

# Package ‘ArArRedux’

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**Title** Rigorous Data Reduction and Error Propagation of Ar40 / Ar39  
Data

**Version** 1.0

**Description** Processes noble gas mass spectrometer data to determine the isotopic composition of argon (comprised of Ar36, Ar37, Ar38, Ar39 and Ar40) released from neutron-irradiated potassium-bearing minerals. Then uses these compositions to calculate precise and accurate geochronological ages for multiple samples as well as the covariances between them. Error propagation is done in matrix form, which jointly treats all samples and all isotopes simultaneously at every step of the data reduction process. Includes methods for regression of the time-resolved mass spectrometer signals to t=0 ('time zero') for both single- and multi-collector instruments, blank correction, mass fractionation correction, detector intercalibration, decay corrections, interference corrections, interpolation of the irradiation parameter between neutron fluence monitors, and (weighted mean) age calculation. All operations are performed on the logs of the ratios between the different argon isotopes so as to properly treat them as 'compositional data', sensu Aitchison [1986, The Statistics of Compositional Data, Chapman and Hall].

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**License** GPL-2

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average	<i>Calculate the arithmetic mean</i>
---------	--------------------------------------

---

### Description

Calculate the arithmetic mean of some logratio data

### Usage

```
average(x, i = NULL, newlabel = NULL)
```

### Arguments

x	an object of class redux or logratios
i	(optional) vector of sample indices
newlabel	(optional) string with the new label to be assigned to the averaged values

**Value**

an object of the same class as x

**Examples**

```
data(Melbourne)
K <- average(Melbourne$X, grep("K:", Melbourne$X$labels), newlabel="K-glass")
plotcorr(K)
```

---

averagebyday

*Average all the data collected on the same day.*

---

**Description**

This function is useful for grouping a number of replicate air shots or calibration experiments

**Usage**

```
averagebyday(x, newlabel)
```

**Arguments**

x                    an object of class timeresolved, logratios, PHdata or redux  
 newlabel            a string with the new label that should be given to the average

**Value**

an object of the same class as x

**Examples**

```
dfile <- system.file("Calibration.csv", package="ArArRedux")
dlabels <- c("H1", "AX", "L1", "L2")
md <- loaddata(dfile, dlabels, PH=TRUE)
ld <- fitlogratios(blankcorr(md))
d <- averagebyday(ld, "DCAL")
plotcorr(d)
```

blankcorr	<i>Apply a blank correction</i>
-----------	---------------------------------

---

## Description

Applies a blank correction to some time-resolved mass spectrometer data

## Usage

```
blankcorr(x, ...)  
  
## Default S3 method:  
blankcorr(x, ...)  
  
## S3 method for class 'timeresolved'  
blankcorr(x, blanklabel = NULL, prefix = "", ...)  
  
## S3 method for class 'PHdata'  
blankcorr(x, blanklabel = NULL, prefix = "", ...)
```

## Arguments

x	an object of class <code>timeresolved</code> or <code>PHdata</code>
...	other arguments
blanklabel	as string denoting the prefix of the blanks
prefix	a string to be prepended to the non-blanks

## Value

an object of class `blankcorrected`

## Examples

```
samplefile <- system.file("Samples.csv",package="ArArRedux")  
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")  
m <- loaddata(samplefile,masses) # samples and J-standards  
blanklabel <- "EXB#"  
l <- fitlogratios(blankcorr(m,blanklabel),"Ar40")  
plotcorr(l)
```

---

blankcorrected	<i>The blankcorrected class</i>
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---

### Description

An object class containing blank-corrected mass spectrometry data

### Details

Extends the class classes `timeresolved` and `PHdata` by adding an additional list item `blankindices` containing the index of the nearest blank. `fitlogratios` uses this information to group the samples during regression to 'time zero'.

