the density-dependent increase in survival associated with a reduction in spawning output. It represents the fraction by which this mortality-like rate is reduced as spawning output is reduced from  $SB_0$  to 0. This is approximately equal to the increase in survival as a fraction of the maximum possible increase in survival. That is:

$$z_{\text{frac}} = \frac{\ln(S_{\text{max}}) - \ln(S_0)}{-\ln(S_0)} \approx \frac{S_{\text{max}} - S_0}{1 - S_0} \quad (12)$$

For example, if  $S_0 = 0.4$ ,  $z_{\text{frac}} = 0.8$ , then the resulting fraction increase in survival is  $(S_{\text{max}} - S_0)/(1 - S_0) = 0.72$ .

The parameter  $\beta$  controls the point where survival changes fastest as a function of spawning depletion. A value of  $\beta = 1$  corresponds to a linear change in natural log survival and an approximately linear relationship between survival and spawning depletion. Values of  $\beta < 1$  have survival increasing fastest at low spawning output (concave decreasing survival) whereas  $\beta > 1$  has the increase in survival occurring fastest closer to the unfished equilibrium (convex decreasing survival).

The steepness ( $h$ ) of the spawner-recruit curve (defined as recruitment relative to  $R_0$  at a spawning depletion level of 0.2) based on pre-recruit survival can be derived from the parameters discussed above according to the relationship and associated inequality:

$$h = 0.2e^{z_0 z_{\text{frac}}(1-0.2^\beta)} < 0.2e^{z_0} = \frac{1}{5S_0} = \frac{SB_0}{5R_0} \quad (13)$$

Unlike the Beverton-Holt stock-recruitment relationship, recruitment can increase above  $R_0$  for stocks that are below  $SB_0$  and thus the steepness is not fundamentally constrained below 1. However, in many cases, steepness will be limited well below 1 by the inequality above, which implies an inverse relationship between the maximum steepness and equilibrium survival. Specifically, the

inequality above bounds steepness below 1 for all cases where  $S_0 > 0.2$ , which are those with the lowest fecundity, an intuitively reasonable result. For example, with  $S_0 = 0.4$ , the steepness is limited below 0.5, regardless of the choice of  $z_{\text{frac}}$  or  $\beta$ . This natural limit on steepness may be one of the most valuable aspects of this stock-recruitment relationship.

Code for the survival based recruitment can be found in [Appendix C](#).

## Shepherd

The Shepherd stock recruit curve is calculated as:

$$R_y = \left( \frac{SB_y}{SB_0} \right) \frac{5h_{adj}R_0(1 - 0.2^c)}{(1 - 5h_{adj}0.2^c) + (5h_{adj} - 1)\left(\frac{SB_y}{SB_0}\right)^c} e^{-0.5b_y\sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim N(0; \sigma_R^2) \quad (14)$$

where  $c$  is the shape parameter for the stock recruitment curve, and  $h_{adj}$  is the transformed steepness parameter defined as:

$$h_{adj} = 0.2 + \left( \frac{h - 0.2}{0.8} \right) \left( \frac{1}{5 * 0.2^c} - 0.2 \right) \quad (15)$$

## Shepherd Re-parameterization

The Shepherd stock recruit curve re-parameterized version. More details can be found in Punt and Cope (2017).

$$R_y = \frac{R_0 SB_y}{SB_0} \left( \frac{5h(1 - 0.2^c)}{1 - 5h0.2^c + (5h - 1)(SB_y/SB_0)^c} \right) \quad (16)$$

where  $c$  is the shape parameter for the stock recruitment curve.

## Ricker Re-parameterization

The Ricker stock recruit curve re-parameterized version. More details can be found in Punt and Cope (2017).

$$R_y = R_0 * (1 - temp) * e^{\ln(5h)(1 - SB_y/SB_0)^\gamma / 0.8^\gamma} \quad (17)$$

where  $\gamma$  is the Ricker shape parameter and  $temp$  is defined as:

$$temp = \begin{cases} 1 - SB_y/SB_0 & \text{if } 1 - SB_y/SB_0 > 0 \\ 0.001 & \text{if } 1 - SB_y/SB_0 \leq 0 \end{cases} \quad (18)$$

where  $temp$  stabilizes recruitment at  $R_0$  if  $SB_y > SB_0$ .

## Recruitment Eras

Conceptually, SS treats the early, data-poor period, the main data-rich period, and the recent/forecast time period as three eras along a continuum. The user has control of the break year between eras. Each era has its own vector. The early era is defined as a vector (prior to V3.10 this was a deviation vector) so it can have zeros during the earliest years not informed by data and then a few years with non-zero values without imposing a zero-centering on this collection of deviations. The main era can be a vector of simple deviations, or a deviation vector but it is normally implemented as a deviation vector so that the spawner-recruitment function is its central tendency. The last era does not force a zero-centered deviation vector so it can have zeros during the actual forecast and non-zero values in last few years of the time series. The early and last eras are optional, but their use can help prevent SS from balancing a preponderance of negative deviations in early years against a preponderance of positive deviations in later years. When the 3 eras are used, it would be typically to turn on the main era during an early model phase, turn on the early era during a later phase, then have the last era turn on in the final phase.

## Recruitment Likelihood with Bias Adjustment

For each year in the total recruitment deviation time series (early, mid, late/forecast) the contribution of that year to the log likelihood is equal to:  $dev^2 / (2.0 * sigmaR^2) + offset * ln(sigmaR)$  where offset is the recruitment bias adjustment between the arithmetic and geometric mean of expected recruitment for that year. With this approach, years with a zero or small offset value do not contribute to the second component.  $\sigma_R$  may be estimable when there is good data to establish the time series of recruitment deviations.

The recruitment bias adjustment implemented in SS is based upon the work documented in Methot et al. (2011) and following the work of Maunder and Deriso (2003). The concept is based upon the following logic.  $\sigma_R$  represents the true variability of recruitment in the population. It provides the constraining penalty for the estimates of recruitment deviations and it is not affected by data. Where data that are informative about recruitment deviations are available, the total variability in recruitment,  $\sigma_R$ , is partitioned into a signal (the variability among the recruitment estimates) and the residual, the variance of each recruitment estimate (see equation below). Where there are no data, no signal can be estimated and the individual recruitment deviations collapse towards 0.0 and the variance of each recruitment deviation approaches  $\sigma_R$ . Conversely, where there highly informative data about the recruitment deviations, then the variability among the estimated recruitment deviations will approach  $\sigma_R$  and the variance of each recruitment deviation will approach zero. Perfect data will estimate the recruitment time series signal perfectly. Of course, we never have perfect data so we should always expect the estimated signal (variability among the recruitment

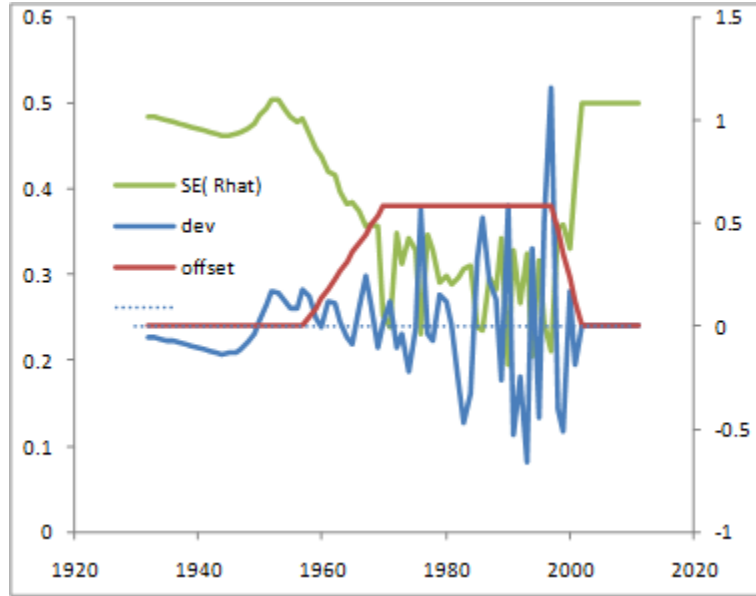
deviations) to be less than the true population recruitment variability.

$$SE(\hat{r}_y)^2 + SD(\hat{r})^2 = \left( \left( \frac{1}{\sigma_d^2} + \frac{1}{\sigma_R^2} \right)^{-1/2} \right)^2 + \left( \frac{\sigma_R^2}{(\sigma_R^2 + \sigma_d^2)^{1/2}} \right)^2 = \sigma_R^2 \quad (19)$$

The correct offset (bias adjustment) to apply to the expected value for recruitment is based on the concept that a time series of estimated recruitments should be mean unbiased, not median unbiased, because the biomass of a stock depends upon the cumulative number of recruits, which is dominated by the large recruitments. The degree of offset depends upon the degree of recruitment signal that can be estimated. Where no recruitment signal can be estimated, the median recruitment is the same as the mean recruitment, so no offset is applied. Where lognormal recruitment signal can be estimated, the mean recruitment will be greater than the median recruitment. The value

$$b_y = \frac{E\left( SD(\hat{r}_y) \right)^2}{\sigma_R^2} = 1 - \frac{SE(\hat{r}_y)^2}{\sigma_R^2} \quad (20)$$

of the offset then depends upon the partitioning of  $\sigma_R$  into between and within recruitment variability. The most appropriate degree of bias adjustment can be approximated from the relationship among  $\sigma_R$ , recruitment variability (the signal), and recruitment residual error.



Because the quantity and quality of data varies during a time series, SS allows the user to control the rate at which the offset is ramped in during the early, data-poor years, and then ramped back to zero for the forecast years.

On output SS calculates the mean bias adjustment during the early and main eras and compares it to the RMSE of estimated recruitment deviations in the report.sso file. A warning is generated if the RMSE is small and the bias adjustment is larger than 2.0 times the ratio of  $rmse^2$  to  $\sigma R^2$ .

In MCMC mode, the model still draws recruitment deviations from the lognormal distribution, so the full offset is used such that the expected mean recruitment from this lognormal distribution will stay equal to the mean from the spawner-recruitment curve. When SS reaches the MCMC and MCEVAL phases, all bias adjustment values are set to 1.0 for all active recruitment deviations because the model is now re-sampling from the full lognormal distribution of each recruitment.

## Recruitment Autocorrelation

The autocorrelation parameter is implemented. It is not performance tested and it has no effect on the calculation of the offsets described in the section above.

## Recruitment Cycle

When SS is configured such that seasons are modeled as years, the concept of season within year disappears. However, there may be reason to still want to model a repeating pattern in expected recruitment to track an actual seasonal cycle in recruitment. If the recruitment cycle factor is set to a positive integer, this value is interpreted as the number of time units in the cycle and this number of full parameter lines will be read. The cyclic effect is modeled as an  $\exp(p)$  factor times  $R_0$ , so a parameter value of 0.0 has nil effect. In order to maintain the same number of total recruits over the duration of the cycle, a penalty is introduced so that the cumulative effect of the cycle produces the same number of recruits as  $N_{cycles} * R_0$ . Because the cyclic factor operates as an exponential, this penalty is different than a penalty that would cause the sum of the cyclic factors to be 0.0. This is done by adding a penalty to the parameter likelihood, where:

$$\begin{aligned} X &= \sum(e^p) \\ Y &= N_{cycle} \\ Penalty &= 100000 * (X - Y)^2 \end{aligned} \tag{21}$$

## Initial Age Composition

A non-equilibrium initial age composition is achieved by setting the first year of the recruitment deviations before the model start year. These pre-start year recruitment deviations will be applied to the initial equilibrium age composition to adjust this composition before starting the time series. The model first applies the initial F level to an equilibrium age composition to get a preliminary N-at-age

vector and the catch that comes from applying the F's to that vector, then it applies the recruitment deviations for the specified number of younger ages in this vector. If the number of estimated ages in the initial age composition is less than maximum age, then the older ages will retain their equilibrium levels. Because the older ages in the initial age composition will have progressively less information from which to estimate their true deviation, the start of the bias adjustment should be set accordingly.

## Fishing Mortality Method

There are three methods available for calculation of fishing mortality: Pope's approximation, Baranov's continuous F with each F as a model parameter, and a hybrid F method that does a Pope's approximation to provide initial values for iterative adjustment of the Baranov continuous F values to closely approximate the observed catch. It is recommended in most cases to use the hybrid F approach. With the hybrid method, the final values are in terms of continuous F, but do not need to be specified as full parameters. In a 2 fishery, low F case, the hybrid method is just as fast as the Pope approximation and produces identical result. However, when F is very high, the problem becomes quite stiff for Pope's and the hybrid method so convergence may slow. It may be better to use F option 2 (continuous F as full parameters) in these high F cases. F as parameter is also preferred for situations where catch is known imprecisely and you are willing to accept a solution in which the final F values do not reproduce the input catch levels exactly. For the F as parameter approach, there is an option to do early phases using hybrid, then switch to F as parameter in later phases and transfer the hybrid F values to the parameter initial values by specifying the phase under the conditional input for F method = 2.

Control file continued:

Typical Value	Description and Options
0.2	F ballpark This value is compared to the sum of the F's for the specified year (defined on the next line). The sum is over all seasons and areas. In older versions of SS, the lambda was automatically set to 0.0 in the final phase, the user now has control over whether to reduce the <a href="#">lambda</a> in later phases.
-1990	F ballpark year Negative value disable F ballpark.
3	F Method 1 = Pope's (discrete); 2 = Baranov (continuous) F as a parameter; and



Typical Value	Description and Options
	3 = Hybrid F (recommended).
2.9	Maximum F This maximum is applied within each season and area. A value of 0.9 is recommended for F method 1, and a value of about 4 is recommended for F method 2 and 3.
COND: F method = 1, no additional input for Pope's approximation.	
COND: F method = 2:	
0.10 1 0	Initial F value, phase, and the number of F detail setup lines to read (example has 0). For phases prior to the phase of the F value becoming active, SS will use the hybrid option and the F values so calculated become the starting values for the F parameters when this phase is reached.
If F method = 2 and N for F detail is > 0	
1 1980 1 0.20 0.05 4	Fleet, year, season, F, SE, phase - these values override the catch standard error values in the data file and the overall starting F value and phase read just above.
COND: F method = 3	
4	Number of tuning iterations in hybrid method. A value of 2 or 3 is sufficient with a single fleet and low Fs. A value of 5 or so may be needed to match the catch near exactly when there are many fleets and high F.

## Initial Fishing Mortality

Read a short parameter setup line for each fishery. The parameters are the fishing mortalities for the initial equilibrium. Do not try to estimate parameters for fisheries with zero initial equilibrium catch. If there is catch, then give a starting value greater than zero and it generally is best to estimate the parameter in phase 1.

In SS3.30, the initial equilibrium year has explicit seasons, so the needed initial F values will also be by season. Initial F values are only needed for fleet/seasons that have catch. So, if no fleet/season combo has catch, then no parameters are needed.

It is possible to use the initial F method to achieve an estimate of the initial equilibrium Z in cases

where the initial equilibrium catch is unknown. To do this:

- Include a positive value for the initial equilibrium catch.
- Set the lambda for the log likelihood for initial equilibrium catch to a nil value (hence causing SS to ignore the lack of fit to the input catch level.
- Allow the initial F parameter to be estimated. It will be influenced by the early age and size comps which should have some information about the early levels of Z.

## Catchability

Catchability is the scaling factor that relates a model quantity to the expected value for some type of data (index). Typically this is used to converted selected numbers or biomass for a fleet into the expected value for a survey or CPUE by that fleet. In SS, the concept has been extended so that, for example, a time series of an environmental factor could be treated as a survey of the time series of deviations for some parameter. This flexibility means that a family of link functions beyond simple proportionality is needed.

For each fishery and survey with an index, enter a row with the entries as described below:

1. Fleet Number
2. Link type or index of deviation vector: An assumed functional form between Q, the expected value, and the survey observation.
  - (a) 1 = simple Q, proportional assumption about Q:  $y = q * x$ .
  - (b) 2 = mirror simple Q - this will mirror the Q value from another fleet. Mirror in Q must refer to a lower number fleet relative to the fleet with the mirrored Q (example: fleet 3 mirror fleet 2). Requires a Q parameter line for the fleet but will not be used.
  - (c) 3 = Q with power, 2 parameters establish a parameter for non-linearity in survey-abundance linkage. Assumes proportional with offset and power function:  $y = qx^c$  where  $q = \exp(\ln Q_{base})$  thus the  $c$  is not related to expected biomass but vulnerable biomass to Q. Therefore,  $c < 0$  leads to hyper-stability and  $c > 0$  leads to hyper-depletion.
  - (d) 4 = mirror Q with offset (2 parameter lines required). The mirrored Q with offset for with be reported as base Q + offset value. Mirror in Q must refer to a lower number fleet relative to the fleet with the mirrored Q. See [mirrored Q with offset](#) below for example set up.

- (e) If the parameter is for an index of a deviation vector (index units = 35), use this column to enter the index of the deviation vector to which the index is related.

3. Extra input for link (i.e., mirror fleet)

- (a) >0 = mirror the Q from another (lower numbered survey designated by referencing the fleet number)

4. Do extra standard error

- (a) 0 = skip (typical); and  
(b) 1 = estimate a parameter that will contain an additive constant to be added to the input standard deviation of the survey variability.

5. Bias adjustment

- (a) 0 = no bias adjustment applied; and  
(b) 1 = apply bias adjustment.

6. Q float

- (a) 0 = no float (parameter is estimated); and  
(b) 1 = float (analytical solution is used, but parameter line still required).  
(c) Additional information regarding the use of and appropriate application of float in Q can be found in the [Float Q](#) section below.

For a setup with a single survey, the Q setup matrix could be:

Fleet Num.	Link Type	Link Info	Extra SD	Bias Adjust	Float	Label
3	1	0	1	1	0	#Survey
-9999	0	0	0	0	0	#End Read

LO	HI	INIT	<other entries>	PHASE	<other entries>	Block Fxn	Parameter Label
-5	5	-0.12	...	1	...	0	#Survey1 LnQ base
0	0.5	0.1	...	-1	...	0	#Survey1 Extra SD

If the Q base parameter specifies that it is time-varying by the annual deviation method, short parameter lines to specify the specifications of the deviation vector come after all the base Q parameters.

## Mirrored Q with offset

Below is an example setup for fleets with a mirrored Q and offset from another fleet (link type = 4):

For a setup with a single survey, the Q setup matrix could be:

Fleet Num.	Link Type	Link Info	Extra SD	Bias Adjust	Float	Label
1	1	0	1	0	0	#Fleet 1
2	4	1	0	0	0	#Fleet 2
-9999	0	0	0	0	0	#End Read

A long parameter line is expected for each link parameter (i.e. Q) and for the

LO	HI	INIT	<other entries>	PHASE	<other entries>	Block Fxn	Parameter Label
-7	5	0.51	...	1	...	0	#Fleet 1 LnQ base
0	0.5	0.1	...	-1	...	0	#Fleet 1 Extra SD
-7	5	-6	...	-1	...	0	#Fleet 2 LnQ base
-8	5	-7	...	-1	...	0	#Fleet 2 Mirror Q offset

## Float Q

The use and development of float in Q has evolved over the life of SS. The original approach in earlier versions of SS (version 3.24 and before) is that with Q "float" the units of the survey or fishery CPUE were treated as dimensionless so the Q was adjusted within each model iteration to maintain a mean difference of 0.0 between observed and expected (usually in natural log space). In contrast, Q as a parameter (float = 0) one had the ability to interpret the absolute scaling of Q and put a prior on it to help guide the model solution. Also, with Q as a parameter the code allowed for Q to be time-varying.

Then midway through the evolution of the SS v.3.24 code lineage a new Q option was introduced based on user recommendations. This option allowed Q to float and to compare the resulting Q value to a prior, hence the information in that prior would pull the model solution in direction of a floated Q that came close to the prior.

Currently, in 3.30, that float with prior capability is fully embraced. All fleets that have any survey or CPUE options need to have a catchability specification and get a base Q parameter in the list. Any of these Q's can be either:

- Fixed: by not floating and not estimating.
- Floating: not estimated as an active parameter, set phase to negative, and not capable of being time-varying. Can have a prior, or not. Future versions of SS may allow Q to be time-varying and then rescaling that Q vector according to the float logic but this is not yet currently implemented.
- Estimated as active parameter: so not floating. Can be time-varying and can have a prior.

Q relates the units of the survey or CPUE to the population abundance, not the population density per unit area. But many surveys and most fishery CPUE is a proportional to mean fish density per unit area. This does not have any impact in a one area model because the role of area is absorbed into the value of Q. In a multi-area model, one may want to assert that the relative difference in CPUE between two areas is informative about the relative abundance between the areas. However, CPUE is a measure of fish density per unit area, so one may want to multiply CPUE by area before putting the data into SS so that asserting the same Q for the two areas will be informative about relative abundance.

In SS v.3.30.13, a new catchability option has been added that allows Q to be mirrored and to add an offset to  $\ln(Q)$  of the primary area when calculating the  $\ln(Q)$  for the dependent area. The offset is a parameter and, hence, can be estimated and have a prior. This option allows the CPUE data to stay in density units and the effect of relative stock area is contained in the value of the  $\ln(Q)$  offset.

## Q Conversion Issues Between SS v.3.24 and v.3.30

In SS v.3.24 it was common to use the deviation approach implemented as if it was survey specific blocks to create a time-varying Q for a single survey. In some cases, only one year's deviation was made active in order to implement, in effect, a block for Q. The transition executable (sstrans.exe) cannot convert this, but an analogous approach is available in SS v.3.30 because true blocks can now be used, as well as environmental links and annual deviations. Also note that deviations in SS v.3.24 were survey specific (so no parameter for years with no survey). In SS v.3.30, deviations are always year-specific, so you might have a deviation created for a year with no survey.

## Selectivity and Discard

For each fleet and survey, read a definition line for size selectivity and retention.

Example Setup for Selectivity:

Size Selectivity:				
Pattern	Discard	Male	Special	Label
1	2	0	0	#Fishery1
1	0	0	0	#Survey1
0	0	0	0	#Survey2

Age Selectivity:				
Pattern	Discard	Male	Special	Label
11	0	0	0	#Fishery1
11	0	0	0	#Survey1
11	0	0	0	#Survey2

### Pattern

Specify the size/age selectivity pattern. See the [Selectivity Pattern](#) section for user options.

### Discard

Discard options:

- Option = 0: no discarding by fleet.
- Option = 1: program will read 4 retention parameters after reading the specified number of selectivity parameters and all discarded fish are assumed dead.
- Option = 2: program will read 4 retention parameters and 4 discard mortality parameters.
- Option = 3: no additional parameters are read and all fish are assumed discarded and dead.
- Option = 4: program will read 7 retention parameters for dome-shaped retention and 4 discard mortality parameters.

- Option = negative fleet number: will mirror the retention and discard mortality pattern of the lower numbered fleet.

## Male

Male specific selectivity options:

- Option = 0: no male specific selectivity parameters required. Male and female selectivity will be the same.
- Option = 1: program will read 4 additional parameters to define the male selectivity relative to the female selectivity. Anytime the male selectivity is caused to be greater than 1.0; the entire male/female matrix of selectivity values is scaled by the max so that the realized max is 1.0. Hopefully this does not cause gradient problems.
- Option 2: main selectivity parameters define male selectivity and female selectivity is estimated as an offset from male selectivity. This alternative is preferable if female selectivity is less than male selectivity.
- Option 3: only available if the selectivity pattern is 1, 20, or 24 and it causes the male selectivity parameters to be offset from the female parameters, rather than the male selectivity being an offset from the female selectivity.

