

# Package ‘numOSL’

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**Type** Package

**Title** Numeric Routines for Optically Stimulated Luminescence Dating

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**Author** Jun Peng [aut, cre],  
Bo Li [aut],  
Jorge More [ctb],  
Burton Garbow [ctb],  
Kenneth Hillstrom [ctb],  
John Burkardt [ctb],  
Paul Gilbert [ctb],  
Ravi Varadhan [ctb]

**Maintainer** Jun Peng <pengjun10@mails.ucas.ac.cn>

**Description** Package for optimizing regular numeric problems in optically stimulated luminescence dating, such as: equivalent dose calculation, dose rate determination, growth curve fitting, decay curve decomposition, statistical age model optimization, and statistical plot visualization.

**License** GPL-3

**Depends** R (>= 2.15.3)

**Imports** graphics, stats, utils, grDevices

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numOSL-package	<i>Package for tackling basic numeric problems in optically stimulated luminescence dating</i>
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**Description**

Package for routine numeric optimization and data visualization in optically stimulated luminescence dating.

**Details**

Package: numOSL  
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**Author(s)**

Jun Peng    Hunan University of Science and Technology (HNUST), Xiangtan, China

Bo Li      University of Wollongong (UOW), Wollongong, Australia

### Package maintainer

Jun Peng <pengjun10@mails.ucas.ac.cn>

### Related package projects

R program KMS <https://github.com/pengjunUCAS/KMS>

R package tgcd <https://CRAN.R-project.org/package=tgcd>

### References

Peng J, Dong ZB, Han FQ, Long H, Liu XJ, 2013. R package numOSL: numeric routines for optically stimulated luminescence dating. *Ancient TL*, 31(2): 41-48.

Peng J, Li Bo, 2017. Single-aliquot Regenerative-Dose (SAR) and Standardised Growth Curve (SGC) Equivalent Dose Determination in a Batch Model Using the R Package 'numOSL'. *Ancient TL*, 35(2): 32-53.

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analyseBINdata

*BIN data analysis*

---

### Description

Analysing signal data records extracted from a BIN file.

### Usage

```
analyseBINdata(obj_pickBIN, nfchn, nlchn, bg = "late",
               me = 2.0, distp = "p", kph = NULL,
               kdc = NULL, dcr = NULL, FR.fchn = NULL,
               FR.mchn = NULL, FR.lchn = NULL,
               signal.type = "LxTx", outfile = NULL)
```

### Arguments

obj_pickBIN	<b>list(required)</b> : an object of S3 class "pickBIN" produced by function <code>pickBINdata</code>
nfchn	<b>integer(required)</b> : number of the first few channels from the initial part of a decay curve. Number of counts summed over channels (Delay+1L):(Delay+nfchn) is calculated as the fast-component plus background signal
nlchn	<b>integer(required)</b> : number of the last few channels from the latter part of a decay curve. If bg="late", number of counts averaged over channels (Delay+0n-nlchn+1L):(Delay+0n) will be calculated as the background signal, if bg="early", number of counts averaged over channels (Delay+nfchn+1L):(Delay+nfchn+nlchn) will be calculated as the background signal. Delay and 0n are obtained internally from the BIN file.

bg	<b>character</b> (with default): background subtraction method, i.e., bg="early" or bg="late"
me	<b>numeric</b> (with default): measurement error of Lx (or Tx) in percent
distp	<b>character</b> (with default): distribution of photon counts, distp="p" denotes Poisson distribution, distp="op" denotes Over Poisson distribution
kph	<b>numeric</b> (optional): correction factor for photon counts
kdc	<b>numeric</b> (optional): correction factor for dark counts
dcr	<b>numeric</b> (optional): dark count rate
FR.fchn	<b>vector</b> (optional): fast-component signal channels, note that those channels are extracted internally from the "ON" channels, i.e., FR.fchn=(Delay+1):(Delay+On)[FR.fchn]. Example: FR.fchn=1:5
FR.mchn	<b>vector</b> (optional): medium-component signal channels, note that those channels are extracted internally from the "ON" channels, i.e., FR.mchn=(Delay+1):(Delay+On)[FR.mchn]. Example: FR.mchn=31:60
FR.lchn	<b>vector</b> (optional): background signal channels, note that those channels are extracted internally from the "ON" channels, i.e., FR.lchn=(Delay+1):(Delay+On)[FR.lchn]. Example: FR.lchn=201:250
signal.type	<b>character</b> (with default): type of signal, "LxTx", "Lx", or "Tx"
outfile	<b>character</b> (optional): if specified, analysis results (i.e., NO, Position, Grain, SAR.Cycle, Dose, Init, BG, Lx, seLx, TInit, TBG, Tx, seTx, LxTx, seLxTx) will be written to a CSV file named "outfile" and saved to the current work directory

## Details

Function `analyseBINdata` is used for signal (i.e., Lx, Tx, and Lx/Tx) calculation. It provides two protocols for background subtraction (i.e., the early and late background subtraction methods).

Standard error of signals are assessed using two methods: if photon counts are assumed to follow Poisson distributions, **Eqn.(3)** of Galbraith (2002) will be applied; if photon counts are over-dispersed, **Eqn.(10)** of Bluszcz et al. (2015) will be applied.

If arguments `FR.fchn`, `FR.mchn`, and `FR.lchn` are provided, fast ratio will be calculated according to Madsen et al. (2009).

## Value

Return an invisible `list` of S3 class object "analyseBIN" containing the following elements:

SARdata	a <code>data.frame</code> containing calculated SAR data sets
criteria	values used as rejection criteria (0-1 values indicating if Tn is more than 3 sigma above BG or not, ratio of initial Tn signal to BG and associated standard error, relative standard error of Tn in percent, fast ratio of Tn and associated standard

	error), NA is produced if the value can not be calculated. Note that in this function rejection criteria are calculated but not applied
Tn	values of Tn and associated standard errors
LnTn.curve	decay curves for Ln and Tn for different aliquots (grains)
TxTn	ratios of Tx to Tn for various SAR cycles
agID	aliquot or grain ID (i.e., NO, Position, and Grain)

SARdata is a [data.frame](#) containing the following elements if `signal.type="LxTx"`:

Element	Description
NO	aliquot (grain) number
SAR.Cycle	SAR cycle (N, R1, R2, R3, ...)
Dose	regenerative dose
LxTx	sensitivity-corrected regenerative-dose signal
seLxTx	standard error of LxTx

SARdata contains the following elements if `signal.type="Lx"`:

Element	Description
NO	aliquot (grain) number
SAR.Cycle	SAR cycle (N, R1, R2, R3, ...)
Dose	regenerative dose
Lx	regenerative-dose signal
seLx	standard error of Lx

SARdata contains the following elements if `signal.type="Tx"`:

Element	Description
NO	aliquot (grain) number
SAR.Cycle	SAR cycle (N, R1, R2, R3, ...)
Dose	regenerative dose
Tx	test-dose signal
seTx	standard error of Tx

### Note

Though function [analyseBINdata](#) is originally designed to analyze CW-OSL data sets, IRSL data sets obtained from the SAR protocol can also be analyzed.

### References

- Ballarini M, Wallinga J, Wintle AG, Bos AJJ, 2007. A modified SAR protocol for optical dating of individual grains from young quartz samples. *Radiation Measurements*, 42(3): 360-369.
- Bluszcz A, Adamiec G, Heer AJ, 2015. Estimation of equivalent dose and its uncertainty in the OSL SAR protocol when count numbers do not follow a Poisson distribution. *Radiation Measurements*, 81: 46-54.

Cunningham AC, Wallinga J, 2010. Selection of integration time intervals for quartz OSL decay curves. *Quaternary Geochronology*, 5(6): 657-666

Duller GAT, 2016. *Analyst* (v4.31.9), User Manual.

Durcan JA, Duller GAT, 2011. The fast ratio: A rapid measure for testing the dominance of the fast component in the initial OSL signal from quartz. *Radiation Measurements*, 46(10): 1065-1072.

Galbraith R, 2002. A note on the variance of a background-corrected OSL count. *Ancient TL*, 20(2): 49-51.

Madsen AT, Duller GAT, Donnelly JP, Roberts HM, Wintle AG, 2009. A chronology of hurricane landfalls at Little Sippewissett Marsh, Massachusetts, USA, using optical dating. *Geomorphology*, 109(1-2): 36-45.

### See Also

[loadBINdata](#); [pickBINdata](#); [pickSARdata](#);  
[calED](#); [calSARED](#); [calSGCED](#);  
[fitGrowth](#); [lsNORM](#); [BIN](#)

### Examples

```
### Example 1 (not run):
# obj_loadBIN <- loadBINdata("foo.bin", view=TRUE)
# obj_pickBIN <- pickBINdata(obj_loadBIN, Position=2, LType="OSL")
# analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)

### Example 2:
data(BIN)
obj_pickBIN <- pickBINdata(BIN, Position=c(2,4,6,8,10),
                           LType="OSL", view=FALSE)
obj_analyseBIN <- analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)
obj_analyseBIN$SARdata
```

---

as\_analyseBIN

*Transform SAR data sets into S3 class object "analyseBIN"*

---

### Description

Transform SAR data sets into S3 class object "analyseBIN".

### Usage

```
as_analyseBIN(SARdata)
```

### Arguments

SARdata **matrix(required)**: SAR data set, it should contain five columns (i.e., NO, SAR.Cycle, Dose, Signal, and Signal.Err), see [SARdata](#) for details

**Value**

Return an invisible [list](#) of S3 class object "analyseBIN" containing the following elements:

SARdata	a <a href="#">data.frame</a> containing SAR data sets
criteria	values used as rejection criteria, here it is set equal to NULL
Tn	values of Tn and associated standard errors, here it is set equal to NULL
LnTn.curve	decay curves of Ln and Tn for different aliquots (grains), here it is set equal to NULL
TxTn	ratios of Tx to Tn for various SAR cycles, here it is set equal to NULL
agID	aliquot or grain ID (i.e., NO, Position, and Grain), here both Position and Grain are set equal to 0

SARdata is a [data.frame](#) containing the following elements:

Element	Description
NO	aliquot (grain) number
SAR.Cycle	SAR cycle (N, R1, R2, R3, ...)
Dose	regenerative dose
Signal	OSL signal
Signal.Err	standard error of OSL signal

**Note**

Function [as\\_analyseBIN](#) transforms SAR data sets (see [SARdata](#)) into S3 class object "analyseBIN". The returned elements such as `criteria`, `Tn`, `LnTn.curve`, and `TxTn` are set equal to NULL.

**See Also**

[analyseBINdata](#); [SARdata](#);  
[calSARED](#); [pickSARdata](#)

**Examples**

```
### Example 1:
data(SARdata)
obj_analyseBIN <- as_analyseBIN(SARdata[1:8, ,drop=FALSE])
res_calSARED <- calSARED(obj_analyseBIN)
res_calSARED$sarED

### Example 2 (not run):
# obj_analyseBIN <- as_analyseBIN(SARdata)
# res_calSARED <- calSARED(obj_analyseBIN, rcy1.range=c(1,1), outpdf="SARED")

### Example 3 (not run):
# obj_analyseBIN <- as_analyseBIN(SARdata)
# res_pickSARdata <- pickSARdata(obj_analyseBIN, fom.up=6, outpdf="SARdata")
# res_pickSARdata$SARdata
```

---

BIN	<i>BIN data</i>
-----	-----------------

---

### Description

BIN data for aeolian sample GL2-1 from the south margin of the Tengger Desert (Peng et al., 2013).

### Usage

```
data(BIN)
```

### Format

A S3 class object "loadBIN" produced by function [loadBINdata](#) that contains the following two elements:

**records** a [list](#) consists of loaded data records for each aliquot (grain)

**tab** a [data.frame](#) used for summarizing loaded data records

### References

Peng J, Han FQ, 2013. Selections of fast-component OSL signal using sediments from the south edge of Tengger Desert. Acta Geoscientica Sinica, 34(6): 757-762.

### See Also

[loadBINdata](#); [pickBINdata](#); [analyseBINdata](#)

### Examples

```
# Not run.  
# data(BIN)  
# class(BIN)
```

---

calDA	<i>Annual dose rate (age) calculation</i>
-------	---

---

### Description

Calculating the annual dose rate and burial age.