---

calibration	<i>Detector calibration</i>
-------------	-----------------------------

---

### Description

Apply the detector calibration for multicollector data

### Usage

```
calibration(X, clabel)
```

### Arguments

X	an object of class <code>redux</code>
clabel	the label of the detector calibration data

### Value

an object of class `redux`

### Examples

```
data(Melbourne)
C <- calibration(Melbourne$X, "DCAL")
plotcorr(C)
```

---

clcorrection	<i>Cl-interference correction</i>
--------------	-----------------------------------

---

**Description**

Apply the interference correction for the Cl-decay products

**Usage**

```
clcorrection(X, irr)
```

**Arguments**

X	an object of class <code>redux</code>
irr	the irradiation schedule

**Value**

an object of class `redux`

**Examples**

```
data(Melbourne)
Cl <- clcorrection(Melbourne$X,Melbourne$irr)
plotcorr(Cl)
```

---

concat	<i>Merge a list of logratio data</i>
--------	--------------------------------------

---

**Description**

Recursively concatenates a list of logratio data into one big dataset

**Usage**

```
concat(lrlist)
```

**Arguments**

lrlist	a list containing items of class <code>logratios</code> or <code>redux</code>
--------	---

**Value**

an object of the same class as x containing the merged dataset

## Examples

```

samplefile <- system.file("Samples.csv",package="ArArRedux")
kfile <- system.file("K-glass.csv",package="ArArRedux")
cafile <- system.file("Ca-salt.csv",package="ArArRedux")
dfile <- system.file("Calibration.csv",package="ArArRedux")
masses <- c("Ar37", "Ar38", "Ar39", "Ar40", "Ar36")
blanklabel <- "EXB#"
Jpos <- c(3,15)
dlabels <- c("H1", "AX", "L1", "L2")

m <- loaddata(samplefile,masses) # samples and J-standards
mk <- loaddata(kfile,masses) # K-interference data
mca <- loaddata(cafile,masses) # Ca interference data
md <- loaddata(dfile,dlabels,PH=TRUE) # detector intercalibrations

# form and fit logratios
l <- fitlogratios(blankcorr(m,blanklabel),"Ar40")
lk <- fitlogratios(blankcorr(mk,blanklabel),"K:"),"Ar40")
k <- getmasses(lk,"Ar39","Ar40") # subset on the relevant isotopes
lca <- fitlogratios(blankcorr(mca,blanklabel),"Ca:"),"Ar37")
ca <- getmasses(lca,c("Ar36","Ar39"),c("Ar37","Ar37")) # subset
ld <- fitlogratios(blankcorr(md))
d <- averagebyday(ld,"DCAL")

# merge all data (except air shots) into one big logratio structure
X <- newredux(concat(list(l,k,ca,d)),Jpos)
data(Melbourne)
if (isTRUE(all.equal(Melbourne$X,X))) {
  print("We just reconstructed the built-in dataset Melbourne$X")}

```

---

decaycorrection	<i>Correct for radioactive decay occurred since irradiation</i>
-----------------	---

---

## Description

Correct for radioactive decay of neutron-induced  $^{37}\text{Ar}$  and  $^{39}\text{Ar}$  occurred since irradiation

## Usage

```
decaycorrection(X, irr, isotope)
```

## Arguments

X	an objects of class redux
irr	the irradiation schedule
isotope	a string denoting the isotope that needs correcting

**Value**

an object of class `redux`

**Examples**

```
data(Melbourne)
C <- calibration(Melbourne$X,"DCAL")
A <- massfractionation(C,Melbourne$fract)
D9 <- decaycorrection(A,Melbourne$irr,"Ar39")
plotcorr(D9)
```

---

fitlogratios

*Extrapolation to 'time zero'*


---

**Description**

This function extrapolates time resolved mass spectrometer data to  $t=0$ . When fed with multicollector data, it forms the ratios of the raw signals, forms their logs and performs linear regression to  $t=0$ . When fed with single collector data, the function first takes their logs and extrapolates them to  $t=0$  before taking ratios, unless `denmass=NULL`, in which case the logs of the raw signals are extrapolated.

**Usage**

```
fitlogratios(x, ...)

## Default S3 method:
fitlogratios(x, ...)

## S3 method for class 'timeresolved'
fitlogratios(x, denmass, ...)

## S3 method for class 'PHdata'
fitlogratios(x, denmass = NULL, ...)
```

**Arguments**

<code>x</code>	an object of class <code>timeresolved</code> or <code>PHdata</code>
<code>...</code>	further arguments (see below)
<code>denmass</code>	a string denoting the denominator isotope

**Value**

an object of class `logratios`



**Examples**

```
samplefile <- system.file("Samples.csv",package="ArArRedux")
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")
m <- loaddata(samplefile,masses) # samples and J-standards
blanklabel <- "EXB#"
l <- fitlogratios(blankcorr(m,blanklabel),"Ar40")
plotcorr(l)
```

---

fractionation	<i>Compute the mass fractionation correction</i>
---------------	--

---

**Description**

Compares the measured  $^{40}\text{Ar}/^{36}\text{Ar}$  ratio of an air shot on a given detector with the atmospheric ratio.