## Special

Special (0/value): This value is used in different ways depending on the context. If the selectivity type is to mirror another selectivity type, then put the index of that source fleet or survey here. It must refer to a lower numbered fleet/survey. If the selectivity type is 6 (linear segment), then put the number of segments here. If the selectivity type is 7, then put a 1 here to keep selectivity constant above the mean average size for old fish of morph 1.

## Age Selectivity

For each fleet and survey, read a definition line for age selectivity. The 4 values to be read are the same as for the size-selectivity.

## Reading the Selectivity and Retention Parameters

Read the required number of parameter setup lines as specified by the definition lines above. The complete order of the parameter setup lines is:

1. Size selectivity for fishery 1;

2. Retention for fishery 1 (if discard specified);
3. Discard Mortality for fishery 1 (if discard specified);
4. Male offsets for size selectivity for fishery 1 (if offsets used);
5. <repeat for additional fleets and surveys>;
6. Age selectivity for fishery 1;
7. Retention for fishery 1 (if discard specified);
8. Discard Mortality for fishery 1 (if discard specified);
9. Male offsets for age selectivity for fishery 1 (if offsets used); and
10. <repeat for additional fleets and surveys>.

The list of parameters to be read from the above setup would be:

LO	HI	INIT	PRIOR	<other entries>	Block Fxn	Parameter Label
19	80	53.5	50	...	0	#SizeSel p1 fishery 1
0.01	60	18.9	15	...	0	#SizeSel p2 fishery 1
20	70	38.6	40	...	0	#Retain p1 fishery 1
0.1	10	6.5	1	...	0	#Retain p2 fishery 1
0.001	1	0.98	1	...	0	#Retain p3 fishery 1
-10	10	1	0	...	0	#Retain p4 fishery 1
0.1	1	0.6	0.6	...	0	#DiscMort p1 fishery 1
-2	2	0	0	...	0	#DiscMort p2 fishery 1
20	70	40	40	...	0	#DiscMort p3 fishery 1
0.1	10	1	1	...	0	#DiscMort p4 fishery 1
19	80	53.5	50	...	0	#SizeSel p1 survey 1
0.01	60	18.9	15	...	0	#SizeSel p2 survey 1
0	40	0	5	...	0	#AgeSel p1 fishery 1
0	40	40	5	...	0	#AgeSel p2 fishery 1
0	40	0	5	...	0	#AgeSel p1 survey 1
0	40	40	5	...	0	#AgeSel p2 survey 1
0	40	0	5	...	0	#AgeSel p1 survey 2
0	40	0	5	...	0	#AgeSel p2 survey 2



## Selectivity Patterns

The currently defined selectivity patterns, and corresponding required number of parameters, are:

SIZE BASED SELECTIVITY		
Pattern	N Parameters	Description
0	0	Selectivity = 1.0 for all sizes.
1	2	Logistic selectivity.
2	8	Discontinued: Double logistic with defined peak (uses IF joiners). Use pattern 8 instead.
4	0	Discontinued: Set size selectivity equal to female fecundity. Use <a href="#">special survey pattern 30</a> located in the index section within the data file instead.
5	2	Mirror another selectivity. The two parameters select bin range.
6	2	Non-parametric
7	8	Discontinued: Double logistic with defined peak, uses smooth joiners; special = 1 causes constant selectivity above $L_{inf}$ for morph 1. Use pattern 8.
8	8	Double logistic, with defined peak, uses smooth joiners; special=1 causes constant selectivity above $L_{inf}$ for morph 1.
9	6	Simple double logistic with no defined peak.
15	0	Mirror another selectivity (same as for age selectivity).
21	2	Non-parametric size selectivity
22	4	Double normal; similar to CASAL.
23	6	Same as the double normal pattern 24 except the final selectivity is now directly interpreted as the terminal selectivity value. Cannot be used with Pope's F method because maximum selectivity may be greater than 1.
24	6	Double normal with defined initial and final selectivity level – Recommended option.
25	3	Exponential-logistic.

Pattern	N Parameters	Description
27	$3 + 2*N$ nodes	Cubic spline with N nodes.
42	$5 + 2*x$	Selectivity pattern 27 but with 2 additional scaling parameters.
43	$4 + x$	Selectivity pattern 6 but with 2 additional scaling parameters.

#### AGE BASED SELECTIVITY

Pattern	N Parameters	Description
0	0	Selectivity = 1.0 for ages 0+.
10	0	Selectivity = 1.0 for all ages beginning at age 1. If it is desired that age-0 fish be selected, then use pattern #11 and set minimum age to 0.0.
11	2	Selectivity = 1.0 for a specified age range.
12	2	Logistic selectivity.
13	8	Double logistic, IF joiners. Use discouraged. Use pattern 18 instead.
14	nages + 1	Separate parameter for each age (empirical), value at age is $\frac{1}{1+exp(-x)}$ .
15	0	Mirror another age-specific selectivity pattern.
16	2	Coleraine single Gaussian
17	nages + 1	Empirical as a random walk from previous age. For all ages in the population beginning with Amin = 1 for the fishery and 2 for the survey, there is a corresponding set of selectivity parameters for each fleet, $p_a$ .
18	8	Double logistic, with defined peak, uses smooth joiners.
19	6	Simple double logistic with no defined peak.
20	6	Double normal with defined initial and final level. Recommended option.
26	3	Exponential logistic.
27	$3 + 2*N$ nodes	Cubic spline in age based on N nodes.

Pattern	N Parameters	Description
41	2 + nages + 1	Selectivity pattern 17 but with 2 additional scaling parameters.
42	5 + 2*N nodes	Selectivity pattern 27 but with 2 additional scaling parameters.
44	4 + nages	Similar to age selectivity pattern 17 but with separate parameters for males and with revised controls.
45	4 + nages	Similar to age selectivity pattern 14 but with separate parameters for males and with revised controls.

### Special Selectivity Options

Special selectivity options (type 30 in size based selectivity) are no longer specified within the control file. Specifying the use of one of these selectivity types is now done within the data file by selecting the survey "units" (see the section on [Index units](#)).

## Selectivity Pattern Details

### Pattern 1 (size) and 12 (age) - Simple Logistic

Within SS logistic selectivity for the primary sex (if selectivity varies by sex) is formulated as:

$$S_l = \frac{1.0}{1 + \exp(-\ln(19)(L_l - p1)/p2)} \quad (22)$$

where  $L_l$  is the length bin. If age based selectivity is selected then the length bin is replaced by the age vector. If sex specific selectivity is specified the non-primary sex the p1 and p2 parameters are estimated as offsets. Note that with a large p2 parameter, selectivity may not reach 1.0 at the largest size bin. The parameters are:

- p1 - size/age at inflection; and
- p2 - width for 95% selection; a negative width causes a descending curve.

### Pattern 5 (size) - Mirror Selectivity

Two parameters select the min and max bin number (not min max size) of the source selectivity pattern. If first parameter has value  $\leq 0$ , then interpreted as a value of 1 (e.g., first bin). If second parameter has value  $\leq 0$ , then interpreted as maximum length bin (e.g., last bin specified in the data file). The mirrored selectivity pattern must have be from a lower fleet number (e.g., already specified before the mirrored fleet).

### Pattern 6 (size) - Non-parametric Selectivity

Non-parametric size selectivity uses a set of linear segments. The first way point is at Length = p1 and the last way point is at Length = p2. The total number of way points is specified by the value of the Special factor in the selectivity set-up, so the N intervals is one less than the number of way points. Intermediate way points are located at equidistant intervals between p1 and p2. Parameters 3 to N are the selectivity values at the way points, entered as logistic, e.g.  $1/(1 + \exp(-x))$ . Ramps from 10 cm to p3 if  $L < p1$ . Constant at Np if  $L > p2$ . Note that prior to version 3.03 the way points were specified in terms of bin number, rather than length.

### Pattern 8 (size) and 18 (age) - Double Logistic

Users are discouraged from using the double logistic selectivity. The double normal selectivity pattern (size pattern 24, age pattern 20) provides similar functionality but with only 6 parameters.

- p1 – peak: size (age) for peak. Should be an integer and should be at bin boundary and not estimated. But options 7 and 18 may allow estimation.
- p2 – initial: selectivity at length bin=1 (minimum length) or age=0.
- p3 – inflection: a logit transform ( $1/(1 + \exp(-x))$ ) is used so that the transformed value will be between 0 and 1. So a p1 value of -1.1 will be transformed to 0.25 and used to set the selectivity equal to 0.5 at a size (age) equal to 0.25 of the way between minimum length and peak.
- p4 – slope1: ln(slope) of left side (ascending) selectivity.
- p5 – final: logit transform for selectivity at maximum length (or maximum age).
- p6 – inflection2: logit transform for size (age) at right side selectivity equal to half way between peak + peak width and maximum length (or maximum age).
- p7 – slope2: ln(slope) of right side (descending) selectivity.
- p8 – peak width: width of flattop.

### Pattern 14 (age) - Revise Age

Age-selectivity pattern 14 to allow selectivity-at-age to be the same as selectivity at the next younger age. When using this option, the range on each parameter should be approximately -5 to 9 to prevent the parameters from drifting into extreme values with nil gradient. SS calculates the age-based

selectivity as where  $a = 1$  to  $a = Amax + 1$ :

$$S_a = \frac{1}{1 + \exp(-(p(a + 1) + temp))} \quad (23)$$

### Pattern 17 (age) - Random Walk

This selectivity pattern provides for a random walk in  $\ln(\text{selectivity})$ . For each age  $a \geq A_{\min}$ , where  $A_{\min}$  is the minimum age for which selectivity is allowed to be non-zero, there is a selectivity parameter,  $p_a$ , controlling the changing selectivity from age  $a - 1$  to age  $a$ .

The selectivity at age  $a$  is computed as

$$S_a = \exp(S'_a - S'_{\max}), \quad (24)$$

where

$$S'_a = \sum_{i=A_{\min}}^a p_i \quad (25)$$

and

$$S'_{\max} = \max\{S'_a\}. \quad (26)$$

Selectivity is fixed at  $S_a = 0$  for  $a < A_{\min}$ .

This formulation has the properties that the maximum selectivity equals 1, positive values of  $p_a$  are associated with increasing selectivity between ages  $a - 1$  and  $a$ , and negative values are associated with decreasing selectivity between those ages and  $p_a = 0$  gives constant selectivity.

The condition that maximum selectivity equals 1 results in one fewer degree of freedom than the number of estimated  $p_a$ . Therefore, at least one parameter should be fixed at an arbitrary value, typically  $p_{A_{\min}} = 0$ .

In typical usage:

- First parameter (for age 0) could have a value of -1000 so that the age 0 fish would get a selectivity of 0.0;
- Second parameter (for age 1) could have a value of 0.0 and not be estimated, so age 1 is the reference age against which subsequent changes occur.
- Next parameters get estimated values. To assure that selectivity increases for the younger ages, the parameter min for these parameters could be set to 0.0 or a slightly negative value.
- If dome-shaped selectivity is expected, then the parameters for older ages could have a range with the max set to 0.0 so they cannot increase further.

- To keep selectivity at a particular age the same as selectivity at the next younger age, set its parameter value to 0.0 and not estimated. This allows for all older ages to have the same selectivity.
- To keep a constant rate of change in selectivity across a range of ages, use the -999 flag to keep the same rate of change in  $\ln(\text{selectivity})$  as for the previous age.
- Code for implementing random walk selectivity within SS can be found in [Appendix C](#).

### Pattern 9 (size) and 19 (age) - Simple Double Logistic with no defined peak

- p1 - inflection1: ascending inflection size (in cm).
- p2 – slope1: ascending slope.
- p3 – inflection2: descending inflection size (in cm).
- p4 – slope2: descending slope.
- p5 – first bin: bin number for the first bin with non-zero selectivity (must be an integer bin number, not a size).
- p6 – offset: enter 0 if p3 is independent of p1; enter 1 if p3 is an offset from p1.

### Pattern 22 (size) - Double Normal with Plateau

- p1 – peak1: beginning size for the plateau (in cm).
- p2 – peak2: ending size for the plateau. Calculated as a fraction of the distance between peak1 and 99% of the lower edge of the last size bin in the model. Transformed as  $(1/(1+\exp(-p2)))$ . So a value of 0 results in peak2 being halfway between peak1 and 99% of the last bin.
- p3 – upslope:  $\ln(\text{variance})$  on ascending side.
- p4 – downslope:  $\ln(\text{variance})$  on descending side.

### Pattern 23 (size) and 24 (size) - Double Normal Selectivity

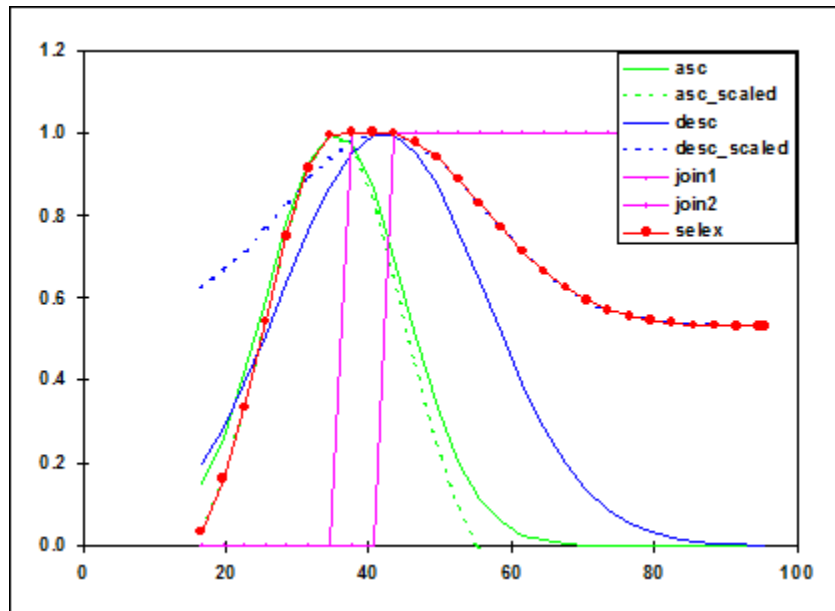
- p1 – peak: beginning size for the plateau (in cm).
- p2 – top: width of plateau, as logistic between peak and maximum length (or age).

- p3 – ascending width: parameter value is  $\ln(\text{width})$ .
- p4 – descending width: parameter value is  $\ln(\text{width})$ .
- p5 – initial:selectivity at first bin, as logistic between 0 and 1.
- p6 – final: selectivity at last bin, as logistic between 0 and 1 (for pattern 24). For pattern 23 age selectivity at last bin, as absolute value, so can be  $> 1.0$ . Warning: do not allow this value to go above 1.0 if the F\_method uses Pope's approximation. It can above 1.0 when F is in exponential form. When this parameter is above 1.0, the overall selectivity pattern will have an intermediate plateau at 1.0 (according to peak and top), then will ascend further to the final value.

Notes for Double Normal Selectivity:

- For the initial selectivity parameter (parameter 5)
  - -999 or -1000: ignore the initial selectivity algorithm and simply decay the small fish selectivity according to p3,
  - $< -1000$ : ignore the initial selectivity algorithm as above and then set selectivity equal to  $1.0e-06$  for size bins 1 through bin = -1001 -value. So a value of -1003 would set selectivity to a nil level for bins 1 through 2 and begin using the modeled selectivity in bin 3.
- For the final selectivity parameter (parameter 6)
  - -999 or -1000: ignore the final selectivity algorithm and simply decay the large fish selectivity according to parameter 4,
  - $< -1000$ : set selectivity constant for bins greater than bin number = -1000 - value.

Selectivity pattern 24, double normal, showing sub-functions and steep logistic joiners:



### Pattern 15 (age) - Mirror

No parameters. Whole age range is mirrored from another fleet. The mirrored selectivity pattern must have be from a lower fleet number (e.g., already specified before the mirrored fleet).

### Pattern 16 - Gaussian (similar to Coleraine)

- p1 – age below which selectivity declines
- p2 – scaling factor for decline

### Pattern 9 (size) and 19 (age) - Simple Double Logistic

- p1 – ascending inflection age/size
- p2 – ascending slope
- p3 – descending inflection age/size
- p4 – descending slope
- p5 – age or size at first selection; this is a specification parameter, so must not be estimated. Enter integer that is age for pattern 19 and is bin number for pattern 9
- p6 – (0/1) where a value of 0 causes the descending inflection to be a standalone parameter,



and a value of 1 causes the descending inflection to be interpreted as an offset from the ascending inflection. This is a specification parameter, so must not be estimated.

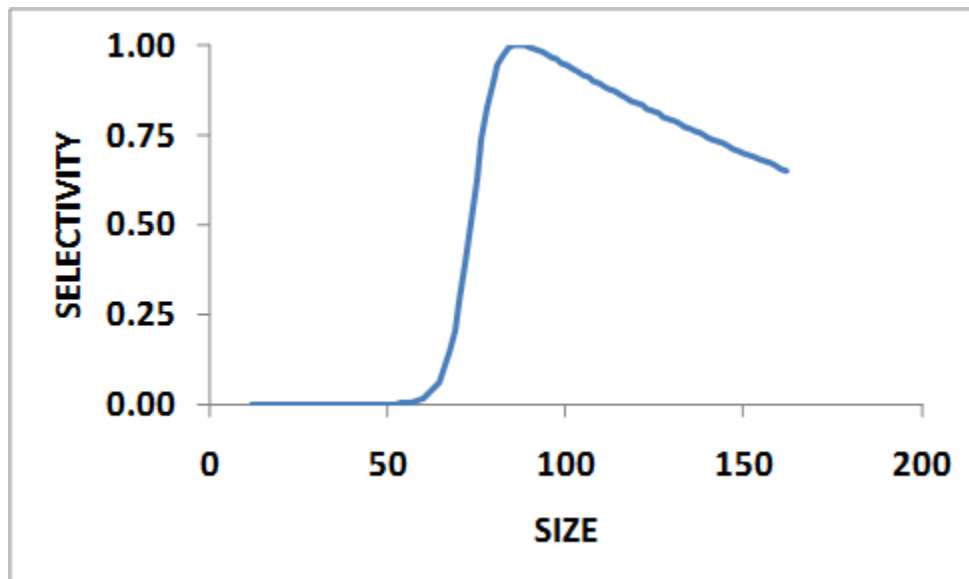
A value of 1.0e-6 is added to the selectivity for all ages, even those below the minimum age.

### Pattern 25 (size) and 26 (age) - Exponential logistic

- p1 – ascending rate, min: 0.02, max: 1.0, reasonable start value: 0.1.
- p2 – peak, as fraction of way between min size and max size. Parameter min value: 0.01; max: 0.99; reasonable start value: 0.5.
- p3 – descending rate, min: 0.001, max: 0.5, reasonable start value: 0.01. A value of 0.001 provides a nearly asymptotic curve. Values above 0.2 provide strongly dome-shaped function in which the p3 and p1 parameters interact strongly.

$$\frac{e^{p3 \cdot p1 \cdot (p2' - size)}}{1 - p3(1 - e^{p1(p2' - size)})} \quad (27)$$

Example: Exponential logistic selectivity with p1 = 0.30, p2 = 0.50, and p3 = 0.02:



### Pattern 27 (size and age)- Cubic Spline

This selectivity pattern uses the ADMB implementation of the cubic spline function. This function requires input of the number of nodes, the positions of those nodes, the parameter values at those nodes, and the slope of the function at the first and last node. In SS, the number of nodes is specified in the "special" column of the selectivity set-up. The pattern number 27 is used to invoke cubic spline

for size selectivity and for age selectivity; the input syntax is identical.

For a 3 node setup, the SS input parameters would be:

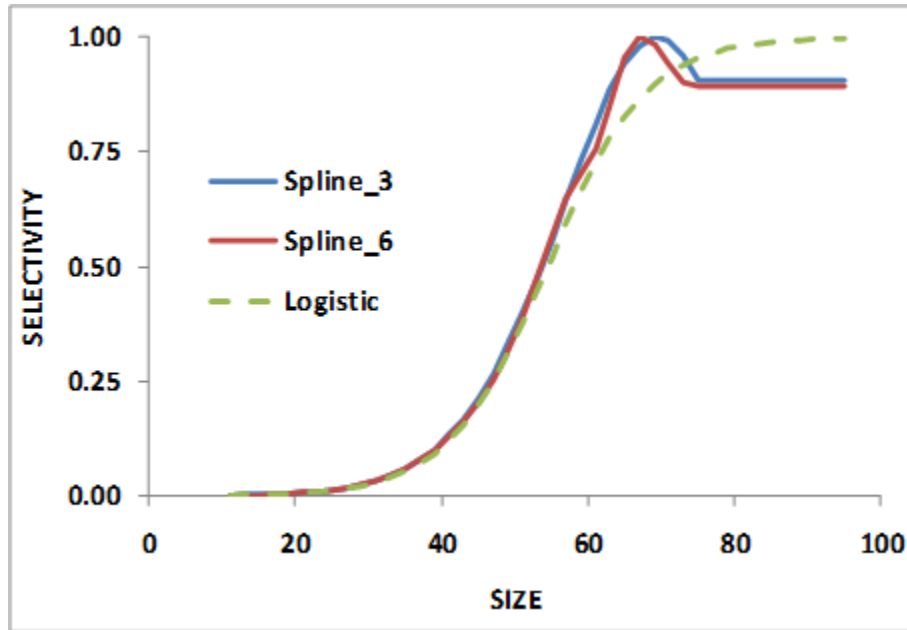
- p1 – code for initial set-up (0, 1 or 2) as explained below
- p2 – gradient at the first node (should be a small positive value)
- p3 – gradient at the last node (should be zero or a small negative value)
- p4-p6 – the nodes in units of cm; must be in rank order and inside of the range of the population length bins. These must be held constant (not estimated, e.g., negative phase value) during a model run.
- p7-p9 – the values at the nodes. Units are  $\ln(\text{selectivity})$ .

Notes:

- There must be at least 3 nodes.
- One of the node selectivity parameter values should be held constant so others are estimated relative to it.
- Selectivity is forced to be constant for sizes greater than the size at the last node.
- The overall selectivity curve is scaled to have a peak equal to 1.0.
- Terminal nodes cannot be at the min or max population length bins.

Code for implementing cubic spline selectivity within SS can be found in [Code Examples in the appendix](#).

The figure below compares a 3 node and a 6 node cubic spline with a 2 parameter logistic function. In fitting these functions, the 2 cubic spline approaches fit slightly better than the logistic, presumably because the data were slightly indicative of a small dome in selectivity.



Auto-Generation of Cubic Spline Control File Set-Up: A New SS feature pioneered with the cubic spline function is a capability to produce more specific parameter labels and to auto-generate selectivity parameter setup. The auto-generation feature is controlled by the first selectivity parameter value for each fleet that is specified to use the cubic spline. There are 3 possible values for this setup parameter:

- 0: no auto-generation, process parameter setup as read.
- 1: auto-generate the node locations based on the specified number of nodes and on the cumulative size distribution of the data for this fleet/survey.
- 2: auto-generate the nodes and also the min, max, prior, initial, and phase for each parameter.