### Usage

```
calDA(dose, minGrainSize, maxGrainSize, Ucontent, Thcontent,  
      Kcontent, Wct, depth, altitude, latitude, longitude,  
      bulkDensity = 2.5, alphaValue = 0.03, nsim = 10000,  
      rdcf = 0.05, rba = 0.05, plot = TRUE)
```



## Arguments

dose	<b>vector(required)</b> : equivalent dose and associated measurement error (unit, Gy)
minGrainSize	<b>numeric(required)</b> : lower limit on grain size (unit, um)
maxGrainSize	<b>numeric(required)</b> : upper limit on grain size (unit, um)
Ucontent	<b>vector(required)</b> : uranium content and its measurement error (unit, ppm)
Thcontent	<b>vector(required)</b> : thorium content and its measurement error (unit, ppm)
Kcontent	<b>vector(required)</b> : potassium content and its measurement error (unit, 1 percent)
Wct	<b>vector(required)</b> : water content and its measurement error (unit, 1 percent)
depth	<b>numeric(required)</b> : sampling depth (unit, m)
altitude	<b>numeric(required)</b> : altitude of the sampling site (unit, m above sea level)
latitude	<b>numeric(required)</b> : latitude of the sampling site (unit, decimal degree)
longitude	<b>numeric(required)</b> : longitude of the sampling site (unit, decimal degree)
bulkDensity	<b>numeric(with default)</b> : average density of bulk sample (unit, g/cm <sup>3</sup> )
alphaValue	<b>numeric(with default)</b> : average alpha efficiency
nsim	<b>integer(with default)</b> : number of Monte Carlo iterations
rdcf	<b>numeric(with default)</b> : constant relative standard error for dose-rate conversion factors (unit, 1 percent)
rba	<b>numeric(with default)</b> : constant relative standard error for beta dose absorption fraction (unit, 1 percent)
plot	<b>logical(with default)</b> : draw a plot or not

## Details

Function `calDA` is used for calculating the annual dose rate and burial age using concentrations of radioactive nuclides (uranium, thorium, potassium) obtained from Neutron Activation Analysis (NAA), grain size, water content, average sample density, geographical parameters (depth, altitude, latitude, longitude), and an equivalent dose value. The elemental concentrations are converted into annual dose rate according to dose-rate conversion factors (Adamiec and Aitken, 1998). Beta dose absorbed fractions are calculated through linear interpolation using published data (Fain et al., 1999). The cosmic ray dose rate is estimated as a function of depth, altitude and geomagnetic latitude (Prescott and Hutton, 1994).

The standard error of an annual dose rate is estimated by a "parametric bootstrap" method. To perform the simulation, dose-rate conversion factors and beta dose absorption factor are assumed to have constant relative standard errors. Arguments such as `dose`, `Ucontent`, `Thcontent`, `Kcontent`, `wct` should be two-element vectors with the form `c(value, sd)`, as their measurement uncertainties are major error sources. Arguments such as `depth`, `altitude`, `latitude`, `longitude`, `bulkDensity`, `alphaValue` can be either a scalar or a two-element vector. This means that uncertainties from these quantities can be either ignored or taken into account during the simulation.

## Value

Return a `matrix` that contains calculated annual dose rate and age

## References

- Adamic G, Aitken M, 1998. Dose-rate conversion factors: update. *Ancient TL*, 16(2): 37-49.
- Fain J, Soumana S, Montret M, Miallier D, Pilleyre T, Sanzelle S, 1999. Luminescence and ESR dating Beta-dose attenuation for various grain shapes calculated by a Monte-Carlo method. *Quaternary Science Reviews*, 18(2): 231-234.
- Prescott JR, Hutton JT, 1994. Cosmic ray contributions to dose rates for Luminescence and ESR dating: large depths and long-term time variations. *Radiation Measurements*, 23(2-3): 497-500.

## Examples

```
calDA(dose=c(25.04,0.68), minGrainSize=90,
      maxGrainSize=180, Ucontent=c(2.86,0.19),
      Thcontent=c(8.63,0.34), Kcontent=c(2.00,0.11),
      Wct=c(0.05,0.05), depth=c(1.1,0.05), altitude=c(1170,58.5),
      latitude=c(37.64,1.88), longitude=c(103.16,5.16),
      bulkDensity=c(2.5,0.1), nsim=10000, rdcf=0.05, rba=0.05)
```

---

calED

*Equivalent dose calculation and error assessment*

---

## Description

Calculating an equivalent dose and assessing its standard error.

## Usage

```
calED(Curvedata, Ltx, model = "gok", origin = FALSE,
      errMethod = "sp", nsim = 500, weight = TRUE,
      trial = FALSE, plot = TRUE, nofit.rgd = NULL,
      agID = NULL, Tn = NULL, Tn3BG = NULL,
      TnBG.ratio = NULL, rseTn = NULL, FR = NULL,
      LnTn.curve = NULL, TxTn = NULL)
```

## Arguments

- |           |  |
|-----------|--|
| Curvedata | <b>matrix(required)</b> : a three-column matrix (i.e., regenerative doses, sensitivity-corrected regenerative-dose signals, and associated standard errors)                                    |
| Ltx       | <b>vector(required)</b> : a two-element vector consists of sensitivity-corrected natural-dose signal and its error   |
| model     | <b>character(with default)</b> : model used for growth curve fitting, see <a href="#">fitGrowth</a> for available models   |
| origin    | <b>logical(with default)</b> : logical value indicating if the growth curve should be forced to pass the origin  |
| errMethod | <b>character(with default)</b> : method used for equivalent dose error assessment. "sp" and "mc" denote error estimation using the Simple Transformation and Monte Carlo methods, respectively |

nsim	<b>integer</b> (with default): desired number of randomly simulated equivalent dose obtained by Monte Carlo simulation
weight	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see function <code>fitGrowth</code> for details
trial	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using other models if the given model fails, see function <code>fitGrowth</code> for details
plot	<b>logical</b> (with default): logical value indicating if the results should be plotted
nofit.rgd	<b>integer</b> (optional): regenerative doses that will not be used during the fitting. For example, if <code>nofit.rgd=1</code> then the first regenerative dose will not be used during growth curve fitting
agID	<b>vector</b> (optional): a three-element vector indicating aliquot (grain) ID, i.e., <code>agID[1]=NO</code> , <code>agID[2]=Position</code> , <code>agID[3]=Grain</code>
Tn	<b>vector</b> (optional): a two-element vector containing value and standard error of Tn
Tn3BG	<b>numeric</b> (optional): 0-1 value indicating if Tn is more than 3 sigma above BG, 1 indicates <code>Tn &gt; 3_sigma_BG</code> , 0 indicates <code>Tn &lt;= 3_sigma_BG</code>
TnBG.ratio	<b>vector</b> (optional): a two-element vector containing value and standard error of ratio of initial Tn signal to BG
rseTn	<b>numeric</b> (optional): relative standard error of Tn in percent
FR	<b>vector</b> (optional): a two-element vector containing value and standard error of fast ratio of Tn
LnTn.curve	<b>list</b> (optional): decay curve data for Ln and Tn, it should contain four elements, i.e., <code>names(LnTn.curve)=c("Ln.x", "Ln.y", "Tn.x", "Tn.y")</code>
TxTn	<b>vector</b> (optional): ratios of Tx to Tn for various SAR cycles

### Details

Function `calED` is used for calculating an equivalent dose and assessing its standard error. The standard errors of an equivalent dose can be assessed using the Simple Transformation or Monte Carlo method (Duller, 2007).

Interpolation is performed using a combination of golden section search and successive parabolic interpolation (**R** function `optimize` in package *stats*) (freely available Fortran 77 source code at <http://www.netlib.org/fmm/fmin.f>). See function `fitGrowth` for more details on growth curve fitting.

### Value

Return an invisible **list** that contains the following elements:

message	return 0 if calculation succeeds, 1 if growth curve fitting fails, 2 if natural-dose signal saturates, 3 if equivalent dose calculation fails, 4 if equivalent dose error assessment fails
fitIDX	Indices of dose points used in growth curve fitting
LMpars	optimized parameters for the growth curve

value	minimized objective for the growth curve
avg.error	average fit error for the growth curve
RCS	reduced chi-square value for the growth curve
FOM	figure of merit value for the growth curve in percent
calED.method	method used for equivalent dose calculation, i.e., "Interpolation" or "Extrapolation"
mcED	randomly simulated equivalent doses
ED	calculated equivalent dose and its standard error
ConfInt	68 percent and 95 percent confidence intervals for the equivalent dose
RecyclingRatio1	the first recycling ratio and its standard error
RecyclingRatio2	the second recycling ratio and its standard error
RecyclingRatio3	the third recycling ratio and its standard error
Recuperation1	the first recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to natural-dose signal) and its standard error in percent
Recuperation2	the second recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to maximum regenerative-dose signal) and its standard error in percent

### Note

Arguments `agID`, `Tn`, `Tn3BG`, `TnBG.ratio`, `rseTn`, `FR`, `LnTn.curve`, and `TxTn` have nothing to do with equivalent dose calculation. They are used only for plotting purpose.

Argument `Tn3BG` indicates if `Tn` (after background subtraction) is more than 3 sigma above `BG`, while argument `TnBG.ratio` denotes the ratio of `Tn` (no background subtraction) to `BG`.

Function `calED` will return `message=3` (i.e., "Failed in equivalent dose calculation") if the equivalent dose to be calculated below  $-50$  ( $<Gy><s>$ ).

68 percent (one sigma) and 95 percent (two sigma) confidence intervals of equivalent doses will be determined respectively using normal approximation and Monte Carlo simulation, for `errMethod="sp"` and `errMethod="mc"`.

Function `sgcED` in previous versions was bundled to function `calSGCED`.

### References

- Duller GAT, 2007. Assessing the error on equivalent dose estimates derived from single aliquot regenerative dose measurements. *Ancient TL*, 25(1): 15-24.
- Duller GAT, 2016. *Analyst* (v4.31.9), User Manual.
- Galbraith RF, Roberts RG, 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: an overview and some recommendations. *Quaternary Geochronology*, 11: 1-27.

**See Also**

[analyseBINdata](#); [fitGrowth](#); [calRcyRcp](#);  
[calSARED](#); [fastED](#); [calSGCED](#)

**Examples**

```
### Example 1:
Curvedata <- cbind(c(0, 18, 36, 54, 72, 0, 18),
                  c(0.026, 1.55, 2.39, 3.46, 4.13, 0.023, 1.61),
                  c(0.005, 0.11, 0.27, 0.22, 0.20, 0.008, 0.24))
Ltx <- c(3.1,0.31)
calED(Curvedata, Ltx, model="exp", origin=FALSE)

### Example 2 (not run):
# data(BIN)
# obj_pickBIN <- pickBINdata(BIN, Position=48,
#                             LType="OSL", view=FALSE)
# obj_analyseBIN <- analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)
# Curvedata <- obj_analyseBIN$SARdata[-1,3:5]
# Ltx <- as.numeric(obj_analyseBIN$SARdata[1,4:5])
# calED(Curvedata, Ltx, model="gok", origin=FALSE)
```

---

calRcyRcp

*Recycling ratio and recuperation calculation*


---

**Description**

Calculating recycling ratio, recuperation, and associated standard errors.

**Usage**

```
calRcyRcp(Curvedata, Ltx)
```

**Arguments**

Curvedata     **matrix(required)**: a three-column matrix (i.e., regenerative doses, sensitivity-corrected regenerative-dose signals, and associated standard errors)

Ltx            **vector(required)**: a two-element vector consists of sensitivity-corrected natural-dose signal and its error

**Value**

Return a [list](#) that contains the following elements:

RecyclingRatio1

the first recycling ratio and its standard error

RecyclingRatio2

the second recycling ratio and its standard error

RecyclingRatio3	the third recycling ratio and its standard error
Recuperation1	the first recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to natural-dose signal) and its standard error in percent
Recuperation2	the second recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to maximum regenerative-dose signal) and its standard error in percent

**Note**

If the sensitivity-corrected signals for the first, second, and third repeated regenerative doses are R1, R2, and R3, respectively, then  $\text{RecyclingRatio1} = R2/R1$ ,  $\text{RecyclingRatio2} = R3/R1$ , and  $\text{RecyclingRatio3} = R3/R2$ .

**References**

Wintle AG, Murray AS, 2006. A review of quartz optically stimulated luminescence characteristics and their relevance in single-aliquot regeneration dating protocols. *Radiation Measurements*, 41(4): 369-391.

