Stock Assessment Model User Manual
SAM v1.1-2014**-** (rev. ****)

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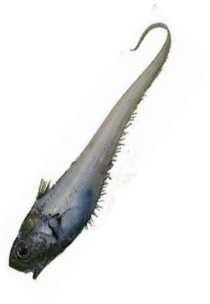
Month 2014



SAM logo being developed by Erika MacKay.

SAM name tbd.

Confirmation of structure and contents order is required in the first instance.

Documentation copied and adapted from CASAL and SPM manuals - requres discussion, checking and rewriting.

Chapters for command and subcommand syntax are auto-generated from the SAM code for Population, Estimation, Observation and Report sections.

Version.tex file required to auto-update version date/time/number.

Citation: Doonan. I.; Dunn, A.; Rasmussen, S.; Large, K.; Bull, B.; Francis, R.I.C.C.; McKenzie, A.; Gilbert, D.J.; Smith, M.H.; Bian, R.; Fu, D. (2014) Stock Assessment Model User Manual, SAM v1.1-2014**-** (rev. ****) . National Institute of Water & Atmospheric Research Ltd. *Unpublished report*. 115 p.

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KL comment: 4th level included for planning purposes, will be removed when order of contents confimed.

Contents

1. Introduction

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SAM (Stock Assessment Model) is a generalised age- or size-structured fish stock assessment model that allows flexibility in specifying population dynamics, paramaeter estimation and model outputs. SAM can model population dynamics for an age-structured population using a range of observations, including tagging, relative abundance, and age frequency data. SAM implements an age-structured population which can have user defined categories (e.g., immature, mature, male, female, etc.), and age range.

This manual describes how to use SAM, including how to run SAM, how to set up an input configuration file. Further, we describe the population dynamics and estimation methods, and describe how to specify and interpret output.

1.1. Version

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This document (last modified 2014-**-**) describes SAM v1.1-2014**-** (rev. ****) . The SAM version number is suffixed with a date/time (yyyy-mm-dd) and revision number, giving the revision control system UTC date and revision number for the most recent modification of the source files. User manual updates will usually be issued for each minor version or date release of SAM, and can be obtained, on request, from the authors.

1.2. Citing SAM

check and confirm text
A suitable reference for SAM and this document is:

Doonan. I.; Dunn, A.; Rasmussen, S.; Large, K.; Bull, B.; Francis, R.I.C.C.; McKenzie, A.; Gilbert, D.J.; Smith, M.H.; Bian, R.; Fu, D. (2014) Stock Assessment Model User Manual, SAM v1.1-2014**-** (rev. ****) . National Institute of Water & Atmospheric Research Ltd. *Unpublished report*. 115 p.

1.3. Software license

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1.4. System requirements

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SAM is available for most IBM compatible machines running 64-bit Linux and Microsoft Windows operating systems.

Several of SAMs tasks are highly computer intensive and a fast processor is recommended. Depending on the model implemented, some of SAMs tasks can take a considerable amount of time (minutes to hours), and in extreme cases can even take several days to estimate a model fit. Some of SAMs tasks can be multi-threaded, and hence multi-core machines may perform some tasks quicker than single core processors.

The program itself requires only a few megabytes of hard-disk space but output files can consume large amounts of disk space. Depending on number and type of user output requests, the output could range from a few hundred kilobytes to several hundred megabytes. When estimating model fits, several hundred megabytes of RAM may be required, depending on the spatial size of the model, number of categories, and complexity of processes and observations. For extremely large models, several gigabytes of RAM may be required.

1.5. Necessary files

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For both 64-bit Linux and Microsoft Windows, only the binary file spm or spm.exe is required to run SAM. No other software is required. We do not compile a version for 32-bit operating systems.

SAM offers little in the way of post-processing of the output, and a package available that allows tabulation and graphing of model outputs is recommended. We suggest software such as Microsoft Excel, S-Plus, or **R** (R Development Core Team 2007). To assist in the post processing of SAM output, we provide the sam **R** package for importing the SAM output into **R** (see Section 14).

1.6. Getting help

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SAM is distributed as unsupported software, however we would appreciate being notified of any problems or errors in SAM. See Section **??** for how to report errors to the authors. Further information about SAM can be obtained by contacting the authors.

1.7. Technical details

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SAM was compiled on Linux using gcc, the C/C++ compiler developed by the GNU Project. The 64-bit Linux version was compiled using gcc version 4.8.1 20130909 (SUSE Linux). Note that SAM is not supported for Linux kernel versions prior to 2.6. The Microsoft Windows version was compiled using Mingw32 gcc (tdm64-1) 4.7.1. The Microsoft Windows installer was built using the Nullsoft Scriptable Install System.

SAM uses two minimisers — the first is closely based on the main algorithm of Dennis Jr and Schnabel (1996), and which which uses finite difference gradients, and the second is an implementation of the differential evolution solver (Storn and Price, 1995), and based on code by Lester E. Godwin of PushCorp, Inc.

The random number generator used by SAM uses an implementation of the Mersenne twister random number generator (Matsumoto and Nishimura, 1998). This, the command line functionality, matrix operations, and a number of other functions use the BOOST C++ library (Version 1.54.0).

Note that the output from SAM may differ slightly on the different platforms due to different precision arithmetic or other platform dependent implementation issues. The source code for SAM is available

either as a part of the installation, or on request from the authors.

Unit tests of the underlying SAM code are carried out at build time, using the BOOST unit testing framework. The unit test framework aims to cover a significant proportion of the key functions and processes within the SAM code base. The unit test code for SAM is available as a part of the underlying source code.

2. Model overview

2.1. Introduction

check and confirm text

The Stock Assessment Model (SAM) is an age-structured population dynamics model. It implements a statistical catch-at-age population dynamics, using a discrete time-step state-space model that represents a cohort-based population age structure .

SAM is run from the console window on Microsoft Windows or from a terminal window on Linux. SAMgets its information from input data files, the main one of which is the *input configuration file*. Commands and subcommands in the input configuration file are used to define the model structure, provide observations, define parameters, and define the outputs (reports) for SAM. Command line switches tell SAM the run mode and where to direct its output. See Section **??** for the details.

We define the model in terms of the *state*. The state consists of two parts, the *partition*, and any *derived quantities* or *derived quantities by cell*. The state will typically change one or more times in every *time-step* of every year, depending on the *processes* defined for each model.

The partition is a representation of the population at an instance in time, and is a matrix of the numbers of individuals within each age, and category. A derived quantity is a cumulative summary of the partition (over all cells) at some point in time. A derived quantity by cell is a cumulative summary of the partition in each of the cells at some point in time. Unlike the partition (which is updated as each new process is applied), each derived quantity records a single value for each year of the model run, and each derived quantity by cell records a layer of values for each year of the model run. Hence, derived quantities build up a vector of values over the model run years. For example, the total number of individuals in a category labelled mature at some point in the annual cycle may be a derived quantity and the total number of individuals in a category labelled mature in each cell of the model at some point in the annual cycle may be a derived quantity by cell. The state is the combination of the partition and any derived quantities or derived quantities by cell at some instance in time. Changes to the state occur by the application of processes. Additions to the vectors of derived quantities occur when a model is requested to add a value to each derived quantity vector.

Running of the model consists of two main parts — first the model state is initialised for a number of iterations (years), then the model runs over a range of predefined years.

The application of processes within each year is controlled by the *annual cycle*. This defines what processes happen in each model year, and in what sequence. Initialisation can be phased, and for each phase, the user need to define the processes that occur in each year, and the order in which they are applied.

For the run years, each year is split up into one or more time-steps (with at least one process occurring in each time-step). You can think of each time-step as representing a particular part of the calendar year, or you can just treat them as an abstract sequence of events.

The division of the year into an arbitrary number of time-steps allows the user to specify the exact order in which processes occur and when observations are evaluated. The user specifies the time-steps, their order, and the processes within each time-step. If more than one process occurs in the same time-step, then the occur in the order that they are specified. Observations are always evaluated at the end of the time-step in which they occur. Hence, time-steps can be used to break processes into groups, and assist in defining the timing of the observations within the annual cycle.

The population structure of SAM follows the usual population modelling conventions and is similar to those implemented in other population models, for example CASAL (Bull et al., 2012). The model

records the numbers of individuals by age and category (e.g., male, female). In general, cohorts are added via a recruitment event, are aged annually, and are removed from the population via various forms of mortality. The population is assumed to be closed (i.e., no immigration or emigration from the modelled area)

A model is implemented in SAM using an input configuration file, which is a complete description of the model structure (i.e., spatial and population processes), observations, estimation methods, and reports (outputs) requested. SAM runs from a console window on Microsoft Windows or from a text terminal on Linux. A model can be either *run*, estimable parameters can be *estimated* or *profiled*, *MCMC* distributions calculated, and these estimates can be used by SAM as parameters of an operating model to *simulate* observations.

A model in SAM is specified by an input configuration file, and comprises of four main components. These are the population section (model structure, population dynamics, etc.), the estimation section (methods of estimation and the parameters to be estimated), the observation section (observational data and associated likelihoods), and the report section (printouts and reports from the model). The input configuration file completely describes a model implemented in SAM. See Sections 8, 9, 10, and 11 for details and specification of SAMs command and subcommand syntax within the input configuration file.

2.2. The population section

check and confirm text
The population section (Section 4) defines the model of the population dynamics. It describes the model structure (i.e. the population structure), initialisation and run years (model period), population processes (for example, recruitment, migration, and mortality), selectivities, and key population parameters.

2.3. The estimation section

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The estimation section (Section 5) specifies the parameters to be estimated, estimation methods, penalties and priors. Estimation is based on an objective function (e.g., negative log posterior). Depending on the run mode, the estimation section is used to specify the methods for finding a point estimate (i.e., the set of parameter values that minimizes the objective function), doing profiles, or MCMC methods and options, etc.

Further, the estimation section specifies the parameters to be estimated within each model run and the estimation methods. The estimation section specifies the choice of estimation method, which model parameters are to be estimated, priors, starting values, and minimiser control values.

Penalties and priors act as constraints on the estimation. They can either encourage or discourage (depending on the specific implementation) parameter estimates that are 'near' some value, and hence influence the estimation process. For example, a penalty can be included in the objective function to discourage parameter estimates that lead to models where the recorded catch was unable to be fully taken.

2.4. The observation section

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Types of observations, their values, and the associated error structures are defined in the observation

section (Section 6). Observations are data which allow us to make inferences about unknown parameters. The observation section specifies the observations, their errors, likelihoods, and when the observations occur. Examples include relative or absolute abundance indices, proportions-at-age frequencies, etc. Estimation uses the observations to find values for each of the estimated parameters so that each observation is 'close' (in some mathematical sense) to a corresponding expected value.

2.5. The report section

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The report section (Section 7) specifies the model outputs. It defines the quantities and model summaries to be output to external files or to the standard output. While `SAM` will provide informational messages to the screen, `SAM` will only produce model estimates, population states, and other data as requested by the report section. Note that if no reports are specified, then no output will be produced.

3. Running SAM

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SAM is run from the console window (i.e., the DOS command line) on Microsoft Windows or from a terminal window on Linux. SAM gets its information from input data files, the key one of which is the input configuration file.

The input configuration file is compulsory and defines the model structure, processes, observations, parameters (both the fixed parameters and the parameters to be estimated), and the reports (outputs) requested. The following sections describe how to construct the SAM configuration file. By convention, the name of the input configuration file ends with the suffix `.tex`, however, any file name is acceptable.

Other input files can, in some circumstances, be supplied to define the starting point for an estimation or as a point estimate from which to simulate observations.

Simple command line arguments are used to determine the actions or *tasks* of SAM, i.e., to run a model with a set of parameter values, estimate parameter values (either point estimates or MCMC), project quantities into the future, simulate observations, etc,. Hence, the *command line arguments* define the *task*. For example, `-r` is the *run*, `-e` is the *estimation*, and `-m` is the *MCMC* task. The *command line arguments* are described in Section 3.4.

3.1. Using SAM

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To use SAM, open a console (i.e. the command prompt) window (Microsoft Windows) or a terminal window (Linux). Navigate to a directory of your choice, where your input configuration files are located. Then type `spm` with any arguments (see Section 3.4 for the the list of possible arguments). SPM will print output to the screen and return you to the command prompt when it completes its task. Note that the SAM executable (binary) must be either in the directory where you run it or somewhere in your PATH. Note that an automated installer is available for SAM on Microsoft Windows. If you use the installer, then it will give you the option of modifying your PATH for you (as well a a number of other options to make using the program a little easier). Otherwise, see your operating system documentation for help on identifying or modifying your PATH.
*need an example here...*a small example of directory navigation and spm with arguments as would be typed in the command prompt window

3.2. The input configuration file

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The input configuration file is made up of four broad sections; the description of the population structure and parameters (the population section), the estimation methods and variables (the estimation section), the observations and their associated likelihoods (the observation section), and the outputs and reports that SAM will return (the report section). The input configuration file is made up of a number of commands (many with subcommands) which specify various options for each of these components.

The command and subcommand definitions in the input configuration file can be extensive (especially when you have a model that has many observations), and can result in a input configuration file that is long and difficult to navigate. To aid readability and flexibility, we can use the input configuration file command `@include` *`file`*. The command causes an external file,

file, to be read and processed, exactly as if its contents had been inserted in the main input configuration file at that point. The file name must be a complete file name with extension, but can use either a relative or absolute path as part of its name. Note that included files can also contain `@include` commands — but be careful that you do not set up a recursive state. See Section 12 for more detail.

3.3. Redirecting standard output

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SAM uses the standard output stream `standard output` to display run-time information. The standard error stream is used by SAM to output the program exit status and run-time errors. We suggest redirecting both the standard output and standard error into files. With the bash shell (on Linux systems), you can do this using the command structure,

```
(\sam [arguments] > out) >& err &
```

It may be useful to redirect the standard input, especially is you're using SAM inside a batch job software, i.e.

```
(\sam [arguments] > out < /dev/null) >& err &
```

On Microsoft Windows systems, you can redirect to standard output using,

```
\sam [arguments] > out
```

And, on some Microsoft Windows systems (e.g., Windows7), you can redirect to both standard output and standard error, using the syntax,

```
\sam [arguments] > out 2> err
```

Note that SAM outputs a few lines of header information to the output. The header consists of the program name and version, the arguments passed to SAM from the command line, the date and time that the program was called (derived from the system time), the user name, and the machine name (including the operating system and the process identification number). These can be used to track outputs as well as identifying the version of SAM used to run the model.

3.4. Command line arguments

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The call to SAM is of the following form.:

sam[-c *config_file*] [*task*] [*options*]

-c *config_file* Define the input configuration file for SAM. If omitted, then SAM looks for a file named `config.spm`.

and where *task* is one of;

-h Display help (this page).

-l Display the reference for the software license (CPLv1.0).

-v Display the SAM version number.

-r *Run* the model once using the parameter values in the input configuration file, or optionally, with the values from the file denoted with the command line argument -i *file*.

-e Do a point *estimate* using the values in the input configuration file as the starting point for the parameters to be estimated, or optionally, with the start values from the file denoted with the command line argument -i *file*.

-p Do a likelihood *profile* using the parameter values in the input configuration file as the starting point, or optionally, with the start values from the file denoted with the command line argument -i *file*.

-m Do an *MCMC* estimate using the values in the input configuration file as the starting point for the parameters to be estimated, or optionally, with the start values from the file denoted with the command line argument -i *file*.

