Spatial Population Model User Manual
SPM v1.00-2009-03-17 (rev. 3056)

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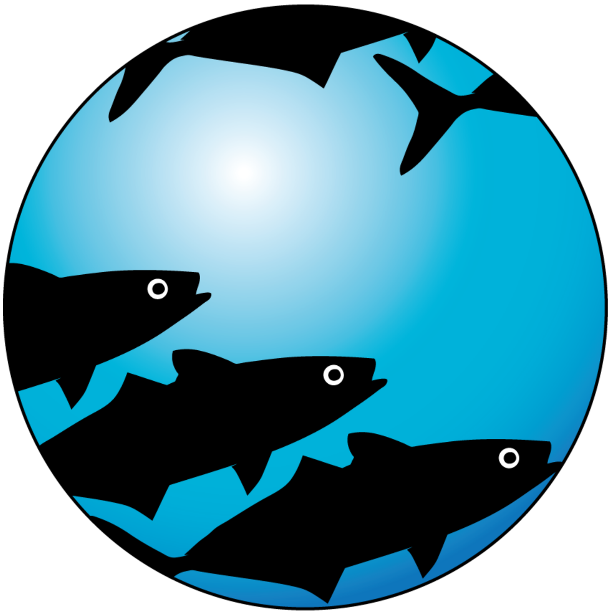

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1 Introduction

The Spatial Population Model (`SPM`) is a generalised spatially explicit age-structured population dynamics and movement model. `SPM` can model population dynamics and movement parameters for an age-structured population using a range of observations, including tagging, relative abundance, and age frequency data. `SPM` implements an age-structured population within an arbitrary shaped spatial structure, which can have user defined categories (e.g., immature, mature, male, female, etc.), and age range. Movement can be modelled as either adjacent cell movements or global movements based on covariates.

This manual describes how to use `SPM`, including how to run `SPM`, how to set up an input configuration file. Further, we describe the population dynamics and estimation methods, and describe how to specify and interpret output. If you are new to `SPM`, then a good place to start is by reading this manual and attempting to replicate the examples (Section 13).

1.1 Version

This document (last modified 2009-04-03) describes `SPM` v1.00-2009-03-17 (rev. 3056) . The `SPM` version number is suffixed with a date/time (`yyyy-mm-dd`) and revision number, giving the revision control system UTC date and revision number for the most recent modification of the source files. User manual updates will usually be issued for each minor version or date release of `SPM`, and can be obtained, on request, from the authors.

1.2 Citing `SPM`

A suitable reference for `SPM` and this document is:

Dunn, A.; Rasmussen, S. (2009) Spatial Population Model User Manual, `SPM` v1.00-2009-03-17 (rev. 3056) . National Institute of Water & Atmospheric Research Ltd. *Unpublished report*. 156 p.

1.3 Software license

This program and the accompanying materials are made available under the terms of the Common Public License v1.0 which accompanies this software (see Section 19).

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1.4 System requirements

`SPM` is available for most IBM compatible machines running Linux and from the command prompt under most Microsoft Windows operating systems.

Several of `SPM`s tasks are highly computer intensive and a fast, powerful processor is recommended. We recommend a minimum of 10 megabytes of free RAM (although, depending on the scope of the problem, you may need much more). Some of `SPM`s tasks can be multi-threaded, and hence multi-core machines may perform some tasks considerably quicker than single core processors. The program itself requires only a few megabytes of hard-disk space but output files can consume large amounts of disk space. Depending on number and type of user output requests, the output could range from a few hundred kilobytes to several hundred megabytes. However, we note that, depending on the model implemented, some of `SPM`s tasks can take a considerable amount of time.

1.5 Necessary files

In Linux, only the executable file `spm` is required to run `SPM` (but, depending on your system, you may need the either the 32- or 64-bit version). For Microsoft Windows, you need the executable file `spm.exe`. There is no 64-bit version for Microsoft Windows.

1.6 Useful add-ons

No software other than the appropriate operating system or emulation package is required to run `SPM`. However, as `SPM` offers little in the way of post-processing of the output, most users will wish to have a package available that allows tabulation and graphing of model outputs. We recommend the use of software packages such as Microsoft Excel, S-Plus, or **R** (R Development Core Team 2007). See Section 14 for details of the `spm` **R** package for extracting `SPM` output.

1.7 Getting help

`SPM` is distributed as unsupported software. The authors do not, as a rule, provide help for users of `SPM`. However, we may be able to offer limited assistance, and we would appreciate being notified of any problems or errors in `SPM`. See Section 15.2 for how to report errors to the authors. Further information about `SPM` can be obtained by contacting the authors.

1.8 Technical details

`SPM` is compiled on Linux using `gcc`, the C/C++ compiler developed by the GNU Project. The 32-bit Linux version has been compiled using `gcc` version 4.1.2 20070115 (prerelease) (SUSE Linux), the 64-bit Linux version uses `gcc` version 4.1.0 (SUSE Linux). Note that `SPM` is not supported for Linux kernel versions prior to 2.6. The Microsoft Windows version is compiled using Mingw32 `gcc` 3.4.5, and should run on most 32-bit WindowsXP and Windows Vista systems. There are no plans to port `SPM` to Microsoft Windows 64-bit platforms.

`SPM` uses two minimisers — the first is closely based on the main algorithm of Dennis Jr and Schnabel (1996), and which which uses finite difference gradients, and the second is an implementation of the differential evolution solver (Storn and Price, 1995), and based on code by Lester E. Godwin of PushCorp, Inc. The random number generator used by `SPM` uses an implementation of the Mersenne twister random number generator (Matsumoto and Nishimura, 1998). This, the command line functionality, matrix operations, and a number of other functions use the BOOST C++ library (Version 1.38.0).

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

2 Model overview

2.1 Introduction

The Spatial Population Model (`SPM`) is a generalised spatially explicit age-structured population dynamics and movement model. It allows the implementation of age-structured population models suitable for the simulation and estimation of parameters in models with a large number of areas. It implements a statistical catch-at-age population dynamics and movement model, using a discrete time-step state-space model that represents a cohort-based population age structure in a spatially explicit manner.

The basic structure of the model is defined in terms of the *state*. The state consists of two parts, the *partition* and *derived quantities*. The state will typically change one or more times in every *time step* of every year, depending on the *processes* defined for each model.

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

The application of processes within each year is controlled by the *annual cycle*. This defines what processes happen in each model year, and in what sequence. Further, each year is split up into one or more *time steps* (with at least one process occurring in each time step). You can think of each time step as representing a particular part of the calendar year, or you can just treat them as an abstract sequence of events.

The division of the year into an arbitrary number of time steps allows the user to specify the exact order in which processes occur and when observations are evaluated. The user specifies the time steps, their order, and the processes within each time step. If more than one process occurs in the same time step, then the occur in the order that they are specified. Observations are always evaluated at the end of a 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.

An `SPM` model can be parametrised by both population processes (for example, ageing, recruitment, and mortality) and movement processes. Movement is by either adjacent cell movements, between cell migrations, or by global movements parametrised as a function of known attributes at each spatial location (termed preference functions — see later). `SPM` is designed to be flexible and to allow for the estimation of both population and movement parameters from local or aggregated spatially explicit observations.

The population structure of `SPM` follows the usual population modelling conventions and is similar to those implemented in other population models, for example CASAL (Bull et al., 2008). The model records the numbers of individuals by age and category (e.g., male, female), as well as the locations of these cohorts within a spatial grid. 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)

The spatial component of `SPM` is designed to allow parametrise movement cohorts and groups of individuals between spatial locations, and hence allow movement parameters to be estimated by incorporating spatially explicit observations.

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

This section gives a quick overview of the model, and how to use it. Detailed descriptions of the components of `SPM`, the model structures, mathematical equations used, and command and subcommand syntax and arguments are given in the following sections.

A model in `SPM` is specified by an input configuration file, and comprises of four main components. These are the population section (model structure, population and spatial dynamics, etc.), the estimation section (methods of estimation and the parameters to be estimated), the observation section (observational data and associated likelihoods), and the report section (printouts and reports from the model). These input configuration file completely describe a model implemented in `SPM`. See Sections 8, 9, 10, and 11 for details and specification of `SPM`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 movement and population dynamics. It describes the model structure (both the spatial and population structure), defines the population and movement processes (for example, recruitment, migration, and mortality), layers (the known attributes of each spatial cell), selectivities, and key population parameters.

2.3 The estimation section

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

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

Penalties and priors act as constraints on the estimation. They can either encourage or discourage (depending on the specific implementation) parameter estimates that are ‘near’ some value, and hence influence the estimation process. For example, the catch-limit penalties can be used to discourage parameter estimates that lead to models where the recorded catch was unable to be fully taken.

2.4 The observation section

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

2.5 The report section

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 `SPM` will provide informational messages to the screen, the `SPM` will only produce model estimates, population states, and other data as requested by the report section. Note that if no reports are specified, then no output will be produced.

3 Running `SPM`

`SPM` is run from the command line in Microsoft Windows or from a terminal window in Linux. `SPM` gets its information from input data files, the key one of which is the input configuration file.

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

Other input files can, in some circumstances, be supplied to define the starting point for an estimation, define the parameters for a projection, or to simulate observations.

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

3.1 Using `SPM`

To use `SPM`, open a command line window (Microsoft Windows) or a terminal window (Linux). Navigate to a directory of your choice, where your input configuration files are located. Then type `spm` with any arguments (see Section 3.4). SPM will print output to the screen, and return you to the command prompt when it completes its task. Note that the `SPM` executable (binary) must be either in the directory where you run it or somewhere in your `PATH`. See your operating system documentation for help on identifying or modifying your `PATH`

3.2 The input configuration file

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

The command and subcommand definitions in the input configuration file can be extensive, and can result in a input configuration file that is long and difficult to navigate. To aid readability and flexibility, we can use the input configuration file command `@include` *`file`*. The command causes an external file, *`file`*, to be read and processed, exactly as if its contents had been inserted in the main input configuration file at that point. The file name must be a complete file name with extension, but can use either a relative or absolute path as part of its name. Note that included files can also contain `@include` commands — but be careful that you do not set up a recursive state. See Section 12 for more detail.

3.3 Redirecting standard output

`SPM` uses the standard out to display run-time information. Standard error is not used by `SPM`, but may be used by the operating system to report an error with `SPM`. We suggest redirecting both the standard out and standard error into files. With the bash shell (on Linux systems), you can do this using the command structure,

```
(spm [arguments] > out) >& err &
```

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

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

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

```
spm [arguments] > out
```

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

```
spm [arguments] > out 2> err
```

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

3.4 Command line arguments

The call to `SPM` is of the following form.:

`spm [-c` *`config_file`*`] [`*`task`*`] [`*`options`*`]`

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

and where *task* is one of;

-h Display help (this page).

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

-v Display the `SPM` version number.

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

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

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

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

-f 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 start values from the file denoted with the command line argument `-i file`.

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

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

-i *file* *Input* one or more sets of estimated parameter values from `file`. See Section 11.1.6 for details about the format of `file`.

-t *number* Number of *threads* to run (i.e., number of processors available for use).

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

-g *seed* Seed the random number *generator* with `seed`, a positive (long) integer value. Note, if `-g` is not specified, then `SPM` looks the command `@Estimation.random_seed` for a random number seed , and if not defined, then automatically generates a random number seed based on the computer clock time.

3.5 Constructing an SPM input configuration file

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

3.5.1 Commands

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

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

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

3.5.2 Subcommands

Subcommands in `SPM` are for defining options and parameter values for commands. They always take an argument which is one of a specific *type*. The types acceptable for each subcommand are defined in Section 8.11, 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. `SPM` may report an error if they are not supplied in this way, however, in some circumstances a different order may result in a valid, but unintended set of actions, leading to possible errors in your expected results.

The arguments for a subcommand are either,

switch true/false

integer an integer number

integer vector a vector of integer numbers

constant a real number (i.e., double)

constant vector a vector of real numbers (i.e., vector of doubles)

estimable a real number that can be estimated (i.e., estimable double)

estimable vector a vector of real numbers that can be estimated (i.e., vector of estimable doubles)

string a categorical (string) value

string vector a vector of categorical values

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

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

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

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

3.5.3 The command-block format

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

`@command`, or

`@command argument`, or

`@command` *`label`*

and then

`subcommand argument`

`subcommand argument`

etc,.

Blank lines are ignored, as is extra white space (i.e., tabs and spaces) between arguments. But don't put extra white space before a `@` character (which must also be the first character on the line), and make sure the file ends with a carriage return. Commands and subcommands consist of letters and/or underscores, must not contain a spaces or full-point ('.').

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

In general, commands, sub-commands, and arguments in the parameter files are case insensitive. But note, however, that if you are on a Linux system then external calls to files are case sensitive (i.e., when using `@include` *`file`*, the argument *`file`* will be case sensitive).

3.5.4 Commenting out lines

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

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

3.5.5 Determining parameter names

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

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

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

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

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

`process[MyRecruitment].r0`

3.6 SPM exit status values

When `SPM` completes its task successfully or errors out gracefully, it returns a single exit status value (0) to the operating system. The operating system will return -1 if `SPM` terminates unexpectedly.

To determine if `SPM` has completed its task successfully, check the standard output for error and information messages.

4 The population section

4.1 Introduction

The population section defines the models structure, movement and population dynamics, and other associated parameters. It describes the model structure (both the spatial and population structure), defines the population (for example, recruitment, migration, and mortality) and movement processes, defines the layers (the known attributes of each spatial cell), selectivities, and model parameters.

The population, at any point in time, is described by the *state*, which comprises of the *partition* and any *derived quantities*. The partition is a 4-dimensional matrix, comprising of the spatial structure, and within each spatial location, the population structure.

The population section consists of several components, including;

- The spatial and population structure
- Model initialisation (i.e., the state of the model at the start of the first year)
- The annual cycle (time steps and processes that are applied in each time step)
- The specifications and parameters of the processes;
  - Population processes (i.e., processes that add, remove, or shift numbers between ages and categories)
  - Spatial processes (i.e., processes that move or shift cohorts between spatial locations but do not alter their ages or categories)
- Layers (used by processes, observations and reports) and their definitions
- Selectivities
- Parameter values and their definitions
- Derived quantities required as parameters for some processes (i.e., spawning stock biomass to resolve the spawner-recruit relationship in a recruitment process)

4.2 Spatial structure

The spatial structure of `SPM` is represented by an $n_{rows} \times n_{cols}$ grid, with rows $i = 1 \dots n_{rows}$ and columns $j = 1 \dots n_{cols}$. Each cell of this matrix records the population structure at that point in space, where the population structure is represented by an $n_{categories} \times n_{ages}$ rectangular matrix (with categories $k = 1 \dots n_{categories}$ and ages $l = 1 \dots n_{ages} = age_{min} \dots age_{max}$. Hence we can describe any spatial and population element of the model as element(i, j, k, l). We define, within the spatial grid $(n_{rows} \times n_{cols})$, locations where the population can and cannot potentially be present using a *layer*.

`SPM` implements a single spatial structure, a grid of *square* cells (Figure 4.1) The spatial grid can be of an arbitrary size, but must be rectangular.

The dimensions of the spatial grid are user defined but must be at least a 1×1 grid (i.e., a single spatial cell). But the largest spatial structure allowed by `SPM` is a grid of 1000×1000 cells. Associated with the spatial structure is the one compulsory layer (see Section 4.4), the *base layer*. This defines the locations where the population can and cannot potentially be present (e.g., in a marine model, the locations associated with the sea and not land) as values within the base layer that are greater than zero. There must be at least one cell in the spatial grid where the population can be present. In addition, the base layer also defines the relative *area* of each spatial cell, as used for density calculations within `SPM`.

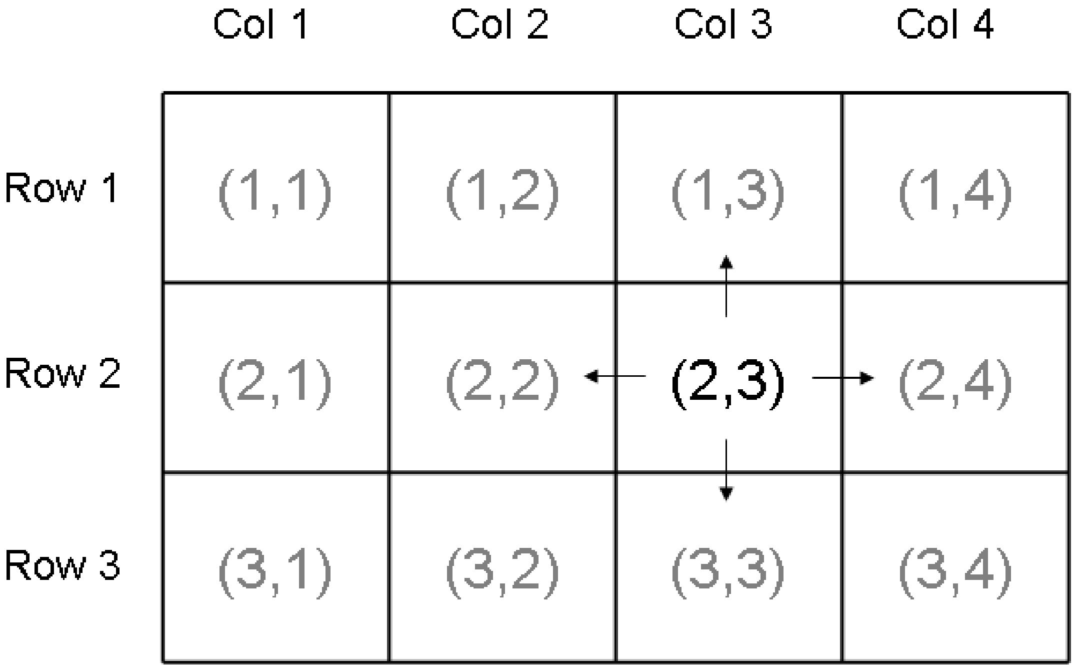

Figure 4.1: An illustration of the *square* spatial structure

Models are implemented as a grid of cells as a rectangular matrix. Distance between cells is determined as the euclidean distance between cell centres, modified by an arbitrary scalar.