**See Also**

[calED](#); [fastED](#); [calSARED](#); [pickSARdata](#)

---

calSARED

*SAR equivalent doses calculation and selection*

---

**Description**

Calculating and selecting a series of equivalent doses in a batch mode according to the single aliquot regenerative-dose (SAR) method (Murray and Wintle, 2000).

**Usage**

```
calSARED(obj_analyseBIN, model = "gok", origin = FALSE,
         errMethod = "sp", nsim = 500, weight = TRUE,
         trial = TRUE, nofit.rgd = NULL, Tn.above.3BG = TRUE,
         TnBG.ratio.low = NULL, rseTn.up = NULL, FR.low = NULL,
         rcy1.range = NULL, rcy2.range = NULL, rcy3.range = NULL,
         rcp1.up = NULL, rcp2.up = NULL, fom.up = NULL,
         rcs.up = NULL, calED.method = NULL, rseED.up = NULL,
         use.se = TRUE, outpdf = NULL, outfile = NULL)
```

**Arguments**

obj_analyseBIN	<b>list(required)</b> : an object of S3 class "analyseBIN" produced by function <a href="#">analyseBINdata</a> or <a href="#">as_analyseBIN</a>
model	<b>character</b> (with default): model used for growth curve fitting, see <a href="#">fitGrowth</a> for available models
origin	<b>logical</b> (with default): logical value indicating if the growth curve should be forced to pass the origin
errMethod	<b>character</b> (with default): method used for equivalent dose error assessment. See function <a href="#">calED</a> for details
nsim	<b>integer</b> (with default): desired number of randomly simulated equivalent dose obtained by Monte Carlo simulation
weight	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see function <a href="#">fitGrowth</a> for details
trial	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using other models if the given model fails, see function <a href="#">fitGrowth</a> for details
nofit.rgd	<b>integer</b> (optional): regenerative doses that will not be used during the fitting. For example, if <code>nofit.rgd=6</code> then the sixth regenerative dose will not be used during growth curve fitting
Tn.above.3BG	<b>logical</b> (with default): logical value indicating if aliquot (grain) with Tn below 3 sigma BG should be rejected
TnBG.ratio.low	<b>numeric</b> (optional): lower limit on ratio of initial Tn signal to BG
rseTn.up	<b>numeric</b> (optional): upper limit on relative standard error of Tn in percent
FR.low	<b>numeric</b> (optional): lower limit on fast ratio of Tn
rcy1.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 1, Example: <code>rcy1.range=c(0.9, 1.1)</code>
rcy2.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 2
rcy3.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 3
rcp1.up	<b>numeric</b> (optional): upper limit on recuperation 1 (i.e., ratio of the sensitivity-corrected zero-dose signal to natural-dose signal) in percent
rcp2.up	<b>numeric</b> (optional): upper limit on recuperation 2 (i.e., ratio of the sensitivity-corrected zero-dose signal to maximum regenerative-dose signal) in percent
fom.up	<b>numeric</b> (optional): upper limit on figure of merit (FOM) values of growth curves in percent
rsc.up	<b>numeric</b> (optional): upper limit on reduced chi-square (RCS) values of growth curves
calED.method	<b>character</b> (optional): method used for equivalent dose calculation, i.e., "Interpolation" or "Extrapolation"
rseED.up	<b>numeric</b> (optional): upper limit on the relative standard error of equivalent dose in percent

use.se	<a href="#">logical</a> (with default): logical value indicating if standard errors of values should be used during application of rejection criteria
outpdf	<a href="#">character</a> (optional): if specified, results of SAR equivalent dose calculation will be written to a PDF file named "outpdf" and saved to the current work directory
outfile	<a href="#">character</a> (optional): if specified, SAR equivalent doses related quantities will be written to a CSV file named "outfile" and saved to the current work directory

### Value

Return an invisible [list](#) that contains the following elements:

LMpars	a <a href="#">list</a> containing optimized parameters of growth curves of calculated (selected) SAR equivalent doses
Tn	values and standard errors of Tn of calculated (selected) SAR equivalent doses
Ltx	sensitivity-corrected natural-dose signals and associated standard errors used for SAR equivalent dose calculation
sarED	calculated (selected) SAR equivalent doses and associated standard errors
ConfInt	68 percent (one sigma) and 95 percent (two sigma) confidence intervals of SAR equivalent doses
agID	aliquot (grain) ID of calculated (selected) SAR equivalent doses
summary.info	a summary of the SAR equivalent dose calculation

### Note

Rejection criteria used to select reliable SAR equivalent dose estimates can be categorized into three groups:

- (1) signal-related criteria, such as `Tn.above.3BG`, `TnBG.ratio.low`, `rseTn.up`, and `FR.low`;
- (2) growth-curve-related criteria, such as `rcy1.range`, `rcy2.range`, `rcy3.range`, `rcp1.up`, `rcp2.up`, `fom.up`, and `rsc.up`;
- (3) equivalent-dose-related criteria, such as `calED.method` and `rseED.up`.

### References

Duller GAT, 2016. Analyst (v4.31.9), User Manual.

Murray AS, Wintle AG, 2000. Luminescence dating of quartz using improved single-aliquot regenerative-dose protocol. *Radiation Measurements*, 32(1): 57-73.

Wintle AG, Murray AS, 2006. A review of quartz optically stimulated luminescence characteristics and their relevance in single-aliquot regeneration dating protocols. *Radiation Measurements*, 41(4): 369-391.

### See Also

[analyseBINdata](#); [fitGrowth](#);  
[calED](#); [calSGCED](#); [pickSARdata](#)



## Examples

```
data(BIN)
obj_pickBIN <- pickBINdata(BIN, Position=c(2,4,6,8,10), Grain=0,
  LType="OSL", view=FALSE)
obj_analyseBIN <- analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)
res_SARED <- calSARED(obj_analyseBIN, model="exp", origin=FALSE)
# plot(res_SARED$Tn[,1], res_SARED$sarED[,1], xlab="Tn", ylab="ED (<Gy>|<s>)")
```

---

 calSGCED

*SGC Equivalent dose calculation and selection*


---

## Description

Calculating and selecting equivalent doses in a batch model according to the "standardised growth curve" (SGC) method suggested by Roberts and Duller (2004) or the "global standardised growth curve" (gSGC) method suggested by Li et al. (2015, 2016).

## Usage

```
calSGCED(obj_analyseBIN, SGCpars, model, origin, avgDev,
  method = "SGC", SAR.Cycle = "N", errMethod = "sp",
  Tn.above.3BG = TRUE, TnBG.ratio.low = NULL,
  rseTn.up = NULL, FR.low = NULL, rseED.up = NULL,
  use.se = TRUE, outpdf = NULL, outfile = NULL)
```

## Arguments

obj_analyseBIN	<b>list(required)</b> : an object of S3 class "analyseBIN" produced by function <a href="#">analyseBINdata</a> or <a href="#">as_analyseBIN</a>
SGCpars	<b>vector(required)</b> : optimized parameters of the SGC obtained using function <a href="#">lsNORM</a> (or <a href="#">fitGrowth</a> )
model	<b>character(required)</b> : fitting model used for obtaining SGCpars
origin	<b>logical(required)</b> : logical value indicating if established SGC passes the origin
avgDev	<b>numeric(required)</b> : average deviation (i.e., average fit error) of the SGC obtained using function <a href="#">fitGrowth</a> or <a href="#">lsNORM</a> . This quantity stands for the uncertainty of established SGC when assessing the equivalent dose error using the simple transformaion method
method	<b>character</b> (with default): method used for equivalent dose calculation, i.e., method="SGC" (for the original SGC method) or method="gSGC" (for the improved SGC method)
SAR.Cycle	<b>character</b> (with default): SAR cycles used for SGC equivalent dose calculation. Example: SAR.Cycle=c("N", "R3")
errMethod	<b>character</b> (with default): method used for equivalent dose error assessment
Tn.above.3BG	<b>logical</b> (with default): logical value indicating if aliquot (grain) with Tn below 3 sigma BG should be rejected

TnBG.ratio.low	<a href="#">numeric</a> (optional): lower limit on ratio of initial Tn signal to BG
rseTn.up	<a href="#">numeric</a> (optional): upper limit on relative standard error of Tn in percent
FR.low	<a href="#">numeric</a> (optional): lower limit on fast ratio of Tn
rseED.up	<a href="#">numeric</a> (optional): upper limit on the relative standard error of equivalent dose in percent
use.se	<a href="#">logical</a> (with default): logical value indicating if standard errors of values should be used during application of rejection criteria
outpdf	<a href="#">character</a> (optional): if specified, results of SGC equivalent dose calculation will be written to a PDF file named "outpdf" and saved to the current work directory
outfile	<a href="#">character</a> (optional): if specified, SGC equivalent doses related quantities will be written to a CSV file named "outfile" and saved to the current work directory

### Value

Return an invisible [list](#) that contains the following elements:

scale.Ltx	scaled standardised natural-dose signals and associated standard errors used for SGC equivalent dose calculation. Note that standardised natural-dose signals will remain un-scaled if method="SGC"
sgcED	calculated SGC equivalent doses
ConfInt	68 percent (one sigma) and 95 percent (two sigma) confidence intervals of SGC equivalent doses
agID	aliquot (grain) ID of calculated (selected) SGC equivalent doses
summary.info	a summary of the SGC equivalent dose calculation

### References

- Li B, Roberts RG, Jacobs Z, Li SH, 2015. Potential of establishing a "global standardised growth curve" (gSGC) for optical dating of quartz from sediments. *Quaternary Geochronology*, 27: 94-104.
- Li B, Jacobs Z, Roberts RG, 2016. Investigation of the applicability of standardised growth curves for OSL dating of quartz from Haua Fteah cave, Libya. *Quaternary Geochronology*, 35: 1-15.
- Roberts HM, Duller GAT, 2004. Standardised growth curves for optical dating of sediment using multiple-grain aliquots. *Radiation Measurements*, 38(2): 241-252.

### See Also

[fitGrowth](#); [lsNORM](#); [SARdata](#);  
[scaleSGCN](#); [calED](#); [calSARED](#)

### Examples

```
data(SARdata)
### (1) gSGC ED calculation:
### gSGCpars were obtained using function "lsNORM".
gSGCpars <- c(137.440874251, 0.007997863, 2.462035263, -0.321536177)
avg.error2 <- 0.1111623
```

```

res <- calSGCED(as_analyseBIN(SARdata), gSGCpars, method="gSGC",
               model="gok", origin=FALSE, avgDev=avg.error2,
               SAR.Cycle=c("N","R3"))
print(res$sgcED)

### (2) SGC ED calculation (not run):
### SGCpars were obtained using function "fitGrowth".
# SGCpars <- c(183.474322547, 0.007038048, 4.254287622, -0.337734151)
# avg.error <- 0.3156259
# calSGCED(as_analyseBIN(SARdata), SGCpars, method="SGC", model="gok",
#          origin=FALSE, avgDev=avg.error, SAR.Cycle="N", outpdf="SGCED")

### (3) gSGC ED calculation and signal-related
### rejection criteria application (not run):
# data(BIN)
# res_pickBIN <- pickBINdata(BIN, LType="OSL")
# res_analyseBIN <- analyseBINdata(res_pickBIN, nfchn=4, nlchn=30)
# res_lsNORM <- lsNORM(res_analyseBIN$SARdata, model="gok", origin=FALSE)

# calSGCED(res_analyseBIN, SGCpars=res_lsNORM$LMpars2[,1],
#          model="gok", origin=FALSE, avgDev=res_lsNORM$avg.error2,
#          method="gSGC", SAR.Cycle=c("N","R3"), Tn.above.3BG=TRUE,
#          TnBG.ratio.low=4, rseTn.up=10, outpdf="foo", outfile="foo")

```

---

 dbED

*De distribution summarization*


---

## Description

Calculating statistical parameters (skewness, kurtosis, quantiles) for a number of equivalent dose values.