-s *number* *Simulate* the *number* of observation sets using values in the input configuration file as the parameter values, or optionally, with the values for the parameters denoted as estimated from the file with the command line argument -i *file*.

In addition, the following are optional arguments [*options*],

-i *file* *Input* one or more sets of free (estimated) parameter values from *file*. See Section **??** for details about the format of *file*.

-o *file* *Output* a report of the free (estimated) parameter values in a format suitable for -i *file*. See Section **??** for details about the format of *file*.

-t *number* Maximum number of *threads* to use when the model includes multi-threaded process.

-q Run *quietly*, i.e., suppress verbose printing of SAM.

-g *seed* Seed the random number *generator* with *seed*, a positive (long) integer value. Note, if -g is not specified, then SAM will generate a random number seed based on the computer clock time.

3.5. Constructing an SAM input configuration file

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The model definition, parameters, observations, and reports are specified in an input configuration file. The population section is described in Section 4 and the population commands in Section 8. Similarly, the estimation section is described in Section 5 and its commands in Section 9, and in Section 7 and Section 11 for the report and report commands.

3.5.1. Commands

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SAM has a range of commands that define the model structure, processes, observations, and how tasks are carried out. There are three types of commands,

1. Commands that have an argument and do not have subcommands (for example, @include *file*)

2. Commands that have a label and subcommands (for example `@process` must have a label, and has subcommands)
3. Commands that do not have either a label or argument, but have subcommands (for example `@model`)

Commands that have a label must have a unique label, i.e., the label cannot be used on more than one command of that type. The labels must start with a letter or underscore, can contain letters, underscores, or numbers. Labels must not contain white-space, a full-point ('.'), or other characters that are not letters, numbers, or an underscore.
need an example here...

3.5.2. Subcommands

check and confirm text
Subcommands in SAM are for defining options and parameter values for commands. They always take an argument which is one of a specific *type*. The types acceptable for each subcommand are defined in Section 8.8.10, and are summarised below.

Like commands (`@command`), subcommands and their arguments are not order specific — except that that all subcommands of a given command must appear before the next `@command` block. SAM may report an error if they are not supplied in this way, however, in some circumstances a different order may result in a valid, but unintended set of actions, leading to possible errors in your expected results.

The arguments for a subcommand are either:

switch	true/false
integer	an integer number,
integer vector	a vector of integer numbers,
integer range	a range of integer numbers separated by a hyphen (-), e.g. 1994-1996 2000 is expanded to an integer vector of values 1994 1995 1996 2000),
constant	a real number (i.e. double),
constant vector	a vector of real numbers (i.e. vector of doubles),
estimable	a real number that can be estimated (i.e. estimable double),
estimable vector	a vector of real numbers that can be estimated (i.e. vector of estimable doubles),
string	a categorical (string) value, or
string vector	a vector of categorical values.

Switches are parameters which are either true or false. Enter *true* as `true` or `t`, and *false* as `false` or `f`.

Integers must be entered as integers (i.e., if `year` is an integer then use 2008, not 2008.0)

Arguments of type integer vector, integer range, constant vector, estimable vector, or categorical vector contain one or more entries on a row, separated by white space (tabs or spaces).

Estimable parameters are those parameters that SAM can estimate, if requested. If a particular parameter is not being estimated in a particular model run, then it acts as a constant. Within SAM only estimable parameters can be estimated. And, you have to tell SAM those that are to be estimated in any particular model. Estimable parameters that are being estimated within a particular model run are called the *estimated parameters*.

3.5.3. The command-block format

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Each command-block either consists of a single command (starting with the symbol) and, for most commands, a label or an argument. Each command is then followed by its subcommands and their arguments, e.g.,

`@command`, or

`@command argument`, or

`@command label`

and then

`subcommand argument`

`subcommand argument`

etc,.

Blank lines are ignored, as is extra white space (i.e., tabs and spaces) between arguments. But don't put extra white space before a `@` character (which must also be the first character on the line), and make sure the file ends with a carriage return.

There is no need to mark the end of a command block. This is automatically recognized by either the end of the file, section, or the start of the next command block (which is marked by the `@` on the first character of a line). Note, however, that the `@include` is the only exception to this rule. See Section 12) for details of the use of `@include`.

Note that in the input configuration file, commands, sub-commands, and arguments are not case sensitive. However, labels and variable values are case sensitive. Also note that if you are on a Linux system then external calls to files are case sensitive (i.e., when using `@include file`, the argument `file` will be case sensitive).

Characters used in labels must be alphanumeric and can include underscores (_). Other characters will result in an error.

3.5.4. Commenting out lines

check and confirm text
Text that follows a # on a line are considered to be comments and are ignored. If you want to remove a group of commands or subcommands using #, then comment out all lines in the block, not just the first line.

Alternatively, you can comment out an entire block or section by placing curly brackets around the text that you want to comment out. Put in a { as the first character on the line to start the comment block, then end it with }. All lines (including line breaks) between { and } inclusive are ignored. (These should ideally be the first character on a line. But if not, then the entire line will be treated as part of the comment block.)
*need an example here.....*short example of comment syntax

3.5.5. Determining parameter names

check and confirm text
When SAM processes a input configuration file, it translates each command and each subcommand into a parameter with a unique name. For commands, this parameter name is simply the command name. For subcommands, the parameter name format is either

`command[label].subcommand` if the command has a label, or

`command.subcommand` if the command has no label, or

`command[label].subcommand(i)` if the command has a label and the subcommand arguments are a vector, and we are accessing the *i*th element of that vector.

The unique parameter name is used to reference the parameter when estimating, applying a penalty, or applying a profile. For example, the parameter name of subcommand `r0` of the command `@process` with the label `MyRecruitment` is

```
process[MyRecruitment].r0
```

3.6. SAM exit status values

check and confirm text

When SAM completes its task successfully or errors out gracefully, it returns a single exit status value (0) to the operating system. The operating system will return (-1) if SAM terminates unexpectedly. To determine if SAM has completed its task successfully, check the standard output for error and information messages.

4. The population section

4.1. Introduction

The population section specifies the model structure, population dynamics, and other associated parameters. It describes the model structure (population structure), defines the population (e.g., recruitment, migration, and mortality), selectivities, and model parameters.

The population section consists of several components, including;

- The population structure;
- Model initialisation (i.e., the state of the model at the start of the first year);
- The years over which the model runs (i.e., the start and end years of the model)
- The annual cycle (time-steps and processes that are applied in each time-step);
- The specifications and parameters of the population processes (i.e. processes that add, remove individuals to or from the partition, or shift numbers between ages and categories in the partition);
- Selectivities;
- Parameter values and their definitions;
- Derived quantities, required as parameters for some processes (e.g. spawning stock biomass to resolve the spawner-recruit relationship in a recruitment process).

4.2. Population structure

The basic structure of a CASAL population model is defined in terms of an annual cycle, time steps, states, and transitions.

The annual cycle defines what processes happen in each model year, and in what sequence. (In line with the New Zealand fisheries management framework, CASAL runs on an annual cycle rather than, for example, a 6-monthly cycle.)

Each year is split into one or more time steps, with at least one process occurring in each time step. Each time step can be thought of as representing a particular part of the calendar year, or you can just treat them as an abstract sequence of events.

The state is the current status of the population, at any given time. The state can change one or more times in every time step of every year. The state object must contain sufficient information to figure out the future course of the fishery (given a model and a complete set of parameters).

There are a number of possible changes in the state, which are called transitions. These include processes such as recruitment, natural mortality, fishing mortality, disease mortality, ageing, migration, tagging events, and semelparous mortality.

The division of the year into an arbitrary number of time steps allows the user to specify the exact order in which processes and observations occur. The user needs to specify the time step in which each process occurs. If more than one process occurs in the same time step, there is a default order in which they occur (see Section 5.3). If you dont want things to happen in this default order, then split the processes into different time steps.

The key element of the state is the partition. This is a broadly applicable concept that can be used to describe many different kinds of fish model. The partition is simply a breakdown of the total number

of fish in the current population into different kinds of fish. (Note that the partition records numbers of fish, not biomass.) The fish are categorised by various characters. The permissible characters are: size class or age class, sex, maturity, area, stock, tag, and growth-path. The user chooses:

- whether the partition is subdivided by size class or age class (not both)
- which of the other characters are included in the partition, e.g., the number of areas, stocks, tagging events, or growth paths (if any of these characters are included in the partition).

The resulting partition can be conceptualised as a matrix, where the columns are size or age classes and the rows represent combinations of the other characters. Then the number in each cell of the matrix is the number of fish with the corresponding combination of characters.

For an example of these ideas, consider a model of a single stock with a spawning and non-spawning fishery. The non-spawning fishery happens over most of the year (say 10 months) in the home area. The mature fish then migrate to the spawning area, where the spawning fishery operates. At the end of spawning, these fish, along with the recruits from the previous year, migrate back to the home area. The modeller decides that fish will be divided in the partition by age, sex, maturity, and area (spawning and home grounds). So the partition has 8 rows (2 sexes (mature or immature) 2 areas) and one column per age class.

KL comment: INSERT TABLE HERE

So they define four time steps, labelled 1 through 4. Step 1 includes the non-spawning fishery. Step 2 includes the migration to the spawning area. Step 3 includes the spawning fishery. Step 4 includes recruitment and the migration back to the home area. (In fact, they could have used only 3 time steps, by using a single step in place of their steps 2 and 3. Because the default order of processes within a time step places migrations before fisheries, the processes would still have occurred in the right order.) There are other details to be sorted out, such as the proportion of natural mortality occurring in each time step, but this gives the basic idea.

This structure can be used to implement complex models, with intermingling of separate stocks, with complex migration patterns over multiple areas, and multiple fisheries using different fishing methods and covering different areas and times. Note that there is little point in using a complex structure to model a stock when there are no observations to support that structure. In other words, use a structure for your model that is compatible with the data available.

The model is run from an initial year up to the current year. It can also be run past the current year to make projections things that happen in the future up to the final year. Alternatively, for yield calculations, it is run over an abstract simulation period.

4.3. The state object and the partition

The key component of the state object is the partition, a matrix of numbers of fish by combinations of characters. The columns can either be age or size classes, the rows are combinations of the following characters:

- Sex (male or female);
- Area (any number of areas, named by the user);
- Stock (any number of stocks, named by the user);
- Maturity (immature or mature);
- Growth-path (any number of growth-paths);

- Tag. (any number of tagging events, but note that CASAL will always create a no_tag member of the partition in addition to those that you specify).

A stock is defined as a subpopulation of fish which recruits separately. See Section 5.11 for the treatment of maturity when it is not a character in the partition.

Growth-paths are a feature used to implement some persistence of size at age in an age-based model that uses some length/size data. Each growth-path has its own growth curve, and the size-based model features will consequently have different effects on different growth-paths. So, you need to tell CASAL the following:

- Whether the model is age- or size-based.
- The number and nature of size classes in a size-based model.
- The minimum and maximum age classes in an age-based model.
- Whether there is a plus group.
- Whether the partition is divided by sex.
- Whether the partition is divided by maturity.
- Whether the partition has growth-paths, and, if so, how many.
- Whether the partition has multiple stocks, and, if so, how many, and their names.
- Whether the partition has multiple areas, and, if so, how many, and their names.
- Whether the partition includes tagged fish, and, if so, how many, and the names of the tag partitions.

Age classes are always 1 year wide, except that the maximum age group can optionally be a plus group. Users need to choose the minimum and maximum age classes. Size classes are defined by the user, and you need to specify how many size classes there are, the lower bound of each size class, and whether the last size class is a plus group, or if not, what its upper bound is. The relevant parameters are `class_mins` and `plus_group`. The `class_mins` parameter contains the lower bound of each class, and concludes with the upper bound of the last class if it is not a plus group. If, for example, size classes of 3040, 4050, 5060, and 6070+ cm were desired, you would set `class_mins 30 40 50 60` and `plus_group true`. Whereas if 3040, 4050, 5060, and 6070 cm were desired, you would set `class_mins 30 40 50 60 70` and `plus_group false`.

The user can specify that some combinations of characters are not possible. For example, immature fish might never occur in the area you have labelled `spawn_ground`. To do this, you use the exclusions parameters. In this case, you would set,

```
exclusions_char1 maturity
exclusions_val1 immature
exclusions_char2 area
exclusions_val2 spawn_ground
```

Its a good idea to use the exclusions parameter wherever appropriate because it reduces the size of the partition (so, with the above example, there will be no rows in the partition corresponding to immature fish in area `spawn_ground`) and can save memory and calculation time.

The other component of the state object in CASAL is a vector of spawning stock biomasses (SSBs, mid-spawning season biomasses of spawning fish) for each stock. CASAL needs to include this in the state object to calculate future recruitments, if there is a stock-recruitment relationship.

4.4. Time sequences

The time sequence of the population model includes the years over which it is to run and the annual cycle for each year. The model runs from the start of year `initial` and runs to the end of year `current`. Projections extend up to the end of year `final`. The annual cycle can contain the following transition processes:

- Ageing (in an age-based model);
- Recruitment;
- Maturation (if maturity is a character in the partition);
- Migration (if the model includes more than one area);
- Growth (in a size-based model);
- Natural and fishing mortality;
- Disease mortality;
- Tag release events;
- Tag shedding rate;
- Semelparous mortality.

If two or more processes are specified for the same time step then they will happen in the above order. This ordering is imposed only to simplify the specification of the annual cycle. It does not restrict the user because it applies only to processes within the same time step. If, for example, it is desired that maturation occur before recruitment then this can be done by putting these processes in separate time steps.

The basic unit of fishing mortality is a fishery, defined as fishing mortality in a single area and time step. You may need to split a single administrative fishery into multiple CASAL fisheries, in which case you will need to partition the catch. (However, this should often be avoidable. If you have an observation partway through a fishery, you can specify that a certain proportion of the mortality occurs before the observation, without needing to split the time step into two.)

If there is more than one stock, recruitment is handled separately for each stock, but all stocks must recruit in the same time step. There can be more than one maturation episode per year, each of which can apply to only one stock, or all stocks equally. Similarly there can be more than one growth episode per year, each of which can apply to only one stock, or all stocks equally. The user can define any number of migrations in a given year.

To specify the time sequence, you need to tell CASAL the following:

- The initial, current, and final years;
- The number of time steps in each year;
- The time step in which recruitment occurs, and the area to which each stock recruits
- How SSB is calculated [1];

[1] The SSB (spawning stock biomass) is a common model output and is also the measure of abundance used in stock-recruitment relationships in CASAL (where applicable). Different models define SSB in quite different ways so we allow several options in CASAL as to how SSB is calculated. By default, SSB is calculated for each stock as the mature biomass (of both sexes), in an area (or areas) of your choice, halfway through the natural and fishing mortality in a time step of your choice. It can alternatively be calculated after some other specified proportion of the mortality (see Section 5.4.6) and/or for one sex only. A proportion spawning multiplier can be applied to the mature biomass to get the SSB (in multi-area models this would typically not be done, instead the appropriate proportion of fish would be migrated to the spawning

- In an age-based model, the time step at which ages are incremented;
- If there are any migrations, the time step at which each migration occurs and the source and destination areas. Note that if there are multiple migrations in a time step and an area is the source of more than one migration, then the migrations will happen in the order that they are defined in the `population.csl` file;
- If maturity is a partition character, the number of maturation episodes per year, and the time step at which each maturation episode occurs;
- In a size-based model, the number of growth episodes per year, and the time step at which each growth episode occurs;
- In an age-based model, the proportion of the years growth which has occurred by the start of each time step [2];
- The proportion of the years natural mortality occurring in each time step;
- The time step and area in which each fishery occurs;
- Whether fishing mortality is instantaneous or uses the Baranov equation [3];
- If there is a disease mortality event, and in which time step this occurs;
- If tagging has been specified, when the tagging event occurs, how many fish by age or size class, in which member of the partition to put the tagged fish, and the tag shedding rates, if defined.