With either the auto-generate option #1 or #2, it still is necessary to include in the parameter file placeholder rows of values so that the `init_matrix` command can input the current number of values because all selectivity parameter lines are read as a single matrix dimensioned as N parameters x 14 columns. The read values of min, max, initial, prior, prior type, prior stddev, and phase will be overwritten.

Cumulative size and age distribution is calculated for each fleet, summing across all samples and both sexes. These distributions are output in `echoinput.sso` and in a new `OVERALL_COMPS` section of `report.sso`.

When the nodes are auto-generated, the first node is placed at the size corresponding to the 2.5% percentile of the cumulative size distribution, the last is placed at the 97.5% percentile of the size distribution, and the remainder are placed at equally spaced percentiles along the cumulative size

distribution. These calculated node values are output into control.ss\_new. So, the user could extract these nodes from control.ss\_new, edit them to desired values, then, insert them into the input control file. Remember to turn off auto-generation in the revised control file.

When the complete auto-generation is selected, the control.ss\_new would look like the table below:

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	2	2.0	...	0	#SizeSpline Code
-0.001	1	0.13	...	0	#SizeSpline GradLo
-1	0.001	-0.03	...	0	#SizeSpline GradHi
11	95	38	...	0	#SizeSpline Knot1
11	95	59	...	0	#SizeSpline Knot2
11	95	74	...	0	#SizeSpline Knot3
-9	7	-3	...	0	#SizeSpline Value1
-9	7	-1	...	0	#SizeSpline Value2
-9	7	-0.78	...	0	#SizeSpline Value3

### Pattern 41 (age) - Random Walk with User-Defined Scaling

Selectivity pattern 17 with two additional parameters. The two additional parameters are the bin numbers to define the range of bins for scaling. All of the selectivity values will be scaled (divided) by the mean value over this range. The low and high bin numbers are defined before the other selectivity parameters.

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	20	10	...	0	#AgeSel_ScaleAgeLo
0	20	20	...	0	#AgeSel_ScaleAgeHi

### Pattern 42 (size and age) - Cubic Spline with User-Defined Scaling

Selectivity pattern 27 with two additional parameters. The two additional parameters are the bin numbers to define the range of bins for scaling. All of the selectivity values will be scaled (divided) by the mean value over this range. The low and high bin numbers are defined before the other selectivity parameters.

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	20	10	...	0	#AgeSpline_ScaleAgeLo

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	20	20	...	0	#AgeSpline_ScaleAgeHi

### Pattern 43 (size) - Non-parametric with User-Defined Scaling

Selectivity pattern 6 with two additional parameters. The two additional parameters are the bin numbers to define the range of bins for scaling. All of the selectivity values will be scaled (divided) by the mean value over this range. The low and high bin numbers are defined before the other selectivity parameters.

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
1	80	50	...	0	#SizeSel_ScaleBinLo
1	80	70	...	0	#SizeSel_ScaleBinHi

### Pattern 44 (age)

Similar to pattern 17 but with separate parameters for males and females. This selectivity pattern provides for a random walk in  $\ln(\text{selectivity})$ . In typical usage:

- p1 - First parameter (for age 0) could have a value of -1000 so that the age 0 fish would get a selectivity of 0.0.
- p2 - The first age for which mean selectivity = 1.
- p3 - The last age for which mean selectivity = 1.
- p4 - Male mean selectivity relative to the female selectivity mean entered as  $\ln(\text{ratio})$  for the male relative female selectivity.
- p5-p<sub>n</sub> - Additional parameter lines for the natural log of the selectivity change between ages corresponding to the user specified number of changes in the "special" column for the selectivity specification for each sex with females entered first then males.
- -999 input indicates to the model to keep the change unchanged from the previous age (keeps same rate of change).
- -1000 input indicates used only for male selectivity indicates to the model to set the change in male selectivity equal to the female change in selectivity.

An example specification and setup for this selectivity option where selectivity is dome-shaped, peaking at age 2 with female and male selectivity are equal with 4 change points per sex:

#Pattern	Discard	Male	Special
44	0	0	4

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	20	0	...	0	#first selex age
0	20	2	...	0	#first age peak selex (mean)
0	20	2	...	0	#last age peak selex (mean)
-1	2	-0.001	...	0	#male ln(ratio)
-10	10	3.01	...	0	#female ln(selex) change 1
-10	10	1.56	...	0	#female ln(selex) change 2
-10	10	-0.15	...	0	#female ln(selex) change 3
-10	10	-0.15	...	0	#female ln(selex) change 4
-1000	10	-1000	...	0	#male ln(selex) change 1
-1000	10	-1000	...	0	#male ln(selex) change 2
-1000	10	-1000	...	0	#male ln(selex) change 3
-1000	10	-1000	...	0	#male ln(selex) change 4

### Pattern 45 (age) - Revise Age

Similar to pattern 14 but with separate parameters for males and females. Age-selectivity pattern 45 to allow selectivity-at-age to be the same as selectivity at the next younger age.

- p1 - is the first age with non-zero selectivity.
- p2 - The first age in mean for peak selectivity
- p3 - The last age in mean for peak selectivity
- p4 - The male mean selectivity relative to the female mean, entered as ln(ratio) for the male relative female selectivity
- -999 input indicates to the model to keep the change unchanged from the previous age (keeps same rate of change).
- -1000 input indicates used only for male selectivity indicates to the model to set the change in male selectivity equal to the female change in selectivity.

An example specification and setup for this selectivity option where selectivity is asymptotic, with female and male selectivity are equal with 4 change points per sex:

#Pattern	Discard	Male	Special
45	0	0	3

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
0	20	2	...	0	#first selex age
0	20	5	...	0	#first age peak selex (mean)
0	20	5	...	0	#last age peak selex (mean)
-1	2	-0.001	...	0	#male ln(ratio)
-10	10	-8.1	...	0	#female ln(selex) change 1
-10	10	-4.1	...	0	#female ln(selex) change 2
-10	10	-1.8	...	0	#female ln(selex) change 3
-1000	10	-1000	...	0	#male ln(selex) change 1
-1000	10	-1000	...	0	#male ln(selex) change 2
-1000	10	-1000	...	0	#male ln(selex) change 3

## Retention

Retention is defined as a logistic function of size or age. It does not apply to surveys. Four parameters (for asymptotic retention) or seven parameters (for dome-shaped retention) are used:

- Asymptotic (4 parameters):
  - p1 – ascending inflection,
  - p2 – ascending slope,
  - p3 – maximum retention controlling the height of the asymptote (smaller values result in lower asymptotes), often a time-varying quantity to match the observed amount of discard,
  - p4 – male offset to ascending inflection (arithmetic, not multiplicative),

- Dome-shaped (add the following 3 parameters):
  - p5 – descending inflection,
  - p6 – descending slope, and
  - p7 – male offset to descending inflection (arithmetic, not multiplicative).

$$\text{Retention} = \left( \frac{P3}{1 + e^{\frac{-(L-(P1+P4*male))}{P2}}} \right) * \left( 1 - \frac{1}{1 + e^{\frac{-(L-(P5+P7*male))}{P6}}} \right) \quad (28)$$

## Discard Mortality

Discard mortality is defined as a logistic function of size such that mortality declines from 1.0 to an asymptotic level as fish get larger. It does not apply to surveys and it does not affect the calculation of expected values for discard data. It is applied so that the total mortality rate is:

$$\text{dead fish} = \text{selectivity} * (\text{retain} + (1.0-\text{retain})*\text{discard mortality})$$

If discard mortality is 1.0, all selected fish are dead; if discard mortality is 0.0, only the retained fish are dead.

Four parameters are used:

- p1 – descending inflection
- p2 – descending slope
- p3 – maximum discard mortality
- p4 – male offset to descending inflection (arithmetic, not multiplicative)

Discard mortality is calculated as:

$$\text{Discard Mortality} = \left( 1 - \frac{1 - P3}{1 + e^{\frac{-(L-(P1+P4*male))}{P2}}} \right) \quad (29)$$

## Sex-Specific Selectivity

There are two approaches to specifying sex specific selectivity. One approach allows male selectivity to be specified as a fraction of female selectivity (or vice versa). This first approach can be used for



any selectivity pattern. The other option allows for separate selectivity parameters for each sex plus an additional parameter to define the scaling of one sex's peak selectivity relative to the other sex's peak. This second approach has only been implemented for a few selectivity patterns.

### Male Selectivity as a Fraction of Female Selectivity (or vice versa):

If the "domale" flag is set to 1, then the selectivity parameters define female selectivity and the offset defined below sets male selectivity relative to female selectivity. The two sexes switch roles if the "domale" flag is set to 2. Generally it is best to select the option so that the dependent sex has lower selectivity, thus obviating the need to rescale for selectivities that are greater than 1.0. Sex specific selectivity is done the same way for all size and age selectivity options.

- p1 – size (age) at which a dogleg occurs (set to an integer at a bin boundary and do not estimate).
- p2 –  $\ln(\text{relative selectivity})$  at minimum length or age = 0. Typically this will be set to a value of 0.0 (for no offset) and not estimated. It would be a rare circumstance in which the youngest/smallest fish had sex-specific selectivity.
- p3 –  $\ln(\text{relative selectivity})$  at the dogleg.
- p4 –  $\ln(\text{relative selectivity})$  at maximum length or max age.

For intermediate ages, the natural log values are linearly interpolated on size (age).

If selectivity for the dependent sex is greater than the selectivity for the first sex (which always peaks at 1.0), then the male-female selectivity matrix is rescaled to have a maximum of 1.0.

### Male Selectivity Estimated as Offsets from Female Selectivity (or vice versa):

A new sex selectivity option (3 or 4) has been implemented for size selectivity patterns 1 (logistic) and 23 and 24 (double normal) or age selectivity pattern 20 (double normal age). Rather than calculate male selectivity as an offset from female selectivity, here the male selectivity is calculated by making the male parameters an offset from the female parameters (option 3), or females are offset from males with option 4. The description below applies to option 3. If the size selectivity pattern is 1 (logistic), then read 3 parameters:

- male parameter 1 is added to the first selectivity parameter (inflection)
- male parameter 2 is added to the second selectivity parameter (width of curve)
- male parameter 3 is the asymptotic selectivity

If the size selectivity pattern is 20, 23 or 24 (double normal), then:

- male parameter 1 is added to the first selectivity parameter (peak)

- male parameter 2 is added to the third selectivity parameter (width of ascending side); then  $\exp(\text{this sum})$  per previous transform
- male parameter 3 is added to the fourth selectivity parameter (width of descending side); then  $\exp(\text{sum})$  per previous transform
- male parameter 4 is added to the sixth selectivity parameter (selectivity at final size bin); then  $1/(1+\exp(-\text{sum}))$  per previous transform
- male parameter 5 is the apical selectivity for males

Note that the male selectivity offsets currently cannot be time-varying because they are offsets from female selectivity, they inherit the time-varying characteristics of the female selectivity.

## Dirichlet Multinomial Error for Data Weighting

If the Dirichlet multinomial error distribution was selected in the data file for either length or age data weighting an additional parameter line is required immediately following the selectivity parameter block.

The list of parameters to be read from the above setup would be:

LO	HI	INIT	<other entries>	Block Fxn	Parameter Label
1	25	1	...	0	#ln(EffN mult) Age or Length 1
1	25	1	...	0	#ln(EffN mult) Age or Length 2

## Time-varying Options

The time-varying options for selectivity parameters are identical to the time-varying options for biology parameters. These options are described below in the [Using Time-Varying Parameter Options](#). After reading the selectivity parameters, which will include possible instructions to create environmental link, blocks, or deviation vectors, then read the following section. Note that all inputs in this section are conditional (COND) on entries in the selectivity parameter section. So if no selectivity parameters invoke any time-varying properties, this section is left blank (or completely commented out with #).

## Two-Dimensional Auto-Regressive Selectivity

A new experimental feature added within SS v.3.30.03.02. Earlier versions do not have this feature and hence this input is not expected. This features allows for auto-correlation by age and/or time. The age based random walk selectivity, pattern 17, should be selected to implement the semiparametric auto-regressive selectivity.

Typical Value	Description and Options									
1	Two-dimensional auto-regressive selectivity: 0 = Not used, 1 = Use 2D AR. COND = 1 Read the following long parameter lines:									
Fleet	Ymin	Ymax	Amin	Amax	Sigma Amax	Use Rho	Len(1)/ Age(2)	Phase	Before Range	After Range
1	1979	2015	2	10	1	1	2	5	1980	2007

continued:

				PRIOR	PRIOR					
LO	HI	INIT	PRIOR	SD	TYPE	PHASE	LABEL			
0	4	1	1	0.1	6	-4	#Sigma selex			
-1	1	0	0	0.1	6	-4	#Rho year			
-1	1	0	0	0.1	6	-4	#Rho age			
#Terminator line of 11 in length indicates the end of parameter input lines										
-9999	1	1	1	1	1	1	1	1	1	1

Parameter Definitions:

- Fleet: Fleet number to which semi-parametric deviations should be added.
- Ymin: First year with deviations.
- Ymax: Last year with deviations.
- Amin: First integer age (or population length bin index) with deviations.
- Amax: Last integer age (or population length bin index) with deviations.

- Sigma Amax: Not currently implemented. It is recommended to set the Sigma Amax equal to the Amin value. In future, Sigma Amax will be set to last age (or population length bin index) for which a separate sigma should be read.
- Use Rho: Use autocorrelation parameters.
- Len(1) / Age(2): 1 or 2 to specify whether the deviations should be applied to length- or age-based selectivity.
- Phase: Phase to begin estimation of the deviation parameters.
- Before Range: How should selectivity be modeled in the years prior to Ymin? Available options are (0) apply no deviations, (1) use deviations from the first year with deviations (Ymin), and (3) use average across all years with deviations (Ymin to Ymax).
- After Range: Similar to Before Range but defines how selectivity should be modeled after Ymax.

## Parameterizing the Two-Dimensional Autoregressive Selectivity

When the two-dimensional autoregressive selectivity feature is turned on for a fleet, the selectivity is calculated as a product of the assumed selectivity pattern and a non-parametric deviation term deviating from this assumed pattern:

$$\hat{S}_{a,t} = S_a \exp^{\epsilon_{a,t}} \quad (30)$$

where  $S_a$  is specified in the corresponding age/length selectivity types section and it can be either parametric (recommended) or non-parametric (including any of the existing selectivity options in SS);  $\epsilon_{a,t}$  is simulated as a two-dimensional first-order autoregressive (2D AR1) process:

$$\text{vec}(\epsilon) \sim MVN(\mathbf{0}, \sigma_s^2 \mathbf{R}_{\text{total}}) \quad (31)$$

where  $\epsilon$  is the two-dimensional deviation matrix and  $\sigma_s^2 \mathbf{R}_{\text{total}}$  is the covariance matrix for the 2D AR1 process. More specifically,  $\sigma_s^2$  quantifies the variance in selectivity deviations and  $\mathbf{R}_{\text{total}}$  is equal to the kronecker product ( $\otimes$ ) of the two correlation matrices for the among-age and among-year AR1 processes:

$$\mathbf{R}_{\text{total}} = \mathbf{R} \otimes \tilde{\mathbf{R}} \quad (32)$$

$$\mathbf{R}_{a,\tilde{a}} = \rho_a^{|a-\tilde{a}|} \quad (33)$$

$$\tilde{\mathbf{R}}_{t,\tilde{t}} = \rho_t^{|t-\tilde{t}|} \quad (34)$$

where  $\rho_a$  and  $\rho_t$  are the among age and among year AR1 coefficients, respectively. When both of them are zero,  $\mathbf{R}$  and  $\tilde{\mathbf{R}}$  are two identity matrices and their Kronecker product,  $\mathbf{R}_{\text{total}}$ , is also an identity matrix. In this case selectivity deviations are essentially identical and mutually independent:

$$\epsilon_{a,t} \sim N(0, \sigma_s^2) \quad (35)$$

## Using the Two-Dimensional Autoregressive Selectivity

First, fix the two AR1 coefficients ( $\rho_a$  and  $\rho_t$ ) at 0 and tune  $\sigma_s$  iteratively to match the relationship:

$$\sigma_s^2 = SD(\epsilon)^2 + \frac{1}{(a_{max} - a_{min} + 1)(t_{max} - t_{min} + 1)} \sum_{a=a_{min}}^{a_{max}} \sum_{t=t_{min}}^{t_{max}} SE(\epsilon_{a,t})^2 \quad (36)$$

The minimal and maximal ages/lengths and years for the 2D AR1 process can be freely specified by users in the control file. However, we recommend specifying the minimal and maximal ages and years to cover the relatively "data-rich" age/length and year ranges only. Particularly we introduce:

$$b = 1 - \frac{\frac{1}{(a_{max}-a_{min}+1)(t_{max}-t_{min}+1)} \sum_{a=a_{min}}^{a_{max}} \sum_{t=t_{min}}^{t_{max}} SE(\epsilon_{a,t})^2}{\sigma_s^2} \quad (37)$$

as a measure of how rich the composition data is regarding estimating selectivity deviations. We also recommend using the Dirichlet-Multinomial method to "weight" the corresponding composition data while  $\sigma_s$  is interactively tuned in this step.

Second, fix  $\sigma_s$  at the value iteratively tuned in the previous step and estimate  $\epsilon_{a,t}$ . Plot both Pearson residuals and  $\epsilon_{a,t}$  out on the age-year surface to check their 2D dimensions. If their distributions seems to be not random but rather be autocorrelated (deviation estimates have the same sign several ages and/or years in a row), users should consider estimating and then including the autocorrelations in  $\epsilon_{a,t}$ .

Third, extract the estimated selectivity deviation samples from the previous step for estimating  $\rho_a$  and  $\rho_t$  externally by fitting the samples to a stand-alone model written in Template-Model Builder (TMB). In this model, both  $\rho_a$  and  $\rho_t$  are bounded between 0 and 1 via applying a logic transformation. If at least one of the two AR1 coefficients are notably different from 0, SS should be run one more time by fixing the two AR1 coefficients at their values externally estimated from deviation samples. The Pearson residuals and  $\epsilon_{a,t}$  from this run are expected to distribute more randomly as the autocorrelations in selectivity deviations can be at least partially included in the 2D AR1 process.

## Tag Recapture Parameters

Specify if tagging data are being used:

Typical Value		Description and Options				
1		Tagging Data Present: 0 = No tagging data, or if tagging data is present in the data file, a value of 0 here will auto-generate the tag parameter section in the control.ss_new file. 1 = Read following lines of tagging data.				
COND = 1 Read the following long parameter lines:						
LO	HI	INIT	PRIOR	<other entries>	Block Fxn	Parameter Label
-10	10	9	9	...	0	#TG loss init 1
-10	10	9	9	...	0	#TG loss chronic 1
1	10	2	2	...	0	#TG loss overdispersion 1
-10	10	9	9	...	0	#TG report fleet 1
-4	0	0	0	...	0	#TG report decay 1

If there are multiple tagging groups or multiple fleets reporting tagged fish the additional needed parameter lines should be entered in order for each parameter type (i.e, TG loss init 1, TG loss init 2, TG loss chronic 1, TG loss chronic 2,..., TG report decay 1, TG report decay 2).

The parameters are defined as:

- Tag group loss init: the tag loss rate immediately following tagging.
- Tag group loss chronic: the long term tag loss rate.
- Tag group loss overdispersion:
- Tag group report fleet: the reporting rate of tags for a specific fleet.
- Tag group report decay: the long-term reporting rate of tags for a specific fleet.

The tagging reporting rate parameter is transformed within SS during estimation to maintain a positive value and is reported according to the transformation:

$$\text{Tagging Reporting Rate} = \frac{e^{\text{input parameter}}}{1 + e^{\text{input parameter}}} \quad (38)$$

Currently, tag parameters cannot be time-varying.

A shortcoming was identified in the recapture calculations when using Pope's F Method and multiple seasons in SS versions prior to 3.30.14. The internal calculations were corrected in version 3.30.14.

Now the Z-at-age is applied internally for calculations of fishing pressure on the population when using the Pope calculations.

## Mirroring of Tagging Parameters

In version 3.30.14, the ability to mirror the tagging parameters from another tag group or fleet was added. With this approach, the user can have just one parameter value for each of the five tagging parameter types and mirror all other parameters. Note that parameter lines are still required for the mirrored parameters and only lower numbered parameters can be mirrored. Mirroring is evoked through the phase input in the tagging parameter section. The options are:

- No mirroring among tag groups or fleets: phase > -1000,
- Mirror the next lower (i.e., already specified) tag group or fleet: phase = -1000 and set other parameter values the same as next lower Tag Group or fleet,
- Mirror a lower (i.e., already specified) tag group or fleet x: phase = -100x and set other parameter values the same as the mirrored tag group or fleet( i.e., if you would like to mirror fleet 1 then the phase should -1001).

To avoid having to specify mirrored parameter lines, the tag parameters can be auto-generated. The control.ss\_new file created after running this model will have a full set of tagging parameter lines to use in future SS runs.

## Variance Adjustment Factors

When doing iterative re-weighting of the input variance factors, it is convenient to do this in the control file, rather than the data file. This section creates that capability.

Read variance adjustment factors to be applied:

Factor	Fleet	Value	Description
1	2	0.5	# Survey CV for survey/fleet 2
4	1	0.25	# Length data for fleet 1
4	2	0.75	# Length data for fleet 2
-9999	0	0	# End read

### Additive Survey CV - Factor 1

The survey input variance (labeled survey CV) is actually the standard deviation of the ln(survey). The variance adjustment is added directly to this standard deviation. Set to 0.0 for no effect. Negative

values are OK, but will crash if adjusted standard deviation value becomes negative.

### Additive Discard - Factor 2

The input variance is the CV of the observation. Because this will cause observations of near zero discard to appear overly precise, the variance adjustment is added to the discard standard deviation, not to the CV. Set to 0.0 for no effect.

### Additive Mean Body Weight - Factor 3

The input variance is in terms of the CV of the observation. Because such data are typically not very noisy, the variance adjustment is added to the CV and then multiplied by the observation to get the adjusted standard deviation of the observation.

### Multiplicative Length Composition - Factor 4

The input variance is in terms of an effective sample size. The variance adjustment is multiplied times this sample size. Set variance adjustment to 1.0 for no effect.

### Multiplicative Age Composition - Factor 5

Age composition is treated the same way as length composition.

### Multiplicative Size-at-Age - Factor 6

Size-at-age input variance is the sample size for the N observations at each age. The variance adjustment is multiplied by these N values. Set to 1.0 for no effect.

### Multiplicative Generalized Size Composition - Factor 7

Generalized size composition input variance is the sample size for each observation. The variance adjustment for each fleet is multiplied by these sample sizes. Set to 1.0 for no effect.

### Variance Adjustment Usage Notes

The report.sso output file contains information in the "FIT\_LEN\_COMPS" and "FIT\_AGE\_COMPS" useful for determining if an adjustment of these input values is warranted to better match the scale of the average residual to the input variance scale.

Because the actual input variance factors are modified, it is these modified variance factors that are used when creating parametric bootstrap data files. So, the control files used to analyze bootstrap generated data files should have the variance adjustment factors reset to null levels.



## Lambdas (Emphasis Factors)

These values are multiplied by the corresponding likelihood component to calculate the overall negative log likelihood to be minimized.

