



# Getting started with CASAL2

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## 1. Introduction

This document is an introductory help guide for CASAL2, a generalised age-structured population dynamic modelling package. CASAL2 is run through the command prompt/terminal where it reads text files (configuration files) which define the model. CASAL2 then prints output to a screen or a file or errors out gracefully. This short document is aimed at users who are new to CASAL2. CASAL2 is primarily used for assessing fish populations, but is by no means specific to fish population dynamics. CASAL2's predecessor is the primary tool used in assessing New Zealand's tier one stocks, it is also the standard tool used by CCAMLR for modelling Antarctic toothfish.

CASAL2 is very general, highly flexible, and therefore can be a bit daunting at first sight. It has a large number of run modes, settings, and user defined population dynamics choices that can be turned on and off, depending on circumstances such as, population life history and available data. While there is no requirement for a user to see or understand the underlying code base, great effort has been put into developing a code base that can be easily interpreted by novice programmers. The code has been well tested.

CASAL2 is open source, and is covered under the GNU GPL 2.0 licence. See the terms and conditions in the CASAL2 Technical User Manual (Rasmussen et al., 2016), or type `casal2 -l` into the command prompt. There is also supplementary information that may be useful when getting familiar with CASAL2. CASAL2 has a comprehensive user manual (Rasmussen et al., 2016) which should be consulted for detail on any model component. CASAL2 also has a contributors guide to help users add any functionality for any problem, the modular structure of the code base can make adding new processes, observations and likelihoods a breeze. If you have any questions, please contact the CASAL2 development team at [casal2@niwa.co.nz](mailto:casal2@niwa.co.nz).

The remaining content of this chapter describes requirements and details about how to run, cite, get licensing and contact info for CASAL2. If you are new to population modelling then section 2 describes the types of data needed to run a CASAL2 model. Section 2 is a good starting point to find out if you have the data for writing a new model. Otherwise you can use CASAL2 as an operating model to simulate data. The remaining content of the document explains how to run CASAL2, the syntax of the input configuration files that CASAL2 finally we run through an example.

### 1.1. Version

CASAL2 can differ between version, especially as issues are fixed or new features added. The CASAL2 version number is suffixed with a date/time stamp (yyyy-mm-dd), giving the revision control system UTC date for the most recent modification of the underlying software source code. User manual updates will usually be issued for each minor version or date release of CASAL2.

### 1.2. Citing the CASAL2 Getting Started Guide

A suitable reference for this document is:

C. Marsh (2019). Getting started with CASAL2. National Institute of Water & Atmospheric Research Ltd.. 22 p.

### 1.3. Software license

This program and the accompanying materials are made available under the terms of the licence GNU GPL v2 which accompanies this software.

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### 1.4. System requirements

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

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

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

### 1.5. Necessary files

For both 64-bit Linux and Microsoft Windows, only the executable file `casal2` or `casal2.exe` is required to run CASAL2 with non-auto differentiable minimisers. If you wish to use the auto differentiable minimisers the `.dll` for windows and `.so` for Linux must be in the same folder as the executable CASAL2 files or in your system path. No other software is required. We do not compile a version for 32-bit operating systems.

CASAL2 offers an **R** library for post-processing of model output, so we suggest users download software such as **R** (R Core Team, 2014) to assist in the post processing of CASAL2 output (see the CASAL2 User Manual Chapter 17 (Post=Processing) for more detail on the **R** package).

### 1.6. Getting help

CASAL2 is distributed as unsupported software, however we would appreciate being notified of any problems or errors in CASAL2. See the CASAL2 User manual (Rasmussen et al., 2016) for the recommended template for reporting issues.



## **2. Data Requirements**

The information that is required to setup and run an age based model in CASAL2, but is by no means the end all and be all (because you can add in any functionality you wish). An age based model refers to how CASAL2 keeps track of the population, this is by keeping track of the numbers at age for each category in the population.