You then need to provide CASAL with details about how each process works. These processes are described individually in *KL comment:* Section 5.4 .

When defining the annual cycle, there are a number of errors can be made. Some of the less obvious ones are listed here. It is an error if:

- the sum of the proportions of the years natural mortality over time steps is not 1,
- in an age-based model, any element of `growth_props` is outside $[0, 1]$; or if `growth_props` is not 0 in the time step in which fish age; or if `growth_props` diminishes between consecutive time steps without age incrementation having taken place,
- in a size-based model, more than one growth episode occurs in the same time step, unless they involve different stocks,

area). If maturity is not in the partition, then the modeller may nevertheless know that all fish in the spawning area should be mature (i.e., because only mature fish are meant to migrate) but the model does not know this because maturity is not persistent. In this case the user can specify that the SSB is the total biomass in the area, rather than using the mature biomass.

[2] Fish growth in an age-based model is handled quite differently from a size-based model. The simplest option is to assume that the mean size of a fish is based on its age, rounded down to the next lowest whole number of years. So, for example, 2-year old fish have the same mean size whether they have just passed their 2nd birthday or whether they are about to turn 3. An alternative is to allow some fish growth between birthdays. You can do this using the `growth_props` parameter. This is a vector with one entry per time step. The mean size of fish of age a years (rounded down) in the *ith* time step is calculated as if their age was (a+`growth_props[i]`). So, if the first entry of `growth_props` is 0.5, then, in time step 1, the mean size of 2-year-old fish is calculated as if they were age 2.5. The default is `growth_props` = 0 (i.e., no growth between birthdays).

[3] Natural mortality and fishing mortality occurring in the same area and time step can be sequenced in two different ways. The first option is to apply half the natural mortality, then to apply the mortalities from all the fisheries instantaneously, then to apply the remaining half of the natural mortality. The second options is to use the Baranov catch equation, which implies that natural and fishing mortalities are simultaneous. We prefer the first option the calculations are more straightforward and the result typically about the same. However you can use Baranov if you want, except that we have not yet implemented the Baranov equation for multiple fisheries in the same area in the same time step. Whichever option you use is applied to all fisheries. More on this in Section 5.4.6.

- you want to use the Baranov equation and there is a time step that includes two or more fisheries in the same area.

4.5. Time sequences

The time sequence of the model is defined in two parts;

- Initialisation
- Run years
- Projection years

4.5.1. Annual cycle

The annual cycle is implemented as a set of processes that occur, in a user-defined order, within each year. Time-steps are used to break the annual cycle into separate components, and allow observations to be associated with different sets of processes. Any number of processes can occur within each time-step, in any order and can occur multiple times within each time-step. Note that time-steps are not implemented during the initialisation phases (effectively, there is only one time-step), and that the annual cycle in the initialisation phases can be different from that which is applied during the model years.

4.5.2. Initialisation

Model initialisation can occur in several phases, each of which iterates through a number of years carrying out the population processes defined for that phase. At the end of the initialisation step, `SAM` runs through the model years carrying out processes in the order defined in the annual cycle, and can evaluate expected values of observations in order to calculate likelihoods, project forward to determine future states, or simulate observations from the current state.

`SAM` initialises the initial equilibrium state as an iterative process: a general solution that initialises complex structured models can be difficult to implement using analytic techniques. However, initialising via iteration for a long-lived species with complex transitions can take many iterations and be slow to run. In `SAM`, we allow for user-defined multi-phased initialisation using iteration to allow the user to optimize models for speed. Each phase of the initialisation can involve any number of processes. Note that the length of the initialisation period may affect the model outputs, and that a period should be chosen to allow the population state to converge.

In addition, each initialisation process can optionally be stopped early if a user defined convergence criteria is met. For a set of user defined years in the initialisation phase, convergence is defined as met if the proportional absolute summed difference between the the state in year $t-1$ and the state in year t ($\widehat{\lambda}$) is less than λ where,

$$\widehat{\lambda} = \frac{\sum_i \sum_j |\text{element}(i,j)_t - \text{element}(i,j)_{t-1}|}{\sum_i \sum_j \text{element}(i,j)_t} \tag{4.1}$$

In each initialisation phase, the processes defined for that phase are carried out and used as the starting point for the following phase or, if it is the last phase, then the years that the model is run over. The first phase is always initialised with each element (i.e., each age and category) set at

zero. Note that this means that recruitment processes where the numbers of recruits is based on a stock recruitment or density dependant relationship will likely fail if used in the first phase of an initialisation.

The multi-phase iteration allows the user to determine if the initialisation has converged in a particular model run. Here, add an additional initialisation phase for, say, 1 year as the last initialisation phase (with the same processes applied). Then, using the initialisation reports (`@report[label].type=initialisation_phase`), print a copy of the partition just before and just after that phase. If the initialisation has converged to an equilibrium state, then the partition at both these time intervals will be the same.

Hence, for initialisation you need to define;

- The initialisation phases
- The number of years in each phase and the processes to apply in each

4.5.3. Model years

Following initialisation, the model then runs over a number of user-defined years. For this part of the model, the annual cycle can be broken into separate time-steps, and observations can be associated with the state of the model at the end of any time-step, i.e., likelihoods for particular observations are evaluated, if required, at the end of each time-step.

Processes are carried out in the order specified within each time-step, and can be the same or different to processes in other initialisation phases of the model. The run years define the years over which the model is to run and the annual cycle within each year. The model runs from the start of year `initial` and runs to the end of year `current`. The projection part then extends the run time up to the end of year `final`.

- The time-steps and the processes applied in each
- The initial year (i.e., the model start year)
- The current year (i.e., the model end year)
- The final year (i.e., the model projection end year)

4.5.4. Projections

`SAM` can project, from a set of parameter estimates, the state of the model into the future. In a projection run, the model is initialised and run through the model years from `initial` to the `current`. Then, the model is run from `current` to `final`.

4.6. Population processes

Population processes are those processes that change the population state of individuals. Processes produce changes in the model partition, by adding, removing or moving individuals between ages or categories. The population processes include recruitment, ageing, mortality events (e.g., natural and exploitation) and category transition processes (i.e., processes that move individuals between categories, while preserving their age structure). See Section 4 for a complete list of available processes.

Each of these processes is carried out in the user-defined prescribed order when initialising the model, and then for a user-defined order in each year in the annual cycle.

4.6.1. Recruitment

Recruitment processes are defined as process that introduces new individuals into the model. `SAM` implements two types of recruitment process, constant recruitment and Beverton-Holt recruitment (**?**).

In the recruitment processes, the number of individuals are added to a single age class within the partition, with the amount defined by the type of recruitment process and its function. If more than one category is defined, then the proportion of recruiting individuals to be added to each category is specified by the `proportions` parameter. For example, if recruiting to categories labelled male and female, then you might set the proportions as 0.5 and 0.5 respectively to denote that half of the recruits recruit to the male category and the remaining half to the female category.

For the constant and Beverton-Holt recruitment processes, the number of individuals following recruitment in year y is,

$$\text{element}(i,j) \leftarrow \text{element}(i,j) + p_j(R_y) \tag{4.2}$$

where age is the age defined as the recruitment age, p_j is the proportion to category k defined to have recruitment, n is the number of spatial locations where recruitment occurs, and the recruitment to each cell is scaled to be proportional to the value of the layer in that cell. See below for how R_y is determined in each of these cases.

Constant Recruitment

In the constant recruitment process the total number of recruits added each year is R_y, and is simply R_0, i.e.

$$R_y = R_0 \tag{4.3}$$

It is equivalent to a Beverton-Holt recruitment process where steepness is set equal to one ($h = 1$).

For example, to specify a constant recruitment process, where individuals are added to the category 'immature' at $age = 1$, and the number to add is $R_0 = 5 \times 10^5$, then the syntax is

```
@process Recruitment
type constant_recruitment
categories immature
proportions 1.0
R0 500000
age 1
```

Beverton-Holt recruitment

In the Beverton-Holt recruitment process the total number of recruits added each year is R_y, and is the product of the average recruitment R_0, the annual year class strength multiplier, YCS, and the stock-recruit relationship i.e.,

$$R_y = R_0 \times YCS_{y-\text{offset}} \times SR(SSB_{y-\text{offset}}) \tag{4.4}$$

where $offset$ is the number of years offset to link the year class with the year of spawning y, and SR is the Beverton-Holt stock-recruit relationship parametrised by the steepness h,

$$SR(SSB_y) = \frac{SSB_y}{B_0} \Big/ \left(1 - \frac{5h-1}{4h}\left(1 - \frac{SSB_y}{B_0}\right)\right) \tag{4.5}$$

Note that the Beverton-Holt recruitment process requires a value for B_0 and SSB_y to resolve the stock-recruitment relationship. Here, a derived quantity (see Section 4.7) must be defined that provides the annual SSB_y for the recruitment process. B_0 is then defined as the value of the SSB at the end of one of the initialisation phases. During initialisation the YCS multipliers are assumed to be equal to one, and recruitment that happens in the initialisation phases that occur before and during the phase when B_0 is determined is assumed to have steepness $h = 1$ (i.e. in those initialisation phases, recruitment is simply equal to R_0). Recruitment in the initialisation phases after the phase where B_0 was determined follow the Beverton-Holt stock-recruit relationship defined above. Recruits are then distributed across cells in proportion to the values in a numeric layer.

For example, assume a Beverton-Holt recruitment process, where individuals are added to the category 'immature' at $age = 1$, the number to add is $R_0 = 5 \times 10^5$. Then `SSB_Biomass` is a derived quantity that specifies the total spawning stock biomass, with B_0 the value of the derived quantity at the end of the initialisation phase labelled `phase1`. The YCS are standardised to have mean one in the period 1994 to 2004, and recruits enter into the model two years following spawning. Then the command specification is

```
@process Recruitment
type BH_recruitment
categories immature
proportions 1.0
R0 500000
steepness 0.75
age 1
B0 phase1
SSB SSB_Biomass
standardise_YCS_years 1994-2004
YCS_years 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006
YCS_values   1    1    1    1    1    1    1    1    1    1    1    1    1
SSB_offset 2
```

Note that if not specified, `SSB_offset` is set at the value of age. This corresponds to cases where recruitment happens after spawning. `SSB_offset` can be user-defined to a different value if needed — for example, if recruitment happens in a time-step before spawning, the offset will need to be specified as $age + 1$.

4.6.2. Ageing

The ageing process simply moves all individuals in the named categories to the next age class. The ageing process is defined as,

$$\text{element}(i, j) \leftarrow \text{element}(i, j-1) \tag{4.6}$$

except that in the case of the plus group (if defined),

$$\text{element}(i, age_{\max}) \leftarrow \text{element}(i, age_{\max}) + \text{element}(i, age_{\max-1}). \tag{4.7}$$

For example, to apply ageing to the categories `immature` and `mature`, then the syntax is,

```
@process Ageing
type ageing
categories immature mature
```

Note that ageing is *not* applied by SAM by default. As with other processes, SAM will not apply a process unless its defined and specified as a process within the annual cycle. Hence, it is possible to specify a model where a category is not aged. SAM will not check or otherwise warn if there is a category defined where ageing is not applied.

4.6.3. Mortality

Three types of mortality processes are permissible in SAM, constant rate, event and biomass-event. These processes remove individuals from the partition, either as a rate, as a total number (abundance), or as a biomass of individuals. SAM does not implement the Baranov catch equation or any other process where both natural and event mortality are applied simultaneously. To approximate concurrent natural and event mortality, the population processes must be defined to remove some natural mortality (e.g. as a constant), then some event mortality (e.g. fishing) in sequence. It is up to the user to specify how this happens.

Constant mortality rate

To specify a constant annual mortality rate ($M = 0.2$) for categories 'male' and 'female', then,

```
@process NaturalMortality
type constant_mortality_rate
categories male female
selectivities One One
M 0.2 0.2
```

Note that the mortality rate process requires a selectivity. To apply the same mortality rate over all age classes, use a selectivity defined as $S_i = 1.0$ for all ages i, e.g.

```
@selectivity One
type constant
c 1
```

Event and biomass-event mortality

The event mortality process and biomass mortality processes act in a similar manner, except that they remove a specified abundance (number of individuals) or biomass respectively, rather than applying mortality as a rate. However, the maximum abundance or biomass to remove is constrained by a maximum exploitation rate.

SAM removes as many individuals or as much biomass as it can while not exceeding the maximum exploitation rate. Event mortality processes require a penalty function to discourage parameter values that do not allow the defined number of individuals to be removed. Here, the model penalises those parameter estimates that result in an insufficient number of individuals in defined categories (after applying selectivities). See Section 5.8 for more information on specifying penalties.

For example, the event mortality applied to user-defined categories i, with the numbers removed at age j determined by a selectivity-at-age S_l is applied as follows:

First, calculate the vulnerable abundance for each category i in $1 \ldots I$ for ages $j = 1 \ldots J$ that are subject to event mortality,

$$V(i,j) = S(j)N(i,j) \tag{4.8}$$

And hence define the total vulnerable abundance V_{total} as,

$$V_{total} = \sum_i \sum_j V(i,j) \tag{4.9}$$

Hence the exploitation rate to apply is

$$U = \begin{cases} C/V_{total}, & \text{if } C/V_{total} \leq U_{max} \\ U_{max}, & \text{otherwise} \end{cases} \tag{4.10}$$

And the number removed R from each age j in category i is,

$$R(i,j) = UV(i,j) \tag{4.11}$$

For example, to specify fishing mortality based on catches given for each year, over categories 'immature' and 'mature', with selectivity 'FishingSel' and assuming a maximum possible exploitation rate of 0.7, then the syntax is

```
@process Fishing
type event_mortality
categories immature mature
years 2000 2001 2002 2003
U_max 0.70
selectivities FishingSel FishingSel
penalty event_mortality_penalty
```

4.6.4. Maturation

KL comment: Text from CASAL, need to rewrite as relevant to SAM

Maturation is the process in which immature fish become mature and are moved accordingly in the partition. See Section 5.11 for how to treat maturity when it is not a character in the partition.

You can specify a single maturation episode in each year, or you can have multiple maturations. Each episode can apply to one stock, or all stocks equally, and can be applied in one area, or all areas equally. Maturation rates are expressed as an ogive (and note that this ogive contains the rates of maturation, not the proportions of mature fish).

If you try to mature fish in an area where fish are constrained to be immature, CASAL will issue a warning, and will not mature those fish.

So, to specify each maturation episode, the following information is required:

- If it applies to only one stock, which is it?
- If it applies to only one area, which is it?
- The maturation rates, as an ogive, optionally by sex.

4.6.5. Migration

KL comment: text from CASAL. Rewrites required?

Migration is the process of moving fish from one area to another. It only occurs in multi-area models. You can specify any number of migrations occurring in each year. If two or more migrations are specified in the same time step then they take place in the order in which they are given.