Hence, the definition of the spatial structure includes;

- The type of spatial grid and its dimensions, n_{rows} and m_{cols}
- The label of a numeric layer to be used as the base layer (defining the locations where the population can be present as well as the area of each cell)
- The length (distance) of a side of the grid cell to be used as the scaler for distance calculations

4.3 Population structure

The population structure in `SPM` is represented by a matrix containing an arbitrary number of user defined categories (rows), and an arbitrary age range (columns). Hence, each spatial cell has a population state described as $n_{categories} \times n_{ages}$ rectangular matrix with categories $k = 1 \ldots n_{categories}$ and ages $l = age_{min} \ldots age_{max}$.

Within each (i, j) element of the spatial grid element (termed spatial *cell*), the population structure in `SPM` is represented by a matrix containing an arbitrary number of user defined categories (rows), and an arbitrary age range (columns). Hence, each spatial cell has a population state described as $n_{categories} \times n_{ages}$ rectangular matrix with categories $k = 1 \ldots n_{categories}$ and ages $l = age_{min} \ldots age_{max}$.

The names and number of categories are user defined, but there just be at least one category in any model. The ages are defined as a sequence from age_{min} to age_{max}, and the last age may optionally be a plus group.

Hence, the definition of the population structure includes;

- The number and labels of the categories, $k_{categories}$
- The minimum and maximum ages that define the ages of the model, l_{ages}
- If the last age is a plus group

4.4 Layers

Layers are used by `SPM` to evaluate locations where the population may be present (via the *base layer*), to provide sets of known attributes of each spatial location (for preference based movements), and to group or categorise cells for use by processes and observations. Layers consist of an $n \times m$ matrix and can be either *numeric* or *categorical*. See Section 4 for further details.

Layers form a key underlying concept in `SPM`. They comprise of a grid of known values, with a value for every spatial cell in the model. Layers are used by processes, observations, and outputs commands to supply spatially explicit covariates and any categorical groupings required.

Every model must define at least one layer, the base later L_B. A layer is defined as a $n_{rows} \times n_{cols}$ grid of values (with one exception — the distance layer, see below), where the value for each cell represents a known quantity. For example layers may represent classifications, physical attributes, or some other assumed quantity. Typically they are provided by the user as a matrix of values, although abundance and distance layers can be calculated by `SPM` as and when required.

Within `SPM`, layers are used in three contexts:

1. The base layer: The base layer L_B is a special layer (there must be exactly one base layer defined within the model) that defines the locations where the population can and cannot potentially be present (e.g., locations associated with the sea and not land in a marine model). Here, we define that a cell may potentially have part of the population present if every element $L_B(i,j) \geq 0$. Further, positive values of the base layer L_B represent the *area* represented by that spatial cell.
2. Covariate layers: A model may have many covariate layers, and these are used as covariates of some population or movement process (e.g., the sea floor depth may be a covariate of some movement process). The values in layers used as covariates must be continuous (i.e., numeric) variables. Covariate layers must have values ≥ 0.
3. Classification layers. A model may have many classification layers, and these are used as a classification or grouping variable for aggregating data over individual spatial cells (i,j), e.g., statistical areas or management areas. Such layers are typically used to aggregate the population within cells into groups so-as to allow comparison with observations. The values in layers used as classification layers must be categorical.

Typically, layers are supplied by the user and are assumed known and constant. `SPM` defines the following types of layer;

1. Numeric layers: A model may have many numeric layers, and these can be used as covariates of a population or movement process (e.g., depth may be a covariate of some movement process), and/or locations of event mortality. Numeric layers can contain only continuous (numeric) variables. Values for a numeric layer must be supplied for each cell by the user.

2. Categorical layers: A model may have many categorical layers, and these are used as a classification or grouping variable for aggregating data over individual cells, e.g., management areas. Such layers are typically used to aggregate the population within cells into groups for comparing with observations. The values in layers used as categorical layers can contain any characters (except white space), and are interpreted as categorical values. Values for a categorical layer must be supplied for each cell by the user.
3. Distance layers: A distance layer is one that defines the distance between any two cells. By default, `SPM` calculates the values of the distance layer as the Euclidean distance (where the grid type is `square`). Here, the distance between cell a and cell b can be defined as,

   $$d(a,b) = \lambda\sqrt{(x_a - x_b)^2 + (y_a - y_b)^2} \tag{4.1}$$

   where x and y represent the x- and y-coordinates of a and b respectively, and λ is an arbitrary scaler representing the length of one side of the square. Unlike other types of layers, distance layers are not a $n_{rows} \times n_{cols}$ grid of values, but rather a matrix of dimension $(n_{rows} \times n_{cols}) \times (n_{rows} \times n_{cols})$ where the distance between each cell and every other cell is evaluated. Note that under this definition, the distance between any cell and itself is 0.
4. Abundance layers: The abundance layer is the sum of the number of individuals within cell a in categories k and with selectivity S_l at age l.

   $$N(a) = \sum_k \sum_l S_l \text{ element}(i,j,k,l) \tag{4.2}$$

   `SPM` calculates the values of the layer when running the model at the point in time where the value is required.
5. Biomass layers: The biomass layer is the sum of the biomass of individuals within cell a in categories k, with selectivity S_l at age l, and mean weight w_{kl}

   $$N(a) = \sum_k \sum_l w_{k,l} S_l \text{ element}(i,j,k,l) \tag{4.3}$$

   `SPM` calculates the values of the layer when running the model at the point in time where the value is required.
6. Abundance-density layers: The abundance density layer is the density of the number of individuals within cell a with area A_a in categories k, with selectivity S_l at age l,

   $$N(a) = \frac{1}{A_a} \sum_k \sum_l S_l \text{ element}(i,j,k,l) \tag{4.4}$$

   `SPM` calculates the values of the layer when running the model at the point in time where the value is required.
7. Biomass-density layers: The biomass-density layer is the density of the biomass of individuals within cell a with area A_a in categories k, with selectivity S_l at age l, and mean weight w_{kl},

   $$N(a) = \frac{1}{A_a} \sum_k \sum_l w_{k,l} S_l \text{ element}(i,j,k,l) \tag{4.5}$$

   `SPM` calculates the values of the layer when running the model at the point in time where the value is required.

8. Meta-layers: In addition to the above types of layer, `SPM` defines a special type of layer known as a *meta-layer*. The meta-layer allows individual layers (of the same type) to be indexed by year, and applied as a single layer within the model. For example, assume that we had a model where we wished to use Sea Surface Temperature (SST) as a layer, perhaps to control some movement process. The SST values for each year of the model would be defined as individual numeric layers, each with a unique label. We could then define a meta-layer that indexed the individual annual SST layers by year, and use the meta-layer as the control layer in the movement process.

However, there are exceptions to this rule — layers of type biomass, quantity, and distance are calculated automatically by `SPM` as required. For example, for the distance layer in a square grid, the distance between cell a and cell b is defined as proportional to $\sqrt{(x_a - x_b)^2 + (y_a - y_b)^2}$, where x and y represent the x- and y-coordinates of a and b respectively.

For the abundance layer, the abundance or biomass of a cell is simply a count of the number (or biomass) of individuals in the cell a within categories K, with selectivity S, e.g., $N(a) = \sum_k \sum_i \text{element}(i, j, k, l)$.

Note that `SPM` does not ‘edit’ or otherwise change layers, including adding or otherwise combining layers that are supplied in the input parameter files.

4.5 Time sequences

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

- Initialisation
- Run years
- Projection years

4.5.1 Annual cycle

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

4.5.2 Model initialisation

`SPM` initialises the initial equilibrium state as an iterative process, because a general solution that initialises complex structured movement models can be difficult to implement using analytic techniques. However, initialising via iteration for a long-lived species with complex movements can also be slow to run. In `SPM`, we allow for user-defined multi-phased initialisation using iteration to allow the user to optimize models for speed. Each phase of the initialisation can involve any number of population and/or movement processes.

The initialisation part can consist of one or more phases, with each phase occurring for at least one year. Within each phase, the processes defined for that phase are carried out, and use as the starting point for the following phase, or if it is the last phase, then the years that the model is run over. The first phase is always initialised with each element (i.e., each age and category within each spatial cell) seeded with a zero. Note that this means that recruitment processes where the numbers of recruits is based on a stock recruitment or density dependant relationship will likely fail.

Hence, you need to define;

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

Model initialisation can occur in several phases, each which iterates through a number of years carrying out the population and/or spatial processes defined for that phase. Analytical initialisation is not implemented in `SPM`, hence equilibrium and initial population states must be evaluated iteratively. At the end of the initialisation, `SPM` runs through the model years carrying out processes in the order defined in the annual cycle, and can evaluate expected values of observations in order to calculate likelihoods, project forward to determine future states, or simulate observations from the current state.

4.5.3 Model years

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

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

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

4.5.4 Projections

To be added...

4.6 Processes

Processes produce changes in the model partition, by adding, removing or moving individuals between spatial cells (movement processes), and ages or categories (population processes). These include processes such as recruitment, mortality, ageing, and movements.

`SPM` has two types of processes, *population* and *movement* processes. Population processes are those processes which modify, move or otherwise change the numbers of individuals *within* a spatial cell, i.e., they do not affect the spatial location of a cohort. Movement processes, on the other hand, move, shift or otherwise modify cohorts *between* spatial cells, but do not affect the age or category of the numbers in each cohort.

The population processes include recruitment, ageing, mortality events (e.g., natural and exploitation) and category transition processes (i.e., processes that move individuals between categories, while preserving their age structure). See Section 4 for a complete list of available processes.

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

`SPM` implements three different types of movement processes;

1. A migration movement rate of cohorts between any two locations, and is roughly analogous to movements between areas as implemented in other population models, such as CASAL (Bull et al., 2008).
2. An adjacent cell movements, parametrised by some function of an underlying layer — equivalent to, for example, movement processes implemented in Fish Heaven (Ball and Constable, 2000, Ball and Williamson, 2003).
3. Movement parametrised as a probability density function. Here, the key underlying idea is that the spatial distribution of cohorts at any point in time and at any location can be represented as a density function based on attributes of that location, local abundance, and/or distance from their previous location (Bentley et al., 2004a,b).

An `SPM` model can be parametrised by both population processes (for example, ageing, recruitment, and mortality), and movement processes. Population processes are those processes which modify, move or otherwise change the numbers of individuals within a spatial cell, i.e., they do not affect the spatial location of a cohort. Movement processes, on the other hand, move, shift or otherwise modify cohorts between spatial cells, but do not affect the age or category of the numbers in each cohort.

4.7 Population processes

Population processes are those processes that change the population state of individuals, but retain their location.

4.7.1 Recruitment

Recruitment processes are defined as process that introduces new individuals into the model. `SPM` implements two types of recruitment process, constant recruitment and Beverton-Holt recruitment (Beverton and Holt, 1957).

In both of the recruitment process, a number of individuals are added to the partition at the age and categories specified. If more than one category is defined, then the proportions of individuals added across categories are user-defined. For example, if recruiting to categories labelled male and female, then you might set the proportions as 0.5 and 0.5 respectively to denote that half of the recruits recruit to the male category and the remaining half to the female category.

For each cell where $\text{cell}(i,j)$ is a member of some layer L_R, the number of fish added in year y is

$$\text{element}(i,j,k,l) \leftarrow \text{element}(i,j,k,l) + p_k(R_y/n) \tag{4.6}$$

where age is the age defined as the recruitment age, p_k is the proportion recruitment to category k defined to have recruitment, and n is the number of spatial locations where recruitment occurs.

In the constant recruitment process, R_y, the number of recruits in year y is simply the product of the average recruitment R_0 and the annual year class strength multiplier, YCS, i.e.,

$$R_y = R_0 \times YCS_{y-offset} \tag{4.7}$$

where $offset$ if the number of years offset to link the year class with the year of spawning.

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

$$R_y = R_0 \times YCS_{y-offset} \times SR(SSB_{y-offset}) \tag{4.8}$$

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

$$SR(SSB) = \frac{SSB}{B_0} / \left(1 - \frac{5h-1}{4h}\left(1 - \frac{SSB}{B_0}\right)\right) \tag{4.9}$$

Note that the Beverton-Holt recruitment process requires a value for SSB to resolve the stock-recruitment relationship. Here, a derived quantity (see Section 4.9) must be defined that provides the SSB for the recruitment process.

4.7.2 Ageing

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

$$\text{element}(i,j,k,l) \leftarrow \text{element}(i,j,k,l-1) \tag{4.10}$$

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

$$\text{element}(i,j,k,age_{max}) \leftarrow \text{element}(i,j,k,age_{max}) + \text{element}(i,j,k,age_{max-1}). \tag{4.11}$$

4.7.3 Mortality

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

Mortalities as rates can depend on a layer. Here only one method of dependence is implemented, the multiplicative method. The multiplicative natural mortality method defines that the value of instantaneous mortality applied to the population state within each cell is the product of the layer value, a selectivity-at-age, and the mortality rate.

For example, let the mortality rate applied to the population at cell a in category k and age l be denoted $M(a,k,l)$, and given a value from a layer L_a at a, a constant morality rate M, and a selectivity-at-age S_l at age l for some user-defined categories k then,

$$M(a,k,l) = ML_aS_l \tag{4.12}$$

And the resulting number of individuals remaining in cell a in category k at age l from applying the constant mortality process is,

$$n'(a,k,l) = n(a,k,l)\exp\left(-M(a,k,l)\right) \tag{4.13}$$

Mortality for the annual rate is similar, except that the rate applied in each year is defined as a separate value.

The event mortality types act in a similar manner, except that it removes a specified abundance (number of individuals) or biomass from the partition, rather than applying a mortality rate. However, the maximum abundance or biomass to remove is constrained by a maximum exploitation rate.

The event mortality types must be defined using a layer. Here, the abundance or biomass to remove from a the population for each cell a is the value of the layer at a (denoted F_a) — except where there are too few individuals for the event mortality to be taken (as defined by the maximum exploitation rate). In this scenario, `SPM` removes as many individuals or as much biomass as it can while not exceeding the maximum exploitation rate.

For example, the event 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 vulnerable abundance for each category k in $1 \ldots K$ for ages $l = 1 \ldots L$ that are subject to event mortality,

$$V(k,l) = S(l)N(k,l) \tag{4.14}$$

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

$$V_{Total} = \sum_K \sum_L V(k,l) \tag{4.15}$$

Hence the exploitation rate to apply is

$$U = \begin{cases} C/V_{total}, & \text{if } C/V_{total} \leq U_{max} \\ U_{max}, & \text{otherwise} \end{cases} \tag{4.16}$$

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

$$R(k,l) = UV(k,l) \tag{4.17}$$

Similarly, the biomass-event mortality type is applied as … **to be added**.

4.7.4 Category transitions

Category transition processes move individuals between categories. `SPM` implements two types, the total number and a rate.

The transition type moves a number n between a source and sink category. The transition process with selectivity S for source category a and sink category b is,

$$\begin{aligned}\text{element}(i,j,a,l) &\leftarrow \text{element}(i,j,a,l) - \frac{nS_l}{\sum\limits_l S_l} \times \text{element}(i,j,a,l)\\ \text{element}(i,j,b,l) &\leftarrow \text{element}(i,j,b,l) + \frac{nS_l}{\sum\limits_l S_l} \times \text{element}(i,j,a,l)\end{aligned} \tag{4.18}$$

The transition rate type moves a proportion p between a source and sink category. The transition rate process with selectivity S for source category a and sink category b is,

$$\begin{aligned}\text{element}(i,j,a,l) &\leftarrow \text{element}(i,j,a,l) - pS_l \times \text{element}(i,j,a,l)\\ \text{element}(i,j,b,l) &\leftarrow \text{element}(i,j,b,l) + pS_l \times \text{element}(i,j,a,l)\end{aligned} \tag{4.19}$$

4.8 Movement processes

Movement processes are those processes that move individuals between cells but retain the their population state, and are defined such that,

$$\text{element}(i,j,k,l) \leftarrow \text{element}(i,j,k,l) + p \times \text{element}(i',j',k,l) \tag{4.20}$$

i.e., each element in cell(i,j) is updated as the sum of itself and some proportion p of a neighbouring element in cell(i',j'). To conserve abundance we also update element(i',j',k,l) as,

$$\text{element}(i',j',k,l) \leftarrow \text{element}(i',j',k,l) - p \times \text{element}(i',j',k,l) \tag{4.21}$$

`SPM` assumes that each movement process occurs simultaneously over all cells (synchronous updating), i.e., all cell updates from each individual movement process are first evaluated for all cells, and then applied to all cells affected.

