



# CASAL2 User Manual

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## 1. Introduction

### 1.1. About CASAL2

CASAL2 is NIWA's open-source integrated assessment tool for modelling the population dynamics of marine species, including fishery stock assessments. CASAL2 expands functionality and increases maintainability relative to its predecessor, CASAL. CASAL2 can be used for quantitative assessments of marine populations, including fish, invertebrates, marine mammals and seabirds.

The CASAL2 software implements a generalised age-structured population model that allows for a great deal of choice in specifying the population dynamics, parameter estimation, and model outputs. CASAL2 is designed for flexibility. It can implement an age-structured model for a single population or multiple populations using user-defined categories such as area, sex, and maturity. These structural elements are generic and not predefined, and are easily constructed. CASAL2 models can be used for a single population with a single anthropogenic event (in a fish population model this would be a single fishery), or for multiple species and populations, areas, and/or anthropogenic or exploitation methods, and including predator-prey interactions.

In CASAL2 the processes in a time period and within an annual cycle are defined by the user. Observation data used for model fitting can be from many different sources, like, removals-at-size or -age from an anthropogenic or exploitation event (e.g., fishery or other human impact), research survey and other biomass indices, and mark-recapture data. Model parameters can be estimated using penalised maximum likelihood or Bayesian methods.

As well as the point estimates of the parameters, CASAL2 can calculate the likelihood or posterior distribution profiles, and can generate Bayesian posterior distributions using Markov chain Monte Carlo methods. CASAL2 can project population status using deterministic or stochastic population dynamics. CASAL2 can also simulate observations from a set of given model structures.

### 1.2. Citing CASAL2

The reference for this document is I. Doonan, A. Dunn, K. Large, C. Marsh, S. Rasmussen (2020). CASAL2 User Manual, v2020-04-01 (rev. d5dc698). National Institute of Water & Atmospheric Research Ltd. *NIWA Technical Report 139*. 215 p.

The peer-reviewed journal article reference for CASAL2 is ([Doonan et al., 2016](#)).

### 1.3. Software license

This program and the accompanying materials are made available under the terms of the GNU General Public License version 2 which accompanies this software (see [Section 17](#)).

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### 1.4. Where to get CASAL2

In the first instance, see <http://www.niwa.co.nz/> for information about CASAL2. The CASAL2 source code is hosted on GitHub, and can be found at <https://github.com/NIWAFisheriesModelling/CASAL2>.

There are installation packages available for Linux and Microsoft Windows. The package includes the CASAL2 executable, the **R** library, the User Manual and other documentation, example models, and other information. The installation packages can be downloaded at <https://github.com/NIWAFisheriesModelling/CASAL2/releases>.

### 1.5. System requirements

CASAL2 is available for most IBM compatible machines running 64-bit Linux and Microsoft Windows operating systems.

Several of CASAL2's tasks are computer intensive and a fast processor is recommended. Depending on the model implemented, some of the CASAL2 tasks can take a considerable amount of processing time (minutes to hours), and in extreme cases may take several days to complete an MCMC estimate.

Output files can be large, and the output from developing a model, sensitivity analyses, and running multiple MCMC chains can take up significant amounts of disk space. Depending on the 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 larger models, several gigabytes of RAM and disk space may occasionally be required.

### 1.6. Necessary files

For both 64-bit Linux and Microsoft Windows, only the binary executable `casal2` or `casal2.exe` is required to run CASAL2. No other software is required. CASAL2 is not available for 32-bit operating systems.

CASAL2 provides few functions for post-processing model output, and a package that allows tabulation and graphing of model outputs is recommended. Software such as **R** ([R Core Team, 2014](#)) is recommended for post-processing CASAL2 output. The CASAL2 **R** package is provided for parsing the CASAL2 output into **R** (see [Section 15](#)), as well as providing some diagnostic and plotting functionality.

### 1.7. Getting help

TODO review with the Project Manager and Project Lead

CASAL2 is distributed as unsupported software. Please notify the CASAL2 Development Team of any issues with or errors in CASAL2. Please contact the `Casal2 Development Team`. See [Section 16.2](#) for the template for reporting issues.

### 1.8. Technical details

CASAL2 was compiled on Linux using `gcc` (<http://gcc.gnu.org>), the C/C++ compiler developed by the GNU Project (<http://gcc.gnu.org>). The 64-bit Linux version was compiled using `gcc` version 4.8.5 20150623 on CentOS 7.7 Linux (<http://www.ubuntu.com/>).

The Microsoft Windows (<http://www.microsoft.com>) version was compiled using MingW (<http://www.mingw.org>) `gcc` 8.1.0 (<http://gcc.gnu.org>). The Microsoft Windows(<http://www.microsoft.com>)

`//www.microsoft.com`) installer was built using the Inno Setup 5 (<http://www.jrsoftware.org/isdl.php>).

CASAL2 includes number of different minimisers; different minimisers may perform better for some models than others. The first three minimisers are non-automatic differentiation minimisers: the first is closely based on the main algorithm of [Dennis Jr and Schnabel \(1996\)](#), and uses finite difference gradients; the second is an implementation of the differential evolution solver ([Storn and Price, 1995](#)), based on code by Lester E. Godwin of PushCorp, Inc.; and the third is Dlib ([King, 2009](#)).

The three automatic differentiation minimisers are: ADOL-C, an auto differentiation minimiser ([Walther et al., 1996](#)); CppAD, an auto differentiation minimiser similar to ADOL-C ([Wächter and Biegler, 2006](#)); and the third is a modified version of an older version of ADOL-C (v1.8.4) that was used as the automatic differentiation minimiser in the first version of CASAL ([Bull et al., 2012](#)).

The random number generator used in CASAL2 uses an implementation of the Mersenne twister random number generator ([Matsumoto and Nishimura, 1998](#)). This functionality, the command line functionality, matrix operations, and a number of other functions use the Boost C++ library (Version 1.58.0).

The output from CASAL2 may differ slightly on the different operating systems and operating system versions due to different precision arithmetic or other platform-dependent implementation details. The source code for CASAL2 is available in the GitHub repository at <https://github.com/NIWAFisheriesModelling/CASAL2>.

Unit tests of the underlying CASAL2 code are carried out at build time, using the Google Test and Mock unit testing and mocking framework. The unit test framework aims to cover a significant proportion of the key functionality within the CASAL2 code base. The unit test code for CASAL2 is available as a part of the underlying source code.





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## 2. Model overview

### 2.1. Introduction

CASAL2 is a generalized age-structured population dynamics modelling framework. It implements statistical catch-at-age population dynamics using a discrete time-step state-space model that represents a cohort-based population age structure.

CASAL2 is run from the console window on Microsoft Windows or from a terminal window on Linux. CASAL2 reads in information from input data files, the main one of which is the *input configuration file*. Commands and subcommands in the input configuration file define the model structure, provide observations, define parameters, and define the outputs (reports) for CASAL2. Command line options and argument set the run mode and where to direct the output. See Section 3 for details.

The model is defined in terms of the *state*. The state consists of two parts, the *partition*, and any *derived quantities*. The state will typically change in each *time-step* of every year, depending on the *processes* defined for those time-steps in the model.

The *partition* is a representation of the population at an point in time, and can be considered a matrix of the numbers of individuals within each category and at each age.

A *derived quantity* is a summary of the abundance or biomass of a selected part of the partition at some point in time. Unlike the partition, which is updated as each new process is applied, a derived quantity records a single value for each year of the model run. Hence, derived quantities build up a vector of values over the time period represented by the model. For example, the total biomass of individuals in categories labelled, say, 'mature' at some point in the annual cycle may be a derived quantity. The derived quantity is then available as an *addressable parameter* to the model, to be reported, or to be an input into another process (e.g., the stock-recruitment relationship) at some point in the model in a subsequent year.

The state at some point in time is the term for the combination of the partition and any derived quantities at that point in time. Throughout the modelled years, changes to the state occur from the application of *processes*. This state then provides the basis for the generation of expected values for *observations*, as well as for reports and other outputs.

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

Initialisation can be in one or more phases, and for each phase, the processes that occur in each year, and the order in which they are applied, need to be defined. The processes that occur is controlled by the *annual cycle*. This configuration defines what processes happen in each model year and in what sequence. Furthermore, the processes in each year are split up into one or more time-steps (with at least one process occurring in each time-step). Each time-step can be conceptualised as representing a particular period of the calendar year, or they can be 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 how/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 a time-step, then the processes are applied in the order that they are specified.

Observations are always linked to a specific time-step, and are evaluated by the model in that time-step. 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 manner in which observations are evaluated and how the expected values are calculated by the model is described in Section 6.

The population structure of CASAL2 follows the usual population modelling conventions and is similar to those implemented in CASAL (Bull et al., 2012). The model records the numbers of individuals by category and age (e.g., numbers of males and females at age). 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 CASAL2 using an input configuration file, which provides a complete description of the model configuration (i.e., the population structure, the initialisation assumptions, and the subsequent population processes), the observations, the estimation methods, and the reports (outputs). CASAL2 runs from a console window on Microsoft Windows or from a terminal on Linux. A model can be either *run*, estimable parameters can be *estimated* or *profiled*, *MCMC* samples can be generated, and parameter estimates can be *projected* or used by CASAL2 as parameters of an operating model to *simulate* observations.

A model in CASAL2 is specified by an input configuration file, comprising four main sections. These are: the population section that defines the model structure, population dynamics, etc.; the estimation section that defines the methods of estimation (minimisation methods or MCMC algorithms) and the model parameters to be estimated; the observation section that defines the observation data and their associated likelihoods; and the report section that defines the outputs and reports from the model and where these are saved. The input configuration file completely describes a model implemented in CASAL2. See Sections 8, 9, 10, and 11 for details and specification of CASAL2's command and subcommand syntax within the input configuration file.

### 2.2. The population section

The population section (Section 4) defines the model of the population dynamics. It describes the population structure, the initialisation method and phases, the run and projection years (model period), population processes (for example, recruitment, migration, and mortality), selectivities, and key population parameters.

### 2.3. The estimation section

The estimation section (Section 5) specifies the parameters to be estimated, estimation methods, the penalties to be applied, and the 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 minimises the objective function), doing likelihood profiles, MCMC methods and options, etc.

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, their priors, their 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

The types of observations, their values, and their associated error structures are defined in the observation section (Section 6). Observations are data which allow for making 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, and tag recapture observations. Estimation generates values for each of the estimated parameters that are the best fit to the data, i.e., where each expected value is 'close' (in some mathematical sense) to the corresponding observed value.

## 2.5. The report section

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 CASAL2 will output helpful and informative messages generated from the source code as the application runs, CASAL2 will produce model estimates, population states, and other data only as configured in the report section. There are no default reports produced. If no reports are specified, then no output will be produced.



---

### 3. Running CASAL2

CASAL2 is run from a console window (i.e., the command line) on Microsoft Windows or from a terminal window on Linux. CASAL2 uses information from input data files -- the *input configuration file* being the main input file.

The input configuration file is required and defines the model structure and processes, the observations and parameters (both the fixed parameters and the parameters to be estimated), and the reports (outputs) requested.

The following sections describe how to construct the CASAL2 configuration file. By convention, the name of the input configuration file ends with the suffix `.csl2`. However, any file name is acceptable. Note that the input configuration file can include other files as a part of its syntax. Collectively, these are called the input configuration file.

Other input files can be included depending on the run mode and what information is required. For example, an input file can define the initial parameter values for estimation, or values from which to simulate observations, or values from which to run projections.

Command line arguments are used to specify the actions or *tasks* of CASAL2, e.g., to run a model with a set of parameter values, to estimate parameter values (either point estimates or MCMC), to project quantities, or to simulate observations. Hence, the *command line arguments* define the *task*. For example, `-r` is the *run* mode, `-e` is the *estimation* mode, and `-m` is the *MCMC* mode. The *command line arguments* are described in Section 3.4.

#### 3.1. Using CASAL2

To use CASAL2, open a console window (i.e. the command prompt) window on Microsoft Windows or a terminal window on Linux. Navigate to the directory where the model input configuration files are located. Then enter `casal2` with arguments for a specific mode to start the CASAL2 mode running; see Section 3.4 for the list of possible arguments. CASAL2 will print output to the screen.

The CASAL2 executable and shared libraries (files with extension `.dll` or `.so`) must either be in the same directory as the input configuration files or in one of the directories in your operating system's `PATH` environment variable. The CASAL2 installer will update `PATH`; see your operating system documentation for help displaying or modifying `PATH`.

#### 3.2. The input configuration file

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 estimated variables (the estimation section),
- the observations and their associated properties and likelihoods (the observation section), and
- the output values and reports that CASAL2 will output (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, particularly if you have a model that has many partitions or timesteps, and can result in a input configuration file that is long and difficult to navigate.

To aid in making the model configuration more readable and flexible, the input configuration file command `!include "filename"` can be used (Figure 3.1). This command specifies that another file, `filename`, be read and processed, exactly as if its contents had been inserted into the main input configuration file at that point. The file name must be the complete file name with extension, and can use either the relative or absolute path as part of its name. Included files can also contain `!include` commands. See Section 12 for more detail.



**Figure 3.1:** Example of using the input configuration file command `!include "filename"`.

### 3.3. Redirecting standard output

CASAL2 uses the standard output stream to display runtime information. The standard error stream is used by CASAL2 to output the program exit status and runtime 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

```
(casal2 [arguments] > run.out) >& run.err &
```

It may be useful to redirect the standard input, especially if you're using CASAL2 inside a batch job, i.e.

```
(casal2 [arguments] > run.out < /dev/null) >& run.err &
```

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

```
casal2 [arguments] > run.out
```

And, on some Microsoft Windows systems (e.g., Windows 10), you can redirect to both standard output and standard error, using the syntax

```
casal2 [arguments] > run.out 2> run.err
```

CASAL2 outputs header information to the output (Figure 3.2). The header consists of the program name and version, the arguments passed to CASAL2 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). This information can be used to track outputs as well as identifying the version of CASAL2 used to run the model.



Figure 3.2: Example of output file header information.

### 3.4. Command line arguments

CASAL2 is called using:

```
casal2[-c config_file] [task] [options]
```

where

**-c *config\_file*** Define the input configuration file for CASAL2 (if this argument is omitted, the default input configuration file is `config.csl2`)

and where *task* must be one of the following ([ ] indicates a secondary label to call the task, e.g. **-h** will execute the same task as **--help**),

**-h [--help]** Display help (this page)

**-l [--licence]** Display the reference for the software license (GPL v2)

**-v [--version]** Display the CASAL2 version number

**-r [--run]** Run the model once using the parameter values in the input configuration file, or optionally with the starting parameter values from the file specified with argument **-i *filename***

**-e [--estimate]** 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 starting parameter values from the file specified with the argument **-i *filename***

**-p [--profiling]** Do a likelihood *profile* using the parameter values in the input configuration file as the starting point, or optionally with the starting parameter values from the file specified with the argument **-i *filename***

**-m [--mcmc]** Do an *MCMC* chain using the values in the input configuration file as the starting point for the parameters to be estimated, or optionally with the starting parameter values from the file specified with the argument **-i *filename***

**-f [--projection]** Project the model *forward* in time using the parameter values in the input configuration file as the starting point for the estimation, or optionally with the starting parameter values from the file specified with the argument **-i *filename***

**-s [--simulation] *number*** Simulate the *number* of observation sets using values in the input configuration file as the parameter values, or optionally with the parameter values from the file specified with the argument **-i *filename***

and where the following optional arguments [*options*] may be specified

- i** [**--input**] *filename* *Input* one or more sets of free (estimated) parameter values from *filename* (see Section 11 for details about the format of *filename*)
- o** [**--output**] *filename* *Output* a report of the free (estimated) parameter values in a format suitable for **-i** *filename* (see Section 11 for details about the format of *filename*)
- g** [**--seed**] *seed* Initialise the random number *generator* with *seed*, a positive (long) integer value (note, if **-g** is not specified, then CASAL2 will generate a random number seed based on the computer clock time)
- loglevel** *arg* = {trace, finest, fine, medium} (see Section 7)
- tabular** Run with **-r** or **-f** command to print @report in tabular format (see Section 7)
- single-step** Run with **-r** to pause the model and ask the user to specify parameters and their values to use for the next iteration (see Section 3.6)
- q** [**--query**] *object type* *Query* an object type to print an extract of the object description and parameter definitions. An object can be defined as *block.type*, e.g. `casal2 --query process.recruitment_constant` will query the constant recruitment block.

### 3.5. Constructing the CASAL2 input configuration files

The model definition, characteristics, parameters, observations, and reports are specified in input configuration files:

- Population input (Section 4) specifies the model structure, population dynamics, and other associated parameters;
- Estimation input (Section 5) defines the objective function, parameters of the model, and the method of estimation (point estimates, Bayesian posteriors, profiles, etc.);
- Observation input (Section 6) specifies the observations data used in the model and describes how the observed values should be formatted, how CASAL2 calculates the expected values, and the likelihoods applied for each set of observations; and
- Report input (Section 7) specifies the output.

The command and subcommand syntax to be used in each of these configuration sections are listed in Sections 8 (Population), 9 (Estimation), 10 (Observation) and 11 (Report).

#### 3.5.1. Commands

CASAL2 has a range of commands that define the model structure, processes, parameters, observations, and how tasks are carried out. There are three types of commands

- Commands that have an argument and do not have subcommands (for example, `!include filename`)
- Commands that have a label and subcommands (for example @process must have a label and has subcommands)
- 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 can contain alpha numeric characters, period ('.'), underscore ('\_') and dash ('-'). Labels must not contain whitespace (tabs or spaces) or other characters that are not letters, numbers, dash, period, or an underscore. For example,

```
@process NaturalMortality
or
!include MyModelSpecification.csl2
```

### 3.5.2. Subcommands

CASAL2 subcommands define options and parameter values related to a particular command. Subcommands always take an argument which is one of a specific *type*. The argument *types* acceptable for each subcommand are defined in Section 12, 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. CASAL2 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 the expected results.

The argument type for a subcommand can be:

<b>switch</b>	true/false
<b>integer</b>	an integer number
<b>integer vector</b>	a vector of integer numbers
<b>integer range</b>	a range of integer numbers separated by a colon, e.g. 1994:1996 is expanded to an integer vector of values (1994 1995 1996)
<b>constant</b>	a real number (i.e., a double)
<b>constant vector</b>	a vector of real numbers (i.e., a vector of doubles)
<b>estimable</b>	a real number that can be estimated (i.e., a double)
<b>estimable vector</b>	a vector of real numbers that can be estimated (i.e., a vector of doubles)
<b>addressable</b>	a real number that can be referenced but not estimated (i.e., an addressable double)
<b>addressable vector</b>	a vector of real numbers that can be referenced but not estimated (i.e., a vector of addressable doubles)
<b>string</b>	a categorical (string) value
<b>string vector</b>	a vector of categorical values.

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

Integers must be entered as whole numbers without decimal points (i.e., if *year* is an integer then it is specified as 2008, not 2008.0)

Arguments of type integer vector, constant vector, estimable vector, addressable vector, or categorical vector must contain one or more entries on a row, separated by whitespace (tabs or spaces). Arguments of type integer range must contain a colon (:) and no whitespace (tabs or spaces).

Parameters are defined in the population section and can be specified as estimable with the subcommand type *estimable* or *estimable vector*. These parameters will be estimated if specified as such in the estimation section. If an estimable parameter is not specified in the estimation section it will instead be treated as a constant (or constant vector). In other words, only estimable parameters can be estimated and the parameter command must explicitly specify that the parameter

is estimable with the `estimable` or `estimable vector` subcommand type.

Parameters defined as addressable with the subcommand type `addressable` or `addressable vector` are usually derived quantities and are not directly estimable. As such, they can be referenced by various processes, or have priors and/or penalties associated with them, but they do not directly contribute to any estimation within the model.

### 3.5.3. The command block format

Each command block consists of a single command which starts with the symbol `@` and, for most commands, a unique label or an argument. Each command is then followed by its subcommands and their arguments, e.g.,

<code>@command</code>	<code>@command argument</code>	<code>@command label</code>
<code>subcommand argument</code>	<code>subcommand argument</code>	<code>subcommand argument</code>
<code>subcommand argument</code>	<code>subcommand argument</code>	<code>subcommand argument</code>
<code>.</code>	<code>.</code>	<code>.</code>
<code>.</code>	<code>.</code>	<code>.</code>
<code>etc.</code>	<code>etc.</code>	<code>etc.</code>

Blank lines are ignored, as is extra whitespace (tabs and spaces) between arguments. However, to start command block the `@` character must be the first character on the line and must not be preceded by any whitespace. Each input file must end with a carriage return.

There is no indicator of the end of a command block. Each command block is delimited by the end of the file, the end of the section, or the start of the next command block (which is marked by the `@` on the first character of a line). The `!include` command is the only exception to this rule (see Section 12 for details of the use of `!include`).

Commands, subcommands, and arguments in the input configuration files are not case sensitive. However, labels and variable values are case sensitive. On Linux, filenames and paths are case sensitive (i.e., when using `!include filename`, the argument `filename` will be case sensitive).

### 3.5.4. Commenting out lines

Text on a line that starts with the symbol `#` is considered to be a comment and is ignored. To comment out a group of commands or subcommands, use `#` at the beginning of each line to be ignored.

Alternatively, to comment out an entire block or section, use `/*` at the beginning of a line to start the comment block, then end the block with `*/`. All lines (including line breaks) between `/*` and `*/` inclusive are ignored.

```
# This line is a comment and will be ignored
@process NaturalMortality
m 0.2
/*
This block of text
is a comment and
will be ignored
*/
```

### 3.5.5. Determining CASAL2 parameter names

When CASAL2 processes the input configuration file it translates each command block and each subcommand block into a CASAL2 object, each with a unique parameter name. For commands, this parameter name is simply the command label. 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 ith element of that vector.
command[label].subcommand{i:j} if the command has a label, and the subcommand arguments
are a vector, and we are accessing the elements from i to j (inclusive) of that vector.
```

The unique parameter name is used to reference that parameter when, e.g., estimating, applying a penalty, projecting, time varying, or profiling. For example, the parameter name of the Natural Mortality rates subcommand `m` of the command `@process` with the label `NaturalMortality` is category related and so, the syntax to reference all `m` related categories is

```
process[NaturalMortality].m
```

The syntax to specify a single category to which the natural mortality process is applied is

```
process[NaturalMortality].m{male}
```

All labels (parameter names) are user specified. As such, naming conventions are non-restrictive and can be model specific.

## 3.6. Single-stepping CASAL2

Single-stepping means CASAL2 can ‘pause’ after each year in the annual cycle during a model run, write reports, then wait and process user input of updated estimable parameters for the next year (see the command line argument `--single-step`).

This enables CASAL2 to implement models for management simulations or scenarios that require feedback and can be used, for example, in operational management procedures (OMPs). The single-stepping process can be automated using **R**, so that CASAL2 may be used with **R** to update input harvest values (e.g., catches from a fishery in a fisheries model) to evaluate a particular harvest control rule.

## 3.7. CASAL2 exit status values

When CASAL2 is run, it will complete its task successfully or output errors. CASAL2 will return a single exit status value ‘completed’ to the standard output. Error messages will be printed to the console. When input file configuration errors are found, CASAL2 will print error messages, along with the associated filename(s) and line number(s) where the errors were identified, for example,

```
#1: At line 15 in Reports.csl2: Parameter '{' is not supported
```



---

## 4. The population section

### 4.1. Introduction

The population section specifies the model of the population dynamics. It describes the model structure, the population partitions and categories, the population processes (e.g., recruitment, ageing, migration, and mortality), the selectivities, and the associated parameters.

The population section includes:

- The population structure, the categories and ages in an age-based model;
- The initialisation process, the state of the partition at the start of the first year;
- The years over which the model runs, the start and end years of the model;
- The annual cycle, the number of time steps and the processes that are applied in each time step;
- The specification of and the parameters for the population processes, processes that add or remove individuals from a partition, or shift individuals between ages and categories in a partition;
- The selectivities;
- The parameters, their definitions, initial values, prior distributions, and other characteristics; and
- Derived quantities, e.g., mature biomass to include in density-dependent processes such as the spawner-recruit relationship

### 4.2. Population structure

The basic structure of the population section of a CASAL2 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. CASAL2 assumes an annual cycle.

Each year is defined by one or more time steps, with at least one process occurring in each time step. Each time step can represent a specific period of the calendar year, or it can be an abstract sequence of events.

The division of the year into time steps allows the user to specify the exact order in which processes and observations occur throughout the year. The user specifies the time step in which each process occurs. If more than one process occurs in the same time step, the order in which to apply each process is specified in the `@time_step` block.

The mortality processes are grouped into a mortality block: in every time step, a mortality block (a group of consecutive mortality-based processes) exists in which individuals are removed from the partition (see Section 4.4.2).

The state is the current status of the population at any given time. The state can change one or more times in each time step in each year. The state object must contain sufficient information to determine how the population changes over time, given a model and a complete set of parameters.

The state can undergo a number of possible changes during the annual cycle, called transitions. Transitions are applied by processes. Transitions include recruitment, natural mortality, fishing

mortality, ageing, migration, tagging events, and maturation. These transitions are repeated for each year of the model, although some processes can be specified to occur in a subset of years only.

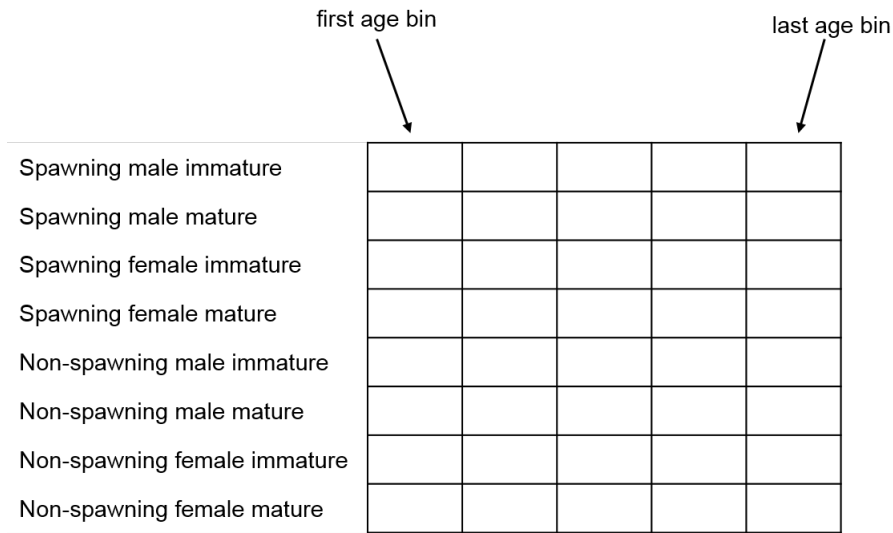
The key element of the state is the partition. The partition separates the total number of individuals in the population into different ages, lengths, and/or categories. The categories include sex, maturity state, area, and species. CASAL2 has no predefined categories; *all* categories are defined by the user, which differs from CASAL (Bull et al., 2012).

The partitions can be conceptualised as a matrix, where each row represents a category and the columns are the age classes (Figure 4.1). Each row represents all individuals that category.

The names of categories are user defined. There must be at least one category defined for each model. The model ages are a sequence from  $age_{min}$  to  $age_{max}$ , with the last age optionally a plus group. The age-length relationship for each category must also be defined for an age-based model, although this relationship could be defined as "none". An example of four categories based on sex and area is:

```
@categories
format mature.sex
names          spawn.male  spawn.female  nonspawn.male  nonspawn.female
age_lengths    male_AL     female_AL     male_AL        female_AL
```

Consider a model of a fish population with a mature fishery and a non-spawning fishery. Assume that the non-spawning fishery occurs in the non-spawning area. The mature fish then migrate to the spawning area, where the spawning fishery occurs. At the end of spawning, these fish, along with the recruits from the previous year, migrate back to the non-spawning area. The fish population can be represented with partitions by age, sex, maturity, and area (spawning and non-spawning areas). So the partition has 8 rows of numbers-at-age, for 2 sexes  $\times$  (mature or immature)  $\times$  2 areas.



	first age bin							last age bin
Spawning male immature								
Spawning male mature								
Spawning female immature								
Spawning female mature								
Non-spawning male immature								
Non-spawning male mature								
Non-spawning female immature								
Non-spawning female mature								

**Figure 4.1: A visual representation of a partition.**

For this example four time steps are defined and labelled 1 through 4: *step1* for the non-spawning fishery period, *step2* for the migration to the spawning area, *step3* for the spawning fishery period, and *step4* for recruitment and migration back to the non-spawning area. The default order of processes within a time step has migrations occurring before fisheries (TODO: check this), so that the processes in steps 2 and 3 could have occurred in one time step. Other details that describe the

population structure are also linked to time steps, such as proportion of natural mortality occurring in each time step and in which time step the observations occur.

The definition and ordering of processes in multiple time steps can be used to represent complex dynamics, with the intermingling of multiple species and stocks, migration patterns occurring over multiple areas, and/or multiple sources of anthropogenic impact using a range of methods which cover different areas and times. However, the complexity of a stock structure definition is constrained by the available data. It is challenging to use a complex structure to model a population when there are no observations to support that structure. For information on how to define categories and use the shorthand syntax see Section 14.2.

The model is run from the start year through the final year. It can also be run past the final year to project the state of the population through the final projection year.

To specify a model with two categories, male and female, population ages 1-20, with the last age a plus group, three time steps, and sex-specific age-length relationships, the `@model` and `@categories` blocks are:

```
@model
start_year 1901
final_year 2000
projection_final_year 2010
base_weight_units tonnes
min_age 1
max_age 20
age_plus_group true
initialisation_phases Equilibrium_phase
time_steps step1 step2 step3

@categories
format sex
names male female
age_lengths male_growth female_growth
```

### 4.3. The state object and the partition

The key component of the state object is the partition, a matrix that stores the numbers of individuals at age or length for each category. A category represents a group of individuals that have the same attributes, e.g., life histories characteristics, growth rates, etc.

- Sex (male or female)
- Area
- Maturity (immature or mature)
- Growth path
- Tagging event
- Stock
- Species

A stock is defined as a population of individuals which recruits to that population. Maturity can either be defined as a separate category in the partition, or calculated from the population at the time required; see Section 4.11 for the treatment of maturity when maturity is not a category in the partition.

Each CASAL2 model requires:

- The minimum and maximum population ages
- Whether the maximum age is a plus group
- The names of all of the categories

The age range is sequential by 1 starting with the minimum age through the maximum age.

CASAL2 allows categories of the partition to exist for a subset of years of a model. This feature enables more efficient computations when models contain categories that do not persist over all model years. A model may define one-off processes that transition individuals from one category into another in a subset of the model initialisation phases or years (e.g., tagging events). Excluding categories for certain years can be more efficient as CASAL2 will not initialise these categories or apply processes to categories in years or time steps in which they do not exist.

The structure of the partition is defined in a configuration block with the `@categories` block (Section 4.2).

Derived quantities are another important component of the state object. An example of a derived quantity is spawning stock biomass (SSB; the biomass of [female] spawning fish calculated at the mid point of the spawning season). CASAL2 calculates derived quantities using the command `@derived_quantity`, which may be required for some processes. In fisheries stock assessment models, a recruitment process which includes a stock-recruitment relationship requires the definition of a derived quantity that specifies the mid-season spawning stock biomass.

### 4.4. Time sequences

The time sequence of the model is defined in:

- The annual cycle
- The mortality blocks
- The initialisation phases
- The model run years
- The projection years

#### 4.4.1. The 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 specific time periods and processes. Any number of processes can occur within each time step, in any order, although there are restrictions for mortality-based processes (see Section 4.4.2); processes can occur multiple times within each time step. Time steps are not implemented during the initialisation phases (effectively there is only one initialisation time step), and the annual cycle in the initialisation phases can be different from the annual cycle specified for the model years.



#### 4.4.2. The mortality blocks

There is an associated *mortality block* for every time step in the annual cycle. Mortality blocks are a key concept in CASAL2.

Mortality blocks are used to define the "point" in the model time sequence when observations (see Section 6) are evaluated, and derived quantities (see Section 4.6) are evaluated.

A mortality block is defined as a consecutive sequence of mortality processes within a time step. The mortality processes are described in Subsection 4.5.3.

CASAL2 requires that each time step has exactly one mortality block. Either all of the mortality processes in a time step must be sequential (i.e., there can not be a non-mortality process between any two mortality processes within any one time step); or, if no mortality processes occur in a time step, then the mortality block is defined to occur at the end of the time step.

CASAL2 will output an error if more than one mortality block occurs in a single time step. Use separate time steps to define a sequence of mortality blocks.



**Figure 4.2: A example sequence for an annual cycle.**

#### 4.4.3. The initialisation phases

Initialisation is the process of determining the model starting state. The initial state can be equilibrium/steady state or some other initial state for the model (e.g., exploited), prior to the start year of the model.

There are multiple options for partition initialisation in CASAL2, including

- Iterative
- Derived
- Cinitial
- Fixed

Model initialisation can also occur in several phases, each of which can use a different method. The initialisations are performed in sequence. At the end of all of the initialisation phases, CASAL2 then

runs through the model years applying the user-defined processes in each time step in the annual cycle.

The multi-phased initialisation allows for flexibility in the number and type of initialisations, for initialising a non-equilibrium starting state, or applying simple processes before applying more complex ones.

Each phase of the initialisation defaults to have the same processes and in the same order as defined in the annual cycle. An initialisation phase can include other processes with the `insert_processes` subcommand.

In each initialisation phase, the processes defined for that phase are applied and used as the starting point for the following phase or, if it is the last phase, the start year of the model.

The *first* initialisation phase is always initialised with each age and category set to zero. Care must be taken when using complex category inter-relationships or density-dependent processes that depend on a previously calculated state, as they may fail when used in the first phase of an initialisation.

Multi-phase iterations can also be used to determine if an initialisation has converged. A second initialisation phase can be added for 1 year, with the same processes applied as in the first phase. The state at the end of the first and second phase is then output. If these states are identical, then it is likely that the initialisation has converged to an equilibrium state.

The subcommands for including or excluding processes are `insert_processes` and `exclude_processes`.

For the `insert_processes` the syntax is:

```
insert_processes time_step_label(process_label_in_annual_cycle) = label_new_process
```

For example, this subcommand could be used in a `@time_step` labelled `Oct_Nov`, which includes the `@process` labelled `predationInit`, and before the `@process` labelled `Instantaneous_Mortality`,

```
insert_processes Oct_Nov(Instantaneous_Mortality)=predationInit
```

To include a process at the end of the time step:

```
insert_processes Oct_Nov()=predationInit
```

To exclude a process from an initialisation phase, use the subcommand `exclude_processes` in a command `@initialisation_phase`,