1. Catch History (currently CASAL2 assumes this is known without error)
2. Time series of relative/absolute abundance/biomass
3. Age/length compositional data (if you want to estimate selectivities or year class strengths)
4. Some recruitment process
5. Biological information (e.g. growth, maturity, life cycle)

In theory recruitment and biological information is all that is needed to run a CASAL2 model, obviously that would not include any anthropogenic exploitation processes and so can be thought of as a equilibrium or steady-state model.

The biological information that would be required will depend on if you are going to need to do weight calculations. For an age based model you will need to specify

1. length at age @age\_length
2. weight at length @length\_weight
3. natural mortality @process



**Figure 2.1: An example of a Von Bertalanffy growth curve.**

### 3. Where to get CASAL2

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

A Microsoft Windows bundle includes the binary, manual, examples and other help guides. It can be downloaded at <ftp://ftp.niwa.co.nz/Casal2/windows/Casal2.zip> for the Microsoft Windows version. The Linux bundle which includes a binary, manual, examples and other help guides can be downloaded at <ftp://ftp.niwa.co.nz/Casal2/linux/Casal2.tar.gz>.

For both 64-bit Linux and Microsoft Windows, only the executable file `casal2` or `casal2.exe` is required to run CASAL2 with non-auto differentiable minimisers. If you wish to use the auto differentiable minimisers the `.so` or `.dll` must be in the same folder as the executable CASAL2files.

If you cannot run the following command `casal2 -h` you may need to shift `casal2_release.so` to `/usr/local/lib/` (which is where your system may expect to find it).

## 4. How it works

CASAL2 is run from a console windows in Microsoft Windows or in a terminal window in Linux, CASAL2 is executed by typing `casal2 -"parameter"`, where "parameter" defines the run type of CASAL2. Once a CASAL2 has been executed with a certain parameter CASAL2 reads in text files. These text files define the model structure and the output wanted. For help on the parameters available and there descriptions type `casal2 --help`, this will print a help screen. There are multiple modes that CASAL2 can be run in. The modes and corresponding parameters include deterministic run `-r`, parameter estimation `-e`, parameter profiling `-p`, mcmc runs `-m`, and projections `-f`. There are two ways of printing output, the default is to print all output to screen, the second is to print output to a file. The second is usually the preferred if you intend on post processing output i.e. create plots. The following example shows how to read in text file that out model is configured in (`My_model.txt`) and run an estimation on some parameters in that model, then print the output to a file named `output.txt`.

```
casal2 -e -c My_model.txt > output.txt
```

CASAL2 calls the program, `-e` tells the program it is going to do an estimation. `-c` is the parameter that gives the name of the text file with the configured model is, and `>` is the command to specify the file name where the output is printed. If the `-c` is not supplied CASAL2 will search for a file names `config.csl2`.

A list of the main run modes in CASAL2 with more of a description.

- `casal2 -r` will run the model from `start_year` to `final_year` with the parameters in the configuration file or will use parameters specified using the `-i` functionality.
- `casal2 -e` will run the model in `-r` many times trying to solve for the global solution.
- `casal2 -f 1` is the projection mode and will run the model from `start_year` to `projection_final_year` applying any `@project` functionality. Because most of the `@project` functionality are stochastic in nature, for a given set of parameters you can do many projections. For example `casal2 -f 50` will do 50 projection runs. If you have multiple candidate parameters (maybe from an mcmc) you could do `casal2 -f 50 -i mcmc_params.out` 50 projections for each set, in theory propagating more uncertainty into future predictions.
- `casal2 -s 1` is the simualtion mode, and CASAL2 will run from `start_year` to `final_year`. It will generate expectations for all `@observation` blocks that will be passed to random number generateors to generate simulated data. You will need to add the neccassary reports that will generate observation files that can be re-estiamted.
- `casal2 -m` is the mcmc mode and will run an MCMC estimation defined by subcommands in the `@mcmc`.

