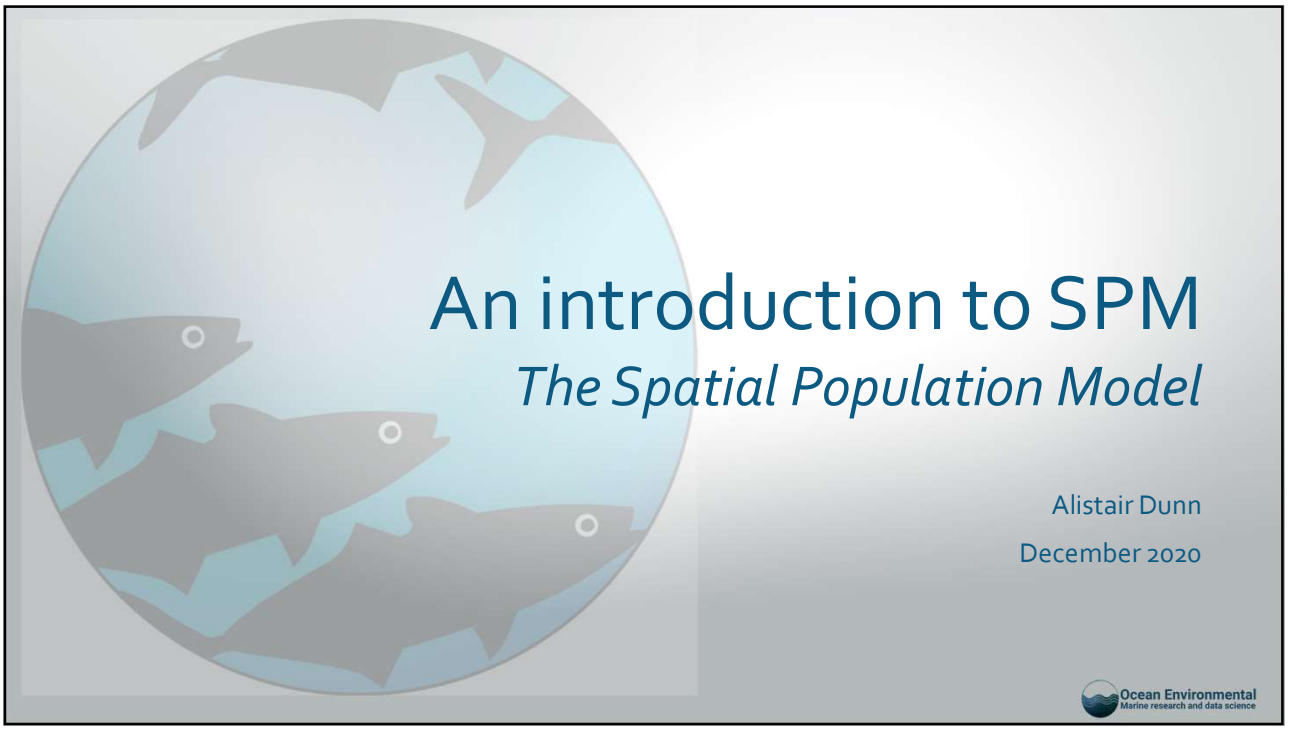
An introduction to SPM
The Spatial Population Model
Alistair Dunn
December 2020
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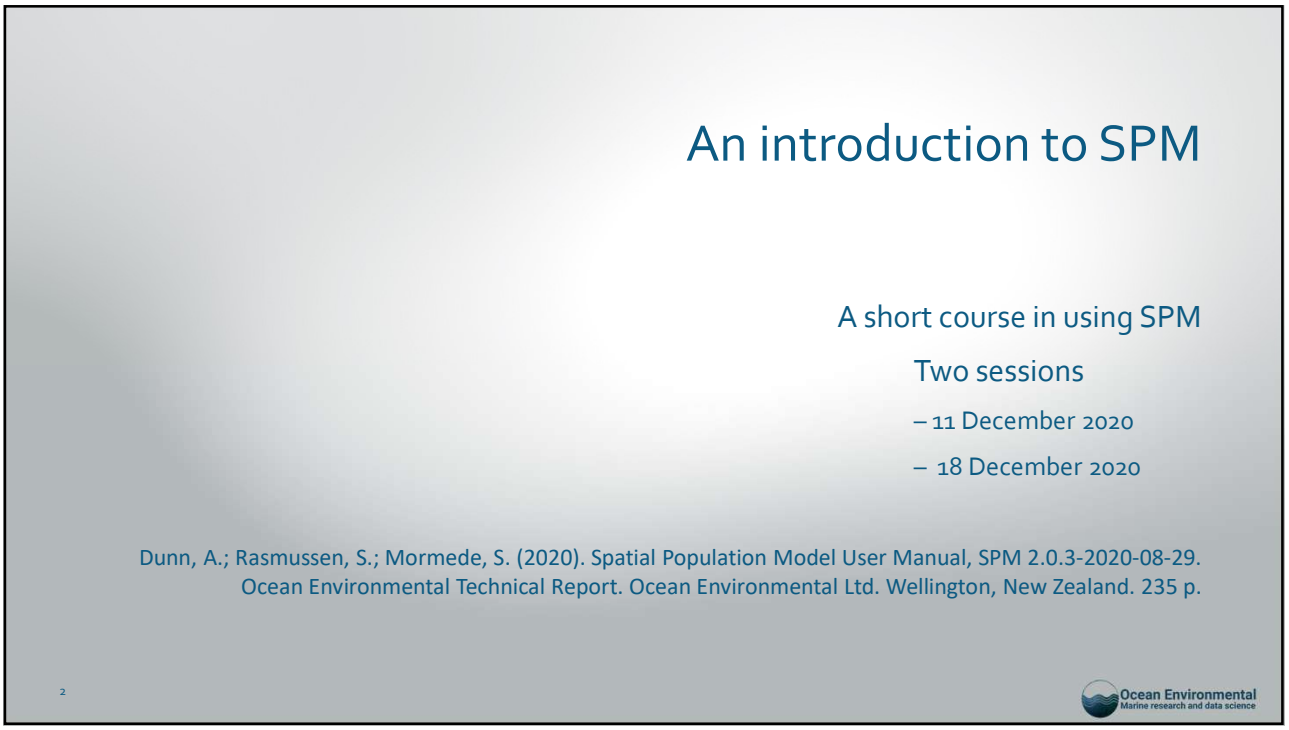
An introduction to SPM
A short course in using SPM
Two sessions
– 11 December 2020
– 18 December 2020
Dunn, A.; Rasmussen, S.; Mormede, S. (2020). Spatial Population Model User Manual, SPM 2.0.3-2020-08-29.
Ocean Environmental Technical Report. Ocean Environmental Ltd. Wellington, New Zealand. 235 p.
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An introduction to SPM
Session 1