## Usage

```

dbED(EDdata, plot = TRUE, typ = "pdf", from = NULL,
     to = NULL, step = NULL, nbin = 15, pcolor = "grey",
     psize = 1.5, outfile = NULL)

```

## Arguments

EDdata	<b>matrix(required)</b> : a two-column matrix (i.e., equivalent dose values and associated standard errors)
plot	<b>logical</b> (with default): draw a plot or not
typ	<b>character</b> (with default): type of plot, typ="pdf" means a probability density plot and typ="hist" means a histogram plot
from	<b>numeric</b> (optional): desired lower limit on x-axis

to	<a href="#">numeric</a> (optional): desired upper limit on x-axis
step	<a href="#">numeric</a> (optional): a step-size used for constructing the probability density plot (if typ="pdf"). Smaller step value gives smoother density curve
nbin	<a href="#">integer</a> (with default): desired number of intervals for the histogram (if typ="hist")
pcolor	<a href="#">character</a> (with default): color of data points, input <a href="#">colors()</a> to see available colors
psize	<a href="#">numeric</a> (with default): size of data points
outfile	<a href="#">character</a> (optional): if specified, calculated probability densities (if typ="pdf") will be written to a CSV file named "outfile" and saved to the current work directory

### Value

Return a [list](#) that contains the following elements:

weight.ED	weighted mean of equivalent dose values and associated standard error
skewness	weighted skewness of equivalent dose values and associated standard error
kurtosis	kurtosis of equivalent dose values and associated standard error
quantile.ED	quantiles of equivalent dose values

### References

- Galbraith RF, 2010. On plotting OSL equivalent doses. *Ancient TL*, 28(1): 1-10.
- Galbraith RF, Roberts RG, 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: an overview and some recommendations. *Quaternary Geochronology*, 11: 1-27.

### See Also

[psRadialPlot](#); [RadialPlotter](#); [EDdata](#)

### Examples

```
data(EDdata)
dbED(EDdata$g111, typ="pdf")
```

---

decomp

*OSL decay curve decomposition*

---

### Description

Decomposing a CW-OSL or LM-OSL decay curve to a given number of first-order exponential components using a combination of differential evolution and Levenberg-Marquardt algorithm suggested by Bluszcz and Adamiec (2006).

**Usage**

```
decomp(Sigdata, delay.off = c(0,0), ncomp = 2,
       constant = TRUE, typ = "cw", control.args = list(),
       weight = FALSE, plot = TRUE, log = "x", lwd = 2,
       curve.no = NULL, SAR.Cycle = NULL, irr.dose = NULL,
       outfile = NULL, transf = TRUE)
```

**Arguments**

Sigdata	<b>matrix(required)</b> : a two-column matrix (i.e., stimulation time and photon count values)
delay.off	<b>vector</b> (with default): a two-elment vector indicating the "Delay" and "Off" values of the decay curves, i.e., <code>delay.off[1]=Delay, delay.off[2]=Off</code>
ncomp	<b>integer</b> (with default): number of decomposed components
constant	<b>logical</b> (with default): logical value indicating if a constant component should be subtracted from the decay curve
typ	<b>character</b> (with default): type of a decay curve (i.e., <code>typ="cw"</code> or <code>typ="lm"</code> )
control.args	<b>list</b> (with default): arguments used in the differential evolution algorithm, see details
weight	<b>logical</b> (with default): logical value indicating if the fit should be performed using a weighted procedure
plot	<b>logical</b> (with default): logical value indicating if the results should be plotted
log	<b>character</b> (with default): a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic
lwd	<b>numeric</b> (with default): width of curves (lines)
curve.no	<b>numeric</b> (optional): decay curve number
SAR.Cycle	<b>numeric</b> (optional): SAR cycle of the decay curve, Example: <code>SAR.Cycle="R1"</code>
irr.dose	<b>numeric</b> (optional): irradiation dose of the decay curve
outfile	<b>character</b> (optional): if specified, decomposed signal values will be written to a CSV file named "outfile" and saved to the current work directory
transf	<b>logical</b> (with default): do not use (for backward compatibility purpose)

**Details**

Function `decomp` decomposes an OSL decay curve to a specified number of components using a combination of differential evolution and Levenberg-Marquardt algorithm. Both CW-OSL and LM-OSL decay curves can be decomposed.

For a CW-OSL decay curve, the fitting model (Bluszcz and Adamiec, 2006) is:

$$I(t) = a_1 * b_1 * \exp(-b_1 * t) + \dots + a_k * b_k * \exp(-b_k * t),$$

where  $k=1, 2, \dots, 7$ ,  $I(t)$  is the luminescence intensity as a function of time,  $a$  is the number of trapped electrons, and  $b$  is the detrapping rate. The constant component is  $c$  if `constant=TRUE`.

For a LM-OSL decay curve, the fitting model (Bulur, 2000) is:

$$I(t) = a_1 * b_1 * (t/P) * \exp[-b_1 * t^2 / (2 * P)] + \dots + a_k * b_k * (t/P) * \exp[-b_k * t^2 / (2 * P)],$$

where  $k=1, 2, \dots, 7$ , and  $I(t)$  is the luminescence intensity as a function of time,  $P$  is the total stimulation time,  $a$  is the number of trapped electrons, and  $b$  is the detrapping rate. The constant component is  $c * (t/P)$  if `constant=TRUE`.

Parameters are initialized using a differential evolution method suggested by Bluszcz and Adamiec (2006), then the Levenberg-Marquardt algorithm (minpack: Fortran 90 version by John Burkardt, freely available at [http://people.sc.fsu.edu/~jburkardt/f\\_src/minpack/minpack.html](http://people.sc.fsu.edu/~jburkardt/f_src/minpack/minpack.html)) will be performed to optimize the parameters. If `weight=TRUE`, the photon counts will be assumed to follow a Poisson distribution with a standard error equal to the square root of the number of photon counts, and the decay curve will be fitted using a weighted procedure. Setting `weight=TRUE` gives more weight to photon counts from slower decaying components.

Arguments in `control.args` that control the differential evolution algorithm include:

- (1) *factor*: the number of population members, `np=factor*ncomp`, default `factor=20`;
- (2) *f*: a weighting factor that lies between 0 and 1.2, default `f=0.5`;
- (3) *cr*: a crossover constant that lies between 0 and 1, default `cr=0.99`;
- (4) *maxiter*: maximum number of iterations, default `maxiter=500`;
- (5) *tol*: tolerance for stopping the iteration, the procedure will be terminated if all relative standard deviations of parameters are smaller than `tol`, default `tol=0.1`.

## Value

Return an invisible [list](#) containing the following elements:

<code>message</code>	return 0 if fit succeeds, else 1
<code>comp.sig</code>	a matrix containing time, signal, and fitted signal values for each component
<code>LMpars</code>	optimized parameters for the decay curve
<code>constant</code>	estimated constant component, it returns 0 if <code>constant=FALSE</code>
<code>value</code>	minimized objective for the decay curve
<code>FOM</code>	figure of merit value for the decay curve in percent

## Note

Arguments `curve.no`, `SAR.Cycle`, and `irr.dose` have nothing to do with decay curve fitting. They are used only for plotting purpose.

The model to be optimized should not be underdetermined. This means that the number of data points should exceed (or at least be equal to) the number of parameters. For a given model, this routine will return an error if any standard errors of parameters cannot be estimated by numerical difference-approximation. Function `decomp` in previous versions was bundled to function [decomp](#).

We would like to thank Professor Andrzej Bluszcz who helps us a lot during the programming of this function. Dr Jeong-Heon Choi is thanked for providing published data sets to test this routine.

## References

Bluszcz A, 1996. Exponential function fitting to TL growth data and similar applications. *Geochronometria*, 13: 135-141.

Bluszcz A, Adamiec G, 2006. Application of differential evolution to fitting OSL decay curves. *Radiation Measurements*, 41(7-8): 886-891.

Bulur E, 2000. A simple transformation for converting CW-OSL curves to LM-OSL curves. *Radiation Measurements*, 32(2): 141-145.

Differential evolution algorithm, [http://en.wikipedia.org/wiki/Differential\\_evolution](http://en.wikipedia.org/wiki/Differential_evolution)

Jain M, Murray AS, Boetter-Jensen L, 2003. Characterisation of blue-light stimulated luminescence components in different quartz samples: implications for dose measurement. *Radiation Measurements*, 37(4-5): 441-449.

More JJ, 1978. "The Levenberg-Marquardt algorithm: implementation and theory," in *Lecture Notes in Mathematics: Numerical Analysis*, Springer-Verlag: Berlin. 105-116.

## Further reading

Adamiec G, 2005. OSL decay curves-relationship between single- and multiple-grain aliquots. *Radiation Measurements*, 39(1): 63-75.

Balian HG, Eddy NW, 1977. Figure-of-merit (FOM), an improved criterion over the normalized chi-squared test for assessing goodness-of-fit of gamma-ray spectral peaks. *Nuclear Instruments and Methods*, 145(2): 389-95.

Choi JH, Duller GAT, Wintle AG, 2006. Analysis of quartz LM-OSL curves. *Ancient TL*, 24(1): 9-20.

Li SH, Li B, 2006. Dose measurement using the fast component of LM-OSL signals from quartz. *Radiation Measurements*, 41(5): 534-541.

Peng J, Dong ZB, Han FQ, Han YH, Dai XL, 2014. Estimating the number of components in an OSL decay curve using the Bayesian Information Criterion. *Geochronometria*, 41(4): 334-341.

## See Also

[Signaldata](#); [pickBINdata](#); [fastED](#)

## Examples

```
### Example 1:
data(Signaldata)
decomp(Signaldata$lm, ncomp=3, typ="lm",
       control.args=list(maxiter=10))

### Example 2 (not run):
# data(BIN)
# obj_pickBIN <- pickBINdata(BIN, Position=2, Run=2, view=TRUE,
#                             LType="OSL", force.matrix=TRUE)
# decomp(obj_pickBIN$BINdata[[1]], ncomp=2, log="xy")
```

---

EDdata	<i>Equivalent dose values</i>
--------	-------------------------------

---

**Description**

Two sets of equivalent dose values.

**Usage**

```
data(EDdata)
```

**Format**

A list that contains two sets of equivalent dose values:

**gl11** 35 equivalent dose values of a sand sample from the Tengger Desert (Peng and Han, 2013)

**al3** 84 equivalent dose values of an alluvial deposit from the andean precordillera (Schmidt et al., 2012)

**References**

Peng J, Han FQ, 2013. Selections of fast-component OSL signal using sediments from the south edge of Tengger Desert. *Acta Geoscientica Sinica*, 34(6): 757-762.

Schmidt S, Tsukamoto S, Salomon E, Frechen M, Hetzel R, 2012. Optical dating of alluvial deposits at the orogenic front of the andean precordillera (Mendoza, Argentina). *Geochronometria*, 39(1): 62-75.

**See Also**

[dbED](#); [psRadialPlot](#); [RadialPlotter](#);  
[mcFMM](#); [mcMAM](#)

**Examples**

```
# Not run.  
# data(EDdata)  
# names(EDdata)
```



---

fastED *Fast-component equivalent dose calculation*

---

### Description

Estimating a fast-component equivalent dose using decay curves obtained from the single aliquot regenerative-dose (SAR) method.

### Usage

```
fastED(Sigdata, Redose, delay.off = c(0,0), ncomp = 2,
       constant = TRUE, control.args = list(), typ = "cw",
       model = "gok", origin = FALSE, errMethod = "sp",
       nsim = 500, weight.decomp = FALSE,
       weight.fitGrowth = TRUE, trial = TRUE,
       nofit.rgd = NULL, outpdf = NULL, log = "x",
       lwd = 2, test.dose = NULL, agID = NULL)
```

### Arguments

Sigdata	<b>matrix(required)</b> : a series of decay curves stored in a matrix column by column, the first column denotes stimulation time values, see details. Data structure of this kind can be obtained using function <a href="#">pickBINdata</a> by setting argument <code>force.matrix=TRUE</code> , see examples
Redose	<b>vector(required)</b> : regenerative dose values. Example: <code>Redose=c(1,2,3,4,0,1)</code>
delay.off	<b>vector(with default)</b> : a two-element vector indicating the "Delay" and "Off" values of the decay curves, i.e., <code>delay.off[1]=Delay, delay.off[2]=Off</code>
ncomp	<b>integer(with default)</b> : number of decomposed components
constant	<b>logical(with default)</b> : logical value indicating if a constant background should be subtracted from the decay curve, see function <a href="#">decomp</a> for details
control.args	<b>list(with default)</b> : arguments used in the differential evolution algorithm, see function <a href="#">decomp</a> for details
typ	<b>character(with default)</b> : type of an OSL decay curve, only CW-OSL decay curve can be analyzed currently
model	<b>character(with default)</b> : model used for growth curve fitting, see function <a href="#">fitGrowth</a> for available models
origin	<b>logical(with default)</b> : logical value indicating if the growth curve should be forced to pass the origin
errMethod	<b>character(with default)</b> : method used for equivalent dose error assessment. See function <a href="#">calED</a> for details
nsim	<b>integer(with default)</b> : desired number of randomly simulated equivalent dose obtained by Monte Carlo simulation
weight.decomp	<b>character(with default)</b> : logical value indicating if the decay curve should be fitted using a weighted procedure, see function <a href="#">decomp</a> for details

weight.fitGrowth	<b>character</b> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see function <a href="#">fitGrowth</a> for details
trial	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using other models if the given model fails, see function <a href="#">fitGrowth</a> for details
nofit.rgd	<b>integer</b> (optional): regenerative doses that will not be used during the fitting. For example, if <code>nofit.rgd=1</code> then the first regenerative dose will not be used during fast-component growth curve fitting
outpdf	<b>character</b> (optional): if specified, results of fast-component equivalent dose calculation will be written to a PDF file named "outpdf" and saved to the current work directory
log	<b>character</b> (with default): a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic
lwd	<b>numeric</b> (with default): width of curves (lines)
test.dose	<b>numeric</b> (optional): test dose of decay curves
agID	<b>vector</b> (optional): a three-element vector indicating aliquot (grain) ID, i.e., <code>agID[1]=NO</code> , <code>agID[2]=Position</code> , <code>agID[3]=Grain</code>

## Details

Function [fastED](#) is used to estimate a fast-component equivalent dose using data sets obtained from the SAR protocol (Murray and Wintle, 2000). The routine tries to decompose a series of decay curves to a specified number of components, then the numbers of trapped electrons from the fast-component will be used to construct the growth curve to estimate a fast-component equivalent dose. See function [decomp](#), [fitGrowth](#), and [calED](#) for more details concerning decay curve decomposition, growth curve fitting, and equivalent dose calculation, respectively.