Typical Value	Description and Options
4	Max lambda phase: read this number of lambda values for each element below. The last lambda value is used for all higher numbered phases.
1	SD offset: 0 = The $\ln(\text{like})$ to omit the $+\ln(s)$ term, 1 = The $\ln(\text{like})$ to include the $\ln(s)$ term for CPUE, discard, growth CV, mean body weight, recruitment deviations. If you are estimating any variance parameters, SD offset must be set to 1.

### Lambda Usage Notes

If the CV for size-at-age is being estimated and the model contains mean size-at-age data, then the flag for inclusion of the  $+\ln(\text{stddev})$  term in the likelihood must be included. Otherwise, the model will always get a better fit to the mean size-at-age data by increasing the parameter for CV of size-at-age.

The reading of the lambda values has been substantially altered with SS v.3.30. Instead of reading a matrix containing all the needed lambda values, SS now just reads those elements that will be given a value other than 1.0. After reading the datafile, SS sets lambda equal to 0.0 if there are no data for a particular fleet/data type, and a value of 1.0 if data exist. So beware if your data files had data but you had set the lambda to 0.0 in a previous version of SS. First read an integer for the number of changes.

Read the lambda adjustments by fleet and data type:

Likelihood Component	Fleet	Phase	Lambda Value	SizeFreq Method
1	2	2	1.5	1
4	2	2	10	1
4	2	3	0.2	1
-9999	1	1	1	1

The codes for component are:

1 = survey

10 = recruitment deviations

2 = discard	11 = parameter priors
3 = mean weight	12 = parameter deviations
4 = length	13 = crash penalty
5 = age	14 = morph composition
6 = size frequency	15 = tag composition
7 = size-at-age	16 = tag negative binomial
8 = catch	17 = F ballpark
9 = initial equilibrium catch	18 = regime shift

---

## Controls for Variance of Derived Quantities

Additional standard deviation reported may be selected:

Typical Value			Description and Options					
1			0 = No additional std dev reporting; and 1 = read values below.					
COND > 0 : Read the 4 following lines:								
Selex Type	Len/Age /Both	Year	Nselex Bins	Growth Pattern	N Growth Ages	NatAge Area	NatAge year	N Natage
1	1	-1	5	1	5	1	-1	5
Vector (length of 5) with selectivity std bin picks (-1 in first bin to self-generate).								
5	15	25	35	43				
Vector (length of 5) with growth std bin picks (-1 in first bin to self-generate).								
1	2	14	26	40				
Vector (length of 5) with NatAge std bin picks (-1 in first bin to self-generate).								
1	2	14	26	40				
999	#End of the control file input							

Where:

- Selex Type: The index of the fleet to be output.
  - 0 = No selectivity variance output; and
  - 1 = Selectivity variance output.
- Len/Age/Both:
  - 1 = Select length selectivity;
  - 2 = Select age selectivity; and
  - 3 = Both length and age selectivity.
- Year:
  - year = Enter a value for the selected year; and
  - -1 = To get the selectivity in the end year.
- N Selex bins: enter the number of bins for which selectivity will be output. This number controls the number of items to be read below, even if the Selex Type is set to zero. In other words, the read occurs even if the effect of the read is disabled.
- Growth pattern: growth pattern is the number of the growth pattern to be output. Note that in a multiple season model, SS will output the size-at-age for the last birth season that gets any recruits within the year. Also, if growth parameters are not estimated, then standard deviation output of mean size-at-age is disabled.
  - positive value = Growth pattern,
  - 0 = No variance output for size-at-age.
- N growth bins: Number of ages for which size-at-age variance is requested. This number controls the number of items to be read below, even if the growth pattern selection is set to zero. In other words, the read occurs even if the effect of the read is disabled.
- Area for Natage: specifies the area for which output of numbers at age is requested.
  - positive value = area to output;
  - 0 = Disables this output; and
  - -1 = Requests that numbers-at-age be summed across all areas. In all cases,

numbers-at-age is summed across all growth patterns and platoons and output for each sex.

- NatAge Year: specifies the year for which numbers-at-age are output.
  - year = The year to output; and
  - -1 = Requests output for year equal to end year + 1, hence the year that starts the forecast period.
- N Natage bins: as with the N growth bins.

## Using Time-Varying Parameters

The approach to allowing parameters to have time-varying values has been completely overhauled in the transition from SS v.3.24 to SS v.3.30. Fortunately, the transition executable (sstrans.exe) will do the conversion for you, but you should review the new control file closely before simply running with it, especially for time-varying catchability parameters.

### Time-Varying Parameter Change from Earlier SS Versions

In SS v.3.24, the group of biology parameters (termed mortality-growth parameters) and the selectivity parameters used the same long parameter line approach, but it was implemented with entirely different code, and hence was inefficient. The spawner-recruitment parameters used short parameter lines and a different approach for linkage to an environmental variable and the R1 offset provided a limited type of block. The catchability parameters also used short parameter lines and had its own approach to doing environmental linkage and random deviations, but not blocks. Then finally, the tagging parameters had long parameter lines, but there was no code to interpret any time-varying info in those lines. The situation was begging for a more modular approach.

### Code Flow Version SS v.3.30

In SS v.3.30, mortality-growth, selectivity, stock recruitment relationship, catchability, and tag (soon but not as of v.3.30.12) base parameters all use long parameter lines and invoke blocks, trends, environmental linkages, and random deviations using identical syntax. As SS v.3.30 executes the SS\_readcontrol code, it calls a function in SS\_global called “create\_timevary” whenever a base parameter has any one of the 4 types of time-varying options. In fact, block/trend, env and devs all can be applied to the same base parameter. Only blocks and trends are mutually exclusive, but any combined effect could be used together judiciously. “Create\_timevary” creates all needed information to describe and index a list of time varying parameter specifications. in fact, if the auto-generation switch has been set to zero, then you will omit all of the needed parameters for implementing the time-varying effect and SS will auto-generate and use the needed parameters and write them out in

the control.ss\_new file. Then as SS gets into iterative parameter updating it starts by calling a function in SS\_timevaryparm that processes each time-varying parameter specification (each of which can contain any combination of block/trend, env and dev specification) and creates a time-series of the parameter value that are used as SS subsequently loops through the years.

## Parameter Order

The order of parameters has changed and the re-ordering is handled by the transition executable (sstrans.exe). Previously, for each of mortality-growth and selectivity parameters all environmental link parameters were listed first, then block/trend parameters and then deviation parameters. In SS v.3.30, these parameters are re-organized such that all parameters that affect a base parameter are clustered together with block/trend first, then environmental, then deviation. So, if mortality-growth (MG) base parameters 3 and 7 had time varying changes, the order would look like:

MG base parameter 3	Block parameter 3-1
	Block parameter 3-2
	Environmental link parameter 3-1
	Deviation se parameter 3
	Deviation rho parameter 3
MG base parameter 7	Block parameter 7-1
	Deviation se parameter 7
	Deviation rho parameter 7

## Link Functions

The functional form by which a time-varying parameter,  $Q$ , changes a base parameter,  $P$ , is a link function:  $P'_y = f(P, Q)$ . Typically, this is additive or multiplicative function, but the parameter mirroring feature is essentially a link that takes no parameter. Another type of link in SS is between a model state variable, such as available biomass, and the expected value for a survey. Typically, this is a simple proportional link taking one parameter,  $q$ , but the  $q$  power feature is essentially a 2 parameter link function. So, a parameter link function can change  $q$  over time, and a survey link function then uses the annual value of  $q$  to link the annual value of a state variable to the expected value for a survey. In SS v.3.24, various usages of positive and negative codes and other conventions were used to invoke additive vs multiplication links and other options. But as SS v.3.30 builds capability to allow an environment index to be a “survey” of a parameter deviation, we need a larger family of link functions such as logistic and even dome-shaped.

The link specifications in SS v.3.30 has been updated from SS v.3.24. Take special note of the environmental linkage specification where two bits of information are coded into one number. The

new specification has the environmental link function denoted by the first environmental index to use specified by two additional. (e.g., environmental link specification of 204 is parsed by SS to use link type 2 using environmental variable 4).

The new available options for time-varying parameters in SS v.3.30 are described below:

- Environmental Link and Variance - Element 8 in parameter setup
  - env\_data is a dvar\_matrix populated with the read environmental data for columns 1-N environmental variables and derived quantities mapped to columns -1 to -4 to density-dependence:
    - \* -1; for  $\ln(\text{relative spawning biomass})$ ;
    - \* -2; for recruitment deviation;
    - \* -3; for  $\ln(\text{relative summary biomass})$  (e.g., current year summary biomass divided by the unfished summary biomass);
    - \* -4; for  $\ln(\text{relative summary numbers})$ .
  - So, environmental input 103 would use link type 1 and apply it to environmental data column 3 and environmental input -103 would use link type 1 and apply it to the "-3" column which is  $\ln(\text{relative summary biomass})$ .
  - These four derived quantities are all calculated at the beginning of each year within the model, so they are available inside SS to use as the basis for time-varying parameter links without violating any order of operations rule.
- Deviation Link - Element 9 in parameter setup
  - 1 = multiplicative ( $P_y * = \exp(\text{dev}_y * \text{dev}_{se})$ ),
  - 2 = additive ( $P_y + = \text{env}_y * \text{dev}_{se}$ ),
  - 3 = random walk options are now implemented by using rho in the objective function. SS now expects the estimated deviations to be normal in distribution and the deviation values are multiplied by the standard error parameter as they are used,
  - 4 = zero reverting random walk with rho. The deviation parameter is now multiplied by the standard error parameter, rather than deviations being penalized according to a specified standard error (the approach in SS v.3.24).
  - The option of applying the final model year deviation value into the forecast period was added in v. 3.30.13. This new option is specified by selecting the appropriate deviation

link option (1, 2, 3, or 4) and appending a 2 at the front (21, 22, 23, or 24) which will use the final year deviation value for all forecast years.

- See [Deviation Link](#) to see the code behind each of these options
- Deviation Minimum Year - Element 10 in parameter setup
  - Year for deviations to start for parameter
- Deviation Maximum Year - Element 11 in parameter setup
  - Year for deviations to end for parameter
- Deviation Phase - Element 12 in parameter setup
  - integer, this available element in the long parameter line is now a deviation vector specific phase control
- Blocks - Element 13 in parameter setup. Currently, there are four options for applying blocks:
  - >0: block index for parameter.
  - -1: trend with final as offset from base parameter and offset values is in natural log space, also inflection year is in natural log space and the offset from  $\ln(0.5)$ . No additional parameter lines are required. Three parameters will be estimated; end trend parameter value logistic offset, inflection year logistic offset, and slope.
  - -2: trend with final as standalone value. No additional parameter lines are required. Three parameters will be estimated; end trend parameter value, inflection year, and slope.
  - -3 end value is a fraction of base parameter maximum - minimum; inflection year is fraction of end year - start year. No additional parameter lines are required. Three parameters will be estimated; end trend parameter value as a fraction, inflection year as a fraction, and slope.
- Block Functional Form: Element 14 in parameter setup
  - 0: multiplicative ( $P_y = P_{base} * \exp(tv\_para)$ ),
  - 1: additive ( $P_y = P_{base} + tv\_para$ ),
  - 2: replace ( $P_y = tv\_para$ ),
  - 3: random walk across blocks ( $P_{block} = P_{block,-1} + tv\_para$ ),
  - 4: mean reverting random walk

## Block Trends

Additional information regarding the options for applying blocks (element 13):

- -1: Trend bounded by base parameter minimum maximum and parameters in transformed units (use with caution),
  - Logistic approach to trend as offset from base parameter
  - Transform the base parameter from the MG parameter section:

$$temp = -0.5 * \ln \left( \frac{MGparm_1(j, 2) - MGparm_1(j, 1) + 0.0000002}{MGparm(j) - MGparm_1(j, 1) + 0.0000001} - 1 \right) \quad (39)$$

- Add the offset. Note, that offset values in in the transform space.

$$temp+ = MGparm(k + 1) \quad (40)$$

- Back transform

$$temp1 = MGparm_1(j, 1) + \frac{MGparm_1(j, 2) - MGparm_1(j, 1)}{1 + e^{-2*temp}} \quad (41)$$

## Parameter Priors

Priors on parameters fulfill two roles in SS. First, for parameters provided with an informative prior, SS is receiving additional information about the true value of the parameter. This information works with the information in the data through the overall log likelihood function to arrive at the final parameter estimate. Second, diffuse priors provide only weak information about the value of a prior and serve to manage model performance during execution. For example, some selectivity parameters may become unimportant depending upon the values of other parameters of that selectivity function. In the double normal selectivity function, the parameters controlling the width of the peak and the slope of the descending side become redundant if the parameter controlling the final selectivity moves to a value indicating asymptotic selectivity. The width and slope parameters would no longer have any effect on the log likelihood, so they would have no gradient in the log likelihood and would drift aimlessly. A diffuse prior would then steer them towards a central value and avoid them crashing into the bounds. Another benefit of diffuse priors is the control of parameters that are given unnaturally wide bounds. When a parameter is given too broad of a bound, then early in a model run it could drift into this tail and potentially get into a situation where the gradient with respect that parameter approaches zero even though it is not at its global best value. Here the diffuse prior helps move the parameter back towards the middle of its range where it presumably will be more influential and estimable.



The options for parameter priors are described as a function of  $Pval$ , the value of the parameter for which a prior is being calculated, as well as the parameter bounds in the case of the beta distribution ( $P_{max}$  and  $P_{min}$ ), and the input values for  $Prior$  and  $Pr\_SD$ , which in some cases are the mean and standard deviation, but interpretation depends on the prior type. The Prior Likelihoods below represent the negative log likelihood in all cases.

## Prior Types

Note that the numbering in SS v.3.30 is different from that used in SS v.3.24 (where confusingly -1 indicated no prior and 0 indicated a normal prior). The calculation of the negative log likelihood is provided below for each prior types, as a function of the following inputs:

$p$	The value of the parameter for which a prior is being calculated
$P_{min}$	The lower bound of the parameter (1st column in control file)
$P_{max}$	The upper bound of the parameter (2nd column in control file)
$Prior$	The input value for the PRIOR input (4th column in control file)
$Pr\_SD$	The input value for the PR_SD input (5th column in control file)

- **Prior Type = 0 = No prior applied**

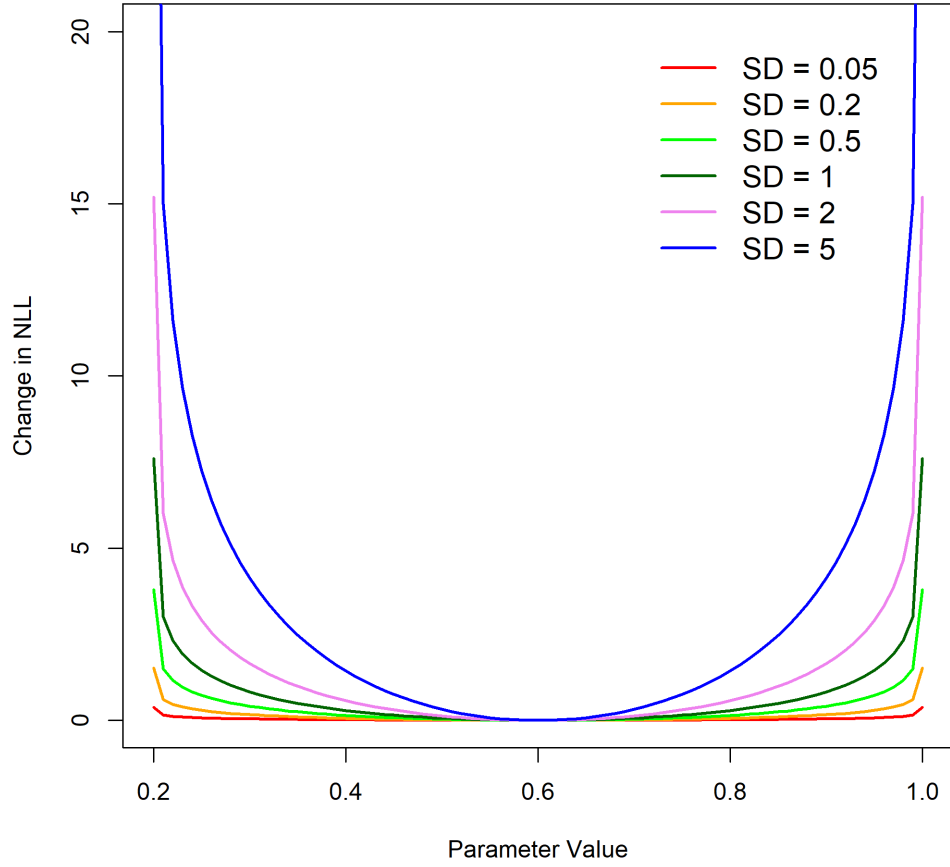
In a Bayesian context this is equivalent to a uniform prior between the parameter bounds.

- **Prior Type = 1 = Symmetric beta prior**

The symmetric beta is scaled between parameter bounds, imposing a larger penalty near the bounds. Prior standard deviation of 0.05 is very diffuse and a value of 5.0 provides a smooth U-shaped prior. The PRIOR input is ignored for this prior type.

$$\mu = -Pr\_SD \cdot \ln \left( \frac{P_{max} + P_{min}}{2} - P_{min} \right) - Pr\_SD \cdot \ln(0.5) \quad (42)$$

$$\begin{aligned} \text{Prior Likelihood} = & -\mu - Pr\_SD \cdot \ln(p - P_{min} + 0.0001) \\ & - Pr\_SD \cdot \ln \left( 1 - \frac{p - P_{min} - 0.0001}{P_{max} - P_{min}} \right) \end{aligned} \quad (43)$$



Prior distributions for the symmetric beta distribution.

- **Prior Type = 2 = Beta prior**

The definition of  $\mu$  is consistent with CASAL's formulation with the  $B_{prior}$  and  $A_{prior}$  corresponding to the  $m$  and  $n$  parameters.

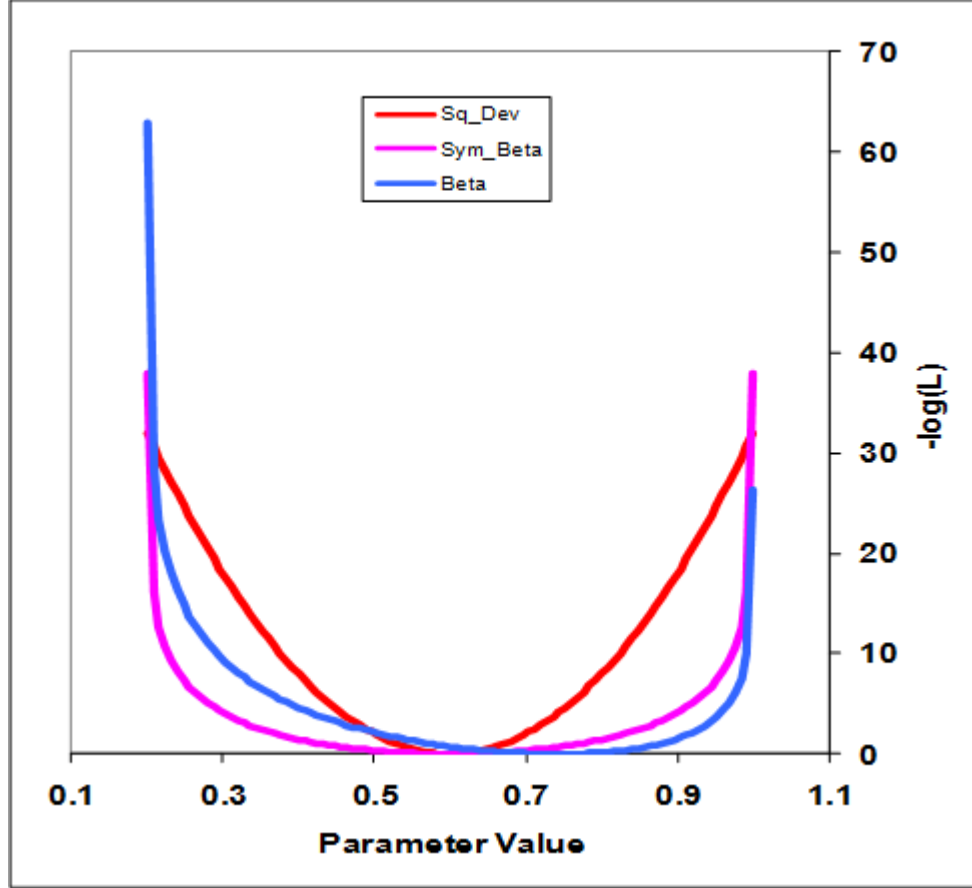
$$\mu = \frac{Prior - P_{min}}{P_{max} - P_{min}} \quad (44)$$

$$\tau = \frac{(Prior - P_{min})(P_{max} - Prior)}{Pr\_SD^2} - 1 \quad (45)$$

$$B_{prior} = \tau \cdot \mu \quad (46)$$

$$A_{prior} = \tau(1 - \mu) \quad (47)$$

$$\begin{aligned}
\text{Prior Likelihood} = & (1 - B_{\text{prior}}) \cdot \ln(0.0001 + p - P_{\min}) \\
& + (1 - A_{\text{prior}}) \cdot \ln(0.0001 + P_{\max} - p) \\
& - (1 - B_{\text{prior}}) \cdot \ln(0.0001 + \text{Prior} - P_{\min}) \\
& - (1 - A_{\text{prior}}) \cdot \ln(0.0001 + P_{\max} - \text{Prior})
\end{aligned} \tag{48}$$



Comparison of the symmetric beta and the beta prior functions

- **Prior Type 3 = Lognormal prior**

Note that this is undefined for  $p \leq 0$  so the lower bound on the parameter must be  $> 0$ . The prior value is input into the parameter line in natural log space while the initial parameter value is defined in normal space (e.g. INIT = 0.20, PRIOR = -1.609438).

$$\text{Prior Likelihood} = \frac{1}{2} \left( \frac{\ln(p) - \text{Prior}}{\text{Pr\_SD}} \right)^2 \tag{49}$$

- **Prior Type 4 = Lognormal prior with bias correction**

This option allows the prior mean value to be entered as the  $\ln(\text{mean})$ . Note that this is undefined for  $p \leq 0$  so the lower bound on the parameter must be  $> 0$ .

$$\text{Prior Likelihood} = \frac{1}{2} \left( \frac{\ln(p) - \text{Prior} + \frac{1}{2} \text{Pr\_SD}^2}{\text{Pr\_SD}} \right)^2 \quad (50)$$

- **Prior Type 5 = Gamma prior**

The lower bound should be 0 or greater.

$$\text{scale} = \frac{\text{Pr\_SD}^2}{\text{Prior}} \quad (51)$$

$$\text{shape} = \frac{\text{Prior}}{\text{scale}} \quad (52)$$

$$\text{Prior Likelihood} = -\text{shape} \cdot \ln(\text{scale}) - \ln(\Gamma(\text{shape})) + (\text{shape} - 1) \cdot \ln(p) - \frac{p}{\text{scale}} \quad (53)$$

- **Prior Type 6 = Normal prior**

Note that this function is independent of the parameter bounds.

$$\text{Prior Likelihood} = \frac{1}{2} \left( \frac{p - \text{Prior}}{\text{Pr\_SD}} \right)^2 \quad (54)$$

## Optional Inputs

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

SS has 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 an explicit switch near the top of the control file. The values are read from a separate file named, wtatage.ss. This file is only required to exist if this option is selected.