**Usage**

```
fractionation(fname, detector, MS = "ARGUS-VI", PH = FALSE)
```

**Arguments**

fname	a .csv file with the air shot data
detector	the name of the ion detector
MS	the type of mass spectrometer
PH	TRUE if the data were recorded in 'peak hopping' mode, FALSE if recorded in multicollector mode.

**Value**

an object of class `logratios`

**Examples**

```
data(Melbourne)
fd37file <- system.file("AirL2.csv",package="ArArRedux")
fd40file <- system.file("AirH1.csv",package="ArArRedux")
fract <- list(fractionation(fd37file,"L2",PH=TRUE),
             fractionation(fd40file,"H1",PH=FALSE))
if (isTRUE(all.equal(Melbourne$fract,fract))){
  print("We just re-created the fractionation correction for the Melbourne dataset")
}
```

---

get4039	<i>Calculate the 40Ar*/39ArK-ratios</i>
---------	---

---

**Description**

Calculate the 40Ar\*/39ArK-ratios of interference corrected logratio intercept data

**Usage**

```
get4039(X, irr)
```

**Arguments**

X	an object of class <code>redux</code> containing some interference corrected logratio intercept data
irr	the irradiation schedule

**Value**

an object of class `link{redux}` containing the 40Ar\*/39ArK-ratios as intercepts and its covariance matrix as `covmat`

**Examples**

```
data(Melbourne)
R <- get4039(Melbourne$X, Melbourne$irr)
plotcorr(R)
```

---

getages	<i>Calculate 40Ar/39Ar ages</i>
---------	---------------------------------

---

**Description**

Calculate 40Ar/39Ar ages from a vector of 40Ar/39Ar-ratios and J-factors

**Usage**

```
getages(RJ)
```

**Arguments**

RJ	an object of class <code>Redux</code> containing the amalgamated $^{40}\text{Ar}/^{39}\text{Ar}_K$ -ratios and J-factors with their covariance matrix
----	---

**Value**

an object of class `results` containing the ages and their covariance matrix

**Examples**

```
data(Melbourne)
R <- get4039(Melbourne$X,Melbourne$irr)
J <- getJfactors(R)
ages <- getages(J)
plotcorr(ages)
```

---

getJfactors

*Calculate the irradiation parameter ('J factor')*


---

**Description**

Interpolate the irradiation parameters for the samples given the  $^{40}\text{Ar}^*/^{39}\text{ArK}$  ratios of the samples and fluence monitors

**Usage**

```
getJfactors(R)
```

**Arguments**

R                      a vector of  $^{40}\text{Ar}^*/^{39}\text{ArK}$  ratios

**Value**

an object of class redux containing, as intercepts, the  $^{40}\text{Ar}^*/^{39}\text{ArK}$  ratios of the samples, the interpolated J-factors, and the  $^{40}\text{K}$  decay constant; and as covmat: the covariance matrix. All other class properties are inherited from R.

**Examples**

```
data(Melbourne)
R <- get4039(Melbourne$X,Melbourne$irr)
J <- getJfactors(R)
plotcorr(J)
```

---

getmasses

*Select a subset of isotopes from a dataset*


---

**Description**

Extracts the intercepts, covariance matrix, etc. of a selection of isotopes from a larger dataset

**Usage**

```
getmasses(x, ...)

## Default S3 method:
getmasses(x, ...)

## S3 method for class 'timeresolved'
getmasses(x, mass, invert = FALSE, ...)

## S3 method for class 'logratios'
getmasses(x, num, den, invert = FALSE, ...)

## S3 method for class 'redux'
getmasses(x, num, den, invert = FALSE, ...)
```

**Arguments**

x	an object of class <code>logratios</code> , <code>timeresolved</code> , <code>PHdata</code> or <code>redux</code> .
...	other arguments
mass	a vector of strings denoting the masses of interest
invert	boolean parameter indicating whether the selection should be inverted (default = FALSE)
num	vector of strings indicating the numerator isotopes
den	vector of string indicating the denominator isotopes