A migration can involve only one stock in an area, or all stocks. You can migrate immature fish only, or mature fish only, or both. You can state that a given proportion of these fish migrate (constant across all age or size classes), or provide an ogive of proportions migrating by age or size class.

You cannot migrate fish to an area where their combination of characters is not allowed (CASAL errors out). So, for example, if moving fish to an area where only mature fish are allowed, you need to specify that only mature fish migrate.

CASAL currently supports two-wave migrations. These migrations consist of two waves in different time steps. If *pi* is the specified proportion of fish migrating from the *ith* partition element, proportion (`pwave` *pi*) will migrate in wave 1 and proportion $(1-\texttt{pwave})pi/(1-(\texttt{pwave}pi))$ will migrate in wave 2. Specify these as two separate migrations, give `pwave` for each, and specify that the first is a '1st wave' and that the second is a '2nd wave'. (No checking is currently carried out that there are two matching waves with the same parameters. Remember that to specify `pwave` for each, not `pwave` for the first and (1-`pwave`) for the second. If you want to estimate `pwave`, you need to set the `estimate.same` parameter to make sure that `pwave` takes the same value for both waves.)

CASAL also supports annual variation in migrations and density-dependent migrations. The annual variation allows the migration rate to be modified in a particular year by some factor F. For density dependent migrations, the rate depends on the fish abundance in the source area, the destination area, or both – so, you can encourage fish to move into an under populated area and/or out of an overpopulated area.

Both annual variation and density dependen migration rates are calculated via an odds ratio, and a single factor (F) is applied to all fish in a given migration in a given year, regardless of age, sex, etc. Now let $P^i_{a,b}(y)$ be the proportion of fish in element i of the partition which migrate from area a to area b in year y, prior to the application of an annual variation or density dependence. (These values depend on the migration rate, or ogive of migration rates, etc.) And let the corresponding odds be

$$O^i_{a,b}(y) = \frac{P^i_{a,b}(y)}{1-P^i_{a,b}(y)} \tag{4.12}$$

Then the effect of the annual variation or density dependence is to change the odds to

$$\vartheta^i_{a,b}(y) = O^i_{a,b}(y) \times F_{a,b}(y) \tag{4.13}$$

and hence the proportion of fish migrating to

$$\Pi^i_{a,b}(y) = \frac{\vartheta^i_{a,b}(y)}{1-\vartheta^i_{a,b}(y)} \tag{4.14}$$

For annually-varying migrations, the factor F is just $\exp(m_y)$, where m_y is the annual variation value

for year y. For density dependent migrations, F is calculated as follows. In each year y, for each density dependent migration from area a to area b

$$F_{a,b}(y) = \exp\left(-S\left(\frac{A_{a,y} - A_{a,0}}{A_{a,0}}\right) - D\left(\frac{A_{b,y} - A_{b,0}}{A_{b,0}}\right)\right) \tag{4.15}$$

where S is a number expressing the dependence on the abundance in the source area (negative values mean that fish are encouraged to leave an overpopulated area. Set $S = 0$ for no dependence); D is a number expressing the dependence on the abundance in the destination area (positive values mean that fish are encouraged to move to an under populated area – set $D = 0$ for no dependence); $A_{j,y}$ is the total abundance of all fish in area j, year y (with $y = 0$ meaning the unfished equilibrium level) just before the migration occurs.

Neither annual variations nor density dependence are applied during the calculation of the initial state. In the calculation of the initial state for a model with annually-varying migration, the above factor F is set to $\exp(\overline{m})$, where $\overline{m}$ is the mean of the annual variation values, m_y, over a user-specified range of years.

The specification of the annual cycle includes the time step, source area, and destination area of each migration. You also need to tell CASAL the following:

- If there are multiple stocks and only one stock migrates, which is it?
- Do only mature fish migrate, or immature fish, or both?
- If a proportion of these fish migrate (constant across age or size classes), what is it? Or, if fish migrate according to an ogive across age or size classes, what is it?
- Is density dependence applied? If so, what are the values of the density dependence parameters S and D?
- Is an annual variation applied? If so, what are the years (`annual_variation_years`) and values (`annual_variation_values`) of the annual variation, and what range of years should be used in calculating ?

Two-wave migrations require more details – see earlier.

4.6.5.1. Tag release events

4.6.5.2. Tag shedding rate

4.7. Derived quantities

4.8. Derived quantities by cell

4.9. Size-age relationship

The age-size relationship defines the size at age (and the weight at size, see Section 4.10) of individuals at age/category within the model. There are three size-age relationships available in `SAM`. The first is the naive no relationship (where each individual has size 1 irrespective of age). The second and third are the von-Bertalanffy and Schnute relationships respectively. The size-at-age relationship is used to determine the size frequency, given age, and then with the size-weight relationship, a weight-at-age of individuals within an age/category.

The three age-size relationships are,

None: where the size of each individual is exactly 1 for all ages, in which case the `none` size-weight relationship must also be used.

von Bertalanffy: where size at age is defined as,

$$\bar{s}(age) = L_\infty \left(1 - \exp\left(-k\left(age - t_0\right)\right)\right) \tag{4.16}$$

Schnute: where size at age is defined as,

$$\bar{s}(age) = \begin{cases} \left[y_1^b + \left(y_2^b - y_1^b\right)\dfrac{1-\exp\left(-a(age-\tau_1)\right)}{1-\exp\left(-a(\tau_2-\tau_1)\right)}\right]^{1/b}, & \text{if } a \neq 0 \text{ and } b \neq 0 \\ y_1 \exp\left[\ln\left(y_2/y_1\right)\dfrac{1-\exp\left(-a(age-\tau_1)\right)}{1-\exp\left(-a(\tau_2-\tau_1)\right)}\right], & \text{if } a \neq 0 \text{ and } b = 0 \\ \left[y_1^b + \left(y_2^b - y_1^b\right)\dfrac{age-\tau_1}{\tau_2-\tau_1}\right]^{1/b}, & \text{if } a = 0 \text{ and } b \neq 0 \\ y_1 \exp\left[\ln\left(y_2/y_1\right)\dfrac{age-\tau_1}{\tau_2-\tau_1}\right], & \text{if } a = 0 \text{ and } b = 0 \end{cases} \tag{4.17}$$

The von Bertalanffy curve is parameterised by L_∞, k, and t_0; the Schnute curve (**?**) by y_1 and y_2, which are the mean sizes at reference ages τ_1 and τ_2, and a and b (when $b = 1$, this reduces to the von Bertalanffy with $k = a$).

When defining size-at-age in `SAM`, you must also define a size-weight relationship (see Section 4.10 below).

4.9.0.3. Calculation of size-at-age (in an age-based model)

4.9.0.4. Interpolation of size-at-age

4.10. Size-weight relationship

There are two size-weight relationship,s available in `SAM`. The first is the naive no relationship. Here, the weight of an individual, regardless of size, is always 1. The second is the basic relationship.

The two size-weight relationships are,

- None: The size-weight relationship where

  $$\text{mean weight} = 1 \tag{4.18}$$

- Basic: The size-weight relationship where the mean weight w of an individual of size l is

  $$w = al^b \tag{4.19}$$

  Note that if a distribution of size-at-age is specified, then the mean weight is calculated over the distribution of sizes, and is

  $$w = (al^b)(1+cv^2)^{\frac{b(b-1)}{2}} \tag{4.20}$$

  where the cv is the c.v. of sizes-at-age. This adjustment is exact for lognormal distributions, and a close approximation for normal distributions if the c.v. is not large (Bull et al., 2012).

Be careful about the scale of a — this can easily be specified incorrectly. If the catch is in tonnes and the growth curve in centimetres, then a should be on the right scale to convert a length in centimetres to a weight in tonnes. Note that there are reports available that can be used to help check that the units specified are plausible (see Section 7).

4.10.0.5. Calculation of mean weight

4.11. Weightless model

4.12. Maturity, in models without maturing in the partition

4.13. Selectivities

A selectivity is a function with a different value for each age class (i.e., for each column of the partition). Selectivities are used throughout SAM to interpret observations (Section 5) or to modify the effects of processes on each age class (Section 4). SAM implements a number of different parametric forms, including logistic, knife edge, and double normal selectivities.

A selectivity is always defined to apply just to one category of the population (i.e, row of the partition). To apply the same selectivity to more than one category, then just repeat the selectivity for each category that it is applied to.

Note that selectivities are indexed by age, with indices from min_age to max_age. For example, you might have an age-based selectivity that was logistic with 50% selected at age 5 and 95% selected at age 7. This would be defined by the type=logistic with parameters $a_{50} = 5$ and $a_{to95} = (7-5) = 2$. Then the value of the selectivity at age $x = 7$ is 0.95 and the selectivity at $x = 3$ is 0.05.

Note that the function values for some choices of parameters for some selectivities can result in an computer numeric overflow error (i.e., the number calculated from parameter values is either too large or too small to be represented in computer memory). SAM implements range checks on some parameters to test for a possible numeric overflow error before attempting to calculate function values. For example, the logistic selectivity is implemented such that if $(a50-x)/ato_95 > 5$ then the value of the selectivity at $x = 0$, i.e., for $a50 = 5$, $ato_95 = 0.1$, then the value of the selectivity at $x = 1$, without range checking would be 7.1×10^{-52}. With range checking, that value is 0 (as $(a50x)/ato_95 = 40 > 5$).

The available selectivities are;

- Constant
- Knife-edge
- All values
- All values bounded
- Increasing
- Logistic
- Inverse logistic
- Logistic producing
- Double normal
- Double exponential
- Cubic spline

The available selectivities are described below.

4.13.1. constant

$$f(x) = C \tag{4.21}$$

The constant selectivity has the estimable parameter C.

4.13.2. knife_edge

$$f(x) = \begin{cases} 0, & \text{if } x < E \\ \alpha, & \text{if } x \geq E \end{cases} \tag{4.22}$$

The knife-edge ogive has the estimable parameter E and a scaling parameter α, where the default value of $\alpha = 1$

4.13.3. all_values

$$f(x) = V_x \tag{4.23}$$

The all-values selectivity has estimable parameters V_{low}, $V_{low+1} \ldots V_{high}$. Here, you need to provide the selectivity value for each age class.

4.13.4. all_values_bounded

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ V_x, & \text{if } L \leq x \leq H \\ V_H, & \text{if } x > H \end{cases} \tag{4.24}$$

The all-values-bounded selectivity has non-estimable parameters L and H. The estimable parameters are V_L, $V_{L+1} \ldots V_H$. Here, you need to provide an selectivity value for each age class from $L \ldots H$.

4.13.5. increasing

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ f(x-1) + \pi_x(\alpha - f(x-1)), & \text{if } L \leq x \leq H \\ f(\alpha), & \text{if } x \geq H \end{cases} \tag{4.25}$$

The increasing ogive has non-estimable parameters L and H. The estimable parameters are π_L, π_{L+1} $\ldots \pi_H$ (but if these are estimated, they should always be constrained to be between 0 and 1). α is a scaling parameter, with default value of $\alpha = 1$. Note that the increasing ogive is similar to the all-values-bounded ogive, but is constrained to be non-decreasing.

4.13.6. logistic

$$f(x) = \alpha / [1 + 19^{(a_{50} - x)/a_{to95}}] \tag{4.26}$$

The logistic selectivity has estimable parameters a_{50} and a_{to95}. α is a scaling parameter, with default value of $\alpha = 1$. The logistic selectivity takes values 0.5α at $x = a_{50}$ and 0.95α at $x = a_{50} + a_{to95}$.

4.13.7. inverse_logistic

$$f(x) = \alpha - \alpha / [1 + 19^{(a_{50} - x)/a_{to95}}] \tag{4.27}$$

The inverse logistic selectivity has estimable parameters a_{50} and a_{to95}. α is a scaling parameter, with default value of $\alpha = 1$. The logistic selectivity takes values 0.5α at $x = a_{50}$ and 0.95α at $x = a_{50} - a_{to95}$.

4.13.8. `logistic_producing`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ \lambda(L), & \text{if } x = L \\ (\lambda(x) - \lambda(x-1)) / (1 - \lambda(x-1)), & \text{if } L < x < H \\ 1, & \text{if } x \geq H \end{cases} \tag{4.28}$$

The logistic-producing selectivity has the non-estimable parameters L and H, and has estimable parameters a_{50} and a_{to95}. α is a scaling parameter, with default value of $\alpha = 1$. For category transitions, $f(x)$ represents the proportion moving, not the proportion that have moved. This selectivity was designed for use in an age-based model to model maturity. In such a model, a logistic-producing maturation selectivity will (in the absence of other influences) make the proportions mature follow a logistic curve with parameters a_{50}, a_{to95}.

4.13.9. `double_normal`

$$f(x) = \begin{cases} \alpha 2^{-[(x-\mu)/\sigma_L]^2}, & \text{if } x \leq \mu \\ \alpha 2^{-[(x-\mu)/\sigma_R]^2}, & \text{if } x \geq \mu \end{cases} \tag{4.29}$$

The double-normal selectivity has estimable parameters a_1, s_L, and s_R. α is a scaling parameter, with default value of $\alpha = 1$. It has values α at $x = a_1$, and 0.5α at $x = a_1 - s_L$ and $x = a_1 + s_R$.

4.13.10. `double_exponential`

$$f(x) = \begin{cases} \alpha y_0 (y_1/y_0)^{(x-x_0)/(x_1-x_0)}, & \text{if } x \leq x_0 \\ \alpha y_0 (y_2/y_0)^{(x-x_0)/(x_2-x_0)}, & \text{if } x > x_0 \end{cases} \tag{4.30}$$

The double-exponential selectivity has non-estimable parameters x_1 and x_2, and estimable parameters x_0, y_0, y_1, and y_2. α is a scaling parameter, with default value of $\alpha = 1$. It can be 'U-shaped'. Bounds for x_0 must be such that $x_1 < x_0 < x_2$. With $\alpha = 1$, the selectivity passes through the points (x_1, y), (x_0, y_0), and (x_2, y_2). If both y_1 and y_2 are greater than y_0 the selectivity is 'U-shaped' with minimum at (x_0, y_0).

4.13.11. `spline`

The spline selectivity implements a cubic spline that has non-estimable knots, and an estimable value for each knot. The cubic spline is either (i) a natural splines where the where the second derivatives are set to 0 at the boundaries, i.e., the values at the boundaries are horizontal, (ii) a spline with a fixed first derivative at the boundaries (linear, but not necessarily horizontal) and (iii) spline which turns into a parabola at the boundaries.

5. The estimation section

5.1. Role of the estimation section

check and confirm text
KL comment: This text from SPM, a rewrite of CASAL. OK to use?

The role of the estimation section is to define the tasks carried out by `SAM`:

1. Define the objective function (see Section 5.2)
2. Define the parameters to be estimated (see Section 5.3)
3. Calculate a point estimate, i.e., the maximum posterior density estimate (MPD) (see Section 5.4).
4. Calculate a posterior profile selected parameters, i.e., find, for each of a series of values of a parameter, allowing the other estimated parameters to vary, the minimum value of the objective function (see Section 5.5).
5. Generate an MCMC sample from the posterior distribution (see Section 5.6).
6. Calculate the approximate covariance matrix of the parameters as the inverse of the minimizer's approximation to the Hessian, and the corresponding correlation matrix (see Section 5.4).

The estimation section defines the objective function, parameters of the model, and the method of estimation (point estimates, Bayesian posteriors, profiles, etc.). The objective function is based on a goodness-of-fit measure of the model to observations, priors and penalties. See the observation section for a description of the observations, likelihoods, priors and penalties.