The first value read is a single integer for the maximum age used in reading this file. So if the maximum age is 40, there will be 41 columns of weight-at-age entries to read, with the first column being for age 0. If the number of ages specified in this table is greater than maximum age in the model, the extra weight-at-age values are ignored. If the number of ages in this table is less than maximum age in the model, the weight-at-age for the number of ages in the file is filled in for all unread ages out to maximum age.

The format of this input file is:

40 Maximum Age								
			Growth		Birth			
Year	Season	Gender	Pattern	Season	Fleet	Age-0	Age-1	...
1971	1	1	1	1	-2	0	0	0.1003
1971	1	1	1	1	-1	0.0169	0.0864	0.2495
1971	1	1	1	1	0	...	...	...
1971	1	1	1	1	1	...	...	...
1971	1	1	1	1	2	...	...	...
-9999	1	1	1	1	0	...	...	...

where:

- Fleet = -2 is age-specific fecundity\*maternity\*weight-at-age, so time-varying fecundity is possible to implement.
- Fleet = -1 is population wt-at-age at middle of the season.N
- Fleet = 0 is population wt-at-age at the beginning of the season.
- There must be an entry for fecundity\*maternity, population wt-at-age at the middle of the season, population wt-at-age at the beginning of the season, and wt-at-age for each fleet (even if these vectors are identical in some cases).
- Fleets that do not use biomass do not need to have wt-at-age assigned.
- Growth pattern and birth season 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
- There is no internal error checking to verify that weight-at-age has been read for every fleet and for every year.
- In the future, there could be an option to use another value of the control file switch to turn off all aspects of growth parameters and size selectivity.

- The values entered for  $\text{endyr} + 1$  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 weight-at-age from the growth input, so there is no way to compare the input weight-at-age from the weight-at-age derived from the growth parameters.
- If weight-at-age is read and size-selectivity is used, a warning is generated.
- If weight-at-age is read and discard/retention is invoked, then a warning is generated because of untested consequences for the body weight of discarded fish.
- Age 0 fish seem to need to have  $\text{weight}=0$  for spawning biomass calculation (code -2).

## User Testing

- Setup a model with age-maturity (option 2) and only age selectivity.
- Take the output calculation of weight-at-age and fecundity-at-age from `report.sso` and put into `wtatage.ss` (as shown above).
- Re-run SS with this input weight-at-age (Maturity\_Option 5) to see if identical results are produced relative to the run that had generated the weight-at-age from the growth parameters.

## runnumber.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.

## profilevalues.ss

This file contains information for changing the value of selected parameters for each run in a batch. In the control 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 control 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 control 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. Also, this options was created before use of R became widespread. You probably can create a more flexible approach using R today.

## Likelihood components

The objective function  $L$  is the weighted sum of the individual components indexed by kind of data  $i$ , and fishery/survey  $f$  as appropriate:

$$L = \sum_{i=1}^I \sum_{f=1}^{A_f} \omega_{i,f} L_{i,f} + \omega_R L_R + \sum_{\theta} \omega_{\theta} L_{\theta} + \sum_P \omega_P L_P \quad (55)$$

where  $L$  is the total objective function,  $i$  is the index of the objective function component,  $A_f$  is the number of fleets,  $L_{i,f}$  is the objective function for data kind  $i$  for the fishery/survey  $f$ ,  $\omega_{i,f}$  is a weighting factor for each objective function component,  $\omega$  is the parameter priors, and  $P$  is the random parameter deviations.

The components of the objective function based on the model set-up and data are:

Index	Source	Kind	Error structure
$i$	fishery/survey $f$	CPUE or Abundance index	user choice
$i$	fishery $f$	Discard biomass	user choice
$i$	fishery/survey $f$	Mean body weight	normal
$i$	fishery/survey $f$	Length composition	multinomial or log-gamma
$i$	fishery/survey $f$	Age composition	multinomial or log-gamma
$i$	fishery/survey $f$	Dirichlet data weighting	gamma in log-space
$i$	fishery/survey $f$	Mean size-at-age	normal

$i$	fishery/survey $f$	Tag-recapture 1	multinomial
$i$	fishery/survey $f$	Tag-recapture 2	negative binomial
$i$	fishery $f$	Initial equilibrium catch	normal
$R$		Recruitment deviations	lognormal
$P$		Random parameter devs.	normal
$\theta$		Parameter priors	user choice
$F_B$		F ballpark penalty	
$C_P$		Crash penalty	

---

## Running SS

### Command Line Interface

The name of the SS executable files often contains the phrase "safe" or "opt" (for optimized). The safe version includes checking for out of bounds values and should always be used whenever there is a change to the data file. The optimized version runs slightly faster but can result in data not being included in the model as intended if the safe version has not been run first. A file named "ss.exe" is typically the safe version unless the result of renaming by the user. In some situations, users may wish to rename the file they are using to ss.exe, but the longer file name can be used.

On Mac and Linux computers, the executable does not include an extension (like .exe on Windows). Running the executable on from the DOS command line in Windows simply require typing the executable name (without the .exe extension):

```
> ss
```

On Mac and Linux computers, the executable name must be preceded by a period and slash (unless it's location has been added to the user's PATH):

```
> ./ss
```

Additional ADMB commands can follow the executable name, such as "-nohess" to avoid calculating the Hessian matrix. To see a full list of options, add "-?" after the executable name (with a space in between).

On all operating systems, a copy of the SS executable can either be located in the same directory as



the model input files or in a central location and referenced either by adding it to the PATH or by a script files. Further discussion on script files for Windows is below. Editing the PATH is not covered here.

## Example of DOS batch input file

One file management approach is to put ss.exe in its own folder (example: C:\SS\_model) and to put your input files in separate folder (example: C:\My Documents \SS\_runs). Then a DOS batch file in the SS\_runs folder can be run at the command line to start ss.exe. All output will appear in SS\_runs folder.

A DOS batch file (e.g. SS.bat) might contain some explicit ADMB commands, some implicit commands, and some DOS commands:

```
c:\SS_model\ss.exe -cbs 5000000000 -gbs 50000000000 %1 %2 %3 %4
del ss.r0*
del ss.p0*
del ss.b0*
```

In this batch file, the -cbs and -gbs arguments allocate a large amount of memory for SS to use (you may need to edit these for your computer and SS configuration), and the %1, %2 etc. allows passing of command line arguments such as -nox or -nohess. You add more items to the list of % arguments as needed.

An easy way to start a command line in your current directory (SS\_runs) is to create a shortcut to the DOS command line prompt. The shortcut's target would be:

```
> %SystemRoot%\system32\cmd.exe
```

And it would start in:

```
> %CURRDIR%
```

An alternative shortcut is to have the executable within the model folder then use Ctrl+Shift+Right Click and then select either "Open powershell window here" or "Open command window here", depending upon your computer. From the command window the executable name can be typed along with additional inputs (e.g., -nohess) and the model run. If using the powershell type cmd and then hit enter prior to calling the model (ss).

## Simple Batch

This first example relies upon having a set of prototype files that can be renamed to starter.ss and then used to direct the running of SS. The example also copies one of the output files to save it from being overwritten. This sequence is repeated 3 times here and can be repeated an unlimited number of times. The batch file can have any name with the .bat extension, and there is no particular limit to the DOS commands invoked. Note that brief output from each run will be appended to cumreport.sso (see below).

```
del ss.cor
del ss.std
copy starter.r01 starter.ss
c:\admodel\ss\ss.exe -sdonly
copy ss.std ss-std01.txt
copy starter.r01 starter.ss
c:\admodel\ss\ss.exe -sdonly
copy ss.std ss-std02.txt
```

## Complicated Batch

This second example processes 25 dat files from a different directory, each time using the same ctl and nam file. The loop index is used in the file names, and the output is searched for particular keywords to accumulate a few key results into the file SUMMARY.TXT. Comparable batch processing can be accomplished by using R or other script processing programs.

```
del summary.txt
del ss-report.txt
copy /Y runnumber.zero runnumber.ss
FOR /L %%i IN (1,1,25) DO (
copy /Y ..\MakeData\A1-D1-%%i.dat Ase1.dat
del ss.std
del ss.cor
del ss.par
c:\admodel\ss\ss.exe
copy /Y ss.par A1-D1-A1-%%i.par
copy /Y ss.std A1-D1-A1-%%i.std
find "Number" A1-D1-A1-%%i.par >> Summary.txt
find "hessian" ss.cor >> Summary.txt)
```

## Running Parameter Profiles

Users will often want to run profiles over specific parameter to evaluate the information in the model to estimate the parameter based on changes in the log likelihood. There are two ways this can be done.

The first option is the use functions within `r4ss` to run the profile, summarize quantities across runs, and plot the output. The `SS_profile()` function will run the profile based on function inputs, `SSgetoutput()` will read quantities from each run Report file, `SSsummarize()` will summarize key model quantities, and the `SSplotProfile()` and `PinerPlot()` functions can be used to visualize results. Additional information regarding `r4ss` can be found on page [173](#).

The second way is to create and run a batch file to profile over parameters. This example will run a profile on natural mortality and spawner-recruitment steepness, of course. Edit the control file so that the natural mortality parameter and steepness parameter lines have the phase set to -9999. Edit `STARTER.SS` to refer to this control file and the appropriate data file.

Create a `PROFILEVALUES.SS` file

```
2 # number of parameters using profile feature
0.16 # value for first selected parameter when runnumber equals 1
0.35 # value for second selected parameter when runnumber equals 1
0.16 # value for first selected parameter when runnumber equals 2
0.40 # value for second selected parameter when runnumber equals 2
0.18 # value for first selected parameter when runnumber equals 3
0.40 # value for second selected parameter when runnumber equals 3
etc.; make it as long as you like.
```

Create a batch file that looks something like this. Or make it more complicated as in the example above.

```
del cumreport.sso
copy /Y runnumber.zero runnumber.ss % so you will start with runnumber=0
C:\SS330\ss.exe
C:\SS330\ss.exe
C:\SS330\ss.exe
```

Repeat as many times as you have set up conditions in the `PROFILEVALUES.SS` file. The summary results will all be collected in the `cumreport.sso` file. Each step of the profile will have an unique run number and its output will include the values of the natural mortality and steepness parameters for that run.

## Re-Starting a Run

SS model runs can be restarted from a previously estimated set of parameter values. In the `starter.ss` file, enter a value of 1 on the first numeric input line. This will cause SS to read the file `ss.par` and use these parameter values in place of the initial values in the control file. This option only works if the number of parameters to be estimated in the new run is the same as the number of parameters in the previous run because only actively estimated parameters are saved to the file `ss.par`. The file `ss.par` can be edited with a text editor, so values can be changed and rows can be added or deleted. However, if the resulting number of elements does not match the setup in the control file, then unpredictable results will occur. Because `ss.par` is a text file, the values stored in it will not give exactly the same initial results as the run just completed. To achieve greater numerical accuracy, SS can also restart from `ss.bar` which is the binary version of `ss.par`. In order to do this, the user must make the change described above to the `starter.ss` file and must also enter `-binp ss.bar` as one of the command line options.

## Debugging Tips

When SS input files are causing the program to crash or fail to produce sensible results, there are a few steps that can be taken to diagnose the problem. Before trying the steps below, examine the `echoinput.sso` file. It is highly annotated, so you should be able to see if SS is interpreting your input files as you intended. Additionally, users should check the `warning.sso` file when attempting to debug a non-running model.

1. Set the `turn_off_phase` switch to 0 in the `starter.ss` file. This will cause the mode to not attempt to adjust any parameters and simply converges a dummy parameter. It will still produce a `Report.sso` file, which can be examined to see what has been calculated from the initial parameter values.
2. Turn the verbosity level to 2 in the `starter.ss` file. This will cause the program to display the value of each likelihood component to the screen on each iteration. So if the program is creating an illegal computation (e.g. divide by zero), it may show you which likelihood component contains the problematic calculation. If the program is producing a `Report.sso` file, you may then see which observation is causing the illegal calculation.
3. Run the program with the command `ss »SSpipe.txt`. This will cause all screen display to go to the specified text file (note, delete this file before running because it will be appended to). Examination of this file will show detailed statements produced during the reading and preprocessing of input files.
4. If SS fails to achieve a proper Hessian it exits without writing the detailed outputs in the `FINAL_SECTION`. If this happens, you can do a run with the `-nohess` option so you can view

the Report.sso to attempt to diagnose the problem.

## Keyboard Tips

Typing "N" during a run will cause ADMB to immediately advance to the next phase of estimation.

Typing "Q" during a run will cause ADMB to immediately go to the final phase. This bypasses estimation of the Hessian and will produce all of the SS outputs, which are coded in the FINAL\_SECTION.

## Running MCMC

Run SS v3.30

- This gives maximum posterior density estimates, report file, Hessian matrix and the .cor file.
- Look for parameters stuck on bounds which will degrade efficiency of MCMC implementation.

Run SS v.3.30 with arguments -mcmc xxxx -mcsave yyyy

- Where: xxxx is the number of iterations for the chain, and yyyy is the thinning interval (1000 is a good place to start).
- MCMC chain starts at the MPD values.
- Recommended: Remove existing .psv files in run directory to generate a new chain.
- Recommended: Set DOS run detail switch in starter file to 0; reporting to screen will dramatically slow MCMC progress.
- Optional: Add -nohess to use the existing Hessian file without re-estimating.
- Optional: To start the MCMC chain from specific values change the par file; run the model with estimation, adjust the par file to the values that the chain should start from, change within the starter file for the model to begin from the par file, and call the MCMC function using ss -mcmc xxxx - mcsave yyyy -nohess -noest.
- Optional: Add -noest -nohess and modify starter file so that run will now start from the converged (or modified) parameter estimates in "ss.par".

Run SS v3.30 with argument -mceval

- This generates the posterior output files.
- Optional: Modify starter file entries to add a burn-in and thinning interval above and beyond the ADMB thinning interval applied at run time.
- Recommended: MCMC always begins with the maximum posterior density values and so a burn-in >0 should always be used.
- This step can be repeated for alternate forecast options (e.g., catch levels) without repeating step 2.

Optional: Run SS v3.30 with arguments -mcr -mcmc xxxx -mcsave yyyy ...

- This restarts and extends an uninterrupted chain previously completed (note that any intermediate runs without the -mcr command in the same directory will break this option).

Note: when SS switches to MCMC or MCEVAL mode, it sets all the bias adjustment factors to 1.0 for any years with recruitment deviations defined. SS does not create a report file after completing MCMC because it would show values based on the last MCMC step.

## Output Files

### Standard ADMB output files

Standard ADMB files are created by SS. These are:

ss.par – This file has the final parameter values. They are listed in the order they are declared in SS. This file can be read back into SS to restart a run with these values (see running SS on page [155](#)).

ss.std – This file has the parameter values and their estimated standard deviation for those parameters that were active during the model run. It also contains the derived quantities declared as standard deviation report variables. All of this information is also report in the covar.sso. Also, the parameter section of Report.sso lists all the parameters with their SS generated names, denotes which were active in the reported run, displays the parameter standard deviations, then displays the derived quantities with their standard deviations.

ss.rep – This report file is created between phases so, unlike Report.sso, will be created even if the hessian fails. It does not contain as much output as shown in Report.sso.

ss.cor – This is the standard ADMB report for parameter and standard deviation report correlations. It is in matrix form and challenging to interpret. This same information is reported in covar.sso.

## SS Summary

The ss\_summary.sso file (available for versions 3.30.08.03 and later) is designed to put key model outputs all in one concise place. It is organized as a list. At the top of the file are some descriptors, followed by the likelihoods for each component, then the parameters and their standard errors, then the derived quantities and their standard errors. The total biomass, summary biomass, and catch were added to the quantities reported in this file in version 3.30.11 and later. This output was created to make it easy to compare the results between different versions of the executable, however, this file could be useful for numerous other uses.

## SIS table

The SIS\_table.sso file contains model output formatted for reading into the NMFS Species Information System (SIS). This file includes an assessment summary for categories of information (abundance, recruitment, spawners, catch estimates) that are input into the SIS database. A time-series of estimated quantities which aggregates estimates across multiple areas and seasons are provided to summarize model results. Access to the SIS database is granted to all NOAA employees and can be accessed as: <https://www.st.nmfs.noaa.gov/sis/>.

## Derived Quantities

Before listing the derived quantities reported to the standard deviation report, there are a couple of topics that deserve further explanation.

### Virgin Spawning Biomass (B0) vs Unfished Spawning Biomass

Unfished is the condition for which reference points (benchmark) are calculated. Virgin Spawning Biomass (B0) is the initial condition on which the start of the time-series depends. If biology or SR parameters are time-varying, then the benchmark year input in the forecast file tells SS which years to average in order to calculate "unfished". In this case, virgin recruitment and/or the virgin spawning biomass will differ from their unfished counterparts. Virgin recruitment and spawning biomass are

reported in the mgmt\_quant portion of the sd\_report and are now labeled as "unfished" for clarity. Note that if  $\ln(R0)$  is time-varying, then this will cause unfished to differ from virgin. However, if regime shift parameter is time-varying, then unfished will remain the same as virgin because the regime shift is treated as a temporary offset from virgin. Virgin spawning biomass is denoted as SPB\_virgin and spawning biomass unfished is denoted as SPB\_unf in the report file.

Virgin Spawning Biomass ( $B_0$ ) is used in four ways within SS:

1. Anchor for the spawner-recruitment relationship as virgin spawning biomass.
2. Basis for the initial equilibrium abundance.
3. Basis against which annual depletion is calculated.
4. Benchmark calculations.

However, if there is time-varying biology, then the 4th usage can have a different  $B_0$  calculation compared to the other usages.

## Metric for Fishing Mortality

A generic single metric of annual fishing mortality is difficult to define in a generalized model that admits multiple areas, multiple biological cohorts, dome-shaped selectivity in size and age for each of many fleets. Several separate indices are provided and others could be calculated by a user from the detailed information in Report.sso.

## Equilibrium SPR

This index focuses on the effect of fishing on the spawning potential of the stock. It is calculated as the ratio of the equilibrium reproductive output per recruit that would occur with the current year's  $F$  intensities and biology, to the equilibrium reproductive output per recruit that would occur with the current year's biology and no fishing. Thus it internalizes all seasonality, movement, weird selectivity patterns, and other factors. Because this index moves in the opposite direction than  $F$  intensity itself, it is usually reported as  $1-SPR$ . A benefit of this index is that it is a direct measure of common proxies used for  $F_{MSY}$ , such as  $F_{40\%}$ . A shortcoming of this index is that it does not directly demonstrate the fraction of the stock that is caught each year. The SPR value is also calculated in the benchmarks (see below). The derived quantities report shows an annual SPR statistic. The options, as specified in the starter.ss file, are:

- 0 = skip



- $1 = (1-SPR)/(1-SPR_{TGT})$
- $2 = (1-SPR)/(1-SPR_{MSY})$
- $3 = (1-SPR)/(1-SPR_{Btarget})$
- 4 = raw SPR

## F std

This index provides a direct measure of fishing mortality. The options are:

- 0 = skip
- 1 = exploitation(Bio)
- 2 = exploitation(Num)
- 3 = sum(Frates)

The exploitation rates are calculated as the ratio of the total annual catch (in either biomass or numbers as specified) to the summary biomass or summary numbers on January 1. The sum of the F rates is simply the sum of all the apical Fs. This makes sense if the F method is in terms of instantaneous F (not Pope's approximation) and if there are not fleets with widely different size/age at peak selectivity, and if there is no seasonality, and especially if there is only one area. In the derived quantities, there is an annual statistic that is the ratio of the can be annual F\_std value to the corresponding benchmark statistic. The available options for the denominator are:

- 0 = raw
- $1 = F/F_{SPR}$
- $2 = F/F_{MSY}$
- $3 = F/F_{Btarget}$

## F-at-Age

Because the annual F is so difficult to interpret as a sum of individual F components, an indirect calculation of F-at-age is reported at the end of the report.sso file. This section of the report calculates Z-at-age simply as  $\ln(N_{a+1,t+1}/N_{a,t})$ . This is done on an annual basis and summed over all areas. It is done once using the fishing intensities as estimated (to get Z), and once with the F

intensities set to 0.0 to get M-at-age. This latter sequence also provides a measure of dynamic Bzero. The user can then subtract the table of M-at-age/year from the table of Z-at-age/year to get a table of F-at-age/year. From this apical F, average F over a range of ages, or other user-desired statistics could be calculated. Further work within SS with this table of values is anticipated.

## MSY and other Benchmark Items

The following quantities are included in the sdreport vector mgmt\_quantities, so obtain estimates of variance. Some additional quantities can be found in the benchmarks section of the forecast\_report.sso.

Benchmark Item	Description
SSB_Unfished	Unfished reproductive potential (SSB is commonly female mature spawning biomass).
TotBio_Unfished	Total age 0+ biomass on January 1.
SmryBio_Unfished	Biomass for ages at or above the summary age on January 1.
Recr_Unfished	Unfished recruitment.
SSB_Btgt	SSB at user specified SSB target.
SPR_Btgt	Spawner potential ratio (SPR) at F intensity that produces user specified SSB target.
Fstd_Btgt	F statistic at F intensity that produces user specified SSB target.
TotYield_Btgt	Total yield at F intensity that produces user specified SSB target.
SSB_SPRtgt	SSB at user specified SPR target (but taking into account the spawner-recruitment relationship).
Fstd_SPRtgt	F intensity that produces user specified SPR target.
TotYield_SPRtgt	Total yield at F intensity that produces user specified SPR target.
SSB_MSY	SSB at F intensity that is associated with MSY; this F intensity may be directly calculated to produce MSY, or can be mapped to F_SPR or F_Btgt.
SPR_MSY	Spawner potential ratio (SPR) at F intensity associated with MSY.
Fstd_MSY	F statistic at F intensity associated with MSY.
TotYield_MSY	Total yield (biomass) at MSY.

Benchmark Item	Description
RetYield_MSY	Retained yield (biomass) at MSY.

## Brief cumulative output

Cum\_Report.sso: contains a brief version of the run output, which is appended to current content of file so results of several runs can be collected together. This is especially useful when a batch of runs is being processed. Unless this file is deleted, it will contain a cumulative record of all runs done in that subdirectory. The first column contains the run number.

## Bootstrap Data Files

Data.ss\_new: contains a user-specified number of data files, generated through a parametric bootstrap procedure, and written sequentially to this file. These can be parsed into individual data files and re-run with the model. The first output provides the unaltered input data file (with annotations added). The second provides the expected values for only the data elements used in the model run. The third and subsequent outputs provide parametric bootstraps around the expected values.

## Forecast and Reference Points (Forecast-report.sso)

The Forecast-report file contains output of fishery reference points and forecasts. It is designed to meet the needs of the Pacific Fishery Management Council's Groundfish Fishery Management Plan, but it should be quite feasible to develop other regionally specific variants of this output.

The vector of forecast recruitment deviations is estimated during an additional model estimation phase. This vector includes any years after the end of the recruitment deviation time series and before or at the end year. When this vector starts before the ending year of the time series, then the estimates of these recruitments will be influenced by the data in these final years. This is problematic, because the original reason for not estimating these recruitments at the end of the time series was the poor signal/noise ratio in the available data. It is not that these data are worse than data from earlier in the time series, but the low amount of data accumulated for each cohort allows an individual datum to dominate the model's fit. Thus, an additional control is provided so that forecast

recruitment deviations during these years can receive an extra weighting in order to counter-balance the influence of noisy data at the end of the time series.