**Value**

an object of the same class as x

**Examples**

```
kfile <- system.file("K-glass.csv", package="ArArRedux")
masses <- c("Ar37", "Ar38", "Ar39", "Ar40", "Ar36")
mk <- loaddata(kfile, masses)
lk <- fitlogratios(blankcorr(mk, "EXB#", "K:"), "Ar40")
k <- getmasses(lk, "Ar39", "Ar40") # subset of the relevant isotopes
plotcorr(k)
```

---

interference

---

*define the interference corrections*


---

**Description**

create a new object of class `logratios` containing the interferences from neutron reactions on Ca and K

**Usage**

```
interference(intercepts, covmat, num, den, irr, label)
```

**Arguments**

intercepts	a vector with logratios
covmat	the covariance matrix of the logratios
num	a vector of strings marking the numerator isotopes of intercepts
den	a vector of strings marking the denominator isotopes of intercepts
irr	an object of class irradiations
label	a string with a name which can be used to identify the interference data in subsequent calculations

**Value**

an object of class logratios

**Examples**

```
samplefile <- system.file("Samples.csv",package="ArArRedux")
irrfile <- system.file("irradiations.csv",package="ArArRedux")
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")
X <- read(samplefile,masses,blabel="EXB#",Jpos=c(3,15))
irr <- loadirradiations(irrfile)
# assume log(36Ar/37Ar) = log(39Ar/37Ar) = 1 in co-irradiate Ca-salt
# with variances of 0.0001 and zero covariances
ca <- interference(intercepts=c(1,1),
                   covmat=matrix(c(0.0001,0,0,0.0001),nrow=2),
                   num=c("Ar39","Ar36"),den=c("Ar37","Ar37"),
                   irr=X$irr[1],label="Ca-salt")
# assume log(39Ar/40Ar) = 4.637788 in co-irradiate K-glass
# with variance 7.9817e-4
k <- interference(intercepts=4.637788,covmat=7.9817e-4,
                  num="Ar39",den="Ar40",irr=X$irr[1],
                  label="K-glass")
ages <- process(X,irr,ca=ca,k=k)
summary(ages)
```

---

loaddata

*Load mass spectrometer data*


---

**Description**

Loads a .csv file with raw mass spectrometer data

**Usage**

```
loaddata(fname, masses, MS = "ARGUS-VI", PH = FALSE)
```

**Arguments**

fname	the file name, must end with .csv
masses	a vector of strings denoting the order of the isotopes listed in the table
MS	the type of mass spectrometer
PH	a boolean indicating whether the data are to be treated as multicollector (PH=FALSE) or 'peak hopping' (PH=TRUE) data. The default is PH=FALSE.

**Value**

if PH=FALSE: an object of class `timeresolved`  
 if PH=TRUE: an object of class `PHdata`

**Examples**

```
samplefile <- system.file("Samples.csv",package="ArArRedux")
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")
m <- loaddata(samplefile,masses) # samples and J-standards
plot(m,"MD2-1a","Ar40")
```

---

loadirradiations	<i>Load the irradiation schedule</i>
------------------	--------------------------------------

---

**Description**

Loads a .csv file with the schedule of a multi-stage neutron irradiation

**Usage**

```
loadirradiations(fname)
```

**Arguments**

fname	file name (in .csv format)
-------	----------------------------

**Value**

a list of irradiations, where each irradiation is a named list containing:  
 tin: vector with the start times of irradiations  
 tout: vector with the end times of irradiations  
 P: vector with the power of the irradiations

**Examples**

```
irrfile <- system.file("irradiations.csv",package="ArArRedux")
irr <- loadirradiations(irrfile)
str(irr)
```

---

logratios	<i>The logratios class</i>
-----------	----------------------------

---

**Description**

An object class containing logratio intercepts

**Details**

A list with the following items:

labels: a vector of strings denoting the names of the runs

num: a vector of strings denoting the numerator isotopes

den: a vector of strings denoting the denominator isotopes

intercepts: a vector of logratio intercepts or values

covmat: the covariance matrix of intercepts

irr: a vector of strings denoting the irradiation runs

pos: a vector of integers with the positions in the irradiation stack

thedata: a vector containing the acquisition dates and times

n1r: a vector with the number of logratios per run

---

massfractionation	<i>Apply the mass fractionation correction</i>
-------------------	--

---

**Description**

Applies the fractionation obtained from air shot data by [fractionation](#) to the denominator detector in order to correct it for the mass difference between the numerator and denominator isotopes.