The Spatial Population Model

Alistair Dunn

December 2020

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Introduction

- What is SPM
  - Where to get SPM
  - Version control and maintenance
  - Using the package
- The C++ codebase
- The config file
  - Model structure and general approach to the package

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What is SPM

SPM (the Spatial Population Model)

SPM (Spatial Population Model) 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/length 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.

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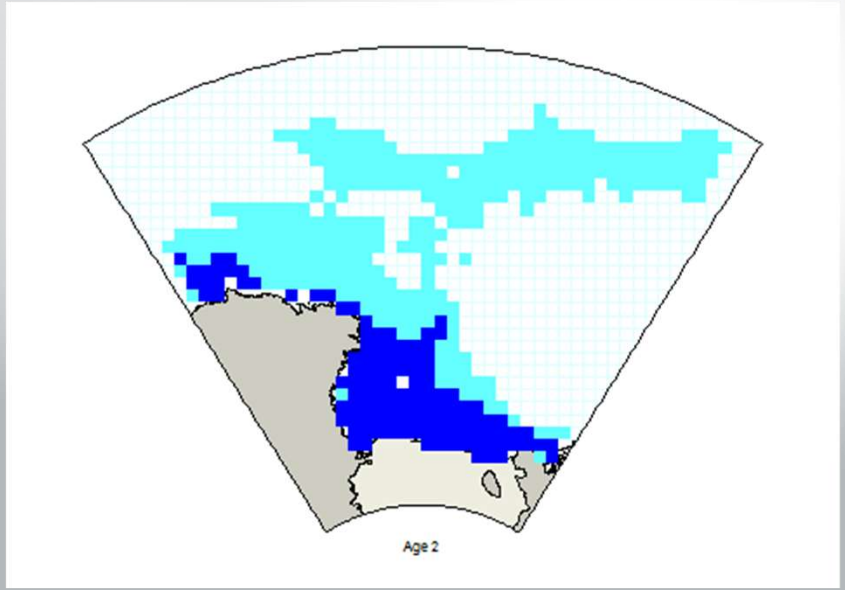
SPM: predictions of the abundance at age for Antarctic toothfish in the Ross Sea



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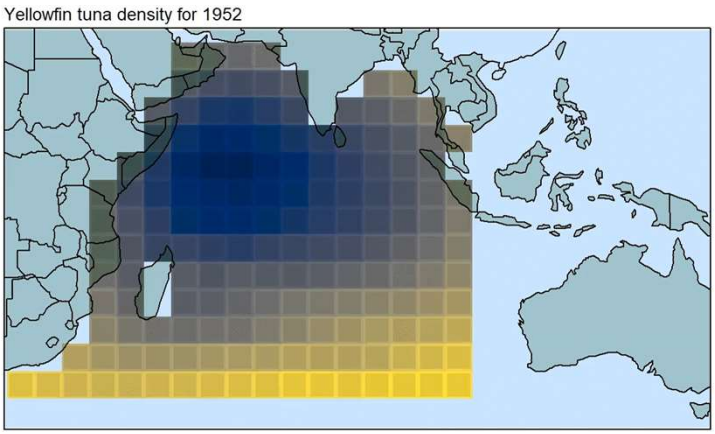
SPM: predictions of the abundance of YFT in the Indian Ocean



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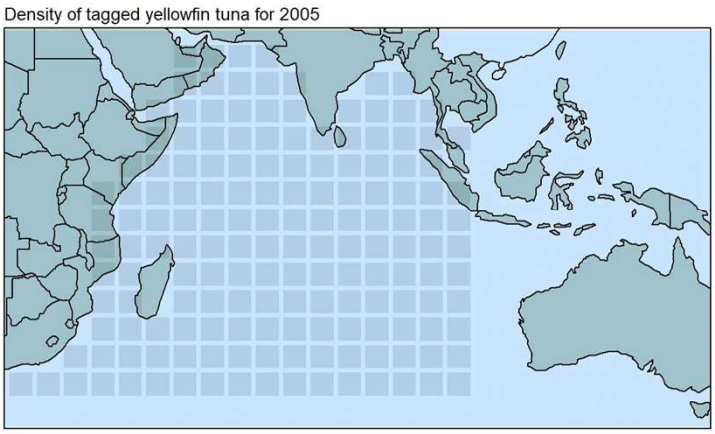
SPM: predictions of the tags of YFT in the Indian Ocean



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Modular code and object based

- SPM is built around the idea of object orientated approach
  - Modula – models are built by combining individual components
    - Processes, Observations, etc.
  - Model size only limited by time and memory (and can be 10 000's of cells in size)
- Flexible and extendable
  - Code base uses modern C_++ and is relatively easy to add new functionality
- But .. some parts are a bit old
  - it would be nice to update these one day
- It can be a bit slow ☹

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Getting SPM

- Most recent version (binaries and Windows installer)
  - https://github.com/alistairdunn1/SPM/releases/tag/v2.0.3-2020-08-26
- GitHub repository
  - https://github.com/alistairdunn1/SPM
- Older (NIWA) version available at
  - https://github.com/NIWAFisheriesModelling/SPM

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About SPM

- Developed at NIWA in mid-2000s to investigate biases with the use of tagging data for the assessment of Antarctic Toothfish in the Ross Sea
- Written in C++. Source code is on GitHub
- Minor development recently to fix issues and add functionality
- Allows generalised structures, with a range of observations types and can
  - **Estimate** a wide range of free parameters
    - Profile, point estimates, and MCMC using Maximum Likelihood and Bayes
  - **Simulate** observations from a given set of parameters and model structure
  - **Flexible**, generalised model structure, model years, annual cycle, processes, and observations

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SPM license

- Open source (Common Public License v1.0)

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

- Pretty much allows you to do anything with the code or program (including sell it!)