Argument `Sigdata` is a column-matrix made up with stimulation time values and a number of decay curves:

Column.no	Description
I	Stimulation time values
II	Natural-dose signal values
III	Test-dose signal values for the natural-dose
IV	The 1th Regenerative-dose signal values
V	Test-dose signal values for the 1th regenerative-dose
VI	The 2th regenerative-dose signal values
VII	Test-dose signal values for the 2th regenerative-dose
...	...

## Value

Return an invisible [list](#) containing the following elements:

<code>decomp.pars</code>	a <a href="#">list</a> containing optimized parameters of successfully fitted decay curves
<code>Curvedata</code>	data sets used for building the fast-component growth curve

Ltx	sensitivity-corrected natural-dose fast-component signal and its standard error
LMpars	optimized parameters for the fast-component growth curve
value	minimized objective for the fast-component growth curve
avg.error	average fit error for the fast-component growth curve
RCS	reduced chi-square value for the fast-component growth curve
FOM	figure of merit value for the fast-component growth curve in percent
calED.method	method used for fast-component equivalent dose calculation, i.e., "Interpolation" or "Extrapolation"
mcED	randomly simulated fast-component equivalent doses
ED	fast-component equivalent dose and its standard error
ConfInt	68 percent and 95 percent confidence interval of fast-component equivalent dose
RecyclingRatio1	the first fast-component recycling ratio and its standard error
RecyclingRatio2	the second fast-component recycling ratio and its standard error
RecyclingRatio3	the third fast-component recycling ratio and its standard error
Recuperation1	the first fast-component recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to natural-dose signal) and its standard error in percent
Recuperation2	the second fast-component recuperation (i.e., ratio of the sensitivity-corrected zero-dose signal to maximum regenerative-dose signal) and its standard error in percent

### Note

Argument `test.dose` and `agID` have nothing to do with fast-component equivalent dose calculation. They are used only for plotting purpose.

The number of trapped electrons that corresponds to the largest decay rate will be regarded as the fast-component signal, which cannot always ensure that a pure fast-component signal be extracted if an ultra-fast decaying component appears.

The authors thank Professor Sheng-Hua Li and Professor Geoff Duller for their helpful discussions concerning fast-component equivalent dose calculation.

### References

- Li SH, Li B, 2006. Dose measurement using the fast component of LM-OSL signals from quartz. *Radiation Measurements*, 41(5): 534-541.
- Murray AS, Wintle AG, 2000. Luminescence dating of quartz using improved single-aliquot regenerative-dose protocol. *Radiation Measurements*, 32(1): 57-73.

### See Also

[pickBINdata](#); [Signaldata](#);  
[fitGrowth](#); [decomp](#); [calED](#)

## Examples

```
### Example 1 (not run):
# data(Signaldata)
# fastED(Signaldata$CW, Redose=c(80,160,240,320,0, 80)*0.13,
#        ncomp=3, constant=FALSE, outpdf="fastED1")

### Example 2 (not run):
# data(BIN)
# obj_pickBIN <- pickBINdata(BIN, Position=6, Grain=0,
#                             LType="OSL", force.matrix=TRUE)
# fastED(obj_pickBIN$BINdata[[1]], ncomp=2, constant=TRUE,
#        Redose=c(100,200,300,400,0,100)*0.13, outpdf="fastED2")
```

---

 fitGrowth

*Growth curve fitting*


---

## Description

Fitting growth curves using the Levenberg-Marquardt algorithm.

## Usage

```
fitGrowth(Curvedata, model = "gok", origin = FALSE,
          weight = TRUE, trial = FALSE, plot = TRUE,
          nofit.rgd = NULL, agID = NULL, Tn = NULL,
          Tn3BG = NULL, TnBG.ratio = NULL, rseTn = NULL,
          FR = NULL, RecyclingRatio1 = NULL,
          RecyclingRatio2 = NULL, RecyclingRatio3 = NULL,
          Recuperation1 = NULL, Recuperation2 = NULL,
          LnTn.curve = NULL, TxTn = NULL)
```

## Arguments

Curvedata	<b>matrix(required)</b> : a three-column matrix (i.e., regenerative doses, sensitivity-corrected regenerative-dose signals, and associated standard errors)
model	<b>character</b> (with default): model used for growth curve fitting, see details
origin	<b>logical</b> (optional): logical value indicating if the growth curve should be forced to pass the origin
weight	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see details
trial	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using other models if the given model fails, see details
plot	<b>logical</b> (with default): logical value indicating if the results should be plotted

nofit.rgd	<b>integer</b> (optional): regenerative doses that will not be used during the fitting. For example, if <code>nofit.rgd=c(5,6)</code> then both the fifth and sixth regenerative doses will not be used during growth curve fitting
agID	<b>vector</b> (optional): a three-element vector indicating aliquot (grain) ID, i.e., <code>agID[1]=NO</code> , <code>agID[2]=Position</code> , <code>agID[3]=Grain</code>
Tn	<b>vector</b> (optional): a two-element vector containing value and standard error of Tn
Tn3BG	<b>numeric</b> (optional): 0-1 value indicating if Tn is more than 3 sigma above BG, 1 indicates $Tn > 3\_sigma\_BG$ , 0 indicates $Tn \leq 3\_sigma\_BG$
TnBG.ratio	<b>vector</b> (optional): a two-element vector containing value and standard error of ratio of initial Tn signal to BG
rseTn	<b>numeric</b> (optional): relative standard error of Tn in percent
FR	<b>vector</b> (optional): a two-element vector containing value and standard error of fast ratio of Tn
RecyclingRatio1	<b>vector</b> (optional): a two-element vector containing value and standard error of the first recycling ratio
RecyclingRatio2	<b>vector</b> (optional): a two-element vector containing value and standard error of the second recycling ratio
RecyclingRatio3	<b>vector</b> (optional): a two-element vector containing value and standard error of the third recycling ratio
Recuperation1	<b>vector</b> (optional): a two-element vector containing value and standard error of the first recuperation
Recuperation2	<b>vector</b> (optional): a two-element vector containing value and standard error of the second recuperation
LnTn.curve	<b>list</b> (optional): decay curve data for Ln and Tn, it should contain four elements, i.e., <code>names(LnTn.curve)=c("Ln.x", "Ln.y", "Tn.x", "Tn.y")</code>
TxTn	<b>vector</b> (optional): ratios of Tx to Tn for various SAR cycles

## Details

In growth curve fitting using function `fitGrowth`, five models are available:

- (1) *"line"*: a linear model,  $y=a*x+b$ ;
- (2) *"exp"*: a single saturation exponential model,  $y=a*[1-\exp(-b*x)]+c$ ;
- (3) *"lexp"*: a single saturation exponential plus linear model,  $y=a*[1-\exp(-b*x)]+c*x+d$ ;
- (4) *"dexp"*: a double saturation exponential model,  $y=a*[1-\exp(-b*x)]+c*[1-\exp(-d*x)]+e$ ;
- (5) *"gok"*: a general order kinetic model (Guralnik et al., 2015),  $y=a*[1-(1+b*c*x)^{-1/c}]+d$ .

The fitting process is performed using the Levenberg-Marquardt algorithm (minpack: Fortran 90 source code by John Burkardt, freely available at [http://people.sc.fsu.edu/~jburkardt/f\\_src/minpack/minpack.html](http://people.sc.fsu.edu/~jburkardt/f_src/minpack/minpack.html)). If `weight=TRUE`, a weighted procedure will be performed through weighting each data point by its inverse variance. User is advised to set argument `plot=TRUE` if possible to visualize the quality of fit.

Argument `trial=TRUE` means that if the growth curve can not be fitted successfully using the user-supplied model, then the procedure will try to fit other models instead:

<b>Model</b>	<b>Tried model</b>
"dexp"	c("dexp", "gok", "exp", "line")
"lexp"	c("lexp", "gok", "exp", "line")
"gok"	c("gok", "exp", "line")
"exp"	c("exp", "line")
"line"	c("line")

For example, if `model="dexp"` and `trial=TRUE`, then a number of models from sequence `c("dexp", "gok", "exp", "line")` will be applied one after another until the fit succeeds.

The required number of data points for each model is (value inside the parentheses denotes the required number of observations if the model passes the origin):

<b>Model</b>	<b>Required NPoints</b>
"dexp"	>=5 (>=4)
"lexp"	>=4 (>=3)
"gok"	>=4 (>=3)
"exp"	>=3 (>=2)
"line"	>=2 (>=1)

If user-provided data is not enough for model fitting (i.e., the number of data points is less than the number of parameters of a given model), then a model with less parameters will be fitted. For example, if 4 data points are fitted using a "dexp" (`origin=FALSE`) model that actually needs at least 5 data points, then a 4-parameter "gok" model will be fitted instead.

### Value

Return a [list](#) that contains the following elements:

<code>message</code>	return 0 if the fit succeeds, else 1
<code>fitIDX</code>	Indices of dose points used in growth curve fitting
<code>LMpars</code>	optimized parameters for the growth curve
<code>value</code>	minimized objective for the growth curve
<code>avg.error</code>	average fit error for the growth curve
<code>RCS</code>	reduced chi-square value for the growth curve
<code>FOM</code>	figure of merit value for the growth curve in percent

### Note

Arguments `agID`, `Tn`, `Tn3BG`, `TnBG.ratio`, `rseTn`, `FR`, `RecyclingRatio1`, `RecyclingRatio2`, `RecyclingRatio3`, `Recuperation1`, `Recuperation2`, `LnTn.curve`, `TxTn` have nothing to do with growth curve fitting. They are used only for plotting purpose.

The model to be optimized should not be underdetermined. This means that the number of data points should exceed (or at least be equal to) the number of parameters. For a given model, the procedure will return an error if any standard errors of parameters cannot be estimated by numerical difference-approximation.

## References

Balian HG, Eddy NW, 1977. Figure-of-merit (FOM), an improved criterion over the normalized chi-squared test for assessing goodness-of-fit of gamma-ray spectral peaks. *Nuclear Instruments and Methods*, 145(2): 389-95.

Guralnik B, Li B, Jain M, Chen R, Paris RB, Murray AS, Li SH, Pagonis V, Valla PG, Herman F, 2015. Radiation-induced growth and isothermal decay of infrared-stimulated luminescence from feldspar. *Radiation Measurements*, 81: 224-231.

More JJ, 1978. "The Levenberg-Marquardt algorithm: implementation and theory" in *Lecture Notes in Mathematics: Numerical Analysis*, Springer-Verlag: Berlin. 105-116.