**Usage**

```
massfractionation(X, fract)
```

**Arguments**

X	an object of class <code>redux</code>
---	---------------------------------------

fract	a list with fractionation data for the detectors used to measure the denominator isotopes
-------	---

**Value**

an object of class `redux`

**Examples**

```
data(Melbourne)
C <- calibration(Melbourne$X,"DCAL")
A <- massfractionation(C,Melbourne$fract)
plotcorr(A)
```

Melbourne

*An example dataset***Description**

Contains all the relevant information needed for the data reduction some ARGUS-IV data from the University of Melbourne

**Author(s)**

David Philips <dphillip@unimelb.edu.au>

**Examples**

```
data(Melbourne)
plotcorr(Melbourne$X)
```

newredux

*Create a new [redux](#) object***Description**

Initialises a new [redux](#) object by packing a [logratios](#) dataset together with all the parameters needed for age calculation

**Usage**

```
newredux(X, Jpos, detectors = list(Ar36 = "H1", Ar37 = "L2", Ar38 = "L1", Ar39
  = "AX", Ar40 = "H1"))
```

**Arguments**

X	an object of class <a href="#">logratios</a>
Jpos	a vector of integers denoting the positions of the fluence monitors in the irradiation stack
detectors	a list of strings denoting the detectors for each argon isotope

**Value**

an object of class [redux](#)



---

param	<i>Set or get Ar-Ar_Redux parameters</i>
-------	--

---

## Description

This function is used to query and modify the half lives, standard ages etc. associated with an object of class `redux`

## Usage

```
param(X, ...)
```

## Arguments

X	an object of class <code>redux</code>
...	any combination of the parameters given below

## Details

`param` grants access to the following parameters:

l0: 40K decay constant (default value = 5.5492e-4 Ma-1, Renne et al. [2010])  
 sl0: standard error of the 40K decay constant (default value = 0.0047e-4 Ma-1)  
 l7: 37Ar decay constant (default value = 7.2438 yr-1, Renne and Norman [2001])  
 sl7: standard error of the 37Ar decay constant (default value = 0.0083 yr-1)  
 l9: 39Ar decay constant (0.002577 yr-1 Stoenner et al. [1965])  
 sl9: standard error of the 39Ar decay constant (0.000014 yr-1)  
 l6: 36Cl decay constant (default value = 2301.3e-9 yr-1)  
 sl6: standard error of the 36Cl decay constant (default value = 7.6e-9 yr-1)  
 pcl: (36Cl/38Cl)-production rate (default value = 252.7 for OSTR reactor, Renne et al. [2008])  
 spcl: standard error of the (36Cl/38Cl)-production rate (default value = 1.8)  
 ts: age of the fluence monitor (default = 28.201 Myr for the Fish Canyon Tuff, Kuiper et al. [2008])  
 sts: standard error of the fluence monitor age (default value = 0.023 Myr)  
 air: atmospheric 40Ar/36Ar ratio (default value = 298.56, Lee et al. [2006])  
 sair: standard error of the atmospheric 40Ar/36Ar ratio (default value = 0.155)

## Value

returns the modified `redux` object OR the current parameter values if no optional arguments are supplied.

## Examples

```
data(Melbourne)
param(Melbourne$X)$air
Y <- param(Melbourne$X,air=295.5)
param(Y)$air
```

---

PHdata

*The PHdata class*


---

### Description

An object class containing time resolved 'peak-hopping' mass spectrometry data

### Details

A list with the following items:

masses: a vector of strings denoting the isotopes monitored in each run

signals: a list with objects of class [timeresolved](#), each corresponding to a detector (i.e. length(signals)==1 for single collector instruments).

### See Also

[loaddata](#)

---

plot.timeresolved

*Plot a time resolved mass spectrometry signal*


---

### Description

Plots the raw signal of a given isotope against time.