See the manual:

Dunn, A.; Rasmussen, S.; Mormede, S. (2020). Spatial Population Model User Manual, SPM 2.0.3-2020-08-29. Ocean Environmental Technical Report. Ocean Environmental Ltd. Wellington, New Zealand. 235 p.

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Using SPM

- SPM is available for Windows and Linux
- Runs from the terminal (command line) – there is no GUI
- Simple command line calls to "do" something
- Multiple command line options `-h -c -e -p -q -m -g` etc. depending on what you want to do (we'll cover this later)
- `spm -h` gives short help of the command line options

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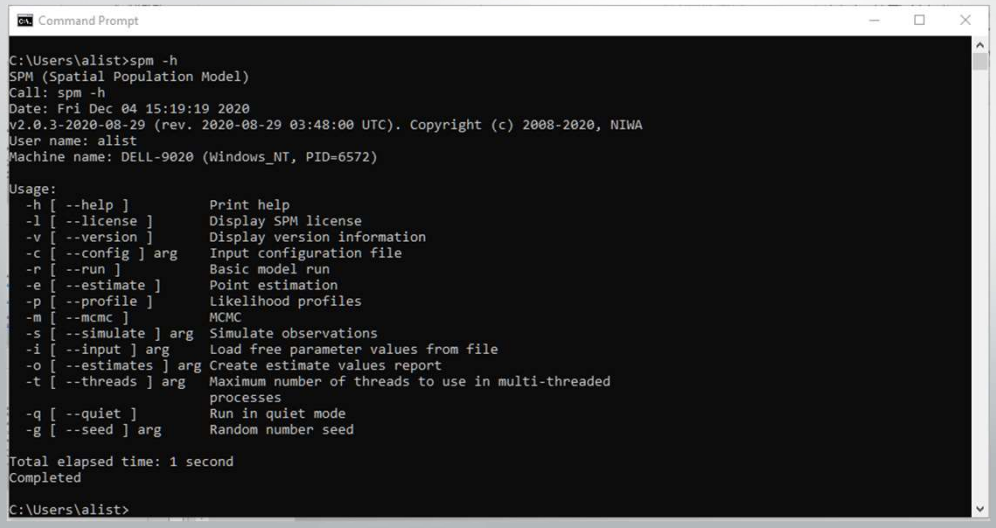

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Typical command lines

- A "run" (without estimation): `spm -r`
- An "estimate" (with estimation): `spm -e`
- "Simulate" observations : `spm -s n_sims`
- Do an MCMC (you probably shouldn't though): `spm -m`
- Etc.

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Versions and reports

- SPM prints to std::out and std::err (although you don't really need to know this)
- std::out gets sent to a file (or many files). This is the output you want to look at
- std::err gets sent to the screen (typically logging of what its doing)
- Almost all output files have a standard header, e.g.,

```
C:\Users\alist>spm -h
SPM (Spatial Population Model)
Call: spm -h
Date: Fri Dec 04 15:19:19 2020
v2.0.3-2020-08-29 (rev. 2020-08-29 03:48:00 UTC). Copyright (c) 2008-2020, NIWA
User name: alist
Machine name: DELL-9020 (Windows_NT, PID=6572)
```

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Redirecting output and standard error

- Modern operating systems allow redirection of std::out and std::err
- Windows

  spm [arguments] > *output_file* 2> *error_file*
- Linux

  (spm [arguments] > *output_file*) >& *error_file* &

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The *config* file

- SPM uses a specific text file and format to specify the model, observations, estimation parameters, and the reports (output)
- These live in the *input parameter configuration* file (the *config* file for short)

  e.g., `spm -c myconfig.spm`
- The default name for this file is `config.spm`
- Other names are allowed but if not the default, then it must be specified

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Config command syntax

- SPM config files contain commands and subcommands.
- Commands are always specified by a leading @ symbol
- Subcommands must follow after the `@command`
- The order of commands and subcommands does not matter
  - Except that subcommands for a command must occur after the command, and before the next command
  - The config file can include other files (which can also include other files) if you want to use multiple files to define the model (see `@include filename`)

this can be useful to manage the files (e.g., the YFT config file is 100 000 lines long!)

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Example of commands and subcommands

```
# Model Structure
@model
nrows 6
ncols 10
layer Base
categories immature mature
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2
initial_year 1995
current_year 2007
cell_length 100
time_steps one two
age_size none none
```

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Documentation is in the manual

- The manual (SPM.pdf) is split into 3 main parts…
  - Introduction and how to use SPM (at the beginning), and summary information (at the end)
  - Descriptions for the model components (split into 4 sections)
    - Population structure, estimation, observations, reports
  - Syntax for commands and subcommands (also split into the same 4 sections)
    - Population structure, estimation, observations, reports
- Its quite long!

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Commands and subcommands from the manual

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 nrows in the spatial structure

Type: Integer

Default: No default

Value: A positive integer, nrows > 0

ncols The number of columns ncols in the spatial structure

Type: Integer

Default: No default

Value: A positive integer, ncols > 0

layer The label for the base layer

Type: String

Default: No default

Value: Must be a label of a numeric layer defined by @layer

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Brief overview: Population section

- Model structure
- Initialisation
- Time steps and processes
- Preference functions (<– a means of moving fish, *see later*)
- Biological information
- Ancillary information (layers, derived parameters, etc.)

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Brief overview: Estimation section

- Estimation methods (and associated parameters)
  - Point estimates, profiles, and MCMCs
- Defining estimated parameters
- Constraints and penalties

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Brief overview: Observation section

- Definitions of observations
  - Observed values
  - Likelihoods and variance/sample sizes
- Proportions-at-age
- Proportions-at-length
- Proportions-by-category
- Proportions-by-category-at-length
- Abundance
- Biomass
- Presence/absence

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Brief overview: Report section

- Determines the information that is written to output
  - Defines the file or files where the get written
- WARNING

  If there are NO @report commands, then SPM will produce NO output!