`SPM` implements three types of movement;

1. A migration movement rate of cohorts between any two locations, and is roughly analogous to movements between areas as implemented in other population models, such as CASAL (Bull et al., 2008).
2. An adjacent cell movements, parametrised by some function of an underlying layer — equivalent to, for example, movement processes implemented in Fish Heaven (Ball and Constable, 2000, Ball and Williamson, 2003).
3. Movement parametrised as a probability density function. Here, the key underlying idea is that the spatial distribution of cohorts at any point in time and at any location can be represented as a density function based on attributes of that location, local abundance, and/or distance from their previous location (Bentley et al., 2004a,b).

4.8.1 Migration movement

The migration process moves individuals from one location to another. A migration can involve one or more categories and movement at age is defined as some proportion multiplies by a selectivity. Migrations are limited in scope to move individuals from one cell to another, and are available to allow compatibility with limited space models such as CASAL Bull et al. (2008).

4.8.2 Adjacent cell movement

The adjacent cell movement simply moves a proportion of individuals to neighbouring cells. It can be applied to a limited range of spatial locations by associating it with a layer.

4.8.3 Preference movement

Preference movements allows movement from any $cell(a) \rightarrow cell(b)$, for $\forall a,b \in L_B$ and is implemented as a function of the product of up to n independent *preference functions*. We define the probability of moving from any cell a to any cell b, for all $a,b \in L_B$, as a function of the relative preference for that cell. Here, we use the term *preference function* (Bentley et al., 2004a,b) to describe the movement probability distributions. We assume that the population and spatial extent are defined, and that there is a preference function that is a function of some (typically estimable) parameters and a spatially explicit set of known attributes.The preference function movement process allows the number of parameters describing movement to to reduced, and results in a movement process that is some function of some underlying property of each location. For example, if we assume that movement between areas was a function of the Euclidean distance between areas, we could model movement between any two areas as a linear decay or exponential decay function (Bentley et al., 2004a). Alternately, if distribution and density were correlated with bathymetric depth for a marine organism, we might model the movement and distribution as a function of depth.

The total preference function

Movement in `SPM` can be defined as a probability distribution based on an underlying preference function. Here, we define the preference for a cell x as the preference function $f_x(\theta_x, P(x))$, where θ_x are the parameters for f_x. So, given a set of n attributes for cell x, we can define a preference function for each, and hence we define the aggregated or total preference function for any cell x as the weighted product of individual preference functions,

$$P_x = f_1(\theta_1, P_1(x))^{\alpha_1} + f_2(\theta_2, P_2(x))^{\alpha_2} + f_3(\theta_3, P_3(x))^{\alpha_3} + \cdots + f_n(\theta_n, P_n(x))^{\alpha_n} \tag{4.22}$$

where α_i is an arbitrary weighting factor for attribute i.

Then we define the probability of moving from cell a to any cell b (where b is defined as the set of all possible cells, including a),

$$p(a \rightarrow b) = \frac{P_a}{\sum\limits_{i \in \forall b} P_i} \tag{4.23}$$

Note that there are three forms of preference function,

1. Those that are a function of some underlying attribute of a cell, as defined by some arbitrary layer L
2. Those that are a function of the abundance (perhaps with a selectivity and for a subset of all categories) of each cell
3. Those that are a function of the distance between the sink and the source cells.

Preference functions of the first type are determined only by the parameters of the preference function and some underlying, fixed, attribute. Preference functions of the others are dynamic, i.e. they depend on the relative locations of the cells or on the density of a cell at a particular point in time.

Preference functions

Preference functions in `SPM` include constant, Normal, double-Normal, logistic, inverse-logistic, Exponential, and threshold. These are defined as,

1. The constant preference function has dependent variable x and has no parameters, and is defined as,
$$f(x) = x, \text{ where } 0 \leq x \leq 1 \tag{4.24}$$
2. The Normal preference function has dependent variable x and parameters $\theta = (\mu, \sigma)$, and is defined as,
$$f(x|\mu,\sigma) = 2^{-[(x-\mu)/\sigma]^2} \tag{4.25}$$
3. The double-Normal preference function has dependent variable x and parameters $\theta = (\mu, \sigma_L, \sigma_R)$, and is defined as,
$$f(x|\mu,\sigma_L,\sigma_R) = \begin{cases} 2^{-[(x-\mu)/\sigma_L]^2}, & \text{if } x \leq \mu \\ 2^{-[(x-\mu)/\sigma_R]^2}, & \text{if } x \geq \mu \end{cases} \tag{4.26}$$
4. The Logistic preference function has dependent variable x and parameters $\theta = (a_{50}, a_{to95})$, and is defined as,
$$f(x|a_{50},a_{to95}) = 1/[1+19^{(a_{50}-x)/a_{to95}}] \tag{4.27}$$
5. The inverse-Logistic preference function has dependent variable x and parameters $\theta = (a_{50}, a_{to95})$, and is defined as,
$$f(x|a_{50},a_{to95}) = 1-1/[1+19^{(a_{50}-x)/a_{to95}}] \tag{4.28}$$
6. The Exponential preference function has dependent variable x and parameters $\theta = (\lambda)$, and is defined as,
$$f(x|\lambda) = \exp(-\lambda x), \text{where } x \geq 0 \text{ and } 0 \text{ otherwise} \tag{4.29}$$
7. The threshold preference function has dependent variable x and parameters $\theta = (N, \lambda)$, and is defined as,
$$f(x|N,\lambda) = \begin{cases} 1, & \text{if } 0 \leq x \leq N \\ 1/\left(\frac{x}{N}^{\lambda}\right), & \text{if } x \geq N \\ 0, & \text{otherwise} \end{cases} \tag{4.30}$$

4.9 Derived quantities

Derived quantities are values, calculated by `SPM` as required, that have a single value for each year of the model. Derived quantities can be calculated as either an abundances or as a biomass. Derived quantities are simply the count or sum of cells within some categories, after applying a selectivity, within cells defined by a layer.

Some processes require, as arguments, a population value derived from the population state. These are termed *derived quantities*. For example, a recruitment process may require the amount of spawning stock biomass to resolve the stock-recruit relationship. In this example, the spawning stock biomass could be 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 described further in the population section (Section 4).

4.10 Size-at-age

This is used to determine length frequencies and hence biomass (using a size-weight relationship) of individuals at age/category. There are two alternative growth curves in `SPM`,

von Bertalanffy where size at age is defined as,

$$\bar{s}(age) = L_\infty \left(1 - \exp\left(-k\left(age - t_0\right)\right)\right) \tag{4.31}$$

Schnute where size at age is defined as,

$$\bar{s}(age) = \begin{cases} \left[y_1^b + (y_2^b - y_1^b)\dfrac{1-\exp\left(-a(age-\tau_1)\right)}{1-\exp\left(-a(\tau_2-\tau_1)\right)}\right]^{1/b}, & \text{if } a \neq 0 \text{ and } b \neq 0 \\ y_1 \exp\left[\ln\left(y_2/y_1\right)\dfrac{1-\exp\left(-a(age-\tau_1)\right)}{1-\exp\left(-a(\tau_2-\tau_1)\right)}\right], & \text{if } a \neq 0 \text{ and } b = 0 \\ \left[y_1^b + \left(y_2^b - y_1^b\right)\dfrac{age-\tau_1}{\tau_2-\tau_1}\right]^{1/b}, & \text{if } a = 0 \text{ and } b \neq 0 \\ y_1 \exp\left[\ln\left(y_2/y_1\right)\dfrac{age-\tau_1}{\tau_2-\tau_1}\right], & \text{if } a = 0 \text{ and } b = 0 \end{cases} \tag{4.32}$$

The von Bertalanffy curve is parameterised by L_∞, k, and t_0; the Schnute curve (Schnute, 1981) by y_1 and y_2, which are the mean sizes at reference ages τ_1 and τ_2, and a and b (when $b = 1$, this reduces to the von Bertalanffy with $k = a$).

The model can incorporate changes in size-at-age during the year (i.e., growth between fish birthdays) by specifying the growth proportions for each time step of the annual cycle.

4.11 Mean weight

The size-weight parameters a and b is calculated as either,

- None: A relationship where the weight of each individual is exactly 1
- Basic: The more usual size-weight relationship, where

$$\text{mean weight} = a(\text{mean size-at-age})^b \tag{4.33}$$

Be careful about the scale of a — this is easily specified incorrectly. If you provide your catch in tonnes, and your growth curve in centimetres, then a should be on the right scale to convert a length in centimetres to a weight in tonnes. Note that there is an option `@report[label].type=weight_at_size` (see Section 7.1.7) that can be used to help check that the units specified are plausible.

If you specify a distribution for the size-at-age relationship, then the mean weight at age is calculated over that distribution, using the following formula, which is exact for lognormal distributions, and a good approximation for a normal distribution (if the c.v. is not large),

$$\text{mean weight} = a \times (\text{mean size at age})^b \times \left(1 + \text{cv}^2\right)^{\frac{b(b-1)}{2}} \tag{4.34}$$

where cv is the c.v. of sizes-at-age.

4.12 Selectivities

A selectivity is a function with a different value for each age class (i.e., for each column of the partition). Selectivities are used throughout `SPM` to interpret observations (Section 5 or to modify the effects of processes on each age class 4. `SPM` implements a number of different parametric forms, including logistic, knife edge, and double normal selectivities. See Section 4.12 for more details.

A selectivity is a function with a different value for each age class (i.e., for each column of the partition). Selectivities are used frequently throughout the SPM population section: for selectivity curves. Selectivities have a number of different parametric forms (types) in SPM and you can use any of these for any selectivity parameter.

A selectivity is always defined to apply just to one category of the population (i.e, row of the partition). To apply the same selectivity to more than one category, the you need to specify the categories that it applied to.

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

Note that the function values for some choices of parameters for some selectivities can result in an computer numeric overflow error (i.e., the number calculated from parameter values is either too large or too small to be represented in computer memory). `SPM` implements range checks on some parameters to test for a possible numeric overflow error before attempting to calculate function values. For example, the logistic selectivity is implemented such that if $(a50-x)/ato_95 > 5$ then the value of the selectivity at $x = 0$, i.e., for $a50 = 5$, $ato_95 = 0.1$, then the value of the selectivity at $x = 1$, without range checking would be $7.1x10-52$. With range checking, that value is 0 (as $(a50x)/ato_95 = 40 > 5$).

The available selectivities are;

- Constant
- Knife-edge
- All values
- All values bounded
- Increasing
- Logistic
- Logistic-producing
- Double-normal
- Double-exponential

The available selectivities are described below.

4.12.1 `constant`

$$f(x) = C \tag{4.35}$$

The constant selectivity has the estimable parameter C.

4.12.2 `knife_edge`

$$f(x) = \begin{cases} 0, & \text{if } x < E \\ \alpha, & \text{if } x \geq E \end{cases} \tag{4.36}$$

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

4.12.3 `all_values`

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

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

4.12.4 `all_values_bounded`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ V_x, & \text{if } L \leq x \leq H \\ V_H, & \text{if } x > H \end{cases} \tag{4.38}$$

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

4.12.5 `increasing`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ f(x-1) + \pi_x(\alpha - f(x-1)), & \text{if } L \leq x \leq H \\ f(\alpha), & \text{if } x \geq H \end{cases} \tag{4.39}$$

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

4.12.6 `logistic`

$$f(x) = \alpha / [1 + 19^{(a_{50} - x)/a_{to95}}] \tag{4.40}$$

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

4.12.7 `logistic_producing`

$$f(x) = \begin{cases} 0, & \text{if } x < L \\ \lambda(L), & \text{if } x = L \\ (\lambda(x) - \lambda(x-1)) / (1 - \lambda(x-1)), & \text{if } L < x < H \\ 1, & \text{if } x \geq H \end{cases} \tag{4.41}$$

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

4.12.8 `double_normal`

$$f(x) = \begin{cases} \alpha 2^{-[(x-\mu)/\sigma_L]^2}, & \text{if } x \leq \mu \\ \alpha 2^{-[(x-\mu)/\sigma_R]^2}, & \text{if } x \geq \mu \end{cases} \tag{4.42}$$

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

4.12.9 `double_exponential`

$$f(x) = \begin{cases} y_0 (y_1/y_0)^{(x-x_0)/(x_1-x_0)}, & \text{if } x \leq x_0 \\ y_0 (y_2/y_0)^{(x-x_0)/(x_2-x_0)}, & \text{if } x > x_0 \end{cases} \tag{4.43}$$

The double-exponential selectivity has non-estimable parameters x_1 and x_2, and estimable parameters x_0, y_0, y_1, and y_2. It can be ‘U-shaped’. Bounds for x_0 must be such that $x_1 < x_0 < x_2$. 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).

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 `SPM`:

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

The estimation section defines The objective function is based on a goodness-of-fit measure of the model to observations, priors and penalties. The observation section describes the objective function, observations, priors and penalties.

5.2 The objective function

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

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

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

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

You will usually want to use penalties to ensure that the exploitation rate constraints on your fisheries are not breached (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), and possibly penalties to encourage estimated values to be similar, smoothed, etc.

5.3 Specifying the parameters to be estimated

You need to tell SPM which of the estimable parameters are to be estimated by using `@estimate` commands (see Section 9). An `@estimate` command-block looks like,

```
@estimate process[MyRecruitment].r0
lower_bound 1000
```

```
upper_bound 100000
prior uniform
```

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

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

5.4 Point estimation

Point estimation is invoked with `spm -e`. Mathematically, it is an attempt to find a minimum of the objective function. SPM has two algorithms for solving (minimising) optimisation problem. The first uses a quasi-Newton minimiser built which is a slightly modified implementation of the main algorithm of Dennis Jr. & Schnabel (Dennis Jr and Schnabel, 1996), while the second uses a genetic algorithm developed by Storn & Price (Storn and Price, 1995).

The minimiser has three kinds of (non-error) exit status:

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

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

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

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

- the Hessian approximation develops over many minimiser steps, so if the minimiser has only run for a small number of iterations the covariance matrix can be a very poor approximation

- the inverse Hessian is not a good approximation to the covariance matrix of the estimated parameters, and may not be useful to construct, for example, confidence intervals.

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

5.5 Posterior profiles

If profiles are requested `spm -p`, `SPM` 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, `SPM` will fix its value at a sequence of n evenly spaced numbers between specified bounds l and u, and calculate a point estimate at each value.

By default $n = 10$, and $(l,u) =$ (lower bound on parameter plus $(range/(2n))$, upper bound on parameter less $(range/(2n))$. Each minimisation starts at the final parameter values from the previous resulting value of the parameter being profiled. `SPM` will report the objective function for each parameter value and all the parameter estimates. The initial point estimate is also inserted into the profile (note that this can serve as a check that none of the other points along the profile have a better objective function value than the initial 'minimum').

You specify which parameters are to be profiled, and optionally n, l, and u values for each. In the case of vector parameters, you will also need to specify the element of the vector being profiled.

TODO: Check the following para

You can also supply the initial point estimate using `spm -i`, so that `SPM` doesn't need to do the first minimisation. Be aware that you are supplying the point estimate, not the minimiser starting point to get to the point estimate (as in other situations where `spm -i` is used).

TODO: Check the following para

If you have specified multi-phase estimation, it is only used for the initial point estimate. Subsequent minimisations are done single-phase, as they should start reasonably close to the endpoint and so shouldn't need multiple phases.

TODO: Check the following para for syntax

If you get an implausible profile, it may be a result of not using enough iterations in the minimiser (in this case, increase `@minimiser.max_iterations` and/or `@minimiser.max_evaluations` and retry), or the convergence criteria may not be strong enough (try setting `@minimiser.gradient_tolerAnce` to a smaller value).

5.6 Bayesian estimation

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

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

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

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

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

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

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

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

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

- Start from the point estimate.
- Start from a random point near the point estimate (the point is generated from a multivariate normal distribution, centred on the point estimate, with covariance equal to the inverse Hessian times a user-specified constant). This is done to prevent the chain from getting 'stuck' at the point estimate.)
- Start from a point specified by the user with `spm -i`.