```
exclude_processes Instantaneous_Mortality
```

This command removes the process labelled `Instantaneous_Mortality` during that particular initialisation phase.

#### 4.4.3.1. Iterative Initialisation

The *Iterative* initialisation is a general solution for initialising the model. The iterative method can be slow to converge, depending on the model, but can work on even complex structured models that may be difficult or impossible to implement using analytic approximations.

The number of iterations in the iterative initialisation can increase the model output, and the number of iterations should be chosen to be large enough to allow the population state to fully converge. A period of about two generation times is recommended to ensure convergence. CASAL2 can be configured to report convergence statistics that can assist in determining convergence properties.

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

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

Hence, for initialisation define:

- The number of initialisation phases,
- The number of years in each phase, and
- The processes to apply in each phase, where the default processes are those applied in the annual cycle

An example with one initialisation phase:

```
@model
...
initialisation_phases Iterative_initialisation

@initialisation_phase Iterative_initialisation
type iterative
years 50
lambda 0.0001
convergence_years 20 40
```

#### 4.4.3.2. Derived Initialisation

The Derived initialisation is an analytical solution that calculates the equilibrium age structure and the plus group using a geometric series solution. The benefit of this method is it can be solved in  $\text{max\_age} - \text{min\_age} + 1$  years/steps/units?, so it is computationally faster than the iterative initialisation phase. Under some process combinations (e.g., one-way migrations) this initialisation does not calculate the exact equilibrium partition. When using this initialisation, confirm that the partition has reached an equilibrium state by either comparing with an iterative initialisation, or by adding a second iterative initialisation phase with a limited number of iterations for comparison.

An example with one initialisation phase:

```
@model
...
initialisation_phases Equilibrium_initialisation

@initialisation_phase Equilibrium_initialisation
type derived
```

#### 4.4.3.3. Cinitia Initialisation

The `Cinitia` initialisation is used only as a second or greater phase initialisation, and can only be applied after `Derived` or `Iterative` initialisation phases. This initialisation can be a method for estimating the non-equilibrium state of population if there is exploitation before the data start. The estimated `Cinitia` factors shift the initial population away from an equilibrium state prior to the start year. It would be helpful to include an observation of age composition data for the first year of the model in order to estimate the non-equilibrium population state.

An example with two initialisation phases:

```
@model
...
initialisation_phases Iterative Cinitia

@initialisation_phase Iterative
type iterative
years 10
lambda 0.0001
convergence_years 10 20

@initialisation_phase Cinitia
type cinitia
categories spawn.male+nonspawn.male spawn.female+nonspawn.female
table n
spawn.male+nonspawn.male      5e7 5e7 7e6 6e6 5e6 4e6 3e6 2e6 1e6 1e6 1e1 1e1 1e1 1e1
spawn.female+nonspawn.female 5e7 5e7 7e6 6e6 5e6 4e6 3e6 2e6 1e6 1e6 1e1 1e1 1e1 1e1
end_table
```

The `Cinitia` factors can also be estimated with the syntax

```
@estimate cinit_male
parameter initialisation_phase[Cinitia].spawn.male+nonspawn.male
same initialisation_phase[Cinitia].spawn.female+nonspawn.female
lower_bound 2e2 2e2 2e2 2e2 2e2 2e2 2e2 2e2 2e2 2e2 2e0 2e0 2e0 2e0
upper_bound 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9 2e9
type uniform
```

#### 4.4.3.4. Fixed Initialisation

The `Fixed` initialisation uses a user-defined table as the initial partition numbers-at-age prior to the start year. Models can be initialised by specifying the numbers-at-age for each category. When initialising models with this type, undefined behaviour may be result if the model applies processes that require derived quantities to be calculated in the initialisation phase.

An example with one initialisation phase:

```
@model
...
initialisation_phases Fixed

@initialisation_phase Fixed
type state_category_by_age
categories male female
```

```

min_age 3
max_age 10
table n
male 1000 900 800 700 600 500 400 700
female 1000 900 800 700 600 500 400 700
end_table

```

#### 4.4.4. Model run years

Following initialisation, the model then runs over the user-defined years, from `start_year` to `final_year`. For this part of the model, the annual cycle can be broken into multiple time steps per year, and observations can be associated with specific time steps.

Processes are applied in the order specified within each time step. These processes can be the same or different from the processes specified for the initialisation phases.

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` to the end of year `final`. The projection then extends the run time up to the end of year `project_final_year`.

The model properties must be specified:

- The number of time steps and the processes applied in each
- The first year, the model start year
- The last year, the model final year
- The last projection year, the model projection final year

An example of the syntax:

```

@model
start_year 1972
final_year 2016
projection_final_year 2021
## Define the ages in the partition
min_age 1
max_age 30
age_plus true
base_weight_units tonnes
initialisation_phases Equilibrium_state
## Define the annual cycle
time_steps Sep_Feb Mar_May Jun_Aug

## Define the "rows" in the partition
## This is a single sex and area population
@categories
format stock
names HAK4
age_lengths age_size

@initialisation_phase Equilibrium_state
type derived

## Define the processes in the annual cycle
## A list of labels in each time step that correspond to a process

```

```
@time_step Sep_Feb
processes Recruitment Instantaneous_Mortality
```

```
@time_step Mar_May
processes Instantaneous_Mortality
```

```
@time_step Jun_Aug
processes Ageing Instantaneous_Mortality
```

#### 4.4.5. Projection years

The Projection functionality runs the model forwards, using stochastic and/or deterministic values for some population parameters, such as recruitments and catches.

The CASAL2 command to run the model in projection mode is `casal2 -f 1`. The number that follows the `-f` parameter indicates the number of projections to generate for each set of parameters supplied. This functionality allows for the exploration of many scenarios with a single set of parameters. The number of projections should be greater than 1 only if applying a projection type that is stochastic.

The `--tabular` flag should be used when running projections after a Bayesian analysis. This option will output a tabular report (see Section 7.21) which can then be analysed in **R**.

Projection years are after the model run years, and are defined as the `final_year + 1` through the `final_projection_year`.

For a projection run in CASAL2 the model is initialised and run through the model years from `start_year` to `final_year`. During this run mode CASAL2 stores all parameter values so that projection classes can allow parameters before `final_year` to be projected. The model then is re-run from `start_year` to `projection_final_year`, where any parameter can either be fixed or drawn from a stochastic distribution or process.

An example of when a parameter is projected before the projection phase has started is for year class parameters. The last few year class parameters may be poorly estimated, which depends on the quality and coverage of the composition data that could inform these parameters or the use of a recruitment index. Thus, users may assume that these parameters are unknown and apply projection methods for the future values.

CASAL2 has no default projection properties for parameters that are specified by year, e.g., year class strength parameters. The projections for these parameters must be specified using the `@project` command block. CASAL2 will produce errors if run in projection mode without a `@project` block for the `ycs_values` parameter being specified.

CASAL2 allows any estimable parameter to be specified in a `@project` block and then used in a projection. The available projection types for these parameters include:

- constant
- lognormal
- empirical-lognormal
- empirical re-sampling
- user-defined

The projection classes available, and examples of their syntax, are in Section 4.13.

The subcommands `years` and `parameter` are common to all projection methods. The argument `multiplier` is a constant which is multiplied with the projected value after it has been generated.

**Note for the year class parameters:** the definition of year applies to the `ycs_years`, not the model years. As defined in Section 4.5.1.2, `ycs_years` are offset between the time of spawning and when individuals are added to the partition.

## 4.5. Population processes

Population processes are processes that change the model state. These processes produce changes in the partition by adding and removing individuals, or by moving individuals between ages and/or categories.

The population processes include:

- recruitment,
- ageing,
- growth,
- maturation,
- mortality events (e.g., natural and fishing), and
- category transition processes, i.e., processes that move individuals between categories while preserving their age structure.

There are two types of processes: (1) processes that occur across multiple time steps in the annual cycle, e.g., `mortality_constant_rate` and `mortality_instantaneous`; and (2) processes that occur only within the time step in which they are defined. These processes are applied in the user-defined order when initialising the model, and then for a user-defined order in each year in the annual cycle.

### 4.5.1. Recruitment

Recruitment processes are defined as processes that add new individuals to the partition. CASAL2 has two options for recruitment processes, constant recruitment and the Beverton-Holt stock-recruitment relationship (Beverton and Holt, 1957).

In the recruitment processes, a number of individuals are added to a single age class within the partition, with the number determined by the type of recruitment process specified. If more than one category (of recruits?) is defined, then the proportion of recruits to be added to each category is specified by the `proportions` property, or multiple recruitment processes can be defined. For example, if recruiting to categories labelled `male` and `female`, then the proportions may be set to 0.5 and 0.5, so that half of the recruits are added to the male category and the other half to the female category.

Recruitment can differ between a spawning event or the creation of a cohort/year class. In a fisheries context, recruitment usually refers to individuals "recruiting" to a fishery. This definition is used because there is usually not a lot of information on younger age classes between the time of spawning and being vulnerable to a survey or fishery for data collection. Thus, the model configuration may specify the population for which data are available.

The offset between spawning and recruitment is parameterised either by the recruitment variable `age`, or `min_age`, which is the default value for the `age` property in the recruitment process. The

CASAL2 parameter `age` is the same as the CASAL parameter `y_enter`.

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

$$N_{y,a,j} \leftarrow N_{y,a-1,j} + p_j(R_y) \quad (4.2)$$

where  $N_{y,a,j}$  is the numbers in year  $y$  and category  $j$  at age  $a$ ,  $p_j$  is the proportion added to category  $j$ , and  $R_y$  is the total number of recruits in year  $y$ .

#### 4.5.1.1. Constant recruitment

In the constant recruitment process the total number of recruits added in each year  $y$  in age  $a$  is  $R_y$ , with  $R_y = R_0$  for all years

$$R_{y,j} = p_j(R_0) \quad (4.3)$$

Constant recruitment is equivalent to a Beverton-Holt recruitment process with steepness ( $h$ ) set to 1.

For example, to specify a constant recruitment process where individuals are added to the male and female immature categories at  $age = 1$  in equal proportion (`proportions = 0.5`), and the number to add is  $R_0 = 5 \times 10^5$ , the syntax is

```
@process Recruitment
type constant_recruitment
categories male.immature female.immature
proportions 0.5 0.5
r0 500000
age 1
```

#### 4.5.1.2. Beverton-Holt recruitment

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

$$R_{y,a,j} = p_j(R_0 \times YCS_{y_{cs\_year}} \times SR(SSB_{y_{cs\_year}})) \quad (4.4)$$

where

$$y_{cs\_year} = y - ssb\_offset \quad (4.5)$$

and  $a$  is age,  $p_j$  is the proportion of recruits to enter category  $j$ , and `ssb_offset` is the number of years lag between spawning and recruitment.



Recruitment refers to recruitment into the population and may differ from the spawning event. See below on more information about `ssb_offset`. In general this parameter should not be specified by the user.

$SR(SSB_y)$  is the Beverton-Holt stock-recruit relationship parametrised by the steepness  $h$ , and based on [Mace and Doonan \(1988\)](#) parametrisation

$$SR(SSB_y) = \frac{SSB_y}{B_0} / \left( 1 - \frac{5h-1}{4h} \left( 1 - \frac{SSB_y}{B_0} \right) \right) \quad (4.6)$$

The Beverton-Holt recruitment process requires a value for  $B_0$  and  $SSB_y$  to calculate the number of recruits. A derived quantity (see Section 4.6) 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, which is defined by the parameter `b0_initialisation_phase`.

During initialisation the  $YCS$  multipliers are assumed to be equal to 1, and recruitment that happens in the initialisation phases that occur before and during the phase when  $B_0$  is determined are assumed to have steepness  $h = 1$  (i.e., in those initialisation phases, recruitment is equal to  $R_0$ ).

Recruitment in the initialisation phases after the phase where  $B_0$  was determined are calculated using the Beverton-Holt stock-recruit relationship.  $R_0$  and  $B_0$  have a direct relationship when there are no density-dependent processes in the annual cycle. Models can thus be initialised using  $B_0$  or  $R_0$ .

The property `ssb_offset` should not be manually specified; CASAL2 determines `ssb_offset` by the order of ageing, recruitment, spawning, and the recruitment parameter `age`

- if the annual time step order is recruitment, ageing, spawning, then `ssb_offset` should equal `age + 1`, or
- if the annual time step order is spawning, ageing, recruitment, then `ssb_offset` should equal `age - 1`, or
- `ssb_offset = age`

There may be scenarios where the user will input these values, e.g., if there are multiple ageing processes in the annual cycle. CASAL2 does not have functionality to accommodate this situation, so in this case `ssb_offset` would be manually defined.

There are two variants of this process and they refer to how the stock recruitment residuals or  $YCS_{y_{cs\_year}}$  are parametrised. This parametrisation can either be in natural space as year class strength ( $YCS$ ) multipliers, or in log space as recruitment deviations. Due to the difference in terminology, these variants are implemented in two separate processes, `recruitment_beverton_holt` and `recruitment_beverton_holt_with_deviations`, respectively.

### YCS ( $YCS_y$ )

The  $YCS$  parameter (`y_{cs\_years}`) is defined in Equation (4.5). The parameter `y_{cs\_values}` is referenced by the `y_{cs\_years}` parameter and is important to note when defining `@estimate`, `@project`, and `@time_varying` blocks for the parameter `y_{cs\_values}`. An example is at the end of the section.

A common practice when estimating  $YCS$  is to standardise using the Haist parametrisation, which was described by V. Haist. CASAL2 will standardise  $YCS$  only if subcommand `standardise_y_{cs\_years}` is defined. The model parameter `y_{cs\_values}` is a vector  $\mathbf{Y}$ , covering the

years from `start_year - ssb_offset` to `final_year - ssb_offset`, as defined by the parameter `ycs_years`. The resulting year class strengths are calculated by  $YCS_i = Y_i / \bar{Y}$ , where the mean is calculated over the user-specified years `standardise_ycs_years`.

$$YCS_i = \begin{cases} Y_i / \text{mean}_{y \in S}(Y_y) & : y \in S \\ Y_i & : y \notin S \end{cases}$$

where  $S$  is the set of years from `standardise_ycs_years`. One effect of this parametrisation is that  $R_0$  is then defined as the mean estimated recruitment over the set of years  $S$ , because the mean  $YCS$  multiplier over these years will always be one.

Typically `standardise_ycs_years` is defined to span the years over which  $YCS$  is reasonably well estimated. For years that are not well estimated,  $Y_y$  can be set to 1 for some or all years  $y \in S$  (which is equivalent to forcing  $R_y = R_0 \times SR(SSB_y)$ ) by setting the lower and upper bounds of these  $Y$  values to 1. An exception to this might occur for the most recent  $YCS$  values, which the user may estimate but not include in the definition of  $R_0$  (because the estimates may be based on too few data). One or more years may be excluded from the range of years for the averaging process of the Haist parametrisation.

The advantage of the Haist parametrisation is that a large penalty is not necessary to force the mean of the  $YCS$  parameter to be 1, although a small penalty should still be used to stop the mean of  $Y$  from drifting. These adjustments may improve MCMC performance. Projected  $YCS$  values are not affected by this feature. A disadvantage with this parametrisation in a Bayesian analysis is that the prior applies to  $Y$ , not  $YCS$ .

An example of the specification of a Beverton-Holt recruitment process, where individuals are added to the category "immature" at  $age = 1$ , and the number added is  $R_0 = 5 \times 10^5$ ; `SSB_derived_quantity` is a derived quantity that specifies the total spawning stock biomass that contributed to the year class, with  $B_0$  the value of the derived quantity at the end of the initialisation phase labelled `phase1`; and  $YCS$  are standardised to have mean one in the period 1995 to 2004, and recruits enter into the model two years following spawning

```
@process Recruitment
type recruitment_beverton_holt
categories immature
proportions 1.0
r0 500000
b0_initialisation_phase phase1
steepness 0.75
age 1
ssb SSB_derived_quantity
standardise_ycs_years 1995:2004
ycs_years 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006
ycs_values 0.65 0.87 1.6 1.13 1.0235 0.385 2.653 1.35 1 1 1 1 1
```

### Recruitment deviations, $\epsilon_y$

Recruitment deviations represent the stock-recruitment relationship residuals in log space, with the link between  $YCS_y$  and  $\epsilon_y$

$$YCS_y = \exp(\epsilon_y - b_y \sigma_R^2 / 2) \quad (4.7)$$

where  $\varepsilon_y \sim N(0, \sigma_R^2)$ ,  $\sigma_R^2$  is the variance of the stock-recruitment residuals, and  $b_y$  is a bias correction defined by [Methot Jr and Taylor \(2011\)](#)

$$b_y = \left\{ \begin{array}{ll} 0, & \text{for } y \leq y_1^b \\ b_{\max}(1 - \frac{y-y_1^b}{y_2^b-y_1^b}), & \text{for } y_1^b < y < y_2^b \\ b_{\max}, & \text{for } y_2^b \leq y \leq y_3^b \\ b_{\max}(1 - \frac{y_3^b-y}{y_4^b-y_3^b}), & \text{for } y_3^b < y < y_4^b \\ 0, & \text{for } y_4^b \leq y \end{array} \right\} \quad (4.8)$$

The  $\varepsilon_y$  values are normally distributed in log space and thus lognormal when back-transformed to the resulting stock-recruitment relationship  $YCS_y$ . Recent work has found that this transformation does not technically lead to the *a priori* assumption that the resulting  $YCS_y$  are lognormal. See [Appendix A](#) for more discussion.

The ramp function described above for the bias correction has the additional subcommands controlling the ramp

- $y_1^b = \text{last\_year\_with\_no\_bias}$
- $y_2^b = \text{first\_year\_with\_bias}$
- $y_3^b = \text{last\_year\_with\_bias}$
- $y_4^b = \text{first\_recent\_year\_with\_no\_bias}$
- $b_{\max} = \text{b\_max}$

```
@process Recruitment
type recruitment_beverton_holt_with_deviations
categories immature
proportions 1.0
r0 500000
last_year_with_no_bias 1940
first_year_with_bias 1950
last_year_with_bias 2016
first_recent_year_with_no_bias 2018
b_max 0.85
b0_initialisation_phase phase1
steepness 0.75
age 1
ssb SSB_derived_quantity
deviation_years 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006
deviation_values 0 -0.2 0.4 0 0 0 0 0 0 0 0 0 0
```

To specify a Beverton-Holt recruitment for each stock, the information required is:

1.  $YCS$ , starting from year (`start_year - ssb_offset`) and extending up to year (`final_year - ssb_offset`)
2. the value of age (which is `y_enter` in CASAL)
3. the steepness parameter `h`
4. in a multi category model, the proportion of recruits for each category
5. a label for the derived quantity

When an `@initialisation_phase` (Section 4.4.3) `type = derived` is specified and the recruitment is defined by `b0`, then all categories must be specified in the `@recruitment` block. Usually in a recruitment processes only the categories that receive recruits need to be defined. For example, a population has a spawning area that is different from the area where recruits enter the population. An area-specific model could then be specified which contains spawning categories and recruiting categories. The recruiting categories would be specified in the subcommand `categories`, as these would be the categories receiving recruits.

If `@initialisation_phase, type=derived` is used, then all categories that are a part of that recruitment process need to be specified as well

```
@process Recruitment
type recruitment_beverton_holt
categories recruits.male recruits.female spawn.male spawn.female
proportions 0.5 0.5 0.0 0.0
r0 500000
ssb SSB
....
```

The `proportions = 0.0` for "spawn.male" and "spawn.female" are needed due to the way the derived initialisation phase works. The derived initialisation finds a solution for when `r0 = 1.0` based on an infinite geometric series for the plus group, and scales the initial partition by `r0`. Thus, if all categories are not specified, then those that are missed would not be initialised to true values and this could lead to inaccurate model outputs. This set-up extends to multiple-stock fisheries model configurations as well, where all of the categories that make up the stock need to be listed.

#### 4.5.2. Ageing

The ageing process "ages" individuals, i.e., this process moves all individuals in the named categories  $j$  from one age class  $a$  to age class  $a + 1$ , or accumulates them if the last age class is a plus group.

The ageing process is defined as,

$$\text{element}(a + 1, j) \leftarrow \text{element}(a, j) \quad (4.9)$$

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

$$\text{element}(a_{\max}, j) \leftarrow \text{element}(a_{\max}, j) + \text{element}(a_{\max-1}, j). \quad (4.10)$$

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

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

**Note:** the ageing process is *NOT* applied by CASAL2 by default. As with other processes, CASAL2 will not apply a process unless it is defined and specified as a process within the annual cycle. Hence, it is possible to specify a model where a category is not aged. CASAL2 *will NOT check or otherwise warn if there is a category defined where ageing is not applied.*

### 4.5.3. Mortality

There are 8 types of mortality processes available in CASAL2:

- constant rate,
- event,
- biomass-event,
- instantaneous,
- instantaneous retained,
- Hollings,
- initialisation, and
- a density-dependent relationship based on prey suitability.

These processes remove individuals from the partition, either as a rate, as a total number (abundance), as a biomass of individuals or, as a combination of these. CASAL2 does not (yet) implement the Baranov catch equation. However, instantaneous mortality is considered an approximation to the Baranov catch equation.

To apply both natural and biomass-event mortality, the mortality type `mortality_instantaneous` can be specified. Note that all mortality processes occur within the mortality block of a time step. See Section 4.4.2 for more information and definitions on mortality blocks.

#### 4.5.3.1. Constant mortality rate

To specify a constant annual mortality rate (e.g.  $M = 0.2$ ) for categories "male" and "female"

```
@process NaturalMortality
type mortality_constant_rate
categories male female
selectivities One One
m 0.2 0.2
```

The total number of individuals removed from a category

$$D_{j,t} = \sum_a N_{a,j,t} [1 - \exp(-S_{a,j} M_{a,j} p_t)] \quad (4.11)$$

where  $D_{j,t}$  is the total number of deaths in category  $j$  in time step  $t$ ,  $N_{a,j,t}$  is the number of individuals in category  $j$  of age  $a$  in time step  $t$ ,  $S_{a,j}$  is the selectivity value for age  $a$  in category  $j$ ,  $M_{a,j}$  is the mortality rate for category  $j$  for age  $a$ , and  $p_t$  is the proportion of the mortality rate to apply in time step  $t$ .

The mortality rate process requires a selectivity. To apply the same mortality rate over all age classes in a category, use a selectivity defined as  $S_{a,j} = 1.0$  for all ages  $a$  in category  $j$

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

Age-specific mortality rates can also be applied. For example, the hypothesis that mortality is higher for younger and older individuals and lowest when individuals are at their optimal fitness could be defined by using a double exponential selectivity (see Section 4.12)

```
@selectivity age_specific_M
type double_exponential
x0 7.06524
x1 1
x2 17
y0 0.182154
y1 1.43768
y2 1.57169
alpha 1.0

@process NaturalMortalityByAge
type mortality_constant_rate
categories male female
selectivities age_specific_M age_specific_M
m 1.0 1.0
```

In this definition `m` is set to 1.0 and the rate is described through the selectivity. This concept can be constructed similarly for other mortality methods such as `instantaneous_mortality`.

#### 4.5.3.2. Event and biomass-event mortality

The event mortality and biomass-event mortality processes are applied in a similar manner, except that they remove a specified abundance (number of individuals) or biomass, respectively. These mortality processes can be used to define mortality events where the numbers of removals are known, e.g., fishing, rather than applying mortality as a rate.

In these cases, the abundance or biomass removed is also constrained by a maximum exploitation rate. CASAL2 removes as many individuals or as much biomass as possible, while not exceeding the maximum exploitation rate.

Event mortality processes require a penalty to avoid estimating parameter values that will not allow the defined number of individuals to be removed. The model penalises those parameter estimates that result in an too low a number of individuals in the defined categories (after applying selectivities) to allow for removals at the maximum exploitation rate, with a similar penalty for biomass. See Section 5.8 for more information on how to specify penalties.

The event mortality applied to user-defined categories  $i$ , with the numbers removed at age  $j$  determined by a selectivity-at-age  $S_j$ :

First, calculate the vulnerable abundance for each category  $j$  in  $1 \dots J$  for ages  $a = 1 \dots A$  that are subject to event mortality

$$V_{a,j} = S_{a,j} N_{a,j} \quad (4.12)$$

and define the total vulnerable abundance  $V_{total}$  as

$$V_{total} = \sum_j \sum_a V_{a,j} \quad (4.13)$$

The exploitation rate to apply is

$$U = \begin{cases} C/V_{total}, & \text{if } C/V_{total} \leq U_{max} \\ U_{max}, & \text{otherwise} \end{cases} \quad (4.14)$$

The number removed  $R_{a,j}$  from each age  $a$  in category  $j$  is,

$$R_{a,j} = UV_{a,j} \quad (4.15)$$

For example, to specify an **abundance-based** fishing mortality process with catches given for a set of specific years over categories "immature" and "mature", with selectivity "FishingSel", and assuming a maximum possible exploitation rate of 0.7, 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
```

and specified similarly for a **biomass-based** fishing mortality process

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

#### 4.5.3.3. Instantaneous mortality

The instantaneous mortality process combines both natural mortality and event biomass mortality into a single process. This allows the simultaneous application of both natural mortality and anthropogenic mortality to occur across multiple time steps. This process applies half the natural mortality in each time step, then the mortalities from all the concurrent removals instantaneously, then half of the natural mortality. In fisheries models this is the most commonly used mortality process.

This process allows for multiple removal events, e.g., a fisheries model with multiple fisheries and/or fleets. A removal method can occur in one time step only, although multiple removals can be defined to cover events during the year.

The equations for instantaneous mortality:

TODO redo equations, as notation is not consistent with that above, e.g.,  $S_{a,j}$

- An exploitation rate (actually a proportion) is calculated for each fishery, as the catch divided by the selected-and-retained biomass,

$$U_f = \frac{C_f}{\sum_a \bar{w}_a S_{f,a} n_a \exp(-0.5tM_a)}$$

- The mortality pressure associated with method  $f$  is defined as the maximum proportion of fish taken from any element of the partition in the area affected by the method  $f$

$$U_{f,obs} = \max_a \left( \sum_k S_{k,a} U_k \right)$$

where the maximum is over all partition elements affected by fishery  $f$ , and the summation is over all methods  $k$  which affect the  $j$ th partition element in the same time step as fishery  $f$ .

In most cases the mortality pressure will be equal to the exploitation rate (i.e.,  $U_{f,obs} = U_f$ ), but can be different if: (a) there is another removal method operating in the same time step as removal method  $f$  and affecting some of the same partition elements, and/or (b) the selectivity  $S_{f,a}$  does not have a maximum value of 1.

There is a maximum mortality pressure limit of  $U_{f,max}$  for each method of removal  $f$ . So, no more than proportion  $U_{f,max}$  can be taken from any element of the partition affected by removal method  $f$  in that time step. Clearly,  $0 \leq U_{max} \leq 1$ . It is an error if two removal methods, which affect the same partition elements in the same time step, do not have the same  $U_{max}$ .

For each  $f$ , if  $U_{f,obs} > U_{f,max}$ , then  $U_f$  is multiplied by  $U_{f,max}/U_{f,obs}$  and the mortality pressures are recalculated. In this case the catch actually taken from the population in the model will differ from the specified catch,  $C_f$ .

- The partition is updated using

$$n'_a = n_a \exp(-tM_a) \left[ 1 - \sum_f S_{f,a} U_f \right]$$

For example, to apply natural mortality of 0.20 across three time steps on both male and female categories, with two methods of removals (fisheries FishingWest and FishingEast) and their respective catches (kg) known for years 1975:1977 (the catches are given in the `catches` table and information on selectivities, penalties, and maximum exploitation rates are given in the `method` table), the syntax is

TODO where is `time_step_ratio` and its usage defined?

```
@process instant_mort
type mortality_instantaneous
m 0.20
time_step_ratio 0.42 0.25 0.33
selectivities One
categories male female
units kgs

table catches
year FishingWest FishingEast
1975 80000 111000
1976 152000 336000
1977 74000 1214000
end table

table method
method      category  selectivity u_max  time_step penalty
FishingWest  stock      westFSel   0.7    step1    CatchPenalty
FishingEast  stock      eastFSel   0.7    step1    CatchPenalty
end_table
```



and for referencing catch parameters for use in projecting, time-varying, and estimating, the syntax is

```
parameter process[mortality_instantaneous].method_"method_label"{2018}
```

where "method\_label" is the label from the catch or method table and continuing the example,

```
parameter process[instant_mort].method_FishingWest{2018}
```

To calculate weight by empirical weight-at-age matrices as described in Section 4.9, the method table would include an additional column to reference weight-at-age objects:

```
@age_weight jan_weight_at_age
type data
table data
year 1 2 3 4
1980 3.4 5.6 7.23 8.123
end_table

table method
method      category  selectivity  u_max  time_step  penalty      age_weight
FishingWest stock     westFSel     0.7    step1      CatchPenalty jan_weight_at_age
FishingEast stock     eastFSel     0.7    step1      CatchPenalty jan_weight_at_age
end_table
```

#### 4.5.3.4. Instantaneous mortality with retained catch and discards

The instantaneous mortality retained process builds on the instantaneous mortality process (4.5.3.3) which has simultaneous applications of fishing and natural mortality, but with all catch-at-sea being landed, i.e., no discarding. The process `mortality_instantaneous_retained` allows for retained catch, discards, and also a mortality to be applied to discards, i.e., some are allowed to survive. The method for taking catch from the partition and the constraints used are the same as in `mortality_instantaneous`.

This process was implemented to address issues with the pot fishery for blue cod which has a minimum legal size and so some catch is discarded at sea and some of these discards are expected to survive (based on some experimental work). There are length data taken at sea, so the total catch selectivity can be estimated, and length and age data taken from the landed catch (retained), so the retention selectivity can also be estimated.

In this mortality process, discard mortality is specified by defining a selectivity to represent mortality by age or length (e.g., constant or asymptotic descending logistic). This discard selectivity is not be estimated since there is no observation class associated with it. If discard mortality is not provided, it is assumed that all discards die. Landed catch, and both the retained and total catch selectivities must be specified.

Extending the example shown in instantaneous mortality process (4.5.3.3) to use retained weight instead of catch, the commands are:

```
@process FishingRetainedCatch
type mortality_instantaneous_retained
# natural mortality
```

```

m 0.20
# the ratio of natural mortality in each of the three time steps
time_step_ratio 0.42 0.25 0.33
selectivities One
#for natural mortality by age
categories male female
units kgs

table catches
# two fisheries, West and East
year FishingWest FishingEast
# the catches are now landed catch
1975 80000 111000
1976 152000 336000
1977 74000 1214000
end table

table method
# all discards die
method      category selectivity retained_selectivity u_max time_step penalty
FishingWest stock    westFSel   westRetainedSel    0.7  step1  CatchPenalty
FishingEast stock    eastFSel   eastRetainedSel    0.7  step1  CatchPenalty
end_table

```

If discard mortality is less than 1.0, use:

```

table method
# 50% discard mortality
method      category selectivity retained_selectivity discard_mortality u_max time_step penalty
FishingWest stock    westFSel   westRetainedSel    DisMort    0.7  step1  CatchPer
FishingEast stock    eastFSel   eastRetainedSel    DisMort    0.7  step1  CatchPer
end_table

@selectivity DisMort
Type constant
# 50% mortality of discards
c 0.5

```

See the instantaneous mortality process (4.5.3.3) for referencing catch parameters and calculating weight using empirical weight-at-age matrices.

The report outputs total catch, actual landed catch, and discards, without and with discard mortality:

```

@report Mortality
type process
process Instantaneous_Mortality_Retained

```

TODO redo notation, as it is not consistent with that above, e.g.,  $S_{a,j}$  and  $R_y$

In the following, fisheries are indexed by  $f$ , and  $a$  indexes both age and category combinations.

The total catch is found by applying a selectivity,  $S_{f,a}$ , in the same way as in the instantaneous mortality process. Retention,  $R_{f,a}$ , is defined by specifying a selectivity, which can be a function

of length or age. The retained catch is the product of these two values,  $R_{f,a} * S_{f,a}$ . If sex is in the partition, then there are potentially two retention curves, one for each sex.

In general, there is a retention curve for each category in the partition. This property does not apply to surveys. Discard mortality is also specified as a selectivity,  $D_{f,a}$ . The fraction of dead fish from fishing activity is  $S_{f,a} * [R_{f,a} + (1.0 - R_{f,a}) * D_{f,a}]$ . If  $D_{f,a}$  is 1.0, then all selected fish are dead, and if it is 0.0, then only the retained fish are dead.

The equations for the `mortality_instantaneous_retained` process:

- Total catch (catch-on-board),  $C_f$ , is calculated by (retained catch) \* VF / VR, where VF is vulnerable retained biomass,  $j$  indexes categories and  $t$  is the proportion of M in the time step, and VR is the full vulnerable biomass,  $VF = \sum_{a,j} \bar{w}_a S_{a,j} n_{a,j} \exp(-0.5tM_{a,j})$ .
- An exploitation rate (actually a proportion) is calculated for each fishery, as the total catch (retained + discards) divided by the selected biomass (VF above) using selectivity  $S_{f,a}$ ,

$$U_f = \frac{C_f}{\sum_a \bar{w}_a S_{f,a} n_a \exp(-0.5tM_a)}$$

- The mortality pressure associated with method  $f$  is defined as the maximum proportion of fish taken from any element of the partition in the area affected by the method  $f$ ,

$$U_{f,obs} = \max_a \left( \sum_k S_{k,a} U_k \right)$$

where the maximum is over all partition elements affected by fishery  $f$ , and the summation is over all methods  $k$  which affect the  $j$ th partition element in the same time step as fishery  $f$ .

In most cases the mortality pressure will be equal to the exploitation rate (i.e.,  $U_{f,obs} = U_f$ ), but can be different if: (a) there is another removal method operating in the same time step as removal method  $f$  and affecting some of the same partition elements, and/or (b) the selectivity  $S_{f,a}$  does not have a maximum value of 1.

There is a maximum mortality pressure limit of  $U_{f,max}$  for each method of removal  $f$ . So, no more than proportion  $U_{f,max}$  can be taken from any element of the partition affected by removal method  $f$  in that time step. Clearly,  $0 \leq U_{max} \leq 1$ . It is an error if two removal methods, which affect the same partition elements in the same time step, do not have the same  $U_{max}$ .

For each  $f$ , if  $U_{f,obs} > U_{f,max}$ , then  $U_f$  is multiplied by  $U_{f,max}/U_{f,obs}$  and the mortality pressures are recalculated. In this case the catch actually taken from the population in the model will differ from the specified catch,  $C_f$ .

- Discard numbers-at-age (including their share of natural mortality) is  $S_{a,j}(1 - R_{a,j})n_{a,j} \exp(-0.5tM_{a,j})$ , and those that die at the end of the time step (updating the partition) are  $D_{a,j}S_{a,j}(1 - R_{a,j})n_{a,j} \exp(-tM_{a,j})$ , where  $D_{f,a}$  is the fraction that die on return to the sea.
- The partition is updated by removing landed catch, natural mortality, and discard mortality

$$n'_a = n_a \exp(-tM_a) \left[ 1 - \sum_f S_{f,a} U_f (R_{f,a} + D_{f,a}(1 - R_{f,a})) \right]$$

#### 4.5.3.5. Holling mortality rate

The density-dependent Hollings mortality process applies the Holling Type II or Type III functions (Holling, 1959), and is generalised by the Michaelis-Menten equation (Michaelis and Menten, 1913).