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Now for some more detail…

- Population section
- Estimation section
- Observation section
- Report section

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Population section (recap)

- Model structure
- Initialisation
- Time steps and processes
- Preference functions (<– a means of moving fish, *see later*)
- Biological information
- Ancillary information (layers, derived parameters, etc.)

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Population section

```
# Model Structure
@model
nrows 6
ncols 10
layer Base
categories immature mature
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2
initial_year 1995
current_year 2007
cell_length 100
time_steps one two
age_size none none
```


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Model structure

- The partition: SPM models a matrix of *categories* by *ages*, inside **each** spatial cell
  - This can take a lot of memory and time!
- Categories are user-defined
  - Species, stocks, sexes, maturity, etc. are all possible
  - Call these categories what you want (e.g., *male*, *female*, *tagged*, *mature*, *bob*, *kate*, *etc.*)
- Updates of the partition occur via *processes (population* or *movement)*
- Observations reference the partition to calculate the 'expected' values

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Partition structure (categories x ages)

Categories	Age=1	Age=2	Age=3	Age=4+
Male_immature	…	…	…	…
Female_immature	…	…	…	…
Male_mature	…	…	…	…
Female_mature	…	…	…	…

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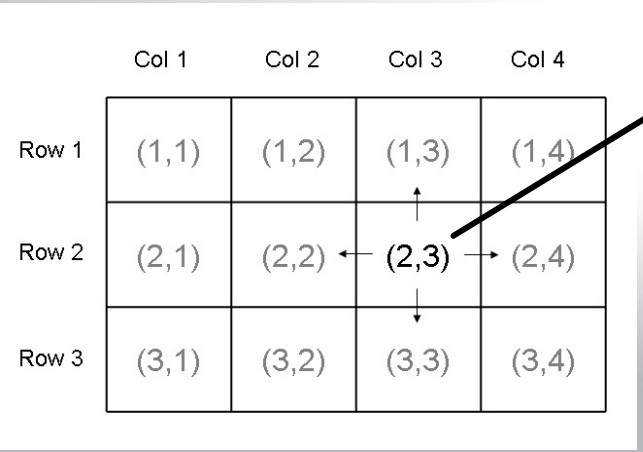
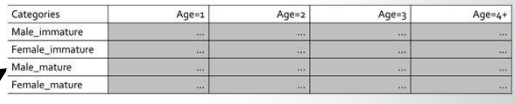
Spatial structure (rows x cols)





Within each spatial cell, we record that cell's population partition

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Population section

- The "action" in the model occurs from of *processes*
- Two types of processes: Population dynamics and movement dynamics
- Population dynamics
  - Biological processes
    - natural mortality, fishing, ageing, recruitment, maturation, etc.
  - Movement processes
    - Preference movement, migration movement, diffusion movement
- We can also include predator-prey interactions, density-dependent processes, etc…

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Population processes

- Similar to other models
  - Recruitment: adds individuals to the "age 1" column in the partition for each spatial cell
  - Ageing: Shifts individuals one column to the right in the partition for each spatial cell
  - Mortality: Removes individuals from the partition for each spatial cell
  - Category transitions: Moves individuals from one (or more) categories, to another for each spatial cell
  - Etc…
- Population processes can be modified for each cell, use selectivities, etc as for a standard model
- Population processes *never* move fish from one spatial cell to another

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Population processes

- There are many sub-types of population process … see the manual
- E.g., for the mortality processes
  - Constant mortality rate (i.e., in y^{-1})
  - Age specific mortality rate
  - Constant exploitation rate (i.e., as a proportion)
  - Annual mortality rate
  - Layer-varying mortality rate
  - Event (abundance) and biomass-event mortality (i.e., fishing)
  - Holling mortality rate (density dependant dynamics using the Michaelis-Menten equation)
  - Prey-suitability mortality rate (predator prey dynamics, Jurado-Molina et al., 2005)

A quick diversion: Layers

- Layers are a key concept in SPM
  - They specify attributes of each cell
  - They must have the same dimensions as the nrows x ncols as the model
  - Most layers are fixed in time, but
    - meta-layers can be used to vary layers over time
    - biomass and abundance layers can be derived (for density dependant processes)
    - layers can be numeric or categorical
    - some layers are compulsory (e.g., the **base** layer)
  - The base layer
    - Defines locations where the population can live or not (and each cell can be non-negative number)
      e.g., water or land for fish
  - Other layers are used as required (e.g., processes and observations)….

Standard layers

```
# Base map
@layer Base
type numeric
data 0 0 0 1 1 1 1 0 0 0
data 0 0 0 1 1 1 1 1 0 0
data 0 1 1 1 1 1 1 1 1 0
data 0 1 1 1 1 1 1 1 1 0
data 1 1 1 1 1 1 1 1 1 1
data 0 0 1 1 1 1 1 1 0 0
```


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Meta-layers

(the way of adding annually varying layers)

```
@layer sst
type numeric_meta
default_layer sst_mean
years 1-256
layers sst_1 sst_2 sst_3 sst_4 sst_5 sst_6 sst_7 sst_8 sst_9 sst_10 sst_11 sst_12 sst_13 sst_14 sst_15 sst_16 sst_17 sst_18 sst_19 sst_20 sst_21 sst_22 sst_23 sst_24 sst_25 sst_26 sst_27
sst_28 sst_29 sst_30 sst_31 sst_32 sst_33 sst_34 sst_35 sst_36 sst_37 sst_38 sst_39 sst_40 sst_41 sst_42 sst_43 sst_44 sst_45 sst_46 sst_47 sst_48 sst_49 sst_50 sst_51 sst_52 sst_53 sst_54
sst_55 sst_56 sst_57 sst_58 sst_59 sst_60 sst_61 sst_62 sst_63 sst_64 sst_65 sst_66 sst_67 sst_68 sst_69 sst_70 sst_71 sst_72 sst_73 sst_74 sst_75 sst_76 sst_77 sst_78 sst_79 sst_80 sst_81
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sst_245 sst_246 sst_247 sst_248 sst_249 sst_250 sst_251 sst_252 sst_253 sst_254 sst_255 sst_256
```