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

- The covariance matrix is taken as the inverse of the approximate Hessian from the quasi-Newton minimiser.
- The covariance matrix is modified so as to decrease all correlations greater than `@MCMC.max_correlation` down to `@MCMC.max_correlation`, and similarly to increase all correlations less than -`@MCMC.max_correlation` up to -`@MCMC.max_correlation` (the `@MCMC.max_correlation` parameter defaults to 0.8). This should help to avoid getting 'stuck' in a lower-dimensional subspace.
- The covariance matrix is then modified either by,

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

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

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

  This allows each estimated parameter to move in the MCMC even if its variance is very small according to the inverse Hessian. In both cases, the `@MCMC.min_diff` parameter defaults to 0.0001.

- The `@MCMC.step_size` (a scalar factor applied to the covariance matrix to improve the acceptance probability) is chosen by the user. The default is $2.4d^{-0.5}$ where d is the number of estimated parameters, as recommended by Gelman et al. (Gelman et al., 1995), though some experimentation suggested that this may be too high and can lead to a low acceptance rate.

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 (`SPM` enforces this). The adaptive mechanisms are as follows:

1. You can request that the step size change adaptively at one or more sample numbers. At each adaptation, the step size is doubled if the acceptance rate since the last adaptation is more than 0.5, or halved if the acceptance rate is less than 0.2. (See Gelman et al. 1995 for justification.) The new step size is recorded in the objectives file.

2. You can request that the entire covariance matrix change adaptively at one or more sample numbers. At each adaptation, it is replaced with a matrix based on the sample covariance of an earlier section of the chain. The theory here is that the covariance of a portion of chain could potentially be a better estimate of the covariance of the posterior distribution than the inverse Hessian.

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

The variance-covariance matrix of this sub-sample of chain is calculated. As above, correlations greater than `@MCMC.MaxCor` are reduced to `@MCMC.MaxCor`, correlations less than `@MCMC.MaxCor` are increased to `@MCMC.MaxCor`, and very small non-zero variances are increased (`@MCMC.CovarianceAdjustment` and `@MCMC.MinDiff`. The result is the new variance-covariance matrix of the proposal distribution.

The step size parameter is now on a completely different scale, and must also be reset. It is set to a user-specified value (which may or may not be the same as the initial step size). We recommend that some of the step size adaptations are set to occur after this, so that the step size 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 probability of acceptance for each jump is 0 if it would move out of the bounds, or 1 if it improves the posterior, or (new posterior/old posterior) otherwise.

You can specify how often the position of the chain is recorded using the keep parameter. For example, with keep 10, only every 10th sample is written to file.

You have the option to specify that some of the estimated parameters are fixed during MCMC. If the chain starts at the point estimate or at a random location, these fixed parameters are set to their values at the point estimate. If you specify the start of the chain using `spm -i`, these fixed parameters are set to the values in the file.

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

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

The posterior sample can also be used for projections (Section XXX) or simulations (Section XXX), allowing the parameter uncertainty, as expressed in the posterior distribution, can be included into the risk or other output estimates.

5.7 Priors

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

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

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

1. Uniform

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

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

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

3. Normal with mean μ and c.v. c

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

4. Normal with mean μ and standard deviation σ

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

5. Lognormal with mean μ and c.v. c

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

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

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

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

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

5.8 Penalties

TODO

6 The observation section

6.1 Observations and likelihoods

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

`SPM` allows the following types of observations;

Observations of proportions by age class within categories

Observations of proportions between categories within age classes

Relative and absolute abundance/biomass observations

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

6.2 Proportions-at-age observations

Proportions-at-age observations are observations of either the relative number of individuals at age or relative biomass at age.

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

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

Proportions-at-age observations can be supplied for a single category, aggregated across categories, or be proportions of multiple categories. For example, for a model with the two categories *male* and *female*, we might supply either (i) observations of the proportions of males (or alternately female) within each age class; (ii) proportions of total individuals (males + females) at each age class, or (iii) the proportions of individuals for both male and female categories simultaneously. In addition, each category must have an associated selectivity, defined by `selectivities`.

The way the categories of the observation are defined specifies which of these alternatives to use. For example, to specify that the observations are of the proportions of male within each age class (example (i) above), then the subcommand `categories` for the `@observation[label].type=proportion_by_age` command is,

```
categories male
```

`SPM` then expects that there will be a vector of proportions supplied, with one proportion for each age class within the defined age range. 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 applying a selectivity at the year and time step specified. Note that the supplied vector of proportions (i.e., in this example, the 8 proportions) must sum to one (with a default tolerance of 0.001).

By default, categories are aggregated. For example, to specify that the observations are of the proportions of total individuals (males + females) at each age class (example (ii) above), then the subcommand `categories` is,

```
categories male female
```

`SPM` then expects that there will be a vector of proportions supplied, with one proportion for each age class within the defined age range. For example, if the age range was 3 to 10, then 8 proportions should be supplied. The expected values will be the expected proportions of selected males plus selected females within each of these age classes, at the year and time step specified. Note that the supplied vector of proportions (i.e., in this example, the 8 proportions) must sum to one (with a default tolerance of 0.001).

Otherwise, to provide proportions for multiple categories simultaneously, you need to spe3cify which categories are aggregated and which are separate. `SPM` uses a : symbol to denote those categories to are separate. For example, to specify that the observations are of the the proportions of individuals for both male and female simultaneously at each age class (example (iii) above), then the subcommand `categories` is,

```
categories male : female
```

`SPM` then expects that there will be a vector of proportions supplied, with one proportion for each age class within the defined age range for males and then females. For example, if the age range was 3 to 10, then 16 proportions should be supplied, the first set of 8 corresponding to the proportions of male (out of male and female combined) and the second 8 to female. The expected values will be the expected proportions of selected males and selected females within each of these age classes, at the year and time step specified. Note that the supplied vector of proportions (i.e., in this example, the 16 proportions) must sum to one (with a default tolerance of 0.001).

The definition of categories can be a combination of the above cases and can become more complex as the number of categories in the model increases. For example, in a model with categories male-immature, male-mature, female-immature, and female-mature, we might supply observations of males (immature and mature combined) and females (immature and mature combined) simultaneously. Here the `categories` subcommand would be;

```
categories male-immature male-mature : female-immature female-mature
```

Assuming that we wanted to supply observations for ages 3 to 10, then `SPM` would expect a vector of 16 proportions for each spatial location — the first eight corresponding to the observed proportions of males aged 3–10, and the second set of eight corresponding to the proportions of females aged 3–10. Further, the proportions would sum to one.

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

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

```
@layer Area
```

```
type categorical
data A A
data B B
```

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

```
@observation MyProportions
...
categories male female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20 0.01 0.05 0.15 0.20 0.03
...
```

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

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

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

`SPM` always evaluates the observations at the end of a time step (i.e., after `SPM` has applied all of the processes for that time step). However, the observation can be applied to the abundance at the start of a time step or part-way through a time step by the use of the `proportion_time_step` subcommand. Here `SPM` stores the state of the partition at the beginning of a time step, and again at the end of the time step. The partition at some point p during the time step is then evaluated as the weighted sum between the start and end of the time step, i.e, for any element i in the partition, $n_i = (1-p)n_i^{start} + pn_i^{end}$.

6.2.1 Likelihoods for proportions-at-age observations

`SPM` implements only one likelihood for proportions-at-age observations, 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 log-likelihood is defined as;

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

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

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

The default value of δ is 1×10^{-11}.

6.3 Proportions-by-category

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

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

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

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

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

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

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

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

```
@layer Area
```

```
type categorical
data A A
data B B
```

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

```
@observation MyProportions
...
categories male
categories2 female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20 0.01 0.05 0.15 0.20 0.03
...
```

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

```
@observation MyProportions
...
categories male
categories2 female
min_age 1
max_age 5
obs A 0.01 0.05 0.10 0.20 0.20 0.01 0.05 0.15 0.20 0.03
obs B 0.02 0.06 0.10 0.21 0.18 0.02 0.05 0.15 0.20 0.01
...
```

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

`SPM` always evaluates the observations at the end of a time step (i.e., after `SPM` has applied all of the processes for that time step). However, the observation can be applied to the abundance at the start of a time step or part-way through a time step by the use of the `proportion_time_step` subcommand. Here `SPM` stores the state of the partition at the beginning of a time step, and again at the end of the time step. The partition at some point p during the time step is then evaluated as the weighted sum between the start and end of the time step, i.e, for any element i in the partition, $n_i = (1-p)n_i^{start} + pn_i^{end}$.

6.3.1 Likelihoods for proportions-by-category observations

`SPM` implements only one likelihood for proportions-by-category observations, the binomial likelihood.

$$\begin{aligned}-\log(L) = -\sum_i & \log(N_i!) - \log((N_i(1-O_i))!) - \log((N_iO_i)!) + N_iO_i\log(Z(E_i,\delta)) \\ & + N_i(1-O_i)\log(Z(1-E_i,\delta))\end{aligned} \tag{6.3}$$

where O_i are the observed proportions for age class i, E_i are the expected proportions for age class i, and N_i is the effective sample size for age class i.

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

$$Z(\theta,\delta) = \begin{cases} \theta, & \text{where } \theta \geq r \\ \delta/(2-\theta/\delta), & \text{otherwise} \end{cases} \tag{6.4}$$

The default value of δ is 1×10^{-11}.

6.4 Abundance

Abundance observations are observations of either a relative or absolute number of individuals from a set of categories after applying a 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. Further, you need to provide the label of the catchability coefficient q, which can either be estimated of fixed. For absolute abundance observations, define a catchability where $q = 1$.

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

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

defines an observation of the abundance of males. `SPM` then expects that there will be a single abundance value supplied. The expected values will be the expected number of males, after applying the selectivities, at the year and time step specified.

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

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

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

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

```
@observation MyAbundance
...
categories male
obs A 1000
...
```

Or, for both A and B as,

```
@observation MyProportions
...
categories male
obs A 1000
obs B 1200
...
```

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

`SPM` always evaluates the observations at the end of a time step (i.e., after `SPM` has applied all of the processes for that time step). However, the observation can be applied to the abundance at the start of a time step or part-way through a time step by the use of the `proportion_time_step` subcommand. Here `SPM` stores the state of the partition at the beginning of a time step, and again at the end of the time step. The partition at some point p during the time step is then evaluated as the weighted sum between the start and end of the time step, i.e, for any element i in the partition, $n_i = (1-p)n_i^{start} + pn_i^{end}$.

6.4.1 Likelihoods for abundance observations

The lognormal likelihood with observations O_i, c.v. c_i, and expected values qE_i, and was,

$$-\log(L) = \sum_i \left(\log(\sigma_i) + 0.5 \left(\frac{\log(O_i/qZ(E_i,\delta))}{\sigma_i} + 0.5\sigma_i \right)^2 \right) \tag{6.5}$$

where

$$\sigma_i = \sqrt{\log\left(1+c_i^2\right)} \tag{6.6}$$

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

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

The default value of δ is 1×10^{-11}.

6.5 Process error

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

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

$$c_i' = \sqrt{c_i^2 + c_{process\_error}^2} \tag{6.8}$$

Similarly, if the likelihood is parameterised by the standard deviation *sigma*,

$$\sigma_i' = \sqrt{\sigma_i^2 + \sigma_{process\_error}^2} \tag{6.9}$$

or by the effective sample size N,

$$N_i' = \frac{1}{1/N_i + 1/N_{process\_error}} \tag{6.10}$$

In all three cases, the process error has more effect on small errors than on large ones. Be clear that a large value for the multinomial process error means a small process error.

6.6 Simulating observations

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

`SPM` generates simulated observations for the observations defined in the input configuration file with `@observation[label].simulate=True`.

First, the model is run using the 'true' parameter values, and a set of fits is produced for each set of observations. If a set of observations uses ageing error, then ageing error is applied to the fits as usual. If there are relative observations, then the catchability coefficient q is applied to the fits as per normal.

Second, each set of observations is randomised, based on (i) the fitted values, (ii) the type of likelihood specified, and (iii) the variability parameters (e.g., `error_value` and `process_error`).

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

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

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

6.7 Pseudo-observations

`SPM` can generate expected values for observations where there is no observed value. These are called pseudo-observations, and can be use to either generate the expected values from `SPM` or as ‘observations’ to be simulated from when using `SPM` as an operating model.

All of the observation types in `SPM` can be used as pseudo-observations. The observation command is `@pseudo-observation`, and the subcommands are then the same as for observations except that;

- Do not provide observed values —these are not required to generate expected values of to simulate observations. Note that if you do provide observed values, `SPM` will ignore them.
- The subcommands `likelihood`, `error_value` and `process_error` will be ignored when generating the expected values for the pseudo-observation. However, if simulating (`spm -s`) then the subcommands `likelihood` and `error_value` are required. In this case, `SPM` needs to know the likelihood and error value to simulate observations. In addition, if the subcommand `process_error` is supplied, `SPM` will modify the the error value (`error_value`) as usual, before generating the simulated observation.

7 The report section

The report section specifies the printouts and other outputs from the model.

7.1 Reporting model outputs

7.1.1 Printing the partition

7.1.2 Printing derived quantities

7.1.3 Printing the objective function

7.1.4 Printing observations, fits, and residuals

7.1.5 Printing layers

7.1.6 Printing selectivities

7.1.7 Verifying the size-weight relationship

7.1.8 Reporting processes

8 Population command and subcommand syntax

8.1 Model structure

`@model` Define the spatial structure, population structure, annual cycle, and model years

`nrows` The number of rows n_{rows} in the spatial structure
Type: Integer
Default: None
Value: A positive integer, $n_{rows} > 0$

`ncols` The number of columns n_{cols} in the spatial structure
Type: Integer
Default: None
Value: A positive integer, $n_{cols} > 0$

`layer` The label for the base layer
Type: String
Default: None
Value: Must be a label of a `numeric` layer defined by `@layer`

`categories` Labels of the categories (rows) of the population component of the partition
Type: Vector of strings, of length $1 \ldots n_{categories}$
Default: None
Value: Names of categories must be unique

`min_age` Minimum age of the population
Type: Integer
Default: None
Value: A non-negative integer, $age_{min} \geq 0$ and $age_{min} \leq age_{max}$

`max_age` Maximum age of the population
Type: Integer
Default: None
Value: A non-negative integer, $age_{max} \geq 0$ and $age_{min} \geq age_{min}$

`age_plus_group` Define the largest age as a plus group
Type: Switch
Default: True
Value: Defines the largest age as a plus group

`cell_length` The length (distance) of one side of a cell
Type: Constant
Default: 1
Value: A positive real number

`size_at_age` Define the label of the associated size-at-age relationship for each category

Type: Vector of strings, of length $1 \ldots n_{categories}$
Default: None
Value: Label names must be unique

`initialisation_phases` Define the labels of the phases of the initialisation
Type: Vector of strings, of length of the number of initialisation phases
Default: None
Value: A valid label defined by `@initialisation_phase`

`initial_year` Define the first year of the model, immediately following initialisation
Type: Integer
Default: None
Value: Defines the first year of the model, ≥ 1, e.g. 1990

`current_year` Define the current year of the model
Type: Integer
Default: None
Value: Defines the current year of the model, i.e., the model is run from `@model..first_year` to `@model.current_year`

`final_year` Define the final year of the model in projections
Type: Integer
Default: None
Value: Defines the final year of the model for use in projections, i.e., the model is run from `@model.first_year` to `@model.current_year`, then projected to `@model.final_year`

`time_steps` Define the `@time_step` labels (in order that they are applied) to form the annual cycle
Type: String vector
Default: None
Value: Defines the labels of the time steps that are run in each year

8.2 Initialisation

The methods for initialisation available are,

- Iterative

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

`@initialisation_phase` *`label`* Define the processes and years of the initialisation phase with label

`type` Define the type of initialisation
Type: String
Default: None
Value: A valid type of initialisation

8.2.1 `@initialisation_phase[label].type=iterative`

`years` Define the number of years to run
Type: Integer
Default: None
Value: A non-negative integer

`processes` Define the processes (in order of occurrence) to run in each year of the initialisation
Type: String vector
Default: None
Value: A valid process label, from one of `@process`

8.3 Time steps

`@time_step` *`label`* Define a time step with label

`processes` Define the process labels, in the order that they are applied, for the time step
Type: String vector
Default: None
Value: Defines the labels of the processes for that time step

8.4 Processes

The population processes available are,

- Constant recruitment process
- Beverton-Holt stock-recruit relationship recruitment process
- Ageing process
- Constant mortality rate process
- Annually varying mortality rate process
- Mortality event (as a number) process
- Mortality event (as a biomass) process
- Category transition process
- Category shift process

The movement processes available are,

- Migration movement
- Adjacent cell movement
- Preference movement

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

`@process` *`label`* Define a process with label

`type` Define the type of process
Type: String
Default: None
Value: A valid type of process

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

`r0` Define the total amount of recruitment at equilibrium abundance levels
Type: Estimable
Default: None
Value: Total amount (in numbers) of recruitment applied across all categories at equilibrium abundances

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`proportions` Define the proportion of recruitment that occurs into each category
Type: Estimable vector of length `categories`
Default: None
Value: Proportion of the annual recruitment that is applied to each category

`ages` Define the ages within each category that receive recruitment
Type: Integer vector
Default: None
Value: The age classes that receive recruitment

`layer` Name of the layer used to determine where recruitment occurs
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then recruitment is in proportion to the layer values. Note that the layer values must be non-negative

8.4.2 `@process[label].type=BH_recruitment`

`r0` Define the total amount of recruitment at equilibrium abundance levels
Type: Estimable
Default: None
Value: Total amount (in numbers) of recruitment applied across all categories at equilibrium abundances

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`proportions` Define the proportion of recruitment that occurs into each category
Type: Estimable vector of length `@process[label].categories`
Default: None
Value: Proportion of the annual recruitment that is applied to each category

`ages` Define the age within each category that receive recruitment
Type: Integer vector
Default: None
Value: The age classes that receive recruitment

`steepness` Define the Beverton-Holt stock recruitment relationship steepness (h) parameter
Type: Estimable
Default: None
Value: Steepness value between 0.2 and 1.0

`sigma_r` Define the recruitment variability σ_R in the stock-recruitment relationship for projections
Type: Estimable
Default: None

`rho` Define the autocorrelation ρ in the recruitment variability in the stock-recruitment relationship for projections
Type: Estimable
Default: None

`SSB` Define the label of the `@derived_quantity` that defines the SSB
Type: String
Default: None
Value: Must be a valid `@derived_quantity` label

`SSB_offset` Define the offset (in years) for the year of the derived quantity that is to be applied as the SSB in the stock-recruit relationship
Type: Integer
Default: None
Value: Must be a value $ge0$

`YCS_values` YCS values
Type: Estimable vector
Default: None
Value: Must be vector
Note: Special values can be used here, i.e., mean, all

`YCS_years` Years for year class strength values
Type: Integer vector
Default: None
Value: Must be vector of length `YCS_values`
Note: Special year ranges (YYYY-YYYY) can be used

`standardise_YCS_year_range` Years for which the year class strength values are defined to have mean 1.0
Type: Integer vector of length 2
Default: None
Value: Must be vector of length 2, with values of years between `@model.initial` to `@model.current`

`layer` Name of the layer used to determine where recruitment occurs
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then recruitment is in proportion to the layer values.