This mortality process removes a number or biomass from a set of categories according to the total (selected) abundance (or biomass) and some "predator" abundance (or biomass), and is constrained by a maximum exploitation rate.

The mortality applied to user-defined categories  $k$ , with the numbers removed at age  $l$ , determined by a selectivity-at-age  $S_l$  is applied as follows:

First, calculate the total predator abundance (or biomass) over all predator categories  $k$  in  $1 \dots K$  and ages  $l = 1 \dots L$  that are applying the mortality

$$P_{k,l} = S_l^{predator} N_{k,l}^{predator} \quad (4.16)$$

And define the total predator abundance (or biomass)  $P_{total}$  as

$$P_{total} = \sum_K \sum_L P_{k,l} \quad (4.17)$$

Then calculate the total vulnerable abundance (or biomass) over all prey categories  $k$  in  $1 \dots K$  and ages  $l = 1 \dots L$  that are subject to the mortality

$$V_{k,l} = S_l^{prey} N_{k,l}^{prey} \quad (4.18)$$

Then define the total vulnerable abundance (or biomass)  $V_{total}$  as

$$V_{total} = \sum_K \sum_L V_{k,l} \quad (4.19)$$

The number to remove is then determined by

$$R_{total} = P_{total} \frac{aV_{total}^{x-1}}{b + V_{total}^{x-1}} \quad (4.20)$$

where  $x = 2$  for the Holling type II function,  $x = 3$  for the Holling type III function, or a different value of  $x \geq 1$  for the generalised Michaelis-Menten function;  $a > 0$  and  $b > 0$  are the Holling function parameters.

The exploitation rate to apply is

$$U = \begin{cases} R_{total}/V_{total}, & \text{if } R_{total}/V_{total} \leq U_{max} \\ U_{max}, & \text{otherwise} \end{cases} \quad (4.21)$$

And the number removed  $R$  from each age  $l$  in category  $k$  is

$$R_{k,l} = UV_{k,l} \quad (4.22)$$

The density-dependent Holling mortality process is applied either as a function of biomass or abundance, depending on the value of the `is_abundance` switch.

For example, a biomass Holling type II mortality process on prey `prey` by predator `predator` has the syntax

```
@process HollingMortality
type Holling_mortality_rate
is_abundance F
a 0.08
b 10000
x 2
categories prey
selectivities One
predator_categories predator
predator_selectivities One
u_max 0.8
```

#### 4.5.3.6. Initialisation-event mortality

Initialisation event mortality is a process that can occur only in the initialisation phase. It applies abundance or biomass mortality events specifically in initialisation phases. This option can be useful if the population is not in equilibrium before model start.

This process applies a single catch value for all iterations within the initialisation phase, and mortality will not be applied outside of the initialisation phase. This process should not be embedded in the annual cycle.

This process should be used in conjunction with the `insert_processes` command in the `@initialisation_phase` block.

Example syntax where the `initialisation_mortality_event` has been specified in the initialisation phase `Predation_state` but not in the annual cycle:

```
initialisation_phases Equilibrium_state Predation_state
time_steps Oct_Nov Dec_Mar
```

```
@initialisation_phase Equilibrium_state
type derived
```

```
@initialisation_phase Predation_state
type iterative
insert_processes Oct_Nov()=predation_Initialisation
```

```
@process predation_Initialisation
type initialisation_mortality_event
categories male.HOKI female.HOKI
catch 90000
selectivities Hakesl Hakesl
```

```
time_step Oct_Nov
processes Mgl Instantaneous_Mortality
```

```
@time_step Dec_Mar
processes Recruitment Instantaneous_Mortality
```

**4.5.3.7. Prey-suitability mortality**

The density-dependent prey-suitability mortality process applies predation mortality from a predator group to its prey groups simultaneously. It removes an abundance (or biomass) from each prey group according to the total (selected) abundance (or biomass) of each prey group, the total (selected) abundance (or biomass) of the other prey groups, some "predator" abundance (or biomass), and the preference (electivity) of the predator for each prey group, constrained by a maximum exploitation rate. The predator-prey suitability functions were based on the multispecies Virtual Population Analysis (MSVPA) functions (Jurado-Molina et al., 2005).

The mortality applied to the user-defined prey group  $g$  of category  $k$ , with the numbers removed at age  $l$  determined by a selectivity-at-age  $S_l$  is applied as follows:

First, calculate the total predator abundance (or biomass) over all predator categories  $k$  in  $1 \dots K$  and ages  $l = 1 \dots L$  that are applying the mortality

$$P_{k,l} = S_l^{predator} N_{k,l}^{predator} \quad (4.23)$$

And define the total predator abundance (or biomass)  $P_{total}$  as

$$P_{total} = \sum_K \sum_L P_{k,l} \quad (4.24)$$

Then, given the total vulnerable abundance (or biomass) of prey group  $g$  over all categories  $k$  in  $1 \dots K$  and ages  $l = 1 \dots L$  that are subject to the mortality

$$V_{g,k,l} = S_l^{prey} N_{k,l}^{prey} \quad (4.25)$$

And define the total vulnerable abundance (or biomass) of each prey group  $V_{total}^g$  as

$$V_{total}^g = \sum_K \sum_L V_{g,k,l} \quad (4.26)$$

And the total availability  $A_{total}^g$  for each prey group as

$$A_{total}^g = \frac{V_{total}^g}{\sum_G V_{total}^g} \quad (4.27)$$

The vulnerable abundance (or biomass) and availability every prey group  $g$  in  $1 \dots G$  is calculated simultaneously. Then the abundance (or biomass) to remove from each prey group  $g$  is a function of its electivity  $E_g$ , the availability of all other prey groups  $i$  in  $1 \dots G$ , the electivity of the predator for each prey group  $E_i$ , and the total consumption rate of the predator  $CR$  and its abundance (or biomass)  $P_{total}$

$$R_{total}^g = P_{total} CR \frac{A_{total}^g E_g}{\sum_G A_{total}^i E_i} \quad (4.28)$$

The exploitation rate to apply to each prey group  $g$  is then

$$U_g = \begin{cases} R_{total}^g / V_{total}^g, & \text{if } R_{total}^g / V_{total}^g \leq U_{max} \\ U_{max}, & \text{otherwise} \end{cases} \quad (4.29)$$

And the number removed  $R^g$  in each prey group  $g$  from each age  $l$  in category  $k$  is

$$R_{g,k,l} = U_g V_{g,k,l} \quad (4.30)$$

Prey suitability choice occurs only between the prey groups specified by the process. The total predator consumption rate represents the consumption of the predator on those prey groups alone. The electivities must sum to 1. Further, the consumption rate can be modified by a layer to be cell specific.

The density-dependent prey-suitability process is applied as either a biomass or an abundance depending on the value of the `is_abundance` switch.

Individual categories can be aggregated into prey groups using the "+" symbol. To indicate that two (or more) categories are to be aggregated, separate them with a "+" symbol.

For example, to specify two prey groups of two species made up of the males and females in each prey group

```
prey_categories maleSpeciesA + femaleSpeciesA maleSpeciesB + femaleSpeciesB
```

This syntax indicates that there are two prey groups, `maleSpeciesA + femaleSpeciesA` and `maleSpeciesB + femaleSpeciesB`, with each group having its own electivity.

For example, a biomass prey-suitability mortality process with an overall consumption rate of 0.8 of prey species A and species B (modelled as males and females) by the predator `predatorSpecies` with electivities between species A and species B of 0.18 and 0.82 has syntax

```
@process PreySuitabilityMortality
type prey-suitability_predation
is_abundance F
consumption_rate 0.8
categories maleSpeciesA + femaleSpeciesA maleSpeciesB + femaleSpeciesB
electivities 0.18 0.82
selectivities One One One One
predator_categories predatorSpecies
predator_selectivities One
u_max 0.8
```

#### 4.5.4. Transition By Category

The transition by category process moves individuals between categories. This process is used to specify transitions such as maturation (individuals move from an immature to mature state) and migration (individuals move from one area to another).

**4.5.4.1. Annual transition by category**

A special process type is the annual transition by category process, which allows a transition to occur in a specific subset of years only, where each year can have a different rate.

In both cases, there is a one-to-one relationship between the "from" category and the "to" category, i.e., for every source category there is one target category only

$$N_{a,j} = N_{a,i} \times P_i \times S_{a,i} \quad (4.31)$$

where  $N_{a,j}$  is the number of individuals that have moved to category  $j$  from category  $i$  in age  $a$ ,  $N_{a,i}$  is the number of individuals in category  $i$ ,  $P_i$  is the proportion parameter for category  $i$ , and  $S_{a,i}$  is the selectivity at age  $a$  for category  $i$ .

To merge categories repeat the "to" category multiple times.

For example, to specify a simple spawning migration of mature males from a western area to an eastern (spawning) area, the syntax is

```
@process Spawning_migration
type transition_category
from West.males
to East.males
selectivities MatureSel
proportions 1
```

where `MatureSel` is a selectivity that describes the proportion of age or length classes that are mature and thus move to the eastern area.

**4.5.5. Tag Release events**

Tagging processes can be age- or length-based processes, whereby numbers of individuals are moved from an untagged category to a tagged category defined in the `@categories` block. Tag release processes can also account for initial tag-induced mortality on individuals.

Age-based tag release events move a known number of individuals tagged for each age to a tagged category, along with applying additional mortality. Individuals are removed from the non-tagged categories and added to tagged categories. Often the ages of tagged individuals are not known, so length-based tag release events are more commonly used.

Length-based tag release processes are more complicated, as the age-length matrix is calculated and the exploitation for each length bin to then move the correct numbers-at-age based on the known lengths of release. CASAL2 also allows for initial tag loss.

The tag-release process:

For each length bin  $l$  of the input vector of numbers-at-length  $\tilde{N}_l$

$$N_{l,j} = \sum_{a=1} N_{a,l,j} * S_a$$

where  $N_{a,l,j}$  is the numbers at age  $a$  and length  $l$  for category  $j$ , and  $S_a$  is the selectivity at age  $a$ .



Calculate the total numbers-at-length  $T_l$  across all source categories at length  $l$ , taking into account the selectivities

$$T_l = \sum_{j=1} N_{l,j}$$

Calculate the transition rate for length bin  $u_l$

$$u_l = \tilde{N}_l / T_l$$

Check that the threshold  $u_{max}$  is not exceeded, which is analogous to the  $u_{max}$  in a mortality processes

$$u_l = \begin{cases} u_{max}, & \text{if } u_l > u_{max} \text{ flag a penalty} \\ u_l, & \text{otherwise} \end{cases}$$

Calculate the numbers-at-age in this category that will be moved by multiplying across the age-length matrix and storing the result by age, for each age accumulated across all length bins. Then move the necessary

$$N_{a,j+} = N_{a,l} * u_l$$

The syntax for an example of tag release by length process

```
@process 2005Tags_shelf
type tag_by_length
years 2005
from male.untagged+female.untagged
to male.2005 female.2005
selectivities ShelfselMale ShelfselFemale
penalty tagging_penalty
initial_mortality 0.1
table proportions
year 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220
2005 0 0 0.0580 0.1546 0.3380 0.1981 0.1643 0.0531 0.0242 0.0097 0 0 0 0 0 0 0 0 0 0
end_table
n 207
U_max 0.999
```

This process moves 207 individuals from a combination of male.untagged and female.untagged categories, based on the combination of growth rates and selectivity, into tagged male and tagged female categories.

#### 4.5.6. Tag Loss

Tag Loss is the process which accounts for tags being lost from a tagged individual due to, for example, tag failure or tags getting knocked off. This process is applied as an instantaneous migration rate that can happen over multiple time steps in the annual cycle. This method assumes that when tags are lost the individuals are transferred from the `from` category to the `to` category.

The tag loss rate is applied depending on whether the individuals were tagged with a single tag only (`tag_number_per_animal = 1`), double tagged (`tag_number_per_animal = 2`), or tagged with  $n$  tags (`tag_number_per_animal = n`).

The syntax for the tag loss is

```
@process Tag_loss
type tag_loss
categories tagged_fish
tag_loss_rate 0.02
time_step_ratio 0.25 0.75
selectivities One
tag_loss_type single
year 1985
```

#### 4.6. Derived quantities

Some processes require a population value derived from the population state as an argument. These values are derived quantities. Derived quantities are values calculated at the end of a specified time step in every year, and thus have a single value for each year of the model.

Derived quantities can be calculated as either a function of abundance or biomass. Abundance-derived quantities are the sum over the categories (after applying a selectivity). Biomass-derived quantities are calculated similarly.

Derived quantities are also calculated during the initialisation phases. Therefore, the time step during each phase must be specified. If the initialisation time steps are not specified, the derived quantity will be calculated during the initialisation phases in every year, at the end of the annual cycle.

Derived quantities are required by some processes, e.g., the Beverton-Holt recruitment process which requires an equilibrium biomass ( $B_0$ ) and annual spawning stock biomass values ( $SSB_y$ ) to calculate the stock-recruit relationship. These derived quantities are defined as the abundance or biomass of a part of the population at some point in the annual cycle for selected ages and categories.

Derived quantities are associated with a mortality block; see section 4.4.2 for more detail on mortality blocks. Derived quantities can be calculated partway through a mortality blocks.

Two derived quantity methods interpolate derived quantities partway through a mortality block. These methods are `weighted_sum` and `weighted_product`, and are defined as

- `weighted_sum`: after proportion  $p$  of the mortality block, the partition elements are given by  $n_{p,j} = (1 - p)n_j + p'_j$
- `weighted_product`: after proportion  $p$  of the mortality block, the partition elements are given by  $n_{p,j} = n_j^{1-p} n'_j{}^p$

where  $n_{p,j}$  is the derived quantity at proportion  $p$  of the mortality block for category  $j$ ,  $n_j$  is the quantity at the beginning of the mortality block, and  $n'_j$  is the quantity at the end of the mortality block.

For example, to define a biomass-derived quantity spawning stock biomass,  $SSB$ , calculated at the end of the first time step (labelled `step_one`), over all "mature" male and female categories and halfway through the mortality block using the `weighted_sum` method, the syntax is

```
@derived_quantity SSB
type biomass
```

```

time_step step_one
categories mature.male mature.female
selectivities One
time_step_proportion 0.5
time_step_proportion_method weighted_sum

```

## 4.7. Age-length relationship

The age-length relationship defines the functional form of the length-at-age (and the weight-at-length; see Section 4.8) of individuals at age/category within the model.

There are three length-age relationship options. The first is the naive "no relationship", where each individual has length 1 regardless of age. The second is the von Bertalanffy relationship, and the third is the Schnute relationship.

The length-at-age relationship is used to calculate the length frequency given age, and with the length-weight relationship, the weight-at-age of individuals within an age/category. When defining length-at-age, the length-weight relationship must also be defined (see Section 4.8).

Changes in length-at-age during the year, i.e., growth between birthdays, are represented by incrementing age as specified by the `time_step_proportions` parameter.

### 4.7.0.1. The "no relationship" relationship, `none`

The length of each individual is 1 for all ages, and the `none` length-weight relationship must also be used.

### 4.7.0.2. The von Bertalanffy relationship, `von_bertalanffy`

$$\bar{s}(\text{age}) = L_{\infty} (1 - \exp(-k(\text{age} - t_0))) \quad (4.32)$$

### 4.7.0.3. The Schnute relationship, `schnute`

$$\bar{s}(\text{age}) = \begin{cases} \left[ y_1^b + (y_2^b - y_1^b) \frac{1 - \exp(-a(\text{age} - \tau_1))}{1 - \exp(-a(\tau_2 - \tau_1))} \right]^{1/b}, & \text{if } a \neq 0 \text{ and } b \neq 0 \\ y_1 \exp \left[ \ln(y_2/y_1) \frac{1 - \exp(-a(\text{age} - \tau_1))}{1 - \exp(-a(\tau_2 - \tau_1))} \right], & \text{if } a \neq 0 \text{ and } b = 0 \\ \left[ y_1^b + (y_2^b - y_1^b) \frac{\text{age} - \tau_1}{\tau_2 - \tau_1} \right]^{1/b}, & \text{if } a = 0 \text{ and } b \neq 0 \\ y_1 \exp \left[ \ln(y_2/y_1) \frac{\text{age} - \tau_1}{\tau_2 - \tau_1} \right], & \text{if } a = 0 \text{ and } b = 0 \end{cases} \quad (4.33)$$

The von Bertalanffy relationship has parameters  $L_{\infty}$ ,  $k$ , and  $t_0$ . The Schnute relationship (Schnute, 1981) has parameters  $y_1$  and  $y_2$ , which are the mean lengths at reference ages  $\tau_1$  and  $\tau_2$ , and  $a$  and  $b$ ; when  $b = 1$ , this relationship reduces to the von Bertalanffy relationship with  $k = a$ .

**4.7.0.4. data**

There is an option to input empirical length at age by year, which is an alternative to using an age-length growth model such as the von Bertalanffy and Schnute model. CASAL2 will interpolate values for missing years across time steps. The calculations of length-at-age throughout the model years occur in the same time step.

**4.8. Length-weight relationship**

There are two length-weight relationships options. The first is the naive "no relationship" relationship, where the weight of an individual is always 1, regardless of length. The second relationship is the "basic" relationship, which is the standard length-weight relationship,  $W = aL^b$ .

**4.8.0.1. The "no relationship" relationship, none**

$$\text{mean weight} = 1 \quad (4.34)$$

**4.8.0.2. The standard length-weight relationship, basic**

The mean weight  $\hat{w}_a$  of an individual of age  $a$  is

$$\hat{w}_a = a\hat{l}_a^b \quad (4.35)$$

where  $\hat{l}_a$  is the mean length at age  $a$ . If a distribution of length-at-age is specified, then the mean weight is calculated over the distribution of lengths

$$\hat{w}_a = (a\hat{l}_a^b)(1 + cv^2)^{\frac{b(b-1)}{2}} \quad (4.36)$$

where the  $cv$  is the coefficient of variation (CV) of the length-at-age relationship. This adjustment is exact for lognormal distributions, and an approximation for normal distributions if the CV is not large (Bull et al., 2012).

For comparing CASAL with CASAL2 results, there is a small difference between the two programs. CASAL adjusted the CVs by\_length only when CVs are used in distribution calculations (length-based selectivities, length-based processes, and [length-based?] observations), and is not done in the above correction.

**Note:** the scale of  $a$  can be specified incorrectly. If the catch is in tonnes and the growth curve is in centimetres, then  $a$  should convert a length in centimetres to a weight in tonnes. There are reports available that can be used to help check that the units specified are plausible (see Section 7).

```
@length_weight length_weight
type basic
units tonnes
a 0.00000123
b 3.132
```

## 4.9. Age-weight relationship

Empirical weight-at-age data can be input. This option is different from the method above as it uses empirical data for weight-at-age, rather than calculating it with the growth functions (`age->length->weight`).

This option specifies the weight-at-age values for categories at a point in time. These values can be used in weight-based derived quantities, processes, and observations.

An example

```
type Data
units tonnes
table data
year 1 2 3 4 5 6 7 8 9 10
1986 0.134 0.686 1.639 2.719 3.649 4.901 6.329 6.591 7.238 7.491
1987 0.132 0.724 1.534 2.829 4.092 4.853 5.705 6.143 7.179 8.089
1988 0.122 0.641 1.533 2.641 3.796 5.054 5.652 6.356 6.95 8.857
1989 0.137 0.722 1.606 2.416 3.629 5.027 5.561 6.35 6.933 7.217
1990 0.138 0.773 1.645 2.74 3.711 4.506 5.684 6.929 7.424 7.479
end_table
```

If weight is defined by the empirical weight-at-age data, then the age-length block in the `@categories` block can be omitted.

```
@categories
format stock
names Stock
```

If a weight- or biomass-based derived quantity, process, or observation has a `age_weight_label` subcommand then the `@age_weight` class can be used to calculate the mean weight-at-age.

## 4.10. Weightless model

To model abundance (i.e., to model the population in numbers and not convert to biomass), the `@length_weight` argument is turned off by specifying the keyword `none` in the `@age_length` block

```
@age_length age_size
type schnute
...
length_weight none
```

In this case any "biomass" generated by CASAL2 will actually be abundance, and care should be taken with interpretation of the output.

## 4.11. Maturity, in models without maturing in the partition

If maturity is not a characteristic of the partition it can be derived using selectivities. The mature individuals in a population can be calculated by applying a maturity selectivity to the partition. These numbers can then be used in processes, in calculating mature biomass (using derived quantities), and in reports for the mature partition as an output.

### 4.12. Selectivities

A selectivity is a function that can have a different value for each age class. Selectivities are used to fit to observations (Section 5) or to modify the effects of processes on each age class (Section 4).

There are a number of different parametric forms as options, including logistic, knife edge, and double normal selectivities. Selectivities are defined in command block (@selectivity), where the unique label of the selectivity is used by observations and processes to identify which selectivity to apply.

Selectivities are indexed by age, with indices from `min_age` to `max_age`. S logistic age-based selectivity with 50% selected at age 5 and 95% selected at age 7 would be defined by the `type=logistic` with parameters  $a_{50} = 5$  and  $a_{t095} = (7 - 5) = 2$ . The value of the selectivity at age  $x = 7$  is 0.95, and the value at age  $x = 3$  is 0.05.

For some selectivities the function values for some choices of parameters can result in numeric overflow or underflow errors (i.e., the number calculated from parameter values is either too large or too small to be well represented). CASAL2 implements range checks on some parameters to test for these errors before calculating function values.

For example, the logistic selectivity is implemented such that if  $(a_{50} - x)/a_{t095} > 5$  then the value of the selectivity at  $x = 0$ , i.e., for  $a_{50} = 5$ ,  $a_{t095} = 0.1$ , then the value of the selectivity at  $x = 1$ , without range checking would be  $7.1 \times 10^{-52}$ . With range checking, that value is 0 (as  $(a_{50} - x)/a_{t095} = 40 > 5$ ).

The selectivities options are:

- Constant
- Knife-edge
- All values
- All values bounded
- Increasing
- Logistic
- Inverse logistic (descending logistic?)
- Logistic producing
- Double normal
- Double exponential

#### 4.12.1. constant

$$f(x) = C \tag{4.37}$$

The constant selectivity has the estimable parameter C.

#### 4.12.2. knife\_edge

$$f(x) = \begin{cases} 0, & \text{if } x < E \\ \alpha, & \text{if } x \geq E \end{cases} \tag{4.38}$$

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

#### 4.12.3. `all_values`

$$f(x) = V_x \quad (4.39)$$

The all-values selectivity has estimable parameters  $V_{low}, V_{low+1} \dots V_{high}$ . The selectivity value for each age class must be set.

#### 4.12.4. `all_values_bounded`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ V_x, & \text{if } L \leq x \leq H \\ V_H, & \text{if } x > H \end{cases} \quad (4.40)$$

The all-values-bounded selectivity has non-estimable parameters  $L$  and  $H$ . The estimable parameters are  $V_L, V_{L+1} \dots V_H$ . Selectivity values for each age class from  $L \dots H$  must be set.

#### 4.12.5. `increasing`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ f(x-1) + \pi_x(\alpha - f(x-1)), & \text{if } L \leq x \leq H \\ f(\alpha), & \text{if } x \geq H \end{cases} \quad (4.41)$$

The increasing ogive has non-estimable parameters  $L$  and  $H$ . The estimable parameters are  $\pi_L, \pi_{L+1} \dots \pi_H$ ; if these are estimated, they should always be constrained to be between 0 and 1.  $\alpha$  is a scaling parameter, with default value of  $\alpha = 1$ . The increasing ogive is similar to the all-values-bounded ogive, and is constrained to be non-decreasing.

#### 4.12.6. `logistic`

$$f(x) = \alpha / [1 + 19^{(a_{50}-x)/a_{t095}}] \quad (4.42)$$

The logistic selectivity has estimable parameters  $a_{50}$  and  $a_{t095}$ .  $\alpha$  is a scaling parameter, with default value of  $\alpha = 1$ . The logistic selectivity takes values  $0.5\alpha$  at  $x = a_{50}$  and  $0.95\alpha$  at  $x = a_{50} + a_{t095}$ .

#### 4.12.7. `inverse_logistic`

$$f(x) = \alpha - \alpha / [1 + 19^{(a_{50}-x)/a_{t095}}] \quad (4.43)$$

The inverse logistic selectivity has estimable parameters  $a_{50}$  and  $a_{t095}$ .  $\alpha$  is a scaling parameter, with default value of  $\alpha = 1$ . The logistic selectivity takes values  $0.5\alpha$  at  $x = a_{50}$  and  $0.95\alpha$  at  $x = a_{50} - a_{t095}$ .

**4.12.8. logistic\_producing**

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ \lambda(L), & \text{if } x = L \\ (\lambda(x) - \lambda(x-1)) / (1 - \lambda(x-1)), & \text{if } L < x < H \\ 1, & \text{if } x \geq H \end{cases} \quad (4.44)$$

The logistic-producing selectivity has non-estimable parameters  $L$  and  $H$ . The estimable parameters are  $a_{50}$  and  $a_{t095}$ .  $\alpha$  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  $a_{50}$  and  $a_{t095}$ .

**4.12.9. double\_normal**

$$f(x) = \begin{cases} \alpha 2^{-[(x-\mu)/\sigma_L]^2}, & \text{if } x \leq \mu \\ \alpha 2^{-[(x-\mu)/\sigma_R]^2}, & \text{if } x \geq \mu \end{cases} \quad (4.45)$$

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

**4.12.10. double\_exponential**

$$f(x) = \begin{cases} \alpha y_0 (y_1/y_0)^{(x-x_0)/(x_1-x_0)}, & \text{if } x \leq x_0 \\ \alpha y_0 (y_2/y_0)^{(x-x_0)/(x_2-x_0)}, & \text{if } x > x_0 \end{cases} \quad (4.46)$$

The double-exponential selectivity has non-estimable parameters  $x_1$  and  $x_2$ . The estimable parameters are  $x_0$ ,  $y_0$ ,  $y_1$ , and  $y_2$ .  $\alpha$  is a scaling parameter, with default value of  $\alpha = 1$ . This selectivity curve 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  $(x_1, y_1)$ ,  $(x_0, y_0)$ , 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  $(x_0, y_0)$ .





**Figure 4.3: Examples of the selectivities**

Selectivities `all_values` and `all_values_bounded` can be included in additional priors using the syntax

```
@selectivity maturity
type all_values
v 0.001 0.1 0.2 0.3 0.4 0.3 0.2 0.1

## encourage ages 3-8 to be smooth.
@additional_prior smooth_maturity
type vector_smooth
parameter selectivity[maturity].values{3:8}
```

### 4.13. Projections

This section lists all the projections classes available, their functionality, and an example of the syntax.

#### 4.13.1. The constant projection class, `constant`

A parameter can either be fixed during all projection years or specified individually for each projection year. This is a deterministic assumption, where the parameter is assumed to be known without error during projection years.

```
@project Future_ycs
type constant
parameter process[Recruitment].ycs_values
years 2012:2016
values 1 2 1 2 0.5
multiplier 1
```

#### 4.13.2. Sampling from a range of years, `empirical_resampling`

Parameters that have time components associated with them can be re-sampled uniformly with replacement over a range of years and used as values for the projected years. The year range to sample from is between `start_year` and `final_year`:

```
@project Future_ycs
type empirical_sampling
parameter process[Recruitment].ycs_values
years 2012:2016
start_year 1988
final_year 2008
multiplier 1
```

#### 4.13.3. Sampling from a lognormal distribution, `lognormal`

The parameters are drawn from a Gaussian distribution in log space and exponentiated to result in the lognormal distribution

$$X_p = \exp(\epsilon_p - \sigma^2/2) \tag{4.47}$$

where  $\epsilon_p \stackrel{iid}{\sim} N(\mu, \sigma)$  and  $X_p$  is the projected value for parameter  $X$ , and  $\mu$  and  $\sigma$  are the mean and standard deviation on the log scale.

An example of applying this process to draw future year class parameters from a lognormal distribution with mean 1 and standard deviation 0.8

```
@project Future_ycs
type lognormal
parameter process[Recruitment].ycs_values
years 2012:2016
```

```
mean 0
sigma 0.8
multiplier 1
```

#### 4.13.4. Sampling from a lognormal distribution defined by values from a range of years, `lognormal_empirical`

This class applies a lognormal draw as in the `LogNormal` class and specifies a year range which is re-sampled uniformly without replacement. These re-sampled values are then used to calculate the standard deviation of the distribution. Then equation (4.47) is used to generate future values with a specified  $\mu$  and empirically calculated  $\sigma$ ,

```
@project Future_ycs
type lognormal_empirical
parameter process[Recruitment].ycs_values
years 2012:2016
mean 0
start_year 1988
final_year 2008
multiplier 1
```

#### 4.13.5. Sample using a user-defined function, `user_defined`

This class uses the equation parser to define the future values of a parameter during projection mode. This was set up to define and apply harvest control rules (i.e., apply a management action such as changing the TACC based on the current or previous state).

In fisheries models, this option can be used to calculate the projected catch based on an exploitation rate multiplied by the vulnerable biomass, where the exploitation rate is based on a rule (Figure 4.4).



**Figure 4.4: Examples of control rules based on current stock status.**

```
@project HCR_2015
type user_defined
parameter process[Instantaneous_Mortality].method_Sub_Ant_F
years 2015
equation if(derived_quantity[SSB].values{2014} / process[Recruitment].b0 <= 0.1, 0.0,
if(derived_quantity[SSB].values{2014} / process[Recruitment].b0 > 0.1 &&
derived_quantity[SSB].values{2014} / process[Recruitment].b0 < 0.2,
derived_quantity[SSB].values{2014} * derived_quantity[SSB].values{2014}
/ process[Recruitment].b0,
derived_quantity[SSB].values{2014} * 0.2))
```

Care should be taken when writing user-defined equations. The above equation is: if  $%B_{2014} \leq 0.1$  then set next year's catch to 0.0, else if  $%B_{2014} > 0.1$  &  $%B_{2014} \leq 0.2$  then set next year's catch equal to  $%B_{2014} \times SSB_{2014}$ , else set next year's catch to  $0.2SSB_{2014}$ .

#### 4.13.6. Projections with catches specified

Catches are unique in that they are known inputs in a table format. For example, to project catches that are in a table

```
# fishing process
@process Fishing
type mortality_instantaneous_retained
m 0.17*6 #0.17 #testing at old values
time_step_ratio 1
selectivities One*6 #for age based M
categories *
table catches
year FishingLine FishingPot Recreation
1900 0 0 0
1901 13.2 0 22.9
1902 26.4 0 23.5
1903 39.6 0 24
end_table

# projection block
@project future_catch
type constant
parameter process[Fishing].method_fishingpot
years 2020:2029
values 4000
```

This uses the syntax `block_type[block_label].method_fishinglabel`. **Note:** the fishing label which is defined in the table needs to be lower case form in the `@projection` block.

#### 4.14. Time-varying Parameters

CASAL2 has the functionality to vary any parameter annually between the start and final year of a model run. This can be for blocks of years or specific years. For years that are not specified the parameter will default to the input, or if in an iterative state such as estimation mode, the value being trialled at that iteration.

Method types for a time-varying parameter are:

- constant,
- random\_walk,
- exogenous,
- linear,
- annual\_shift, and
- random\_draw.

This option allows for a parameter to be known in a year, or be the result of a deterministic or stochastic equation. **Note:** the stochastic time-varying functionality was added for simulation purposes. It has not been tested in an estimation context.

To implement hierarchical models, estimated the prior parameter values with hyperpriors. To implement a hierarchical model using the time-varying functionality, use MCMC estimation to calculate the integral which is required to obtain unbiased estimates. In an MCMC context a Gibbs sampler is assumed. That is, every draw is from a conditional distribution and so every draw is a candidate value.

When allowing removals with annually varying catchabilities, selectivities, and/or other model components, simulated observations more closely model real data and associated conclusions

become more useful. Implementing time-varying parameters also allows for mean or location parameters of selectivities to change between years based on an explanatory variable. An example of this is in the New Zealand Hoki fishery where the  $\mu$  and  $a_{50}$  parameters are allowed to shift depending on when the fishing season occurs. Descriptive analysis showed that when fishing was earlier relative to other years smaller fish were caught and vice versa. This can be shown in the CASAL2/Examples/2stock directory, implemented at line: 382 in the `population.csl2` file.

#### 4.14.1. constant

This option allows a parameter to have an alternative value during certain years, which can be estimated.

```
@time_varying q_time_var
type constant
parameter catchability[survey_q].q
years 1975:1988
values 0.001
```

These year values can be estimated using the syntax

```
@estimate q_time_var
type uniform
parameter time_varying[q_time_var].values(1975:1976)
lower_bound 1e-6 1e-6
upper_bound 2 2
```

**Caution:** do not estimate both the actual parameter and its time-varying counterpart, as the time-varying value will overwrite the actual parameter making the actual value unidentifiable.

#### 4.14.2. random\_walk

A random deviate drawn from a standard normal distribution is added to the previous value. This option has an estimable parameter  $\sigma_p$  for each time-varying parameter  $p$ . For reproducible modelling when using stochastic functionality, set the random seed (see Section 3.4).

```
@time_varying q_time_var
type random_walk
parameter catchability[survey_q].q
distribution normal
mean 0
sigma 3
```

If the parameter specified in the `@time_varying` block is associated with an `@estimate` block, then the parameter is constrained to stay within the lower and upper bounds of the `@estimate` block.

**WARNING:** if the parameter does not have an associated `@estimate` block then there is no safeguard against the application of a random deviate resulting in parameter values which cause the model to fail, i.e., generates NA or INF values. To avoid this, specify an `@estimate` block even though the parameter is not actually being estimated; see the example syntax below.

A constraint whilst using this functionality is that a parameter cannot be less than 0.0. If it is then CASAL2 sets it equal to 0.01.

```
@estimate survey_q_est
type uniform
parameter catchability[survey_q].q
lower_bound 1e-6
upper_bound 10
```

This configuration will insure the random walk time-varying process will set the any new candidate values within the lower and upper bound of the @estimate block.

#### 4.14.3. annual\_shift

A parameter generated in year  $y$  ( $\theta'_y$ ) depends on the value specified by the user ( $\theta_y$ ) along with three coefficients  $a$ ,  $b$ , and  $c$

$$\bar{\theta}_y = \frac{\sum_y^Y \theta_y}{Y} \quad (4.48)$$

$$\theta'_y = a\bar{\theta}_y + b\bar{\theta}_y^2 + c\bar{\theta}_y^3 \quad (4.49)$$

#### 4.14.4. exogenous

Parameters are shifted based on an exogenous variable. An example of this is an exploitation selectivity parameters that may vary between years based on known changes in exploitation behaviour such as season, start time, and average depth of exploitation.

$$\delta_y = a(E_y - \bar{E}) \quad (4.50)$$

$$\theta'_y = \theta_y + \delta_y \quad (4.51)$$

where  $\delta_y$  is the shift or deviation in parameter  $\theta_y$  in year  $y$  to generate the new parameter value in year  $y$  ( $\theta'_y$ ).  $a$  is an estimable shift parameter,  $E$  is the exogenous variable, and  $E_y$  is the value of this variable in year  $y$ . For more information readers can see [Francis et al. \(2003\)](#).