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Other special types of layers

```
@layer SSB
type biomass
categories mature
selectivities one
```

```
@layer distance
type distance
```


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Movement processes

- Movement processes move individuals from one cell to another
- Movement processes *never* change the categories or age of individuals
- Three types of movement
  - Preference based movement (see next slides)
  - Migration (specify the source and the sink cell)
  - Diffusion ("diffuses" fish to a neighbourhood cell)

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Preference movement

- A tricky concept to explain…
  - Based on the idea that movement is driven by underlying environmental (or other) layers
  - Movement can be 'near' or 'far'
    - Attempt to reduce the problem that cell 'size' is a factor that determines rates of movement
    - Preference movement is a product of many interactions from individual preference functions

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

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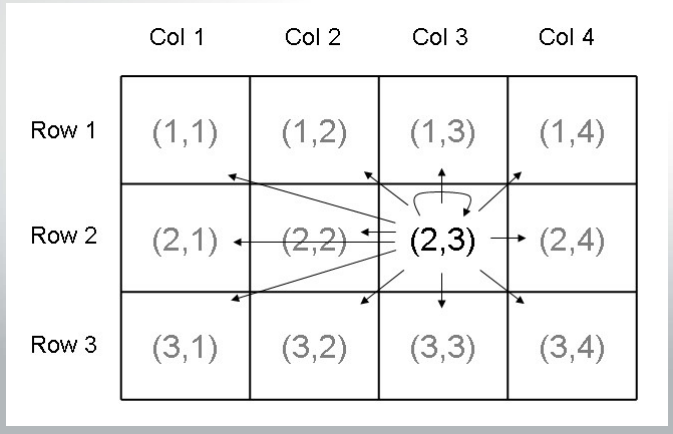
The preference movement process



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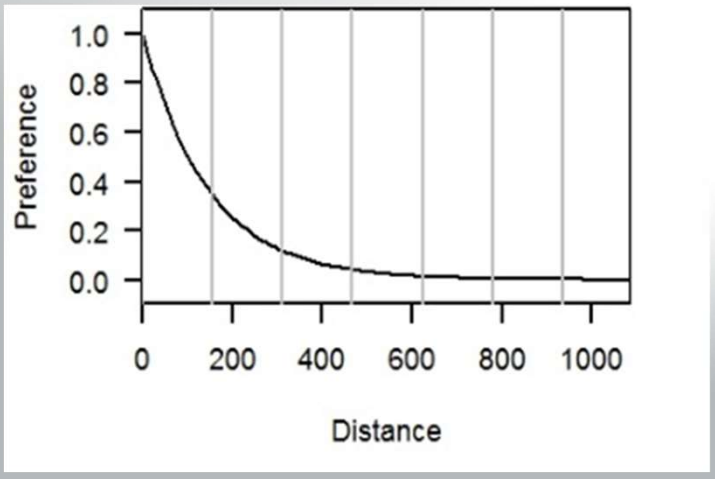
A simple preference function (distance)



This is an exponential decay function, implemented as a function of distance (see **distance** layer earlier), parameterised by lambda

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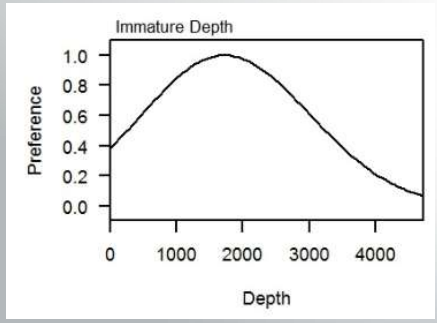
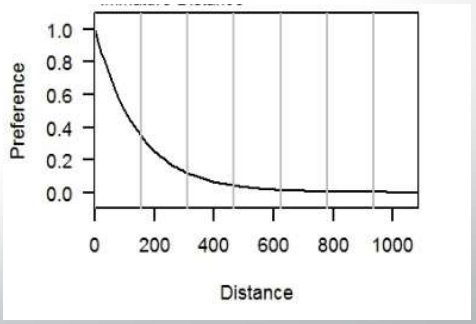
Total preference function





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Preference function

- The total preference function is the product of many individual preference functions
- Individual preference functions are functions of a **layer** (or layers)
  - E.g., we evaluate the relative preference of cells based on the total product of the individual preference functions evaluated at each cell, using the parameters and the value of layers in those cells
- Movement from a cell is defined by the relative preference of each cell according to the total preference function value
- It can apply to a specific age group or range of ages (via a selectivity) and to one or more categories

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Preference functions available

- A range of functions are available
  - Constant
  - Normal
  - Double normal
  - Logistic
  - Inverse-logistic
  - Exponential
  - Threshold
  - Knife-edge
  - Categorical
- Copula preference also available to include a dependence between two variables

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An example…

```
@process moveMature
type preference
categories mature mature_tag
preference_functions distanceMature SSTmature CLOmature
```

```
@preference_function distanceMature
type exponential
alpha 1
lambda 0.001
layer distance

@preference_function SSTmature
type logistic
alpha 1
a50 20
ato95 5
layer sst

@preference_function CLOmature
type logistic
alpha 1
a50 -4
ato95 2
layer clo
```

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Aside: most parameters in SPM can be estimated (if required)

```
@estimate preference_function[distanceMature].lambda
lower_bound 1e-06
upper_bound 10
type uniform

@estimate preference_function[SSTmature].a50
lower_bound 5
upper_bound 60
type uniform

@estimate preference_function[SSTmature].ato95
lower_bound 1
upper_bound 100
type uniform
```

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Annual cycle and time-steps

- Flexible start and final year (i.e., user defined)
- Flexible *annual cycle* with discrete *time steps*
  - Defines the processes that occur, in what order, and when observations are evaluated
- Note the initialisation annual cycle and time steps can be different (handy for phased initialisation to improve speed)