## See Also

[analyseBINdata](#); [SARdata](#);  
[calED](#); [calSARED](#); [fastED](#);  
[pickSARdata](#); [lsNORM](#); [calSGCED](#)

## Examples

```
### Example 1:
Curvedata <- cbind(c(0, 18, 36, 54, 72, 0, 18),
                  c(0.026, 1.55, 2.39, 3.46, 4.13, 0.023, 1.61),
                  c(0.005, 0.11, 0.27, 0.22, 0.20, 0.008, 0.24))
fitGrowth(Curvedata, model="gok", origin=FALSE, plot=TRUE)

### Example 2 (not run):
# data(SARdata)
# Curvedata <- SARdata[!is.element(SARdata[,2], "N"),3:5]
# fitGrowth(Curvedata, model="gok", origin=FALSE)
```

---

loadBINdata

*BIN file loading (importing)*

---

## Description

Loading (importing) a BIN file into the R platform.

## Usage

```
loadBINdata(filename, view = TRUE)
```

## Arguments

filename	<b>character(required)</b> : name(s) of file(s) (with file extension ".BIN", ".bin", "BINX", or "binx"), the file(s) must be available from the current working directory. Example: filename=c("foo1.bin", "foo2.binx")
view	<b>logical(optional)</b> : logical value indicating if the loaded data should be visualized in a Summary Table

## Details

Function `loadBINdata` is used for loading BIN (BINX) files into the R platform. Five versions of binary files (V3, V4, V6, V7, and V8) are loadable. It can load a single BIN (BINX) file or a number of files into R simultaneously.

Items reserved during the loading process include:

- (1) *Position*: Carousel position;
- (2) *Grain*: Grain number;
- (3) *Run*: Run number;
- (4) *Set*: Set number;
- (5) *DType*: Data type, includes: Natural, N+dose, bleach, Bleach+dose, Natural(Bleach), N+dose(Bleach), Dose, Background;
- (6) *IRRTime*: Irradiation time;
- (7) *NPoints*: number of data points;
- (8) *LType*: Luminescence type, includes: TL, OSL, IRSL, M-IR, M-VIS, TOL, TRPOSL, RIR, RBR, USER, POSL, SGOSL, RL, XRF;
- (9) *Low*: Low (temperature, time, wavelength);
- (10) *High*: High (temperature, time, wavelength);
- (11) *Rate*: Rate (temperature, time, wavelength);
- (12) *Temperature*: Sample temperature;
- (13) *Delay*: TOL "delay" channels;
- (14) *On*: TOL "on" channels;
- (15) *Off*: TOL "off" channels;
- (16) *LightSource*: Light source, includes: None, Lamp, IRDiodes, CalibrationLED, BlueDiodes, WhiteLight, GreenLaser, IRLaser;
- (17) *AnTemp*: Annealing temperature;
- (18) *TimeSinceIrr*: Time since irradiation;
- (19) *Time*: Data collection time;
- (20) *Date*: Data collection date.

## Value

Return an invisible `list` of S3 class object "loadBIN" containing the following elements:

records	a <code>list</code> containing loaded data records
tab	a table ( <code>data.frame</code> ) summarizing items of loaded data records



**Note**

We would like to appreciate Dr Lei Gao who prompts me to write this function and provides measured data sets to test this procedure.

**References**

Duller GAT, 2016. Analyst (v4.31.9), User Manual.

**See Also**

[pickBINdata](#); [analyseBINdata](#); [BIN](#)

**Examples**

```
### Not run.
### Ensure that file "foo.bin" is available
### from the current working directory.
# obj_loadBIN <- loadBINdata("foo.bin", view=TRUE)
# class(obj_loadBIN)
# obj_loadBIN$records
```

---

lsNORM

*Regenerative-dose signal optimization using the LS-normalisation procedure*

---

**Description**

Optimizing standardised regenerative-dose signals according to the least-squares normalisation (LS-normalisation) procedure using an iterative scaling and fitting procedure proposed by Li et al. (2016).

**Usage**

```
lsNORM(SARdata, model = "gok", origin = FALSE,
       weight = FALSE, natural.rm = TRUE,
       norm.dose = NULL, maxiter = 10,
       plot = TRUE)
```

**Arguments**

SARdata	<b>matrix(required)</b> : SAR data used for performing the LS-normalisation procedure, it should contain five columns (i.e., NO, SAR.Cycle, Dose, Signal, and Signal.Err), see <a href="#">SARdata</a> for details
model	<b>character</b> (with default): model used for growth curve fitting, see <a href="#">fitGrowth</a> for available models
origin	<b>logical</b> (with default): logical value indicating if the growth curve should be forced to pass the origin

weight	<a href="#">logical</a> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see function <a href="#">fitGrowth</a> for details
natural.rm	<a href="#">logical</a> (with default): logical value indicating if the standardised natural-dose signal should be removed from SARdata
norm.dose	<a href="#">numeric</a> (optional): regenerative-dose used for re-scaling established gSGC. For example, if norm.dose=100, then the signal value for a dose value of 100 (Gy/s) will be re-scaled to unity
maxiter	<a href="#">integer</a> (with default): allowed maximum number of iterations during the LS-normalisation optimization process
plot	<a href="#">logical</a> (with default): logical value indicating if the results should be plotted

### Details

Function [lsNORM](#) is used for optimizing regenerative-dose signal data from a number of grains (aliquots) according to the least-squares normalisation (LS-normalisation) procedure outlined by Li et al. (2016) using an iterative scaling and fitting procedure.

The LS-normalisation procedure for growth curve optimization involves the following steps:

- (1) Fit standardised regenerative-dose signals from all of the aliquots;
- (2) Re-scale the individual growth curve from each aliquot using a scaling factor. The scaling factor for each aliquot is determined in a way such that the sum of squared residuals is minimized. Each aliquots is treated individually, and different scaling factors are calculated for different aliquots.
- (3) Iterate the fitting (step 1) and re-scaling (step 2). The iterative procedure is performed repeatedly until there is negligible change in the relative standard deviation of the normalised growth curve data.

### Value

Return an invisible [list](#) that contains the following elements:

norm.SARdata	SAR data sets optimized using the LS-normalisation procedure
sf	scaling factor of standardised regenerative-dose signals
iter	number of iterations required
LMpars1	optimized parameters for the growth curve before LS-normalisation
value1	minimized objective for the growth curve before LS-normalisation
avg.error1	average fit error for the growth curve before LS-normalisation
RCS1	reduced chi-square value for the growth curve before LS-normalisation
FOM1	figure of merit value for the growth curve before LS-normalisation in percent
LMpars2	optimized parameters for the growth curve after LS-normalisation
value2	minimized objective for the growth curve after LS-normalisation
avg.error2	average fit error for the growth curve after LS-normalisation
RCS2	reduced chi-square value for the growth curve after LS-normalisation
FOM2	figure of merit value for the growth curve after LS-normalisation in percent

## References

Li B, Jacobs Z, Roberts RG, 2016. Investigation of the applicability of standardised growth curves for OSL dating of quartz from Haua Fteah cave, Libya. *Quaternary Geochronology*, 35: 1-15.

## See Also

[analyseBINdata](#); [fitGrowth](#); [SARdata](#)  
[scaleSGCN](#); [calSGCED](#)

## Examples

```
### Example 1:
data(SARdata)
# Use only the first five aliquots of SARdata.
Data <- SARdata[1:40,]
res_lsNORM <- lsNORM(Data, model="gok")
res_lsNORM$norm.SARdata

### Example 2 (not run):
# data(BIN)
# obj_pickBIN <- pickBINdata(BIN, Position=1:48, Grain=0,
#                             LType="OSL", view=FALSE)
# obj_analyseBIN <- analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)
# lsNORM(obj_analyseBIN$SARdata, norm.dose=300)
```

---

mcFMM

*Finite mixture age model optimization (using a Markov chain Monte Carlo method)*

---

## Description

Sampling from the joint-likelihood functions of finite mixture age models (include the central age model) using a Markov chain Monte Carlo (MCMC) method.

## Usage

```
mcFMM(EDdata, ncomp = 1, addsigma = 0, iflog = TRUE,
      nsim = 50000, inis = list(), control.args = list())
```

## Arguments

EDdata            [matrix](#)(**required**): a two-column matrix (i.e., equivalent dose values and associated standard errors)

ncomp            [integer](#)(with default): number of components (1 denotes the central age model)

addsigma        [numeric](#)(with default): additional uncertainty

iflog	<b>logical</b> (with default): transform equivalent dose values to log-scale or not
nsim	<b>integer</b> (with default): desired number of iterations
inis	<b>list</b> (with default): initial state of parameters. Example: <code>inis=list(p1=1,p2=1,mu1=5,mu2=10)</code> in FMM2 (the sum of p1 and p2 will be normalized to 1 during the simulation)
control.args	<b>list</b> (with default): arguments used in the Slice Sampling algorithm, see details

## Details

Function **mcFMM** is used for sampling from the joint-likelihood functions of finite mixture age models (include the central age model) using a Markov chain Monte Carlo sampling algorithm called Slice Sampling (Neal, 2003). Three arguments (`control.args`) are used for controlling the sampling process:

- (1) *w*: size of the steps for creating an interval from which to sample, default  $w=1$ ;
- (2) *m*: limit on steps for expanding an interval,  $m \leq 1$  means no limit on the expansion,  $m > 1$  means the interval is expanded with a finite number of iterations, default  $m=-100$ ;
- (3) *nstart*: maximum number of trials for updating a variable in an iteration. It can be used for monitoring the stability of the simulation. For example, a MAM4 is likely to crash down for data sets with small numbers of data points or less dispersed distributions (see section 8.3 of Galbraith and Roberts, 2012 for a discussion), and sometimes more than one trial (i.e., using  $nstart > 1$ ) is required to complete the sampling process, default  $nstart=1$ .

## Value

Return an invisible **list** of S3 class object "mcAgeModels" including the following elements:

EDdata	equivalent dose values
addsigma	additional uncertainty
model	fitting model
iflog	transform equivalent dose values to log-scale or not
nsim	number of iterations
chains	simulated samples

## References

Galbraith RF, Green P, 1990. Estimating the component ages in a finite mixture. International Journal of Radiation Applications and Instrumentation. Part D. Nuclear Tracks and Radiation Measurements, 17: 197-206.

Neal RM, 2003. "Slice sampling" (with discussion). Annals of Statistics, 31(3): 705-767. Software is freely available at <http://www.cs.utoronto.ca/~radford/slice.software.html>.

## See Also

[mcMAM](#); [reportSAM](#);  
[RadialPlotter](#); [EDdata](#)

## Examples

```
# Not run.
# data(EDdata)
# Construct a MCMC chain for FMM3.
# obj<-mcFMM(EDdata$gl111,ncomp=3,nsim=5000)
# reportSAM(obj,thin=2,burn=1e3)
```

---

mcMAM	<i>Minimum age model optimization (using a Markov chain Monte Carlo method)</i>
-------	---

---

## Description

Sampling from the joint-likelihood function of the minimum age model using a Markov chain Monte Carlo (MCMC) method .

## Usage

```
mcMAM(EDdata, ncomp = -1, addsigma = 0, iflog = TRUE,
      nsim = 50000, inis = list(), control.args = list())
```

## Arguments

EDdata	<b>matrix(required)</b> : a two-column matrix (i.e., equivalent dose values and associated standard errors)
ncomp	<b>integer</b> (with default): number of components, -1=MAM3, -2=MAM4
addsigma	<b>numeric</b> (with default): additional uncertainty
iflog	<b>logical</b> (with default): transform equivalent dose values to log-scale or not
nsim	<b>integer</b> (with default): desired number of iterations
inis	<b>list</b> (with default): initial state of parameters. Example: <code>inis=list(p=0.1,gamma=20,sigma=0.5)</code> in MAM3
control.args	<b>list</b> (with default): arguments used by the Slice Sampling algorithm, see function <a href="#">mcFMM</a> for details

## Value

Return an invisible **list** of S3 class object "mcAgeModels". See [mcFMM](#) for details.

## References

Galbraith RF, Roberts RG, Laslett GM, Yoshida H, Olley JM, 1999. Optical dating of single grains of quartz from Jinmium rock shelter, northern Australia. Part I: experimental design and statistical models. *Archaeometry*, 41(2): 339-364.

Neal RM, 2003. "Slice sampling" (with discussion). *Annals of Statistics*, 31(3): 705-767. Software is freely available at [http://www.cs.utoronto.ca/~radford/slice\\_software.html](http://www.cs.utoronto.ca/~radford/slice_software.html).