### 4.15. Equation Parser

CASAL2 has equation parser functionality, which is currently implemented in Projections (section 4.13), Derived quantities (section 4.6), and Reports (section 7).

Examples of syntax for implementing the equation parser are below. For more information on the parser, see <https://github.com/nickgammon/parser/blob/master/parser.cpp>

TODO what does this first example do?

```
equation process[Recruitment].r0 * (2-1)
```

mathematical functions such as `sqrt()`, `log()`, `exp()`, `cos()`, `sin()`, and `tan()` can be used

```
equation sqrt(process[Recruitment].r0)
```

exponents can be used with `pow()`

```
equation pow(2, 3)
```

the absolute value of an equation using `abs()`

```
equation abs(sqrt(process[Recruitment].r0) * 1.33)
```

if-else statements can be used

```
equation if(process[Recruitment].r0 > 23, 44, 55)
## if R0 is greater than 23 return 44 else return 55
```

if-else statements can also be linked, more complex syntax

```
equation if(process[Recruitment].r0 > 23, 44,
            if(process[Recruitment].r0 > 10, 55, 66))
## if R0 is greater than 23 return 44 else if R0 less than 23 but greater than 10 return 55,
else R0 must be less than 10 return 66
```

Only single values can be referenced, so an equation cannot be applied to a vector, e.g., `process[Recruit].yrs_values{1974:1980}` cannot be referenced. More information on which parameters can be included in an equation parser is available (Section 12). Any subcommand that has a type `estimable` could be referenced with the equation parser.

**Note:** the equation parser will not catch all user configuration errors, such as checking whether a parameter that exists in the system has been populated when it is required.

For example, the wrong year could be misspecified in the case of removals in year  $y$  which is based on the state of the population in year  $y - 1$

```
parameter process[removals].catch
year 2015
equation derived_quantity[percent_b0].values{2020}
```

This example is a valid equation but it will have nonsensical results, since a value for 2020 is to be calculated using values for 2015. Although the equation parser adds flexibility, it is easy to misspecify equations.



---

## 5. The estimation section

### 5.1. Role of the estimation section

The role of the estimation section is to define the tasks carried out by CASAL2:

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 on selected parameters, i.e., for each of a series of values of a parameter, minimise the objective function, allowing the other estimated parameters to vary (see Section 5.5)
5. Generate MCMC samples 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, the assumed priors, and the penalties. See the observation section for a description of the observations, likelihoods, priors, and penalties.

### 5.2. The objective function

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

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

where  $\pi$  is the joint prior density of the parameters  $p$ .

The contribution to the objective function from the likelihood components is described in Section 6.2. In addition to likelihoods, priors (see Section 5.7) and penalties (see Section 5.8) are components of the objective function. Note that if the priors are specified as uniform, then the prior contribution is zero and the optimisation is now a penalised likelihood and not Bayesian.

Penalties can be used to ensure that the estimated parameter values and derived quantities meet certain restrictions. For example, exploitation rate constraints on mortality events (i.e., fisheries) that are not violated (otherwise there is nothing to prevent the model from having abundances so low that the recorded catches could not have been taken); penalties on category transitions (to ensure there are enough individuals to move); penalties such that estimated values are similar or smooth, etc.

Equation 5.1 can be reduced to a penalised likelihood equation if all priors are assumed to be uniform. This is because uniform priors have no contribution to the objective function so Equation 5.1 reduces to the likelihood components plus penalties.

### 5.3. Specifying the parameters to be estimated

The parameters to be estimated (estimables) are defined using `@estimate` commands (see Section 9).

For example, a `@estimate` command block

```
@estimate male.m
parameter process[NaturalMortality].m{male}
lower_bound 0.1
upper_bound 0.4
type uniform
```

See Section 3.5.5 for information on how to specify the parameter name. At least one parameter is required to be estimated if doing an estimation `-e`, profile `-p`, or MCMC `-m` run. Initial values for the parameters to be estimated are required, and these values are used as the starting values for the minimiser. However, these values may be overwritten if a set of alternative starting values is provided (i.e., using `casal2 -i`, see Section 3.4).

All parameters are estimated within the specified bounds. For each parameter estimated, the lower and upper bounds and the prior (`type`) (Section 5.7) must be specified. The bounds and the prior should be chosen carefully as they affect the values over which the minimisers search. Some minimisers convert the lower and upper bounds into a minimisation space (for example `-1,1` space for the numerical differences algorithm). If estimating only some elements of a vector, either define each element of the vector to be estimated (see 3.5.5) or fix the others by setting the lower and upper bounds to the same value as the initial value.

### 5.4. Point estimation

Point estimation is invoked with `casal2 -e`, which attempts to find a minimum of the objective function. CASAL2 has multiple minimisation algorithms. There are three automatic differentiation (AD) minimisers: ADOL-C, CppAD, and BetaDiff (the minimiser used in CASAL). There are also three non-automatic differentiation minimisers: numerical differences, differential evolution minimiser (`de_solver`), and the dlib minimiser (see Section 1.8). AD minimisers are recommended for more complex models as they are on average much faster and tend to find a more robust minimum when exploring a complex objective surface.

An important input parameter for most minimisers is the `tolerance` parameter. This is one of the stopping rules that minimisers use to define when they have found a 'solution' (although a solution may be a local minimum and not the global minimum). To evaluate the robustness of a solution, use a set of different starting values, with the `-i parameter_file.txt` option.

Start with the default `tolerance` parameter value of 0.002 and decrease it while developing a model. For a given model, the parameter estimates when minimising with tolerance value 0.0000002 may be quite different from those with the default tolerance value. This is not robust model behaviour and more investigative and diagnostic work may be required to determine what parameters are causing this behaviour. *Note:* this issue will also affect the covariance matrix. When a different tolerance value and/or minimiser is used, a different approximate Hessian matrix which is inverted to solve for the covariance matrix may be produced. The effect that this behaviour has on MCMC samples is not well-determined.

### 5.4.1. The numerical differences minimiser

The minimiser has three kinds of (non-error) exit status, depending on the minimiser:

- Successful convergence (suggests a local minimum has been found, at least).
- Convergence failure (a local minimum has not been found, although the results may be 'close enough').
- Convergence unclear (the minimiser halted but was unable to determine if convergence occurred. The result may be a local minimum, although this can be checked by restarting the minimiser at the final values of the estimated parameters).

The maximum number of quasi-Newton iterations and objective function evaluations allowed can be specified. If either limit is exceeded, the minimiser exits with a convergence failure. Set the maximum number of evaluations and iterations to values larger than the defaults of 300 and 1000, unless convergence is reached with fewer. An alternative starting point of the minimiser can be specified using `casal2 -i`.

The minimisers are local optimisation algorithms trying to solve a global optimisation problem. What this means is that, even if a 'successful convergence' is reached, the solution may be only a local minimum, and not a global one. To diagnose this problem, start multiple runs from different starting points and comparing the results, or do profiles of one or more key parameters and seeing if any of the profiled estimates finds a better optimum 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.

Note 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; and
- 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.

```
@minimiser numerical_diff
type numerical_differences
tolerance 1e-6
iterations 2500
evaluations 4000
```

### 5.4.2. The differential evolution minimiser

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 (TODO reference?).

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 terminates 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 the model, this value can be set to a lower value and still find a robust solution.

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. Some results suggest 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 automatic differentiation minimisers or other more sophisticated algorithms have not been made.

```
@minimiser DE_solver
type de_solver
tolerance 1e-6
iterations 2500
evaluations 4000
```

#### 5.4.3. The BetaDiff minimiser

An automatic differentiation minimiser for non-linear models, This is the minimiser from the original CASAL package, based on ADOL-C.

```
@minimiser beta_diff
type beta_diff
tolerance 1e-6
iterations 2500
evaluations 4000
```

#### 5.4.4. The ADOL-C minimiser

An automatic differentiation minimiser for non-linear models. See <https://projects.coin-or.org/ADOL-C> for more information.

```
@minimiser ADOLC
type adolc
step_size 1e-6
iterations 2500
evaluations 4000
tolerance 1e-6
```

### 5.4.5. The CppAD minimiser

An automatic differentiation minimiser for non-linear models using the MUMPS solver. See <https://coin-or.github.io/CppAD/doc/cppad.htm> and [https://www.coin-or.org/CppAD/Doc/ipoft\\_solve.htm](https://www.coin-or.org/CppAD/Doc/ipoft_solve.htm) for more information.

```
@minimiser CPPAD
type cppad
```

CppAD has an implicit tolerance value of  $1e-9$ .

Some results suggest that this solver may be one of the quickest solvers for models that have a reasonably well-defined solution, i.e., the data are informative with respect to determining the estimated parameters.

### 5.4.6. The Dlib minimiser

Non-automatic differentiation minimiser. See <http://dlib.net/> for more information.

```
@minimiser Dlib
type dlib
tolerance 1e-6
iterations 2500
evaluations 4000
```

## 5.5. Posterior profiles

If profiles are run using the command `casal2 -p`, CASAL2 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, CASAL2 will fix its value at a sequence of  $n$  evenly spaced numbers (*step*) between the specified lower and upper bounds  $l$  and  $u$ , and calculate a point estimate at each value.

By default  $step = 10$ , and  $(l, u) = (\text{lower bound on parameter plus } (range/(2n)), \text{upper bound on parameter less } (range/(2n)))$ . Each minimisation starts at the final parameter values from the previous resulting value of the parameter being profiled. CASAL2 will report the objective function for each parameter value. The initial point estimate should be compared with the profile results, to check at least that none of the other points along the profile have a better objective function value than the initial 'minimum'.

The parameters to be profiled are specified, and optionally the number of steps, and lower bound and upper bound, for each parameter. In the case of vector parameters, the element(s) of the vector to be profiled are specified.

The initial starting point for the estimation can also be specified using `casal2 -i file`, which may improve the minimiser performance for the profiles.

If the profile results are not reasonable, 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 may also be useful to try other minimisers and compare the results.

## 5.6. Bayesian estimation

CASAL2 can use Markov chain Monte Carlo (MCMC) functionality to generate a sample from the posterior distribution of the estimated parameters with command `casal2 -m` and output the sampled values to a file, optionally keeping only every  $n$ th set of values.

As CASAL2 has no post-processing capabilities. CASAL2 cannot produce MCMC convergence diagnostics. To calculate these diagnostics, use a package such as BOA, plot/summarize the posterior distributions of the output quantities, and/or use a general-purpose statistical package such as R.

Bayesian methodology and MCMC are both large and complex topics. 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 briefly describes the MCMC algorithms used in CASAL2. See Section 9.3 for a description of the sequence of CASAL2 commands used in a full Bayesian analysis.

CASAL2 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  $\pi$ , scaled by an unknown constant. The algorithm generates a 'chain' or sequence of values. Typically the beginning of the chain is discarded (the burn-in period) and every  $N$ th 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:

1. Draw a candidate step  $s$  from a proposal distribution  $J$ , which should be symmetric i.e.,  $J(-s) = J(s)$
2. Calculate  $r = \min(\pi(x_i + s)/\pi(x_i), 1)$
3. 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 starting point of the point estimate minimiser can be specified using the command `casal2 -i`. Don't start it too close to the actual estimate (either by using `casal2 -i`, or by changing the initial parameter values in input configuration file) as it takes a few iterations to determine a reasonable approximation to the Hessian.

There are currently two options for the starting point of the MCMC:

- Start from the point estimate; or
- Restart a chain given a covariance matrix and a previous starting point.

The chain moves in natural space, i.e., no transformations are applied to the estimated parameters. The default proposal distribution is a multivariate Student's  $t$  distribution centred on the current point, with covariance matrix equal to a matrix based on the approximate covariance produced by the minimiser, multiplied by a stepsize factor.

The following steps define how the initial covariance matrix of the proposal distribution is calculated:

1. The covariance matrix is taken as the inverse of the approximate Hessian from the quasi-Newton minimiser.
2. 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.
3. The covariance matrix is then modified either by
  - `@mcmc.adjustment_method=covariance`: that if the variance of the  $i$ th parameter is non-zero and less than `@mcmc.min_difference` multiplied by the difference between the parameters' lower and upper bound, then the variance is changed, without changing the associated correlations, to  $k = \min\_diff(upper\_bound_i - lower\_bound_i)$ . This is done by setting

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

for  $i \neq j$ , and  $\text{var}(i)' = k$

- `@mcmc.adjustment_method=correlation`: that if the variance of the  $i$ th parameter is non-zero and less than `@mcmc.min_difference` multiplied by the difference between the parameters' lower and upper bounds, 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  $i$ th 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.

4. The `@mcmc.stepsize` (a scalar factor applied to the covariance matrix to improve the acceptance probability) is set 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, 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:

- The stepsize changes adaptively at one or more sample numbers (See next paragraph for details on the stepsize adaptation methods)
- The entire covariance matrix changes adaptively at one or more sample numbers. At each adaptation, the covariance matrix is replaced with an empirical covariance matrix, derived from the MCMC chain. The idea is that an empirical covariance is a better approximation of the proposal distribution than the inverse of the Hessian matrix, and can improve convergence and mixing of the chain.

The two options to adapt the step size are `double_half` or `ratio`, which is chosen with the input parameter `adapt_stepsize_method`. The `double_half` method is used in CASAL (see Gelman et al. (Gelman et al., 1995) for justification).

The algorithm for `double_half` is, 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. The `ratio` is taken from SPM. It adapts the current step size by the acceptance rate since the last adaptation multiplied by 4.1667 to reach an acceptance rate of  $\approx 0.24$ . See [Sherlock and Roberts \(2009\)](#) for justification on that acceptance rate.

The stepsize parameter is now on a completely different scale, and must be rescaled. It is set to a user-specified value (which may or may not be the same as the initial stepsize). Set the stepsize adaptations to occur after this, so that the stepsize can be readjusted to an appropriate value which gives good acceptance probabilities with the new matrix.

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.

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.

The procedure used to choose the sample of points is that, to start, all points on the chain so far are taken. (TODO reword this paragraph) 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 CASAL2 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 had at least this number of transitions, then it is also a fatal error. If this test is passed, the set of points is systematically sub-sampled down to 1000 points (and it must be at least this long to start with).

The probability of acceptance for each jump is 0 if the jump would move a parameter value outside of its bounds, 1 if it improves the posterior, or  $(\text{newposterior}/\text{oldposterior})$  otherwise. How often the position of the chain is recorded is specified with the `keep` parameter. For example, with `keep 10`, only every 10th sample is recorded.

The option to specify that some of the estimated parameters are fixed during the MCMC is available. 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 the start of the chain is specified with the command `casal2 -i`, these fixed parameters are set to the values in the file.

Restarting an MCMC chain: in the case where an MCMC chain was halted or interrupted, the MCMC chain can be restarted from where it finished with

```
casal2 -m --resume --objective-file Objective_file_name --sample-file Sample_file_name
```

where `Objective_file_name` is the file name for the objective function report and `Sample_file_name` is the file name for the sample report from a MCMC chain.

The posterior sample can be used for (projections (Section 4.4.5)) or simulations (Section 6.6) with the values supplied with the command `casal2 -i file`.

A multivariate Student's  $t$  distribution is used as an alternative to the multivariate normal proposal distribution. If you request multivariate Student's  $t$  proposals, change the degrees of freedom from the default of 4. As the degrees of freedom decreases, the  $t$  distribution becomes more heavy tailed.



This may lead to better convergence properties. Note the default is the multivariate Student's  $t$ .

Given a posterior (sub)sample, CASAL2 can calculate a list of output quantities for each sample point (see Section 7 specifically tabular report). These quantities can be output to a file (with the command `casal2 -r -tabular`) 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 4.4.5). The advantage of this is that the parameter uncertainty, as expressed in the posterior distribution, can be included into the risk estimates.

## 5.7. Priors

In a Bayesian analysis, a prior is required for every parameter that is being estimated. There are no default priors.

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 the bounds are applied. The moments of the prior after the bounds are applied may differ.

CASAL2 has the following priors (expressed in terms of their contribution to the objective function):

1. Uniform

$$-\log(\pi(p)) = 0 \quad (5.2)$$

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

$$-\log(\pi(p)) = \log(p) \quad (5.3)$$

3. Normal with mean  $\mu$  and c.v.  $c$

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

4. Normal with mean  $\mu$  and standard deviation  $\sigma$

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

5. Lognormal with mean  $\mu$  and c.v.  $c$

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

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

6. Beta with mean  $\mu$  and standard deviation  $\sigma$ , and range parameters  $A$  and  $B$

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

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

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. Example of syntax to define the estimation of a parameter and the prior assumed:

```
## uniform-log example estimate
@estimate B0
type uniform_log # this command "type" defines the prior type.
parameter process[Recruitment].b0 # "Recruitment" is the label of your process
upper_bound 20000
lower_bound 1000

## Lognormal YCS estimation
@estimate year_class_strengths_1990_1995
type lognormal
parameter process[Recruitment].yces_values{1990:1995}
# ycs_year 1990 1991 1992 1993 1994 1995
mu 1 1 1 1 1 1
cv 0.9 0.9 0.9 0.9 0.9 0.9
lower_bound 0.01 0.01 0.01 0.01 0.01 0.01
upper_bound 9 9 9 9 9 9
```

## 5.8. Penalties

Penalties are associated with processes and can be used to enforce parameter value or derived quantity restrictions or model outputs that are invalid by adding a penalty to the objective function. For example, estimated parameter values can be restricted so that a known mortality event removes enough individuals from the population within an event mortality process. CASAL2 requires penalty functions for processes that remove or shift a *number* of individuals between categories or from the partition. Many of the penalties that were available in CASAL have been moved to be additional priors in CASAL2(see Section 5.9).

For most penalties, a multiplier is required to be specified, and the objective function is increased by this multiplier multiplied by the penalty value. In some cases the multiplier may need to be quite large to prohibit some model behaviour.

Penalties are implemented for the processes

- `@process[label].type=event_mortality,`
- `@process[label].type=mortality_instantaneous,`
- `@process[label].type=tag_by_length,`
- `@process[label].type=tag_by_length,` and

- `@process[label].type=category_transition`

For these processes, two types of penalties can be defined: on the natural scale (the default) and on the log scale. Both of these types add a penalty value of the squared difference between the observed value (e.g., 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), multiplied by the penalty multiplier.

The natural scale penalty calculates the squared difference on a natural scale, and the log scale penalty calculates the squared difference of the logged values.

For example:

```
@process Mortality
type mortality_instantaneous
penalty CatchMustBeTaken

# define the penalty in an @penalty block
@penalty CatchMustBeTaken
type process
log_scale True
multiplier 10000
```

Penalties are added to the objective function in the following ways;

$$Penalty = (X_1 - X_2)^2 \quad (5.8)$$

or if `log_scale true`

$$Penalty = (\log(X_1) - \log(X_2))^2 \quad (5.9)$$

where, for example,  $X_1$  is observed catch biomass and  $X_2$  is the estimated catch biomass. Penalties are usually applied in situations when numbers or weight are known. Another example is for tagging, where the number of individuals that were tagged in a given year is known, so a penalty can be used to restrict the model to estimate reasonable values for the numbers of tagged individuals in that year.

## 5.9. Additional Priors

Additional priors can be thought of as the inverse of penalties (TODO please rephrase). For CASAL models, most of the legacy `@penalty` blocks have now been implemented as `@additional_prior` blocks. They restrict parameters in user-defined spaces (TODO please rephrase).

The types of additional priors available in CASAL2 are `vector_smoothing`, `vector_averaging`, `uniform_log`, `lognormal`, `element_difference`, and `Beta`:

- `vector_averaging`

This prior can be applied to a vector parameter. Sum of squares of  $r^{th}$  differences, optionally on a log scale. This encourages the vector to be like a polynomial of degree  $(r - 1)$ . A range of the vector to be "smoothed" can be specified (and if not, the smoother is applied to the entire vector). However, this restriction must be specified by an index of the vector and must be between 1 and the length of the vector, inclusive.

- `vector_smoothing`

This prior can be applied to a vector parameter. Square of  $(\text{mean}(\text{vector})-k)$ , or of  $(\text{mean}(\log(\text{vector}))-l)$ , or of  $(\log(\text{mean}(\text{vector})/m))$ . Restricts the vector to average arithmetically to  $k$  or  $m$ , or geometrically to  $\exp(l)$ . Typically used for YCS with  $k=1$  or  $m=1$  or  $l=0$ , to restrict the YCS to centre on 1. Optionally, indices can be chosen or excluded outside a given set of bounds.

- `lognormal` with mean  $\mu$  and c.v.  $c$

$$-\log(\pi(p)) = \log(p) + 0.5 \left( \frac{\log(p/\mu)}{s} + \frac{s}{2} \right)^2 \quad (5.10)$$

- `uniform_log`

$$-\log(\pi(p)) = \log(p) \quad (5.11)$$

- `element_difference`

$$-\log(\pi(p_1, p_2)) = \sum_{i=1}^n (p_{1,i} - p_{2,i})^2 \quad (5.12)$$

- `Beta`

Beta with mean  $\mu$  and standard deviation  $\sigma$ , and range parameters  $A$  and  $B$ , for parameter value =  $p$

$$-\log(\pi(p)) = (1-m)\log(p-A) + (1-n)\log(B-p) \quad (5.13)$$

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

Methods available for the type `vector_average` are `l`, `k`, `m`. For a target vector parameter  $\mathbf{X}$  and target mean  $k$ , the contribution to the objective score is

- `method k`

$$-\log(\pi(p)) = (\bar{X} - k)^2$$

- `method l`

$$-\log(\pi(p)) = \left( \overline{\ln(X)} - k \right)^2$$

- `method m`

$$-\log(\pi(p)) = (\ln(\bar{X}) - k)^2$$

where  $\overline{\ln(X)}$  is the mean of the logged values.

There are a range of parameters and derived values that additional priors can be applied to. Here are a list of non-estimated (all parameters that can be estimated can have an additional prior attached to them) parameters that additional priors can be applied to.

- `selectivity[Selectivity_label].values{i:j}`.

This subcommand applies a selectivity (???) to the actual selectivity value by age (for ages  $i$  through  $j$ ). This option is available only for certain types of selectivities (`all_values`, `all_values_bounded`, `double_exponential`). See the Hoki stock assessment for an example of applying additional priors on selectivities.

- `catchability[Catchability_label].q`

This subcommand is for catchabilities that are of type nuisance only. Since nuisance  $qs$  are not free parameters, additional priors can be applied to replicate CASAL models with `@estimate` blocks in nuisance  $qs$ . If a CASAL model applied a uniform prior, then this has a null effect and this functionality can be ignored when converting to a CASAL2 model.

This list may be useful for users who are trying to apply the equivalent CASAL penalties in a CASAL2 model.

## 5.10. Parameter Transformations

CASAL2 has multiple methods to transform a parameter, with some methods developed for legacy purposes. Transformations are implemented to try and achieve 'better' model optimisation. Complex population models can have highly correlated parameters so transforming them to be orthogonal or to be in a different space is a way of addressing correlations, and to allow the minimiser to find a 'global' minimum quicker. To read more about transformations and get a better understanding of why they are used, see [Gilks et al. \(1995\)](#), specifically chapter 6.

There are two main transformation methods available in CASAL2, `transform_with_jacobian` and `prior_applies_to_transform`. When using `transform_with_jacobian`, priors are defined on parameters in natural/model space (the usual priors) but when the parameter is passed to the minimiser it gets transformed and a Jacobian is added to the objective function to account for this transformation. The second method is when bounds and prior parameters on the parameters can be specified in transformed space. Note that both `prior_applies_to_transform` and `transform_with_jacobian` cannot be set to true.

There are two ways that transformations can be applied. The first is within the `@estimate` block, which is for univariate (simple) transformations only. For more complex transformations a `@estimate_transformation` block must be specified to describe the transformation.

For example:

```
## simple transformation
@estimate log_R0
type lognormal
transformation log
parameter process[Recruitment].r0
transform_with_jacobian true
mu 442413
cv 0.2
lower_bound 3000
upper_bound 24154953

## more complex transformation
@estimate R0
type lognormal
```

```

parameter process[Recruitment].r0
mu 442413
cv 0.2
lower_bound 3000
upper_bound 24154953

@estimate_transformation Log_R0
type log
estimate_label log_R0
transform_with_jacobian true

```

### Transform with Jacobian

The support of a random variable  $X$  with density  $p_X(x)$  is that subset of values for which it has non-zero density,

$$\text{supp}(X) = \{x | p_X(x) > 0\} \quad (5.14)$$

If  $f$  is a transformation function defined on the support of  $X$ , then  $Y = f(X)$  is a new random variable (transformed variable).

This section shows the available transformations in CASAL2 and the probability density function of  $Y$ .

Suppose  $X$  is one dimensional and  $f: \text{supp}(X) \rightarrow \mathbf{R}$  is a one-to-one, monotonic function with a differentiable inverse  $f^{-1}$ . Then the density of  $Y$  is

$$p_Y(y) = p_X(f^{-1}(y)) \left| \frac{\partial}{\partial y} f^{-1}(y) \right| \quad (5.15)$$

where  $\left| \frac{\partial}{\partial y} f^{-1}(y) \right|$  is the Jacobian term. The Jacobian measures how the scale of the transformed variable changes with respect to the underlying variable. This can be expanded to the multivariate case where the Jacobian becomes a matrix of partial derivatives.

In equation 5.15 the term  $p_X(f^{-1}(y)) = p_X(X)$  and in a Bayesian context is the prior of the untransformed variable/parameter. **Note:** if this functionality is in use be careful interpreting the covariance matrix as this will be related to the transformed variable not the variable space, e.g., if natural mortality ( $M$ ) is estimated as  $Y = M/2$ , then the covariance matrix will be described for  $Y$ .

```

@estimate log_R0
type lognormal
transformation log
parameter process[Recruitment].r0
transform_with_jacobian true
mu 442413
cv 0.2
lower_bound 3000
upper_bound 24154953

```

### Transform without Jacobian but prior defined in transformed space

This transformation is where the priors are defined in transformed space. This class of transformations contains functionality that was implemented in the CASAL.

If  $f()$  is a transformation function defined on the support of  $X$ , then  $Y = f(X)$  is a new random variable (transformed variable). In this class *a priori* information is specified with regard to  $p_Y(y)$  and  $X$  can be thought of as a derived quantity.

For example:

```
@estimate log_R0
type lognormal
parameter process[Recruitment].r0
prior_applies_to_transform true
mu 13
cv 0.5
lower_bound 8
upper_bound 17
```

### Transformation types

- **log : natural logarithm transformation**

```
is_simple = true
jacobian defined = true
 $Y = \ln(X)$ 
 $\left| \frac{\partial}{\partial y} f^{-1}(y) \right| = X^{-1}$ 
```

- **inverse**

```
is_simple = true
jacobian defined = true
 $Y = X^{-1}$ 
 $\left| \frac{\partial}{\partial y} f^{-1}(y) \right| = -X^{-2}$ 
```

- **sqrt : square root transformation**

```
is_simple = true
jacobian defined = true
 $Y = \sqrt{X}$ 
 $\left| \frac{\partial}{\partial y} f^{-1}(y) \right| = -X^{-1.5}$ 
```

- **average\_difference : two parameters  $\theta_1$  and  $\theta_2$  are transformed to  $Y_1$  and  $Y_2$ , where  $Y_1$  is the average of the original parameters and  $Y_2$  is the difference between the mean and each parameter.**

```
is_simple = false
jacobian defined = false
 $Y_1 = \frac{\theta_1 + \theta_2}{2}$ 
 $Y_2 = (Y_1 - \theta_2)2$ 
```

Restore transformations

$$\theta_1 = Y_1 + 0.5Y_2$$

$$\theta_2 = \theta_1 - 0.5Y_2$$

$$\left| \frac{\partial}{\partial y} f^{-1}(y) \right| \text{ Hasn't been assessed (i.e it could exist) (TODO ?????)}$$

- `log_sum` : two parameters  $\theta_1$  and  $\theta_2$  are transformed to  $Y_1$  and  $Y_2$ , where  $Y_1$  is the natural logarithm of the sum of  $\theta_1$  and  $\theta_2$ .  $Y_2$  describes the proportion of the sum with respect to  $\theta_1$

`is_simple = false`

`jacobian defined = false`

$$Y_1 = \ln(\theta_1 + \theta_2)$$

$$Y_2 = \theta_1 / (\theta_1 + \theta_2)$$

Restore transformations

$$\theta_1 = \exp(Y_1)Y_2$$

$$\theta_2 = \exp(Y_1)(1 - Y_2)$$

$$\left| \frac{\partial}{\partial y} f^{-1}(y) \right| \text{ Hasn't been assessed (i.e it could exist) (TODO ?????)}$$

- `orthogonal` : two parameters  $\theta_1$  and  $\theta_2$  are transformed to  $Y_1$  and  $Y_2$ , where  $Y_1$  is the multiplication of  $\theta_1$  and  $\theta_2$ .  $Y_2$  is the division of  $\theta_1$  and  $\theta_2$

`is_simple = false`

`jacobian defined = true`

$$Y_1 = \theta_1 \theta_2$$

$$Y_2 = \theta_1 / \theta_2$$

Restore transformations

$$\theta_1 = \sqrt{Y_1 Y_2}$$

$$\theta_2 = \sqrt{Y_1 / Y_2}$$

$$\left| \frac{\partial}{\partial y} f^{-1}(y) \right| = 2Y_2$$

- `SumToOne` : given two parameters  $\theta_1$  and  $\theta_2$  that have the constraint  $\sum_{i=1}^2 \theta_i$ , estimate  $\theta_1$  only

given  $\theta_2 = 1 - \theta_1$

`is_simple = false`

`jacobian defined = false`



---

## 6. The observation section

### 6.1. Observations

The objective function calculates the goodness-of-fit of the model to the observation data. Observations are typically supplied at an instance in time, over a group of aggregated categories. Most observations are sampled over time, i.e., data which were recorded for one or more years, in the same format each year. Examples of time series data types include relative abundance indices, commercial catch length frequencies, and survey numbers-at-age.

Definitions for each type of observation are described below, including how the observed values should be formatted, how CASAL2 calculates the expected values, and the likelihoods that are available for each type of observation.

There are two main types of observations available in CASAL2. The first type is observations that are associated with a **mortality block**. The second type is observations that are associated with a specific process. These observations use the `type` subcommand.

If an observation begins with `process` it is an observation that is associated with a process. If an observation does **not** begin with `process` it is associated with the mortality block of the defined time step. For example, the observation type `process_abundance` is a process-based observation, whereas `process_abundance abundance` is an observation that is associated with a mortality block.

There are two types of process observations. **Specific process observations** are observations that are associated with a specific process (e.g., `process_proportions_migrating`), and **general process observations** are observations that can be associated with any process (e.g., `process_proportions_at_age`). The observation types are described in different sections.

#### 6.1.1. Mortality block associated observations

All observations within this class are calculated similarly. That is, the expected values are calculated at the beginning of the mortality block and at the end of the mortality block. CASAL2 then uses a linear interpolation to approximate the expected values part way through a mortality block using the subcommand `time_step_proportion`. This feature could be useful if a survey occurs part way through an exploitation phase, which may be part way through a fishing season when modelling a fish population. Each observation in this class will evaluate different expectations of the partition (explained in the following descriptions).

The observation types available with this class of observations are:

- `abundance`
- `biomass`
- `proportions_at_age`
- `proportions_at_length`
- `proportions_by_category`
- `tag_recapture_by_length`
- `tag_recapture_by_age`

### 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 observation 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 the number of individuals.

Each observation is for a given year and time-step, for some selected age classes of the population (for a range of ages multiplied by a selectivity), for aggregated categories. Furthermore, the label of the catchability coefficient  $q$  is required;  $q$  can either be estimated or 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*, an observation of the total abundance/biomass (male + female) or male-only abundance/biomass could be provided. 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`. CASAL2 then requires that an observation is 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.

CASAL2 calculates the expected values by summing over the defined ages (via the age range and selectivity) and categories at both the beginning and end of a mortality block. CASAL2 will approximate the expectation part way through the mortality block using the `time_step_proportion`. The default `time_step_proportion` value is 0.5. CASAL2 does linear interpolation between the start and end abundance (or biomass) from the mortality block.

For an abundance observation the expected value is

$$E_{i,1} = \sum_{c=1}^C \sum_{a=1}^A S_{a,c} N_{a,c,i,1} \quad (6.1)$$

$$E_{i,2} = \sum_{c=1}^C \sum_{a=1}^A S_{a,c} N_{a,c,i,2} \quad (6.2)$$

Where  $E_{i,1}$  is the expectation at the beginning of time step and  $E_{i,2}$  is the expectation at the end of the time-step.  $S_a$  is the selectivity for age  $a$  and category  $c$ . If there is no mortality related to this observation then  $E_i$  which is used in the likelihood contribution is  $E_{i,1}$ . If this was a biomass observation, then  $N_{a,c,i,1}$  in Equations (6.1) and (6.2) is replaced with  $N_{a,c,i,1} \bar{w}_{a,c}$ , where  $\bar{w}_{a,c}$  is the mean weight of category  $c$  at age  $a$ . If the user wishes to apply 100% mortality then  $E_i = E_{i,2}$ .

For applying quantities of mortality between these values ( $M_i$ ), the linear interpolation is

$$E_i = |E_{i,1} - E_{i,2}| M_i \quad (6.3)$$

```
@observation MyAbundance
type abundance
years 1999
...
categories male
obs 1000
...
```

Or, for an observation aggregated over multiple categories,

```
@observation MyAbundance
type abundance
years 1990 1991
...
categories male+female
table obs
1990 1000
1991 1200
end_table
...
```

To define a biomass observation instead of an abundance observation, use

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

### Proportions-at-age

Proportions-at-age observations are observations of the relative number of individuals 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); the upper end of the age range can optionally be a plus group, which must be either the same as or less than the plus group defined for the partition.

Proportions-at-age observations can be supplied as

- a set of proportions for a single category,
- a set of proportions for multiple categories, or
- a set of proportions across aggregated categories.

The method of evaluating expectations are the same for all three types of proportions. The definitions of these proportions and the expected dimensions of observation and error inputs that CASAL2 expects for each respective proportion type are described below with examples.

Like all types of observations that are associated with the mortality block, CASAL2 will evaluate the numbers at age before and after the mortality block for the specified time step of the observation,

and applying the user-defined selectivity. CASAL2 then generates the expectations from the partition part way through the mortality block using the subcommand `time_step_proportion`. This approximation is a linear interpolation of the numbers-at-age over the mortality block.

The ageing error is then applied, if the user has specified it. Finally, CASAL2 converts the numbers-at-age to proportions-at-age by dividing all numbers in an age bin by the total numbers. The likelihood for the proportions-at-age observation is then calculated.

