

# Package ‘CASAL2’

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**Title** CASAL2 extract package

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**Description** A set of R functions for extracting and plotting from CASAL2 output files.

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check_short_hand	<i>Utility extract function</i>
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Description

Utility extract function

Usage

check\_short\_hand(x)

Author(s)

Craig Marsh

---

convert.to.lines	<i>Utility extract function</i>
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Description

Utility extract function

Usage

convert.to.lines(filename)

Author(s)

Dan Fu

---

DoubleExponential	<i>Calculate the Double-Exponential Selectivity used in Casal2</i>
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---

**Description**

This function calculates the Double-Exponential selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
DoubleExponential(age_or_length, x0, x1, x2, y0, y1, y2, alpha = 1)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
x0	"numeric" See manual for formal definition of these parameters
x1	"numeric"
x2	"numeric"
y0	"numeric"
y1	"numeric"
y2	"numeric"
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

DoubleNormal	<i>Calculate the Double-Normal Selectivity used in Casal2</i>
--------------	---

---

**Description**

This function calculates the Double-Normal selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
DoubleNormal(age_or_length, alpha = 1, mu, sigma_l, sigma_r)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
mu	"numeric" Mean of the selectivity
sigma_l	"numeric" left hand standard deviation of the selectivity
sigma_r	"numeric" Right hand standard deviation of the selectivity

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

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evalit	<i>Utility plot function</i>
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**Description**

Utility plot function

**Usage**

```
evalit(x)
```

**Author(s)**

Craig Marsh

---

extract	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
extract(file, path = "")
```

**Arguments**

file	the name of the input file containing model output to extract
path	Optionally, the path to the file
validate	Optionally, validate the structure of each element in the report section
conversion	Optionally, where possible, convert elements from list_element and data.frame into numeric

**Author(s)**

Dan Fu

---

extract.csl2.file	<i>Model configuration write function</i>
-------------------	---

---

**Description**

This function reads a Casal2 configuration file and returns a list object in R. Where each element is a command and subcommand from the configuration file

**Usage**

```
extract.csl2.file(file, path = "")
```

**Arguments**

file	the name of the input file containing model configuration
path	Optionally, the path to the file

**Author(s)**

Craig Marsh

---

get.casal2_list	<i>Utility function</i>
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---

**Description**

Utility function

**Usage**

```
get.casal2_list()
```

**Author(s)**

Craig Marsh

---

get.line.label	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
get.line.label(line)
```

**Author(s)**

Dan Fu

---

get.line.type	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
get.line.type(line)
```

**Author(s)**

Dan Fu

---

get.lines	<i>Utility extract function</i>
-----------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
get.lines(lines, from = -1, to = -1, contains = "", starts.with = "",  
clip.to = "", clip.from = "", clip.to.match = "",  
clip.from.match = "", ...)
```

**Author(s)**

Dan Fu

---

Increasing

---

*Calculate the Increasing Selectivity used in Casal2*


---

**Description**

This function calculates the Increasing selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
Increasing(age_or_length, alpha = 1, v, low, high)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
v	"vector<numeric>" A vector of selectivities, must have a one for one relationship with age_or_length.
low	"numeric" age or length at which selectivity is set = 0 below
high	"numeric" age or length at which selectivity is set = alpha above

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

InverseLogistic

---

*Calculate the Inverse-Logistic Selectivity used in Casal2*


---

**Description**

This function calculates the Inverse-Logistic selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
InverseLogistic(age_or_length, alpha = 1, a50, ato95)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
a50	"numeric" age or length where selectivity 50%
ato95	"numeric" age or length difference where selectivity goes from 50% - 95% selective

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

is.all.numeric	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
is.all.numeric(x, what = c("test", "vector"), extras = c(".", "NA", "na",
  "null", "NULL"))
```

**Author(s)**

Dan Fu (not really)

---

is.even	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
is.even(x)
```

**Author(s)**

Dan Fu



---

is.in	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
is.in(x, y)
```

**Author(s)**

Dan Fu

---

is.odd	<i>Utility extract function</i>
--------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
is.odd(x)
```

**Author(s)**

Dan Fu

---

KnifeEdge	<i>Calculate the KnifeEdge Selectivity used in Casal2</i>
-----------	---

---

**Description**

This function calculates the KnifeEdge selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
KnifeEdge(age_or_length, alpha = 1, Edge)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
edge	"numeric" age or length at which selectivity is 0 to the left or alpha to the right

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

Logistic

*Calculate the Logistic Selectivity used in Casal2*

---

**Description**

This function calculates the Logistic selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
Logistic(age_or_length, alpha = 1, a50, ato95)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
a50	"numeric" age or length where selectivity 50%
ato95	"numeric" age or length difference where selectivity goes from 50% - 95% selective

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

LogisticProducing	<i>Calculate the Logistic-Producing Selectivity used in Casal2</i>
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---

**Description**

This function calculates the Logistic-Producing selectivity and should be used to plot up the form of the selectivity when estimating the parameters in the model.