**See Also**

[mcFMM](#); [reportSAM](#); [RadialPlotter](#); [EDdata](#)

**Examples**

```
# Not run.
# data(EDdata)
# Construct a MCMC chain for MAM3.
# obj<-mCMAM(EDdata$al3,ncomp=-1,addsigma=0.1,nsim=5000)
# reportSAM(obj,burn=1e3,thin=2)
#
# The convergence of the simulations may be diagnosed with
# the Gelman and Rubin's convergence diagnostic.
# library(coda) # Only if package "coda" has been installed.
# args<-list(nstart=50)
# inis1<-list(p=0.01,gamma=26,mu=104,sigma=0.01)
# inis2<-list(p=0.99,gamma=100,mu=104,sigma=4.99)
# obj1<-mCMAM(EDdata$al3,ncomp=-2,nsim=3000,inis=inis1,control.args=args)
# obj2<-mCMAM(EDdata$al3,ncomp=-2,nsim=3000,inis=inis2,control.args=args)
# chain1<-mcmc(obj1$chains)
# chain2<-mcmc(obj2$chains)
# chains<-mcmc.list(chain1,chain2)
# gelman.plot(chains)
```

---

pickBINdata

*BIN data set selection*

---

**Description**

Extracting data sets from a loaded BIN (BINX) file.

**Usage**

```
pickBINdata(obj_loadBIN, Position = NULL, Grain = NULL,
            Run = NULL, Set = NULL, DType = NULL,
            IRRTime = NULL, NPoints = NULL, LType = NULL,
            Low = NULL, High = NULL, Rate = NULL,
            Temperature = NULL, Delay = NULL, On = NULL,
            Off = NULL, LightSource = NULL, AnTemp = NULL,
            TimeSinceIrr = NULL, view = TRUE,
            manual.select = FALSE, force.matrix = FALSE)
```

**Arguments**

`obj_loadBIN` **list(required)**: an object of S3 class "loadBIN" produced by function [loadBINdata](#)

`Position` **vector(optional)**: carousel position, Example: Position=1:48

`Grain` **vector(optional)**: grain number

Run	<b>vector</b> (optional): run number
Set	<b>vector</b> (optional): set number
DType	<b>character</b> (optional): a character vector indicating data type, Example: DType=c("Natural", "N+dose")
IRRTIME	<b>vector</b> (optional): irradiation time
NPoints	<b>vector</b> (optional): number of data points
LType	<b>character</b> (optional): a character vector indicating luminescence types, Example: LType="OSL"
Low	<b>vector</b> (optional): lower limit on temperature, time, or wavelength
High	<b>vector</b> (optional): upper limit on temperature, time, or wavelength
Rate	<b>vector</b> (optional): increasing rate of temperature, time, or wavelength
Temperature	<b>vector</b> (optional): a vector indicating the sample temperatures
Delay	<b>vector</b> (optional): TOL "delay" channels
On	<b>vector</b> (optional): TOL "on" channels
Off	<b>vector</b> (optional): TOL "off" channels
LightSource	<b>character</b> (optional): a character vector indicating light source, Example: LightSource="BlueDiodes"
AnTemp	<b>vector</b> (optional): annealing temperature
TimeSinceIrr	<b>vector</b> (optional): time since irradiation
view	<b>logical</b> (with default): logical value indicating if the loaded data should be visualized in a Summary Table
manual.select	<b>logical</b> (with default): logical value indicating if the loaded data should be selected manually using a Summary Table
force.matrix	<b>logical</b> (with default): logical value indicating if the picked data sets of an aliquot (grain) should be transformed into a matrix

## Details

Function `pickBINdata` is used for pick up data sets from an object of S3 class "loadBIN" generated using function `loadBINdata`. Set `force.matrix=TRUE` will transform data sets of an aliquot (grain) into a matrix, the transformation fails if data sets have different x (temperature, time, or wavelength) coordinates. Transformed data sets stored in a matrix can be visualize via `matplot` (see examples).

## Value

Return an invisible **list** of S3 class object "pickBIN" containing two elements:

BINdata	selected BIN data
agID	Aliquot or grain ID (i.e., c("NO", "Position", "Grain")) of selected data sets, it returns NULL if <code>force.matrix=TRUE</code>

## References

Duller GAT, 2016. Analyst (v4.31.9), User Manual.

**See Also**

[loadBINdata](#); [analyseBINdata](#); [BIN](#);  
[decomp](#); [fastED](#)

**Examples**

```
### Example 1 (visualize decay curves for Position=2):
data(BIN)
obj_pickBIN <- pickBINdata(BIN, Position=2, view=FALSE,
                           LType="OSL", force.matrix=TRUE)
matplot(obj_pickBIN$BINdata[[1]][,1],
        obj_pickBIN$BINdata[[1]][,-1],
        main="Decay curves",
        xlab="Stimulation time (s)",
        ylab="Photon counts",
        type="l", log="xy")

### Example 2 (visualize test-dose decay curves for Position=2):
obj_pickBIN <- pickBINdata(BIN, Position=2, Run=c(5,11,17,23,29,34,40),
                           view=FALSE, LType="OSL", force.matrix=TRUE)
matplot(obj_pickBIN$BINdata[[1]][,1],
        obj_pickBIN$BINdata[[1]][,-1],
        main="Test-dose decay curves",
        xlab="Stimulation time (s)",
        ylab="Photon counts",
        type="l", log="xy")

### Example 3 (visualize regenerative-dose decay curves for Position=2):
obj_pickBIN <- pickBINdata(BIN, Position=2, Run=c(8,14,20,26,31,37),
                           view=FALSE, LType="OSL", force.matrix=TRUE)
matplot(obj_pickBIN$BINdata[[1]][,1],
        obj_pickBIN$BINdata[[1]][,-1],
        main="Regenerative-dose decay curves",
        xlab="Stimulation time (s)",
        ylab="Photon counts",
        type="l", log="xy")
```

---

pickSARdata

*SAR data set selection*

---

**Description**

Selecting SAR data sets (growth curves) in a batch model according to specified rejection criteria.

**Usage**

```
pickSARdata(obj_analyseBIN, model = "gok", origin = FALSE,
            weight = TRUE, trial = TRUE, nofit.rgd = NULL,
```



```
Tn.above.3BG = TRUE, TnBG.ratio.low = NULL,
rseTn.up = NULL, FR.low = NULL, rcy1.range = NULL,
rcy2.range = NULL, rcy3.range = NULL,
rcp1.up = NULL, rcp2.up = NULL, fom.up = NULL,
rcs.up = NULL, use.se = TRUE, norm.dose = NULL,
outpdf = NULL, outfile = NULL)
```

## Arguments

obj_analyseBIN	<b>list(required)</b> : an object of S3 class "analyseBIN" produced by function <a href="#">analyseBINdata</a> or <a href="#">as_analyseBIN</a>
model	<b>character</b> (with default): model used for growth curve fitting, see <a href="#">fitGrowth</a> for available models
origin	<b>logical</b> (with default): logical value indicating if the growth curve should be forced to pass the origin
weight	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using a weighted procedure, see function <a href="#">fitGrowth</a> for details
trial	<b>logical</b> (with default): logical value indicating if the growth curve should be fitted using other models if the given model fails, see function <a href="#">fitGrowth</a> for details
nofit.rgd	<b>integer</b> (optional): regenerative doses that will not be used during the fitting. For example, if <code>nofit.rgd=2</code> then the second regenerative dose will not be used during growth curve fitting
Tn.above.3BG	<b>logical</b> (with default): logical value indicating if aliquot (grain) with Tn below 3 sigma BG should be rejected
TnBG.ratio.low	<b>numeric</b> (optional): lower limit on ratio of initial Tn signal to BG
rseTn.up	<b>numeric</b> (optional): upper limit on relative standard error of Tn in percent
FR.low	<b>numeric</b> (optional): lower limit on fast ratio of Tn
rcy1.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 1, Example: <code>rcy1.range=c(0.9, 1.1)</code>
rcy2.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 2
rcy3.range	<b>vector</b> (optional): a two-element vector indicating the lower and upper limits on recycling ratio 3
rcp1.up	<b>numeric</b> (optional): upper limit on recuperation 1 (i.e., ratio of the sensitivity-corrected zero-dose signal to natural-dose signal) in percent
rcp2.up	<b>numeric</b> (optional): upper limit on recuperation 2 (i.e., ratio of the sensitivity-corrected zero-dose signal to maximum regenerative-dose signal) in percent
fom.up	<b>numeric</b> (optional): upper limit on figure of merit (FOM) values of growth curves in percent
rcs.up	<b>numeric</b> (optional): upper limit on reduced chi-square (RCS) values of growth curves
use.se	<b>logical</b> (with default): logical value indicating if standard errors of values should be used during application of rejection criteria

norm.dose	<b>numeric</b> (optional): dose value used for SAR data set re-normalisation, for example, if norm.dose=100, then sensitivity-corrected signal for Redose=100 obtained through growth curve fitting will be used to re-normalise a SAR data set
outpdf	<b>character</b> (optional): if specified, results of growth curve fitting will be written to a PDF file named "outpdf" and saved to the current work directory
outfile	<b>character</b> (optional): if specified, SAR data related quantities will be written to a CSV file named "outfile" and saved to the current work directory

### Value

Return an invisible **list** that contains the following elements:

LMpars	a <b>list</b> containing optimized parameters of growth curves of selected SAR data sets
SARdata	a <b>data.frame</b> containing selected SAR data sets
norm.SARdata	a <b>data.frame</b> containing re-normalised SAR data sets, it returns NULL if norm.dose=NULL
agID	aliquot or grain ID (i.e., c("NO", "Position", "Grain")) of selected SAR data
summary.info	a summary of the SAR data selection

### See Also

[analyseBINdata](#); [fitGrowth](#);  
[lsNORM](#); [calSARED](#)

### Examples

```
# Not run.
# data(BIN)
# obj_pickBIN <- pickBINdata(BIN, Position=1:48, Grain=0,
#                             LType="OSL", view=FALSE)
# obj_analyseBIN <- analyseBINdata(obj_pickBIN, nfchn=3, nlchn=20)
# pickSARdata(obj_analyseBIN, model="gok", fom.up=3, outpdf="SARdata")
```

---

psRadialPlot

*Pseudo radial plot drawing*

---

### Description

Drawing a pseudo (simplified) radial plot.

### Usage

```
psRadialPlot(EDdata, addsigma = 0, dose = NULL,
             zmin = NULL, zmax = NULL, ntick = 6,
             digits = 2, pcolor = "blue", psize = 1,
             rg = 2, zlabel = "De (Gy)")
```

### Arguments

EDdata	<b>matrix(required)</b> : a two-column matrix (i.e., equivalent dose values and associated standard errors)
addsigma	<b>numeric</b> (with default): additional uncertainty
dose	<b>vector</b> (optional): dose population(s) to be drawn
zmin	<b>numeric</b> (with default): lower limit on z-axis
zmax	<b>numeric</b> (with default): upper limit on z-axis
ntick	<b>integer</b> (with default): desired number of ticks in z-axis
digits	<b>integer</b> (with default): number of decimal places or significant digits for values shown in z-axis
pcolor	<b>character</b> (with default): color of a data point, input <code>colors()</code> to see more available colors
psize	<b>numeric</b> (with default): size of a data point
rg	<b>integer</b> (with default): range of a dose population, 0=dose, 1=dose+/-sigma, 2=dose+/-2sigma
zlabel	<b>character</b> (with default): title for the z-axis

### Details

Function `psRadialPlot` is used for drawing a simplified radial plot in which the z-axis is a straight line. The pseudo radial plot is easier to construct compared to the regular radial plot. This function can be adopted to display estimates that have different error estimates in any field of the analytical sciences. Note that the function handles datasets in log-scale, so any minus observation is not allowed.

### Value

Return a pseudo radial plot

### References

- Galbraith RF, 1988. Graphical display of estimates having differing standard errors. *Technometrics*, 30(3): 271-281.
- Galbraith RF, 1994. Some applications of radial plots. *Journal of the American Statistical Association*, 89(428): 1232-1242.
- Galbraith RF, 2010. On plotting OSL equivalent doses. *Ancient TL*, 28(1): 1-10.
- Galbraith RF, Roberts RG, Laslett GM, Yoshida H, Olley JM, 1999. Optical dating of single grains of quartz from Jinmium rock shelter, northern Australia. Part I: experimental design and statistical models. *Archaeometry*, 41(2): 339-364.