## 5. Syntax of a CASAL2 file

A general structure of CASAL2 files are that they are split into blocks of subcommands. A block always starts with @ symbol. Blocks describe different aspects of the model, fundamental blocks to have in the model are @model, @initialisation\_phase, @categories, @time\_step, and @process. Within each block there will be subcommands some will be optional and important subcommands will be mandatory. An example of subcommand is shown for the @model block,

```
@model
type age ## is the model age or length based?
min_age 1 ## minimum age in model
max_age 17 ## maximum age in model
age_plus true ## is the last age group a plus group?
start_year 1972 ## the first year of the model
final_year 2013 ## the first year of the model
initialisation_phases phase1
## The label for the block @intialisation_phase
time_steps step1 step2
## Labels for the block @time_step
```

The subcommands are all the options that follow @model, then there is a space which is where the value for the subcommand goes, i.e. min\_age specifies the minimum age in the model and we have set that equal to one but could be any integer. This brings up a useful concept to understand. Different subcommands can take different types of parameters, they can be of type int, double, string and vector. For information about which parameter type a subcommand takes, you should read the syntax section of the manual, there is a field labelled type. If you use the wrong type for a subcommand, for example min\_age 1.5, you will get an error. A line beginning with # is a comment and that line is ignored by CASAL2. To comment out multi-lines the user can use the C++ syntax of /\* and \*/ everything between these braces will be ignored by CASAL2. It is a useful tool for annotating models.

## 6. Components of a model

Components of a model that are important to know before setting up a CASAL2 model are, How many categories are in the partition, what processes occur to which categories in which order, where observations fit in to the model, and what the assumed state of the partition is before the model years run. CASAL2 runs in yearly cycles each year is split up by time steps, So processes such as fishing and spawning seasons will have an effect on how to specify time steps and so will observations such as annual surveys. The next section runs through a very simple example.

Identifying the partition is an important part and will be usually constrained by the information available. Categories in the partition should be included if they have varying biological characteristics, or life-history traits. Some examples why you would have multiple categories in the partition.

1. Varying growth
2. spatially, temporally varying exploitation (a fishery may target habitats physical characteristics that are more associated with some categories than others.)
3. Disproportional recruitment (60% males 40% females)
4. Tracking maturity
5. Tracking tagged fish - this related to observations

## 7. Examples

### 7.1. Simple Example

In the following example describe a situation then go on to configure a CASAL2 file to run. In this example we have a single area, single stock that has one fishery associated with it. We assume that the partition is made up of a single category (no sex or maturity in the partition). Processes and observations that occur in a typical year in the following order.

1. Recruitment
2. Fishing mortality with natural mortality
3. A survey takes place out of the fishing season and in the spawning season
4. More natural mortality
5. At the end of the year all the fish are aged.

The following model would have the following structure.

```
@model
start_year 1975 # Start year
final_year 2012 # Current year
min_age 1 # min age of all categories
max_age 30 # max age of all categories
age_plus true # is the last age a plus group
base_weight_units tonnes
initialisation_phases Equilibrium_state
time_steps Sep_Feb Mar_May Jun_Aug ## Defines the time steps

@categories
format Stock ## format of the category labels
names CHAT4 ## category labels
age_lengths CHAT4_AL ## Labels of age-length relationship for each category
```

The `@categories` command defines the label, number and age-length relationship of categories that make up the partition. A category is a group of individuals that have the same attributes, some examples of such attributes are, life history and growth paths. Characters in a populations that cause differing attributes can be, sex, maturity, multiple area, multiple stock's and tagging information. An example of the `@categories` block for a simple two area model with male and female in the partition.

```
@time_step Sep_Feb
processes Recruitment Instantaneous_Mortality

@time_step Mar_May
processes Instantaneous_Mortality

@time_step Jun_Aug
processes Ageing Instantaneous_Mortality
```

The `@time_step` command describes which processes are implemented and in what order. We will continue on from the `@model` block example, where we defined two time steps in the annual cycle