An additional control is provided for the fraction of the log-bias adjustment to apply to the forecast recruitments. Recall that  $R$  is the expected mean level of recruitment for a particular year as specified by the spawner-recruitment curve and  $R'$  is the geometric mean recruitment level calculated by discounting  $R$  with the log-bias correction factor  $e^{-0.5s^2}$ . Thus a lognormal distribution of recruitment deviations centered on  $R'$  will produce a mean level of recruitment equal to  $R$ . During the modeled time series, the virgin recruitment level and any recruitments prior to the first year of recruitment deviations are set at the level of  $R$ , and the lognormal recruitment deviations are centered on the  $R'$  level. For the forecast recruitments, the fraction control can be set to 1.0 so that 100% of the log-bias correction is applied and the forecast recruitment deviations will be based on the  $R'$  level. This is certainly the configuration to use when the model is in MCMC mode. Setting the fraction to 0.0 during maximum likelihood forecasts would center the recruitment deviations, which all have a value of 0.0 in maximum likelihood mode, on  $R$ . Thus would provide a mean forecast that would be more comparable to the mean of the ensemble of forecasts produced in MCMC mode. Further work on this topic is underway.

Note:

- Cohorts continue growing according to their specific growth parameters in the forecast period rather than staying static at the end year values.
- Environmental data entered for future years can be used to adjust expected recruitment levels. However, environmental data will not affect growth or selectivity parameters in the forecast.

The top of the Forecast-report file shows the search for  $F_{SPR}$  and the search for  $F_{MSY}$ , allowing the user to verify convergence. Note: if the STD file shows aberrant results, such as all the standard deviations being the same value for all recruitments, then check the  $F_{MSY}$  search for convergence. The  $F_{MSY}$  can be calculated, or set equal to one of the other  $F$  reference points per the selection made in starter.ss.

## Main Output File, Report.sso

This is the primary output file. Its major sections are listed below.

The sections of the output file are:

- SS version number with date compiled. Time and date of model run. This info appears at the top of all output files.
- Comments

- Input file lines starting with #C are echoed here.
- Keywords
  - List of keywords used in searching for output sections.
- Fleet Names
  - List of fishing fleet and survey names assigned in the data file.
- Likelihood
  - Final values of the negative log(likelihood) are presented.
- Input Variance Adjustments
  - The matrix of input variance adjustments is output here because these values affect the log likelihood calculations.
- Parameters
  - The parameters are listed here. For the estimated parameters, the display shows: Num (count of parameters), Label (as internally generated by SS), Value, Active\_Cnt, Phase, Min, Max, Init, Prior, Prior\_type, Prior\_SD, Prior\_Like, Parm\_StD (standard deviation of parameter as calculated from inverse Hessian), Status (e.g. near bound), and Pr\_atMin (value of prior penalty if parameter was near bound). The Active\_Cnt entry is a count of the parameters in the same order they appear in the ss.cor file.
- Derived Quantities
  - This section starts by showing the options selected from the starter.ss and forecast.ss input files:
    - \* SPR ratio basis
    - \* F report basis
    - \* B ratio denominator

Then the time series of output, with standard deviation of estimates, are produced with internally generated labels. Note that these time series extend through the forecast era. The order of the output is: spawning biomass, recruitment, SPRratio, Fratio, Bratio, management quantities, forecast catch (as a target level), forecast catch as a limit level (OFL), Selex\_std, Grow\_std, NatAge\_std. For the three "ratio" quantities, there is an additional column of output showing a Z-score calculation of the probability that the ratio differs from 1.0. The "management quantities" section is designed to meet

the terms of reference for west coast groundfish assessments; other formats could be made available upon request. The standard deviation quantities at the end are set up according to specifications at the end of the control input file. In some cases, a user may specify that no derived quantity output of a certain type be produced. In those cases, SS substitutes a repeat output of the virgin spawning biomass so that vectors of null length are not created.

ADMB note, while vectors of null length are very useful for controlling optional model inputs, they cannot be used with current version of ADMB for sdreport quantities.

- Mortality-growth parameter by year after adjustments
  - This block shows the time series of mortality-growth parameters by year after adjustment by environmental links, blocks and deviations.
- Selectivity parameters (size) by year after adjustments
  - This block shows the size selectivity parameters, after adjustment, for each year in which a change occurs.
- Selectivity parameters (age) by year after adjustments
  - This block shows the age selectivity parameters, after adjustment, for each year in which a change occurs.
- Recruitment Distribution
  - This block shows the distribution of recruitment across growth patterns, genders, birth seasons, and areas in the end year of the model.
- Platoon Indexing
  - This block shows the internal index values for various quantities. It can be a useful reference for complex model setups. The vocabulary is: Bio\_Pattern refers to a collection of cohorts with the same defined growth and natural mortality parameters; sex is the next main index. If recruitment occurs in multiple seasons, then birth season is the index for that factor. The index labeled "Platoon" is used as a continuous index across all the other factor-specific indices. If sub-platoons are used, they are nested within the Bio\_Pattern x Sex x Birth Season platoon. However, some of the output tables use the column label "platoon" as a continuous index across platoons and sub-platoons. Note that there is no index here for area. Each of the cohorts is distributed across areas and they retain their biological characteristics as they move among areas.
- Size Frequency Translation
  - If the generalized size frequency approach is used, this block shows the translation

probabilities between population length bins and the units of the defined size frequency method. If the method uses body weight as the accumulator, then output is in corresponding units.

- Movement
  - This block shows movement rate between areas in a multi-area model.
- Exploitation
  - This block shows the time series of the selected  $F_{std}$  unit and the  $F$  multiplier for each fleet in terms of harvest rate (if Pope's approximation is used) or fully selected  $F$ .
- Index 2
  - This section reports the observed and expected values for each index. All are reported in one list with index number included as a selection field. At the bottom of this section, the root mean squared error of the fit to each index is compared to the mean input error level to assist the user in gauging the goodness-of-fit and potentially adjusting the input level of imprecision.
- Index 3
  - This section shows the parameter number assigned to each parameter used in this section.
- Discard
  - This is the list of observed and expected values for the amount (or fraction) discard.
- Mean Body Wt
  - This is the list of observed and expected values for the mean body weight.
- Fit Len Comps
  - This is the list of the goodness of fit to the length compositions. The input and output levels of effective sample size are shown as a guide to adjusting the input levels to better match the model's ability to replicate these observations.
- Fit Age Comps
  - This has the same format as the length composition section.
- Fit Size Comps
  - This has the same format as the length composition section and is used for the

generalized size composition summary.

- Len Selex
  - Here is the length selectivity and other length specific quantities for each fishery and survey.
- Age Selex
  - Here is reported the time series of age selectivity and other age-related quantities for each fishery and survey. Some are directly computed in terms of age, and others are derived from the combination of a length-based factor and the distribution of size-at-age.
- Environmental Data
  - The input values of environmental data are echoed here. In the future, the summary biomass in the previous year will be mirrored into environmental column –2 and that the age zero recruitment deviation into environmental column –1. Once so mirrored, they may enable density-dependent effects on model parameters.
- Numbers at Age
  - The output (in thousands of fish) is shown for each cohort tracked in the model.
- Numbers at Length
  - The output is shown for each cohort tracked in the model.
- Catch at Age
  - The output is shown for each fleet. It is not necessary to show by area because each fleet operates in only one area.
- Biology
  - The first biology section shows the length-specific quantities in the ending year of the time series only. The derived quantity spawn is the product of female body weight, maturity and fecundity per weight. The second section shows natural mortality.
- Growth Parameters
  - This section shows the growth parameters, and associated derived quantities, for each year in which a change is estimated.
- Biology at Age



- This section shows derived size-at-age and other quantities. It is the basis for the Bio report page of the Excel output processor.
- Mean Body Wt (begin)
  - This section reports the time series of mean body weight for each platoon. Values shown are for the beginning of each season of each year.
- Mean Size Time series
  - This section shows the time series of mean length-at-age for each platoon. At the bottom is the average mean size as the weighted average across all platoons for each gender.
- Age Length Key
  - This is reported for the midpoint of each season in the ending year.
- Age Age Key
  - This is the calculated distribution of observed ages for each true age for each of the defined ageing keys.
- Selectivity Database
  - This section contains the selectivities organized as a database, rather than as a set of vectors.
- Spawning Biomass Report 2, etc.
  - The section shows annual total spawning biomass, then numbers-at-age at the beginning of each year for each Bio\_Pattern and Sex as summed over sub-platoons and areas. Then Z-at-age is reported simply as  $\ln(N_{t+1,a+1}N_{t,a})$ . Then the Report\_1 section loops back through the time series with all F values set to zero so that a dynamic Bzero, N-at-age, and M-at-age can be reported. The difference between Report\_1 and Report\_2 can be used to create an aggregate F-at-age.
- Composition Database
  - This section is reported to a separate file, compreport.sso, and contains the length composition, age composition, and mean size-at-age observed and expected values. It is arranged in a database format, rather than an array of vectors. Software to filter the output allows display of subsets of the database.

## Using R To View Model Output (r4ss)

A collection of functions developed as a package, `r4ss`, for the statistical software R has been created to explore SS model output. The functions include tools for summarizing and plotting results, manipulating files, visualizing model parameterizations, and various other tasks. Currently, information on the code, including installation instructions, can be found at [github.com/r4ss/r4ss](https://github.com/r4ss/r4ss). The software package is under constant development to maintain compatibility with new versions of SS and to improve functionality.

Two of the most commonly used functions for model diagnostics are `SS_output` and `SS_plots`. After running a model using SS, the report can be read into R by the `SS_output` function which stores quantities in a list with named objects. This list can then be passed to the `SS_plots` function which creates a series of over 100 plots that are useful to visualize output such as model fit to the data and time series of quantities of interest.

The latest `r4ss` version on CRAN can be installed using a command like:

```
> install.packages("r4ss")
```

However, more frequent enhancements and bug fixes are posted to the GitHub project. The latest version of `r4ss` can be installed directly from GitHub at any time via the `devtools` package in R with the following commands:

```
> install.packages("devtools")
> devtools::install_github("r4ss/r4ss")
```

Note: `devtools` will give this message: *"WARNING: Rtools is required to build R packages, but is not currently installed."*. However, `Rtools` is not required for installing `r4ss` via `devtools`, so ignore this warning.

Once you have installed the `r4ss` package, it can be loaded in the regular manner:

```
> library(r4ss)
```

The results from a model run can be read in and plots created using the following commands:

```
> setwd("C:\\directory where model was run")
> base.model = SS_output(getwd())
> SS_plots(base.model)
```

The `SS_output()` function reads the Report file and stores this information in a list. The function by default will print select items to the screen that can be useful for evaluating a model (e.g., likelihood, estimated parameter with warnings if they hit bounds, parameters with high gradients).

This list created by `SS_output()` can be passed to other functions in the `r4ss` package to allow visualization of results.

The `SS_plots()` function will create plots from the list created by the `SS_output()` function that can be used to visualize model results. The plots by default will be written inside a "plots" folder inside the folder with the model files read by the `SS_output()` function. Additionally, an html file is written which allows for visualization of all plots created.

The functions included in `r4ss` ranging from general use to functions developed for specific model applications:

Core Functions	
<code>SS_output</code>	A function to create a list object for the output from Stock Synthesis
<code>SS_plots</code>	Plot many quantities related to output from Stock Synthesis
Plot functions called by <code>SS_plots</code> :	
<code>SSplotBiology</code>	Plot biology related quantities from Stock Synthesis model output, including mean weight, maturity, fecundity, and spawning output.
<code>SSplotCatch</code>	Plot catch related quantities
<code>SSplotCohorts</code>	Plot cumulative catch by cohort
<code>SSplotComps</code>	Plot composition data and fits
<code>SSplotData</code>	Timeline of presence/absence data by type, year, and fleet
<code>SSplotDiscard</code>	Plot fit to discard fraction
<code>SSplotIndices</code>	Plot indices of abundance and associated quantities
<code>SSplotMnwt</code>	Plot mean weight data and fits
<code>SSplotMovementMap</code>	Show movement rates on a map
<code>SSplotMovementRates</code>	Show movement rates on a map
<code>SSplotNumbers</code>	Plot numbers-at-age related data and fits
<code>SSplotRecdevs</code>	Plot recruitment deviations
<code>SSplotRecdist</code>	Plot of recruitment distribution among areas and seasons
<code>SSplotSelex</code>	Plot selectivity
<code>SSplotSexRatio</code>	Plot sex ratios

SSplotSummaryF	Plot time series summary of F (or harvest rate)
SSplotSpawnrecruit	Plot spawner-recruit curve
SSplotSPR	Plot SPR quantities
SSplotTags	Plot tagging data and fits
SSplotTimeseries	Plot time series data
SSplotYield	Plot yield and surplus production
SS_html	Create HTML files to view figures in browser
SS_fitbiasramp	Estimate bias adjustment for recruitment deviates
Model Comparisons and other diagnostics:	
SSplotPars	Plot distributions of priors, posteriors, and estimates
SSplotProfile	Plot likelihood profile results
PinerPlot	Plot fleet-specific contributions to likelihood profile
SSplotRetroRecruits	Make retrospective pattern of recruitment estimates (a.k.a. squid plot) as seen in Pacific hake assessments
Functions related to MCMC diagnostics:	
mcmc_nuisance	Summarize nuisance MCMC output
mcmc_out	Summarize, analyze, and plot key MCMC output
SSgetMCMC	Read MCMC output
SSplotMCMC_ExtraSelex	Plot uncertainty around chosen selectivity ogive from MCMC
Interactive tools for exploring functional forms:	
movepars	Explore movement parameterization
selfit	A function to visualize parameterization of double normal and double logistic selectivity in SS
selfit_spline	Visualize parameterization of cubic spline selectivity in SS
sel_line	A function for drawing selectivity curves
File manipulation for inputs:	
SS_readdat	Read data file

SS_readforecast	Read forecast file
SS_readstarter	Read starter file
SS_writedat	Write data file
SS_writeforecast	Write forecast file
SS_writestarter	Write starter file
SS_makedatlist	Make a list for SS data
SS_parlines	Get parameter lines from SS control file
SS_changepars	Change parameters in the control file
SSmakeMmatrix	Create inputs for entering a matrix of natural mortality by age and year
SS_profile	Run a likelihood profile in SS (incomplete)
NegLogInt_Fn	Calculated variances of time-varying parameters using SS implementation of the Laplace Approximation
File manipulations for outputs:	
SS_recdevs	Insert a vector of recruitment deviations into the control file
SS_splitdat	Split apart bootstrap data to make input file
Minor plotting functions:	
bubble3	Create a bubble plot
make_multifig	Create multi-figure plots
Make_multifig_sexratio	Create multi-figure plots of sex ratios
plotCI	Plot points with confidence intervals
rich_colors_short	Make a vector of colors
stackpoly	Plot stacked polygons
mountains	Make shaded polygons with a mountain-like appearance
Really specialized functions:	
DoProjectPlots	Make plots from Rebuilder program
IOTCmove	Make a map of movement for a 5-area Indian Ocean model

SSFishGraph	A function for converting SS output to the format used by FishGraph
TSCplot	Create a plot for the TSC report

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## Special Set-ups

### Continuous seasonal recruitment

It is awkward in SS to set up a seasonal model such that recruitment can occur with similar and independent probability in any season of any year. Consequently, some users have attempted to setup SS so that each quarter appears as a year. They have set up all the data and parameters to treat quarters as if they were years (i.e. each still has a duration of 1.0 time step). This can work, but requires that all rate parameters be re-scaled to be correct for the quarters being treated as years.

Another option is available. If there is one season per year and the season duration is set to 3 (rather than the normal 12), then the season duration is calculated to be  $3/12$  or 0.25. This means that the rate parameters can stay in their normal per year scaling and this shorter season duration makes the necessary adjustments internally. Some other adjustments to make when doing quarters as years include:

- Re-index all "year seas" inputs to be in terms of quarter-year because all are now season 1; increase endyr value in sync with this.
- Increase max age because age is now in quarters.
- In the age error definitions, increase the number of entries in accord with new max age
- In the age error definitions, recode so that each quarter-age gets assigned to the correct agebin. This is because the age data are still in terms of age bins; i.e. the first 4 entries for quarter-ages 1 through 4 will all be assigned to age bin 1.5; the next four to age bin 2.5; you cannot accomplish the same result by editing the age bin values because the standard deviation of ageing error is in terms of age bin.
- In the control file, multiple the natural mortality age breakpoints and growth  $A_{min}$  and  $A_{max}$  values by  $1/\text{season duration}$ .

- Decrease the R0 parameter starting value because it is now the average number of recruitments per quarter year.
- Edit the rec\_dev start and end years to be in terms of quarter year.
- Edit any age selectivity parameters that refer to age to now refer to quarter age.
- If there needs to be some degree of seasonality to recruitment or some parameter, then you could create a cyclic pattern in the environmental input and make recruitment or some other parameter a function of this cyclic pattern.

A good test showing comparability of the 3 approaches to setting up a quarterly model should be done.

## Change Log

This section has been removed from the user manual. Information on changes to SS is now recorded in the spreadsheet database, SS\_Changes.xlsx available on VLAB ([vlab.ncep.noaa.gov/group/stock-synthesis/home](http://vlab.ncep.noaa.gov/group/stock-synthesis/home)). Fields include date, version number, category (e.g. growth, selectivity), type (e.g. new, clarify, fix). Occasional model tips will be added with the type="Tip".

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## Appendix A: Recruitment Variability and Bias Correction

Recruitments in SS are defined as lognormal deviates around a log-bias adjusted spawner-recruitment curve. The magnitude of the log-bias adjustment is calculated from the level of  $\sigma_R$ , which is the standard deviation of the recruitment deviations (in log-space). There are 5 segments of the time series in which to consider the effect of the log-bias adjustment: virgin; initial equilibrium; early data-poor period; data-rich period; very-recent/forecast. The choice of break points between these segments need not correspond directly with the settings for the bias adjustment, although some alignment might be desired. Methot et al. (2011) provide more detailed discussion of the bias adjustment than what is provided below but do not address the separation of time periods into separate segments. The approach is illustrated with figures associated the assessment for darkblotched rockfish (Gertseva and Thorson, 2013).

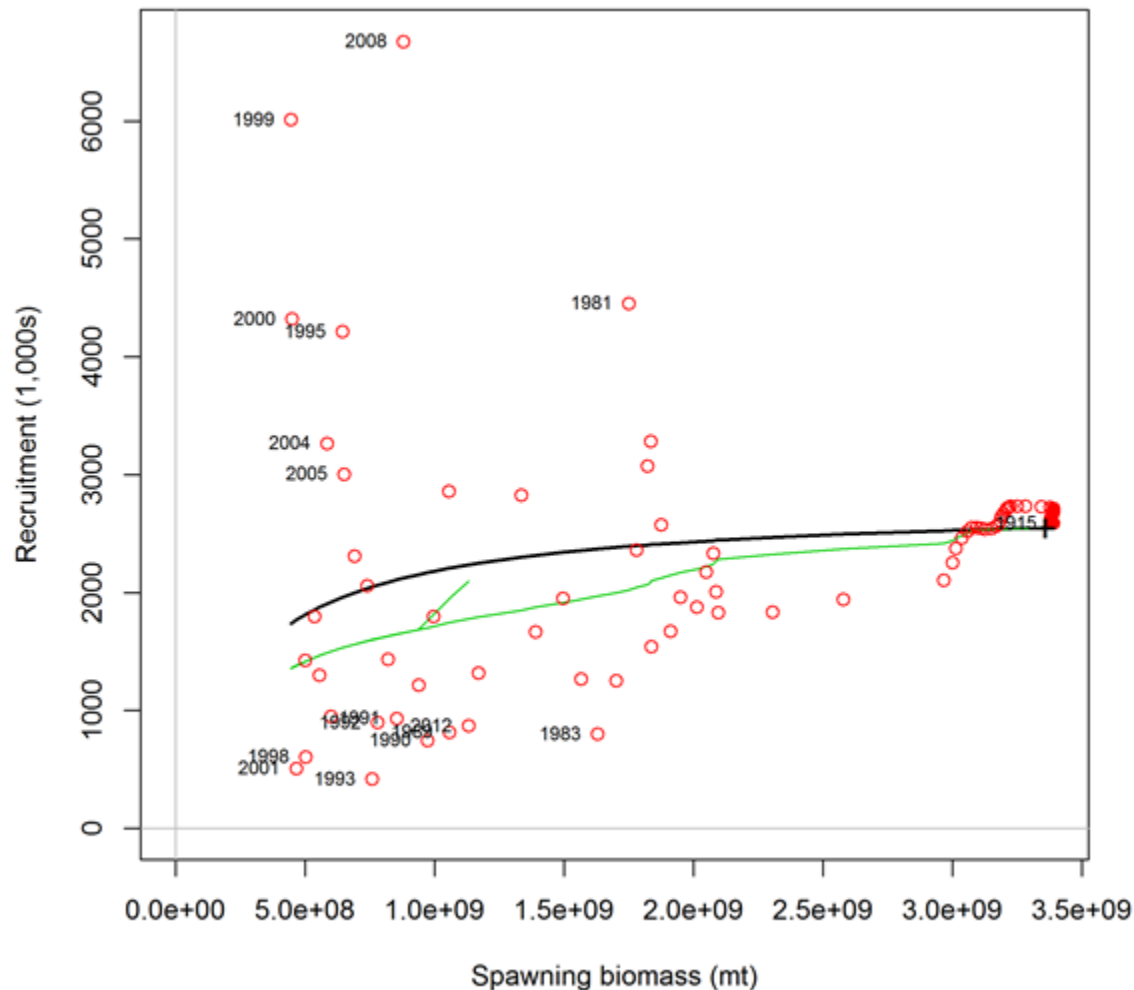


Figure A.1. Spawner-recruitment relationship for darkblotched rockfish (Gertseva and Thorson, 2013). Red points represent estimated recruitments, the solid black line is the stock-recruit relationship and the green line represents the adjustment to this relationship after adjustment to account for the lognormal distribution associated with each year. The "+" symbol labeled 1915 near the right side represents both the virgin and initial equilibrium of the model. The numerous red points close to the initial conditions correspond to the early years of the model with low harvest rates.