5.2. The objective function

check and confirm text
KL comment: This text from SPM. Does not cover all text in S6.7 of CASAL, e.g. max likelihood. OK to use? Additions required?

In Bayesian estimation, the objective function is a negative log-posterior,

$$Objective(p) = -\sum_i \log\left[L\left(\mathbf{p}|O_i\right)\right] - \log\left[\pi\left(\mathbf{p}\right)\right] \tag{5.1}$$

where π is the joint prior density of the parameters p.

The contribution to the objective function from the likelihoods are defined in Section 6.1. In addition to likelihoods, priors (see Section 5.7) and penalties (see Section 5.8) are components of the objective function.

Penalties can be used to ensure that the exploitation rate constraints on mortality events (i.e., fisheries) are not breached (otherwise there is nothing to prevent the model from having abundances so low that the recorded mortalities could not have been taken), penalties on category transitions (to ensure there are enough individuals to move), and possibly penalties to encourage estimated values to be similar or smooth, etc.

5.3. Specifying the parameters to be estimated

check and confirm text
KL comment: This text from SPM. Does not cover all the text in CASAL, e.g. catchabilities. OK to use? Additions required?

The estimable parameters that will be estimated are defined using `@estimate` commands (see Section 9). An `@estimate` command-block looks like,

```
@estimate process[MyRecruitment].r0
lower_bound 1000
upper_bound 100000
prior uniform
```

See Section 3.5.5 for instructions on how to generate the parameter name. At least one parameter to be estimated if doing an estimation, profile, or MCMC run. Initial values for the parameters to be estimated will still need to be provided, and these are used as the starting values for the minimiser. However, these may be overwritten if you provide a set of alternative starting values (i.e., using `sam -i`, see Section 3.4).

All parameters are estimated within bounds. For each parameter to be estimated, you need to specify the bounds and the prior (Section 5.7). Note that the bounds and prior for each parameter refer to the values of the parameters, not the actual values resulting from the application of the parameter to an equation. If estimating only some elements of a vector, either define the elements of the vector to be estimated (see 3.5.5) or fix the others by setting the bounds equal.

The estimation of parameters can be phased. Here, some of the estimated parameters are initially held fixed, and a minimisation is carried out. Next, some or all of the remaining parameters that were initially held fixed are freed, and another minimisation is carried out. This process continues until all phases have been carried out.

5.4. Point estimation

check and confirm text
KL comment: This text from SPM. A rewrite of what's in CASAL and set out differntly. OK to use? Additions required?

Point estimation is invoked with `sam -e`. Mathematically, it is an attempt to find a minimum of the objective function. SPM has two algorithms for solving (minimising) the optimisation problem. The first uses a quasi-Newton minimiser built which is a slightly modified implementation of the main algorithm of Dennis Jr. & Schnabel (Dennis Jr and Schnabel, 1996), while the second uses a genetic algorithm developed by Storn & Price (Storn and Price, 1995), the differential evolution minimiser . However, the second minimiser does not produce an estimate of the covariance matrix, and hence cannot be used to start an MCMC.

5.4.1. The numerical differences minimiser

check and confirm text
The minimiser has three kinds of (non-error) exit status:

1. Successful convergence (suggests you have found a local minimum, at least).

2. Convergence failure (you have not reached a local minimum, though you may deem yourself to be 'close enough' at your own risk).
3. Convergence unclear (the minimiser halted but was unable to determine if convergence occurred. You may be at a local minimum, although you should check by restarting the minimiser at the final values of the estimated parameters).

You can choose the maximum number of quasi-Newton iterations and objective function evaluations allotted to the minimiser. If it exceeds either limit, it exits with a convergence failure. We recommend large numbers of evaluations and iterations (at least the defaults of 300 and 1000) unless you successfully reach convergence with less. You can also specify an alternative starting point of the minimiser using `sam -i`.

We want to stress that this is a local optimisation algorithm trying to solve a global optimisation problem. What this means is that, even if you get a 'successful convergence' message, your solution may be only a local minimum, not a global one. To diagnose this problem, try doing multiple runs from different starting points and comparing the results, or doing profiles of one or more key parameters and seeing if any of the profiled estimates finds a better optimum than than the original point estimate.

The approximate covariance matrix of the estimated parameters can be calculated as the inverse of the minimiser's approximation to the Hessian, and the corresponding correlation matrix is also calculated. Be aware that

- the Hessian approximation develops over many minimiser steps, so if the minimiser has only run for a small number of iterations the covariance matrix can be a very poor approximation
- the inverse Hessian is not a good approximation to the covariance matrix of the estimated parameters, and may not be useful to construct, for example, confidence intervals.

Also note that if an estimated parameter has equal lower and upper bounds, it will have entries of '0' in the covariance matrix and `NaN` or `-1.#IND` (depending on the operating system) in the correlation matrix.

5.4.2. The differential evolution minimiser

check and confirm text

The differential evolution minimiser is a simple population based, stochastic function minimizer, but is claimed to be quite powerful in solving minimisation problems. It is a method of mathematical optimization of multidimensional functions and belongs to the class of evolution strategy optimizers. Initially, the procedure randomly generates and evaluates a number of solution vectors (the population size), each with p parameters. Then, for each generation (iteration), the algorithm creates a candidate solution for each existing solution by random mutation and uniform crossover. The random mutation generates a new solution by multiplying the difference between two randomly selected solution vectors by some scale factor, then adding the result to a third vector. Then an element-wise crossover takes place with probability P_{cr}, to generate a potential candidate solution. If this is better than the initial solution vector, it replaces it, otherwise the original solution is retained. The algorithm is terminated after either a predefined number of generations (`max_generations`) or when the maximum difference between the scaled individual parameters from the candidate solutions from all populations is less than some predefined amount `tolerance`.

The differential evolution minimiser can be good at finding global minimums in surfaces that may have local minima. However, the speed of the minimiser, and the ability to find a good minima

depend on the number of initial 'populations'. Some authors recommend that the number of populations be set at about $10 * p$, where p is the number of free parameters. However, depending on your problem, you may find that you may need more, or that less will suffice.

We note that there is no proof of convergence for the differential evolution solver, but several papers have found it to be an efficient method of solving multidimensional problems. Our (limited) experience suggests that it can often find a better minima and may be faster or longer (depending on the actual model specification) at finding a solution when compared with the numerical differences minimiser. Comparisons with auto-differentiation minimisers or other more sophisticated algorithms have not been made.

5.5. Posterior profiles

check and confirm text
KL comment: This text from SPM. A rewrite of what's in CASAL, except for par. 5 and 7. OK to use? Additions required?

If profiles are requested `sam -p`, SAM will first calculate a point estimate. For each scalar parameter or, in the case of vectors or selectivities, the element of the parameter to be profiled, SAM will fix its value at a sequence of n evenly spaced numbers ($step$) between a specified lower and upper bounds l and u, and calculate a point estimate at each value.

By default $step = 10$, and $(l,u) =$ (lower bound on parameter plus $(range/(2n))$, upper bound on parameter less $(range/(2n))$. Each minimisation starts at the final parameter values from the previous resulting value of the parameter being profiled. SAM will report the objective function for each parameter value. Note that an initial point estimate should be compared with the profile, not least to check that none of the other points along the profile have a better objective function value than the initial 'minimum'.

You specify which parameters are to be profiled, and optionally the number of steps, lower bound, and upper bound for each. In the case of vector parameters, you will also need to specify the element of the vector being profiled.

You can also supply the initial starting point for the estimation using `sam -i file` — this may improve the minimiser performance for the profiles.

If you get an implausible profile, it may be a result of not using enough iterations in the minimiser or a poor choice of minimiser control variables (e.g., the minimiser tolerance). It also may be useful to try both if the minimisers in SAM and compare the results.

5.6. Bayesian estimation

check and confirm text
KL comment: This text is from SPM and is nearly verbatim S6.5 in CASASL, but two large sections exluded: ...request covariate matrix change adaptively... and from ...multivariate t dist... onwards. OK to use/ Additions required?

SAM can use a Monte Carlo Markov Chain (MCMC) to generate a sample from the posterior distribution of the estimated parameters `sam -m` and output the sampled values to a file (optionally keeping only every nth set of values).

As SAM has no post-processing capabilities. SAM cannot produce MCMC convergence diagnostics (use a package such as BOA) or plot/summarize the posterior distributions of the output quantities (for example, using a general-purpose statistical or spreadsheet package such as S-Plus, **R**, or

Microsoft Excel).

Bayesian methodology and MCMC are both large and complex topics, and we do not describe either properly here. See Gelman et al. (1995) and Gilks et al. (1994) for details of both Bayesian analysis and MCMC methods. In addition, see Punt & Hilborn (2001) for an introduction to quantitative fish stock assessment using Bayesian methods.

This section only briefly describes the MCMC algorithms used in `SAM`. See Section 9.3 for a better description of the sequence of `SAM` commands used in a full Bayesian analysis.

`SAM` uses a straightforward implementation of the Metropolis-Hastings algorithm (Gelman et al., 1995, Gilks et al., 1994). The Metropolis-Hastings algorithm attempts to draw a sample from a Bayesian posterior distribution, and calculates the posterior density π, scaled by an unknown constant. The algorithm generates a 'chain' or sequence of values. Typically the beginning of the chain is discarded and every Nth element of the remainder is taken as the posterior sample. The chain is produced by taking an initial point x_0 and repeatedly applying the following rule, where x_i is the current point:

- Draw a candidate step s from a proposal distribution J, which should be symmetric i.e., $J(-s) = J(s)$.
- Calculate $r = min(\pi(x_i + s)/\pi(x_i), 1)$.
- Let $x_i + 1 = x_i + s$ with probability r, or x_i with probability $1 - r$.

An initial point estimate is produced before the chain starts, which is done so as to calculate the approximate covariance matrix of the estimated parameters (as the inverse Hessian), and may also be used as the starting point of the chain.

The user can specify the starting point of the point estimate minimiser using `sam -i`. Don't start it too close to the actual estimate (either by using `sam -i`, or by changing the initial parameter values in input configuration file) as it takes a few iterations to form a reasonable approximation to the Hessian.

There are two options for the starting point of the Markov Chain:

- Start from the point estimate.
- Start from a random point near the point estimate (the point is generated from a multivariate normal distribution, centred on the point estimate, with covariance equal to the inverse Hessian times a user-specified constant). This may be useful if the chain gets 'stuck' at the point estimate, or if you wish to generate multiple chains from for later MCMC diagnostic tests.
- Start from a point specified by the user with `sam -i` *(was NYI, to be included?)*

The chain moves in natural space, i.e., no transformations are applied to the estimated parameters. The default proposal distribution is a multivariate t centred on the current point, with covariance matrix equal to a matrix based on the approximate covariance produced by the minimiser, times some stepsize factor. The following steps define the initial covariance matrix of the proposal distribution:

- The covariance matrix is taken as the inverse of the approximate Hessian from the quasi-Newton minimiser.
- The covariance matrix is modified so as to decrease all correlations greater than `@mcmc.max_correlation` down to `@mcmc.max_correlation`, and similarly to increase all correlations less than `-@mcmc.max_correlation` up to `-@mcmc.max_correlation` (the

`@mcmc.max_correlation` parameter defaults to 0.8). This should help to avoid getting 'stuck' in a lower-dimensional subspace.

- The covariance matrix is then modified either by,
  - if `@mcmc.adjustment_method=covariance`: that if the variance of the ith parameter is non-zero and less than `@mcmc.min_difference` times the difference between the parameters' lower and upper bound, then the variance is changed, without changing the associated correlations, to $k = \text{min\_diff}(upper\_bound_i - lower\_bound_i)$. This is done by setting

    $$\text{Cov}(i,j)' = \text{sqrt}(k)\,\text{Cov}(i,j)/\text{sd}(i)$$

    for $i \neq j$, and $\text{var}(i)' = k$
  - if `@mcmc.adjustment_method=correlation`: that if the variance of the ith parameter is non-zero and less than `@mcmc.min_difference` times the difference between the parameters' lower and upper bound, then its variance is changed to $k = min\_diff(upper\_bound_i - lower\_bound_i)$. This differs from (i) above in that the effect of this option is that it also modifies the resulting correlations between the ith parameter and all other parameters.

  This allows each estimated parameter to move in the MCMC even if its variance is very small according to the inverse Hessian. In both cases, the `@mcmc.min_difference` parameter defaults to 0.0001.
- The `@mcmc.stepsize` (a scalar factor applied to the covariance matrix to improve the acceptance probability) is chosen by the user. The default is $2.4d^{-0.5}$ where d is the number of estimated parameters, as recommended by Gelman et al. (Gelman et al., 1995). However, you may find that a smaller value may often be better.

The proposal distribution can also change adaptively during the chain, using two different mechanisms. Both are offered as means of improving the convergence properties of the chain. It is important to note that any adaptive behaviour must finish before the end of the burn-in period, i.e., the proposal distribution must be finalised before the kept portion of the chain starts. The adaptive mechanisms are as follows:

1. You can request that the stepsize change adaptively at one or more sample numbers. At each adaptation, the stepsize is doubled if the acceptance rate since the last adaptation is more than 0.5, or halved if the acceptance rate is less than 0.2. (See Gelman et al. (Gelman et al., 1995) for justification.)
2. You can request that the entire covariance matrix change adaptively at one or more sample numbers. At each adaptation, it is replaced with a matrix based on the sample covariance of an earlier section of the chain. The theory here is that the covariance of a portion of chain could potentially be a better estimate of the covariance of the posterior distribution than the inverse Hessian. *(was NYI, to be included?)*

The procedure used to choose the sample of points is as follows. First, all points on the chain so far are taken. All points in an initial user-specified period are discarded. The assumption is that the chain will have started moving during this period - if this is incorrect and the chain has still not moved by the end of this period, it is a fatal error and `SAM` stops. The remaining set of points must contain at least some user-specified number of transitions - if this is incorrect and the chain has not moved this often, it is again a fatal error. If this test is passed, the set of points is systematically sub-sampled down to 1000 points (it must be at least this long to start with). *(was NYI, to be included?)*

The variance-covariance matrix of this sub-sample of chain is calculated. As above, correlations greater than `@mcmc.max_correlation` are reduced to `@mcmc.max_correlation`, correlations less than `@mcmc.max_correlation` are increased to `@mcmc.max_correlation`, and very small non-zero variances are increased (`@mcmc.covariance_adjustment` and `@mcmc.min_difference`. The result is the new variance-covariance matrix of the proposal distribution. *(was NYI, to be included?)*

The stepsize parameter is now on a completely different scale, and must be reset. It is set to a user-specified value (which may or may not be the same as the initial stepsize). We recommend that some of the stepsize adaptations are set to occur after this, so that the stepsize can be readjusted to an appropriate value which gives good acceptance probabilities with the new matrix. *(was NYI, to be included?)*

All modified versions of the covariance matrix are printed to the standard output, but only the initial covariance matrix (inverse Hessian) is saved to the objectives file. The number of covariance modifications by each iteration is recorded as a column on the objectives file. *(was NYI, to be included?)*

The probability of acceptance for each jump is 0 if it would move out of the bounds, or 1 if it improves the posterior, or (new posterior/old posterior) otherwise. You can specify how often the position of the chain is recorded using the keep parameter. For example, with keep 10, only every 10th sample is recorded.

You have the option to specify that some of the estimated parameters are fixed during the MCMC. If the chain starts at the point estimate or at a random location, these fixed parameters are set to their values at the point estimate.