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

`categories` Define the categories that ageing is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

8.4.4 `@process[label].type=constant_mortality_rate`

`m` Define the constant mortality rate to be applied
Type: Estimable
Default: None
Value: A real number ≥ 0 and ≤ 1

`categories` Define the categories that mortality is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then mortality applied is the mortality rate times the value of the layer. Note that the layer values must be non-negative

8.4.5 `@process[label].type=annual_mortality_rate`

`years` Define the years when the mortality rates are applied
Type: Constant vector
Default: None
Value: Valid model years

`m` Define the mortality rate to be applied for each year
Type: Estimable vector
Default: None
Value: A real number ≥ 0 and ≤ 1

`categories` Define the categories that mortality is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then mortality applied is the mortality rate times the value of the layer. Note that the layer values must be non-negative

8.4.6 `@process[label].type=event_mortality`

`categories` Define the categories that the event mortality is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`years` Define the years where the mortality even is applied
Type: Integer vector
Default: None
Value: Valid years for the model

`layers` Define the layers that specify the event mortality (as the abundance) in each year
Type: String vector, of length years
Default: None
Value: Valid layers defined by `@layer`. Note that the layer values must be non-negative

`U_max` Define the maximum exploitation rate

Type: Estimable
Default: None
Value: Must be ≥ 0 and ≤ 1

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`penalty` Define the event mortality penalty label
Type: String
Default: None
Value: Valid penalty label defined by `@penalty`

8.4.7 `@process[label].type=biomass_event_mortality`

`categories` Define the categories that the event mortality is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`size_at_age` Define the age-weight relationships for each of the categories that the event mortality is applied to
Type: String vector
Default: None
Value: Valid labels from `@size_at_age`

`years` Define the years where the mortality event is applied
Type: Integer vector
Default: None
Value: Valid years for the model

`layers` Define the layers that specify the event mortality (as a biomass) in each year
Type: String vector, of length years
Default: None
Value: Valid layers defined by `@layer`. Note that the layer values must be non-negative

`U_max` Define the maximum exploitation rate
Type: Constant
Default: None
Value: Must be ≥ 0 and ≤ 1

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`penalty` Define the event mortality penalty label
Type: String
Default: None
Value: Valid penalty label defined by `@penalty`

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

`from` Define the categories that are the source of the transition process
Type: String vector
Default: None
Value: A valid list of categories from `@model.categories`

`selectivities` Define the selectivities applied to the source categories
Type: String vector
Default: None
Value: A valid list of selectivity labels defined by `@selectivity`

`to` Define the categories that are the sink of the transition process
Type: String vector
Default: None
Value: A valid list of categories from `@model.categories`

`years` Define the years where the category transition is applied
Type: Integer vector
Default: None
Value: Valid years for the model

`layers` Define the layers that specify the event mortality (as N for each cell) in each year
Type: String vector
Default: None
Value: Valid layers defined by `@layer`. Note that the layer values must be non-negative

`penalty` Define the penalty to encourage models parameter values away from those which result in not enough individuals to move
Type: String
Default: None
Value: Valid penalty label defined by `@penalty`

8.4.9 `@process[label].type=category_transition_rate`

`from` Define the category that is the source of the transition process
Type: String
Default: None
Value: A valid category from `@model.categories`

`selectivities` Define the selectivities applied to the source categories
Type: String vector
Default: None
Value: A valid list of selectivity labels defined by `@selectivity`

`to` Define the category that is the sink of the transition process
Type: String
Default: None
Value: A valid category from `@model.categories`

`proportion` Define the proportion of individuals to move
Type: Estimable
Default: None
Value: A value ≥ 0 and ≤ 1

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then rate applied to each cell is multiplied by the value of the layer. Note that the layer values must be non-negative

8.4.10 `@process[label].type=migration_movement`

`categories` Define the categories that the migration movement event is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`source_layer` Define the label of a layer that defines the source cells of the migration movement event
Type: String
Default: None
Value: A valid layer defined by `@layer`

`sink_layer` Define the label of a layer that defines the sink cells of the migration movement event
Type: String
Default: None
Value: A valid layer defined by `@layer`

`proportions` Define the constant multiplier for the proportions that migrate
Type: Estimable
Default: 1.0
Value: A real number between 0 and 1, inclusive

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then rate applied to each cell is multiplied by the value of the layer.

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

8.4.11 @process[label].type=adjacent_cell_movement

Not yet implemented. No subcommands have been defined.

8.4.12 @process[label].type=preference

`categories` Define the categories that the preference function movement is applied to
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`preference_functions` Define the labels of the individual preference functions that make up the total preference function
Type: String vector
Default: None
Value: Valid preference function labels defined by `@preference_function`

8.5 Preference functions

The individual preference functions available are,

- Constant
- Normal
- Double-normal
- Logistic
- Inverse logistic
- Exponential
- Threshold
- Threshold-biomass

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

@preference_function *label* Define a preference function with label

`type` Define the type of preference function
Type: String
Default: None
Value: A valid type of preference function

8.5.1 @preference_function[label].type=constant

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

8.5.2 @preference_function[label].type=normal

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

`mu` Defines the μ parameter of the normal preference function
Type: Estimable
Default: None

`sigma` Defines the σ parameter of the normal preference function
Type: Estimable
Default: None

8.5.3 @preference_function[label].type=double_normal

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

`mu` Defines the μ parameter of the double-normal preference function
Type: Estimable
Default: None

`sigma_l` Defines the σ_L parameter of the double-normal preference function
Type: Estimable
Default: None

`sigma_r` Defines the σ_R parameter of the double-normal preference function
Type: Estimable
Default: None

8.5.4 `@preference_function[label].type=logistic`

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

`a50` Defines the a_{50} parameter of the logistic preference function
Type: Estimable
Default: None

`ato95` Defines the a_{to95} parameter of the logistic preference function
Type: Estimable
Default: None

8.5.5 `@preference_function[label].type=inverse_logistic`

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α

Type: Estimable
Default: None

`a50` Defines the a_{50} parameter of the inverse-logistic preference function
Type: Estimable
Default: None

`ato95` Defines the a_{to95} parameter of the inverse-logistic preference function
Type: Estimable
Default: None

8.5.6 `@preference_function[label].type=exponential`

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

`lambda` Defines the λ parameter of the exponential preference function
Type: Estimable
Default: None

8.5.7 `@preference_function[label].type=threshold`

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`categories` Define the categories are used to calculate the abundance
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`alpha` Defines the multiplicative constant α

Type: Estimable
Default: None

`n` Defines the *N* parameter of the threshold preference function
Type: Estimable
Default: None

`lambda` Defines the λ parameter of the threshold preference function
Type: Estimable
Default: None

8.5.8 `@preference_function[label].type=threshold_biomass`

`layer` Defines the layer which supplies the preference function independent variable
Type: String
Default: None
Value: A valid layer defined by `@layer`

`categories` Define the categories are used to calculate the biomass
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`size_at_age` Define the age-weight relationships for each of the categories that the biomass is calculated from
Type: String vector
Default: None
Value: Valid labels from `@size_at_age`

`alpha` Defines the multiplicative constant α
Type: Estimable
Default: None

`biomass` Defines the *B* biomass parameter of the threshold biomass preference function
Type: Estimable
Default: None

`lambda` Defines the λ parameter of the threshold biomass preference function
Type: Estimable
Default: None

8.6 Layers

The available layer types are,

- Numeric
- Categorical
- Distance
- Abundance
- Biomass
- Abundance-density
- Biomass-density
- Meta-layer

`@layer` *`label`* Define a layer function with label

`type` Define the type of layer
Type: String
Default: None
Value: A valid type of layer

8.6.1 `@layer[label].type=numeric`

`data` Define the values of the layer
Type: Constant vector, with total length `@model.ncols` × `@model.nrows`
Default: None
Value: A vector of values of length equal to the number of elements defined for the spatial structure

8.6.2 `@layer[label].type=categorical`

`data` Define the values of the layer
Type: Constant vector, with total length `@model.ncols` × `@model.nrows`
Default: None
Value: A vector of values of length equal to the number of elements defined for the spatial structure

8.6.3 `@layer[label].type=distance`

There are no other subcommands for `@layer[label].type=distance`.

8.6.4 `@layer[label].type=abundance`

`categories` Define the categories are used to calculate the abundance
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

8.6.5 `@layer[label].type=biomass`

`categories` Define the categories are used to calculate the biomass
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`size_at_age` Define the age-weight relationships for each of the categories that the biomass is calculated from
Type: String vector
Default: None
Value: Valid labels from `@size_at_age`

8.6.6 `@layer[label].type=abundance_density`

`categories` Define the categories are used to calculate the abundance
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

8.6.7 `@layer[label].type=biomass_density`

`categories` Define the categories are used to calculate the biomass
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`size_at_age` Define the age-weight relationships for each of the categories that the biomass is calculated from
Type: String vector
Default: None
Value: Valid labels from `@size_at_age`

8.6.8 `@layer[label].type=meta`

`years` Define the years
Type: Constant vector, with values for each year of the model
Default: None

`layers` Define the layer labels for each of the years
Type: String vector, with values for each `year` specified
Default: None
Condition: Listed layers cannot be `@layer[label].type=meta_layer`

`initialisation_layer` Define the layer label to use during the initialisation
Type: String
Default: None
Condition: Listed layers cannot be `@layer[label].type=meta`

8.7 Derived quantities

The individual types of derived quantities available are,

- Abundance
- Biomass

`@derived_quantity` *`label`* Define a derived quantity with label

`type` Define the type of derived quantity
Type: String
Default: None
Value: A valid type of derived quantity

8.7.1 @derived_quantity[label].type=abundance

`categories` Define the categories are used to calculate the derived quantity
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivity` Define the selectivities
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`time_step` Define the time step at the end of which, the derived quantity is calculated
Type: String
Default: None
Value: A valid time step label from `@time_step`

`time_step_proportion` Define the proportion of the time step through which the derived quantity has been calculated
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then value is the sum of the each cell is multiplied by the value of the layer.

8.7.2 @derived_quantity[label].type=biomass

`categories` Define the categories are used to calculate the derived quantity
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities
Type: String vector
Default: None
Value: Valid selectivity labels from `@selectivity`

`time_step` Define the time step at the end of which, the derived quantity is calculated
Type: String
Default: None
Value: A valid time step label from `@time_step`

`layer` Name of the layer
Type: String
Default: None
Value: A valid layer as defined by `@layer`. If a numeric layer, then value is the sum of the each cell biomass multiplied by the value of the layer.

8.8 Size-at-age

The individual types of size-at-age relationship available are,

- von Bertalanffy
- Schnute

`@size_at_age` *`label`* Define a size-at-age relationship with label

`type` Define the type of relationship
Type: String
Default: None
Value: A valid type of size-at-age relationship

8.8.1 `@size_at_age[label].type=von_Bertalanffy`

`Linf` Define the L_∞ parameter of the von Bertalanffy relationship
Type: Estimable
Default: None
Value: A positive real number

`k` Define the k parameter of the von Bertalanffy relationship
Type: Estimable
Default: None
Value: A positive real number

`t0` Define the t_0 parameter of the von Bertalanffy relationship
Type: Estimable
Default: None
Value: A real number

`distribution` Define the distribution of sizes-at-age around the mean

Type: String
Default: Normal
Value: Either normal or lognormal

`by_length` Specifies if the linear interpolation of c.v.s is a linear function of mean size or of age
Type: Logical
Default: True
Value: If true, the the c.v. is a function of length, else a function of age

`cv` Define the c.v. of the distribution of sizes-at-age around the mean
Type: Estimable
Default: None
Value: A positive real number

`growth_proportions` Define the proportion of the year for each time step for evaluating size
Type: Constant vector
Default: None
Value: A vector of values, ≤ 1 of length equal to the number of time steps

`size_weight` Define the label of the associated size-weight relationship
Type: String
Default: None
Value: A valid label from `@size_weight`

8.8.2 `@size_at_age[label].type=Schnute`

`y1` Define the y_1 parameter of the Schnute relationship
Type: Estimable
Default: None
Value: A positive real number

`y2` Define the y_2 parameter of the Schnute relationship
Type: Estimable
Default: None
Value: A positive real number

`tau1` Define the τ_1 parameter of the Schnute relationship
Type: Estimable
Default: None
Value: A real number

`tau2` Define the τ_2 parameter of the Schnute relationship
Type: String
Default: Normal
Value: Either normal or lognormal

`a` Define the *a* parameter of the Schnute relationship
Type: String
Default: Normal
Value: Either normal or lognormal

`b` Define the *b* parameter of the Schnute relationship
Type: String
Default: Normal
Value: Either normal or lognormal

`by_length` Specifies if the linear interpolation of c.v.s is a linear function of mean size or of age
Type: Logical
Default: True
Value: If true, the the c.v. is a function of length, else a function of age

`cv` Define the c.v. of the distribution of sizes-at-age around the mean
Type: Estimable
Default: None
Value: A positive real number

`growth_proportions` Define the proportion of the year for each time step for evaluating size
Type: Constant vector
Default: None
Value: A vector of values, ≤ 1 of length equal to the number of time steps

`size_weight` Define the label of the associated size-weight relationship
Type: String
Default: None
Value: A valid label from `@size_weight`

8.9 Size-weight

The individual types of size-weight relationship available are,

- None
- Basic

`@size_weight` *`label`* Define a size-weight relationship with label

`Type` Define the type of relationship
Type: String
Default: None
Value: A valid type of size-weight relationship

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

There are no other subcommands for `@size_weight[label].type=none`.