Defining an observation for a single category 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
```

CASAL2 then requires 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 omitting males aged less than 3 and 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.

```
@observation MyProportions
type proportions_at_age
...
categories male
min_age 3
max_age 9
years 1990
table obs
1990 0.01 0.09 0.20 0.20 0.35 0.10 0.05
end_table
...
```

Defining an observation for multiple categories extends the single category observation definition. 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
```

CASAL2 then requires 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 across all ages and categories.

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 females within each of these age classes (after omitting those aged less than 3 and 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,

```
@observation MyProportions
type proportions_at_age
...
categories male female
min_age 1
max_age 5
years 1990 1991
table obs
1990 0.01 0.05 0.10 0.20 0.20 0.01 0.05 0.15 0.20 0.03
1991 0.02 0.06 0.10 0.21 0.18 0.02 0.03 0.17 0.20 0.01
end_table
...
```

Defining an observation across aggregated categories 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
```

CASAL2 then requires 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 omitting those aged less than 3 and 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.

For example,

```
@observation MyProportions
type proportions_at_age
...
years 1990 1991
categories male+female
min_age 1
max_age 5
table obs
1990 0.02 0.13 0.25 0.30 0.30
1991 0.02 0.06 0.18 0.35 0.39
end_table
...
```

The latter 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 through 4, a total of 12 proportions are required

```
@observation MyProportions
type proportions_at_age
...
categories male_immature male_mature female_immature+female_mature
min_age 1
max_age 4
years 1990
table obs
year 1990 0.05 0.15 0.15 0.05 0.02 0.03 0.08 0.04 0.05 0.15 0.15 0.08
end_table
...
```

### Proportions-at-length

Functionality for defining combinations of categories and aggregated categories directly translates from proportions-at-age to proportions-at-length. The difference is the observation is over length bins instead of age classes. CASAL2 calculates the expected numbers-at-length by converting the numbers-at-age to numbers-at-length by using the age-length relationship and distribution specified for the category specified in the @age\_length block.

Instead of supplying a minimum and maximum age users must supply a vector of length bins. If there is no plus group, i.e., length\_plus=false, then CASAL2 requires a vector of proportions for each year of length  $n - 1$ , where  $n$  is the number of lengths supplied. If length\_plus=true then CASAL2 expects a vector of proportions for each year of length  $n$ . The last proportion represents the numbers from the last length bin to the maximum length the age-length relationship allows.

```
@observation Observed_Length_frequency_Chatham_east
type process_removals_by_length
years 1991 1992
likelihood multinomial
time_step Summer
fishery EastChathamRise
process instant_mort
categories male
length_plus false
length_bins 0 20 40 60 80 110
table obs
1991 0.2 0.25 0.15 0.2 0.2
1992 0.12 0.25 0.28 0.25 0.1
end_table
table error_values
1991 25
1992 37
end_table
```

### Proportions-by-category observations

TODO 'between categories' or 'within categories'?

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 selected age classes of the population (i.e., for a range of ages multiplied by a selectivity).

The age range must be ages defined in the partition (i.e., between @model.min\_age and @model.max\_age inclusive); 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*, observations of the proportions of males in the population at each age class might be provided. 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.

For example,

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

defines the proportion of males in each age class as a proportion of males + females. CASAL2 then requires 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 ages 3, 4, 5, 6, 7, 8, 9, and 10). The expected values will be the expected ratios 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. CASAL2 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,

```
@observation MyProportions
type proportions_by_category
years 1990 1991
...
categories male
categories2 female
min_age 1
max_age 5
table obs
1990 0.01 0.05 0.10 0.20 0.20
1991 0.02 0.06 0.10 0.21 0.18
end_table
...
```

### Tag Recapture by length

Tag data is primarily used to estimate the population abundance of fish. In some models, this estimation can only be made outside the model and the result is used as an estimate of abundance in

the model. But in CASAL2 the tagging data can, alternatively, be fitted within the model.

Before adding a tag-recapture time series, a tag-release process (Section 4.5.5) needs to be defined. Tagging events list the labels of the tags which are modelled, and define the events where fish are tagged (i.e., CASAL2 moves fish into the section of the partition corresponding to a specific tag).

The observations are divided into two parts: (i) the number of fish that were scanned, and (ii) the number of tags that were recaptured. Each number can be specified by categories, or for combinations of categories. The precise content of the scanned and recaptured observations depends on the sampling method.

The available options are:

- age: both the scanned and recaptured are vectors containing numbers-at-age. Only available in an age-based model. The selectivity ogive is redundant and cannot be supplied.
- size: both the scanned and recaptured are vectors containing numbers-at-size. Can be used in either an age- or size-based model. The selectivity ogive is redundant and cannot be supplied.

When defining the tag-recapture time series, the following are also required:

- the time step,
- the years (unlike a tag-release process, the tag-recapture observations can occur over several years),
- the probability that each scanned tagged fish is detected as tagged (may be less than 1 if the observers are not infallible). The expected number of tags detected is calculated by multiplying this number by the number of tagged fish in the sample,
- the tagged category or categories (Make up the recaptures),
- the categories scanned (All the fish sampled for tags),
- A selectivity used in the recapture process,
- the size classes if the observations are size-based in an age-based model.

An example of a tag recapture observation:

```
## For the following partition
@categories
format sex.area.tag
names    male.Areal.2011,notag female.Areal.2011,notag

@observation Tag_2011_Areal_recap_2012 ## individuals tagged in 2011 and recaptured in 2012
## in Areal
type tag_recapture_by_length
categories format=*.Areal.*+ ## scanned categories in Areal
tagged_categories *.Areal.2011+ ## male and female tagged categories
detection 0.85 ## detection probability
likelihood binomial ## likelihood choice
selectivities One ## label of selectivity for tagged
tagged_selectivities One ## label of selectivity for scanned
years 2012 ## years to apply observation
time_step step2 ## time_step to apply observation
time_step_proportion 0.5 ## proportion of mortality applied before observation is calculated

table scanned
```



```

2012 281271 41360 30239 12234
end_table

table recaptured
2012 15 20 12 2
end_table

delta 1e-11 ## robustification value
dispersion 6.3 ## dispersion factor

```

The observed ( $O_{y,l}$ ) and expected ( $E_{y,l}$ ) values in year  $y$  and length  $l$  of this observation are:

$$O_{y,l} = \frac{R_{y,l}}{S_{y,l}} \quad (6.4)$$

where  $R_{y,l}$  is the number of recaptures in year  $y$  at length  $l$  and  $S_{y,l}$  are the scanned values.

$$E_{y,l} = d \frac{\tilde{N}_{y,l,t} + (\tilde{N}_{y,l,t+1} - \tilde{N}_{y,l,t}) \times p}{N_{y,l,t} + (N_{y,l,t+1} - N_{y,l,t}) \times p} \quad (6.5)$$

where  $\tilde{N}_{y,l,t}$  is an element in the tagged categories at the beginning of time step  $t$  and  $\tilde{N}_{y,l,t+1}$  is an element in the tagged categories at the end of time step  $t$ ,  $N_{y,l,t}$  is the sum of the categories that were vulnerable to sampling when the observation occurred,  $p$  is the proportion of the time step that the observation was taken, and  $d$  is the detection probability.

For observations with multiple tagged categories and multiple categories that were vulnerable to sampling:

$$\tilde{N}_{y,l,t} = \sum_{j=1}^J N_{y,l,t,j} \quad (6.6)$$

where  $j = \{1, 2, 3, \dots, J\}$  are all the tagged categories, the same method is applied to the vulnerable categories to calculate  $N_{y,l,t}$ . The tagged categories should be defined in the vulnerable categories. In an extreme case where every individual in the population is tagged, this result would be divided by zero. So, to constrain the expectation to be between 0 and 1, the numerator must be in the denominator.

The tag-recapture likelihood (binomial) is specified below. It is a modified version of the more general binomial. Note that this likelihood does not have any user-set precision parameters such as  $N$  or  $c.v.$ , although there are user-specified robustification and dispersion parameters available. The factorials are calculated using the log-gamma function, to allow for non-integer arguments where necessary (and to avoid overflow errors).

### 6.1.2. General process observations

A list of types that are associated with this set of observations:

- process\_abundance

- `process_biomass`
- `process_proportions_at_age`
- `process_proportions_at_length`
- `process_proportions_by_category`

These observations have the same expectations as the mortality block versions described in Section 4.4.2. With the exception that instead of wrapping a mortality block they can wrap any process type available in CASAL2.

### 6.1.3. Specific process observations

A list of types that are associated with this set of observations are:

- `process_removals_by_age`
- `process_removals_by_age_retained`
- `process_removals_by_age_retained_total`
- `process_removals_by_length`
- `process_removals_by_length_retained`
- `process_removals_by_length_retained_total`
- `process_proportions_migrating`

#### Process removals by age

Removals-at-age observations are observations of the relative number of individuals at age, part way through a process of type `mortality_instantaneous`. This observation is exclusively associated with the process of type `mortality_instantaneous`, and will produce an error if it is associated with any other process type.

The observation is supplied for a given year and time-step, for selected age classes of the population (i.e., for a range of ages multiplied by a selectivity that is associated with the process).

The age range must be ages defined in the partition (i.e., between `@model.min_age` and `@model.max_age` inclusive); 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.

The expectations from this observation are generated whilst the process is being executed. The expectation of numbers at age  $a$  for category  $c$  from exploitation method  $m$  ( $E[N_{a,c,m}]$ ) are

$$E[N_{a,c,m}] = N_{a,c} U_{a,m} S_{a,c,m} 0.5 M_{a,c} \quad (6.7)$$

where  $N_{a,c}$  are the numbers-at-age in category  $c$  before the process is executed,  $U_{a,m}$  is the exploitation rate for age  $a$  from method  $m$ ,  $S_{a,c,m}$  is the selectivity, and  $M$  is the natural mortality.

The observation class accesses the variable  $E[N_{a,c,m}]$  and applies ageing error if the user has specified it. Then the observations are aggregated by method and category depending on how

the user specifies the observation, before converting numbers-at-age to proportions-at-age and then calculating the likelihood.

Likelihoods that are available for this observation class are the multinomial, Dirichlet, and the lognormal. See Section 6.2 for information on the respected likelihood.

### Process removals by age retained

Observations of retained and total catches by age can be included, using the labels `process_removals_by_age_retained` and `process_removals_by_age_retained_total`, respectively. Examples of two such observations are given below, with the associated process `Instantaneous_Mortality_Retained` having the form of the example in Section 4.5.3.4.

For retained catch:

```
@observation potFishAFtotal #test syntax get catch AF out
type process_removals_by_age_retained_total
mortality_instantaneous_process Instantaneous_Mortality_Retained
method_of_removal FishingPot
years 2005
time_step 1
categories male
### ageing_error Normal_ageing
min_age 3
max_age 15
plus_group True
table obs
2005 0.0002814574 0.0095351205 0.1661896098 0.2701718827 0.2214454177 0.1661869474 0.1107930285 0.
end_table
table error_values
2005 651
end_table
likelihood multinomial
delta 1e-11
```

For total catch:

```
@observation potFishAFretained #test syntax --> fits to discards not catch
type process_removals_by_age_retained
mortality_instantaneous_process Instantaneous_Mortality_Retained
method_of_removal FishingPot
years 2005
time_step 1
categories male
# ageing_error Normal_ageing
min_age 3
max_age 15
plus_group True
table obs
2005 1.650990e-10 7.566419e-07 1.771126e-03 1.962050e-01 3.192775e-01 2.413644e-01 1.609208e-01 8.
end_table
table error_values
2005 651
end_table
likelihood multinomial
```

```
delta 1e-11
```

### Process removals by length

Removals by length observations are observations of the relative number of individuals at length, part way through a process of type `mortality_instantaneous`. This observation is exclusively associated with the process of type `mortality_instantaneous`, and will produce an error if associated with any other process type.

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 that is associated with the process).

The expectations from this observation are generated whilst the process is being executed. The expectation of numbers at age  $a$  for category  $c$  from exploitation method  $m$  ( $E[N_{a,c,m}]$ ) are

$$E[N_{a,c,m}] = N_{a,c} U_{a,m} S_{a,c,m} 0.5 M_{a,c} \quad (6.8)$$

where  $N_{a,c}$  are the numbers at age in category  $c$  before the process is executed,  $U_{a,m}$  is the exploitation rate for age  $a$  from method  $m$ ,  $S_{a,c,m}$  is the selectivity, and  $M$  is the natural mortality.

The observation class accesses the variable  $E[N_{a,c,m}]$  from the process and applies the age-length relationship specified in the model. This converts numbers-at-age to numbers-at-age and -length, which are then converted to numbers-at-length. The observations are aggregated by method and category depending on how the user specifies the observation, before converting numbers-at-age to proportions and calculating the likelihood.

```
@observation observation_fishery_LF
type process_removals_by_length
...
years 1993 1994 1995
method_of_removal FishingEast
mortality_instantaneous_process instant_mort
length_plus false
length_bins 0 20 40 60 80 110
delta 1e-5
table obs
1993 0.0 0.05 0.05 0.10 0.80
1994 0.05 0.1 0.05 0.05 0.75
1995 0.3 0.4 0.2 0.05 0.05
end_table

table error_values
1993 31
1994 34
1995 22
end_table
```

Likelihoods that are available for this observation are the multinomial, Dirichlet and the lognormal. See Section 6.2 for information on the likelihoods.

### Process removals by age retained

Observations of retained and total catches by length can be included, using the labels `process_removals_by_length_retained` and `process_removals_by_length_retained_total` respectively. Examples of two such observations are given below, with the associated process `Instantaneous_Mortality_Retained` having the form of the example in [Section 4.5.3.4](#).

For retained catch:

```
@observation potFishLFtotal #test syntax get catch LF out
type process_removals_by_length_retained_total
mortality_instantaneous_process Instantaneous_Mortality_Retained
method_of_removal FishingPot
years 2005
time_step 1
categories male
length_bins 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 # for LF in catch
length_plus False
table obs
2005 0.05344612 0.06432242 0.07357780 0.08050385 0.08473451 0.08619620 0.08502982 0.08152921 0.076
end_table
table error_values
2005 651
end_table
likelihood multinomial
delta 1e-11
```

For total catch:

```
@observation potFishLFretained #test syntax get retained LF out
type process_removals_by_length_retained
mortality_instantaneous_process Instantaneous_Mortality_Retained
method_of_removal FishingPot
years 2005
time_step 1
categories male
length_bins 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 # for LF in catch
length_plus False
table obs
2005 0.02462879 0.03536036 0.04759163 0.06025858 0.07205340 0.08169356 0.08817806 0.09095124 0.089
end_table
table error_values
2005 651
end_table
likelihood multinomial
delta 1e-11
```

### Proportions migrating

This observation is of the proportion migrating from one area to another. This observation is exclusively associated with the process type `transition_category`, and will produce an error when associated with any other process type. This observation is used to inform migration rates in migration processes. This observation class is used in the Hoki stock

assessment see [Francis et al. \(2003\)](#) for more information on how these observations are collected and a situation that uses it.

This observation calculates an expectation  $E_a$  of proportions for each age class  $a$  that have migrated, by

$$E_a = \frac{N_a - N'_a}{N_a} \quad (6.9)$$

where  $N_a$  are the numbers of individuals in age  $a$  before the migration process occurs, and  $N'_a$  are the number of individuals after the migration process occurs.

The likelihoods that are allowed for this observation are the lognormal, multinomial, and Dirichlet.

A section of the Hoki stock assessment model:

```
@observation pspawn_1993
type process_proportions_migrating
years 1993
time_step step4
process Wspmng ## migration process that the observation is associated with
age_plus true
min_age 4
max_age 9
likelihood lognormal
categories male.west+female.west ## Categories to evaluate the prportion for
ageing_error Normal_offset ## label for an @ageing_error block
table obs
#age    4    5    6    7    8    9
1993 0.64 0.58 0.65 0.66 0.71 0.60
end_table

table error_values
## if lognormal these are c.v.'s
1993 0.25
end_table
```

## 6.2. Likelihoods

### 6.2.1. Likelihoods for proportions-at-age observations

CASAL2 implements three likelihoods for proportions-at-age observations, the multinomial likelihood, the Dirichlet, 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:

$$-\log(L) = -\log(N!) + \sum_i \log((NO_i)!) - NO_i \log(Z(E_i, \delta)) \quad (6.10)$$

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  $\delta > 0$ .

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.11)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

### The Dirichlet 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:

$$-\log(L) = -\log(\Gamma(\sum_i \alpha_i)) + \sum_i \log(\Gamma(\alpha_i)) - \sum_i (\alpha_i - 1) \log(Z(O_i, \delta)) \quad (6.12)$$

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

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.13)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

### 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;

$$-\log(L) = \sum_i \left( \log(\sigma_i) + 0.5 \left( \frac{\log(O_i / Z(E_i, \delta))}{\sigma_i} + 0.5 \sigma_i \right)^2 \right) \quad (6.14)$$

where

$$\sigma_i = \sqrt{\log(1 + c_i^2)} \quad (6.15)$$

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  $\delta > 0$ .

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.16)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

### 6.2.2. Likelihoods for abundance and biomass observations

Abundance and biomass observations are expected as an annual time series in CASAL2, where they select the same categories over that time series. The parameters and inputs needed to use this observation class are: a observation  $O_i$ , c.v.  $c_i$ , catchability coefficient  $q$ , where  $i$  indexed the year. CASAL2 calculates an expectation  $E_i$  and scales it by  $q$  before comparing it to  $O_i$ . This means that the value chosen for  $q$  will determine whether the observation is relative ( $q \neq 1$ ) or absolute  $q = 1$ . Before we describe each of the likelihoods we will discuss the methods available to handle  $qs$ :

- The  $qs$  can be treated as 'nuisance' parameters. For each set of values of the free parameters, the model uses the values of the  $qs$  which minimise the objective function. These optimal  $qs$  are calculated algebraically (see Section 6.4). If one of the  $qs$  falls outside the bounds specified by the user, it is set equal to the closest bound. This approach reduces the size of the parameter vector and hence should improve the performance of the estimation method. However, it is not correct when calculating a sample from the posterior in a Bayesian analysis (except asymptotically, see Walters and Ludwig (1994)) and we offer the following alternative;
- The  $qs$  can be treated as ordinary free parameters.

For both options, it is necessary to evaluate the contribution of  $O_i$  to the negative log likelihood for a given value of  $q$ . Each observation  $O_i$  varies about  $qE_i$ , which expresses the variability of  $O_i$  in terms of its c.v.  $c_i$  (or in one case, its standard deviation  $\sigma_i$ ). Here are the likelihoods, which are expressed on the objective-function scale of  $-\log(L)$ :

#### The lognormal likelihood

The negative log likelihood for the lognormal is

$$-\log(L) = \sum_i \left( \log(\sigma_i) + 0.5 \left( \frac{\log(O_i/qZ(E_i, \delta))}{\sigma_i} + 0.5\sigma_i \right)^2 \right) \quad (6.17)$$

where

$$\sigma_i = \sqrt{\log(1 + c_i^2)} \quad (6.18)$$

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

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2 - \theta/\delta), & \text{otherwise} \end{cases} \quad (6.19)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

This formulation reflects the distributional assumptions that  $O_i$  has the lognormal distribution, that the mean of  $O_i$  is  $qE_i$  and the c.v. of  $O_i$  is  $c_i$ .



### The normal likelihood

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

$$-\log(L) = \sum_i \left( \log(c_i E_i) + 0.5 \left( \frac{O_i - E_i}{Z(c_i E_i, \delta)} \right)^2 \right) \quad (6.20)$$

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

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.21)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

This reflects the distributional assumptions that  $O_i$  has the normal distribution, that the mean of  $O_i$  is  $qE_i$  and the c.v. of  $O_i$  is  $c_i$ .

### 6.2.3. Likelihoods for tag recapture by age and length observations

#### The binomial likelihood

This likelihood is for situations where the size frequencies or age frequencies of the recaptured tagged fish and of the scanned fish are known. Available in both age or size based models.

The likelihood is defined as a binomial, but based on sizes, rather than ages

$$-\log(L)' = -\sum_i \left[ \log(n_i!) - \log((n_i - m_i)!) - \log((m_i)!) + m_i \log \left( Z \left( \frac{M_i}{N_i}, \delta \right) \right) \right. \\ \left. + (n_i - m_i) \log \left( Z \left( 1 - \frac{M_i}{N_i}, \delta \right) \right) \right] \quad (6.22)$$

where

$n_i$  = number of fish at size or age  $i$  that were scanned

$m_i$  = number of fish at size or age  $i$  that were recaptured

$N_i$  = number of fish at size or age  $i$  in the available population (tagged and untagged)

$M_i$  = number of fish at size or age  $i$  in the available population that have the tag after a detection probability  $p_d$  has been applied,  $M_i = M'_i p_d$ , where  $M'_i$  is the expected available population that have the tag.

$Z(x, \delta)$  is a robustifying function with parameter  $r > 0$  (to prevent division by zero errors).

$$Z(x, \delta) = \begin{cases} x & \text{where } x \geq \delta \\ \frac{\delta}{(2 - x/\delta)} & \text{otherwise} \end{cases}$$

If a dispersion parameter ( $\tau$ ) is described in the observation then the final negative log likelihood  $-\log(L)$  contribution is

$$-\log(L) = -\log(L)' / \tau$$

#### 6.2.4. Likelihoods for proportions-by-category observations

CASAL2 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

$$-\log(L) = -\sum_i [\log(N_i!) - \log((N_i(1 - O_i))!) - \log((N_i O_i)!) + N_i O_i \log(Z(E_i, \delta)) + N_i(1 - O_i) \log(Z(1 - E_i, \delta))] \quad (6.23)$$

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

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.24)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

##### 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;

$$-\log(L) = \sum_i \log\left(\sqrt{Z(E_i, \delta) Z(1 - E_i, \delta) / N_i}\right) + \frac{1}{2} \left( \frac{O_i - E_i}{\sqrt{Z(E_i, \delta) Z(1 - E_i, \delta) / N_i}} \right)^2 \quad (6.25)$$

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

$$Z(\theta, \delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta / (2 - \theta / \delta), & \text{otherwise} \end{cases} \quad (6.26)$$

The default value of  $\delta$  is  $1 \times 10^{-11}$ .

### 6.3. Process error

Additional 'process error' can be defined for any 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 the likelihood is parameterised by the c.v., the process error can be specified for a given set of observations as a c.v., in which case all the c.v.s  $c_i$  are changed to

$$c'_i = \sqrt{c_i^2 + c_{process\_error}^2} \quad (6.27)$$

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  $N$ ,

$$N'_i = \frac{1}{1/N_i + 1/N_{process\_error}} \quad (6.28)$$

Note that this requires that  $N_{process\_error} > 0$ , but the special case of  $N_{process\_error} = 0$  is valid, and  $N_{process\_error} = 0$  represents 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. Note that a large value for the  $N$  process error means a small process error.

### 6.4. Calculating nuisance $q$ parameters

This section describes the theory used to calculate nuisance (analytical) catchability coefficients  $qs$  (see Section 6.2.2). From the user's point of view, the essence is that you can use nuisance  $qs$  in the following situations:

- With maximum likelihood estimation
- With Bayesian estimation, providing that the additional prior on  $q$  is one of the following:
  - None (default)
  - Uniform-log
  - Lognormal with observations distributed lognormal, robustified lognormal

The scenarios in which the nuisance catchability  $q$  can be used in a Bayesian analysis (Table 6.1):

**Table 6.1: Equations used to calculate nuisance  $qs$ . (\*=no analytic solution found.)**

Distribution of observations	Maximum Likelihood	None	Uniform-log	Normal	lognormal
Normal	(6.29)	(6.29)	(6.31)	*	*
Lognormal	(6.32)	(6.32)	(6.36)	*	(6.37)

Note that  $qs$  are calculated for robustified lognormal likelihoods as if they were ordinary lognormal likelihoods.

Let  $\sigma_i = \sqrt{\log(1 + c_i^2)}$  throughout, and let  $n$  be the number of observations in the time series. The case of multiple time series sharing the same  $q$ , and the modifications required for the assumption of curvature, are addressed at the end of this subsection.

First, consider maximum likelihood estimation. When the  $(O_i)$  are assumed to be normally distributed

$$-\log(L) = \sum_i \log(c_i q E_i) + 0.5 \sum_i \left( \frac{O_i - q E_i}{c_i q E_i} \right)^2 \quad (6.29)$$

The value of  $q$  which minimises the objective function is found by solving for  $q$  under the following condition,  $\partial/\partial q(-\log(L)) = 0$

$$\frac{\partial}{\partial q}(-\log(L)) = \frac{n}{q} + \frac{1}{q^2} \sum_i \frac{O_i}{c_i^2 E_i} - \frac{1}{q^3} \sum_i \left( \frac{O_i}{c_i E_i} \right)^2 \quad (6.30)$$

hence

$$\hat{q} = \frac{-S_1 + \sqrt{S_1^2 + 4nS_2}}{2n} \quad (6.31)$$

where  $S_1 = \sum_i (O_i/c_i^2 E_i)$  and  $S_2 = \sum_i (O_i/c_i E_i)^2$

When the  $(O_i)$  are assumed to be lognormally distributed,

$$-\log(L) = \sum_i \log(\sigma_i) + 0.5 \sum_i \left( \frac{\log(O_i) - \log(q E_i) + 0.5 \sigma_i^2}{\sigma_i} \right)^2 \quad (6.32)$$

$$\frac{\partial}{\partial q}(-\log(L)) = \frac{-1}{q} \sum_i \left( \frac{\log(O_i/E_i) - \log(q) + 0.5 \sigma_i^2}{\sigma_i^2} \right) \quad (6.33)$$

$$\hat{q} = \exp \frac{0.5n + S_3}{S_4} \quad (6.34)$$

where  $S_3 = \sum_i (\log(O_i/E_i)/\sigma_i^2)$  and  $S_4 = \sum_i (1/\sigma_i^2)$ .

Next, consider Bayesian estimation, where a prior for  $q$  must be specified.

The effects of the prior on the equations are to replace likelihood  $L$  by posterior  $P$  throughout, to add  $-\log(\pi(q))$  to the equation for  $-\log(P)$  and  $\partial/\partial q(-\log(-\pi(q)))$  to the equation for  $\partial/\partial q(-\log(P))$

This last term is 0 for a uniform prior on  $q$ ,  $1/q$  for a log-uniform prior, and  $\frac{1}{q} \left( 1.5 + \frac{\log(q) - \log(\mu_q)}{\sigma_q^2} \right)$  for a lognormal prior, where  $\mu_q$  and  $c_q$  are the mean and c.v. of the prior on  $q$ , respectively, and  $\sigma_q = \sqrt{\log(1 + c_q^2)}$ . Since the prior is uniform, the equation for  $\hat{q}$  is the same as the maximum likelihood estimation.

When the  $(O_i)$  are assumed to be normally distributed and the prior is log-uniform equation (6.31) becomes,

$$\hat{q} = \frac{-S_1 + \sqrt{S_1^2 + 4(n+1)S_2}}{2(n+1)} \quad (6.35)$$

but  $\hat{q}$  with either a normal or lognormal prior cannot be solved for.

When the  $O_i$  are assumed to be lognormally distributed and the prior is log-uniform, equation (6.34) becomes

$$\hat{q} = \exp \frac{0.5n - 1 + S_3}{S_4} \quad (6.36)$$

and if the prior is lognormal,

$$\hat{q} = \exp \frac{0.5n - 1.5 + \log(\mu_q)/\sigma_q^2 + S_3}{S_4 + 1/\sigma_q^2} \quad (6.37)$$

However, it is not possible to solve for  $\hat{q}$  with a normal prior.

An example of specifying the syntax and an equivalent additional prior

```
@catchability chatTANq
type nuisance
upper_bound 0.6
lower_bound 0.0001

@additional_prior chatTANq_prior
type lognormal
parameter catchabilityp[chatTANq].q
mu 0.3
cv 0.2
```

## 6.5. Ageing error

CASAL2 can apply ageing error to expected age frequencies estimated by the model. The ageing error is applied as a misclassification matrix, which has the effect of 'smearing' the expected age frequencies. This is mimicking the error involved in identifying the age of individuals. For example, fish species are aged by reading the ear bones (otoliths) which can be quite difficult depending on the species. These age frequencies 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 7.14 for reporting the misclassification matrix at the end of model run.

The ageing error models implemented are

- None: The default model is to apply no ageing error.
- 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'.
- 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.

The expected values (fits) reported by CASAL2 for observations with ageing error will have had the ageing error applied.

## 6.6. Simulating observations

CASAL2 can generate simulated observations for a given model with a set of parameter values using `casal2 -s 1` (To simulate one set of simulated observations). Simulated observations are randomly generated values, which are generated with the error distributions 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 CASAL2 uses for simulating observations is to use the 'true' parameter values and generate the expected values. Then, if a set of observations use 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 the simulated values, depend on the specific likelihood type of each observation.

- 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  $E_i c_i$ .
- 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  $\delta$  is ignored.
- 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  $\delta$  is ignored. Then,
  1. A sample of  $N$  values from 1 to  $n$  is generated using the multinomial distribution, using sample probabilities proportional to the values of  $E_i$ .
  2. Each simulated observation value  $S_i$  is calculated as the proportion of the  $N$  sampled values equalling  $i$
  3. The simulated observation values  $S_i$  are then rescaled so that their sum is equal to 1
- 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  $\delta$  is ignored. Then,
  1. A sample of  $N_i$  independent binary variates is generated, equalling 1 with probability  $E_i$
  2. The simulated observation value  $S_i$  is calculated as the sum of these binary variates divided by  $N_i$

**An important note when simulating:** CASAL2 will **not** automatically report simulated observations when using a `casal2 -s 1` run. A report must be defined using the

`simulated_observation report (@report[label].type=observation)`. See Section 7 for more information on how to write this report.

## 6.7. Pseudo-observations

CASAL2 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 CASAL2 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. CASAL2 can also generate simulated observations from pseudo-observations. Note that

- Output will be generated only if a report command `@report[label].type=observation` is specified.
- The observed values should be supplied (even if they are 'dummy' observations). These observation values will be processed by CASAL2 as if they were actual observation values, and must be in the same format as actual observation values.
- The subcommands `likelihood`, `obs`, `error_value`, and `process_error` have no effect when generating the expected values for the pseudo-observation.
- When simulating observations, the subcommand `simulation_likelihood` to indicate the 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.

## 6.8. Residuals

CASAL2 will print the default residual values (i.e., observed less fitted) only when the report type `@report.type=observation` is used. For an observation  $O$  and  $F$  the corresponding fit ( $=qE$  for relative observations), then

- Residuals =  $O - F$

Pearson and normalised residuals can be generated using the CASAL2 **R** package. For specific **R** functions see Section 15.

The definitions used in the calculations are

- *Pearson residuals* attempt to express the residual relative to the variability of the observation, and are defined as  $(O-F)/\text{std.dev.}(O)$ , where  $\text{std.dev.}(O)$  is calculated as
  - $F \times \text{cv}$  for normal, lognormal, robustified lognormal, and normal-log error distributions.
  - $s$  for normal-by-standard deviation error distributions.
  - $\sqrt{\frac{Z(F,r)(1-Z(F,r))}{N}}$  for multinomial or binomial likelihoods.
  - $\sqrt{\frac{(F+r)(1-F+r)}{N}}$  for binomial-approx likelihood likelihoods.
- *Normalised residuals* to express the residual on a standard normal scale, and are defined as:
  - Equal to the Pearson residuals for normal error distributions.
  - $(\log(O/F)+0.5\sigma^2)/\sigma$  for lognormal (including robustified lognormal) error distributions, where  $\sigma = \sqrt{\log(1 + \text{cv}^2)}$ .

- $\log(O/F)/\sigma$  for normal-log error distributions, again with  $\sigma = \sqrt{\log(1 + cv^2)}$ .
- And are otherwise undefined.

where  $Z(F, r)$  is the robustifying term on  $F$  (fit or expectation of the observation). This robustifying function is described earlier in the likelihood section.



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## 7. The report section

The report section specifies the printouts and other output from the model. CASAL2 does not, in general, produce any output unless specified by a valid `@report` block.

### 7.1. Report command block format

Reports from CASAL2 can be defined to print partition and states objects at a particular point in time, observation summaries, estimated and derived parameter values, and objective function values.

```
@report observation_age ## label of report
type observation ## Type of report
observation age_1990 ## label corresponding to an @observation report, shown below

@observation age_1990
type proportion_at_age
year 1990
plus_group
etc ...
```

### 7.2. Report block output format

Reports from CASAL2 have a standard style (with one exception, the `output_parameters` report, see below). The standard style is that reports are prefixed with an asterisk followed by a user-defined label and type of report in brackets (e.g., `*label (type)`), with the report ending with the line `*end`. For example,

```
*My_report (type)
...
*end
```

This report block output format should make it easier for other software packages to read and process CASAL2 output. The `extract` functions in the **R** CASAL2 package use this information to identify and read CASAL2 output.

The `output_parameters` report does not print either a header or `*end` at the end of the report block. This is because the `output_parameters` report is designed to provide a single line vector of the estimated parameter values, or multiple lines for more than one set, which can be read by CASAL2 with the command `casal2 -i`. This is a specialised report for the `casal2 -o filename` command.

For estimated values in standard output use the `type=estimate_value` report.

Reports can be defined in a `@report` command block but may not be output, e.g., a report to print the partition for a year and/or timestep that does not exist, or reporting the covariance matrix when not estimation run mode.

Certain reports are associated with certain CASAL2 run modes. These reports are ignored by CASAL2 and the program will not generate any output for these reports, although they must still conform to CASAL2 syntax requirements.

Not all reports will be generated in all run modes. Some reports are only available in some run modes. For example, when simulating, only the simulation reports will be output.

### 7.3. Print the partition at the end of an initialisation

This report prints the partition following the initialisation phase, which includes the numbers of individuals in each age class and category in the partition. This report will print out in run modes `-r`, `-e`, `-f`.

### 7.4. Print the partition

This report prints the numbers of individuals in each age class and category in the partition for each given year or given years and timestep. This report is evaluated at the end of the timestep in the given year(s). This report will print out in run modes `-r`, `-e`, `-f`.

### 7.5. Print the age length and length weight values

This report prints the length and weight value for each age class and category in the partition for each given year or given years and timestep. This report is evaluated at the end of the timestep in the given year(s). This report will print out in run modes `-r`, `-e`, `-f`.