### Usage

```
## S3 method for class 'timeresolved'
plot(x, label, mass, ...)
```

```
## S3 method for class 'PHdata'
plot(x, label, mass, ...)
```

### Arguments

x	an object of class <a href="#">timeresolved</a> or <a href="#">PHdata</a>
label	a string with the name of the run
mass	a string indicating the isotope of interest
...	optional parameters

**Examples**

```
samplefile <- system.file("Samples.csv",package="ArArRedux")
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")
mMC <- loaddata(samplefile,masses)
plot(mMC,"MD2-1a","Ar40")
mPH <- loaddata(samplefile,masses,PH=TRUE)
plot(mPH,"MD2-1a","Ar40")
```

plotcorr

*Plot a matrix with correlation coefficients***Description**

Converts the covariance matrix to a correlation matrix and plots this as a coloured image for visual inspection.

**Usage**

```
plotcorr(X)
```

**Arguments**

X a data structure (list) containing an item called 'covmat' (covariance matrix)

**Examples**

```
data(Melbourne)
plotcorr(Melbourne$X)
```

process

*Process logratio data and calculate  $^{40}\text{Ar}/^{39}\text{Ar}$  ages***Description**

Performs detector calibration, mass fractionation correction, decay corrections, interference corrections, interpolates J-factors and calculates ages.

**Usage**

```
process(X, irr, fract = NULL, ca = NULL, k = NULL)
```

**Arguments**

X	an object of class <code>redux</code>
irr	the irradiation schedule
fract	list with air shot data (one item per denominator isotope)
ca	an object of class <code>logratios</code> with Ca-interference data (not necessary if interferences are included in X)
k	an object of class <code>logratios</code> with K-interference data (not necessary if interferences are included in X)

**Examples**

```
data(Melbourne)
ages <- process(Melbourne$X, Melbourne$irr, Melbourne$fract)
summary(ages)
```

---

read	<i>Read mass spectrometer data</i>
------	------------------------------------

---

**Description**

Reads raw mass spectrometer data and parses it into a `redux` format for further processing.

**Usage**

```
read(xfile, masses, blabel, Jpos, kfile = NULL, cafile = NULL,
     dfile = NULL, dlabels = NULL, MS = "ARGUS-VI")
```

**Arguments**

xfile	a .csv file with samples and fluence monitor data
masses	a list which specifies the order in which the isotopes are recorded by the mass spectrometer
blabel	a prefix string denoting the blanks
Jpos	a vector of integers denoting the positions of the fluence monitors in the irradiation stack
kfile	a .csv file with the K-interference monitor data (optional)
cafile	a .csv file with the Ca-interference monitor data (optional)
dfile	a .csv file with the detector calibration data (optional)
dlabels	a list which specifies the names of the detectors and the order in which they were recorded by the mass spectrometer
MS	a string denoting the type of mass spectrometer. At the moment only the ARGUS-IV is listed. Please contact the author to add other file formats to Ar-Ar_Redux.

## Value

an object of class `redux`.

## Examples

```
samplefile <- system.file("Samples.csv",package="ArArRedux")
kfile <- system.file("K-glass.csv",package="ArArRedux")
cafile <- system.file("Ca-salt.csv",package="ArArRedux")
dfile <- system.file("Calibration.csv",package="ArArRedux")
masses <- c("Ar37","Ar38","Ar39","Ar40","Ar36")
dlabels <- c("H1","AX","L1","L2")
X <- read(samplefile,masses,"EXB#",c(3,15),kfile,cafile,dfile,dlabels)
plotcorr(X)
```

---

redux

*The redux class*

---

## Description

An object class that is used throughout Ar-Ar\_Redux

## Details

A list with the following items:

- labels: a vector of strings denoting the names of the runs
- num: a vector of strings denoting the numerator isotopes
- den: a vector of strings denoting the denominator isotopes
- intercepts: a vector of logratio intercepts or values
- covmat: the covariance matrix of intercepts
- irr: a vector of strings denoting the irradiation runs
- pos: a vector of integers with the positions in the irradiation stack
- thedata: a vector containing the acquisition dates and times
- nlr: a vector with the number of logratios per run
- param: a list of global parameters