If you specify the start of the chain using `sam -i`, these fixed parameters are set to the values in the file. *(was NYI, to be included?)*

The posterior sample can be used for (projections (Section 4.5.4)*(was NYI, to be included?)*) or simulations (Section 6.7) with the values supplied using `sam -i file`.

(following from CASAL, to be included?)

```
A multivariate t distribution is available as an alternative to the multivariate normal
    proposal distribution. If you request multivariate t proposals, you may want to change the
     degrees of freedom from the default of 4. As the degrees of freedom decrease, the t
    distribution becomes more heavy tailed. This may lead to better convergence properties.

Having produced one or more Markov chains and looked at the diagnostics, reload all the chain
    output files into CASAL and use them to generate a single posterior sample (using -C). At
    this stage, the first burn_in iterations for each chain are discarded (so, with keep 10,
    burn_in 1000, the first 1000 recorded samples are discarded for each chain). Unless a very
     large value of keep was originally chosen, it will be necessary to further reduce the
    size of the posterior sample (possibly down to several hundred) such that it can be
    analysed in a reasonable amount of time. This is done by sub-sampling. You specify the
    size of the sub-sample to be produced (or else no sub-sampling is done). You have the
    option to generate a systematic sub-sample (i.e., every nth point is kept) or a random sub
    -sample (the former is recommended except with prior re-weighting, when the latter must be
     used).

Given a posterior (sub)sample, CASAL can calculate a list of output quantities for each sample
     point (see Section 7.2). These quantities can be dumped into a file (using casal -v) and
    read into an external software package where the posterior distributions can be plotted
    and/or summarised.

The posterior sample can also be used for projections (Section 7.3) and stochastic yield
    calculations (Section 7.5). The advantage of this is that the parameter uncertainty, as
    expressed in your posterior distribution, can be included into the risk and yield
    estimates.
```

```
It is possible to investigate the results that would have been obtained if a different prior
    had been specified This is called prior re-weighting and is done by calculating the ratio
    of the new prior to the original prior for each point in the posterior sample, then using
    these ratios as probability weights when generating a random (not systematic) sub-sample
    with casal -C. Prior re-weighting is applicable only if the new prior is zero in every
    part of the parameter space for which the original prior was zero. Also, it is likely to
    be numerically unstable unless the new prior is very small in every part of the parameter
    space for which the original prior was very small.
```

5.7. Priors

In a Bayesian analysis, you need to give a prior for every parameter that is being estimated. There are no default priors.

Note that when some of these priors are parameterised in terms of mean, c.v., and standard deviation, these refer to the parameters of the distribution before bounds are applied. The moments of the prior after the bounds are applied may differ.

SAM has the following priors (expressed in terms of their contribution to the objective function):

1. Uniform

$$-\log(\pi(p)) = 0 \tag{5.2}$$

2. Uniform-log (i.e., $\log(p) \sim$ uniform)

$$-\log(\pi(p)) = \log(p) \tag{5.3}$$

3. Normal with mean μ and c.v. c

$$-\log(\pi(p)) = 0.5\left(\frac{p-\mu}{c\mu}\right)^2 \tag{5.4}$$

4. Normal with mean μ and standard deviation σ

$$-\log(\pi(p)) = 0.5\left(\frac{p-\mu}{\sigma}\right)^2 \tag{5.5}$$

5. Lognormal with mean μ and c.v. c

$$-\log(\pi(p)) = \log(p) + 0.5\left(\frac{\log(p/\mu)}{s} + \frac{s}{2}\right)^2 \tag{5.6}$$

where s is the standard deviation of $\log(p)$ and $s = \sqrt{\log(1+c^2)}$.

(following from CASAL, to be included?)

```
6. Normal-log with log(p) having mean m and standard deviation s,
```

6. Beta with mean μ and standard deviation σ, and range parameters A and B

$$-\log(\pi(p)) = (1-m)\log(p-A) + (1-n)\log(B-p) \tag{5.7}$$

where $\nu = \frac{\mu-A}{B-A}$, and $\tau = \frac{(\mu-A)(B-\mu)}{\sigma^2} - 1$ and then $\mu = \tau\nu$ and $n = \tau(1-\nu)$. Note that the beta prior is undefined when $\tau \leq 0$.

(following from CASAL, to be included?)

```
Vectors of parameters can be independently (but not necessarily identically) distributed
    according to any of the above forms, in which case the joint negative-log-prior for the
    vector is the sum of the negative-log-priors of the components. Values of each parameter
    need to be specified for each element of the vector.

In addition, for a vector p of n identically distributed parameters (for example, YCS) the
    following priors are allowed:

1. Multivariate normal from a stationary AR(1) process with parameters
.
.
.

2. Multivariate normal-log, where log(p) forms a stationary AR(1) process as per 1. above,
    with parameters
.
.
.
3. Multivariate normal-log with mean 1, where E(pi)=1 and log(p) forms a stationary AR(1)
    process as for the multivariate normal above, with parameters
.
.
.
```

5.8. Penalties

check and confirm text
KL comment: This text from SPM, currently iSAM coded as described here. CASAL documentation (S6.7.6) includes 11 penalties. Will this be included?

Penalties can be used to encourage or discourage parameter values or model outputs that are unlikely to be sensible, by adding a penalty to the objective function. For example, parameter estimates that do not allow a known mortality event to remove enough individuals from the population can be discouraged with an event mortality penalty. `SAM` requires penalty functions for processes that move or shift a *number* of individuals between categories or from the partition.

For most penalties, you need to specify a multiplier, and the objective function is increased by this multiplier times the penalty value as described below. In some cases you will need to make the multiplier quite large to prohibit some model behaviour.

Currently, the penalties for the processes `@process[label].type=event_mortality` and `@process[label].type=category_transition` are the only penalties implemented.

For both of these processes, two types of penalty can be defined, natural scale (the default) and log scale. Both of these types add a penalty value of the squared difference between the observed value

(i.e., the actual number of individuals to be removed in an event mortality process or the actual number of individuals to shift in a category transition process), and the number that were moved (if less than or equal), times the penalty multiplier.

The natural scale penalty just uses at the squared difference on a natural scale, while the log scale penalty uses the squared difference of the logged values.

6. The observation section

6.1. Observations and likelihoods

Observations are typically supplied as observations at an instance in time, over some spatially aggregated area. Time series of observations can be supplied as separate observations for each year or point in time.

`SAM` allows the following types of observations;

- Observations of proportions by age class within categories
- Observations of proportions between categories within age classes
- Relative and absolute abundance/biomass observations

The definitions for each type of observation are described below, including how the observed values should be supplied, how `SAM` calculates the expected values, and the likelihoods that are available for each type of observation.

`SAM` evaluates the observations at the end of a time-step (i.e., after all of the processes for that time-step have been applied). However, the observation can be applied to the abundance at the start of a time-step or part-way through a time-step by the use of the `proportion_time_step` subcommand.

By default (i.e., if `proportion_method = mean`), the partition at some point p during the time-step is then evaluated as the weighted sum between the start and end of the time-step, i.e, for any element i in the partition, $n_i = (1-p)n_i^{start} + pn_i^{end}$. Note that it may not be sensible to use a value other than one, depending on the processes that happen during the time-step (for example, if the time-step contains an ageing process).

If the `proportion_method = difference`, then the observation is of the *difference* between the population state at the start of the time-step and the end. This can be used to generate expected values for observations of, for example removals due to a mortality event, by only having a single process in the time-step. In this case, the proportion_time_step is simply a multiplier of the population state.

6.2. Proportions-at-age observations

Proportions-at-age observations are observations of either the relative number of individuals at age or relative biomass at age, via some selectivity.

The observation is supplied for a given year and time-step, for some selected age classes of the population (i.e., for a range of ages multiplied by a selectivity), for categories aggregated over a set of spatial cells. Note that the categories defined in the observations must have an associated selectivity, defined by `selectivities`.

The age range must be ages defined in the partition (i.e., between `@model.min_age` and `@model.max_age` inclusive), but the upper end of the age range can optionally be a plus group — which must be either the same or less than the plus group defined for the partition.

Proportions-at-age observations can be supplied as;

1. a set of proportions for a single category,
2. a set of proportions for multiple categories, or
3. a set of proportions across aggregated categories.

For example, for a model with the two categories *male* and *female*, we might supply either (i) a

set of proportions for a single category (i.e., males) within each age class; (ii) a set of proportions describing the proportions of individuals within each age class across multiple categories (i.e., males and females) simultaneously, or (iii) a set of proportions for the total number of individuals over the aggregated categories (i.e., males + females) combined, within each age class.

The way the categories of the observation are defined specifies which of these alternatives are used. It is also possible to have an observation with multiple and aggregated categories simultaneously.

Proportions-at-age for a single category

This form of defining the observation is the simplest, and is used to model a set of proportions of a single category by age class. For example, to specify that the observations are of the proportions of male within each age class, then the subcommand `categories` for the `@observation[label].type=proportion_by_age` command is,

```
categories male
```

`SAM` then expects that there will be a single vector of proportions supplied, with one proportion for each age class within the defined age range, and that these proportions sum to one.

For example, if the age range was 3 to 10, then 8 proportions should be supplied (one proportion for each of the the ages 3, 4, 5, 6, 7, 8, 9, and 10). The expected values will be the expected proportions of males within each of these age classes (after ignoring any males aged less than 3 or older than 10), after applying a selectivity at the year and time-step specified. The supplied vector of proportions (i.e., in this example, the 8 proportions) must sum to one, which is evaluated with a default tolerance of 0.001.

The observations must be also supplied using all or some of the the values of defined by some *categorical* layer. `SAM` calculates the expected values by summing over the defined ages (via the age range and selectivity) and categories for those spatial cells where the categorical layer has the same value as defined for each vector of observations.

For example, in a 2×2 spatial model a categorical layer (e.g., with label Area) may define that cells $(1,1)$ and $(1,2)$ have value *A* and cells $(2,1)$ and $(2,2)$ have value *B*, i.e.,

```
@layer Area
type categorical
data A A
data B B
```

The observations for those spatial cells where the categorical layer has value *A* would be,

```
@observation MyProportions
type proportions_at_age
layer Area
...
categories male
min_age 1
max_age 5
obs A 0.01 0.09 0.20 0.30 0.40
...
```

Or, for both *A* and *B* as,

```
@observation MyProportions
type proportions_at_age
layer Area
...
categories male
min_age 1
max_age 5
obs A 0.01 0.09 0.20 0.30 0.40
obs B 0.02 0.06 0.12 0.25 0.55
...
```

Note that to have an observation for each individual spatial cell in a model, then define a categorical layer that has a single, unique value for each spatial cell for use in the observation.

Proportions-at-age for multiple categories

This form of the observation extends the idea above for multiple categories. It is used to model a set of proportions over several categories by age class. For example, to specify that the observations are of the proportions of male or females within each age class, then the subcommand `categories` for the `@observation[label].type=proportion_by_age` command is,

```
categories male female
```

`SAM` then expects that there will be a single vector of proportions supplied, with one proportion for each category and age class combination, and that these proportions sum to one.

For example, if there were two categories and the age range was 3 to 10, then 16 proportions should be supplied (one proportion for each of the the ages 3, 4, 5, 6, 7, 8, 9, and 10, for each category male and female). The expected values will be the expected proportions of males and within each of these age classes (after ignoring those aged less than 3 or older than 10), after applying a selectivity at the year and time-step specified. The supplied vector of proportions (i.e., in this example, the 16 proportions) must sum to one, which is evaluated with a default tolerance of 0.001.

For example, using the earlier spatial model with a categorical layer that has label Area, the observations for those spatial cells where the categorical layer has value *A* would be,

```
@observation MyProportions
type proportions_at_age
layer Area
...
categories male female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20 0.01 0.05 0.15 0.20 0.03
obs B 0.02 0.06 0.10 0.21 0.18 0.02 0.05 0.15 0.20 0.01
...
```

Proportions-at-age across aggregated categories

This form of the observation extends the idea above, but allows categories to be aggregated before the proportions are calculated. It is used to model a set of proportions from several categories that have been combined by age class. To indicate that two (or more) categories are to be aggregated, separate them with a '+' symbol. For example, to specify that the observations are of the proportions of male and females combined within each age class, then the subcommand `categories` for the `@observation[label].type=proportion_by_age` command is,

```
categories male + female
```

SAM then expects that there will be a single vector of proportions supplied, with one proportion for each age class, and that these proportions sum to one.

For example, if there were two categories and the age range was 3 to 10, then 8 proportions should be supplied (one proportion for each of the the ages 3, 4, 5, 6, 7, 8, 9, and 10, for the sum of males and females within each age class). The expected values will be the expected proportions of males + females within each of these age classes (after ignoring those aged less than 3 or older than 10), after applying a selectivity at the year and time-step specified. The supplied vector of proportions (i.e., in this example, the 16 proportions) must sum to one, which is evaluated with a default tolerance of 0.001.

For example, using the earlier spatial model with a categorical layer that has label Area, the observations for those spatial cells where the categorical layer has value *A* would be,

```
@observation MyProportions
type proportions_at_age
layer Area
...
categories male + female
min_age 1
max_age 5
obs A 0.02 0.13 0.25 0.30 0.30
obs B 0.02 0.06 0.18 0.35 0.39
...
```

The later form can then be extended to include multiple categories, or multiple aggregated categories. For example, to describe proportions for the three groups: immature males, mature males, and all females (immature and mature females added together) for ages 1–4, a total of 12 proportions are required

```
@observation MyProportions
type proportions_at_age
layer Area
...
categories male_immature male_mature female_immature + female_mature
min_age 1
max_age 4
obs A 0.05 0.15 0.15 0.05 0.02 0.03 0.08 0.04 0.05 0.15 0.15 0.08
...
```

6.2.1. Likelihoods for proportions-at-age observations

SAM implements two likelihoods for proportions-at-age observations, the multinomial likelihood and the lognormal likelihood.

The multinomial likelihood

For the observed proportions at age O_i for age classes i, with sample size N, and the expected proportions at the same age classes E_i, the negative log-likelihood is defined as;

$$-\log(L) = -\log(N!) + \sum_i \log((NO_i)!) - NO_i \log(Z(E_i, \delta)) \tag{6.1}$$

where $\sum_i O_i = 1$ and $\sum_i E_i = 1$. $Z(\theta, \delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta, \delta)$ is defined as,

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta/\delta), & \text{otherwise} \end{cases} \tag{6.2}$$

The default value of δ is 1×10^{-11}.

The lognormal likelihood

For the observed proportions at age O_i for age classes i, with c.v. c_i, and the expected proportions at the same age classes E_i, the negative log-likelihood is defined as;

$$-\log(L) = \sum_i \left(\log(\sigma_i) + 0.5 \left(\frac{\log(O_i / Z(E_i, \delta))}{\sigma_i} + 0.5\sigma_i \right)^2 \right) \tag{6.3}$$

where

$$\sigma_i = \sqrt{\log\left(1 + c_i^2\right)} \tag{6.4}$$

and the c_i's are the c.v.s for each age class i, and $Z(\theta, \delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta, \delta)$ is defined as,

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta/\delta), & \text{otherwise} \end{cases} \tag{6.5}$$

The default value of δ is 1×10^{-11}.

6.3. Proportions-by-category observations

Proportions-by-category observations are observations of either the relative number of individuals between categories within age classes, or relative biomass between categories within age classes.