```
@report length_weight_at_age
type partition_mean_weight
time_step step2
years 1900:2013
```

### 7.6. Print a process summary

Depending on the process, different summaries are produced. These reports typically detail the type of process, its parameters and other options, and any associated details. This report will print out in run modes `-r`, `-e`, `-f`.

### 7.7. Print derived quantities

This report prints the description of the derived quantity, and the values of the derived quantity as recorded in the model state, for each year of the model, and for all years in the initialisation phase. This report will print out in run modes `-r`, `-e`, `-f`.

### 7.8. Print the estimated parameters

This report prints a summary of the estimated parameters using the type `estimate_summary`, including the parameter name, lower and upper bounds, the label of the prior, and its value. This report will print out in run modes `-r`, `-e`.

### 7.9. Print the estimated parameters in a vector format

This report prints the estimated parameter values out as a vector. The `estimate_values` report prints the name of the parameter, followed by the value for that run. This report will print out in run modes `-r`, `-e`.

### 7.10. Print the objective function

This report prints the total objective function value, the value of all observation likelihood components, the values of all priors, and the value of any penalties that have been incurred. If an individual model run does not incur a penalty, then the penalty will not be reported. This report will print out in run modes `-r`, `-e`, `-f`.

### 7.11. Print the covariance matrix

This report prints the Hessian and covariance matrices if in estimation run mode and if the covariance has been requested by `@minimiser[label].covariance=true`.

### 7.12. Print observations, fits, and residuals

This report prints, for each category or combination of categories, the expected values, residuals (observed – expected), the error value, process error, the total error (i.e., the error value as modified by any additional process error), and the contribution to the total objective function of that individual datum in the observation.

Constants in the likelihood components are often ignored in the objective function score of individual observation values. Hence, the total score from an observation equals the contribution of the objective function scores from each individual observation value plus a constant term (if applicable). In likelihood components without a constant term, the total score from an observation will equal the contribution of the objective function scores from each individual observation value.

If CASAL2 is in simulation run mode, then the contribution to the objective function of each observation is reported as zero.

```
@report Tan_at_age_obs
type observation
observation TAN_AT_AGE
```

### 7.13. Print simulated observations

This report prints a complete set of observation values in the form specified by `@report[label].type=observation`, with observed values replaced by randomly generated simulated values. The output is in a form suitable for use within a CASAL2 input configuration file, reproducing the command and subcommands from the input configuration file. This report will print out in run mode `-s`.

**7.14. Print the ageing error misclassification matrix**

This report prints the ageing error misclassification matrix used to offset observations within during model the model fitting procedure.

**7.15. Print selectivities**

This report prints the values of a selectivity for each age in the partition, for a given year and at then end of a given timestep.

**7.16. Print the random number seed**

This report prints the random number seed used by CASAL2 to initialise the generated random number sequence. Additional runs which use the same random number seed and the same model will produce identical outputs.

**7.17. Print the results of an MCMC**

This report prints the MCMC samples, objective function values, and proposal covariance matrix following an MCMC. This report will print out in run mode `-m`.

**7.18. Print the MCMC samples as they are calculated**

This report prints the MCMC samples for each new *i*th sample as they are calculated while doing an MCMC. The output file will be appended with each new sample as it is calculated by CASAL2. This report will print out in run mode `-m`.

**7.19. Print the MCMC objective function values as they are calculated**

This report prints the MCMC objective function values, along with the proposal covariance matrix, for each new *i*th sample as they are calculated while doing an MCMC. The output file will be appended with each new set of objective function values as it is calculated by CASAL2. This report will print out in run mode `-m`.

**7.20. Print time varying parameters**

This report prints all `@time_varying` blocks with the values and years in which they were specified. This report will print out in run modes `-r`, `-e`, `-m`.

```
@report time_varying_parameters
type time_varying
```

**7.21. Tabular reporting format**

An alternative reporting framework to the standard output is the tabular reporting format. Tabular reporting is used with multi-line `-i` input files (like the MCMC sample or `-o` outputs). Tabular reports will print out a row that will correspond with each row of the `-i` input files.

Tabular reporting is specified using the `--tabular` argument (`casal2 -r --tabular -i file_name`).

Derived quantities, processes, observations, and `estimate_values` are the only report types that can be output with this format. For each input file the output will begin with the names of each column followed by a multi-line report ending with the `*end` syntax.

These tables can be read with **R** using the `CASAL2` package. An example usage is reading in files of MCMC posterior values of derived quantities, which can then be plotted. This command is the same as running `casal -v` in `CASAL`.



---

## 8. Population command and subcommand syntax

### 8.1. Model structure

**@model** *label*     Define an object of type *model*

**start\_year**     The first year of the model, immediately following initialisation

Type: non-negative integer

Default: No Default

Value: R, Defines the first year of the model,  $\geq 1$ , e.g. 1990,

**final\_year**     The final year of the model, excluding years in the projection period

Type: non-negative integer

Default: No Default

Value: Defines the last year of the model, i.e., the model is run from start\_year to final\_year

**min\_age**     The minimum age of individuals in the population

Type: non-negative integer

Default: 0

Value: R,  $0 \leq \text{age}_{\min} \leq \text{age}_{\max}$ ,

**max\_age**     The maximum age of individuals in the population

Type: non-negative integer

Default: 0

Value: R,  $0 \leq \text{age}_{\min} \leq \text{age}_{\max}$ ,

**age\_plus**     The oldest age or extra length midpoint ,plus group size, as a plus group

Type: boolean

Default: false

Value: true, false

**initialisation\_phases**     The labels of the phases of the initialisation

Type: string vector

Default: true

Value: R, A list of valid labels defined by @initialisation\_phase,

**time\_steps**     The labels of the time steps, in the order that they are applied, to form the annual cycle

Type: string vector

Default: No Default

Value: R, A list of valid labels defined by @time\_step,

**projection\_final\_year**     The final year of the model in projection mode

Type: non-negative integer

Default: 0

Value: R, Defines the last year of the projection period, i.e., the projection period runs from final\_year+1 to projection\_final\_year. For the default, 0, no projections are run.,

`length_bins`      The minimum length in each length bin

Type: non-negative integer vector

Default: true

Value:  $R, 0 \leq \text{length}_{\min} \leq \text{length}_{\max}$ ,

`length_plus`      Specify whether there is a length plus group or not

Type: boolean

Default: true

Value: true, false

`length_plus_group`      Mean length of length plus group

Type: non-negative integer

Default: 0

Value:  $R, \text{length}_{\max}, \text{length\_plus\_group}$ ,

`base_weight_units`      The units for the base weight. This will be the default unit of any weight input parameters

Type: string

Default: tonnes

Value: grams, kgs or tonnes

Allowed Values: grams, tonnes, kgs

## 8.2. Initialisation

**@initialisation\_phase** *label*      Define an object of type *initialisation\_phase*

*label*      The label of the initialisation phase

Type: string

Default: No Default

*type*      The type of initialisation

Type: string

Default: iterative

### 8.2.1. @initialisation\_\_phase[label].type=cinitial

*categories*      The list of categories for the Cinitial initialisation

Type: string vector

Default: No Default



**8.2.2. @initialisation\_\_phase[label].type=derived**

`insert_processes` Additional processes not defined in the annual cycle that are to be inserted into this initialisation phase

Type: string vector

Default: true

`exclude_processes` Processes in the annual cycle to be excluded from this initialisation phase

Type: string vector

Default: true

`casal_initialisation_switch` Run an extra annual cycle to evaluate equilibrium SSBs. Warning - if true, this may not correctly evaluate the equilibrium state. Set to true if replicating a CASAL model

Type: boolean

Default: false

**8.2.3. @initialisation\_\_phase[label].type=iterative**

`years` The number of iterations ,years, over which to execute this initialisation phase

Type: non-negative integer

Default: No Default

`insert_processes` Processes in the annual cycle to be included in this initialisation phase

Type: string vector

Default: true

`exclude_processes` Processes in the annual cycle to be excluded from this initialisation phase

Type: string vector

Default: true

`convergence_years` The iteration ,year, when the test for convergence ,lambda, is evaluated

Type: non-negative integer vector

Default: true

`lambda` The maximum value of the absolute sum of differences ,lambda, between the partition at year-1 and year that indicates successful convergence

Type: constant

Default: 0.0

**8.2.4. @initialisation\_\_phase[label].type=state\_category\_by\_age**

`categories` The list of categories for the category state initialisation

Type: string vector

Default: No Default

`min_age`      The minimum age of values supplied in the definition of the category state  
Type: non-negative integer  
Default: No Default

`max_age`      The maximum age of values supplied in the definition of the category state  
Type: non-negative integer  
Default: No Default

### 8.3. Categories

**@categories** *label*      Define an object of type *categories*

`format`      The format that the category names use  
Type: string  
Default: No Default

`names`      The names of the categories to be used in the model  
Type: string vector  
Default: No Default

`years`      The years that individual categories will be active for. This overrides the model values  
Type: string vector  
Default: true

`age_lengths`      R, The labels of `age_length` objects that are assigned to categories,  
Type: string vector  
Default: true

`length_weight`      R, The labels of the `length_weight` objects that are assigned to categories,  
Type: string vector  
Default: true

`age_weight`      R, The labels of the `age_weight` objects that are assigned to categories,  
Type: string vector  
Default: true

### 8.4. Time-steps

**@time\_step** *label*      Define an object of type *time\_step*

`label`      The label of the timestep  
Type: string  
Default: No Default

`processes`      The labels of the processes for this time step in the order that they occur  
Type: string vector  
Default: No Default

## 8.5. Processes

**@process** *label*      Define an object of type *process*

`label`      The label of the process  
Type: string  
Default: No Default

`type`      The type of process  
Type: string  
Default: ""

### 8.5.1. @process[label].type=ageing

`categories`      The labels of the categories  
Type: string vector  
Default: No Default

### 8.5.2. @process[label].type=growth\_basic

`categories`      The labels of the categories  
Type: string vector  
Default: No Default

`number_of_growth_episodes`      The number of growth episodes per year  
Type: non-negative integer  
Default: No Default

`growth_time_steps`      The time step in which each growth episode occurs  
Type: string vector  
Default: No Default

`cv`      C.V. for the growth model  
Type: constant  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

`sigma_min`      The lower bound on sigma for the growth model

Type: constant  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

### 8.5.3. **@process[label].type=maturation**

from     List of categories to mature from  
Type: string vector  
Default: No Default

to     List of categories to mature to  
Type: string vector  
Default: No Default

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

years     The years to be associated with rates  
Type: non-negative integer vector  
Default: No Default

rates     The rates to mature for each year  
Type: estimable vector  
Default: No Default

### 8.5.4. **@process[label].type=mortality\_constant\_rate**

categories     List of categories labels  
Type: string vector  
Default: No Default

m     Mortality rates  
Type: estimable  
Default: No Default  
Lower Bound: 0.0 (inclusive)

time\_step\_ratio     Time step ratios for the mortality rates  
Type: constant vector  
Default: true  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

**8.5.5. @process[label].type=mortality\_event**

categories      Categories

Type: string vector

Default: No Default

years      Years in which to apply the mortality process

Type: non-negative integer vector

Default: No Default

catches      The number of removals ,catches, to apply for each year

Type: estimable vector

Default: No Default

u\_max      The maximum exploitation rate , $U_{max}$ ,

Type: estimable

Default: 0.99

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

selectivities      The list of selectivities

Type: string vector

Default: No Default

penalty      The label of the penalty to apply if the total number of removals cannot be taken

Type: string

Default: ""

**8.5.6. @process[label].type=mortality\_event\_biomass**

categories      Category labels

Type: string vector

Default: No Default

selectivities      The labels of the selectivities for each of the categories

Type: string vector

Default: No Default

years      The years in which to apply the mortality process

Type: non-negative integer vector

Default: No Default

catches      The biomass of removals ,catches, to apply for each year

Type: estimable vector

Default: No Default

`u_max`      The maximum exploitation rate  $U_{max}$ ,  
 Type: estimable  
 Default: 0.99  
 Lower Bound: 0.0 (exclusive)  
 Upper Bound: 1.0 (exclusive)

`penalty`      The label of the penalty to apply if the total biomass of removals cannot be taken  
 Type: string  
 Default: ""

### 8.5.7. `@process[label].type=mortality_holling_rate`

`prey_categories`      Prey Categories labels  
 Type: string vector  
 Default: No Default

`predator_categories`      Predator Categories labels  
 Type: string vector  
 Default: No Default

`is_abundance`      Is vulnerable amount of prey and predator an abundance [true] or biomass [false]  
 Type: boolean  
 Default: true

`a`      Parameter a  
 Type: estimable  
 Default: No Default  
 Lower Bound: 0.0 (inclusive)

`b`      Parameter b  
 Type: estimable  
 Default: No Default  
 Lower Bound: 0.0 (inclusive)

`x`      This parameter controls the functional form, Holling function type 2  $x=2$ , or 3  $x=3$ , or generalised Michaelis Menten,  $x=1$ ,  
 Type: estimable  
 Default: No Default  
 Lower Bound: 1.0 (inclusive)

`u_max`      The maximum exploitation rate  $U_{max}$ ,

Type: constant  
Default: No Default  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

prey\_selectivities      Selectivities for prey categories  
Type: string vector  
Default: true

predator\_selectivities      Selectivities for predator categories  
Type: string vector  
Default: true

penalty      Label of penalty to be applied  
Type: string  
Default: ""

years      Years in which to apply the mortality process  
Type: non-negative integer vector  
Default: No Default

#### **8.5.8. @process[label].type=mortality\_initialisation\_event**

categories      Categories  
Type: string vector  
Default: No Default

catch      The number of removals ,catches, to apply for each year  
Type: estimable  
Default: No Default

u\_max      The maximum exploitation rate , $U_{max}$ ,  
Type: estimable  
Default: 0.99  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

selectivities      The list of selectivities  
Type: string vector  
Default: No Default

penalty      The label of the penalty to apply if the total number of removals cannot be taken  
Type: string  
Default: ""

### 8.5.9. @process[label].type=mortality\_initialisation\_event\_biomass

categories      Categories

Type: string vector

Default: No Default

catch      The number of removals ,catches, to apply for each year

Type: estimable

Default: No Default

u\_max      The maximum exploitation rate , $U_{max}$ ,

Type: estimable

Default: 0.99

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

selectivities      The list of selectivities

Type: string vector

Default: No Default

penalty      The label of the penalty to apply if the total number of removals cannot be taken

Type: string

Default: ""

### 8.5.10. @process[label].type=mortality\_instantaneous

categories      Categories for instantaneous mortality

Type: string vector

Default: No Default

m      Natural mortality rates for each category

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

time\_step\_ratio      Time step ratios for natural mortality

Type: constant vector

Default: true

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

selectivities      The selectivities to apply on the categories for natural mortality

Type: string vector

Default: No Default



**8.5.11. @process[label].type=mortality\_instantaneous\_retained**

categories      Categories for instantaneous mortality

Type: string vector

Default: No Default

m      Natural mortality rates for each category

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

time\_step\_ratio      Time step ratios for natural mortality

Type: constant vector

Default: true

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

selectivities      The selectivities to apply on the categories for natural mortality

Type: string vector

Default: No Default

**8.5.12. @process[label].type=mortality\_preysuitability**

prey\_categories      Prey Categories labels

Type: string vector

Default: No Default

predator\_categories      Predator Categories labels

Type: string vector

Default: No Default

consumption\_rate      Predator consumption rate

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

electivities      Prey Electivities

Type: estimable vector

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

u\_max      U max

Type: constant  
Default: No Default  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

prey\_selectivities      Selectivities for prey categories  
Type: string vector  
Default: No Default

predator\_selectivities      Selectivities for predator categories  
Type: string vector  
Default: No Default

penalty      Label of penalty to be applied  
Type: string  
Default: ""

years      Year that process occurs  
Type: non-negative integer vector  
Default: No Default

### **8.5.13. @process[label].type=recruitment\_beverton\_holt**

categories      Category labels  
Type: string vector  
Default: No Default

r0      R0  
Type: estimable  
Default: false  
Lower Bound: 0.0 (inclusive)

b0      B0  
Type: estimable  
Default: false  
Lower Bound: 0.0 (inclusive)

proportions      Proportions  
Type: estimable  
Default: No Default

age      Age at recruitment  
Type: non-negative integer  
Default: true

ssb\_offset      Spawning biomass year offset  
Type: non-negative integer  
Default: true

steepness      Steepness  
Type: estimable  
Default: 1.0  
Lower Bound: 0.2 (inclusive)  
Upper Bound: 1.0 (inclusive)

ssb      SSB label ,derived quantity,  
Type: string  
Default: No Default

b0\_initialisation\_phase      Initialisation phase label that B0 is from  
Type: string  
Default: ""

ycs\_values      YCS Values  
Type: estimable vector  
Default: No Default

ycs\_years      Recruitment years. A vector of years that relates to the year of the spawning event  
that created this cohort  
Type: non-negative integer vector  
Default: false

standardise\_ycs\_years      Years that are included for year class standardisation  
Type: non-negative integer vector  
Default: true

#### **8.5.14. @process[label].type=recruitment\_beverton\_holt\_with\_deviations**

categories      Category labels  
Type: string vector  
Default: No Default

r0      R0  
Type: estimable  
Default: false  
Lower Bound: 0.0 (inclusive)

b0      B0

Type: estimable

Default: false

Lower Bound: 0.0 (inclusive)

proportions      Proportions

Type: estimable

Default: No Default

age      Age to recruit at

Type: non-negative integer

Default: true

ssb\_offset      Spawning biomass year offset

Type: non-negative integer

Default: true

steepness      Steepness

Type: estimable

Default: 1.0

Lower Bound: 0.2 (inclusive)

ssb      SSB Label ,derived quantity,

Type: string

Default: No Default

sigma\_r      Sigma R

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

b\_max      Maximum bias adjustment

Type: estimable

Default: 0.85

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

last\_year\_with\_no\_bias      Last year with no bias adjustment

Type: non-negative integer

Default: false

first\_year\_with\_bias      First year with full bias adjustment

Type: non-negative integer

Default: false

last\_year\_with\_bias      Last year with full bias adjustment

Type: non-negative integer  
Default: false

`first_recent_year_with_no_bias`      First recent year with no bias adjustment  
Type: non-negative integer  
Default: false

`b0_initialisation_phase`      Initialisation phase label that b0 is from  
Type: string  
Default: ""

`deviation_values`      Recruitment deviation values  
Type: estimable vector  
Default: No Default

`deviation_years`      Recruitment years. A vector of years that relates to the year of the spawning event that created this cohort  
Type: non-negative integer vector  
Default: false

#### **8.5.15. @process[label].type=recruitment\_constant**

`categories`      Categories  
Type: string vector  
Default: No Default

`proportions`      Proportions  
Type: estimable  
Default: true

`length_bins`      The length bins that recruits are uniformly distributed over at the time of recruitment  
Type: non-negative integer vector  
Default: No Default

`r0`      R0  
Type: estimable  
Default: No Default  
Lower Bound: 0.0 (inclusive)

### 8.5.16. @process[label].type=survival\_constant\_rate

categories      List of categories

Type: string vector

Default: No Default

s      Survival rates

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

time\_step\_ratio      Time step ratios for S

Type: constant vector

Default: true

Lower Bound: 0.0 (exclusive)

Upper Bound: 1.0 (inclusive)

selectivities      Selectivity label

Type: string vector

Default: No Default

### 8.5.17. @process[label].type=tag\_by\_age

from      Categories to transition from

Type: string vector

Default: No Default

to      Categories to transition to

Type: string vector

Default: No Default

min\_age      Minimum age to transition

Type: non-negative integer

Default: No Default

max\_age      Maximum age to transition

Type: non-negative integer

Default: No Default

penalty      Penalty label

Type: string

Default: ""

u\_max      U Max

Type: constant  
Default: 0.99  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (inclusive)

years      Years to execute the transition in  
Type: non-negative integer vector  
Default: No Default

initial\_mortality  
Type: constant  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

initial\_mortality\_selectivity  
Type: string  
Default: ""

loss\_rate  
Type: constant vector  
Default: No Default

loss\_rate\_selectivities  
Type: string vector  
Default: true

selectivities  
Type: string vector  
Default: No Default

n  
Type: constant vector  
Default: true

#### **8.5.18. @process[label].type=tag\_by\_length**

from      Categories to transition from  
Type: string vector  
Default: No Default

to      Categories to transition to  
Type: string vector  
Default: No Default

penalty      Penalty label

Type: string  
Default: ""

u\_max      U Max  
Type: constant  
Default: 0.99  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (inclusive)

initial\_mortality  
Type: constant  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

initial\_mortality\_selectivity  
Type: string  
Default: ""

selectivities  
Type: string vector  
Default: No Default

n  
Type: constant vector  
Default: true

### 8.5.19. @process[label].type=tag\_loss

categories      List of categories  
Type: string vector  
Default: No Default

tag\_loss\_rate      Tag Loss rates  
Type: constant vector  
Default: No Default  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

time\_step\_ratio      Time step ratios for Tag Loss  
Type: constant vector  
Default: true  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

tag\_loss\_type      Type of tag loss



Type: string  
Default: No Default

selectivities      Selectivities  
Type: string vector  
Default: No Default

year      The year the first tagging release process was executed  
Type: non-negative integer  
Default: No Default

#### **8.5.20. @process[label].type=transition\_category**

from      From category  
Type: string vector  
Default: No Default

to      To category  
Type: string vector  
Default: No Default

proportions      Proportions  
Type: estimable  
Default: No Default  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

selectivities      Selectivity names  
Type: string vector  
Default: No Default

#### **8.5.21. @process[label].type=transition\_category\_by\_age**

from      Categories to transition from  
Type: string vector  
Default: No Default

to      Categories to transition to  
Type: string vector  
Default: No Default

min\_age      Minimum age to transition  
Type: non-negative integer  
Default: No Default

`max_age`      Maximum age to transition  
Type: non-negative integer  
Default: No Default

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

`u_max`      U max  
Type: constant  
Default: 0.99  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (inclusive)

`years`      Years to execute the transition in  
Type: non-negative integer vector  
Default: No Default

### 8.6. Time varying parameters

**@time\_varying** *label*      Define an object of type *time\_varying*

`label`      The time-varying label  
Type: string  
Default: No Default

`type`      The time-varying type  
Type: string  
Default: ""

`years`      Years in which to vary the values  
Type: non-negative integer vector  
Default: No Default

`parameter`      The name of the parameter to time vary  
Type: string  
Default: No Default

### 8.7. Derived quantities

**@derived\_quantity** *label*      Define an object of type *derived\_quantity*

`label`      Label of the derived quantity

Type: string  
Default: No Default

`type`      Type of derived quantity  
Type: string  
Default: No Default

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

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

`selectivities`      A list of one selectivity  
Type: string vector  
Default: No Default

`time_step_proportion`      Proportion through the mortality block of the time step when calculated  
Type: constant  
Default: 0.5  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

`time_step_proportion_method`      Method for interpolating for the proportion through the mortality block  
Type: string  
Default: `weighted_sum`  
Allowed Values: `weighted_sum`, `weighted_product`

`values`  
Type: Addressable vector  
Default: No Default

**8.7.1. `@derived__quantity[label].type=abundance`**

**8.7.2. `@derived__quantity[label].type=biomass`**

## **8.8. Age-length relationship**

**`@age_length label`**      Define an object of type *age\_length*

`label`      Label of the age length relationship

Type: string  
Default: No Default

`type`      The type of age length relationship  
Type: string  
Default: No Default

`time_step_proportions`      The fraction of the year applied in each time step that is added to the age for the purposes of evaluating the length, i.e., a value of 0.5 for a time step will evaluate the length of individuals at age+0.5 in that time step  
Type: constant vector  
Default: true  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

`distribution`      The assumed distribution for the growth curve  
Type: string  
Default: normal

`cv_first`      The CV for the first age class  
Type: estimable  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

`cv_last`      The CV for last age class  
Type: estimable  
Default: 0.0  
Lower Bound: 0.0 (inclusive)

`casal_switch`      If true, use the ,less accurate, equation for the cumulative normal function as was used in the legacy version of CASAL.  
Type: boolean  
Default: false

`by_length`      Specifies if the linear interpolation of CVs is a linear function of mean length at age. Default is by age only  
Type: boolean  
Default: true

### **8.8.1. @age\_\_length[label].type=data**

`external_gaps`  
Type: string  
Default: mean  
Allowed Values: mean, nearest\_neighbour

internal\_gaps

Type: string

Default: mean

Allowed Values: mean, nearest\_neighbour, interpolate

length\_weight      The label from an associated length-weight block

Type: string

Default: No Default

time\_step\_measurements\_were\_made      The time step label for which size-at-age data are provided

Type: string

Default: No Default

### **8.8.2. @age\_\_length[label].type=none**

### **8.8.3. @age\_\_length[label].type=schnute**

y1      The y1 parameter of the Schnute relationship

Type: estimable

Default: No Default

y2      The y2 parameter of the Schnute relationship

Type: estimable

Default: No Default

tau1      The  $\tau_1$  parameter of the Schnute relationship

Type: estimable

Default: No Default

tau2      The  $\tau_2$  parameter of the Schnute relationship

Type: estimable

Default: No Default

a      The  $a$  parameter of the Schnute relationship

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

b      The  $b$  parameter of the Schnute relationship

Type: estimable

Default: No Default

Lower Bound: 0.0 (exclusive)

length\_weight      The label of the associated length-weight relationship

Type: string  
Default: No Default

#### 8.8.4. @age\_\_length[label].type=von\_bertalanffy

`linf` Define the  $L_{infinity}$  parameter of the von Bertalanffy relationship  
Type: estimable  
Default: No Default  
Lower Bound: 0.0 (inclusive)

`k` Define the  $k$  parameter of the von Bertalanffy relationship  
Type: estimable  
Default: No Default  
Lower Bound: 0.0 (inclusive)

`t0` Define the  $t_0$  parameter of the von Bertalanffy relationship  
Type: estimable  
Default: No Default

`length_weight` Define the label of the associated length-weight relationship  
Type: string  
Default: No Default

### 8.9. Length-weight

**@length\_weight** *label* Define an object of type *length\_weight*

`label` The label of the length-weight relationship  
Type: string  
Default: No Default

`type` The type of the length-weight relationship  
Type: string  
Default: No Default

### 8.10. Selectivities

**@selectivity** *label* Define an object of type *selectivity*

`label` The label for this selectivity  
Type: string  
Default: No Default

`type` The type of selectivity

---

Type: string  
Default: No Default

`length_based`      Is the selectivity length based  
Type: boolean  
Default: false

`intervals`      Number of quantiles to evaluate a length based selectivity over the age length distribution  
Type: non-negative integer  
Default: 5

`partition_type`      The type of partition this selectivity will support. Defaults to same as the model  
Type: string  
Default: model  
Allowed Values: model, age, length, hybrid

`values`  
Type: Addressable vector  
Default: No Default

`length_values`  
Type: Addressable vector  
Default: No Default

## 9. Estimation command and subcommand syntax

### 9.1. Estimation methods

**@estimate** *label*      Define an object of type *estimate*

`label`      The label of the estimate  
Type: string  
Default: ""

`type`      The prior type for the estimate  
Type: string  
Default: No Default

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

`lower_bound`      The lower bound for the parameter

Type: constant  
Default: No Default

`upper_bound`      The upper bound for the parameter  
Type: constant  
Default: No Default

`same`      List of parameters that are constrained to have the same value as this parameter  
Type: string vector  
Default: ""

`estimation_phase`      The first estimation phase to allow this to be estimated  
Type: non-negative integer  
Default: 1

`mcmc`      Indicates if this parameter is estimated at the point estimate but fixed during MCMC estimation run  
Type: boolean  
Default: false

`transformation`      Type of simple transformation to apply to estimate  
Type: string  
Default: ""

`transform_with_jacobian`      Apply jacobian during transformation  
Type: boolean  
Default: false

`prior_applies_to_transform`      Does the prior apply to the transformed parameter? a legacy switch, see Manual for more information  
Type: boolean  
Default: false

## 9.2. Point estimation

**@*minimiser*** *label*      Define an object of type *minimiser*

*label*      The minimiser label  
Type: string  
Default: No Default

*type*      The type of minimiser to use  
Type: string  
Default: No Default



`active`      Indicates if this minimiser is active  
Type: boolean  
Default: false

`covariance`      Indicates if a covariance matrix should be generated  
Type: boolean  
Default: true

### 9.3. Markov chain Monte Carlo (MCMC)

**@mcmc** *label*      Define an object of type *mcmc*

`label`      The label of the MCMC  
Type: string  
Default: No Default

`type`      The type of MCMC  
Type: string  
Default: ""

`length`      The number of iterations in for the MCMC chain  
Type: non-negative integer  
Default: No Default

`active`      Indicates if this is the active MCMC algorithm  
Type: boolean  
Default: true

`step_size`      Initial stepsize ,as a multiplier of the approximate covariance matrix,  
Type: constant  
Default: 0.02

### 9.4. Profiles

**@profile** *label*      Define an object of type *profile*

`label`      Label  
Type: string  
Default: ""

`steps`      The number of steps between the lower and upper bound  
Type: non-negative integer  
Default: No Default

`lower_bound`      The lower bounds

Type: constant  
 Default: No Default

`upper_bound`      The upper bounds  
 Type: constant  
 Default: No Default

`parameter`      The system parameter to profile  
 Type: string  
 Default: No Default

`same`      A parameter that is constrained to have the same value as the parameter being profiled  
 Type: string  
 Default: ""

## 9.5. Defining catchability constants

**@catchability** *label*      Define an object of type *catchability*

`label`      Label of the catchability  
 Type: string  
 Default: No Default

`type`      The type of catchability  
 Type: string  
 Default: No Default

## 9.6. Defining penalties

**@penalty** *label*      Define an object of type *penalty*

`label`      The label of the penalty  
 Type: string  
 Default: No Default

`type`      The type of penalty  
 Type: string  
 Default: No Default

## 9.7. Defining priors on parameter ratios, differences, and means

**@additional\_prior** *label*      Define an object of type *additional\_prior*

`parameter`      Name of the parameter to generate additional prior on

---

Type: string  
Default: No Default

label      Label for the additional prior  
Type: string  
Default: No Default

type      Type of additional prior  
Type: string  
Default: No Default

## 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 by category and 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 of type *observation*

label      Label  
Type: string  
Default: No Default

type      Type of observation  
Type: string  
Default: No Default

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

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

delta      Robustification value ,delta, for the likelihood  
Type: constant  
Default: DELTA  
Lower Bound: 0.0 (inclusive)

simulation\_likelihood      Simulation likelihood to use  
Type: string  
Default: ""

likelihood\_multiplier      Likelihood score multiplier  
Type: constant  
Default: double  
Lower Bound: 0.0 (inclusive)

error\_value\_multiplier      Error value multiplier for likelihood  
Type: constant  
Default: double  
Lower Bound: 0.0 (inclusive)

### 10.1.1. @observation[label].type=abundance

selectivities      Labels of the selectivities  
Type: string vector  
Default: true

time\_step      The label of time-step that the observation occurs in  
Type: string  
Default: No Default

### 10.1.2. @observation[label].type=biomass

catchability      The time-step of the observation  
Type: string  
Default: No Default

time\_step      The label of time-step that the observation occurs in  
Type: string  
Default: No Default

obs      The observed values  
Type: string vector  
Default: No Default

years      The years of the observed values  
Type: non-negative integer vector  
Default: No Default

error\_value      The error values of the observed values ,note the units depend on the likelihood,

Type: constant vector

Default: No Default

`selectivities`      Labels of the selectivities

Type: string vector

Default: true

`process_error`      Value for process error

Type: estimable

Default: 0.0

Lower Bound: 0.0 (inclusive)

`age_weight_labels`      R, The labels for the `@age_weight` block which corresponds to each category, to use the weight calculation method for biomass calculations,

Type: string vector

Default: ""

### 10.1.3. `@observation[label].type=process_removals_by_age`

`min_age`      Minimum age

Type: non-negative integer

Default: No Default

`max_age`      Maximum age

Type: non-negative integer

Default: No Default

`plus_group`      Use age plus group

Type: boolean

Default: true

`time_step`      The label of time-step that the observation occurs in

Type: string vector

Default: No Default

`tolerance`      Tolerance

Type: constant

Default: double

Lower Bound: 0.0 (exclusive)

Upper Bound: 1.0 (exclusive)

`years`      Years for which there are observations

Type: non-negative integer vector

Default: No Default

`process_errors`      Label of process error to use  
Type: estimable vector  
Default: true

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

`method_of_removal`      Label of observed method of removals  
Type: string vector  
Default: ""

`mortality_instantaneous_process`      The label of the mortality instantaneous process for the observation  
Type: string  
Default: No Default

#### **10.1.4. `@observation[label].type=process_removals_by_age_retained`**

`min_age`      Minimum age  
Type: non-negative integer  
Default: No Default

`max_age`      Maximum age  
Type: non-negative integer  
Default: No Default

`plus_group`      Use age plus group  
Type: boolean  
Default: true

`time_step`      The label of time-step that the observation occurs in  
Type: string vector  
Default: No Default

`tolerance`      Tolerance  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (exclusive)

`years`      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

`process_errors`      Label of process error to use  
Type: estimable vector  
Default: true

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

`method_of_removal`      Label of observed method of removals  
Type: string vector  
Default: ""

`mortality_instantaneous_process`      The label of the mortality instantaneous process for the observation  
Type: string  
Default: No Default

#### **10.1.5. `@observation[label].type=process_removals_by_age_retained_total`**

`min_age`      Minimum age  
Type: non-negative integer  
Default: No Default

`max_age`      Maximum age  
Type: non-negative integer  
Default: No Default

`plus_group`      Use age plus group  
Type: boolean  
Default: true

`time_step`      The label of time-step that the observation occurs in  
Type: string vector  
Default: No Default

`tolerance`      Tolerance  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (exclusive)

`years`      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

`process_errors`      Label of process error to use  
Type: estimable vector  
Default: true

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

`method_of_removal`      Label of observed method of removals  
Type: string vector  
Default: ""

`mortality_instantaneous_process`      The label of the mortality instantaneous process for the observation  
Type: string  
Default: No Default

#### **10.1.6. `@observation[label].type=process_removals_by_length`**

`length_bins`      Length bins  
Type: constant vector  
Default: No Default

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

`length_plus`      Is the last bin a plus group  
Type: boolean  
Default: true

`tolerance`      Tolerance for rescaling proportions  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (exclusive)

`years`      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

`process_errors`      the value of process error  
Type: estimable vector  
Default: true



method\_of\_removal      Label of observed method of removals  
Type: string  
Default: ""

mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation  
Type: string  
Default: No Default

### 10.1.7. @observation[label].type=process\_removals\_by\_length\_retained

length\_bins      Length bins  
Type: constant vector  
Default: No Default

time\_step      Time step to execute in  
Type: string  
Default: No Default

length\_plus      Is the last bin a plus group  
Type: boolean  
Default: true

tolerance      Tolerance for rescaling proportions  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (exclusive)

years      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

process\_errors      the value of process error  
Type: estimable vector  
Default: true

method\_of\_removal      Label of observed method of removals  
Type: string  
Default: ""

mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation  
Type: string  
Default: No Default

**10.1.8. @observation[label].type=process\_removals\_by\_length\_retained\_total**

length\_bins      Length bins

Type: constant vector

Default: No Default

time\_step      Time step to execute in

Type: string

Default: No Default

length\_plus      Is the last bin a plus group

Type: boolean

Default: true

tolerance      Tolerance for rescaling proportions

Type: constant

Default: double

Lower Bound: 0.0 (exclusive)

Upper Bound: 1.0 (exclusive)

years      Years for which there are observations

Type: non-negative integer vector

Default: No Default

process\_errors      the value of process error

Type: estimable vector

Default: true

method\_of\_removal      Label of observed method of removals

Type: string

Default: ""

mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation

Type: string

Default: No Default

**10.1.9. @observation[label].type=proportions\_at\_age**

min\_age      Minimum age

Type: non-negative integer

Default: No Default

`max_age`      Maximum age  
Type: non-negative integer  
Default: No Default

`plus_group`    Use age plus group  
Type: boolean  
Default: true

`time_step`    The label of time-step that the observation occurs in  
Type: string  
Default: No Default

`tolerance`    Tolerance on the constraint that for each year the sum of proportions in each age must equal 1, e.g., if tolerance = 0.1 then  $1 - \text{Sum,Proportions}$ , can be as great as 0.1  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)  
Upper Bound: 1.0 (exclusive)

`years`        The years of the observed values  
Type: non-negative integer vector  
Default: No Default

`selectivities`   Labels of the selectivities  
Type: string vector  
Default: true

`process_errors`   Process error  
Type: constant vector  
Default: true

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

#### **10.1.10. @observation[label].type=proportions\_at\_length**

`time_step`    The label of time-step that the observation occurs in  
Type: string  
Default: No Default

`tolerance`    Tolerance for rescaling proportions  
Type: constant  
Default: double  
Lower Bound: 0.0 (exclusive)

years      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

selectivities      The labels of the selectivities  
Type: string vector  
Default: true

process\_errors      Process error  
Type: constant vector  
Default: true

#### 10.1.11. @observation[label].type=proportions\_by\_category

min\_age      Minimum age  
Type: non-negative integer  
Default: No Default

max\_age      Maximum age  
Type: non-negative integer  
Default: No Default

time\_step      The label of time-step that the observation occurs in  
Type: string  
Default: No Default

plus\_group      Use age plus group  
Type: boolean  
Default: true

years      Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

selectivities      The labels of the selectivities  
Type: string vector  
Default: true

categories2      Target Categories  
Type: string vector  
Default: No Default

selectivities2      Target Selectivities

Type: string vector  
Default: No Default

#### 10.1.12. `@observation[label].type=proportions_mature_by_age`

`min_age` Minimum age  
Type: non-negative integer  
Default: No Default

`max_age` Maximum age  
Type: non-negative integer  
Default: No Default

`time_step` The label of time-step that the observation occurs in  
Type: string  
Default: No Default

`plus_group` Use age plus group  
Type: boolean  
Default: true

`years` Years for which there are observations  
Type: non-negative integer vector  
Default: No Default

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

`total_categories` All category labels that were vulnerable to sampling at the time of this observation ,not including the categories already given,  
Type: string vector  
Default: true

`time_step_proportion` Proportion through the mortality block of the time step when the observation is evaluated  
Type: constant  
Default: double  
Lower Bound: 0.0 (inclusive)  
Upper Bound: 1.0 (inclusive)

**10.1.13. @observation[label].type=proportions\_migrating**

min\_age      Minimum age

Type: non-negative integer

Default: No Default

max\_age      Maximum age

Type: non-negative integer

Default: No Default

time\_step    The label of time-step that the observation occurs in

Type: string

Default: No Default

plus\_group   Use age plus group

Type: boolean

Default: true

years        Years for which there are observations

Type: non-negative integer vector

Default: No Default

process\_errors   Process error

Type: constant vector

Default: true

ageing\_error    Label of ageing error to use

Type: string

Default: ""

process       Process label

Type: string

Default: No Default

**10.1.14. @observation[label].type=tag\_recapture\_by\_age**

min\_age      Minimum age

Type: non-negative integer

Default: No Default

max\_age      Maximum age

Type: non-negative integer

Default: No Default

plus\_group   Use age plus group

Type: boolean

Default: true

years      Years for which there are observations

Type: non-negative integer vector

Default: No Default

categories2      The available categories in the partition

Type: string vector

Default: No Default

selectivities      The labels of the selectivities

Type: string vector

Default: true

time\_step      The label of time-step that the observation occurs in

Type: string

Default: No Default

selectivities2      The categories of tagged individuals for the observation

Type: string vector

Default: No Default

detection      Probability of detecting a recaptured individual

Type: constant

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

time\_step\_proportion      Proportion through the mortality block of the time step when the observation is evaluated

Type: constant

Default: double

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

#### **10.1.15. @observation[label].type=tag\_recapture\_by\_length**

years      Years for which there are observations

Type: non-negative integer vector

Default: No Default

length\_bins      Length bins

Type: non-negative integer vector

Default: true

`length_plus`      Is the last bin a plus group

Type: boolean

Default: model

`selectivities`      The labels of the selectivities used for untagged categories

Type: string vector

Default: true

`tagged_selectivities`      The labels of the tag category selectivities

Type: string vector

Default: No Default

`detection`      Probability of detecting a recaptured individual

Type: constant

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

`dispersion`      Over-dispersion parameter  $\phi$ ,

Type: constant

Default: double

Lower Bound: 0.0 (inclusive)

`time_step_proportion`      Proportion through the mortality block of the time step when the observation is evaluated

Type: constant

Default: double

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

## 10.2. Likelihoods

**@likelihood** *label*      Define an object of type *likelihood*

## 10.3. Defining ageing error

The methods for including ageing error into estimation with observations are:

- None
- Data
- 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 of type *ageing\_error*

*label* The label of the ageing error

Type: string

Default: No Default

*type* The type of ageing error

Type: string

Default: No Default

**10.3.1. @ageing\_\_error[label].type=data**

**10.3.2. @ageing\_\_error[label].type=none**

**10.3.3. @ageing\_\_error[label].type=normal**

*cv* CV of the misclassification matrix

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

*k* *k* defines the minimum age of individuals which can be misclassified, i.e., individuals of age less than *k* have no ageing error

Type: non-negative integer

Default: 0u

Lower Bound: 0u (inclusive)

**10.3.4. @ageing\_\_error[label].type=off\_by\_one**

*p1* The proportion misclassified as one year younger, e.g., the proportion of age 3 individuals that were misclassified as age 2

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

*p2* The proportion misclassified as one year older, e.g., the proportion of age 3 individuals that were misclassified as age 4

Type: estimable

Default: No Default

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

*k* The minimum age of animals which can be misclassified, i.e., animals of age less than *k* are

assumed to be correctly classified

Type: non-negative integer

Default: 0u

Lower Bound: 0.0 (inclusive)

Upper Bound: 1.0 (inclusive)

## 11. Report command and subcommand syntax

### 11.1. Report commands and subcommands

**@report** *label* Define an object of type *report*

*label* The label for the report

Type: string

Default: No Default

*type* The type of report

Type: string

Default: No Default

*file\_name* The File Name for this report to be in a separate file

Type: string

Default: ""

*write\_mode* The write mode

Type: string

Default: overwrite

Allowed Values: overwrite, append, incremental\_suffix

#### 11.1.1. @report [*label*] .type=*age\_length*

*time\_step* Time Step label

Type: string

Default: ""

*years* Years

Type: non-negative integer vector

Default: true

*age\_length*

Type: string

Default: No Default

*category*

Type: string  
Default: No Default

#### **11.1.2. @report[label].type=ageing\_error\_matrix**

ageing\_error      Ageing Error label  
Type: string  
Default: No Default

#### **11.1.3. @report[label].type=initialisation\_partition\_mean\_weight**

#### **11.1.4. @report[label].type=partition**

time\_step      Time Step label  
Type: string  
Default: ""

years      Years  
Type: non-negative integer vector  
Default: true

#### **11.1.5. @report[label].type=partition\_biomass**

time\_step      Time Step label  
Type: string  
Default: ""

years      Years  
Type: non-negative integer vector  
Default: true

#### **11.1.6. @report[label].type=partition\_mean\_weight**

time\_step      Time Step label  
Type: string  
Default: ""

years      Years  
Type: non-negative integer vector  
Default: true

### 11.1.7. `@report[label].type=partition_year_cross_age_matrix`

## 12. Including commands from other files

**@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.csl2"`

Note: `@include` does not denote the end of the previous command block as is the case for all other commands

---

### 13. Tips for setting up Casal2 model based on an existing CASAL model

Many users of CASAL2 may be starting with a functioning CASAL model. This section focuses on transitioning from CASAL to CASAL2.

There are a range of reasons why CASAL2 will output different values when comparing model output to CASAL models. There are also reasons why values will differ that are not so obvious such as, reasons caused from using different compilers on different machines where over/underflow might occur. It is assumed that the latter reasons should be rare, and the 'overall' behaviour when it comes to estimation will be the same between CASAL and CASAL2.

Reasons why there may be different values reported between CASAL and CASAL2 include:

- Report rounding. There are settings with respect to output in CASAL that set the number of significant figures for writing to files. So if values look truncated, this might be the reason.
- Priors on parameters that are turned off with `upper_bound = lower_bound`. In both CASAL and CASAL2 the estimation of parameters can be turned off by setting the bounds equal. CASAL will evaluate the prior value and add this to the objective function. This contribution is a constant value so it will not affect parameter inference. It may however be confusing when comparing output between the two models.
- Default values. There are a lot of switches in these programs, and options like the `delta` in CASAL2 or `r` parameter in CASAL for robustifying likelihoods can cause differences.
- The order of processes. CASAL has a predefined sequence in which it executes processes within a time step (i.e., ageing, recruitment, maturation, migration, growth, natural and fishing mortality, disease mortality, tag release events, tag shedding rate, and semelparous mortality), whereas CASAL2 is completely user defined.
- Length-based processes or observations. CASAL2 has updated the cumulative normal distribution calculation (CASAL used the approximated no closed form solution) with better approximations.
- Age-based observations. CASAL2 does not have the `sum_to_one` subcommand implemented, and CASAL makes this adjustment implicitly. Check that this flag is set to 'false' in the CASAL model for a more accurate comparison.
- Tag penalties. CASAL applies a penalty to the sum of squares on total tagged fish in a 'tagging episode' from the model compared to observed number of tagged fish. CASAL2 applies a penalty on the transition rate by length. If tags are applied in a length bin that does not have individuals, e.g., a model configuration which tags 2 individuals of length  $l$  when there are no individuals in that length bin will include a penalty.

Many of the flags and options in CASAL and CASAL2 are the same or similar. The syntax section of this document (Sections 8) provides more details about the CASAL2 functionality and behaviour. Check that the programs produce the same results with a **range** of parameter values using the deterministic run command (`casal2 -r`), before doing an estimation run (`casal2 -e`).

The first outputs to check when comparing CASAL2 and CASAL versions of the same model are the stock dynamics outputs, ignoring the fits to observations. That is, check the initial age structure, the SSB and YCS values and patterns,  $R_0$ ,  $B_0$ , etc. If these outputs differ, then the fits to the observations will likely also be different.

There are a few linkages with certain stock dynamics outputs to check to determine if processes are misspecified. Differences between the proportions in the initial age structure, assuming an equilibrium state, are due to  $M$ , natural mortality. Differences in the initial equilibrium recruitment

value,  $R_0$ , are due to growth (@age\_length or @length\_weight). Many models estimate  $B_0$  so that  $R_0$  is a back calculation through the growth curve.

If the initial age structure is the same, next check the derived quantities such as the SSB values. Differences in these values are generally caused by how fishing and recruitment processes are specified. Check which *YCS* values are estimated or standardised, the definition and designation of selectivities, etc.

Once the stock dynamics outputs match, check the results with a few different sets of starting parameter values by using the `-i` command line option. Next, check the fits to the observation data by comparing the expected values. Assuming the observations in both models match, the differences in the objective function value come from the expected values and the likelihood configurations. This is where subcommands such as the robustification values and the default values may differ between CASAL and CASAL2.

Once the stock dynamics outputs and the fits to the observation data are the same, do an estimation run (`casal2 -e`). If CASAL and CASAL2 do not optimise to the same parameter values, then use the parameter values from CASAL and do a deterministic run with CASAL2 using the CASAL estimated parameter values (`casal2 -r -i CASAL_mpd_pars.txt`). Then check the stock dynamics outputs and the fits to the observation data and determine where the differences in the parameter estimates and outputs are.

The next question is, how close do the parameter estimates, expected values, and objective function values have to be to say that the models are equivalent? This is an ongoing topic of discussion. Previously, subjective qualitative measures have been used to decide whether the models are equivalent. A recorded comparison for the hake stock assessment can be found at Appendix B in [Horn \(2017\)](#).

---

## 14. Syntax conventions, examples and niceties

### 14.1. Input File Specification

The file format used for CASAL2 is based on the command block formats used in CASAL and SPM. It is a text file that contains definitions organised into blocks.

Every object specified in a configuration file is part of a block. At the top level blocks have a one-to-one relationships with components in the system.

Example:

```
@block1 label
parameter value
parameter value_1 value 2

@block2 label
parameter value
table table_name
column_1 column_2
data_1 data_2
data_3 data_4
end_table
```

Some general notes about configuration files:

- Whitespace can be used freely. Tabs and spaces are both valid.
- A block ends only at the beginning of a new block or at the end of the final configuration file.
- Configuration files can include other configuration files.
- Included files are placed in-line, so a block can be continued in a new file.
- The configuration files support in-line declarations of objects.

#### 14.1.1. Keywords And Reserved Characters

In order to allow efficient creation of input files, the CASAL2 file format has special keywords and characters that cannot be used for labels.

##### @Block Definitions

Each block in the configuration file must start with the block definition character, which is the "@" character.

Example:

```
@block1 <label>
type <type>

@block2 <label>
type <type>
```

**The 'type' Keyword**

The 'type' keyword is used for declaring the sub-type of a defined block. Any block object that has multiple sub-types will use the `type` keyword.

Example:

```
@block1 <label>
type <sub_type>

@block2 <label>
type <sub_type>
```

**# (Single Line Comments)**

Comments are supported in the configuration file on one line (to the end of that line) or over multiple lines. Comments on single lines start with the "#" character.

Example:

```
@block <label>
type <sub_type> # Descriptive comment
# parameter <value_1> *** This whole line is commented out
parameter <value_1> # <value_2> *** value_2 is commented out
```

**/\* \*/ (Multiple Line Comments)**

Multiple line comments are supported by surrounding the comments in `/*` and `*/`

Example:

```
@block <label>
type <sub_type>
parameter <value_1>
parameter <value_1> <value_2>

/*
Do not load this process
@block <label>
type <sub_type>
parameter <value_1>
parameter <value_1> <value_2>
*/
```

**{ } (Indexing Parameters)**

Individual elements of a vector can be referenced using the { } syntax. For example, when estimating `ycs_values` a range or block of YCS values can be referenced.

Example:

```
@estimate YCS
parameter process[Recruitment].ycs_values{1975:2012}
type uniform
lower_bound
upper_bound
```



**':' (Range Specifier)**

The range specifier ":" allows specifying a range of values instead of specifying each value explicitly. Ranges can be either incremental or decremental.

Example:

```
@process my_recruitment_process
type constant_recruitment
# With the range specifier
years_to_run 1999:2009

@process my_mortality_process
type natural_mortality
# Without the range specifier
years_to_run 2000 2001 2002 2003 2004 2005 2006 2007
```

**',' (List Specifier)**

When a parameter supports multiple values in a single entry, the list specifier "," can be used to define multiple values as a single parameter.

Example:

```
@categories
format sex.stage
# With the list specifier
names male,female.immature,mature

@categories
format sex.stage
# Without the list specifier
names male,immature male,mature female,immature female,mature
```

**'table' and 'end\_table' Keyword**

The table keyword `table` is used to define a tabular block of values used as a parameter. The first line following the `table` declaration must contain a list of columns to be used. The subsequent lines are rows of the table. Each row must have the same number of values as the number of columns specified. The table definition must end with the `"end_table"` keyword on its own line.

Example:

```
@block <label>
type <sub_type>
parameter <value_1>
table <table_label>
<column_label_1> <column_label_2> ... <column_label_N>
<row1_value_1> <row1_value_2> ... <row1_value_N>
<row2_value_1> <row2_value_2> ... <row2_value_N>
end_table
```

**[ ] (in-line Declarations)**

When an object takes the label of a target object as a parameter, the label can be replaced with an in-line declaration. An in-line declaration "[ ]" is a complete declaration of an object on one line. This feature is designed to allow simplifying the configuration definition.

Example:

```
@model
# With in-line declaration with label specified for time step
time_steps step_one=[type=iterative; processes=recruitment ageing]

@model
# With in-line declaration with default label (model.1)
time_steps [type=iterative; processes=recruitment ageing]

# Without in-line declaration
@model
time_steps step_one

@time_step step_one
processes recruitment ageing
```

**Categories**

The CASAL2 population representation is essentially a 2-dimensional structure. The partition is:

**Categories x Ages or Lengths**

Each category allows for a different range of ages or lengths and accessibility during different time periods.

Because each category can be quite complicated, the syntax for defining categories has been structured to allow for complex definitions using a simple shorthand structure.

The "format" parameter allows for defining the structure of the category labels. Using a "." (period) character between each segment allows for shorthand lookups of categories.

The "names" parameter is a list of the category names. The syntax of these names is required to match the "format" parameter so CASAL2 can organise and search on them. Using the "list specifier" and range characters this parameter can be shortened.

Example:

```
@categories
format sex.stage.tag
names male.immature.notag male.immature.2001 male.mature.notag male.mature.2001

names male.immature # Invalid: No tag information
names female # Invalid: no stage of tag information
names female.immature.notag.1 # Invalid: Additional format segment not defined

names male,female.immature,mature.notag,2001:2005 # Valid
# Without the shorthand syntax these categories would be written:
names male.immature.notag male.immature.2001 male.immature.2002 male.immature.2003 male.immature.2004
```

Specific data for a year in a category can be set up so that this category is not to be processed during specific years or in the initialisation phases. A list of years can be provided for each category to indicate in which year(s) it is to be available. These years which will override the default setting of all years in the model. Any category with the default years overridden will no longer be accessible in the initialisation phases.

Examples:

```
@model
start_year 1998
final_year 2010

@categories
format sex.stage.tag
names male,female.immature,mature.notag,2001:2005 # Valid
# Categories with the tag value "2001" are available in years 1999, 2000, 2001, 2002, 2003
# Categories with the tag value "2005" are available in years 2003, 2004, 2005, 2006, 2007
years tag=2001=1999:2003 tag=2005=2003:2007
```

## 14.2. More examples of shorthand syntax and use of reserved and key characters

### Categories

CASAL2 allows for many user-defined categories so shorthand syntax has been added to aid in the definition of complex configuration labelling and partition structures. For example, when defining categories a comma "," can be used to shorten lists of categories.

This syntax is the long way:

```
@categories
format sex.stage
names male.immature male.mature female.immature female.mature
```

For the exact same partition structure specified in a shorter way:

```
@categories
format sex.stage
names male,female.immature,mature
```

CASAL2 requires categories in processes and observations so that the correct model dynamics can be applied to the correct elements of the partition.

An example of a process where categories are required as an input command is for ageing

```
# 1. The standard way
@ageing my_ageing
categories male.immature male.mature female.immature female.mature

# 2. The first shorthand way
@ageing my_ageing
categories male,female.immature,mature

# 3. Wild Card (all categories)
```

```
@ageing my_ageing
categories *

# 4. The second shorthand way
@ageing my_ageing
categories sex=male sex=female
```

To combine/aggregate categories together, use the "+" special character. For example, this feature can be used to specify that the total biomass of the population is made up of both males and females.

For example,

```
@observation CPUE
type biomass
catchability Fishq
time_step one
categories male+female
selectivities FishSel
likelihood lognormal
years 1992:2001
time_step_proportion 1.0
obs 1.50 1.10 0.93 1.33 1.53 0.90 0.68 0.75 0.57 1.23
error_value 0.35
```

This combination/aggregation functionality can be used to compare an observation to the total combined population:

```
@observation CPUE
type biomass
catchability Fishq
time_step one
categories *+
selectivities FishSel
likelihood lognormal
years 1992:2001
time_step_proportion 1.0
obs 1.50 1.10 0.93 1.33 1.53 0.90 0.68 0.75 0.57 1.23
error_value 0.35
```

If male and female are the only categories in a population, then this is the same syntax as the command block above it.

Shorthand syntax can be useful when applying processes to a select group of categories from the partition.

For example, to apply a spawning migration to the mature categories in the partition and the partition was defined:

```
@categories
format area.maturity.tag
names north.immature.notag,2011 north.mature.notag,2011 south.immature.notag,2011
south.mature.notag,2011
```

Then, to migrate a portion of the mature population from the southern area to the northern area:

```
@process spawn_migration
type transition_category
from format=south.mature.*
to format=north.mature.*
proportions 1.0
selectivities One
```

### Parameters

CASAL2 also allows parameters that are of type vector or map to be referenced and estimated fully or partially. An example of a parameter that is type vector is `ycs_values` in a recruitment process.

For example, a recruitment block:

```
@process WestRecruitment
type recruitment_beverton_holt
r0 400000
years
ycs_values 1 1 1 1 1 1 1 1
ycs_years 1975:1983
# An alternative method to specify a sequence of values
# use an asterix to represent a vector of repeating integers
ycs_values 1*8
steepness 0.9
age 1
```

To estimate the last four years of the parameter `process[WestRecruitment].ycs_values` only can be specified as

```
@estimate
parameter process[WestRecruitment].ycs_values{1980:1983}
type uniform
lower_bound 0.1 0.1 0.1 0.1
upper_bound 10 10 10 10
```

Note that the first element of a vector is indexed by 1. This syntax can be applied to parameters that are of type map as well. For information on what type a parameter is see the syntax section.

An example of a parameter that is of type map is `@time_varying[label].type=constant`.

For a `@time_varying` block

```
@time_varying q_step1
type constant
parameter catchability[Fishq].q
years 1992 1993 1994 1995
value 0.2 0.2 0.2 0.2
```

For example, to estimate only one element of the map (say 1992), and force all other years to be the same as the one estimate, can be done in the `@estimate` block using `same`:

```
@estimate
parameter time_varying[q_step1].value{1992}
same time_varying[q_step1].value{1993:1995}
type uniform
lower_bound 0.1 0.1 0.1 0.1
upper_bound 10 10 10 10
```

**In-line declaration**

In-line declarations can help shorten models by passing @ blocks.

For example,

```
@observation chatCPUE
type biomass
catchability [q=6.52606e-005]
time_step one
categories male+female
selectivities chatFselMale chatFselFemale
likelihood lognormal
years 1992:2001
time_step_proportion 1.0
obs 1.50 1.10 0.93 1.33 1.53 0.90 0.68 0.75 0.57 1.23
error_value 0.35

@estimate
parameter catchability[chatTANbiomass.one].q
type uniform_log
lower_bound 1e-2
upper_bound 1
```

In the above code catchability is defined and estimated without explicitly creating a @catchability block.

When an in-line declaration is made, the new object will be created with the name of the creator's label.index, where index is the word "one" through "nine" if it is 1 through 9, and the number if it is 10+.

For example,

```
@mortality halfm
selectivities [type=constant; c=1]

would create
@selectivity halfm.one
```

If there are 10 categories, each with its own selectivity, the 10<sup>th</sup> selectivity is labelled

```
@selectivity halfm.10
```

**14.3. Processes**

Processes are special in how they can be defined. Throughout this document specifying a process has been

```
@process Recruitment
type recruitment_beverton_holt
```

However, for convenience and clarity, this block can also be specified as

```
@recruitment Recruitment
type beverton_holt
```

The difference is that the keyword `process` can be replaced with the first word of the process type. In the example above this is the `recruitment` process. This option can be used to create more succinct model configurations.

More examples:

```
@mortality Fishing_and_M
type instantaneous
```

```
@transition Migration
type category
```

## 14.4. An example of a simple model

This example describes a single species and area model, with recruitment, maturation, natural and fishing mortality, and an annual age increment. The population structure has ages 1 – 30<sup>+</sup> with a single category.

The default CASAL2 configuration filename is `config.csl2`. In this example, `config.csl2` specifies the files to include to run the CASAL2 model from the current directory using the `!include` command.

```
!include "population.csl2"
!include "reports.csl2"
!include "observation.csl2"
!include "estimation.csl2"
```

It is recommended to separate the sections of a CASAL2 model for enhancing readability and error checking, and including the files in a version control system.

The file `population.csl2` contains the population information. The model years are from 1975 through 2012, with 3 time steps. The model is initialised over a 120 year period prior to 1975 and applies the following processes

- A Beverton-Holt recruitment process, recruiting a constant number of individuals to the first age class (i.e.,  $age = 1$ ).
- A constant mortality process representing natural mortality( $M$ ). This process is repeated in all 3 time steps, so that a proportion of  $M$  is applied in each time step.
- An ageing process, where all individuals are aged by one year, and with a plus group accumulator age class at  $age = 30$ .

Following initialisation, the model runs from the years 1975 to 2012 iterating through 3 time steps.

The first time step applies processes of recruitment, and  $\frac{1}{2}M_1 + F + \frac{1}{2}M_1$  processes, where  $M_1$  is the proportion of  $M$  applied in the first time step. The exploitation process (fishing) is applied in the years 1975 - 2012. Catches are defined in the catches table and attributes for each fishery, such as selectivity and time step they are implemented, are in the fisheries table in the `@process` block.

The second time step applies an age increment and the remaining natural mortality.

The third time step applies TODO.

The first 28 lines of the main section of the `population.csl2`:

```

#THE MODEL constraints
@model
start_year 1975
final_year 2012
min_age 1
max_age 30
age_plus true
base_weight_units tonnes
initialisation_phases Equilibrium_state
time_steps Sep_Feb Mar_May Jun_Aug ##
length_bins 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230
            240 250

#CATEGORIES
@categories
format stock ## Single sex and area population
names HAK4
age_lengths age_size

@initialisation_phase Equilibrium_state
type derived

## Define the processes in the Annual Cycle
## This is a list of labels that correspond to a process
@time_step Sep_Feb
processes Recruitment Instantaneous_Mortality

@time_step Mar_May
processes Instantaneous_Mortality

```

To run the model to verify that the model runs without any syntax errors, use the command `casal2 -r`. Since CASAL2 reads in the default filename `config.csl2`, this filename can be overridden. For example, if the model is in file `Mymodel.txt`, then this filename would be specified using the `-c` option, `casal2 -r -c Mymodel.txt`.

To estimate the parameters defined in the file `estimation.csl2` (the catchability constant  $q$ , recruitment  $R_0$ , and the selectivity parameters  $a_{50}$  and  $a_{t095}$ ), use `casal2 -e`. The output has been redirected to file `estimate.log` using the command `casal2 -e > estimate.log`. Reports for the user-defined reports `reports.csl2` from the final iteration of the estimation are output to the file `estimate.log`, and successful convergence is printed to the screen

```

Total elapsed time: 1 second
Completed

```

The main output from the estimation run is summarised in the file `estimate.log`, and the final MPD parameter values can also be redirected as a separate report, in this case named `paramaters.out`, using the command `casal2 -e -o paramaters.out > estimate.log`.

A profile on the  $R_0$  parameter can be run, using `casal2 -p > profile.log`. See the examples folder for the example of the output.



---

## 15. Post-processing output using R

**R** (<https://www.r-project.org/>) is the main application used to process and visualise output from a CASAL2 model. **R** is free and can be downloaded from <https://cran.r-project.org/>. Once you have installed **R** you can install the `casal2` **R** package from the file (`casal2_1.0.tar.gz`) which is part of the CASAL2 download.

The CASAL2 **R** package has functionality to parse CASAL2 output into a list. It also has diagnostic, plotting, and summarising functions.

There are three types of output that CASAL2 can produce, depending on the type of analysis run. These outputs are: Standard, MCMC, and Derived Quantity.

The Standard outputs are the reports that are produced in most CASAL2 run modes, with the exception of `-s` and `-m`. The Standard output can be split into two additional categories, a single parameter run (`casal2 -r`) or a multi-parameter run (`casal2 -r -i many_pars.out`), or running in projection mode (`-f 1`). The Standard outputs can be read into **R** using the `extract.mpd()` function.

The second type of output is generated when doing an MCMC analysis (`casal2 -m`), which can generate two files, `mcmc_objective.out` and `mcmc_samples.out`. The MCMC outputs can be used to summarise convergence properties or chain behaviour, and can also be used to view marginal posteriors and quantify parameter uncertainty.

The third output type is the Derived Quantity outputs, also referred to as tabular output. The Derived Quantity output can be generated after an MCMC analysis is done, to produce the marginal posteriors for derived quantities. A commonly reported derived quantity in fisheries stock assessment modelling is the time series of spawning stock biomass. To get the posterior distributions for these derived quantities use the `--tabular` flag (e.g., `casal2 -r -i mcmc_samples.out --tabular > Tabular_report.out`). This output can then be read into **R** using the `extract.tabular()` function.

CASAL2's reported output is written so that each `@report` will start with a `'*`' and end with `'*end'`. This format can be used as the basis to construct functions that read CASAL2 output to identify and read individual reports for post-processing.

The CASAL2 **R** `extract()` functions differ by how the expected output is structured and they each create a different `casal2` object. The `summary()` and `plot()` functions will generate different plots for the different `casal2` objects. Objects produced by the `extract()` function can be queried with `class(object)`.

The list of `casal2` **R** functions include:

- `extract.mpd()`, which parses the CASAL2 default output into a list
- `extract.mcmc()`, which parses the CASAL2 MCMC output into a list
- `extract.tabular()`, which parses the CASAL2 tabular output into a list
- `extract.parameters()`, which parses the CASAL2 parameter files into a list
- `generate.starting.pars()`, which reads in a file that contains the `@estimate` blocks and generates 'N' starting values to test convergence (???)
- `burn.in.tabular()`, which omits the first 'N' rows from a `casal2TAB` object
- `plot.derived_quantities()`, which plots the derived quantities
- `plot.selectivities()`, which plots the selectivities

- `plot.ycs()`, which plots the true YCS strengths
- `plot.pressure()`, which plots the fishing pressures
- `summary()`, which summarises a model run
- `extract.csl2.file()`, which reads a CASAL2 .csl2 (configuration) file into a list
- `write.csl2.file()`, which writes a CASAL2 .csl2 (configuration) file from (???)
- `ReadSimulatedData()`, which parses CASAL2 output from a `casal2 -s` run
- `Method.TA1.8()`, which returns a weighting factor for age or length composition data. See [Francis \(2011\)](#) for more detail.
- `apply.dataweighting.to.csl2()`, which parses a CASAL2 .csl2 (configuration) file that contains `@observation` blocks, applies a weighting factor to an age or length composition data set, and generates a new .csl2 file with modified effective sample size values

The required and optional arguments for these functions can be queried after loading the CASAL2 **R** library with `library(casal2)` and using the standard **R** help syntax `?` (e.g., `?param.profile()`). Many of the help files have example code and data to demonstrate function syntax.

### Standard diagnostic functions and plots for model output

TODO (functionality description)

```
plot.derived_quantity()
```

When comparing model output either: different parameters for the same model structure are being compared (Situation 1), or outputs from multiple model structures are being compared (Situation 2). These functions can be useful for both comparison types.

- `plot.selectivities()`
- `plot.pressure()`
- `plot.fit()`
- `plot.ycs()`

### Data weighting

An important component of fisheries stock assessment modelling is addressing data conflicts through the use of data weighting. There are a range of methods that can be used ([Francis \(2011\)](#)). The CASAL2 **R** function is `Method.TA1.8()`. An additional function `apply.dataweighting.to.csl2()` automatically applies a weighting factor to a specific age or length composition data in an `@observation` block, and generates a new .csl2 file with modified effective sample size values.