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

`a` Define the *a* parameter of the basic relationship
Type: Estimable
Default: None
Value: A positive real number

`b` Define the *b* parameter of the basic relationship
Type: Estimable
Default: None
Value: A positive real number

8.10 Selectivities

The individual selectivity functions available are,

- Constant
- Knife-edge
- All-values
- All-values-bounded
- Increasing
- Logistic
- Logistic-producing
- Double-normal
- Double-exponential

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

`@selectivity` *`label`* Define a selectivity function with label

`type` Define the type of selectivity function
Type: String
Default: None
Value: A valid type of selectivity function

8.10.1 `@selectivity[label].type=constant`

`c` Defines the *C* parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

8.10.2 `@selectivity[label].type=knife_edge`

`e` Defines the *E* parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

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

`v` Defines the *V* parameters (one for each age class) of the selectivity function
Type: Estimable vector
Default: None
Value: A vector of positive real numbers, of length equal to the number of age classes

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

`l` Defines the *L* parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number

`h` Defines the *H* parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number, must be greater than *L*

`v` Defines the *V* parameters (one for each age class from *L* to *H*) of the selectivity function
Type: Estimable vector
Default: None
Value: A vector of positive real numbers, of length equal to the number of age classes from *L* to *H*

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

`alpha` Defines the α parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`l` Defines the *L* parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number

`h` Defines the H parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number, must be greater than L

`v` Defines the V parameters (one for each age class from L to H) of the selectivity function
Type: Estimable vector
Default: None
Value: A vector of positive real numbers, of length equal to the number of age classes from L to H

8.10.6 `@selectivity[label].type=logistic`

`alpha` Defines the α parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`a50` Defines the a_{50} parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`ato95` Defines the a_{to95} parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

8.10.7 `@selectivity[label].type=logistic_producing`

`alpha` Defines the α parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`l` Defines the L parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number

`h` Defines the H parameter of the selectivity function
Type: Integer
Default: None
Value: A positive real number, must be greater than L

`a50` Defines the a_{50} parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`ato95` Defines the a_{to95} parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

8.10.8 @selectivity[label].type=double_normal

`alpha` Defines the α parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`mu` Defines the μ parameter of the selectivity function
Type: Estimable
Default: None

`sigma_l` Defines the σ_L parameter of the selectivity function
Type: Estimable
Default: None

`sigma_r` Defines the σ_R parameter of the selectivity function
Type: Estimable
Default: None

8.10.9 @selectivity[label].type=double_exponential

`alpha` Defines the α parameter of the selectivity function
Type: Estimable
Default: None
Value: A positive real number

`x1` Defines the x_1 parameter of the selectivity function
Type: Integer
Default: None

`x2` Defines the x_2 parameter of the selectivity function
Type: Integer
Default: None

`x0` Defines the x_0 parameter of the selectivity function
Type: Estimable
Default: None

`y0` Defines the y_0 parameter of the selectivity function
Type: Estimable
Default: None

`y1` Defines the y_1 parameter of the selectivity function
Type: Estimable
Default: None

`y2` Defines the y_2 parameter of the selectivity function
Type: Estimable
Default: None

8.11 Joint selectivities

How this works has yet to be defined...

`@joint_selectivity` *`label`* Define a joint selectivity

`selectivities` Define the labels of the selectivities to be defined as 'joint'
Type: String vector
Default: None
Value: Valid `@selectivity` labels

9 Estimation command and subcommand syntax

9.1 Estimation methods

`@Estimation`

`minimiser` The label of the minimiser to use, if doing a point estimate
Type: String
Default: None
Value: A valid label from `@minimiser`

`MCMC` The label of the MCMC to use, of doing an MCMC
Type: String
Default: None
Value: A valid label from `@MCMC`

`profile` The labels of the profiles to use, if doing a profile
Type: String
Default: None
Value: A valid label from `@MPD`

`random_seed` Defines the random number generator seed
`value` The random number generator seed value
Type: Integer
Default: None
Value: An integer between 0 and 10000 inclusive

9.2 Point estimation

Two methods of minimising when doing a point estimate are,

- Numerical differences minimiser
- Differential evolution minimiser

Note that point estimates are required for

- MPDs
- To generate the starting values and covariance matrix for an MCMC
- To calculate the point estimates for profiles

Each type of minimiser requires a set of subcommands and arguments specific to that minimiser. Different minimisers can be called for different model runs or for different run modes (i.e., MCMC, MPDs, or profiles).

`@Minimiser` *`label`* Define the an minimiser estimator with label

`type` Define the type of minimiser
Type: String
Default: numerical_differences
Value: A valid type of minimiser, either numerical_differences or DE_solver

9.2.1 @minimiser[label].type=numerical_differences

`max_iterations` Define the maximum number of iterations for the minimiser
Type: Integer
Default: 1000
Value: A positive integer

`max_evaluations` Define the maximum number of evaluations for the minimiser
Type: Integer
Default: 4000
Value: A positive integer

`step_size` Define the step-size for the minimiser
Type: Constant
Default: 1e-6
Value: A positive real number

`gradient_tolerance` Define the gradient tolerance for the minimiser
Type: Constant
Default: 0.0002
Value: A positive real number

9.2.2 @minimiser[label].type=DE_solver

`max_iterations` Define the maximum number of iterations for the minimiser
Type: Integer
Default: 1000
Value: A positive integer

`max_evaluations` Define the maximum number of evaluations for the minimiser
Type: Integer
Default: 4000
Value: A positive integer

`step_size` Define the step-size for the minimiser
Type: Constant
Default: 1e-6
Value: A positive real number

`gradient_tolerance` Define the gradient tolerance for the minimiser

Type: Constant
Default: 0.0002
Value: A positive real number

9.3 Monte Carlo Markov Chain (MCMC)

Only one method of carrying out MCMCs is available, Monte Carlo Markov Chain using Metropolis-Hastings

`@MCMC` *`label`* Define the MCMC estimation arguments

`type` Define the method of MCMC
Type: String
Default: Metropolis_Hastings
Value: A valid type of MCMC, currently only Metropolis-Hastings is available

9.3.1 `@MCMC.type=Metropolis_Hastings`

`start` Covariance multiplier for the starting point of the Markov chain
Type: Constant
Default: 0
Value: If 0, defines the starting point of the chain as the point estimate. If ¿0, defines the starting point as randomly generated, with covariance matrix equal to the approximate covariance (inverse Hessian) times the value of this start parameter

`length` Length of the Markov chain
Type: Integer
Default: None
Value: Defines the length of the Markov chain (as a number of iterations)

`keep` Spacing between recorded values in the chain
Type: Integer
Default: 1
Value: Defines the spacing between recorded values in the chain. Samples from the posterior are written to file only if their sample number is evenly divisible by `keep`

`max_correlation` Maximum absolute correlation in the covariance matrix of the proposal distribution
Type: Constant
Default: 0.8
Value: Defines the maximum correlation in the covariance matrix of the proposal distribution. Correlations greater than max_correlation are decreased to max_correlation, and those less than -max_correlation are increased to -max_correlation

`correlation_adjustment_method` Method for adjusting small variances in the covariance

proposal matrix
Type: String
Default: correlation
Value: Defines the method (either correlation or covariance) for the adjusting small variances in the covariance matrix of the proposal distribution

`correlation_adjustment_diff` Minimum non-zero variance times the range of the bounds in the covariance matrix of the proposal distribution
Type: Constant
Default: 0.0001
Value: Defines the minimum non-zero variance times the difference in the bounds of each parameter in the covariance matrix of the proposal distribution

`step_size` Initial step-size (as a multiplier of the approximate covariance matrix)
Type: Constant
Default: $2.4d^{-0.5}$ where d is the number of estimated parameters
Value: The covariance of the proposal distribution is the approximate covariance (inverse Hessian) times this step-size parameter

`proposal_distribution` The shape of the proposal distribution (either *t* or normal)
Type: String
Default: t
Value: Either `t` or `normal`. Defines whether the proposal distribution should be multivariate t rather than multivariate normal

`df` Degrees of freedom of the multivariate t proposal distribution
Type: Integer
Default: 4
Value: Defines the degrees of freedom of the multivariate t proposal distribution

9.4 Profiles

`@profile` *`label`* Define the profile parameters and arguments

`parameter` Name of the parameter to be profiled
Type: String
Default: None
Value: Defines the name of the parameter to be profiled

`n` Number of values at which to profile the parameter
Type: Integer
Default: 10
Value: Defines the number of values at which to profile the parameter

`lower_bound` lower bound on parameter

Type: Integer
Default: None
Value: Defines the lower bound on the range of the parameter to profile

`upper_bound` Upper bound on parameter
Type: Integer
Default: None
Value: Defines the upper bound on the range of the parameter to profile

9.5 Defining the parameters to be estimated and their priors

`@estimate` *`parameter_name`* Estimate an estimable parameter *`parameter_name`*
The `SPM` name of the parameter to estimate
Type: string
Default: None
Value: A valid `SPM` parameter name

`same` Names of the other parameters which are constrained to have the same value
Type: String Vector
Default: None
Value: Defines the names of all the other parameters which are constrained to have the same value as this parameter

`estimation_phase` Phase at which this parameter should be estimated, in point estimation
Type: Integer
Default: 1
Value: Defines the phase at which this parameter should be freed

`lower_bound` Lower bounds on this parameter
Type: Constant vector, of length equal to the parameter length
Default: None
Value: Defines the lower bound(s) on this parameter

`upper_bound` Upper bound on this parameter
Type: Constant vector, of length equal to the parameter length
Default: None
Value: Defines the upper bound(s) on this parameter

`MCMC_fixed` Should this parameter be fixed during MCMC?
Type: Switch
Default: False
Value: Define this parameter as fixed during MCMC (i.e., considered a constant for the MCMC)

`prior` Defines the label for the prior for this parameter

Type: String
Default: No default
Value: Defines the label of the prior on this parameter

9.6 Priors

The available priors are,

- uniform
- uniform-log
- normal
- normal-by-sd
- lognormal
- Beta

`@prior` *`label`* Define the prior label

`type` Define the type of prior
Type: String
Default: None
Value: A valid type of prior

9.6.1 `@prior[label].type=uniform`

The command `@prior[label].type=uniform` has no other subcommands.

9.6.2 `@prior[label].type=uniform_log`

The command `@prior[label].type=uniform_log` has no other subcommands.

9.6.3 `@prior[label].type=normal`

`mu` Defines the mean μ of the normal prior
Type: Constant
Default: No default
Value: Defines the mean of the normal prior

`cv` Defines the c.v. c of the normal prior
Type: Constant
Default: No default
Value: Defines the c.v. of the normal prior

9.6.4 `@prior[label].type=normal_by_sd`

`mu` Defines the mean μ of the normal by standard deviation prior
Type: Constant
Default: No default
Value: Defines the mean of the normal by standard deviation prior

`sd` Defines the standard deviation σ of the normal by standard deviation prior
Type: Constant
Default: No default
Value: Defines the standard deviation of the normal by standard deviation prior

9.6.5 `@prior[label].type=lognormal`

`mu` Defines the mean μ of the lognormal prior
Type: Constant
Default: No default
Value: Defines the mean of the lognormal prior

`cv` Defines the c.v. c of the lognormal prior
Type: Constant
Default: No default
Value: Defines the c.v. of the lognormal prior

9.6.6 `@prior[label].type=beta`

`A` The lower value of the range parameter A of the Beta prior
Type: Constant
Default: No default
Value: Defines the lower value of the range parameter A of the Beta prior

`B` The upper value of the range parameter B of the Beta prior
Type: Constant
Default: No default
Value: Defines the upper value of the range parameter B of the Beta prior

`mu` Defines the mean μ of the Beta prior
Type: Constant
Default: No default
Value: Defines the mean of the Beta prior

`sd` Defines the standard deviation σ of the Beta prior
Type: Constant
Default: No default
Value: Defines the standard deviation of the Beta prior

9.7 Defining ageing error

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

- None
- Normal
- Off-by-one

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

`@ageing_error` *`label`* Define ageing error with `label`

`type` The type of ageing error
Type: String
Default: None
Value: Defines the type of ageing error to use, currently only normal is defined

9.7.1 `@ageing_error[label].type=none`

The `@ageing_error[label].type=none` has no other subcommands.

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

`c` Parameter of the normal ageing error model
Type: Constant
Default: None
Value: Define the c.v. of misclassification

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

`k` The k parameter of the off-by-one ageing error model
Type: Integer
Default: 0
Value: p1 and p2 define the proportions of misclassifications down and up by 1 year respectively. k defines the minimum age of fish which can be misclassified - fish under age k have no ageing error

`p1` The p_1 parameter of the off-by-one ageing error model
Type: Constant
Default: None
Value: p1 and p2 define the proportions of misclassifications down and up by 1 year respectively. k defines the minimum age of fish which can be misclassified - fish under age k have no ageing error

`p2` The p_2 parameter of the off-by-one ageing error model

Type: Constant
Default: None
Value: p1 and p2 define the proportions of misclassifications down and up by 1 year respectively. k defines the minimum age of fish which can be misclassified - fish under age k have no ageing error

9.8 Defining catchability constants

`@catchability` *`label`* Define a catchability constant with `label`

`q` Value of the q parameter
Type: Estimable
Default: None
Value: Defines the value of the catchability q parameter, a real positive number

9.9 Defining penalties

To be written...

10 Observation command and subcommand syntax

10.1 Observation types

The observation types available are,

Observations of a mortality event proportions of individuals by age class

Observations of proportions of individuals by age class

Observations of proportions of individuals between categories within each age class

Relative and absolute abundance observations

Relative and absolute biomass observations

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

`@observation` *`label`* Define an observation

`type` Define the type of observation
Type: String
Default: None
Value: A valid type of observation

10.1.1 `@observation[label].type=event_mortality_at_age`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`process_label` Define the label of the event mortality process
Type: String
Default: None
Value: A valid label of `@process` where `@process[label].type=event_mortality`

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`min_age` Define the minimum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation

Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a layer of type=categorical

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
Type: Constant vector
Default: None
Value: The label is valid value from the associated observation layer. It is followed by a vector of values giving the proportions at age. This subcommand is repeated for each unique value of label

`tolerance` Define the tolerance on the sum-to-one error check in `SPM`
Type: Constant
Default: 0.001
Value: The tolerance on the sum to one error check. If $abs(1-\sum O_i) >$ `tolerance` then `SPM` will report an error

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood
Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term

Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

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

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`categories` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`min_age` Define the minimum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a layer of type=categorical

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
Type: Constant vector
Default: None
Value: The label is valid value from the associated observation layer. It is followed by a vector of values giving the proportions at age. This subcommand is repeated for each unique value of label

`tolerance` Define the tolerance on the sum-to-one error check in `SPM`
Type: Constant
Default: 0.001
Value: The tolerance on the sum to one error check. If $abs(1-\sum O_i) >$ `tolerance` then `SPM` will report an error

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood
Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.1.3 @observation[label].type=proportions_by_category

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`categories` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`categories2` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`selectivities2` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`min_age` Define the minimum age for the observation

Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
Type: Constant vector
Default: None
Value: The label is valid value from the associated observation layer. It is followed by a vector of values giving the proportions at age. This subcommand is repeated for each unique value of label

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood
Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.1.4 `@observation[label].type=abundance`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`catchability` Define the catchability constant label for the observation
Type: String
Default: None
Value: A valid `@catchability` label

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`obs [label]` Define the following data as observations for the categorical layer with value

`[label]`
Type: Constant vector
Default: None
Value: The label is valid value from the associated observation layer. It is followed by a vector of values giving the proportions at age. This subcommand is repeated for each unique value of label

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood
Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.1.5 @observation[label].type=biomass

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the

observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`catchability` Define the catchability constant label for the observation
Type: String
Default: None
Value: A valid `@catchability` label

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
Type: Constant vector
Default: None
Value: The label is valid value from the associated observation layer. It is followed by a vector of values giving the proportions at age. This subcommand is repeated for each unique value of label

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood

Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.2 Pseudo-observations

`@pseudo-observation` *`label`* Define a pseudo-observation

`type` Define the type of pseudo-observation
Type: String
Default: None
Value: A valid type of pseudo-observation

10.2.1 `@pseudo-observation[label].type=event_mortality_at_age`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`process_label` Define the label of the event mortality process
Type: String
Default: None
Value: A valid label of `@process` where `@process[label].type=event_mortality`

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`min_age` Define the minimum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a layer of type=categorical

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.2.2 `@pseudo-observation[label].type=proportions_at_age`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to

Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`categories` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`min_age` Define the minimum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a layer of type=categorical

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.2.3 `@pseudo-observation[label].type=proportions_by_category`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`categories` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`categories2` Define the categories
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category

Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`selectivities2` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`min_age` Define the minimum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`max_age` Define the maximum age for the observation
Type: Integer
Default: None
Value: A valid age in the range `@model.min_age` and `@model.max_age`

`age_plus_group` Define is the the maximum age for the observation is a plus group
Type: Switch
Default: None
Value: Either true or false

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.2.4 `@pseudo-observation[label].type=abundance`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`catchability` Define the catchability constant label for the observation
Type: String
Default: None
Value: A valid `@catchability` label

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`error_value [label]` Define the following data as error values (e.g., N for multinomial

likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`delta` Define the delta robustifying constant for the likelihood
Type: Constant
Default: 1e-11
Value: A non-negative real number

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

10.2.5 `@pseudo-observation[label].type=biomass`

`year` Define the year that the observation applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the observation applies to
Type: Integer
Default: None
Value: A valid time-step

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
Type: Constant
Default: 1.0
Value: A real number between 0 and 1, inclusive

`catchability` Define the catchability constant label for the observation

Type: String
Default: None
Value: A valid `@catchability` label

`categories` Define the categories into which recruitment occurs
Type: String vector
Default: None
Value: Valid categories from `@model.categories`

`selectivities` Define the selectivities applied to each category
Type: String vector
Default: None
Value: Valid selectivity labels defined by `@selectivity`

`layer` Name of the categorical layer used to group the spacial cells for the observation
Type: String
Default: None
Value: A valid layer as defined by `@layer`. Must be a categorical layer

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
Type: Constant
Default: None
Value: A valid value from the associated observation layer. This subcommand is repeated for each unique value of label

`likelihood` Define the likelihood for the observation
Type: String
Default: None
Value: A valid likelihood

`process_error` Define the process error term
Type: Constant
Default: 0
Value: A non-negative real number

`simulate` Defines if this observation should be simulated when doing simulations
Type: Switch
Default: True
Value: True/False

11 Report command and subcommand syntax

11.1 Reports

The report types available are,

Print the map (i.e., row and column labels of each spatial cell) of the spatial structure

Print the partition

Print a summary of a process

Print a derived quantity

Print the estimated parameters in a vector format (suitable for use with `spm -i`)

Print a summary of the estimated parameters

Print the objective function values

Print an observation values, fits, and residuals

Print the covariance matrix

Print a layer

Print a selectivity's values

Print the weight-at-size using the size-weight relationship

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

`@report` *`label`* Define an output report

`type` Define the type of report
Type: String
Default: None
Value: A valid type of report

11.1.1 `@report[label].type=spatial_map`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

11.1.2 `@report[label].type=partition`

`year` Define the year that the partition report applies to
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step that the partition report applies to
Type: Integer
Default: None
Value: A valid time-step

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.3 `@report[label].type=initialisation`

`initialisation_phase` Define the phase of initialisation that the partition report applies to
Type: string
Default: None
Value: A valid phase label, from `@initialisation_phase`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.4 `@report[label].type=process`

`process` Define the label of the process to summarise
Type: String
Default: None
Value: A valid label from `@process`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.5 `@report[label].type=derived_quantity`

`derived_quantity` Define the label of the derived quantity to print
Type: String
Default: None
Value: A valid label from `@derived_quantity`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.6 `@report[label].type=estimate_value`

Prints the estimated parameters in a format suitable for use with `spm -i`.