**Usage**

```
LogisticProducing(age_or_length, alpha = 1, a50, ato95, high, low)
```

**Arguments**

age_or_length	"vector<numeric>" A vector of ages and or lengths to calculate the selectivity over.
alpha	"numeric" The capping parameter of the selectivity, to move the max away from one
a50	"numeric" age or length where selectivity 50%
ato95	"numeric" age or length difference where selectivity goes from 50% - 95% selective
high	"numeric" age or length at which selectivity is set = alpha above
low	"numeric" age or length at which selectivity is set = 0 below

**Value**

"vector<numeric>" selectivity values over the age/length range and parameters supplied

**Author(s)**

Craig Marsh

---

make.complete_vector	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
make.complete_vector(lines)
```

**Author(s)**

Dan Fu

---

make.data.frame	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
make.data.frame(lines)
```

**Author(s)**

Dan Fu

---

make.list	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
make.list(lines)
```

**Author(s)**

Dan Fu

---

make.list_element	<i>Utility extract function</i>
-------------------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
make.list_element(lines)
```

**Author(s)**

Dan Fu

---

make.matrix	<i>Utility extract function</i>
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---

**Description**

Utility extract function

**Usage**

```
make.matrix(lines)
```

**Author(s)**

Dan Fu

---

make.named_complete_vector	<i>Utility extract function</i>
----------------------------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
make.named_complete_vector(lines)
```

**Author(s)**

Dan Fu

---

make.vector	<i>Utility extract function</i>
-------------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
make.vector(lines)
```

**Author(s)**

Dan Fu

---

param.profile	<i>Generate an objective score profile plot for a particular parameter as a consequence from a casal2 -p run</i>
---------------	--

---

## Description

This function reads an extracted list from Casal2 and plots the likelihood/objective profile for one or many observations over the specified parameters range. This range is defined in the profile block of the Casal2 configuration file. Casal2 calculates the profile steps as even intervals between the upper and lower bound by  $= (\text{upper\_bound} - \text{lower\_bound}) / (\text{steps} + 1)$

## Usage

```
param.profile(obs, param, extract_list, Rescale = F,
  ylab = "Objective contribution", xlab = "Parameter", y_min = -0.5)
```

## Arguments

obs	"vector<string>" A vector of report labels that correspond to observations that you would like to plot the profile for. Can be many observations
param	"string" The parameter label that the profile was run for. It should follow the syntax that is used in Casal2 that is, "block[label].parameter" e.g. process[Recruitment].b0
extract_list	"string" The name of the R object that was extracted into R using the extract() function.
Rescale	"bool/logical" If true it will rescale the likelihoods to have a minimum on 0. This is done by subtracting off the minimum value of the likelihood series.
ylab	"string" optional, y-axis label
xlab	"string" optional, x-axis label
ymin	"numeric" optional, minimum value parsed to the ylim parameter in plot()

## Author(s)

Craig Marsh

## Examples

```
library(CASAL2)
Profile = extract("profile.log") ## this is an output file from a casal2 -p run
param.profile(obs = c("Tangaroa_propn_at_age_Jan", "trawl_propn_at_age"),
  param = "process[Instantaneous_Mortality].m(male)", extract_list = "Profile",
  Rescale = T, ylab = "Objective contribution", xlab = "M")
```

---

param.profile.by.cohort

*Generate an objective score profile plot for a particular parameter and age compositional dataset as a consequence from a casal2 -p run.*

---

## Description

This function reads an extracted list from Casal2 and plots the likelihood/objective profile for an age compositional observation over the specified parameters range. This range is defined in the profile block of the Casal2 configuration file. Casal2 calculates the profile steps as even intervals between the upper and lower bound by  $(\text{upper\_bound} - \text{lower\_bound}) / (\text{steps} + 1)$ . The plot will generate a line for each cohort and category. The reason I made this function was for the specific investigation of the natural mortality parameter M. Sometimes running a profile of aggregated compositional data on a parameter is not that informative. The aim of this plot is to show which cohorts are suggestive of certain parameters values, this will either create more confusion (most likely) or at least give the user something interesting to think about (perhaps cohort based processes).