```
library(casal2)

## read in the reported output from a "casal2 -e" run
## ensure there is a @report block for the observation of interest.
mpd <- extract.mpd(file = "estimate.log")

## calculate weighting factor from Francis method
WeightingFactor <- Method.TA1.8(model = mpd, observation_labels = "chatTANage")

## Apply the weighting factor to the block in the Observation.csl2 file
```

---

```
## this call generates a new file (Observation.csl2.0) with the re-weighted effective sample
  sizes
apply.dataweighting.to.csl2(weighting_factor = WeightingFactor,
                             Observation_csl2_file = "Observations.csl2",
                             Observation_label = "chatTANage",
                             Observation_out_filename = "Observation.csl2.0")
```

### Automating the data weighting process:

```
library(casal2)

mpd <- extract.mpd(file = "estimate.log")

ModelFactor <- Method.TA1.8(mpd, observation_labels = c("ObserverProportionsAtAge"))

## make a back-up copy of the file Observation.csl2 before running this section

while(abs(ModelFactor - 1) > 0.01) {
  shell("betadiff & casal2 -e > estimate.log 2> log.out")

  new_mpd <- extract.mpd(file = "estimate.log")

  ModelFactor <- Method.TA1.8(new_mpd, observation_labels = c("ObserverProportionsAtAge"))

  apply.dataweighting.to.csl2(weighting_factor = ModelFactor,
                               Observation_csl2_file = "Observation.csl2",
                               Observation_out_filename = "Observation.csl2",
                               Observation_label = c("ObserverProportionsAtAge"))

  print(ModelFactor)
}
```

## Troubleshooting the **casal2** R package

### If you get this error when using one of the `extract()` functions

```
Read 1 item
Warning messages:
1: In scan(filename, what = "", sep = "\n", fileEncoding = fileEncoding) :
  embedded nul(s) found in input
2: In extract.mpd(file = "results.txt", fileEncoding = "") :
  File is empty, no reports found
```

You may be able to resolve this issue by using an alternative UTF format by specifying this format with the `fileEncoding` parameter

```
MyOutput <- extract.mpd(file = "Estimate.log", path = getwd(), fileEncoding = "UTF-16LE")
```



---

## 16. Troubleshooting

This section is to aid users in debugging models. If you cannot resolve an issue using these guidelines then please contact the development team. To report an issue please follow the format described in Section 16.2.1.

Most user errors should be well documented and CASAL2 should produce informative error messages. There are runtime options that users can enable to attempt to resolve or at least isolate an error or bug, including different levels of logging.

### 16.1. Logging

CASAL2's internal logging system can be invoked at the command line with argument `-loglevel` followed by one of these options: `trace`, `finest`, `fine`, `medium`.

An example of logging with trace level output:

- On Windows: `casal2 -r -loglevel trace > output.log 2> log.out`
- On Linux: `casal2 -r -loglevel trace > output.log 2&> log.out`

This argument will output CASAL2's reports to the file "output.log", and the "2>" or "2&>" syntax will print the error logged information to the file "log.out". You should be able to see where CASAL2 is exiting by going to the end of the "log.out" file.

The optimal level of logging will depend on what run mode you are using and the granularity of information that you would like to see. There is an ordering in the options, with `medium` being the most coarse, and `trace` being the finest level, with `fine` and `finest` in between. We suggest that if you are running CASAL2 in an iterative state such as for estimation (`casal2 -e`) or MCMC you use `medium` level. This is because the logging can print a lot of information for a single model run, so an estimation which could comprise thousands of model runs can produce very large text files with the finer logging option specified. For a single iteration run such as `casal2 -r` each of the logging options can be useful during different phases of model development.

You can see how CASAL2 creates these reports by looking in the ".cpp" files in the Observation or Processes source code subdirectories and see code such as in `Model/Model.cpp`,

```
LOG_FINE() « "Model: State change to Execute";
```

### 16.2. Reporting errors

If you find a bug or error in CASAL2, please submit an issue in the GitHub repository at <https://github.com/NIWAFisheriesModelling/CASAL2/issues>.

Please follow the guidelines below so that the bug or error can be reproduced. It is helpful to be as detailed and specific as possible when describing the observed behavior as well as the expected behaviour.

#### 16.2.1. Guidelines for reporting an error with CASAL2

1. Ensure you are using the most recent version of CASAL2, as the bug or error you are having may have already been resolved.

2. Provide the version of CASAL2 you are using, e.g., "CASAL2 v2020-04-01 (rev. d5dc698)". The version is output by CASAL2 with the command `casal2 -v`.
3. Provide the operating system you are using, e.g., "IBM-PC Intel CPU with Microsoft Windows 10 Enterprise".
4. Provide a brief description of the problem, e.g., "a segmentation fault was produced".
5. If the problem is reproducible, please describe in detail the steps required to cause it, and include the CASAL2 configuration files, other input files, and any output files generated. Specify the *exact* command line arguments that were used, e.g., "Using the command `casal2 -e -q` produced a segmentation fault. The input configuration files are attached."
6. If the problem is not reproducible (it happened only once, or occasionally for no apparent reason), please describe in detail the circumstances in which it occurred and the behaviour observed, e.g., "CASAL2 crashed, but I have not been able to reproduce the issue. It seemed to be related to a local network crash but I cannot be sure."
7. If the problem produced any error messages, please give the *exact* text displayed, e.g., "segmentation fault (core dumped)".
8. Attach all relevant input and output files so that the problem can be reproduced; these files can be compressed into a single file e.g., a zip file, and uploaded to GitHub.

---

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## 18. Acknowledgements

We thank the developers of CASAL ([Bull et al., 2012](#)) for their ideas that led to the development of CASAL2. The CASAL2 logo was designed by Ian Doonan and Erika Mackay (NIWA).

Much of the structure of CASAL2, equations, and documentation in this manual draw heavily on similar components of the fisheries population model CASAL ([Bull et al., 2012](#)) and the spatial model SPM ([Dunn et al., 2015](#)). We thank the authors of CASAL and SPM for their permission to use their work as the basis for parts of CASAL2 and allow the use of the definitions, concepts, and documentation.

TODO rewrite this The development of CASAL2 was funded by the New Zealand Ministry for Primary Industries and the National Institute of Water & Atmospheric Research Ltd. (NIWA) under NIWAs Fisheries Centre Research Programme 1.



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## 21. Quick reference

**@additional\_prior** *label* Define an object of type *additional\_prior*

parameter Name of the parameter to generate additional prior on

label Label for the additional prior

type Type of additional prior

**@ageing\_error** *label* Define an object of type *ageing\_error*

label The label of the ageing error

type The type of ageing error

**@ageing\_\_error[label].type=data**

**@ageing\_\_error[label].type=none**

**@ageing\_\_error[label].type=normal**

cv CV of the misclassification matrix

k k defines the minimum age of individuals which can be misclassified, i.e., individuals of age less than k have no ageing error

**@ageing\_\_error[label].type=off\_by\_one**

p1 The proportion misclassified as one year younger, e.g., the proportion of age 3 individuals that were misclassified as age 2

p2 The proportion misclassified as one year older, e.g., the proportion of age 3 individuals that were misclassified as age 4

k The minimum age of animals which can be misclassified, i.e., animals of age less than k are assumed to be correctly classified

**@age\_length** *label* Define an object of type *age\_length*

label Label of the age length relationship

type The type of age length relationship

time\_step\_proportions The fraction of the year applied in each time step that is added to the age for the purposes of evaluating the length, i.e., a value of 0.5 for a time step will evaluate the length of individuals at age+0.5 in that time step

distribution The assumed distribution for the growth curve

cv\_first The CV for the first age class

cv\_last The CV for last age class

casal\_switch If true, use the ,less accurate, equation for the cumulative normal function as was used in the legacy version of CASAL.

by\_length Specifies if the linear interpolation of CVs is a linear function of mean length at age. Default is by age only

**@age\_\_length[label].type=data**

external\_gaps

internal\_gaps

length\_weight The label from an associated length-weight block

time\_step\_measurements\_were\_made The time step label for which size-at-age data are provided

**@age\_\_length[label].type=none**

**@age\_\_length[label].type=schnute**

y1     The y1 parameter of the Schnute relationship

y2     The y2 parameter of the Schnute relationship

tau1    The  $\tau_1$  parameter of the Schnute relationship

tau2    The  $\tau_2$  parameter of the Schnute relationship

a     The  $a$  parameter of the Schnute relationship

b     The  $b$  parameter of the Schnute relationship

length\_weight     The label of the associated length-weight relationship

**@age\_\_length[label].type=von\_bertalanffy**

linf    Define the  $L_{infinity}$  parameter of the von Bertalanffy relationship

k     Define the  $k$  parameter of the von Bertalanffy relationship

t0    Define the  $t_0$  parameter of the von Bertalanffy relationship

length\_weight     Define the label of the associated length-weight relationship

**@catchability label**     Define an object of type *catchability*

label    Label of the catchability

type    The type of catchability

**@categories label**     Define an object of type *categories*

format    The format that the category names use

names    The names of the categories to be used in the model

years    The years that individual categories will be active for. This overrides the model values

age\_lengths     R, The labels of age\_length objects that are assigned to categories,

length\_weight     R, The labels of the length\_weight objects that are assigned to categories,

age\_weight     R, The labels of the age\_weight objects that are assigned to categories,

**@derived\_quantity label**     Define an object of type *derived\_quantity*

label    Label of the derived quantity

type    Type of derived quantity

time\_step    The time step in which to calculate the derived quantity after

categories    The list of categories to use when calculating the derived quantity

selectivities    A list of one selectivity

time\_step\_proportion     Proportion through the mortality block of the time step when calculated

time\_step\_proportion\_method     Method for interpolating for the proportion through the mortality block

values

**@derived\_\_quantity[label].type=abundance**

**@derived\_\_quantity[label].type=biomass**

**@estimate label**     Define an object of type *estimate*

label    The label of the estimate

---

type      The prior type for the estimate  
 parameter      The name of the parameter to estimate in the model  
 lower\_bound      The lower bound for the parameter  
 upper\_bound      The upper bound for the parameter  
 same      List of parameters that are constrained to have the same value as this parameter  
 estimation\_phase      The first estimation phase to allow this to be estimated  
 mcmc      Indicates if this parameter is estimated at the point estimate but fixed during MCMC estimation run  
 transformation      Type of simple transformation to apply to estimate  
 transform\_with\_jacobian      Apply jacobian during transformation  
 prior\_applies\_to\_transform      Does the prior apply to the transformed parameter? a legacy switch, see Manual for more information  
**@estimate\_transformation** *label*      Define an object of type *estimate\_transformation*  
 label      Label for the transformation block  
 type      The type of transformation  
 transform\_with\_jacobian      Apply Jacobian during transformation  
**@initialisation\_phase** *label*      Define an object of type *initialisation\_phase*  
 label      The label of the initialisation phase  
 type      The type of initialisation

**@initialisation\_\_phase[label].type=cinitial**

categories      The list of categories for the Cinitial initialisation

**@initialisation\_\_phase[label].type=derived**

insert\_processes      Additional processes not defined in the annual cycle that are to be inserted into this initialisation phase  
 exclude\_processes      Processes in the annual cycle to be excluded from this initialisation phase  
 casal\_initialisation\_switch      Run an extra annual cycle to evaluate equilibrium SSBs. Warning - if true, this may not correctly evaluate the equilibrium state. Set to true if replicating a CASAL model

**@initialisation\_\_phase[label].type=iterative**

years      The number of iterations ,years, over which to execute this initialisation phase  
 insert\_processes      Processes in the annual cycle to be included in this initialisation phase  
 exclude\_processes      Processes in the annual cycle to be excluded from this initialisation phase  
 convergence\_years      The iteration ,year, when the test for convergence ,lambda, is evaluated  
 lambda      The maximum value of the absolute sum of differences ,lambda, between the partition at year-1 and year that indicates successful convergence

**@initialisation\_\_phase[label].type=state\_category\_by\_age**

categories      The list of categories for the category state initialisation  
 min\_age      The minimum age of values supplied in the definition of the category state  
 max\_age      The maximum age of values supplied in the definition of the category state  
**@length\_weight** *label*      Define an object of type *length\_weight*  
 label      The label of the length-weight relationship

`type`      The type of the length-weight relationship  
**@likelihood** *label*      Define an object of type *likelihood*  
**@mcmc** *label*      Define an object of type *mcmc*  
`label`      The label of the MCMC  
`type`      The type of MCMC  
`length`      The number of iterations in for the MCMC chain  
`active`      Indicates if this is the active MCMC algorithm  
`step_size`      Initial stepsize ,as a multiplier of the approximate covariance matrix,  
**@minimiser** *label*      Define an object of type *minimiser*  
`label`      The minimiser label  
`type`      The type of minimiser to use  
`active`      Indicates if this minimiser is active  
`covariance`      Indicates if a covariance matrix should be generated  
**@model** *label*      Define an object of type *model*  
`start_year`      The first year of the model, immediately following initialisation  
`final_year`      The final year of the model, excluding years in the projection period  
`min_age`      The minimum age of individuals in the population  
`max_age`      The maximum age of individuals in the population  
`age_plus`      The oldest age or extra length midpoint ,plus group size, as a plus group  
`initialisation_phases`      The labels of the phases of the initialisation  
`time_steps`      The labels of the time steps, in the order that they are applied, to form the annual cycle  
`projection_final_year`      The final year of the model in projection mode  
`length_bins`      The minimum length in each length bin  
`length_plus`      Specify whether there is a length plus group or not  
`length_plus_group`      Mean length of length plus group  
`base_weight_units`      The units for the base weight. This will be the default unit of any weight  
**input parameters**  
**@observation** *label*      Define an object of type *observation*  
`label`      Label  
`type`      Type of observation  
`likelihood`      Type of likelihood to use  
`categories`      Category labels to use  
`delta`      Robustification value ,delta, for the likelihood  
`simulation_likelihood`      Simulation likelihood to use  
`likelihood_multiplier`      Likelihood score multiplier  
`error_value_multiplier`      Error value multiplier for likelihood  
  
**@observation[label].type=abundance**  
`selectivities`      Labels of the selectivities  
`time_step`      The label of time-step that the observation occurs in  
  
**@observation[label].type=biomass**  
`catchability`      The time-step of the observation



---

time\_step    The label of time-step that the observation occurs in  
obs        The observed values  
years       The years of the observed values  
error\_value    The error values of the observed values ,note the units depend on the likelihood,  
selectivities    Labels of the selectivities  
process\_error    Value for process error  
age\_weight\_labels    R,The labels for the @age\_weight block which corresponds to each category, to use the weight calculation method for biomass calculations,

**@observation[label].type=process\_removals\_by\_age**

min\_age    Minimum age  
max\_age    Maximum age  
plus\_group    Use age plus group  
time\_step    The label of time-step that the observation occurs in  
tolerance    Tolerance  
years       Years for which there are observations  
process\_errors    Label of process error to use  
ageing\_error    Label of ageing error to use  
method\_of\_removal    Label of observed method of removals  
mortality\_instantaneous\_process    The label of the mortality instantaneous process for the observation

**@observation[label].type=process\_removals\_by\_age\_retained**

min\_age    Minimum age  
max\_age    Maximum age  
plus\_group    Use age plus group  
time\_step    The label of time-step that the observation occurs in  
tolerance    Tolerance  
years       Years for which there are observations  
process\_errors    Label of process error to use  
ageing\_error    Label of ageing error to use  
method\_of\_removal    Label of observed method of removals  
mortality\_instantaneous\_process    The label of the mortality instantaneous process for the observation

**@observation[label].type=process\_removals\_by\_age\_retained\_total**

min\_age    Minimum age  
max\_age    Maximum age  
plus\_group    Use age plus group  
time\_step    The label of time-step that the observation occurs in  
tolerance    Tolerance  
years       Years for which there are observations  
process\_errors    Label of process error to use  
ageing\_error    Label of ageing error to use  
method\_of\_removal    Label of observed method of removals  
mortality\_instantaneous\_process    The label of the mortality instantaneous process for the observation

**@observation[label].type=process\_removals\_by\_length**

length\_bins      Length bins  
time\_step      Time step to execute in  
length\_plus      Is the last bin a plus group  
tolerance      Tolerance for rescaling proportions  
years      Years for which there are observations  
process\_errors      the value of process error  
method\_of\_removal      Label of observed method of removals  
mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation

**@observation[label].type=process\_removals\_by\_length\_retained**

length\_bins      Length bins  
time\_step      Time step to execute in  
length\_plus      Is the last bin a plus group  
tolerance      Tolerance for rescaling proportions  
years      Years for which there are observations  
process\_errors      the value of process error  
method\_of\_removal      Label of observed method of removals  
mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation

**@observation[label].type=process\_removals\_by\_length\_retained\_total**

length\_bins      Length bins  
time\_step      Time step to execute in  
length\_plus      Is the last bin a plus group  
tolerance      Tolerance for rescaling proportions  
years      Years for which there are observations  
process\_errors      the value of process error  
method\_of\_removal      Label of observed method of removals  
mortality\_instantaneous\_process      The label of the mortality instantaneous process for the observation

**@observation[label].type=proportions\_at\_age**

min\_age      Minimum age  
max\_age      Maximum age  
plus\_group      Use age plus group  
time\_step      The label of time-step that the observation occurs in  
tolerance      Tolerance on the constraint that for each year the sum of proportions in each age must equal 1, e.g., if tolerance = 0.1 then 1 - Sum,Proportions, can be as great as 0.1  
years      The years of the observed values  
selectivities      Labels of the selectivities  
process\_errors      Process error  
ageing\_error      Label of ageing error to use

---

**@observation[label].type=proportions\_at\_length**

time\_step     The label of time-step that the observation occurs in  
tolerance     Tolerance for rescaling proportions  
years        Years for which there are observations  
selectivities   The labels of the selectivities  
process\_errors   Process error

**@observation[label].type=proportions\_by\_category**

min\_age     Minimum age  
max\_age     Maximum age  
time\_step     The label of time-step that the observation occurs in  
plus\_group     Use age plus group  
years        Years for which there are observations  
selectivities   The labels of the selectivities  
categories2     Target Categories  
selectivities2   Target Selectivities

**@observation[label].type=proportions\_mature\_by\_age**

min\_age     Minimum age  
max\_age     Maximum age  
time\_step     The label of time-step that the observation occurs in  
plus\_group     Use age plus group  
years        Years for which there are observations  
ageing\_error   Label of ageing error to use  
total\_categories   All category labels that were vulnerable to sampling at the time of this  
observation ,not including the categories already given,  
time\_step\_proportion   Proportion through the mortality block of the time step when the  
observation is evaluated

**@observation[label].type=proportions\_migrating**

min\_age     Minimum age  
max\_age     Maximum age  
time\_step     The label of time-step that the observation occurs in  
plus\_group     Use age plus group  
years        Years for which there are observations  
process\_errors   Process error  
ageing\_error   Label of ageing error to use  
process     Process label

**@observation[label].type=tag\_recapture\_by\_age**

min\_age     Minimum age

max\_age      Maximum age  
plus\_group    Use age plus group  
years        Years for which there are observations  
categories2    The available categories in the partition  
selectivities    The labels of the selectivities  
time\_step     The label of time-step that the observation occurs in  
selectivities2    The categories of tagged individuals for the observation  
detection     Probability of detecting a recaptured individual  
time\_step\_proportion    Proportion through the mortality block of the time step when the observation is evaluated

**@observation[label].type=tag\_recapture\_by\_length**

years        Years for which there are observations  
length\_bins    Length bins  
length\_plus    Is the last bin a plus group  
selectivities    The labels of the selectivities used for untagged categories  
tagged\_selectivities    The labels of the tag category selectivities  
detection     Probability of detecting a recaptured individual  
dispersion    Over-dispersion parameter  $\phi$ ,  
time\_step\_proportion    Proportion through the mortality block of the time step when the observation is evaluated

**@penalty label**    Define an object of type *penalty*

label        The label of the penalty

type        The type of penalty

**@process label**    Define an object of type *process*

label        The label of the process

type        The type of process

**@process[label].type=ageing**

categories    The labels of the categories

**@process[label].type=growth\_basic**

categories    The labels of the categories

number\_of\_growth\_episodes    The number of growth episodes per year

growth\_time\_steps    The time step in which each growth episode occurs

cv        C.V. for the growth model

sigma\_min    The lower bound on sigma for the growth model

**@process[label].type=maturation**

from        List of categories to mature from

to        List of categories to mature to

selectivities    List of selectivities to use for maturation

years        The years to be associated with rates

rates        The rates to mature for each year

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**@process[label].type=mortality\_constant\_rate**

categories     List of categories labels  
m     Mortality rates  
time\_step\_ratio     Time step ratios for the mortality rates

**@process[label].type=mortality\_event**

categories     Categories  
years     Years in which to apply the mortality process  
catches     The number of removals ,catches, to apply for each year  
u\_max     The maximum exploitation rate , $U_{max}$ ,  
selectivities     The list of selectivities  
penalty     The label of the penalty to apply if the total number of removals cannot be taken

**@process[label].type=mortality\_event\_biomass**

categories     Category labels  
selectivities     The labels of the selectivities for each of the categories  
years     The years in which to apply the mortality process  
catches     The biomass of removals ,catches, to apply for each year  
u\_max     The maximum exploitation rate , $U_{max}$ ,  
penalty     The label of the penalty to apply if the total biomass of removals cannot be taken

**@process[label].type=mortality\_holling\_rate**

prey\_categories     Prey Categories labels  
predator\_categories     Predator Categories labels  
is\_abundance     Is vulnerable amount of prey and predator an abundance [true] or biomass [false]  
a     Parameter a  
b     Parameter b  
x     This parameter controls the functional form, Holling function type 2 , $x=2$ , or 3 , $x=3$ , or generalised ,Michaelis Menten,  $x=1$ ,  
u\_max     The maximum exploitation rate , $U_{max}$ ,  
prey\_selectivities     Selectivities for prey categories  
predator\_selectivities     Selectivities for predator categories  
penalty     Label of penalty to be applied  
years     Years in which to apply the mortality process

**@process[label].type=mortality\_initialisation\_event**

categories     Categories  
catch     The number of removals ,catches, to apply for each year  
u\_max     The maximum exploitation rate , $U_{max}$ ,  
selectivities     The list of selectivities  
penalty     The label of the penalty to apply if the total number of removals cannot be taken

**@process[label].type=mortality\_initialisation\_event\_biomass**

categories     Categories

catch      The number of removals ,catches, to apply for each year  
u\_max      The maximum exploitation rate , $U_{max}$ ,  
selectivities      The list of selectivities  
penalty      The label of the penalty to apply if the total number of removals cannot be taken

**@process[label].type=mortality\_instantaneous**

categories      Categories for instantaneous mortality  
m      Natural mortality rates for each category  
time\_step\_ratio      Time step ratios for natural mortality  
selectivities      The selectivities to apply on the categories for natural mortality

**@process[label].type=mortality\_instantaneous\_retained**

categories      Categories for instantaneous mortality  
m      Natural mortality rates for each category  
time\_step\_ratio      Time step ratios for natural mortality  
selectivities      The selectivities to apply on the categories for natural mortality

**@process[label].type=mortality\_prey\_suitability**

prey\_categories      Prey Categories labels  
predator\_categories      Predator Categories labels  
consumption\_rate      Predator consumption rate  
electivities      Prey Electivities  
u\_max      U max  
prey\_selectivities      Selectivities for prey categories  
predator\_selectivities      Selectivities for predator categories  
penalty      Label of penalty to be applied  
years      Year that process occurs

**@process[label].type=recruitment\_beverton\_holt**

categories      Category labels  
r0      R0  
b0      B0  
proportions      Proportions  
age      Age at recruitment  
ssb\_offset      Spawning biomass year offset  
steepness      Steepness  
ssb      SSB label ,derived quantity,  
b0\_initialisation\_phase      Initialisation phase label that B0 is from  
ycs\_values      YCS Values  
ycs\_years      Recruitment years. A vector of years that relates to the year of the spawning event that created this cohort  
standardise\_ycs\_years      Years that are included for year class standardisation

**@process[label].type=recruitment\_beverton\_holt\_with\_deviations**

categories      Category labels

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r0     R0  
 b0     B0  
 proportions     Proportions  
 age     Age to recruit at  
 ssb\_offset     Spawning biomass year offset  
 steepness     Steepness  
 ssb     SSB Label ,derived quantity,  
 sigma\_r     Sigma R  
 b\_max     Maximum bias adjustment  
 last\_year\_with\_no\_bias     Last year with no bias adjustment  
 first\_year\_with\_bias     First year with full bias adjustment  
 last\_year\_with\_bias     Last year with full bias adjustment  
 first\_recent\_year\_with\_no\_bias     First recent year with no bias adjustment  
 b0\_initialisation\_phase     Initialisation phase label that b0 is from  
 deviation\_values     Recruitment deviation values  
 deviation\_years     Recruitment years. A vector of years that relates to the year of the spawning event that created this cohort

**@process[label].type=recruitment\_constant**

categories     Categories  
 proportions     Proportions  
 length\_bins     The length bins that recruits are uniformly distributed over at the time of recruitment  
 r0     R0

**@process[label].type=survival\_constant\_rate**

categories     List of categories  
 s     Survival rates  
 time\_step\_ratio     Time step ratios for S  
 selectivities     Selectivity label

**@process[label].type=tag\_by\_age**

from     Categories to transition from  
 to     Categories to transition to  
 min\_age     Minimum age to transition  
 max\_age     Maximum age to transition  
 penalty     Penalty label  
 u\_max     U Max  
 years     Years to execute the transition in  
 initial\_mortality  
 initial\_mortality\_selectivity  
 loss\_rate  
 loss\_rate\_selectivities  
 selectivities  
 n

**@process[label].type=tag\_by\_length**

from    Categories to transition from  
to      Categories to transition to  
penalty    Penalty label  
u\_max    U Max  
initial\_mortality  
initial\_mortality\_selectivity  
selectivities  
n

**@process[label].type=tag\_loss**

categories    List of categories  
tag\_loss\_rate    Tag Loss rates  
time\_step\_ratio    Time step ratios for Tag Loss  
tag\_loss\_type    Type of tag loss  
selectivities    Selectivities  
year    The year the first tagging release process was executed

**@process[label].type=transition\_category**

from    From category  
to    To category  
proportions    Proportions  
selectivities    Selectivity names

**@process[label].type=transition\_category\_by\_age**

from    Categories to transition from  
to    Categories to transition to  
min\_age    Minimum age to transition  
max\_age    Maximum age to transition  
penalty    Penalty label  
u\_max    U max  
years    Years to execute the transition in

**@profile label**    Define an object of type *profile*

label    Label  
steps    The number of steps between the lower and upper bound  
lower\_bound    The lower bounds  
upper\_bound    The upper bounds  
parameter    The system parameter to profile  
same    A parameter that is constrained to have the same value as the parameter being profiled

**@project label**    Define an object of type *project*

label    Label  
type    Type  
years    Years to recalculate the values  
parameter    Parameter to project  
multiplier    Multiplier that is applied to the projected value

**@report label**    Define an object of type *report*

label    The label for the report



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type      The type of report  
file\_name      The File Name for this report to be in a separate file  
write\_mode      The write mode

**@report[label].type=age\_length**

time\_step      Time Step label  
years      Years  
age\_length  
category

**@report[label].type=ageing\_error\_matrix**

ageing\_error      Ageing Error label

**@report[label].type=initialisation\_partition\_mean\_weight**

**@report[label].type=partition**

time\_step      Time Step label  
years      Years

**@report[label].type=partition\_biomass**

time\_step      Time Step label  
years      Years

**@report[label].type=partition\_mean\_weight**

time\_step      Time Step label  
years      Years

**@report[label].type=partition\_year\_cross\_age\_matrix**

**@selectivity label**      Define an object of type *selectivity*

label      The label for this selectivity  
type      The type of selectivity  
length\_based      Is the selectivity length based  
intervals      Number of quantiles to evaluate a length based selectivity over the age length  
distribution  
partition\_type      The type of partition this selectivity will support. Defaults to same as the  
model  
values  
length\_values

**@simulate label**      Define an object of type *simulate*

label      Label  
type      Type  
years      Years to recalculate the values  
parameter      Parameter to simulate  
**@time\_step label**      Define an object of type *time\_step*  
label      The label of the timestep

processes     The labels of the processes for this time step in the order that they occur  
**@time\_varying** *label*     Define an object of type *time\_varying*  
label     The time-varying label  
type     The time-varying type  
years     Years in which to vary the values  
parameter     The name of the parameter to time vary

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# Appendices

## A. Investigating two options for YCS prior distribution formulations

There are two common ways of parameterising the lognormal prior distribution of year class strength (YCS) when fitting models.

Let  $YCS_y$  represent the YCS for year  $y$ . The two parameterisations used are:

1.  $YCS_y \sim LN(\mu, \sigma_R^2)$ , with  $\mu$  chosen so that  $E(YCS_y) = 1$ .
2.  $YCS_y = e^{\varepsilon_y - \frac{1}{2}\sigma_R^2}$ , where  $\varepsilon_y \sim N(0, \sigma_R^2)$ .

To check whether the two representations are equivalent, we will determine, in each case the density function of  $YCS_y$  on the log-scale.

Note that, in general, if  $Y \sim LN(\mu, \sigma_R^2)$  (i.e., random variable  $Y$  has a lognormal distribution with parameters  $\mu$  and  $\sigma_R^2$ ), then the expectation,  $E(Y)$ , and variance,  $Var(Y)$ , of  $Y$  are given by

$$E(Y) = e^{\mu + \frac{1}{2}\sigma_R^2},$$

and

$$Var(Y) = \left[ e^{\sigma_R^2} - 1 \right] e^{2\mu + \sigma_R^2}.$$

The lognormal distribution can be expressed on the log scale:

$$\log Y \sim \text{Normal}(\mu, \sigma_R^2).$$

**Option 1:**  $YCS_y \sim LN(\mu, \sigma_R^2)$ , with  $E(YCS_y) = 1$

Setting  $E(YCS_y) = 1$  implies

$$\begin{aligned} e^{\mu + \frac{1}{2}\sigma_R^2} &= 1 \\ \Rightarrow \mu + \frac{1}{2}\sigma_R^2 &= \log 1 \\ \Rightarrow \mu &= -\frac{1}{2}\sigma_R^2 \end{aligned} \tag{A.1}$$

and

$$\begin{aligned} Var(YCS_y) &= \left[ e^{\sigma_R^2} - 1 \right] e^{2\mu + \sigma_R^2} \\ &= \left[ e^{\sigma_R^2} - 1 \right] e^{2(-\frac{1}{2}\sigma_R^2) + \sigma_R^2} \\ &= \left[ e^{\sigma_R^2} - 1 \right] e^0 \\ &= e^{\sigma_R^2} - 1. \end{aligned} \tag{A.2}$$

So, on the log scale:

$$\log YCS_y \sim N\left(-\frac{1}{2}\sigma_R^2, \sigma_R^2\right).$$

**Option 2:**  $YCS_y = e^{\varepsilon_y - \frac{1}{2}\sigma_R^2}$ , where  $\varepsilon_y \sim N(0, \sigma_R^2)$

In this case,  $YCS_y = e^{\varepsilon_y - \frac{1}{2}\sigma_R^2}$  implies

$$\log YCS_y = \varepsilon_y - \frac{1}{2}\sigma_R^2$$

and

$$E(\log YCS_y) = E\left(\varepsilon_y - \frac{1}{2}\sigma_R^2\right) = -\frac{1}{2}\sigma_R^2,$$

since  $E(\varepsilon_y) = 0$ .

Also:

$$\begin{aligned} \text{Var}(\log(YCS_y)) &= \text{Var}\left(\varepsilon_y - \frac{1}{2}\sigma_R^2\right) \\ &= \text{Var}(\varepsilon_y) \\ &= \sigma_R^2 \end{aligned} \tag{A.3}$$

Therefore

$$\log YCS_y \sim N\left(-\frac{1}{2}\sigma_R^2, \sigma_R^2\right).$$

Therefore, the two parameterisations result in exactly the same distribution for  $YCS_y$  values and should give the same results **if expressed correctly** in MCMC algorithms.

To illustrate that these two distributions are exactly the same, we first use simulations to show that we get the same  $YCS_y$  values when generating sequences from these two formulations. One is generated directly from the lognormal distribution, while the other is obtained by transforming a normal random variable.

### Investigating prior specification

Given the two different representations, the question is, how should their prior distribution contributions to the negative log posterior be specified?

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## Prior based on Option 1

For Option 1, this is straight-forward. The  $YCS_y$ s are generated from a lognormal distribution, so the contribution to the log posterior is based on the lognormal density function. That is, if we let  $Y = YCS_y$ , then the density function of  $Y$  is given by

$$f(y) = \frac{1}{y\sigma_R\sqrt{2\pi}} e^{-\frac{1}{2\sigma_R^2}(\log y - \mu)^2}.$$

Since  $\mu = -\frac{1}{2}\sigma_R^2$  as shown in Equation A.1, we have

$$-\log f(y) = \log y + \log \sigma_R + \frac{1}{2} \log 2\pi + \frac{1}{2\sigma_R^2} \left( \log y - \left(-\frac{1}{2}\sigma_R^2\right) \right)^2. \quad (\text{A.4})$$

## Prior based on Option 2

For Option 2, we will look at two ways used to specify the prior and say which one is correct.

### Prior 2 - Normal distribution for $\epsilon_y$

In this approach, we have

$$YCS_y = e^{\epsilon_y - \frac{1}{2}\sigma_R^2}, \text{ where } \epsilon_y \sim N(0, \sigma_R^2).$$

What is sometimes done is to then express the contribution to the negative log posterior using  $-\log f(\epsilon_y)$ , where

$$f(\epsilon_y) = \frac{1}{\sigma_R\sqrt{2\pi}} e^{-\frac{1}{2\sigma_R^2}\epsilon_y^2},$$

and therefore

$$-\log f(\epsilon_y) = \log \sigma_R + \frac{1}{2} \log 2\pi + \frac{1}{2\sigma_R^2}\epsilon_y^2. \quad (\text{A.5})$$

However, this contribution is based on the density function for  $\epsilon_y$  and not for  $Y$ . Such an approach is incorrect. The two contributions are different as seen in Equations A.4 and A.5, and as shown below.

So what does this mean in practice?

The overall model is based on  $YCS_y$ , rather than  $\epsilon_y$ . Using a negative log posterior based on  $f(\epsilon_y)$  gives incorrect weights to the  $YCS_y$  values in the model, meaning that in MCMC steps, acceptance probabilities will be incorrect. When using the specification based on  $\epsilon_y$ , the correct approach is to use variable transformation methods to obtain probability densities for the  $YCS_y$  values. These density values based on  $f(Y)$  are the ones to use in the negative log posterior.

### Prior 3 - Variable transformation to obtain $f(Y)$ based on $f(\epsilon_y)$

Given  $Y = e^{\epsilon_y - \frac{1}{2}\sigma_R^2}$ , where  $\epsilon_y \sim N(0, \sigma_R^2)$ , we need to find  $g(y)$ , the distribution of the transformed variable  $YCS_y$ .

Variable transformation theory tells us that:

$$g(y) = f(s(y)) \left| \frac{ds(y)}{dy} \right|,$$

where  $s(y) = \epsilon_y(y)$  is the result of the conversion from  $Y$  to  $\epsilon_y$ , and  $\left| \frac{ds(y)}{dy} \right|$  is the Jacobian of the transformation.

We find  $s(y)$  by expressing  $\epsilon_y$  as a function of  $y$ :

$$\begin{aligned} y &= e^{\epsilon_y - \frac{1}{2}\sigma_R^2} \\ \Rightarrow \log y &= \epsilon_y - \frac{1}{2}\sigma_R^2 \\ \Rightarrow \epsilon_y &= \log y + \frac{1}{2}\sigma_R^2. \end{aligned} \tag{A.6}$$

Therefore

$$\frac{ds(y)}{dy} = \frac{d\epsilon_y(y)}{dy} = \frac{d}{dy} \left( \log y + \frac{1}{2}\sigma_R^2 \right) = \frac{1}{y}.$$

Then

$$\begin{aligned} g(y) &= \frac{1}{\sigma_R \sqrt{2\pi}} e^{-\frac{1}{2\sigma_R^2} [\log y + \frac{1}{2}\sigma_R^2]^2} \cdot \left| \frac{1}{y} \right| \\ &= \frac{1}{y\sigma_R \sqrt{2\pi}} \exp \left\{ -\frac{[\log y - (-\frac{1}{2}\sigma_R^2)]^2}{2\sigma_R^2} \right\}. \end{aligned} \tag{A.7}$$

This is the density function of a lognormal distribution with parameters  $\mu = -\frac{1}{2}\sigma_R^2$  and  $\sigma_R^2$ , that is,

$$Y \sim LN \left( -\frac{1}{2}\sigma_R^2, \sigma_R^2 \right)$$

and from equation A.7 we see that

$$-\log g(y) = \log y + \log \sigma_R + \frac{1}{2} \log 2\pi + \frac{1}{2\sigma_R^2} \left( \log y - \left( -\frac{1}{2}\sigma_R^2 \right) \right)^2. \tag{A.8}$$

---

which is exactly the same expression as that for  $-\log f(y)$  in equation A.4.

Therefore if used correctly, Option 2 parameterisation results in the same contribution,  $-\log g(y)$ , to the negative log posterior as Option 1,  $-\log f(y)$ .

Note that  $-\log f(y) = -\log f(\epsilon_y)$  only for  $Y = 1$ .

We will carry out a brief simulation exercise to illustrate the point. We will use the density functions derived above, rather than existing R functions and calculate  $-\log f(y) = -\log g(y)$  and  $-\log f(\epsilon_y)$  for a sequence of  $YCS_y$  values.

The simulation results indicate that  $-\log f(y) = -\log g(y) = -\log f(\epsilon_y)$  only for  $Y = 1$ . For other values of  $Y$ , the size of the difference between  $-\log f(y)$  and  $-\log f(\epsilon_y)$  is given by  $|\log y|$  and does not depend on  $\sigma_R^2$ . Therefore, the differences increase in size as the  $YCS$  value diverges further from 1.

What is the implication of this?

Incorrect use of the prior based on  $\epsilon_y$  (i.e., using  $-\log f(\epsilon_y)$  in place of  $-\log g(y)$ ) results in prior contributions to the negative log-posterior that are lower or higher by  $\log YCS_y$  than what they should be.