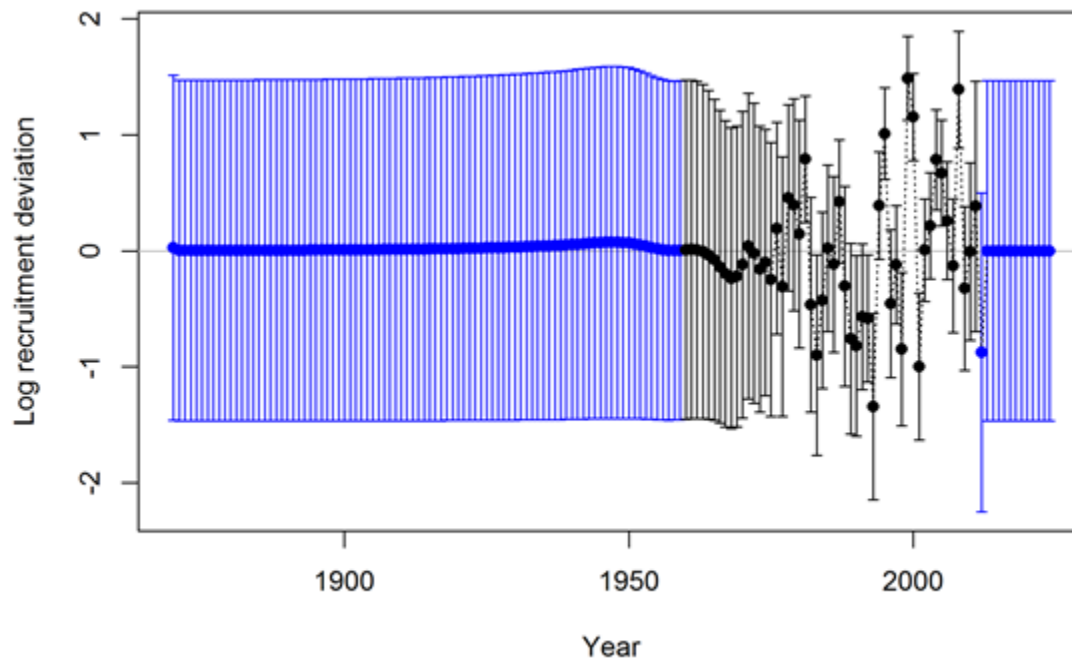


Figure A.2. Timeseries of log recruitment deviations for darkblotched rockfish with 95% uncertainty intervals. The start year of the model is 1915, but recruitment deviations are estimates starting in 1870. The 45 deviation estimates for 1870–1914 inform the age structure used in the start year. The black color for the years 1960–2011 indicates the "main" recruitment deviation vector, while the blue color for the years 1870–1959 and 2012–2024 indicates the "early" and "late/forecast" recruitment deviation vectors, respectively.

## Virgin Biomass

The  $R_0$  level of recruitment is a parameter of the spawner-recruitment curve. This recruitment and the corresponding spawning biomass are expected to represent the long-term arithmetic mean.

## Initial Equilibrium

The level of recruitment is typically maintained at the  $R_0$  level even though the initial equilibrium catch will reduce the spawning biomass below the virgin level. If steepness is moderately low or the initial  $F$  is high, then the lack of response in recruitment level may appear paradoxical. The logic is

that building in the spawner-recruitment response to initial  $F$  would significantly complicate the calculations and would imply that the initial equilibrium catch level had been going on for multiple generations. If the lack of response is considered to be problematic in a particular application, then start the model at an earlier year and with a lower initial equilibrium catch so that the dynamics of the spawner-recruitment response get captured in the early period, rather than getting lost in the initial equilibrium.

## Early Data-Poor Period

This is the early part of the time series where the only data typically are landed catch. There are no data to inform the model about the specific year-to-year fluctuations in recruitment, although the ending years of this period will begin to be influenced by the data. The "early time period" is not a formal concept. It is up to the user to decide whether to start estimating recruitment deviations beginning with the first year of the model, or to delay such estimation until the data become more informative. Modeling recruitment deviations in this period may lead to a more realistic portrayal of the uncertainty in depletion, but can also lead to spurious patterns in estimated recruitments that may be driven by the fit to index data or other sources that would not be expected to have accurate information on recruitment.

- Option A: Do not estimate recruitment deviations during this early period. During years prior to the first year of recruitment deviations, the model will set the recruitment equal to the level of the spawner-recruitment curve. Thus, it is a mean-based level of recruitment. Because these annual parameters are fixed to the level of the spawner-recruitment curve, they have no additional uncertainty and make no contribution to the variance of the model. This approach may produce relatively large, or small, magnitude deviations at the very beginning of the subsequent period, as the model "catches up" to any slight signal that could not be captured through estimated deviations in the early data-poor period. There may be some effect on the estimate of  $R_0$  as a result of lack of model flexibility in balancing early period removals with signal in the early portion of the data-rich period.
- Option B: Estimate recruitment deviations for all the early years. Each of these recruitment deviations is now a deviation parameter so will have a variance that contributes to the total model variance. The estimated standard deviation of each of these deviation parameters should be similar to  $\sigma_R$  because  $\sigma_R$  is the only constraint on these parameters (however, the last few in the sequence will begin to feel the effect of the data so may have lower standard deviations).

## Data-Rich Period

Here the length and or age data inform the model on the year-to-year level of recruitment. These fluctuations in recruitment are assumed to have a lognormal distribution around the log-bias adjusted spawner-recruitment curve. The level of  $\sigma_R$  input to the model should match this level of fluctuation to a reasonable degree. Because the recruitments are lognormal, they produce a mean biomass level that is comparable to the virgin biomass and thus the depletion level can be calculated without bias.

However, if the early period has recruitment deviations estimated by maximum posterior density, then the depletion levels during the early part of the data-rich period may have some lingering effect of negative bias during the early time period. The level of  $\sigma_R$  should be at least as large as the level of variability in these estimated recruitments. If too high a level of  $\sigma_R$  is used, then a bias can occur in the estimate of spawner-recruitment steepness, which determines the trend in recruitment. This occurs when the early recruitments are taken directly from the spawner-recruitment curve, so are mean unbiased, then the later recruitments are estimated as deviations from the log-bias adjusted curve. If  $\sigma_R$  is too large, then the bias-adjustment is too large, and the model may compensate by increasing steepness to keep the mean level of recent recruitments at the correct level.

### Recent Years/Forecast

Here the situation is very similar to the early time period in that there are no data to inform the model about the year-to-year pattern in recruitment fluctuations so all deviations will be pulled to a zero level in the maximum posterior density. The structure of SS creates no sharp dividing line between the estimation period and the forecast period. In many cases one or more recruitments at the end of the time series will lack appreciable signal in the data and should therefore be treated as forecast recruit deviations. To the degree that some variability is observed in these recruitments, partial or full bias correction may be desirable for these deviations separate from the purely forecast deviations, there is therefore an additional control for the level of bias correction applied to forecast deviations occurring prior to end year + 1.

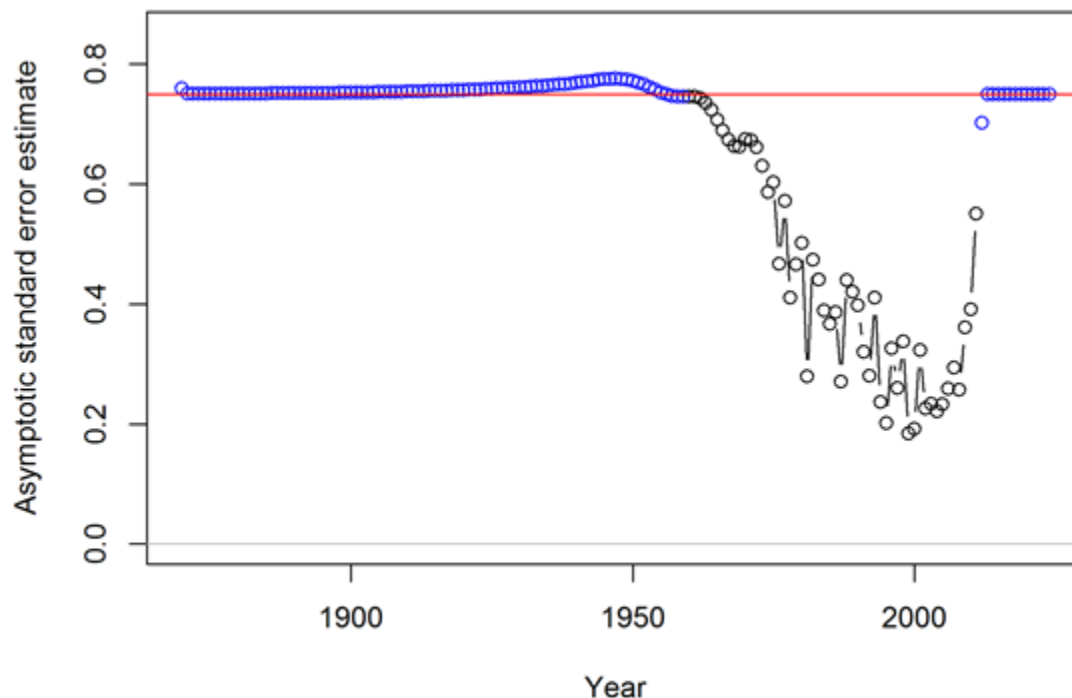


Figure A.3. Timeseries of standard error estimates for the log recruitment deviations for

darkblotched rockfish with 95% uncertainty intervals. As in Figure A.2, the black color indicates the main recruitment period. This period with lower standard error is associated with higher variability among deviations (Figure A.2). The red line at 0.75 indicates the  $\sigma_R$  value in this model.

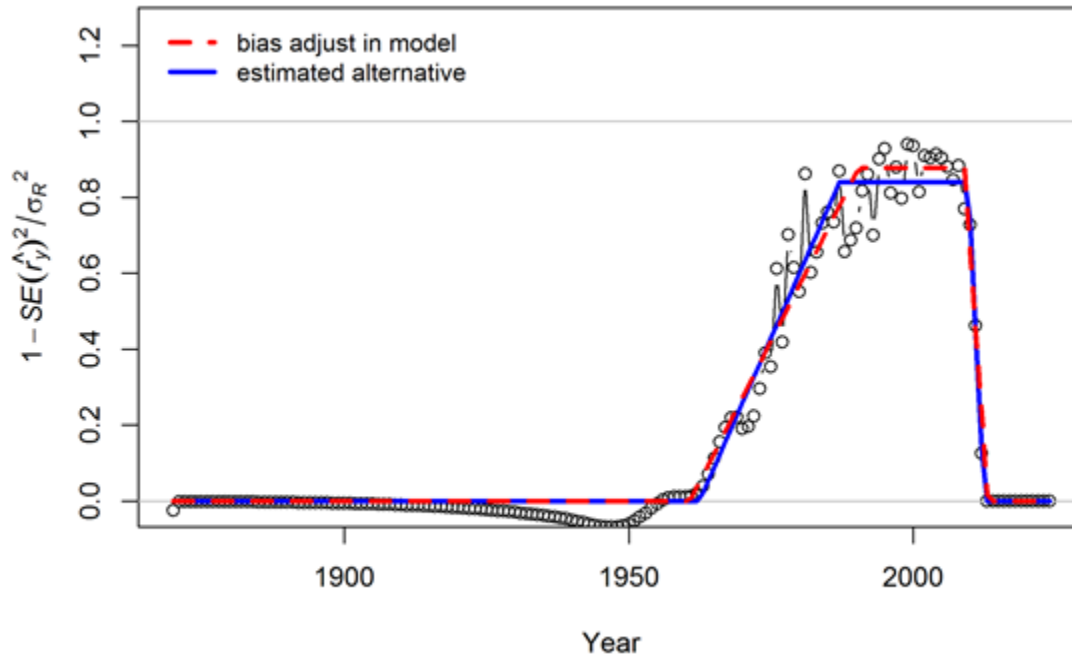


Figure A.4. Transformation of the standard error estimates (shown in Figure A.3) for darkblotched rockfish following the approach suggested by Methot et al. (2011). These values were used to set the 5 values controlling the degree of bias adjustment (as a fraction of  $\sigma_R/2$ ) to account for differences in the mean and median of the lognormal distribution from which the recruitment deviations are drawn. The red line indicates a bias adjustment of 0 up to the 1960.75, ramping up to a maximum adjustment level of 0.877 for the period 1990.4–2008.98, and reducing back to 0 starting in 2013.08. Note that these values controlling the bias adjustment need not be integer year values. Also the break points in the bias adjustment function need not match the break points between early, main, and late/forecast recruitment deviation vectors (indicated by blue and black colors in Figures A.2 and A.3). The blue line indicates a functional form that minimizes the sum of squared differences between the bias adjustment function and the transformed standard error values. The subtle differences between red and blue lines are unlikely to have any appreciable effect on the model results.

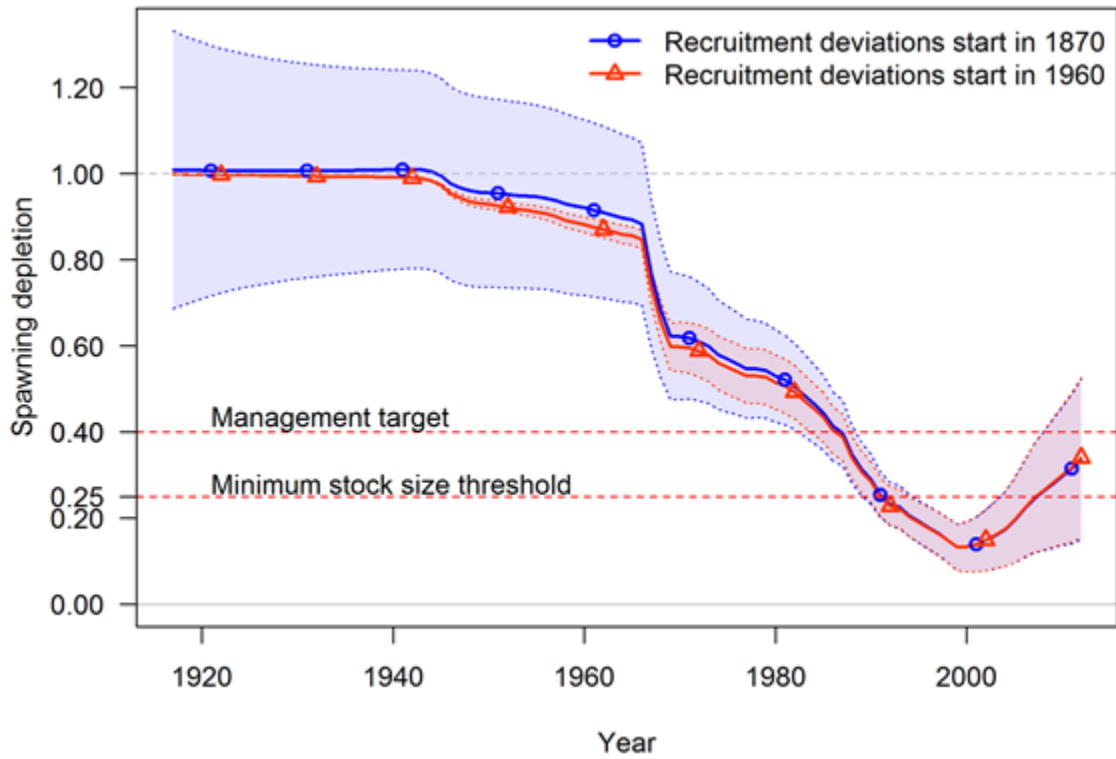


Figure A.5. Comparison of timeseries of spawning depletion for darkblotched rockfish models with early recruitment deviations (starting in 1870) and without early deviations (only main recruitment deviations starting in 1960). The point estimates are similar, but the 95% uncertainty intervals are substantially different. With no recruitment deviations for the early period, the estimates of spawning depletion in the early years are very precise and uncertainty increases as the stock moves into the data rich period. In contrast, the addition of the early recruitment deviations results in a large uncertainty in spawning depletion for the early years and an increase in precision as the stock moves into the data rich period. In this application, the uncertainty associated with the recent years is independent of the assumptions about early recruitments.

## Issues with Including Environmental Effects

The expected level of recruitment is a function of spawning biomass, an environmental time series, and a log-bias adjustment.

$$E(\text{Recruitment}) = f(\text{SpBio}) * \exp(\beta * \text{envdata}) * \exp(-0.5 * \sigma_R^2) \quad (56)$$

$\sigma_R$  is the variability of the deviations, so it is in addition to the variance "created" by the environmental effect. So, as more of the total recruitment variability is explained by the environmental effect, the residual  $\sigma_R$  should be decreased. The model does not do this automatically.

The environmental effect is inherently lognormal. So when an environmental effect is included in the model, the arithmetic mean recruitment level will be increased above the level predicted by  $f(\text{SpBio})$  alone. The consequences of this have not yet been thoroughly investigated, but there probably should be another bias correction based on the variability of the environmental data as scaled by the estimated linkage parameter,  $\beta$ . It is also problematic that the environmental effect time series used as input is assumed to be measured without error.

The preferred approach to including environmental effects on recruitment is not to use the environmental effect in the direct calculation of the expected level of recruitment. Instead, the environmental data would be used as if it was a survey observation of the recruitment deviation. This approach is similar to using the environmental index as if it was a survey of age 0 recruitment abundance because by focusing on the fit to the deviations it removes the effect of SpBio on recruitment. In this alternative, the  $\sigma_R$  would not be changed by the environmental data; instead the environmental data would be used to explain some of the total variability represented by  $\sigma_R$ . This approach may also allow greater uncertainty in forecasts, as the variability in projected recruitments would reflect both the uncertainty in the environmental observations themselves and the model fit to these observations.

## Initial Age Composition

If the first year with recruitment deviations is set less than the start year of the model, then these early deviations will modify the initial age composition. The amount of information on historical recruitment variability certainly will degrade as the model attempts to estimate deviations for older age groups in the initial equilibrium. So the degree of bias correction is reduced linearly in proportion to age so that the correction disappears when maximum age is reached. The initial age composition approach normally produces a result that is indistinguishable from a configuration that starts earlier in the time series and estimates a longer time series of recruitments. However, because the initial equilibrium is calculated from a recruitment level unaffected by spawner-recruitment steepness and initial age composition adjustments are applied after the initial equilibrium is calculated, it is possible that the initial age composition approach will produce a slightly different result than if the time series was started earlier and the deviations were being applied to the recruitment levels predicted from the spawner-recruitment curve.

## Appendix B: Data Weighting

In 2015 there was a CAPAM workshop dedicated to data-weighting. Description of the workshop can be found at [capamresearch.org/data-weighting/workshop](http://capamresearch.org/data-weighting/workshop). The presentations from the workshop are available through that website and many of them were included in a special issue of Fisheries Research a [sciencedirect.com/journal/fisheries-research/vol/192](http://sciencedirect.com/journal/fisheries-research/vol/192).

Currently, there are three main methods for weighting length and data applied for U.S. West Coast assessments using Stock Synthesis.

1. **McAllister - Ianelli:** Effective sample size is calculated from fit of observed to expected length or age compositions. Tuning algorithm is intended to make the arithmetic mean of the input sample size equal to the harmonic mean of the effective sample size (McAllister and Ianelli, 1997).
2. **Francis:** Based on variability in the observed mean length or age by year, where the sample sizes are adjusted such that the fit of the expected mean length or age should fit within the uncertainty intervals at a rate which is consistent with variability expected based on the adjusted sample sizes (Method "TA1.8") (Francis and Hilborn, 2011)
3. **Dirichlet-Multinomial:** A new likelihood (as opposed to the standard multinomial) which includes an estimable parameter ( $\theta$ ) which scales the input sample size. In this case, the term "Effective sample size" has a different interpretation than in the McAllister-Ianelli approach (Thorson et al., 2017).

## Applying the methods

### McAllister-Ianelli

The "Length\_Comp\_Fit\_Summary" and "Age\_Comp\_Fit\_Summary" sections in the Report file include information on the harmonic mean of the effective sample size and arithmetic mean of the input sample size used in this tuning method. In the r4ss package, these tables are returned by the SS\_output function as `$Length_comp_Eff_N_tuning_check` and `$Age_comp_Eff_N_tuning_check`.

A convenient way to process these values into the format required by the control file is to use the function:

```
SS_tune_comps(replist, option = "MI")
```

where the input "replist" is the object created by SS\_output. This function will return a table and also write a matching file called "suggested\_tuning.ss" to the directory where the model was run.

For models using SS version 3.30, the table created by SS\_tune\_comps can be pasted into the bottom of the control file in the section labeled "Input variance adjustments", followed by the terminator line which indicates the end of the section.

Also see the help page for the r4ss function SS\_varadjust which can be used to automatically write a new control file if you want to streamline the process of applying multiple iterations of this tuning



method.

If the tuning has been implemented, the green lines in the figure below would approximately intersect at a point which is on the black 1-to-1 diagonal line in this figure created by the `r4ss` function `SS_plots`.

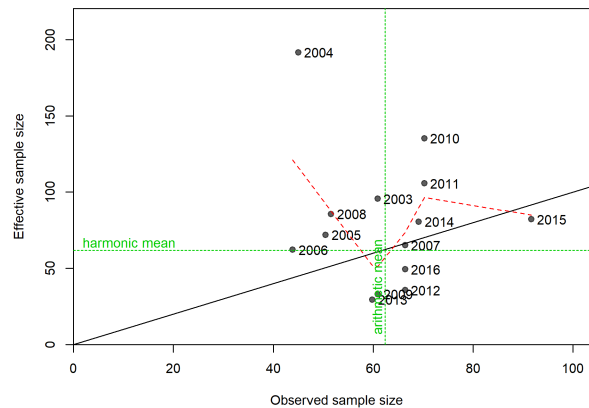


Figure B.1. Input N vs. Effective N comparison, Length composition data as plotted by `r4ss`.

There are a couple of challenges posed by the McAllister-Ianelli data-weighting approach:

1. Subjective choice of how many iterations to take to achieve adequate convergence. Often just one iteration is applied.
2. Takes time to implement so tuning is rarely repeated during retrospective or sensitivity analyses.

## Francis

Implementation: recommended adjustments are calculated by the `r4ss` functions `SSMethod.TA1.8` and `SSMethod.Cond.TA1.8`. These functions are rarely used alone but are called by the `SS_plots` function when making plots like the one below. For `SS v.3.30` models, the simplest way to get the adjustments in the format required by the control file is to use the `SS_tune_comps` function (described above under the McAllister-Ianelli method), but with a different option specified:

```
SS_tune_comps(replist, option = "Francis")
```

The figure below shows the estimated 95% intervals around the observed mean length by year based on the input sample size (thick lines) and the increase in that uncertainty which would occur if the sample sizes were adjusted according to the proposed multiplier.

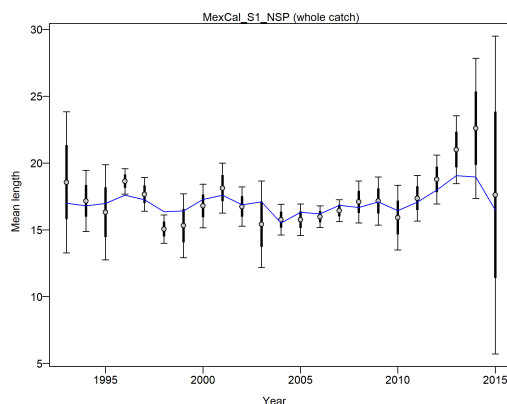


Figure B.2. Mean length for Fleet1 with 95% confidence intervals based on current samples sizes. Francis data weighting method TA1.8: thinner intervals (with capped ends) show result of further adjusting sample sizes based on suggested multiplier (with 95% interval) for len data from Fleet1: 0.2739 (0.1661-0.6305)

There are a several of challenges posed by the Francis data-weighting approach:

1. Subjective choice of how many iterations to take to achieve adequate convergence. Often just one iteration is applied.
2. Takes time to implement so tuning is rarely repeated during retrospective or sensitivity analyses.
3. Recommended adjustment can be sensitive to outliers (remove a few years of anomalous composition data can lead to large change in recommended adjustment).