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.7 `@report[label].type=estimate_summary`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.8 `@report[label].type=objective_function`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.9 `@report[label].type=observation`

`observation` Define the label of the observation to print
Type: String
Default: None
Value: A valid label from `@Observation`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.10 `@report[label].type=layer`

`layer` Define the label of the layer to print
Type: String
Default: None
Value: A valid label from `@Layer`

`year` Define the year for the printing of the layer
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step for the printing of the layer
Type: Integer
Default: None
Value: A valid time-step

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.11 `@report[label].type=selectivity`

`selectivity` Define the label of the selectivity to print
Type: String
Default: None
Value: A valid label from `@Selectivity`

`year` Define the year for the printing of the selectivity
Type: Integer
Default: None
Value: A positive integer between `@model.initial_year` and `@model.current_year`

`time_step` Define the time-step for the printing of the selectivity
Type: Integer
Default: None
Value: A valid time-step

`file_name` Define the name of the output file where the report is written

Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.12 `@report[label].type=random_number_seed`

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

11.1.13 `@report[label].type=weight_at_size`

`size_weight` Define the label of the size-weight relationship print
Type: String
Default: None
Value: A valid label from `@size_weight`

`sizes` Define the label of the size-weight relationship print
Type: Constant
Default: None
Value: Values of sizes to calculate the size-weight relationship for

`file_name` Define the name of the output file where the report is written
Type: String
Default: None
Value: A valid file name. If not supplied, then output is directed to the standard out

`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to
Type: Switch
Default: True
Value: Either True of False

12 Other commands and subcommands

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

`file` The name of the external file to include

Type: string

Default: None

Value: A valid external file

Condition: The file name must be enclosed in double quotes

Example: `@include "my_file.txt"`

Note: `@include` does not denote the end of the previous command block as is the case for all other commands

13 Examples

13.1 An example of a simple 1×1 non-spatial model

```
categories male female
min_age 2
max_age 25
age_plus_group True
initialisation_phases Phase1
initial_year 1975
current_year 2002
final_year 2007
cell_length 11
time_steps one two three

time_steps 3 # There are three time steps: Oct-Aug, Sep, Sep
recruitment_time 2 # Recruitment occurs in time step 2
recruitment_areas chat # in the area "chat" (the only area defined)
spawning_time 2 # Spawning occurs in time step 2
spawning_part_mort 0.5 # and SSBs are calculated after spawning fish have undergone
    0.5 of the mortality assigned to this time step
spawning_areas chat # Spawning occurs in the area "chat"
spawning_ps 1 # and all mature fish spawn
aging_time 3 # Age incrementation occurs in time step 3
growth_props 1.00 1.00 0.00 # All fish growth occurs in time step 1
M_props 1.00 0.00 0.00 # All natural mortality occurs in time step 1
baranov false # The baranov equation is not used
midmortality_partition weighted_sum
fishery_names chatFishery # The fishery has the label "chatFishery
fishery_times 1 # and occurs in the first time step
fishery_areas chat # in the area labelled "chat"
n_migrations 0 # No migrations are defined

# Initialisation
@initialisation_phase Phase1
years 200
processes Recruitment Spawning halfM halfM Ageing
```

13.2 An example of a simple 10×10 spatial model

```
categories immature mature spawning
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2 Phase3
initial_year 1994
Current_year 2008
final_year 2108
cell_length 155.749
time_steps one two

# Initialisation
@initialisation_phase Phase1
years 200
processes Recruitment Spawning Maturation halfM halfM Postspawning Ageing
```

```
@initialisation_phase Phase2
years 1
processes Recruitment Spawning Maturation halfM halfM InitialMoveImmature
    InitialMoveMature InitialMoveSpawning Ageing Postspawning

@initialisation_phase Phase3
years 20
processes Recruitment Spawning Maturation halfM halfM MoveImmature MoveMature
    MoveSpawning Ageing Postspawning

# Annual Cycle
@time_step one
processes Recruitment Spawning Maturation halfM fishing halfM

@time_step two
processes MoveImmature MoveMature MoveSpawning PostSpawning Ageing

# Population processes
@process Ageing
```

13.3 An example of a more complex 10×10 spatial model

```
categories immature mature spawning
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2 Phase3
initial_year 1994
Current_year 2008
final_year 2108
cell_length 155.749
time_steps one two

# Initialisation
@initialisation_phase Phase1
years 200
processes Recruitment Spawning Maturation halfM halfM Postspawning Ageing

@initialisation_phase Phase2
years 1
processes Recruitment Spawning Maturation halfM halfM InitialMoveImmature
    InitialMoveMature InitialMoveSpawning Ageing Postspawning

@initialisation_phase Phase3
years 20
processes Recruitment Spawning Maturation halfM halfM MoveImmature MoveMature
    MoveSpawning Ageing Postspawning

# Annual Cycle
@time_step one
processes Recruitment Spawning Maturation halfM fishing halfM

@time_step two
processes MoveImmature MoveMature MoveSpawning PostSpawning Ageing

# Population processes
@process Ageing
```

14 Post processing output using R

The **R** package `spm` contains a set of **R** functions for reading `SPM` output, and is available as a precompiled binary for Microsoft Windows (.zip file) or as a source package (.gz file) for Linux. To check the version number and date of the `spm` **R** package (useful for checking that you have the most recent version), use the function `spm.version()`.

The `spm` **R** package includes a range of extract and write functions to aid post-processing of `SPM` input configuration files and output. The main extract functions are briefly described below. In addition, the package also has a number of undocumented helper functions, that could be useful for writing you own analysis functions. See the the **R** help for more detail e.g., `help(spm)`

15 Troubleshooting

15.1 Introduction

`SPM` is a complex system, providing many opportunities for error — either because your parameter files do not correctly specify your model, or because the model you tried to specify does not work as you expect. When in doubt, ask an experienced user. Debugging versions of `SPM` can also be compiled that help to track down cryptic errors.

When `SPM` generates an error and the error message makes no sense, please let the `SPM` authors know. Even if you manage to fix the problem yourself, we may be able to implement a more helpful error message and make life easier for the next person to encounter the problem. Guidelines for reporting an error are given in Section 15.3.

Some parameter values of functions or selectivities can result in either very large or very small numbers. These can, on occasion, generate internal numeric overflow errors within `SPM`. This is the most common cause of an overflow error, and can result in parameter estimates of `NaN`. The work-around to this type of error is to impose bounds on parameters that exclude the possibility of an overflow error.

15.2 Reporting errors

If you wish to report a bug or problem with `SPM`, then please send a bug report to the authors. Use the text `SPM:` as the start of the subject line in the email. Note that following these guidelines will assist the `SPM` authors identify, reproduce, and hopefully solve any reported bugs.

Note that `SPM` is distributed as unsupported software. We will not, as a rule, provide help for users of `SPM` outside of National Institute of Water & Atmospheric Research Ltd. — although we will usually endeavour to try. And, while we would appreciate being notified of any problems or errors in `SPM`, please note that we may not be able to provide timely solutions.

15.3 Guidelines for reporting a bug in `SPM`

1. Detail the version of `SPM` are you using? e.g., "`SPM` v1.00-2009-03-17 (rev. 3056) Microsoft Windows executable"
2. What operating system or environment are you using? e.g., "IBM-PC Intel CPU running Microsoft Windows XP Service Pack 3".
3. Give a brief one-line description of the problem, e.g., "a segmentation fault was reported".
4. If the problem is reproducible, please list the exact steps required to cause it, remembering to include the relevant `SPM` configuration file, other input files, and any out generated. Specify the *exact* command line arguments that were used, e.g., "Using the command `spm -e config.spm -q > logfile.out` reports a segmentation fault. The input configuration files are attached."
5. If the problem is not reproducible (only happened once, or occasionally for no apparent reason), please describe the circumstances in which it occurred and the symptoms observed (but note it is much harder to reproduce and hence fix non-reproducible bugs, but if several reports are made over time that relate to the same thing, then this may help to track down the problem), e.g., "SPM crashed, but I cannot reproduce how I did it. It seemed to be related to a local network crash but I cannot be sure."

6. If the problem causes any error messages to appear, please give the *exact* text displayed, e.g., `segmentation fault (core dumped)`.
7. Remember to attach all relevant input and output files so that the problem can be reproduced (it can helpful to compress these into a single file). Without these, it may not be possible to determine the cause of the problem. Note that it is helpful to be as specific as possible when describing the problem.

16 Acknowledgements

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Much of the structure of `SPM`, equations, and documentation in this manual draw heavily on similar components of the population model CASAL (Bull et al., 2008). We thank the authors of CASAL for their permission to use their work as the basis for parts of `SPM` and allow the use of software code, concepts, and documentation from CASAL in `SPM`.

The development of `SPM` was funded by the New Zealand Ministry of Fisheries, the Foundation for Research, Science and Technology, and the National Institute of Water & Atmospheric Research Ltd. (NIWA).

17 Quick reference

17.1 Population command and subcommand syntax

`@model` Define the spatial structure, population structure, annual cycle, and model years

`nrows` The number of rows n_{rows} in the spatial structure
`ncols` The number of columns n_{cols} in the spatial structure
`layer` The label for the base layer
`categories` Labels of the categories (rows) of the population component of the partition
`min_age` Minimum age of the population
`max_age` Maximum age of the population
`age_plus_group` Define the largest age as a plus group
`cell_length` The length (distance) of one side of a cell
`size_at_age` Define the label of the associated size-at-age relationship for each category
`initialisation_phases` Define the labels of the phases of the initialisation
`initial_year` Define the first year of the model, immediately following initialisation
`current_year` Define the current year of the model
`final_year` Define the final year of the model in projections
`time_steps` Define the `@time_step` labels (in order that they are applied) to form the annual cycle

`@initialisation_phase` *`label`* Define the processes and years of the initialisation phase with label

`type` Define the type of initialisation

`@initialisation_phase[label].type=iterative`

`years` Define the number of years to run
`processes` Define the processes (in order of occurrence) to run in each year of the initialisation

`@time_step` *`label`* Define a time step with label

`processes` Define the process labels, in the order that they are applied, for the time step

`@process` *`label`* Define a process with label

`type` Define the type of process

`@process[label].type=constant_recruitment`

`r0` Define the total amount of recruitment at equilibrium abundance levels
`categories` Define the categories into which recruitment occurs
`proportions` Define the proportion of recruitment that occurs into each category
`ages` Define the ages within each category that receive recruitment
`layer` Name of the layer used to determine where recruitment occurs

`@process[label].type=BH_recruitment`

`r0` Define the total amount of recruitment at equilibrium abundance levels `categories` Define the categories into which recruitment occurs

`proportions` Define the proportion of recruitment that occurs into each category

`ages` Define the age within each category that receive recruitment

`steepness` Define the Beverton-Holt stock recruitment relationship steepness (h) parameter

`sigma_r` Define the recruitment variability σ_R in the stock-recruitment relationship for projections

`rho` Define the autocorrelation ρ in the recruitment variability in the stock-recruitment relationship for projections

`SSB` Define the label of the `@derived_quantity` that defines the SSB

`SSB_offset` Define the offset (in years) for the year of the derived quantity that is to be applied as the SSB in the stock-recruit relationship

`YCS_values` YCS values

`YCS_years` Years for year class strength values

`standardise_YCS_year_range` Years for which the year class strength values are defined to have mean 1.0

`layer` Name of the layer used to determine where recruitment occurs

@process[label].type=ageing

`categories` Define the categories that ageing is applied to

@process[label].type=constant_mortality_rate

`m` Define the constant mortality rate to be applied

`categories` Define the categories that mortality is applied to

`selectivities` Define the selectivities applied to each category

`layer` Name of the layer

@process[label].type=annual_mortality_rate

`years` Define the years when the mortality rates are applied

`m` Define the mortality rate to be applied for each year

`categories` Define the categories that mortality is applied to

`selectivities` Define the selectivities applied to each category

`layer` Name of the layer

@process[label].type=event_mortality

`categories` Define the categories that the event mortality is applied to

`years` Define the years where the mortality even is applied

`layers` Define the layers that specify the event mortality (as the abundance) in each year

`U_max` Define the maximum exploitation rate

`selectivities` Define the selectivities applied to each category

`penalty` Define the event mortality penalty label

@process[label].type=biomass_event_mortality

`categories` Define the categories that the event mortality is applied to

`size_at_age` Define the age-weight relationships for each of the categories that the event

mortality is applied to
`years` Define the years where the mortality event is applied
`layers` Define the layers that specify the event mortality (as a biomass) in each year
`U_max` Define the maximum exploitation rate
`selectivities` Define the selectivities applied to each category
`penalty` Define the event mortality penalty label

@process[label].type=category_transition

`from` Define the categories that are the source of the transition process
`selectivities` Define the selectivities applied to the source categories
`to` Define the categories that are the sink of the transition process
`years` Define the years where the category transition is applied
`layers` Define the layers that specify the event mortality (as N for each cell) in each year
`penalty` Define the penalty to encourage models parameter values away from those which result in not enough individuals to move

@process[label].type=category_transition_rate

`from` Define the category that is the source of the transition process
`selectivities` Define the selectivities applied to the source categories
`to` Define the category that is the sink of the transition process
`proportion` Define the proportion of individuals to move
`layer` Name of the layer

@process[label].type=migration_movement

`categories` Define the categories that the migration movement event is applied to
`source_layer` Define the label of a layer that defines the source cells of the migration movement event
`sink_layer` Define the label of a layer that defines the sink cells of the migration movement event
`proportions` Define the constant multiplier for the proportions that migrate
`layer` Name of the layer
`selectivities` Define the selectivities applied to each category

@process[label].type=adjacent_cell_movement

@process[label].type=preference

`categories` Define the categories that the preference function movement is applied to
`preference_functions` Define the labels of the individual preference functions that make up the total preference function

@preference_function *`label`* Define a preference function with label

`type` Define the type of preference function

@preference_function[label].type=constant

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α

`@preference_function[label].type=normal`

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α
`mu` Defines the μ parameter of the normal preference function
`sigma` Defines the σ parameter of the normal preference function

`@preference_function[label].type=double_normal`

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α
`mu` Defines the μ parameter of the double-normal preference function
`sigma_l` Defines the σ_L parameter of the double-normal preference function
`sigma_r` Defines the σ_R parameter of the double-normal preference function

`@preference_function[label].type=logistic`

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α
`a50` Defines the a_{50} parameter of the logistic preference function
`ato95` Defines the a_{to95} parameter of the logistic preference function

`@preference_function[label].type=inverse_logistic`

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α
`a50` Defines the a_{50} parameter of the inverse-logistic preference function
`ato95` Defines the a_{to95} parameter of the inverse-logistic preference function

`@preference_function[label].type=exponential`

`layer` Defines the layer which supplies the preference function independent variable
`alpha` Defines the multiplicative constant α
`lambda` Defines the λ parameter of the exponential preference function

`@preference_function[label].type=threshold`

`layer` Defines the layer which supplies the preference function independent variable
`categories` Define the categories are used to calculate the abundance
`selectivities` Define the selectivities applied to each category
`alpha` Defines the multiplicative constant α
`n` Defines the N parameter of the threshold preference function
`lambda` Defines the λ parameter of the threshold preference function