(time\_steps Sep\_Feb Mar\_May Jun\_Aug). In each year we have two time steps, within each time step we have processes each process must be derined in @process block the following processes are described.

```
@process Recruitment
type recruitment_beverton_holt
categories HAK4
proportions 1
b0 44000
yces_years 1974:2011
yces_values      1*38
steepness 0.9
ssb SSB
age 1
standardise_yces_years 1975:2009
```

```
@process Instantaneous_Mortality
type mortality_instantaneous
m 0.2
time_step_ratio 0.42 0.25 0.33
selectivities One
categories HAK4
table catches
year FishingWest FishingEest
1975 80 111
1976 152 336
1977 74 1214
1978 28 6
1979 103 506
1980 481 269
1981 914 83
1982 393 203
1983 154 148
1984 224 120
1985 232 312
1986 282 80
1987 387 122
1988 385 189
1989 386 418
1990 309 689
end_table
```

```
table fisheries
fishery category selectivity u_max time_step penalty
Fishing CHAT4 FSel 0.7 step1 Catchmustbetaken
end_table
```

```
@process Ageing
type ageing
categories CHAT4_AL
```

The above defines all the processes that occur to the partition. In the process Mortality we associate a selectivity to natural mortality and in the fisheries table FSel, this would be defined as follows.

```
@selectivity One
```



```

type constant
c 1

@selectivity FSel
type double_normal
mu 3.82
sigma_l 1.63
sigma_r 17

```

If a age-length relationship is specified in the @categories block then the @age\_length block needs to be defined, this block is used to convert age to length which is then used to convert length to weight in an age based model, it is specified as follows,

```

@age_length CHAT4_AL
type von_bertalanffy
length_weight CHAT4_LW ## label for @length_weight block
k 0.164
t0 -2.16
linf 100.8

@length_weight CHAT4_LW ## label from @age_length block
type basic
units tonnes
a 4.79e-09
b 2.89

```

The last important block to complete the population text file, is the @initialisation\_phase. This block of commands specifies how you initialise your partition. This describes the state of the partition before start\_year of the model, usually this is an equilibrium state. The subcommands available for this block are as follows,

```

@initialisation_phase phase1
type iterative ## Type of initialisation method see manual for more
years 100 ## How many years to run for

```

In the above example we have an iterative initialisation type. This will default to iterating your annual cycle for 100 years, which may or may not cause your partition to hit an equilibrium state. **N.B.** when using this initialisation method you as the user must check if the partition has reached an acceptable equilibrium state.

The next section we are defining is the observation section. We have a survey that occurs in the second time step, which is of relative abundance, this would be defined as follows.

```

@observation Survey ## label of observation
type biomass ## tyoe of observation
time_step Sep_Feb ## which time step the observation occurs
time_step_proportion 0.5 ## the observation occurs half way through the time step
categories CHAT4
selectivities One
catchability q ## The label for @catchability block
years 1992 1993 1994 1995
obs 2950 3353 3303 2457
error_value 0.41 0.52 0.91 0.61
likelihood lognormal ## likelihood to use for the objective function

```

```
@catchability q ## label from @observation  
type free  
q 0.001 ## The value
```

If you would like to see a complete model configuration of the model we have just started to go through, go to the `CASAL2/Examples/Simple`. To run the simple example which is located in `CASAL2/Examples/Simple`. [shift] + right click — > open command window in the above directory. Type in the command window `casal2 -r` and output should print to screen.

## 8. Analyses of output

An important note about CASAL2 is that there are no default reports. That is if you don't specify a `@report` block CASAL2 will not report any output. So before you run a CASAL2 model do check you have at least one `@report`.

CASAL2 has an **R** library **casal2** which imports CASAL2 output files into **R** as a list. This library can be found in the directory where you installed the program. There is also another library that helps pull out compress useful information such SSB's and Objective scores for datasets.

```
library(casal2)
output = extract.mpd(file = "Output_file.txt", path = "Directory_of_file")
```

## 9. References

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## 10. Acknowledgements

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