## Dirichlet-Multinomial

Change the choice of likelihood and set parameter choices in the data file:

- In the specification of the length and/or age data, change "CompError" column in age and length comp specifications from 0 to 1 and "ParmSelect" from 0 to a sequence of numbers from 1 to N where N is the total number of combinations of fleet and age/length.
- Resulting input should look similar to:

```
#_mintailcomp addtocomp combM+F CompressBins CompError ParmSelect minsamplesize
-1 0.001 0 0 1 1 0.01 #_fleet:1_Fishery
-1 0.001 0 0 1 2 0.01 #_fleet:2_ASHOP
-1 0.001 0 0 0 0 0.01 #_fleet:3_Foreign
-1 0.001 0 0 1 3 0.01 #_fleet:4_POP
-1 0.001 0 0 1 4 0.01 #_fleet:5_Triennial
```

- The ParmSelect column can also have repeated values so that multiple fleets share the same log(theta) parameter.
- If you have both length and age data, the ParmSelect should have separate numbers for each, e.g. 1 and 2 for the length comps and 3 and 4 for the age comps for the same two fleets.

Add parameter lines to the control file:

- Add as many parameter lines as the maximum numbers in the ParmSelect column. The new parameter lines go after the main selectivity parameters but before any time-varying selectivity parameters
- Jim Thorson initially recommended bounds of -5 to 20, with a starting value of 0 (which corresponds to a weight of about 50% of the input sample size). However, parameter estimates above 5 are associated with 99-100% weight with little information in the likelihood about the parameter value. Therefore, an upper bound of 5 may help identify cases that otherwise would have convergence issues.
- Example parameter lines are below:

```
# Dirichlet parameters
#_LO HI INIT PRIOR PR_SD PR_type PHASE ... Blk_Fxn # Parm_name
-5 20 -0.2 0 50 0 2 ... 0 # ln(EffN_mult)_fishery - Dirichlet
-5 20 -0.2 0 50 0 2 ... 0 # ln(EffN_mult)_ashop - Dirichlet
-5 20 -0.2 0 50 0 2 ... 0 # ln(EffN_mult)_pop - Dirichlet
-5 20 -0.2 0 50 0 2 ... 0 # ln(EffN_mult)_tri - Dirichlet
-5 20 -0.2 0 50 0 2 ... 0 # ln(EffN_mult)_afsc - Dirichlet
```

- Reset any existing variance adjustments factors that might have been used for the McAllister-Ianelli or Francis tuning methods. In 3.24 this means setting the values to 1, in SS version 3.30, you can simply delete or comment-out the rows with the adjustments.

The SS\_output function in r4ss returns table like the following:

```
$Dirichlet_Multinomial_pars
      Value Phase Min Max      Theta Theta/(1+Theta)
ln(EffN_mult)_1 12.7638000      2 -5 15 3.493397e+05 0.9999971
ln(EffN_mult)_2  2.5263600      2 -5 15 1.250789e+01 0.9259692
ln(EffN_mult)_3 11.6519000      2 -5 15 1.149095e+05 0.9999913
ln(EffN_mult)_4  1.9373900      2 -5 15 6.940612e+00 0.8740651
ln(EffN_mult)_5 10.2865000      2 -5 15 2.933393e+04 0.9999659
ln(EffN_mult)_6 11.5556000      2 -5 15 1.043598e+05 0.9999904
```

The ratio shown in the final column is the estimated multiplier which can be compared to the sample size adjustment estimated in the other tuning methods above (the New\_Var\_adj column in the table produced by the SS\_tune\_comps function in r4ss).

If the reported  $\theta/(1 + \theta)$  ratio is close to 1.0, that indicates that the model is trying to tune the sample size as high as possible. In this case, the  $\ln(\theta)$  parameters should be fixed at a high value, like the upper bound of 20, which will result in 100% weight being applied to the input sample sizes. An alternative would be to manually change the input sample sizes to a higher value so that the estimated weighting will be less than 100

There are a several of challenges posed by the Dirichlet-Multinomial data-weighting approach:

1. Not yet widely used so little guidance is available.
2. Does not allow weights above 100% (by design) so it is not yet clear how best to deal with the situation when the estimated weight is close to 100%.
3. Parameterization has potential to cause convergence issues or inefficient MCMC sampling when weights are close to 100% (Jim Thorson has proposed a prior distribution that may help with this, but has not yet been tested).

## Appendix C: Forecast Module

### Introduction

SS version 3.20 introduced substantial upgrades to the benchmark and forecast module. The general intent was to make the forecast outputs more consistent with the requirement to set catch limits that have a known probability of exceeding the overfishing limit. In addition, this upgrade addressed several inadequacies with the previous module, including:

- The average selectivity and relative F was the same for the benchmark and the forecast calculations;
- The biology-at-age in  $\text{endyr}+1$  was used as the biology for the benchmark, but biology-at-age propagated forward in the forecast if there was time-varying growth;
- The forecast module had a kluge approach to calculation of overfishing limit (OFL) conditioned on previously catching ABC;
- The forecast module implementation of catch caps was incomplete and applied some caps on a seasonally, rather than the more logical annual basis;
- The  $F_{\text{mult}}$  scalar for fishing intensity presented a confusing concept for many users;
- No provision for specification of catch allocation among fleets;

- The forecast allowed for a blend of fixed input catches and catches calculated from target  $F$ ; this is not optimal for calculation of the variance of  $F$  conditioned on a catch policy that sets annual catch limits (ACLs).

The V3.20 module addressed these issues by:

- Providing for unique specification of a range of years from which to calculate average selectivity for benchmark, average selectivity for forecast, relative  $F$  for benchmark, and relative  $F$  for forecast;
- Create a new specification for the range of years over which to average size-at-age and fecundity-at-age for the benchmark calculation. In a setup with time-varying growth, it may make sense to do this over the entire range of years in the time series. Note that some additional quantities still use their endyr values, notably the migration rates and the allocation of recruitments among areas. This will be addressed shortly;
- Create a multiple pass approach that rectifies the OFL calculation;
- Improve the specification of catch caps and implement specification of catch allocations so that there can be an annual cap for each fleet, an annual cap for each area, and an annual allocation among groups of fleets (e.g. all recreational fleets vs. all commercial fleets);
- Introduce capability to have implementation error in the forecast catch (single value applied to all fleets in all seasons of the year).

## Multiple Pass Forecast

The most complicated aspect of the changes is with regard to the multiple pass aspect of the forecast. This multiple pass approach is needed to calculate both OFL and ABC in a single model run. More importantly, the multiple passes are needed in order to mimic the actual sequence of assessment-management action – catch over a multi-year period. The first pass calculates OFL based on catching OFL each year, so presents the absolute maximum upper limit to catches. The second pass forecasts a catch based on a harvest policy, then applies catch caps and allocations, then updates the  $F$ 's to match these catches. In the third pass, stochastic recruitment and catch implementation error are implemented and SS calculates the  $F$  that would be needed in order to catch the adjusted catch amount previously calculated in the second pass. With this approach, SS is able to produce improved estimates of the probability that  $F$  would exceed the overfishing  $F$ . In effect it is the complement of the  $P^*$  approach. Rather than the  $P^*$  approach that calculates the stream of annual catches that would have an annual probability of  $F > F_{limit}$ , SS calculates the expected time series of  $P^*$  that would result from a specified harvest policy implemented as a buffer between  $F_{target}$  and  $F_{limit}$ .

The sequence of multiple forecast passes is as follows:

1. Pass 1 (a.k.a. Fcast\_Loop1)

(a) Loop Years

i. SubLoop (a.k.a. ABC\_Loop) = 1

- A.  $R=f(SSB)$  with no deviations
- B.  $F=F_{limit}$
- C. Fixed input catch amounts ignored
- D. No catch adjustments (caps and allocations)
- E. No implementation error
- F. Result: OFL conditioned on catching OFL each year

2. Pass 2

(a) Loop Years

i. SubLoop = 1

- A.  $R=f(SSB)$  with no deviations
- B.  $F=F_{limit}$
- C. Fixed input catch amounts ignored
- D. No catch adjustments (caps and allocations)
- E. No implementation error
- F. Result: OFL conditioned on catching ABC previous year. Stored in `std_vector`.

ii. SubLoop = 2

- A.  $R=f(SSB)$  with no deviations
- B.  $F=F_{target}$  to get catch for each fleet in each season
- C. Fixed input catch amounts replace catch from step 2

- D. Catch adjustments (caps and allocations) applied on annual basis (after looping through seasons and areas within this year). These adjustments utilize the logistic joiner approach common in SS so the overall results remain completely differentiable.
  - E. No implementation error
  - F. Result: ABC as adjusted for caps and allocations
- iii. SubLoop = 3
- A.  $R=f(SSB)$  with no deviations
  - B. Catches from Pass 2 multiplied by the random term for implementation error
  - C.  $F$ =adjusted to match the catch\*error while taking into account the random recruitments. This is most easily visualized in a MCMC context where the recruitment deviation and the implementation error deviations take on non-zero values in each instance. In MLE, because the forecast recruitments and implementation error are estimated parameters with variance, their variance still propagates to the derived quantities in the forecast.
  - D. Result: Values for  $F$ ,  $SSB$ , Recruitment, Catch are stored in std-vectors
    - In addition, the ratios  $F/Flimit$  and  $SSB/SSBlimit$  or  $SSB/SSBtarget$  are also stored in std\_vectors.
    - Estimated variance in these ratios allows calculation of annual probability that  $F>Flimit$  or  $B<Blimit$ . This is essentially the realized  $P^*$  conditioned on the specified harvest policy.

## Example Effects on Correlations

An example that illustrates the above process was conducted. The situation was a low  $M$ , late-maturing species, so changes are not dramatic. The example conducted a 10 year forecast and examined correlations with derived quantities in the last year of the forecast. This was done once with the full set of 3 passes as described above, and again with only 2 passes and stochastic recruitment occurring in pass 2, rather than 3. This alternative setup is more similar to forecasts done using previous model versions.

2 Forecast Passes with $F$ from ABC and random recruitment	2 Forecast Passes with catch from target $F$ and equilibrium recruitment
---	---

	Factor X	Factor Y	Corr		Factor X	Factor Y	Corr
A1	F 2011	RecrDev 2002	-0.126	A2	F 2011	RecrDev 2002	0.090
B1	F 2011	Recr 2002	0.312	B2	F 2011	Recr 2002	0.518
C1	ForeCatch 2011	RecrDev 2002	0.000	C2	ForeCatch 2011	RecrDev 2002	0.129
D1	ForeCatch 2011	Recr 2002	0.455	D2	Forecatch 2011	Recr 2002	0.555

Correlation A2 shows a small positive correlation between the recruitment deviation in 2002 and the F in 2011. This is probably due to the fact that a positive deviation in recruitment in 2002 will reduce the chances that the biomass in 2011 will be below the inflection point in the control rule. This occurs because in calculating catch from F, the model effectively "knows" the future recruitments. I predict that this B1 correlation would be near zero if there was no inflection in the control rule.

Correlation A1 shows this turning into a negative correlation. This is because the future catches are first calculated from equilibrium recruitment, then when random recruitments are implemented, a positive recruitment deviation will cause a negative deviation in the F needed to catch that now "fixed" amount of future catch.

Correlations B1 and B2 are in terms of absolute recruitment, not recruitment deviation. Now overall model conditions that cause a higher absolute recruitment level will also result in a higher forecast level. No surprise there, and the correlation is stronger when variance is based on catch is calculated from F (B2).

Correlation C2 shows a positive correlation between recruitment deviation in 2002 and forecast catch in 2011. However, correlation C1 is 0.0 because the forecast catch in 2011 is set based on equilibrium recruitment and is not influenced by the recruitment deviations.

## Future Work

- More testing with high M, rapid turnover conditions
- Testing without inflection in control rule
- Consider separating implementation error into a pass #4 so results will more clearly show effect of assessment uncertainty separate from implementation uncertainty
- Consider adding a random "assessment" error which essentially is a random variable that scales



population abundance before passing into the forecast stage. Complication is figuring out how to link it to the correlated error in the benchmark quantities

- Because all of these calculations occur only in the sdphase or the mceval phase, it would be feasible for mceval calls to add an additional pass that is implemented many times and in which random forecast recruitment draws are made.
- Factors like selectivity and fleet relative F levels are calculated as an average of these values during the time series. This is internally consistent if these factors do not vary during the time series (although clearly this is a stiff model that will underestimate process variance). However, if these factors do vary over time, then the average used for the forecast will under-represent the variance. A better approach would be to set up the parameters of selectivity as a random process that extends throughout the forecast period, and to update estimated selectivity in each year of the forecast based upon the random realization of these parameters.

## Appendix D: Code Examples

### Ageing Error Estimation

```
/* SS_Label_FUNCTION 45 get_age_age */
FUNCTION void get_age_age(const int Keynum, const int AgeKey_StartAge, const int AgeKey_Linear1, const int AgeKey_Linear2)
{
  // FUTURE: calculate adjustment to oldest age based on continued ageing of old fish
  age_age(Keynum).initialize();
  dvariable age;
  dvar_vector age_err_parm(1,7);
  dvariable temp;

  if(Keynum==Use_AgeKeyZero)
  {
    // SS_Label_45.1 set age_err_parm to mgp_adj, so can be time-varying according to MGparm options
    for (a=1;a<=7;a++)
    {age_err_parm(a)=mgp_adj(AgeKeyParm-1+a);}
    age_err(Use_AgeKeyZero,1)(0, AgeKey_StartAge)=r_ages(0, AgeKey_StartAge)+0.5;
    age_err(Use_AgeKeyZero,2)(0, AgeKey_StartAge)=age_err_parm(5)*(r_ages(0, AgeKey_StartAge)+0.5)/
    (age_err_parm(1)+0.5);
    // SS_Label_45.3 calc ageing bias
    if(AgeKey_Linear1==0)
    {
      age_err(Use_AgeKeyZero,1)(AgeKey_StartAge,nages)=0.5 + r_ages(AgeKey_StartAge,nages) +
      age_err_parm(2)+(age_err_parm(3)-age_err_parm(2))*(1.0-mfexp(-age_err_parm(4)*
      (r_ages(AgeKey_StartAge,nages)-age_err_parm(1)))) / (1.0-mfexp(-age_err_parm(4)*
      (r_ages(nages)-age_err_parm(1))));
    }
    else
    {
      age_err(Use_AgeKeyZero,1)(AgeKey_StartAge,nages)=0.5 + r_ages(AgeKey_StartAge,nages) +
      age_err_parm(2)+(age_err_parm(3)-age_err_parm(2))*
      (r_ages(AgeKey_StartAge,nages)-age_err_parm(1))/(r_ages(nages)-age_err_parm(1));
    }
  }
  // SS_Label_45.4 calc ageing variance
```

```

if (AgeKey_Linear2==0)
{
age_err(Use_AgeKeyZero,2)(AgeKey_StartAge,nages)=age_err_parm(5)+(age_err_parm(6)-age_err_parm(5))*
(1.0-mfexp(-age_err_parm(7)*(r_ages(AgeKey_StartAge,nages)-age_err_parm(1)))) /
(1.0-mfexp(-age_err_parm(7)*(r_ages(nages)-age_err_parm(1))));
}
else
{
age_err(Use_AgeKeyZero,2)(AgeKey_StartAge,nages)=age_err_parm(5)+(age_err_parm(6)-age_err_parm(5))*
(r_ages(AgeKey_StartAge,nages)-age_err_parm(1))/(r_ages(nages)-age_err_parm(1));
}
}

```

## Survival Based SRR Code

Code for the survival based recruitment is shown below:

```

// SS_Label_43.3.7 survival based
case 7: // survival based, so constrained such that recruits cannot exceed fecundity
{

SRZ_0=log(1.0/(SSB_virgin_adj/Recr_virgin_adj));
SRZ_max=SRZ_0+SR_parm_work(2)*(0.0-SRZ_0);
SRZ_surv=mfexp((1.-pow((SSB_curr_adj/SSB_virgin_adj),SR_parm_work(3)))*(SRZ_max-SRZ_0)+SRZ_0); // survival
NewRecruits=SSB_curr_adj*SRZ_surv;
exp_rec(y,1)=NewRecruits; // expected arithmetic mean recruitment

// SS_Label_43.3.7.1 Do variation in recruitment by adjusting survival
if(recdev_cycle>0)
{
gg=y - (styr+(int((y-styr)/recdev_cycle))*recdev_cycle)+1;
SRZ_surv*=mfexp(recdev_cycle_parm(gg));
}
exp_rec(y,2)=SSB_curr_adj*SRZ_surv;
SRZ_surv*=mfexp(-biasadj(y)*half_sigmaRsq); // bias adjustment
exp_rec(y,3)=SSB_curr_adj*SRZ_surv;
if(y <=recdev_end)
{
if(recdev_doit(y)>0) SRZ_surv*=mfexp(recdev(y)); // recruitment deviation
}
else if(Do_Forecast>0)
{
SRZ_surv *= mfexp(Fcast_recruitments(y));
}
join=1./(1.+mfexp(100*(SRZ_surv-1.)));
SRZ_surv=SRZ_surv*join + (1.-join)*1.0;
NewRecruits=SSB_curr_adj*SRZ_surv;
exp_rec(y,4) = NewRecruits;
break;
}

```

## Random Walk Selectivity: Pattern 17

Code for selectivity pattern 17, random walk shown below:

```
// SS_Label_Info_22.7.17 #age selectivity: each age has parameter as random walk
// #41 each age has parameter as random walk scaled by average of values at low age through high age
// transformation as selex=exp(parm); some special codes */
case 41:
scaling_offset = 2;
case 17:          //
{
lastsel=0.0; // value is the change in log(selex); this is the reference value for age 0
tempvec_a=-999.;
tempvec_a(0)=0.0; // so do not try to estimate the first value
int lastage;
if(seltype(f,4)==0)
{lastage=nages;}
else
{lastage=abs(seltype(f,4));}

for (a=1;a<=lastage;a++)
{
// with use of -999, lastsel stays constant until changed, so could create a linear change in ln(selex)
// use of (a+1) is because the first element, sp(1), is for age zero
if(sp(a+1+scaling_offset)>-999.) {lastsel=sp(a+1+scaling_offset);}
tempvec_a(a)=tempvec_a(a-1)+lastsel; // cumulative log(selex)
}
if (scaling_offset == 0)
{
temp=max(tempvec_a); // find max so at least one age will have selex=1.
}
else
{
int low_bin = int(value(sp(1)));
int high_bin = int(value(sp(2)));
if (low_bin < 0)
{
low_bin = 0;
N_warn++; warning<<" selex pattern 41; value for low bin is less than 0, so set to 0 "<<endl;
}
if (high_bin > nages)
{
high_bin = nages;
N_warn++; warning<<" selex pattern 41; value for high bin is greater than "<<nages<<" , so set to "<<nages<<" "<<endl;
}
if (high_bin < low_bin) high_bin = low_bin;
if (low_bin > high_bin) low_bin = high_bin;
sp(1) = low_bin;
sp(2) = high_bin;
temp=mean(tempvec_a(low_bin,high_bin));
}
sel_a(y,fs,1)=mfexp(tempvec_a-temp);
a=0;
while(sp(a+1+scaling_offset)==-1000) // reset range of young ages to selex=0.0
{
sel_a(y,fs,1,a)=0.0;
a++;
}
scaling_offset = 0; // reset scaling offset
if(lastage<nages)
{
for (a=lastage+1;a<=nages;a++)
```

```
{
if(seltype(f,4)>0)
{sel_a(y,fs,1,a)=sel_a(y,fs,1,a-1);}
else
{sel_a(y,fs,1,a)=0.0;}
}
}
break;
}
```

# Cubic Spline Selectivity

Code for cubic spline selectivity, option 42, shown below:

```
// SS_Label_Info_22.7.27 #age selectivity: cubic spline
// #42 cubic spline scaled by average of values at low age through high age
case 42:
scaling_offset = 2;
case 27:
{
k=seltype(f,4); // n points to include in cubic spline
for (i=1;i<=k;i++)
{
splineX(i)=value(sp(i+3+scaling_offset)); // "value" required to avoid error, but values should be always fixed anyway
splineY(i)=sp(i+3+k+scaling_offset);
}
z=nages;
while(r_ages(z)>splineX(k)) {z--;}
j2=z+1; // first age beyond last node
vcubic_spline_function splinefn=vcubic_spline_function(splineX(1,k),splineY(1,k),sp(2+scaling_offset),sp(3+scaling_offset));
tempvec_a= splinefn(r_ages); // interpolate selectivity at each age
if (scaling_offset == 0)
{
temp=max(tempvec_a(0,j2));
}
else
{
int low_bin = int(value(sp(1)));
int high_bin = int(value(sp(2)));
if (low_bin < 0)
{
low_bin = 0;
N_warn++; warning<<" selex pattern 42; value for low bin is less than 0, so set to 0 "<<endl;
}
if (high_bin > nages)
{
high_bin = nages;
N_warn++; warning<<" selex pattern 42; value for high bin is greater than "<<nages<<" , so set to "<<nages<<" "<<endl;
}
if (high_bin < low_bin) high_bin = low_bin;
if (low_bin > high_bin) low_bin = high_bin;
sp(1) = low_bin;
sp(2) = high_bin;
temp=mean(tempvec_a(low_bin,high_bin));
scaling_offset = 0; // reset scaling offset
}
tempvec_a-=temp; // rescale to get max of 0.0
tempvec_a(j2+1,nages) = tempvec_a(j2); // set constant above last node
sel_a(y,fs,1)=mfexp(tempvec_a);
break;
}
```

# Deviation Link

Code for alternative deviation links shown below:

```
case 1 (multiplicative):
{
  for (j=timevary_setup(10);j<=timevary_setup(11);j++)
  {
    parm_timevary(tvary,j)*=mfexp(parm_dev(k,j)*parm_dev_stddev(k));
  }
  break;
}

case 2 (additive):
{
  for (j=timevary_setup(10);j<=timevary_setup(11);j++)
  {
    parm_timevary(tvary,j)+=parm_dev(k,j)*parm_dev_stddev(k);
  }
  break;
}

case 3 (random walk):
{
  parm_dev_rwalk(k,timevary_setup(10))=parm_dev(k,timevary_setup(10))*parm_dev_stddev(k);
  parm_timevary(tvary,timevary_setup(10))+=parm_dev_rwalk(k,timevary_setup(10));
  for (j=timevary_setup(10)+1;j<=timevary_setup(11);j++)
  {
    parm_dev_rwalk(k,j)=parm_dev_rwalk(k,j-1)+parm_dev(k,j)*parm_dev_stddev(k);
    parm_timevary(tvary,j)+=parm_dev_rwalk(k,j);
  }
  break;
}

case 4 (mean reverting random walk)
{
  parm_dev_rwalk(k,timevary_setup(10))=parm_dev(k,timevary_setup(10))*parm_dev_stddev(k);
  parm_timevary(tvary,timevary_setup(10))+=parm_dev_rwalk(k,timevary_setup(10));
  for (j=timevary_setup(10)+1;j<=timevary_setup(11);j++)
  {
    //      =(1-rho)*mean + rho*prevval + dev    //   where mean = 0.0
    parm_dev_rwalk(k,j)=parm_dev_rho(k)*parm_dev_rwalk(k,j-1)+parm_dev(k,j)*parm_dev_stddev(k);
    parm_timevary(tvary,j)+=parm_dev_rwalk(k,j);
  }
  break;
}
```