## Usage

```
param.profile.by.cohort(obs, param, extract_list, Rescale = F,
  ylab = "Objective contribution", xlab = "Parameter", y_min = -0.5,
  threshold = 10)
```

## Arguments

obs	"string" A report label that correspond to the age compositional observation that you would like to plot the profile for. Can be many observations
param	"string" The parameter label that the profile was run for. It should follow the syntax that is used in Casal2 that is, "block[label].parameter" e.g. process[Recruitment].b0
extract_list	"string" The name of the R object that was extracted into R using the extract() function.
Rescale	"bool/logical" If true it will rescale the likelihoods to have a minimum on 0. This is done by subtracting off the minimum value of the likelihood series.
ylab	"string" optional, y-axis label
xlab	"string" optional, x-axis label
threshold	"numeric" the minimum number of years a cohort is seen in the observation, for being used in the plot. if threshold = 5 then any cohort that has been sampled for a minimum of 5 years will be automatically plotted.
ymin	"numeric" optional, minimum value parsed to the ylim parameter in plot()

## Author(s)

Craig Marsh

## Examples

```
library(CASAL2)
Profile = extract("profile.log") ## this is an output file from a casal2 -p run
param.profile.by.cohort(obs = c("Tangaroa_propn_at_age_Jan"), param = "process[Instantaneous_Mortality].m(ma
```

---

Paste	<i>Utility plot function</i>
-------	------------------------------

---

**Description**

Utility plot function

**Usage**

```
Paste(..., sep = "")
```

**Author(s)**

Craig Marsh

---

pos	<i>Utility extract function</i>
-----	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
pos(vector, x)
```

**Author(s)**

Dan Fu

---

pos.match	<i>Utility extract function</i>
-----------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
pos.match(vector, regexp)
```

**Author(s)**

Dan Fu



---

pow

*Utility extract function*

---

### Description

Utility extract function

### Usage

```
pow(x, exponent)
```

### Author(s)

Craig Marsh

---

ReadSimulatedData

*Read in multiple sets of Simualted data for a single observation*

---

### Description

This function reads in a set of simulated observations generated from Casal2 in simulation mode. These functions read in all the simulated obs as a list, for visualising and summarising in R

### Usage

```
ReadSimulatedData(filename, path = "")
```

### Arguments

filename      the name of simulated obs for an observation. For example if you generated 100 sets of simulated observations named "SubAntarticObs". Casal2 will generate 100 of these with the following extensions SubAntarticObs.001, SubAntarticObs.002, SubAntarticObs.003,,,. SubAntarticObs.100. filename = SubAntarticObs.

path            Optionally, the path to the file, default is current working directory.

### Author(s)

Craig Marsh

---

regex.in	<i>Utility extract function</i>
----------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
regex.in(vector, regex)
```

**Author(s)**

Dan Fu

---

Regexpr	<i>Utility extract function</i>
---------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
Regexpr(x, y, fixed = T)
```

**Author(s)**

Dan Fu

---

remove.first.words	<i>Utility extract function</i>
--------------------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
remove.first.words(string, words = 1)
```

**Author(s)**

Dan Fu

---

string.to.vector.of.numbers  
*Utility extract function*

---

**Description**

Utility extract function

**Usage**

string.to.vector.of.numbers(string)

**Author(s)**

Dan Fu

---

string.to.vector.of.words  
*Utility extract function*

---

**Description**

Utility extract function

**Usage**

string.to.vector.of.words(string)

**Author(s)**

Dan Fu

---

strip  
*Utility for extract function*

---

**Description**

Utility for extract function

**Usage**

strip(x)

**Author(s)**

Craig Marsh

---

Sum	<i>Utility plot function</i>
-----	------------------------------

---

**Description**

Utility plot function

**Usage**

```
Sum(..., na.rm = T)
```

**Author(s)**

Craig Marsh

---

unpaste	<i>Utility extract function</i>
---------	---------------------------------

---

**Description**

Utility extract function

**Usage**

```
unpaste(string, sep)
```

**Author(s)**

Dan Fu

---

write.csl2.file	<i>Model configuration write function</i>
-----------------	---

---

**Description**

This function will write a Casal2 configuration file based on a list object in R. Ususally this function will be used once a model has been read into R using extract.csl2.file and modified. This function will then print our the configuration to a new file where it can be re run into Casal2

**Usage**

```
write.csl2.file(object, file, path = "")
```

**Arguments**

object	An R list object that follows the same structure that extract.csl2.file would produce
file	Optionally, the file name
path	Optionally, the path to ouput the file

**Author(s)**

Craig Marsh

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