The observation is supplied for a given year and time-step, for some selected age classes of the population (i.e., for a range of ages multiplied by a selectivity), for categories aggregated over a set of spatial cells.

The age range must be ages defined in the partition (i.e., between `@model.min_age` and `@model.max_age` inclusive), but the upper end of the age range can optionally be a plus group — which may or may not be the same as the plus group defined for the partition.

Proportions-by-category observations can be supplied for any set of categories as a proportion of themselves and any set of additional categories. For example, for a model with the two categories *male* and *female*, we might supply observations of the proportions of males in the population at each age class. The subcommand `categories` defines the categories for the numerator in the calculation of the proportion, and the subcommand `categories2` supplies the additional categories to be used in the denominator of the calculation. In addition, each category must have an associated selectivity, defined by `selectivities` for the numerator categories and `selectivities2` for the additional categories used in the denominator, e.g.,

```
categories male
```

```
categories2 female
selectivities male-selectivity
selectivities2 female-selectivity
```

defines that the proportion of males in each age class as a proportion of males + females. SAM then expects that there will be a vector of proportions supplied, with one proportion for each age class within the defined age range, i.e., if the age range was 3 to 10, then 8 proportions should be supplied (one proportion for each of the the ages 3, 4, 5, 6, 7, 8, 9, and 10). The expected values will be the expected proportions of male to male + female within each of these age classes, after applying the selectivities at the year and time-step specified.

The observations must be supplied using all or some of the values defined by a categorical layer. SAM calculates the expected values by summing over the ages (via the age range and selectivity) and categories for those spatial cells where the categorical layer has the same value as defined for each vector of observations.

For example, in a 2×2 spatial model a categorical layer (e.g., with label Area) may define that cells $(1,1)$ and $(1,2)$ have value *A* and cells $(2,1)$ and $(2,2)$ have value *B*, i.e.,

```
@layer Area
type categorical
data A A
data B B
```

Here we supply observations for those spatial cells where the categorical layer has value *A* as,

```
@observation MyProportions
type proportions_by_category
layer Area
...
categories male
categories2 female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20
...
```

Or, for both *A* and *B* as,

```
@observation MyProportions
type proportions_by_category
layer Area
...
categories male
categories2 female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20
obs B 0.02 0.06 0.10 0.21 0.18
...
```

To supply an observation for individual spatial cells, then you will need to define a categorical layer with a single, unique value for each spatial cell.

6.3.1. Likelihoods for proportions-by-category observations

SAM implements two likelihoods for proportions-by-category observations, the binomial likelihood, and the normal approximation to the binomial (binomial-approx).

The binomial likelihood

For observed proportions O_i for age class i, where E_i are the expected proportions for age class i, and N_i is the effective sample size for age class i, then the negative log-likelihood is defined as;

$$\begin{aligned} -\log(L) = -\sum_i [\, &\log(N_i!) - \log((N_i(1-O_i))!) - \log((N_i O_i)!) + N_i O_i \log(Z(E_i,\delta)) \\ &+ N_i(1-O_i)\log(Z(1-E_i,\delta))\,] \end{aligned} \tag{6.6}$$

where $Z(\theta,\delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta,\delta)$ is defined as,

$$Z(\theta,\delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2-\theta/\delta), & \text{otherwise} \end{cases} \tag{6.7}$$

The default value of δ is 1×10^{-11}.

The normal approximation to the binomial likelihood

For observed proportions O_i for age class i, where E_i are the expected proportions for age class i, and N_i is the effective sample size for age class i, then the negative log-likelihood is defined as;

$$-\log(L) = \sum_i \log\left(\sqrt{Z(E_i,\delta)Z(1-E_i,\delta)/N_i}\right) + \frac{1}{2}\left(\frac{O_i - E_i}{\sqrt{Z(E_i,\delta)Z(1-E_i,\delta)/N_i}}\right)^2 \tag{6.8}$$

where $Z(\theta,\delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta,\delta)$ is defined as,

$$Z(\theta,\delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2-\theta/\delta), & \text{otherwise} \end{cases} \tag{6.9}$$

The default value of δ is 1×10^{-11}.

6.4. Abundance or biomass observations

Abundance (or biomass) observations are observations of either a relative or absolute number (or biomass) of individuals from a set of categories after applying a selectivity. The observations classes are the same, except that a biomass observation will use the biomass as the observed (and expected) value (calculated from mean weight of individuals within each age and category) while an abundance observation is just the number of individuals.

Each observation is for a given year and time-step, for some selected age classes of the population (i.e., for a range of ages multiplied by a selectivity), for categories aggregated over a set of spatial cells. Further, you need to provide the label of the catchability coefficient q, which can either be estimated of fixed. For absolute abundance or absolute biomass observations, define a catchability where $q = 1$.

The observations can be supplied for any set of categories. For example, for a model with the two categories *male* and *female*, we might supply an observation of the total abundance/biomass (male + female) or just male abundance/biomass. The subcommand `categories` defines the categories used to aggregate the abundance/biomass. In addition, each category must have an associated selectivity, defined by `selectivities`. For example,

```
categories male
selectivities male-selectivity
```

defines an observation for males after applying the selectivity male-selectivity. SAM then expects that there will be a single observation supplied. The expected values for the observations will be the expected abundance (or biomass) of males, after applying the selectivities, at the year and time-step specified.

The observations must be supplied using all or some of the the values of defined by a categorical layer. SAM calculates the expected values by summing over the defined ages (via the age range and selectivity) and categories for those spatial cells where the categorical layer has the same value as defined for each vector of observations.

For example, in a 2×2 spatial model a categorical layer (e.g., with label Area) may define that cells $(1,1)$ and $(1,2)$ have value *A* and cells $(2,1)$ and $(2,2)$ have value *B*, i.e.,

```
@layer Area
type categorical
data A A
data B B
```

Here we supply abundance observations for those spatial cells where the categorical layer has value *A* as,

```
@observation MyAbundance
type abundance
layer Area
...
categories male
obs A 1000
...
```

Or, for both *A* and *B* as,

```
@observation MyAbundance
type abundance
layer Area
...
categories male
obs A 1000
obs B 1200
...
```

To supply an observation for individual spatial cells, then you will need to define a categorical layer with a single, unique value for each spatial cell.

Note that, to define a biomass observation instead of an abundance observation, use

```
@observation MyBiomass
type biomass
...
```

6.4.1. Likelihoods for abundance observations

The lognormal likelihood

For observations O_i, c.v. c_i, and expected values qE_i, the negative log-likelihood is defined as;

$$-\log(L) = \sum_i \left(\log(\sigma_i) + 0.5 \left(\frac{\log(O_i/qZ(E_i,\delta))}{\sigma_i} + 0.5\sigma_i \right)^2 \right) \tag{6.10}$$

where

$$\sigma_i = \sqrt{\log\left(1+c_i^2\right)} \tag{6.11}$$

and $Z(\theta,\delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta,\delta)$ is defined as,

$$Z(\theta,\delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2-\theta/\delta), & \text{otherwise} \end{cases} \tag{6.12}$$

The default value of δ is 1×10^{-11}.

The normal likelihood

For observations O_i, c.v. c_i, and expected values qE_i, the negative log-likelihood is defined as;

$$-\log(L) = \sum_i \left(\log(c_i E_i) + 0.5 \left(\frac{O_i - E_i}{Z(c_i E_i,\delta)} \right)^2 \right) \tag{6.13}$$

and $Z(\theta,\delta)$ is a robustifying function to prevent division by zero errors, with parameter $\delta > 0$. $Z(\theta,\delta)$ is defined as,

$$Z(\theta,\delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2-\theta/\delta), & \text{otherwise} \end{cases} \tag{6.14}$$

The default value of δ is 1×10^{-11}.

6.5. Process error

Additional 'process error' can be defined for each set of observations. Additional process error has the effect of increasing the observation error in the data, and hence of decreasing the relative weight given to the data in the fitting process.

For observations where where the likelihood is parameterised by the c.v., you can specify the process error for a given set of observations as a c.v., in which case all the c.v.s c_i are changed to

$$c_i' = \sqrt{c_i^2 + c_{process\_error}^2} \tag{6.15}$$

Note that $c_{process\_error} \geq 0$, and that $c_{process\_error} = 0$ is equivalent to no process error.

Similarly, if the likelihood is parameterised by the effective sample size N,

$$N_i' = \frac{1}{1/N_i + 1/N_{process\_error}} \tag{6.16}$$

Note that this requires that $N_{process\_error} > 0$, but we allow the special case of $N_{process\_error} = 0$, and define $N_{process\_error} = 0$ as no process error (i.e., defined to be equivalent to $N_{process\_error} = \infty$).

For both the c.v. and N process errors, the process error has more effect on small errors than on large ones. Be clear that a large value for the N process error means a small process error.

6.6. Ageing error

SAM can apply ageing error age frequency observations. Ageing error is applied to the expected values for proportions-at-age observations. The ageing error is applied as a misclassification matrix, which has the effect of 'smearing' the age frequencies. These are used in calculating the fits to the observed values, and hence the contribution to the total objective function.

Ageing error is optional, and if it is used, it may be omitted for any individual time series. Different ageing error models may be applied for different observation commands. See Section **??** for reporting the misclassification matrix.

The ageing error models implemented are,

1. None: The default model is to apply no ageing error.
2. Off by one: Proportion p_1 of individuals of each age a are misclassified as age $a-1$ and proportion p_2 are misclassified as age $a+1$. Individuals of age $a < k$ are not misclassified. If there is no plus group in the population model, then proportion p_2 of the oldest age class will 'fall off the edge' and disappear.
3. Normal: Individuals of age a are classified as ages which are normally distributed with mean a and constant c.v. c. As above, if there is no plus group in the population model, some individuals of the older age classes may disappear. If c is high enough, some of the younger age classes may 'fall off the other edge'. Individuals of age $a < k$ are not misclassified.

Note that the expected values (fits) reported by SAM for observations with ageing error will have had the ageing error applied.

6.7. Simulating observations

SAM can generate simulated observations for a given model with given parameter values (using `spm -s`). Simulated observations are randomly distributed values, generated according to the error assumptions defined for each observation, around fits calculated from one or more sets of the 'true' parameter values. Simulating from a set of parameters can be used to generate observations from an operating model or as a form of parametric bootstrap.

The procedure SAM uses for simulating observations is to first run using the 'true' parameter values and generate the expected values. Then, if a set of observations uses ageing error, ageing error is applied. Finally a random value for each observed value is generated based on (i) the expected values, (ii) the type of likelihood specified, and (iii) the variability parameters (e.g., `error_value` and `process_error`).

Methods for generating the random error, and hence simulated values, depend on the specific likelihood type of each observation.

1. Normal likelihood parameterised by c.v.: Let E_i be the fitted value for observation i, and c_i be the corresponding c.v. (adjusted by the process error if applicable). Each simulated observation value S_i is generated as an independent normal deviate with mean E_i and standard deviation $E_i c_i$.

2. Log-normal likelihood: Let E_i be the fitted value for observation i and c_i be the corresponding c.v. (adjusted by the process error if applicable). Each simulated observation value S_i is generated as an independent lognormal deviate with mean and standard deviation (on the natural scale, not the log-scale) of E_i and $E_i c_i$ respectively. The robustification parameter δ is ignored.
3. Multinomial likelihood: Let E_i be the fitted value for observation i, for i between 1 and n, and let N be the sample size (adjusted by process error if applicable, and then rounded up to the next whole number). The robustification parameter δ is ignored. Then,
   (a) A sample of N values from 1 to n is generated using the multinomial distribution, using sample probabilities proportional to the values of E_i.
   (b) Each simulated observation value S_i is calculated as the proportion of the N sampled values equalling i
   (c) The simulated observation values S_i are then rescaled so that their sum is equal to 1
4. Binomial and the normal approximation to the binomial likelihoods: Let E_i be the fitted value for observation i, for i between 1 and n, and N_i the corresponding equivalent sample size (adjusted by process error if applicable, and then rounded up to the next whole number). The robustification parameter δ is ignored. Then,
   (a) A sample of N_i independent binary variates is generated, equalling 1 with probability E_i
   (b) The simulated observation value S_i is calculated as the sum of these binary variates divided by N_i

Note that `SAM` will report simulated observations using the usual observation report (`@report[label].type=observation`). The report `@report[label].type=simulated_observation` will generate simulated observations in a form suitable for use as input within a `SAM` input configuration file. See Section 7 for more detail.

6.8. Pseudo-observations

`SAM` can generate expected values for observations without them contributing to the total objective function. These are called pseudo-observations, and can be used to either generate the expected values from `SAM` for reporting or diagnostic purposes. To define an observation as a pseudo-observation, use the command `@observation[label].likelihood=none`. Any observation type can be used as a pseudo-observation. `SAM` can also generate simulated observations from pseudo-observations. Note that;

- Output will only be generated if a report command `@report[label].type=observation` is specified.
- The observed values should be supplied (even if they are 'dummy' observation). These will be processed by `SAM` as if they were actual observation values, and must conform to the validations carried out for the other types of likelihood.
- The subcommands `likelihood`, `obs`, `error_value` and `process_error` have no effect when generating the expected values for the pseudo-observation.
- When simulating observations, `SAM` needs the subcommand `simulation_likelihood` to tell it what sort of likelihood to use. In this case, the `obs`, `error_value` and `process_error` are used to determine the appropriate terms to use for the likelihood when simulating.