Example of the annual cycle and time steps

```
# Model Structure
@model
nrows 6
ncols 10
layer Base
categories immature mature
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2
initial_year 1995
current_year 2007
cell_length 100
time_steps one two
age_size none none
```

```
@time_step one
processes BHrecruitment Maturation M Fishing

@time_step two
processes MoveImmature MoveMature Ageing
```

Initialisation

- Iterative initialisation
- Can be
  - Multiphase: iteratively resolve one part of the problem, before adding in others
  - Can have a different annual cycle during each phase of initialisation
    - But be careful here!
- Can have early 'stopping' rules if the iterative process resolved more quickly than anticipated

```
@initialisation_phase Phase1
years 100
time_steps one two three
lambda 1e-10
lambda_years 50 60 70 80 90 100
```


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Initialisation

- An alternative to iterative initialisation is to define the (starting) state
- The **category_state_by_age** process

```
@process initialise-immature
type category_state_by_age
category immature
layer Area
min_age 1
max_age 5
data A 2 5 15 8 12
data B 2 5 20 20 8
```

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


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Initialisation

- An alternative to iterative initialisation is to define the starting state
- The **category_state_by_age** process

```
@process initialise-immature
type category_state_by_age
category immature
layer Area
min_age 1
max_age 5
data A 2 5 15 8 12
data B 2 5 20 20 8
```

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

cell	age=1	age=2	age=3	age=4	age=5	age=6
r1-c1	1	2.5	7.5	4	6	0
r1-c2	1	2.5	7.5	4	6	0
r2-c1	1	2.5	10	10	4	0
r2-c2	1	2.5	10	10	4	0

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Biological processes

```
@process Maturation
type category_transition_rate
from immature
to mature
proportions 1.0
selectivities Maturation

@selectivity Maturation
type logistic_producing
l 5
h 30
a50 12.2
ato95 2.8
```

```
@process M
type constant_mortality_rate
categories immature mature
m 0.13 0.13
selectivities One One

@selectivity One
type constant
c 1
```


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Recap: model structure

```
# Model Structure
@model
nrows 6
ncols 10
layer Base
categories immature mature
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2
initial_year 1995
current_year 2007
cell_length 100
time_steps one two
age_size VB VB
```


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Biological parameters

```
@age_size VB
type von_bertalanffy
size_weight basic
k      0.091
t0     -0.117
linf   174.545

@size_weight basic
type basic
a 1.051e-008
b 3.036
```


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Derived quantities

- Some processes require a "derived quantity". These can be a 'total' (or a value by cell). E.g., SSB is a derived quantity needed for the Beverton-Holt stock recruit relationship

```
@derived_quantity SSB
type biomass
time_step step_one
initialisation_time_steps step_one step_one
categories mature
selectivities One
layer spawning_ground
```


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Derived quantities by cell

- Useful for
  - "Local" recruitment process (i.e., benthic organisms)
  - Density dependent processes, predator prey interactions, etc.
- The same as a derived quantity, but 'recorded' for each cell, rather than the total overall

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Selectivities

- A range of selectivity ogives are available
  - Constant
  - Knife-edge
  - All-values (a vector or values by age)
  - All values-bounded (a vector of values by age, but for a subset of ages)
  - Increasing
  - Logistic (and inverse logistic and logistic producing)
  - Double normal (and double exponential)
  - Splines (a variety of types)

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Putting the population section together

```
# Example 2: 10x6 spatial model with preference movement processes

# Model Structure
@model
nrows 6
ncols 10
layer Base
categories immature mature
min_age 1
max_age 30
age_plus_group True
initialisation_phases Phase1 Phase2
initial_year 1995
current_year 2007
cell_length 100
time_steps one two
age_size none none

@age_size none
…

@size_weight none
…

# Initialisation
@initialisation_phase Phase1
…
@initialisation_phase Phase2
…

@time_step initial_step_one
…
@time_step initial_step_two
…

# Annual Cycle
@time_step one # Summer
…
@time_step two # Winter
…

# Derived quantities
@derived_quantity SSB
…

# Population processes
@process Ageing
…
@process BHrecruitment
…
@process M
…
@process Fishing
…
@process Maturation
…
# Movement processes
…
@process MoveMature
…
@preference_function ImmatureDistance
…
@preference_function ImmatureDepth
…
@preference_function ImmatureLatitude
…
@preference_function MatureDistance
…
@preference_function MatureDepth
…
@preference_function MatureLatitude
…

# Definition of layers
@include "layers/Base.spm"
@include "layers/Cell.spm"
@include "layers/Constant.spm"
@include "layers/CPUE.spm"
@include "layers/Depth.spm"
@include "layers/Fishing_1998.spm"
@include "layers/Fishing_1999.spm"
@include "layers/Fishing_2000.spm"
@include "layers/Fishing_2001.spm"
@include "layers/Fishing_2002.spm"
@include "layers/Fishing_2003.spm"
@include "layers/Fishing_2004.spm"
@include "layers/Fishing_2005.spm"
@include "layers/Fishing_2006.spm"
@include "layers/Fishing_2007.spm"
@include "layers/Latitude.spm"
@include "layers/Recruitment.spm"
@include "layers/SSRU.spm"

@layer Distance
…
@layer Abundance
…
@layer Abundance-density
…

# Definition of selectivities
@selectivity One
…
@selectivity Maturation
…
@selectivity FishingSel
…

# Catchability
@catchability CPUEq

# Includes
@include "estimation.spm"
@include "observations.spm"
@include "report.spm"
```


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Observation section

- Definitions of observations
  - Observed values
  - Likelihoods and variance/sample sizes
- Types of observation
  - Proportions-at-age
  - Proportions-at-length
  - Proportions-by-category
  - Proportions-by-category-at-length
  - Abundance
  - Biomass
  - Presence/absence

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Observations (1)

- Each observation is an observation of *something* in a year, at a time step, across a number of spatial cells
- Observations can

  contribute to the likelihood, *or*

  be included as pseudo-observations, *or*

  be included as observations for the purposes of simulation

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Observations (2)

