

# 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> |
|------------------|---------------------------------|

---

**Description**

Utility extract function

**Usage**

```
convert.to.lines(filename)
```

**Author(s)**

Dan Fu

---

|             |                    |
|-------------|--------------------|
| CV.for.CPUE | <i>CV.for.CPUE</i> |
|-------------|--------------------|

---

**Description**

This function is useful for deciding on a c.v. to be used with a CPUE series in a stock assessment model. Originally written in Chris Francis's DataWeighting Package, this has been copied over and modified so that users can use this functionality with Casal2 models/output.

**Usage**

```
CV.for.CPUE(year, cpue, f, plot.it = TRUE)
```

**Arguments**

|         |  |
|---------|--|
| year    | vector of years with CPUE indices  |
| cpue    | CPUE indices   |
| f       | degree of lowess smoothing (0 = no smoothing, 1 = maximum smoothing)   |
| plot.it | If TRUE, plot the index and the smoothed fit. Otherwise, return a dataframe of the year, index, smoothed fitted value, and cv) |

**Value**

The function either plots the CPUE, together with a lowess line fitted to it, and returns the c.v. of the residuals to the fit. Or returns a dataframe of the lowess line fits and associated c.v.s for each point.

**Author(s)**

Chris Francis

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

---

### 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

---

|        |                              |
|--------|------------------------------|
| evalit | <i>Utility plot function</i> |
|--------|------------------------------|

---

**Description**

Utility plot function

**Usage**

```
evalit(x)
```

**Author(s)**

Craig Marsh

---

|                   |   |
|-------------------|---|
| 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

extract.mcmc

*extract.mcmc function for casal2 output***Description**

An extract function that reads objective and sample output that are produced from a 'casal2 -m' model run. This function also create a 'casal2.mcmc' class which can be used in plotting and summary functions.

**Usage**

```
extract.mcmc(samples.file = "mcmc_samples.out.0",
             objectives.file = "mcmc_objectives.out.0", path = "",
             return_covariance = F)
```

**Arguments**

samples.file     <string> the name of the input file containing the samples.file output by casal2  
 objectives.file     <string> the name of the input file containing the objectives.file output by casal2  
 path             Optional<string>, the path to the file  
 return\_covariance     Optional<bool>, Whether you want to extract the covariance matrix with the mcmc object?

**Value**

a 'casal2MCMC' that can be integrated using the str() function.

**Author(s)**

C. Marsh

extract.mpd

*extract MPD function for readin in Casal2 output that has been generated from a -r, -e, -f, -p run mode.***Description**

An extract function that reads Casal2 output that are produced from a '-r' or '-e' or '-f' or '-p' model run. This function also create a 'casal2.mpd' class which can be used in plotting and summary functions. See the casal2 manual for more information.

**Usage**

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

**Arguments**

|      |   |
|------|---|
| file | the name of the input file containing model output to extract |
| path | Optionally, the path to the file                              |

**Value**

a 'casal2MPD' object which is essentially a list, that can be integrated using the str() function.

**Author(s)**

Dan Fu

---

|                    |  |
|--------------------|--|
| extract.parameters | <i>Utility extract.parameters function</i> |
|--------------------|--|

---

**Description**

This function reads in a parameter file that would be generated using the -o syntax.

**Usage**

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

**Arguments**

|      |   |
|------|---|
| file | the name of the input file containing model output to extract |
| path | Optionally, the path to the file                              |

**Value**

Data <"data.frame"> of parameters that are from a -i format.

**Author(s)**

Craig Marsh

---

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

---

**Description**

Utility function

**Usage**

```
get.casal2_list()
```

**Author(s)**

Craig Marsh

---

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

---

**Description**

Utility extract function

**Usage**

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

**Author(s)**

Dan Fu

---

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

---

**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> |
|----------------|---------------------------------|

---

**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> |
|---------|---------------------------------|

---

**Description**

Utility extract function

**Usage**

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

**Author(s)**

Dan Fu

---

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

---

**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> |
|-------------------|--|

---

**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> |
|----------------------|---------------------------------|

---

**Description**

Utility extract function

**Usage**

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

**Author(s)**

Dan Fu

---

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

---

**Description**

Utility extract function

**Usage**

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

**Author(s)**

Dan Fu

---

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

---

**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> |
|-------------|---------------------------------|

---

**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

Method.TA1.10

*Method.TA1.10***Description**

This function is useful for deciding on the data weights of one or more at-age or at-length data sets with assumed lognormal error structure in a stock assessment. Originally written in Chris Francis's DataWeighting Package, this has been copied over and modified so that users can use this functionality with Casal2 models/output.

**Usage**

```
Method.TA1.10(model, Observation_label, pe.cv.stg1, plotit = F, xlim = NULL,
              ylim = NULL, trial.pe.cvs = seq(0, 2, 0.05))
```

**Arguments**

|                                |  |
|--------------------------------|--|
| <code>model</code>             | Casal2 output that is the result of a -r, -e run.  |
| <code>Observation_label</code> | Label of the observation you want to apply the weighting too.  |
| <code>pe.cv.stg1</code>        | process-error c.v. assumed or estimated in stage 1 ("This can be extracted from the report")                                   |
| <code>xlim</code>              | x-axis limits for the illustrative plot  |
| <code>ylim</code>              | y-axis limits for the illustrative plot  |
| <code>trial.pe.cvs</code>      | vector of trial stage-2 process-error c.v.s (the default value will usually be OK; if not, an error message is output)         |
| <code>plot.it</code>           | If TRUE, plot the index and the smoothed fit. Otherwise, return a dataframe of the year, index, smoothed fitted value, and cv) |

**Value**

Outputs a stage-2 process-error c.v. for the data set. Returns a 2-vector containing the process-error c.v. assumed or estimated in stage 1, and that estimated using TA1.10 for stage 2

**Note**

Method TA1.10 is described in Appendix A of the following paper Francis, R.I.C.C. (2011). Data weighting in statistical fisheries stock assessment models. Canadian Journal of Fisheries and Aquatic Sciences 68: 1124-1138. (With corrections to the equation in Francis R.I.C.C. (2011) Corrigendum: Data weighting in statistical fisheries stock assessment models. Haven't exported this function because I don't think it works even in Chris's DataWeighting package.