7. The report section

8. Population command and subcommand syntax

8.1. Model structure

`@model` *`label`* Define an object type Model

`initialisation_phases` List of initialisation phases to execute
Type: string
Default: true

`start_year` The first year of the model
Type: unsigned
Default: No default

`age_plus` True if the model supports an age-plus group
Type: bool
Default: false

`min_age` The default minimum age for the population
Type: unsigned
Default: No default

`max_age` The default maximum age for the population
Type: unsigned
Default: No default

`final_year` The last year of the model
Type: unsigned
Default: No default

`time_steps` List of time steps to execute
Type: string
Default: No default

`projection_final_year` The final year of the model in projection mode
Type: unsigned
Default: 0

8.2. Initialisation

`@initialisation_phase` *`label`* Define an object type Initialisation_Phase

`processes` A list of processes to execute during this phase
Type: string
Default: true

`label` Label
Type: string
Default: No default

`time_steps` A list of time steps to execute during this phase
Type: string
Default: true

`years` The number of iterations to execute this phase for
Type: unsigned
Default: No default

8.3. Time-steps

`@time_step` *`label`* Define an object type Time_Step

`processes` Processes
Type: string
Default: No default

`label` Label
Type: string
Default: No default

8.4. Processes

`@process` *`label`* Define an object type Process

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: ””

`print_report` Print parameter report
Type: bool
Default: false

8.4.1. `@process[label].type=ageing`

`categories` Categories
Type: string
Default: No default

8.4.2. @process[label].type=maturation

`from` List of categories to mature from
Type: string
Default: No default

`rates` The rates to mature for each year
Type: double
Default: No default

`selectivities` List of selectivities to use for maturation
Type: string
Default: No default

`to` List of categories to mature too
Type: string
Default: No default

`years` The years to be associated with rates
Type: unsigned
Default: No default

8.4.3. @process[label].type=maturation_rate

`from` From
Type: string
Default: No default

`selectivities` Selectivity names
Type: string
Default: No default

`to` To
Type: string
Default: No default

`proportions` Proportions
Type: double
Default: No default

8.4.4. @process[label].type=mortality_constant_rate

`m` Mortality rates
Type: double
Default: No default

`selectivities` Selectivities
Type: string
Default: No default

`categories` List of categories
Type: string
Default: No default

8.4.5. @process[label].type=mortality_event

`penalty` Penalty label
Type: string
Default: ""

`u_max` U Max
Type: double
Default: 0.99

`categories` Categories
Type: string
Default: No default

`selectivities` List of selectivities
Type: string
Default: No default

`years` Years
Type: unsigned
Default: No default

`catches` Catches
Type: double
Default: No default

8.4.6. @process[label].type=mortality_event_biomass

`penalty` Penalty label
Type: string
Default: ""

`u_max` U Max
Type: double
Default: 0.99

`categories` Category labels
Type: string
Default: No default

`selectivities` Selectivity labels
Type: string
Default: No default

`years` Years to apply mortality
Type: unsigned
Default: No default

`catches` Catches for each year
Type: double
Default: No default

8.4.7. @process[label].type=recruitment_beverton_holt

`r0` R0
Type: double
Default: No default

`ssb_offset` SSB Offset (year offset)
Type: unsigned
Default: No default

`standardise_ycs_years`
Type: unsigned
Default: true

`ycs_values` YCS Values
Type: double
Default: No default

`age` Age to recruit at

Type: unsigned
Default: true

`b0` B0 Label
Type: string
Default: ””

`steepness` Steepness
Type: double
Default: 1.0

`ssb` SSB Label (derived quantity)
Type: string
Default: No default

`categories` Category labels
Type: string
Default: No default

`proportions` Proportions
Type: double
Default: No default

8.4.8. `@process[label].type=recruitment_constant`

`r0` R0
Type: double
Default: No default

`age` Age
Type: unsigned
Default: No default

`proportions` Proportions
Type: double
Default: true

`categories` Categories
Type: string
Default: No default

8.5. Derived quantities

`@derived_quantity` *`label`* Define an object type Derived_Quantity

`time_step` The time step to calculate the derived quantity after
Type: string
Default: No default

`initialisation_time_steps` The initialisation time steps to calculate the derived quantity after
Type: string
Default: true

`selectivities` The list of selectivities to use when calculating the derived quantity. 1 per category
Type: string
Default: No default

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: No default

`categories` The list of categories to use when calculating the derived quantity
Type: string
Default: No default

8.5.1. `@derived_quantity[label].type=abundance`

8.5.2. `@derived_quantity[label].type=biomass`

8.6. Age-size relationship

`@age_size` *`label`* Define an object type Age_Size

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: No default

8.6.1. @age_size[label].type=none

size_weight Not Implemented
Type: string
Default: No default

8.6.2. @age_size[label].type=schnute

tau2 TBA
Type: double
Default: No default

tau1 TBA
Type: double
Default: No default

y1 TBA
Type: double
Default: No default

distribution TBA
Type: string
Default: normal

y2 TBA
Type: double
Default: No default

cv TBA
Type: double
Default: 0.0

by_length TBA
Type: bool
Default: true

a TBA
Type: double
Default: No default

size_weight TBA
Type: string
Default: No default

b TBA

Type: double
Default: No default

8.6.3. @age_size[label].type=von_bertalanffy

`linf` TBA
Type: double
Default: No default

`distribution` TBA
Type: string
Default: normal

`t0` TBA
Type: double
Default: No default

`cv` TBA
Type: double
Default: 0.0

`k` TBA
Type: double
Default: No default

`by_length` TBA
Type: bool
Default: true

`size_weight` TBA
Type: string
Default: No default

8.7. Size-weight

`@size_weight` *`label`* Define an object type Size_Weight

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: No default

8.7.1. `@size_weight[label].type=basic`

`a` A
Type: double
Default: No default

`b` B
Type: double
Default: No default

8.7.2. `@size_weight[label].type=none`

8.8. Selectivities

`@selectivity` *`label`* Define an object type Selectivity

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: No default

8.8.1. `@selectivity[label].type=all_values`

`v` V
Type: double
Default: No default

8.8.2. `@selectivity[label].type=all_values_bounded`

`l` L
Type: unsigned
Default: No default

`v` V
Type: double
Default: No default

`h` H
Type: unsigned
Default: No default

8.8.3. @selectivity[label].type=constant

`c` C
Type: double
Default: No default

8.8.4. @selectivity[label].type=double_exponential

`y1` Y1
Type: double
Default: No default

`y0` Y0
Type: double
Default: No default

`y2` Y2
Type: double
Default: No default

`x2` X2
Type: double
Default: No default

`alpha` Alpha
Type: double
Default: 1.0

`x0` X0
Type: double
Default: No default

`x1` X1
Type: double
Default: No default

8.8.5. @selectivity[label].type=double_normal

`mu` Mu
Type: double
Default: No default

`sigma_l` Sigma L

Type: double
Default: No default

`sigma_r` Sigma R
Type: double
Default: No default

`alpha` Alpha
Type: double
Default: 1.0

8.8.6. `@selectivity[label].type=increasing`

`l` Low
Type: unsigned
Default: No default

`v` V
Type: double
Default: No default

`h` High
Type: unsigned
Default: No default

`alpha` Alpha
Type: double
Default: 1.0

8.8.7. `@selectivity[label].type=inverse_logistic`

`alpha` Alpha
Type: double
Default: 1.0

`a50` A50
Type: double
Default: No default

`ato95` aTo95
Type: double
Default: No default

8.8.8. @selectivity[label].type=knife_edge

`e` Edge
Type: double
Default: No default

`alpha` Alpha
Type: double
Default: 1.0

8.8.9. @selectivity[label].type=logistic

`alpha` Alpha
Type: double
Default: 1.0

`a50` A50
Type: double
Default: No default

`ato95` Ato95
Type: double
Default: No default

8.8.10. @selectivity[label].type=logistic_producing

`l` Low
Type: unsigned
Default: No default

`alpha` Alpha
Type: double
Default: 1.0

`h` High
Type: unsigned
Default: No default

`ato95` Ato95
Type: double
Default: No default

`a50` A50

Type: double
Default: No default

9. Estimation command and subcommand syntax

9.1. Estimation methods

`@estimate` *`label`* Define an object type Estimate

`lower_bound` The lowest value the parameter is allowed to have
Type: double
Default: No default

`same` A list of parameters that are bound to the value of this estimate
Type: string
Default: ""

`prior` The name of the prior to use for the parameter
Type: string
Default: ""

`upper_bound` The highest value the parameter is allowed to have
Type: double
Default: No default

`label` Label
Type: string
Default: No default

`parameter` The name of the variable to estimate in the model
Type: string
Default: No default

`type` Type
Type: string
Default: No default

`estimation_phase` TBA
Type: unsigned
Default: 1u

`mcmc` TBA
Type: bool
Default: ""

9.1.1. @estimate[label].type=beta

`m` M
Type: double
Default: No default

`sigma` Sigma
Type: double
Default: No default

`a` A
Type: double
Default: No default

`b` B
Type: double
Default: No default

9.1.2. @estimate[label].type=lognormal

`mu` Mu
Type: double
Default: No default

`cv` Cv
Type: double
Default: No default

9.1.3. @estimate[label].type=normal

`mu` Mu
Type: double
Default: No default

`cv` Cv
Type: double
Default: No default

9.1.4. @estimate[label].type=normal_by_stdev

`mu` Mu
Type: double
Default: No default

`sigma` Sigma
Type: double
Default: No default

9.1.5. `@estimate[label].type=normal_log`

`mu` Mu
Type: double
Default: No default

`sigma` Sigma
Type: double
Default: No default

9.1.6. `@estimate[label].type=uniform`

9.1.7. `@estimate[label].type=uniform_log`

9.2. Point estimation

`@minimiser` *`label`* Define an object type Minimiser

`active` True if this minimiser is active
Type: bool
Default: false

`label` Label
Type: string
Default: No default

`type` Type of minimiser to use
Type: string
Default: No default

`covariance` True if a covariance matrix should be created
Type: bool
Default: true

9.2.1. `@minimiser[label].type=beta_diff`

9.2.2. `@minimiser[label].type=d_e_solver`

`population_size` The number of candidate solutions to have in the population
Type: unsigned
Default: No default

`difference_scale` The scale to apply to new solutions when comparing candidates
Type: double
Default: 0.02

`tolerance` The total variance between the population and best candidate before acceptance
Type: double
Default: 0.01

`crossover_probability` TBA
Type: double
Default: 0.9

`method` The type of candidate generation method to use
Type: string
Default: ""
Value: not_yet_implemented

`max_generations` The maximum number of iterations to run
Type: unsigned
Default: No default

9.2.3. `@minimiser[label].type=d_lib`

9.2.4. `@minimiser[label].type=gamma_diff`

`tolerance` Tolerance of the gradient for convergence
Type: double
Default: 0.02

`step_size` Minimum Step-size before minimisation fails
Type: double
Default: 1e-7

`evaluations` Maximum number of evaluations
Type: int
Default: 4000

`iterations` Maximum number of iterations
Type: int
Default: 1000

9.3. Monte Carlo Markov Chain (MCMC)

@mcmc *label* Define an object type MCMC

`step_size` TBA
Type: double
Default: 0.0

`covariance_adjustment_method` TBA
Type: string
Default: covariance

`length` The number of chain links to create
Type: unsigned
Default: No default

`adapt_stepsize_at` TBA
Type: unsigned
Default: true

`correlation_adjustment_diff` TBA
Type: double
Default: 0.0001

`keep` TBA
Type: unsigned
Default: 1u

`df` TBA
Type: unsigned
Default: 4

`proposal_distribution` TBA
Type: string
Default: t

`max_correlation` TBA
Type: double
Default: 0.8

`start` TBA
Type: double
Default: 0.0

9.4. Profiles

`@profile` *`label`* Define an object type Profile

`steps` The number of steps to take between the lower and upper bound
Type: unsigned
Default: No default

`lower_bound` The lower bounds
Type: double
Default: No default

`upper_bound` The upper bounds
Type: double
Default: No default

`label` Label
Type: string
Default: No default

`parameter` The system parameter to profile
Type: string
Default: ""

9.5. Defining catchability constants

`@catchability` *`label`* Define an object type Catchability

`label` Label
Type: string
Default: No default

`q` The catchability amount
Type: double
Default: No default

9.6. Defining penalties

`@penalty` *`label`* Define an object type Penalty

`label` Label
Type: string
Default: No default

`log_scale` Log scale

Type: bool
Default: false

`multiplier` Multiplier
Type: double
Default: 1.0

10. Observation command and subcommand syntax

10.1. Observation types

The observation types available are,

Observations of proportions of individuals by age class

Observations of proportions of individuals between categories within each age class

Relative and absolute abundance observations

Relative and absolute biomass observations

Each type of observation requires a set of subcommands and arguments specific to that process.

`@observation` *`label`* Define an object type Observation

`time_step` Time step to execute in
Type: string
Default: No default

`time_step_proportion_method` Method of proportioning to use
Type: string
Default: mean

`selectivities` Selectivity labels to use
Type: string
Default: true

`label` Label
Type: string
Default: No default

`type` Type of observation
Type: string
Default: No default

`categories` Category labels to use
Type: string
Default: true

`simulation_likelihood` Simulation likelihood to use
Type: string
Default: ""

`likelihood` Type of likelihood to use
Type: string
Default: No default

`time_step_proportion` Proportion through the time step to analyse the partition from
Type: double
Default: 1.0

10.1.1. @observation[label].type=abundance

`process_error` Process error
Type: double
Default: 0.0

`obs` Observation values
Type: string
Default: No default

`years` Years to execute in
Type: unsigned
Default: No default

`catchability` TBA
Type: string
Default: No default

`error_value` The error values to use against the observation values
Type: double
Default: No default

`delta` Delta value for error values
Type: double
Default: 1e-10

10.1.2. @observation[label].type=biomass

`process_error` Process error
Type: double
Default: 0.0

`obs` Observation values
Type: string
Default: No default

`years` Years to execute in
Type: unsigned
Default: No default

`catchability` TBA
Type: string
Default: No default

`error_value` The error values to use against the observation values
Type: double
Default: No default

`delta` Delta value for error values
Type: double
Default: 1e-10

10.1.3. `@observation[label].type=proportions_at_age`

`age_plus` Use age plus group
Type: bool
Default: true

`process_error` Process error
Type: double
Default: 0.0

`min_age` Minimum age
Type: unsigned
Default: No default

`obs` Observation values
Type: string
Default: No default

`tolerance` Tolerance
Type: double
Default: 0.001

`error_value` Error values
Type: double
Default: No default

`max_age` Maximum age
Type: unsigned
Default: No default

`year` Year to execute in
Type: unsigned
Default: No default

`ageing_error` Label of ageing error to use
Type: string
Default: ""

`delta` Delta
Type: double
Default: DELTA

10.1.4. @observation[label].type=proportions_by_category

10.2. Likelihoods

`@likelihood` *`label`* Define an object type Likelihood

10.2.1. @likelihood[label].type=binomial

10.2.2. @likelihood[label].type=binomial_approx

10.2.3. @likelihood[label].type=log_normal

10.2.4. @likelihood[label].type=log_normal_with_q

10.2.5. @likelihood[label].type=multinomial

10.2.6. @likelihood[label].type=normal

10.2.7. @likelihood[label].type=pseudo

10.3. Defining ageing error

Three methods for including ageing error into estimation with observations are,

- None
- Normal
- Off-by-one

Each type of ageing error requires a set of subcommands and arguments specific to its type.

`@ageing_error` *`label`* Define an object type Ageing_Error

`label` Label
Type: string
Default: No default

`type` Type
Type: string
Default: No default

10.3.1. `@ageing_error[label].type=normal`

`cv` TBA
Type: double
Default: No default

`k` TBA
Type: unsigned
Default: 0u

10.3.2. `@ageing_error[label].type=off_by_one`

11. Report command and subcommand syntax

11.1. Available reports

The report types available are,

1.
2.
3.
4.
5.
6.
7.
8.

Each type of report requires a set of subcommands and arguments specific to that report.

11.2. Report commands and subcommands

`@report` *`label`* Define an object type Report

`time_step` Time Step label
Type: string
Default: ""

`label` Label
Type: string
Default: No default

`years` Years
Type: unsigned
Default: true

`overwrite` Overwrite file
Type: bool
Default: true

`type` Type
Type: string
Default: No default

`file_name` File Name
Type: string
Default: ""

11.2.1. @report[label].type=category_info

11.2.2. @report[label].type=derived_quantity

11.2.3. @report[label].type=estimate_summary

11.2.4. @report[label].type=estimate_value

11.2.5. @report[label].type=mcmc_chain

11.2.6. @report[label].type=objective_function

11.2.7. @report[label].type=observation

`observation` Observation label
Type: string
Default: No default

11.2.8. @report[label].type=partition

11.2.9. @report[label].type=partition_mean_weight

11.2.10. @report[label].type=simulated_observation

`observation` Observation label
Type: string
Default: No default

11.2.11. @report[label].type=standard_header

12. Other commands and subcommands

`@include` *`file`* Include an external file

`file` The name of the external file to include

Type: string
Default: No default
Value: A valid external file
Condition: The file name must be enclosed in double quotes
Example: `@include "my_file.txt"`
Note: `@include` does not denote the end of the previous command block as is the case for all other commands

13. Examples

14. Post processing output using R

15. Troubleshooting

16. Acknowledgements

17. Quick reference

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