- Observations are supplied as observations at an instance in time (possibly over some spatially aggregated area)
- Time series of observations can be supplied as separate observations for each year or point in time
- Observations are evaluated at the end of a time step
  - But the expected values can be inferred at any point in time between the start and the end of a time step. Seep **proportion_method** in each observations class

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Observation section

- Composition frequencies
  - Proportions-at-age: Observations of proportions at age within categories
  - Proportions-at-length: Observations of proportions at length bin within categories
- Proportions between categories (i.e., proportions mature)
  - Proportions-by-category: Observations of proportions by categories within age classes
  - Proportions-by-category-at-length: Observations of proportions by categories within age classes
- Biomass and abundance observations (CPUE, surveys, etc)
  - Abundance: Relative and absolute abundance (number of fish)
  - Biomass: Relative and absolute biomass (biomass of fish)
- Other
  - Presence/absence: relative proportions present

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Example observation

```
@observation CAA-1998
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True
layer cell
obs r2-c5 0 0 0 0.00409 0.02146 0.00831 0.03836 0.08325 0.06242 0.0854 0.04601 0.11228 0.10244 0.10034 0.05299 0.08555 0.03529 0.02007 0.02677 0.01919 0.01346 0.00775 0.01172 0.01619 0.00961
                0.00835 0.0102 0.00139 0.0051 0.01201
obs r3-c5 0 0 0 0.0106 0.05965 0.06659 0.08638 0.09012 0.05422 0.07038 0.03536 0.07119 0.08309 0.06637 0.05554 0.06758 0.03451 0.02003 0.01972 0.01173 0.0076 0.02246 0.00401 0.01228 0.01052
                0.00861 0.01125 0.00187 0.00479 0.01356
obs r3-c6 0 0 0 0.00292 0.02815 0.02446 0.0929 0.09571 0.05486 0.09705 0.04577 0.07974 0.08562 0.06695 0.05308 0.08523 0.03656 0.03178 0.02135 0.01951 0.01904 0.01915 0.00374 0.00666 0.003
                0.00518 0.01215 0.00148 0 0.00498
obs r4-c3 0 0 0.09996 0.09197 0.19014 0.05221 0.06872 0.09092 0.00622 0.05409 0.05004 0.05407 0.03955 0.04152 0.00656 0.03235 0.00656 0 0 0.00983 0.01748 0.00983 0.00874 0.01967 0.00361
                0.00874 0.00983 0.00361 0 0
obs r4-c4 0 0 0.04694 0.10581 0.23716 0.06041 0.07292 0.09645 0.06859 0.07861 0.03401 0.05064 0.03765 0.02733 0.01321 0.02297 0.0058 0.00757 0.00392 0.00069 0.00262 0.00358 0.00173 0.00116
                0.007 0 0.00153 0 0.00129 0.00095
obs r4-c6 0 0 0 0 0 0.00435 0.00435 0 0 0.00725 0.01812 0.02754 0.05072 0.12319 0.07029 0.11014 0.03551 0.06232 0.07935 0.07645 0.02826 0.05725 0.02029 0.05942 0.02899 0.05072 0.02391 0.0087
                0.02029 0.03261
error_value r2-c5 148
error_value r3-c5 132
error_value r3-c6 119
error_value r4-c3 35
error_value r4-c4 157
error_value r4-c6 58
likelihood multinomial
delta 1e-11
```


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Proportions-at-age (1)

```
@observation CAA-1998
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True
layer cell
obs r2-c5 0 0 0 0.00409 0.02146 0.00831 …
obs r3-c5 0 0 0 0.0106 0.05965 0.06659 …
obs r3-c6 0 0 0 0.00292 0.02815 0.02446 …
obs r4-c3 0 0 0.09996 0.09197 0.19014 …
obs r4-c4 0 0 0.04694 0.10581 0.23716 …
obs r4-c6 0 0 0 0 0 0.00435 0.00435 0 …
error_value r2-c5 148
error_value r3-c5 132
error_value r3-c6 119
error_value r4-c3 35
error_value r4-c4 157
error_value r4-c6 58
likelihood multinomial
delta 1e-11

@report CAA-1998
type observation
observation CAA-1998
```

Note the names of the "spatial cells"

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Proportions-at-age (1)

```
@observation CAA-1998
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True
layer cell
obs r2-c5 0 0 0 0.00409 0.02146 0.00831 …
obs r3-c5 0 0 0 0.0106 0.05965 0.06659 …
obs r3-c6 0 0 0 0.00292 0.02815 0.02446 …
obs r4-c3 0 0 0.09996 0.09197 0.19014 …
obs r4-c4 0 0 0.04694 0.10581 0.23716 …
obs r4-c6 0 0 0 0 0 0.00435 0.00435 0 …
error_value r2-c5 148
error_value r3-c5 132
error_value r3-c6 119
error_value r4-c3 35
error_value r4-c4 157
error_value r4-c6 58
likelihood multinomial
delta 1e-11

@report CAA-1998
type observation
observation CAA-1998
```

Note the names of the "spatial cells"

```
# Base cell reference map
@layer cell
type categorical
data r1-c1 r1-c2 r1-c3 r1-c4 r1-c5 r1-c6 r1-c7 r1-c8 r1-c9 r1-c10
data r2-c1 r2-c2 r2-c3 r2-c4 r2-c5 r2-c6 r2-c7 r2-c8 r2-c9 r2-c10
data r3-c1 r3-c2 r3-c3 r3-c4 r3-c5 r3-c6 r3-c7 r3-c8 r3-c9 r3-c10
data r4-c1 r4-c2 r4-c3 r4-c4 r4-c5 r4-c6 r4-c7 r4-c8 r4-c9 r4-c10
data r5-c1 r5-c2 r5-c3 r5-c4 r5-c5 r5-c6 r5-c7 r5-c8 r5-c9 r5-c10
data r6-c1 r6-c2 r6-c3 r6-c4 r6-c5 r6-c6 r6-c7 r6-c8 r6-c9 r6-c10
```