**Author(s)**

Chris Francis



---

|              |                     |
|--------------|---------------------|
| Method.TA1.8 | <i>Method.TA1.8</i> |
|--------------|---------------------|

---

## Description

This function is useful for deciding on the data weights of one or more at-age or at-length data sets with assumed multinomial error structure in a stock assessment. Can produce a diagnostic plot if the analysis is for a single data set

## Usage

```
Method.TA1.8(model, observation_labels, plot.it = F, xlim = NULL,
             ylim = NULL)
```

## Arguments

|                                 |   |
|---------------------------------|---|
| <code>model</code>              | Casal2 output that is the result of a -r, -e run.   |
| <code>observation_labels</code> | vector<string> Labels of the observations you want to apply the iterative weighting too, can be multiple datasets as in in Chris's original package <code>multiple = T</code> . |
| <code>plot.it</code>            | If TRUE, plot the index and the smoothed fit. Otherwise, return a dataframe of the year, index, smoothed fitted value, and cv)  |
| <code>xlim</code>               | x-axis limits for the illustrative plot   |
| <code>ylim</code>               | y-axis limits for the illustrative plot   |

## Value

Outputs a multiplier,  $w$ , so that  $N_{2y} = w \times N_{1y}$ , where  $N_{1y}$  and  $N_{2y}$  are the stage-1 and stage-2 multinomial sample sizes for the data set in year  $y$ .

## Note

Method TA1.8 is described in Appendix A of the following paper Francis, R.I.C.C. (2011). Data weighting in statistical fisheries stock assessment models. Canadian Journal of Fisheries and Aquatic Sciences 68: 1124-1138. (With corrections to the equation in Francis R.I.C.C. (2011) Corrigendum: Data weighting in statistical fisheries stock assessment models.

## Author(s)

Chris Francis

---

|                      |                                     |
|----------------------|-------------------------------------|
| mpd_derived_quantity | <i>Utility function for summary</i> |
|----------------------|-------------------------------------|

---

**Description**

Utility function for summary

**Usage**

```
mpd_derived_quantity(filename)
```

**Author(s)**

C Marsh This is a utility function that will summarise a derived quantity report for a Casal2MPD class

---

|               |  |
|---------------|--|
| 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

---

```
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

---

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

---

**Description**

Utility plot function

**Usage**

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

**Author(s)**

Craig Marsh

---

|                         |  |
|-------------------------|--|
| plot.derived_quantities | <i>plot.derived_quantities default</i> |
|-------------------------|--|

---

**Description**

A plotting function to plot SSB's for the 'casal2TAB' and 'casal2MPD' objects.

**Usage**

```
plot.derived_quantities(model, type = "number", report_label = "", xlim,
  ylim, xlab, ylab, main, col, plot.it = T, ...)

## S3 method for class 'casal2MPD'
plot.derived_quantities(model, type = "number",
  report_label = "", xlim, ylim, xlab, ylab, main, col, plot.it = T, ...)
```

**Arguments**

|              |   |
|--------------|---|
| model        | <casal2MPD, casal2TAB> object that are generated from one of the extract() functions. |
| type         | <string> whether numbers or scaled by B0.   |
| report_label | <string>  |
| ...          | remaining plotting functions.   |

**Value**

NULL

**Author(s)**

C. 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 | <i>Utility extract function</i> |
|-----|---------------------------------|

---

**Description**

Utility extract function

**Usage**

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

**Author(s)**

Craig Marsh

---

|                   |   |
|-------------------|---|
| ReadSimulatedData | <i>Read in multiple sets of Simualted data for a single observation</i> |
|-------------------|---|

---

### 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

---

|                             |  |
|-----------------------------|--|
| reformat.compositional.data | <i>Reformat Casal2 compositional observations so they are in the same format as the legacy Casal observations.</i> |
|-----------------------------|--|

---

### Description

This function will take a compositional observation that has been generated by Casal2 and re-format it so that it has the same structure as a CASAL reported compositional observation. The purpose for this function is to reformat the Casal2 observations so we can then feed them into packages that have been tailored for Casal observations, such as Chris Francis's DataWeighting library.

### Usage

```
reformat.compositional.data(extract_list, comp_label)
```

### Arguments

|              |   |
|--------------|---|
| extract_list | the r object that has been extracted using the extract() function.      |
| comp_label   | <string> the label of the report for the observation you want converted |

### 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

---

|                 |                        |
|-----------------|------------------------|
| summary.default | <i>summary default</i> |
|-----------------|------------------------|

---

**Description**

A summary function for 'casal2MCMC' 'casal2TAB' and 'casal2MPD' objects.

**Usage**

```
summary.default(model)

## S3 method for class 'casal2MPD'
summary(model)
```

**Arguments**

model                    <casal2MPD, casal2TAB, casal2MCMC> object that are generated from one of the extract() functions.

**Value**

NULL

**Author(s)**

C. 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 <code>extract.csl2.file</code> would produce |
| file   | Optionally, the file name  |
| path   | Optionally, the path to ouput the file   |

**Author(s)**

Craig Marsh

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