`@preference_function[label].type=threshold_biomass`

`layer` Defines the layer which supplies the preference function independent variable
`categories` Define the categories are used to calculate the biomass
`selectivities` Define the selectivities applied to each category
`size_at_age` Define the age-weight relationships for each of the categories that the biomass is

calculated from
`alpha` Defines the multiplicative constant α
`biomass` Defines the B biomass parameter of the threshold biomass preference function
`lambda` Defines the λ parameter of the threshold biomass preference function

@layer *label* Define a layer function with label

`type` Define the type of layer

@layer[label].type=numeric

`data` Define the values of the layer

@layer[label].type=categorical

`data` Define the values of the layer

@layer[label].type=distance

@layer[label].type=abundance

`categories` Define the categories are used to calculate the abundance
`selectivities` Define the selectivities applied to each category

@layer[label].type=biomass

`categories` Define the categories are used to calculate the biomass
`selectivities` Define the selectivities applied to each category
`size_at_age` Define the age-weight relationships for each of the categories that the biomass is calculated from

@layer[label].type=abundance_density

`categories` Define the categories are used to calculate the abundance
`selectivities` Define the selectivities applied to each category

@layer[label].type=biomass_density

`categories` Define the categories are used to calculate the biomass
`selectivities` Define the selectivities applied to each category
`size_at_age` Define the age-weight relationships for each of the categories that the biomass is calculated from

@layer[label].type=meta

`years` Define the years
`layers` Define the layer labels for each of the years
`initialisation_layer` Define the layer label to use during the initialisation

@derived_quantity *label* Define a derived quantity with label

`type` Define the type of derived quantity

@derived_quantity[label].type=abundance

`categories` Define the categories are used to calculate the derived quantity
`selectivity` Define the selectivities
`time_step` Define the time step at the end of which, the derived quantity is calculated
`time_step_proportion` Define the proportion of the time step through which the derived quantity has been calculated
`layer` Name of the layer

@derived_quantity[label].type=biomass

`categories` Define the categories are used to calculate the derived quantity
`selectivities` Define the selectivities
`time_step` Define the time step at the end of which, the derived quantity is calculated
`layer` Name of the layer

@size_at_age *label* Define a size-at-age relationship with label

`type` Define the type of relationship

@size_at_age[label].type=von_Bertalanffy

`Linf` Define the L_∞ 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
`distribution` Define the distribution of sizes-at-age around the mean
`by_length` Specifies if the linear interpolation of c.v.s is a linear function of mean size or of age
`cv` Define the c.v. of the distribution of sizes-at-age around the mean
`growth_proportions` Define the proportion of the year for each time step for evaluating size
`size_weight` Define the label of the associated size-weight relationship

@size_at_age[label].type=Schnute

`y1` Define the y_1 parameter of the Schnute relationship
`y2` Define the y_2 parameter of the Schnute relationship
`tau1` Define the τ_1 parameter of the Schnute relationship
`tau2` Define the τ_2 parameter of the Schnute relationship
`a` Define the a parameter of the Schnute relationship
`b` Define the b parameter of the Schnute relationship
`by_length` Specifies if the linear interpolation of c.v.s is a linear function of mean size or of age
`cv` Define the c.v. of the distribution of sizes-at-age around the mean
`growth_proportions` Define the proportion of the year for each time step for evaluating size
`size_weight` Define the label of the associated size-weight relationship

@size_weight *label* Define a size-weight relationship with label

`Type` Define the type of relationship

@size_weight[label].type=none

@size_weight[label].type=basic

`a`	Define the a parameter of the basic relationship
`b`	Define the b parameter of the basic relationship

@selectivity *`label`* Define a selectivity function with label

`type`	Define the type of selectivity function

@selectivity[label].type=constant

`c`	Defines the C parameter of the selectivity function

@selectivity[label].type=knife_edge

`e`	Defines the E parameter of the selectivity function

@selectivity[label].type=all_values

`v`	Defines the V parameters (one for each age class) of the selectivity function

@selectivity[label].type=all_values_bounded

`l`	Defines the L parameter of the selectivity function
`h`	Defines the H parameter of the selectivity function
`v`	Defines the V parameters (one for each age class from L to H) of the selectivity function

@selectivity[label].type=increasing

`alpha`	Defines the α parameter of the selectivity function
`l`	Defines the L parameter of the selectivity function
`h`	Defines the H parameter of the selectivity function
`v`	Defines the V parameters (one for each age class from L to H) of the selectivity function

@selectivity[label].type=logistic

`alpha`	Defines the α parameter of the selectivity function
`a50`	Defines the a_{50} parameter of the selectivity function
`ato95`	Defines the a_{to95} parameter of the selectivity function

@selectivity[label].type=logistic_producing

`alpha`	Defines the α parameter of the selectivity function
`l`	Defines the L parameter of the selectivity function
`h`	Defines the H parameter of the selectivity function
`a50`	Defines the a_{50} parameter of the selectivity function
`ato95`	Defines the a_{to95} parameter of the selectivity function

@selectivity[label].type=double_normal

`alpha`	Defines the α parameter of the selectivity function

`mu` Defines the μ parameter of the selectivity function
`sigma_l` Defines the σ_L parameter of the selectivity function
`sigma_r` Defines the σ_R parameter of the selectivity function

`@selectivity[label].type=double_exponential`

`alpha` Defines the α parameter of the selectivity function
`x1` Defines the x_1 parameter of the selectivity function
`x2` Defines the x_2 parameter of the selectivity function
`x0` Defines the x_0 parameter of the selectivity function
`y0` Defines the y_0 parameter of the selectivity function
`y1` Defines the y_1 parameter of the selectivity function
`y2` Defines the y_2 parameter of the selectivity function

`@joint_selectivity` *`label`* Define a joint selectivity

`selectivities` Define the labels of the selectivities to be defined as 'joint'

17.2 Estimation command and subcommand syntax

`@Estimation`

`minimiser` The label of the minimiser to use, if doing a point estimate
`MCMC` The label of the MCMC to use, of doing an MCMC
`profile` The labels of the profiles to use, if doing a profile
`random_seed` Defines the random number generator seed

`@Minimiser` *`label`* Define the an minimiser estimator with label

`type` Define the type of minimiser

`@minimiser[label].type=numerical_differences`

`max_iterations` Define the maximum number of iterations for the minimiser
`max_evaluations` Define the maximum number of evaluations for the minimiser
`step_size` Define the step-size for the minimiser
`gradient_tolerance` Define the gradient tolerance for the minimiser

`@minimiser[label].type=DE_solver`

`max_iterations` Define the maximum number of iterations for the minimiser
`max_evaluations` Define the maximum number of evaluations for the minimiser
`step_size` Define the step-size for the minimiser
`gradient_tolerance` Define the gradient tolerance for the minimiser

`@MCMC` *`label`* Define the MCMC estimation arguments

`type` Define the method of MCMC

`@MCMC.type=Metropolis_Hastings`

`start` Covariance multiplier for the starting point of the Markov chain
`length` Length of the Markov chain
`keep` Spacing between recorded values in the chain
`max_correlation` Maximum absolute correlation in the covariance matrix of the proposal distribution
`correlation_adjustment_method` Method for adjusting small variances in the covariance proposal matrix
`correlation_adjustment_diff` Minimum non-zero variance times the range of the bounds in the covariance matrix of the proposal distribution
`step_size` Initial step-size (as a multiplier of the approximate covariance matrix)
`proposal_distribution` The shape of the proposal distribution (either *t* or normal)
`df` Degrees of freedom of the multivariate t proposal distribution

@profile *label* Define the profile parameters and arguments

`parameter` Name of the parameter to be profiled
`n` Number of values at which to profile the parameter
`lower_bound` lower bound on parameter
`upper_bound` Upper bound on parameter

@estimate *parameter_name* Estimate an estimable parameter

`same` Names of the other parameters which are constrained to have the same value
`estimation_phase` Phase at which this parameter should be estimated, in point estimation
`lower_bound` Lower bounds on this parameter
`upper_bound` Upper bound on this parameter
`MCMC_fixed` Should this parameter be fixed during MCMC?
`prior` Defines the label for the prior for this parameter

@prior *label* Define the prior label

`type` Define the type of prior

@prior[label].type=uniform

@prior[label].type=uniform_log

@prior[label].type=normal

`mu` Defines the mean μ of the normal prior
`cv` Defines the c.v. c of the normal prior

@prior[label].type=normal_by_sd

`mu` Defines the mean μ of the normal by standard deviation prior
`sd` Defines the standard deviation σ of the normal by standard deviation prior

@prior[label].type=lognormal

`mu` Defines the mean μ of the lognormal prior
`cv` Defines the c.v. c of the lognormal prior

`@prior[label].type=beta`

`A` The lower value of the range parameter A of the Beta prior
`B` The upper value of the range parameter B of the Beta prior
`mu` Defines the mean μ of the Beta prior
`sd` Defines the standard deviation σ of the Beta prior

`@ageing_error` *`label`* Define ageing error with `label`

`type` The type of ageing error

`@ageing_error[label].type=none`

`@ageing_error[label].type=normal`

`c` Parameter of the normal ageing error model

`@ageing_error[label].type=off_by_one`

`k` The k parameter of the off-by-one ageing error model
`p1` The p_1 parameter of the off-by-one ageing error model
`p2` The p_2 parameter of the off-by-one ageing error model

`@catchability` *`label`* Define a catchability constant with `label`

`q` Value of the q parameter

17.3 Observation command and subcommand syntax

`@observation` *`label`* Define an observation

`type` Define the type of observation

`@observation[label].type=event_mortality_at_age`

`year` Define the year that the observation applies to
`process_label` Define the label of the event mortality process
`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
`min_age` Define the minimum age for the observation
`max_age` Define the maximum age for the observation
`age_plus_group` Define is the the maximum age for the observation is a plus group
`layer` Name of the categorical layer used to group the spacial cells for the observation
`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
`tolerance` Define the tolerance on the sum-to-one error check in `SPM`
`error_value [label]` Define the following data as error values (e.g., N for multinomial

likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
`likelihood` Define the likelihood for the observation
`delta` Define the delta robustifying constant for the likelihood
`process_error` Define the process error term
`simulate` Defines if this observation should be simulated when doing simulations

`@observation[label].type=proportions_at_age`

`year` Define the year that the observation applies to
`time_step` Define the time-step that the observation applies to
`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
`categories` Define the categories
`selectivities` Define the selectivities applied to each category
`min_age` Define the minimum age for the observation
`max_age` Define the maximum age for the observation
`age_plus_group` Define is the the maximum age for the observation is a plus group
`layer` Name of the categorical layer used to group the spacial cells for the observation
`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
`tolerance` Define the tolerance on the sum-to-one error check in `SPM`
`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
`likelihood` Define the likelihood for the observation
`delta` Define the delta robustifying constant for the likelihood
`process_error` Define the process error term
`simulate` Defines if this observation should be simulated when doing simulations

`@observation[label].type=proportions_by_category`

`year` Define the year that the observation applies to
`time_step` Define the time-step that the observation applies to
`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
`categories` Define the categories
`categories2` Define the categories
`selectivities` Define the selectivities applied to each category
`selectivities2` Define the selectivities applied to each category
`min_age` Define the minimum age for the observation
`max_age` Define the maximum age for the observation
`age_plus_group` Define is the the maximum age for the observation is a plus group
`layer` Name of the categorical layer used to group the spacial cells for the observation
`obs [label]` Define the following data as observations for the categorical layer with value `[label]`
`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
`likelihood` Define the likelihood for the observation
`delta` Define the delta robustifying constant for the likelihood
`process_error` Define the process error term
`simulate` Defines if this observation should be simulated when doing simulations

`@observation[label].type=abundance`

`year` Define the year that the observation applies to

`time_step` Define the time-step that the observation applies to

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to

`catchability` Define the catchability constant label for the observation

`categories` Define the categories into which recruitment occurs

`selectivities` Define the selectivities applied to each category

`layer` Name of the categorical layer used to group the spacial cells for the observation

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`

`likelihood` Define the likelihood for the observation

`delta` Define the delta robustifying constant for the likelihood

`process_error` Define the process error term

`simulate` Defines if this observation should be simulated when doing simulations

`@observation[label].type=biomass`

`year` Define the year that the observation applies to

`time_step` Define the time-step that the observation applies to

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to

`catchability` Define the catchability constant label for the observation

`categories` Define the categories into which recruitment occurs

`selectivities` Define the selectivities applied to each category

`layer` Name of the categorical layer used to group the spacial cells for the observation

`obs [label]` Define the following data as observations for the categorical layer with value `[label]`

`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`

`likelihood` Define the likelihood for the observation

`delta` Define the delta robustifying constant for the likelihood

`process_error` Define the process error term

`simulate` Defines if this observation should be simulated when doing simulations

`@pseudo-observation` *`label`* Define a pseudo-observation

`type` Define the type of pseudo-observation

`@pseudo-observation[label].type=event_mortality_at_age`

`year` Define the year that the observation applies to

`process_label` Define the label of the event mortality process

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to

`min_age` Define the minimum age for the observation

`max_age` Define the maximum age for the observation

`age_plus_group` Define is the the maximum age for the observation is a plus group

`layer` Name of the categorical layer used to group the spacial cells for the observation

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`

`likelihood` Define the likelihood for the observation

`process_error` Define the process error term

`simulate` Defines if this observation should be simulated when doing simulations

@pseudo-observation[label].type=proportions_at_age

`year` Define the year that the observation applies to

`time_step` Define the time-step that the observation applies to

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to

`categories` Define the categories

`selectivities` Define the selectivities applied to each category

`min_age` Define the minimum age for the observation

`max_age` Define the maximum age for the observation

`age_plus_group` Define is the the maximum age for the observation is a plus group

`layer` Name of the categorical layer used to group the spacial cells for the observation

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`

`likelihood` Define the likelihood for the observation

`process_error` Define the process error term

`simulate` Defines if this observation should be simulated when doing simulations

@pseudo-observation[label].type=proportions_by_category

`year` Define the year that the observation applies to

`time_step` Define the time-step that the observation applies to

`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to

`categories` Define the categories

`categories2` Define the categories

`selectivities` Define the selectivities applied to each category

`selectivities2` Define the selectivities applied to each category

`min_age` Define the minimum age for the observation

`max_age` Define the maximum age for the observation

`age_plus_group` Define is the the maximum age for the observation is a plus group

`layer` Name of the categorical layer used to group the spacial cells for the observation

`error_value [label]` Define the following data as error values (e.g., *N* for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`

`likelihood` Define the likelihood for the observation

`process_error` Define the process error term

`simulate` Defines if this observation should be simulated when doing simulations

@pseudo-observation[label].type=abundance

`year` Define the year that the observation applies to
`time_step` Define the time-step that the observation applies to
`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
`catchability` Define the catchability constant label for the observation
`categories` Define the categories into which recruitment occurs
`selectivities` Define the selectivities applied to each category
`layer` Name of the categorical layer used to group the spacial cells for the observation
`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
`likelihood` Define the likelihood for the observation
`delta` Define the delta robustifying constant for the likelihood
`process_error` Define the process error term
`simulate` Defines if this observation should be simulated when doing simulations

`@pseudo-observation[label].type=biomass`

`year` Define the year that the observation applies to
`time_step` Define the time-step that the observation applies to
`proportion_time_step` Define the interpolated proportion of the time-step passes that the observation applies to
`catchability` Define the catchability constant label for the observation
`categories` Define the categories into which recruitment occurs
`selectivities` Define the selectivities applied to each category
`layer` Name of the categorical layer used to group the spacial cells for the observation
`error_value [label]` Define the following data as error values (e.g., N for multinomial likelihoods, c.v. for lognormal likelihoods, etc.) for the categorical layer with value `[label]`
`likelihood` Define the likelihood for the observation
`process_error` Define the process error term
`simulate` Defines if this observation should be simulated when doing simulations

17.4 Report command and subcommand syntax

`@report` *`label`* Define an output report

`type` Define the type of report

`@report[label].type=spatial_map`

`file_name` Define the name of the output file where the report is written

`@report[label].type=partition`

`year` Define the year that the partition report applies to
`time_step` Define the time-step that the partition report applies to
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=initialisation`

`initialisation_phase` Define the phase of initialisation that the partition report applies to
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=process`

`process` Define the label of the process to summarise
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=derived_quantity`

`derived_quantity` Define the label of the derived quantity to print
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=estimate_value`

`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=estimate_summary`

`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=objective_function`

`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=observation`

`observation` Define the label of the observation to print
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=layer`

`layer` Define the label of the layer to print

`year` Define the year for the printing of the layer
`time_step` Define the time-step for the printing of the layer
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=selectivity`

`selectivity` Define the label of the selectivity to print
`year` Define the year for the printing of the selectivity
`time_step` Define the time-step for the printing of the selectivity
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=random_number_seed`

`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

`@report[label].type=weight_at_size`

`size_weight` Define the label of the size-weight relationship print
`sizes` Define the label of the size-weight relationship print
`file_name` Define the name of the output file where the report is written
`overwrite` Specify if any previous file with the same name as the output file should be overwritten or appended to

17.5 Other commands and subcommands

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

18 References

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