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Proportions-at-age (3)

```
@observation CAA-1998
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True
layer SSRU
obs 881M 0 0 0 0.00409 0.02146 0.00831 …
obs 881J 0 0 0 0.0106 0.05965 0.06659 …
obs 882A 0 0 0 0.00292 0.02815 0.02446 …
obs 881K 0 0 0.09996 0.09197 0.19014 …
obs 881C 0 0 0.04694 0.10581 0.23716 …
obs 881D 0 0 0 0 0 0.00435 0.00435 0 …
error_value 881M 148
error_value 881J 132
error_value 882A 119
error_value 881K 35
error_value 881C 157
error_value 881D 58
likelihood multinomial
delta 1e-11

@report CAA-1998
type observation
observation CAA-1998
```

```
# SSRUs
@layer SSRU
type categorical
data Other Other Other 881M 881J 881L 882B 882C 882D 882D
data Other Other Other 881M 881J 881K 882A 882B 882C 882D
data Other Other 881F 881H 881H 881I 882A 882B 882B 882C
data Other 881D 881E 881E 881G 881C 882A 882A 882B 882C
data 881A 881A 881A 881A 881B 881C 882A 882A 882B 882B
data Other 881A 881A 881B 881C 881C 882A Other Other
```

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Proportions-at-age (4)

```
@observation CAA-1998
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True
layer cell
obs r2-c5 0 0 0 0.00409 0.02146 0.00831 0.03836 0.08325 0.06242 0.0854 0.04601 0.11228 0.10244 0.10034 0.05299 0.08555 0.03529 0.02007 0.02677 0.01919 0.01346 0.00775 0.01172 0.01619 0.00961
                0.00835 0.0102 0.00139 0.0051 0.01201
obs r3-c5 0 0 0 0.0106 0.05965 0.06659 0.08638 0.09012 0.05422 0.07038 0.03536 0.07119 0.08309 0.06637 0.05554 0.06758 0.03451 0.02003 0.01972 0.01173 0.0076 0.02246 0.00401 0.01228 0.01052
                0.00861 0.01125 0.00187 0.00479 0.01356
obs r3-c6 0 0 0 0.00292 0.02815 0.02446 0.0929 0.09571 0.05486 0.09705 0.04577 0.07974 0.08562 0.06695 0.05308 0.08523 0.03656 0.03178 0.02135 0.01951 0.01904 0.01915 0.00374 0.00666 0.003
                0.00518 0.01215 0.00148 0 0.00498
obs r4-c3 0 0 0.09996 0.09197 0.19014 0.05221 0.06872 0.09092 0.00622 0.05409 0.05004 0.05407 0.03955 0.04152 0.00656 0.03235 0.00656 0 0 0.00983 0.01748 0.00983 0.00874 0.01967 0.00361
                0.00874 0.00983 0.00361 0 0
obs r4-c4 0 0 0 0.04694 0.10581 0.23716 0.06041 0.07292 0.09645 0.06859 0.07861 0.03401 0.05064 0.03765 0.02733 0.01321 0.02297 0.0058 0.00757 0.00392 0.00069 0.00262 0.00358 0.00173 0.00116
                0.007 0 0.00153 0 0.00129 0.00095
obs r4-c6 0 0 0 0 0 0.00435 0.00435 0 0 0.00725 0.01812 0.02754 0.05072 0.12319 0.07029 0.11014 0.03551 0.06232 0.07935 0.07645 0.02826 0.05725 0.02029 0.05942 0.02899 0.05072 0.02391 0.0087
                0.02029 0.03261
error_value r2-c5 148
error_value r3-c5 132
error_value r3-c6 119
error_value r4-c3 35
error_value r4-c4 157
error_value r4-c6 58
likelihood multinomial
delta 1e-11
process_error 50
```

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Proportions-at-age (5)

```
@observation CAA-1998a
type proportions_at_age
year 1998
time_step one
categories immature + mature
selectivities FishingSel FishingSel
min_age 1
max_age 30
tolerance 0.01
age_plus_group True


@observation CAA-1998b
…
categories immature  mature
…

@observation CAA-1998c
…
categories male_immature  + male_mature   female_immature + female_immature
…
```

Combined categories

Separate categories

Combined & separate categories

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Proportions-by-category

```
# Proportions mature (2002)
@observation mature-2002
type proportions_by_category
year 2002
time_step one
categories mature
categories2 immature
selectivities FishingSel
selectivities2 FishingSel
min_age 1
max_age 30
age_plus_group True
layer cell
obs r1-c6 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
obs r1-c7 0 0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 1 1 0 1 1 1 0 0 1 0 1
error_value r1-c6 0 0 0 0 0 0 0 0 0 0 0 0 0.787321602766333 0.34561403690674 1.13656511836189 0.339598241696144 1.97260446913269
        1.63108455705452 2.61832196981598 1.89204376675641 0.617082446534434 1.01619406867846 0.506579197325262 1.04978500403117
        1.35523207671698 0.26735423045293 0.313148903242939 1.25399868831737 0.363334993774255 0.303227308894021
        0.312798722780255
error_value r1-c7 0 0 0 0 0 0 0 0 0 0 0 0 0.351374171679312 0.00564558759137334 0.895055623231706 0.87507361556791 0.928122482467766
        1.53171257719831 0.695603300220298 0.903583975480345 1.68662506324844 0.0348463028891523 0.53670383340713
        0.430556416668389 0.478921468852145 0 0 0.333738157718646 0 0.410913872452334
likelihood binomial
delta 1e-11
```


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Likelihoods

- Different likelihoods available (and depending the observation)
- Does allow likelihood modifiers
  - Likelihood (defines the likelihood for the observation)
  - process_error (modifies the c.v.s or the N)
  - likelihood_multiplier (scaler on the likelihood)
  - simulation_likelihood (define the likelihood for simulations, if different)

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Other observations

- Other observations
  - Proportions-at-length
  - Proportions-by-category-at-length
  - Abundance
  - Biomass
  - Presence/absence
- Slightly different syntax (as required for the different types)

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Next week

- Recap on the population section
- More on the observation, estimation, and report sections
  - Tag data
- Additional SPM command line arguments
- The R library (for reading and writing)
- Examples
- Issues and questions

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