## See Also

param

---

redux2isoplotr	<i>Export ArArRedux data to IsoplotR</i>
----------------	--

---

## Description

Creates a data object compatible with the IsoplotR package

## Usage

```
redux2isoplotr(x, irr, fract = NULL, ca = NULL, k = NULL, format = 1,
  file = NULL)
```

## Arguments

x	an object of class <a href="#">redux</a>
irr	the irradiation schedule
fract	list with air shot data (one item per denominator isotope)
ca	an object of class <a href="#">logratios</a> with Ca-interference data (not necessary if interferences are included in X)
k	an object of class <a href="#">logratios</a> with K-interference data (not necessary if interferences are included in X)
format	input format for IsoplotR. I.e. one of 1: 39/40, s[39/40], 36/40, s[36/40], 39/36, s[39/36] (other formats will be added later)
file	optional (.csv) file name to write the output to.

## Value

an object of class ArAr, i.e. a table with the following columns: 'Ar4036', 'errAr4036', 'Ar3936', 'errAr3936', 'Ar4039', and 'errAr4039'

## Examples

```
data(Melbourne)
print(redux2isoplotr(Melbourne$X, Melbourne$irr))
```

---

results	<i>The results class</i>
---------	--------------------------

---

### Description

A list with the following items:

### Details

labels: a vector of strings denoting the names of the runs  
intercepts: a vector of ages  
covmat: the covariance matrix of intercepts  
thedata: a vector containing the acquisition dates and times

---

subset.timeresolved	<i>Select a subset of some data</i>
---------------------	-------------------------------------

---

### Description

Extracts those intercepts, covariances etc. that match a given list of indices or labels.

### Usage

```
## S3 method for class 'timeresolved'
subset(x, i = NULL, labels = NULL, invert = FALSE,
       include.J = FALSE, ...)

## S3 method for class 'logratios'
subset(x, i = NULL, labels = NULL, invert = FALSE,
       include.J = FALSE, ...)

## S3 method for class 'redux'
subset(x, i = NULL, labels = NULL, invert = FALSE,
       include.J = FALSE, ...)

## S3 method for class 'results'
subset(x, i = NULL, labels = NULL, invert = FALSE, ...)
```

### Arguments

x	an object of class <code>timeresolved</code> , <code>logratios</code> , <code>redux</code> or <code>results</code>
i	a vector with indices of the selected runs
labels	a string or a vector of strings with sample names

invert            boolean flag indicating whether the selection should be inverted, i.e. whether the selected indices or labels should be removed rather than retained

include.J        if TRUE, automatically adds the irradiation monitors to the selection

...              other arguments

**Value**

an object of the same class as x

**Examples**

```
data(Melbourne)
ages <- process(Melbourne$X,Melbourne$irr,Melbourne$fract)
MD <- subset(ages,labels=c("MD2-1","MD2-2","MD2-3","MD2-4","MD2-5"))
plotcorr(MD)
```

---

summary.results	Summary table
-----------------	---------------

---

**Description**

Plots the ages and their standard errors

**Usage**

```
## S3 method for class 'results'
summary(object, ...)
```

**Arguments**

object            an object of class [results](#)

...               no other arguments

**Examples**

```
data(Melbourne)
ages <- process(Melbourne$X,Melbourne$irr,Melbourne$fract)
summary(ages)[1:5,]
```



---

timeresolved	<i>The timesresolved class</i>
--------------	--------------------------------

---

### Description

An object class containing time resolved multi-collector mass spectrometry data

### Details

A list with the following items:

masses: a vector of strings denoting the isotopes monitored in each run

irr: a vector of strings denoting the irradiation runs

pos: a vector of integers with the positions in the irradiation stack

thedata: a vector containing the acquisition dates and times

d: a data table

thetime: a matrix with the measurement times

### See Also

[loaddata](#)

---

weightedmean	<i>Calculate the weighted mean age</i>
--------------	--

---

### Description

Computes the error weighted mean and MSWD of some samples taking into covariances.

### Usage

```
weightedmean(ages, prefix = NULL)
```

### Arguments

ages                    an object of class results

prefix                is either a string with the prefix of the samples that need to be averaged, or a vector of sample names.

### Value

a list with items:

avgt: the weighted mean age

err: the standard error of avgt

MSWD: the Mean Square of the Weighted Deviates

**Examples**

```
data(Melbourne)
ages <- process(Melbourne$X,Melbourne$irr,Melbourne$fract)
weightedmean(ages,"MD2-1")
```

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