### See Also

[dbED](#); [RadialPlotter](#); [EDdata](#)

## Examples

```
data(EDdata)
psRadialPlot(EDdata$a13, addsigma=0.10,
             dose=c(39.14, 51.27, 79.14), digits=1,
             zmin=30, zmax=100, ntick=10, rg=1)
```

---

RadialPlotter	<i>Statistical age model optimization (with a Maximum Likelihood Estimation method)</i>
---------------	---

---

## Description

Depending on the specified number of components, this function performs statistical age models analysis reviewed in Galbraith and Roberts (2012) dynamically using a Maximum Likelihood Estimation method. Age models that can be applied include: central age model (CAM), minimum age model (MAM), and finite mixture age model (FMM).

## Usage

```
RadialPlotter(EDdata, ncomp = 0, addsigma = 0,
             maxcomp = 6, algorithm = c("port", "lbfgsb"),
             plot = TRUE, pcolor = "blue", psize = 1.5,
             kratio = 0.3, zscale = NULL)
```

## Arguments

EDdata	<b>matrix(required)</b> : a two-column matrix (i.e., equivalent dose values and associated standard errors)
ncomp	<b>integer</b> (with default): number of components, -1=MAM3, -2=MAM4, 1=CAM, 0 means fitting FMM automatically, and >=1 means fitting FMM with a given number of components
addsigma	<b>numeric</b> (with default): additional uncertainty
maxcomp	<b>integer</b> (with default): maximum number of components in FMM
algorithm	<b>character</b> (with default): algorithm used for optimizing MAM, default algorithm="port"
plot	<b>logical</b> (with default): draw a radial plot or not
pcolor	<b>character</b> (with default): color of a data point, input <code>colors()</code> to see more available colors
psize	<b>numeric</b> (with default): size of a data point
kratio	<b>numeric</b> (with default): argument controlling the shape of zscale
zscale	<b>vector</b> (optional): argument controlling the scale of z-axis. Example: <code>zscale=seq(min(EDdata), max(EDdata), by=3L)</code>

## Details

Both CAM and FMM are fitted using a iterative Maximum Likelihood Estimation procedure outlined by Galbraith (1988), while MAM can be estimated using either the "L-BFGS-B" algorithm (**R** function `optim` in package *stats*) or the "port" algorithm (**R** function `nlminb` in package *stats*).

## Value

Return an object of S3 class "RadialPlotter" that contains the following elements:

<code>pars</code>	optimized parameters
<code>bic</code>	calculated Bayesian Information Criterion (BIC) value
<code>maxlik</code>	optimized maximum logged likelihood value

## Note

Function `RadialPlotter` was given the same name as the *Java* package *RadialPlotter* written by Pieter Vermeesch (Vermeesch, 2009). Note that this function fits a model in log-scale, hence any minus equivalent dose value is not allowed, and that the procedure will return an error if any standard error of a parameter cannot be estimated by numerical difference-approximation.

The original *S* code for drawing a radial plot was written by Rex Galbraith and was transformed to **R** by Sebastian Kreuzer. The code for drawing radial plot in this function was modified from package *Luminescence* written by Kreuzer et al. (2012). We thank Dr Rex Galbraith for his permission to modify and bundle the code to this function. We also thank Dr Silke Schmidt, Dr Helena Rodnight, Dr Xian-Jiao Ou, and Dr Amanda Keen-Zebert for providing published OSL data sets to test this routine.

## References

- Galbraith RF, 1988. Graphical display of estimates having differing standard errors. *Technometrics*, 30(3): 271-281.
- Galbraith RF, 1990. The radial plot: Graphical assessment of spread in ages. *International Journal of Radiation Applications and Instrumentation. Part D. Nuclear Tracks and Radiation Measurements*, 17(3): 207-214.
- Galbraith RF, Green P, 1990. Estimating the component ages in a finite mixture. *International Journal of Radiation Applications and Instrumentation. Part D. Nuclear Tracks and Radiation Measurements*, 17: 197-206.
- Galbraith RF, Laslett GM, 1993. Statistical models for mixed fission track ages. *Nuclear Tracks And Radiation Measurements*, 21(4): 459-470.
- Galbraith RF, 1994. Some applications of radial plots. *Journal of the American Statistical Association*, 89(428): 1232-1242.
- Galbraith RF, Roberts RG, Laslett GM, Yoshida H, Olley JM, 1999. Optical dating of single grains of quartz from Jinnium rock shelter, northern Australia. Part I: experimental design and statistical models. *Archaeometry*, 41(2): 339-364.
- Galbraith RF, 2005. *Statistics for fission track analysis*. Chapman & Hall/CRC Press.
- Galbraith RF, 2010. On plotting OSL equivalent doses. *Ancient TL*, 28(1): 1-10.

Galbraith RF, Roberts RG, 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: an overview and some recommendations. *Quaternary Geochronology*, 11: 1-27.

### Further reading

Duller GAT, 2008. Single-grain optical dating of Quaternary sediments: why aliquot size matters in luminescence dating. *Boreas*, 37(4): 589-612.

Kreutzer S, Schmidt C, Fuchs MC, Dietze M, Fischer M, Fuchs M, 2012. Introducing an R package for luminescence dating analysis. *Ancient TL*, 30(1): 1-8. Software is freely available at <https://CRAN.R-project.org/package=Luminescence>.

Rodnight H, 2008. How many equivalent dose values are needed to obtain a reproducible distribution? *Ancient TL*, 26(1): 3-10.

Rodnight H, Duller GAT, Wintle AG, Tooth S, 2006. Assessing the reproducibility and accuracy of optical dating of fluvial deposits. *Quaternary Geochronology*, 1(2): 109-120.

Schmidt S, Tsukamoto S, Salomon E, Frechen M, Hetzel R, 2012. Optical dating of alluvial deposits at the orogenic front of the andean precordillera (Mendoza, Argentina). *Geochronometria*, 39(1): 62-75.

Vermeesch P, 2009. RadialPlotter: a Java application for fission track, luminescence and other radial plots. *Radiation Measurements*, 44: 409-410. Software is freely available at <http://www.ucl.ac.uk/~ucfbpve/radialplotter/>.

### See Also

[mcMAM](#); [mcFMM](#);  
[dbED](#); [psRadialPlot](#); [EDdata](#)

### Examples

```
data(EDdata)
# Find out the appropriate number of components
# in FMM and fit automatically.
RadialPlotter(EDdata$a13,zscale=seq(24,93,7))

# Fit MAM3 (not run).
# RadialPlotter(EDdata$g111,ncomp=-1,zscale=seq(20,37,3))
```

---

reportSAM

*Reporting MCMC outputs for statistical age models*

---

### Description

Summarizing distributions of parameters simulated from statistical age models.

### Usage

```
reportSAM(obj, burn = 10000, thin = 5,
          plot = TRUE, outfile = NULL, ...)
```

## Arguments

obj	<b>list(required)</b> : an object of S3 class "mcAgeModels", which is produced by function <a href="#">mcFMM</a> or <a href="#">mcMAM</a>
burn	<b>integer</b> (with default): number of iterations (i.e., the initial, non-stationary portion of the chain) to be discarded
thin	<b>integer</b> (with default): take every thin-th iteration
plot	<b>logical</b> (with default): plot the MCMC output or not
outfile	<b>character</b> (optional): if specified, simulated parameters will be written to a CSV file named "outfile" and saved to the current work directory
...	do not use

## Details

Function [reportSAM](#) summarizes the output of a Markov chain (the mean values, the standard deviations, and the 95 percent confidence intervals). The initial  $i$  (burn= $i$ ) samples may have been affected by the initial state and has to be discarded ("burn-in"). Autocorrelation of simulated samples can be reduced by taking every  $j$ -th (thin= $j$ ) iteration ("thining").

## Value

Return a [list](#) that contains the following elements:

pars	parameters and relevant statistics
quantile	quantiles of simulated parameters
maxlik	calculated maximum logged likelihood value

## References

Lunn D, Jackson C, Best N, Thomas A, Spiegelhalter D, 2013. The BUGS book: a practical introduction to bayesian analysis. Chapman & Hall/CRC Press.

Gelman A, Carlin JB, Stern HS, Dunson DB, Vehtari A, Rubin DB, 2013. Bayesian data analysis. Chapman & Hall/CRC Press.

## See Also

[mcFMM](#); [mcMAM](#)

---

SARdata

*Data sets used for SAR equivalent dose calculation*

---

### Description

SAR data sets for individual aliquots from the "later" group of sample HF11 from Haua Fteah cave, Libya (Li et al., 2016).

### Usage

```
data(SARdata)
```

### Format

A [data.frame](#) with 840 observations containing the following 5 variables:

**NO** aliquot (grain) number

**SAR.Cycle** SAR cycles

**Dose** regenerative doses

**Signal** OSL signals

**Signal.Err** standard error of OSL signals

### References

Li B, Jacobs Z, Roberts RG, 2016. Investigation of the applicability of standardised growth curves for OSL dating of quartz from Haua Fteah cave, Libya. *Quaternary Geochronology*, 35: 1-15.

### See Also

[fitGrowth](#); [lsNORM](#); [calSGCED](#);  
[as\\_analyseBIN](#)

### Examples

```
# Not run.  
# data(SARdata)  
# head(SARdata)
```



---

scaleSGCN	<i>Natural-dose signal re-scaling</i>
-----------	---------------------------------------

---

### Description

Re-scaling sensitivity-corrected natural-dose signals according to the "global standardised growth curve" (gSGC) method suggested by Li et al. (2015, 2016).

### Usage

```
scaleSGCN(obj_analyseBIN, SGCpars, model, origin,
          SAR.Cycle, Tn.above.3BG = TRUE,
          TnBG.ratio.low = NULL, rseTn.up = NULL,
          FR.low = NULL, use.se = TRUE, outfile = NULL)
```

### Arguments

obj_analyseBIN	<b>list(required)</b> : an object of S3 class "analyseBIN" produced by function <a href="#">analyseBINdata</a> or <a href="#">as_analyseBIN</a>
SGCpars	<b>vector(required)</b> : optimized parameters of the SGC obtained using function <a href="#">fitGrowth</a> or <a href="#">lsNORM</a>
model	<b>character(required)</b> : fitting model used for obtaining SGCpars
origin	<b>logical(required)</b> : logical value indicating if established SGC passes the origin
SAR.Cycle	<b>character(required)</b> : a two-element character vector containing SAR cycles used for natural-dose signal re-scaling. Example: SAR.Cycle=c("N", "R3")
Tn.above.3BG	<b>logical(with default)</b> : logical value indicating if aliquot (grain) with Tn below 3 sigma BG should be rejected
TnBG.ratio.low	<b>numeric(optional)</b> : lower limit on ratio of initial Tn signal to BG
rseTn.up	<b>numeric(optional)</b> : upper limit on relative standard error of Tn in percent
FR.low	<b>numeric(optional)</b> : lower limit on fast ratio of Tn
use.se	<b>logical(with default)</b> : logical value indicating if standard errors of values should be used during application of rejection criteria
outfile	<b>character(optional)</b> : if specified, scaled SGC data related quantities will be written to a CSV file named "outfile" and saved to the current work directory

### Details

Sensitivity-corrected natural-dose signals are re-scaled according to **Eqn.(10)** of Li et al. (2015).

### Value

Return an invisible [list](#) that contains the following elements:

scale.Ltx	scaled natural-dose signals and associated standard errors
agID	aliquot (grain) ID of scaled natural-dose signals

**References**

Li B, Roberts RG, Jacobs Z, Li SH, 2015. Potential of establishing a "global standardised growth curve" (gSGC) for optical dating of quartz from sediments. *Quaternary Geochronology*, 27: 94-104.

Li B, Jacobs Z, Roberts RG, 2016. Investigation of the applicability of standardised growth curves for OSL dating of quartz from Haua Fteah cave, Libya. *Quaternary Geochronology*, 35: 1-15.

**See Also**

[lsNORM](#); [calSGCED](#)

**Examples**

```
# Not run.
data(SARdata)
gSGCpars <- c(137.440874251, 0.007997863, 2.462035263, -0.321536177)
scaleSGCN(as_analyseBIN(SARdata), SGCpars=gSGCpars, model="gok",
          origin=FALSE, SAR.Cycle=c("N", "R3"))
```

---

Signaldata

*Decay curves datasets*

---

**Description**

CW-OSL and LM-OSL decay curves.

**Usage**

```
data(Signaldata)
```

**Format**

A list that contains CW-OSL and LM-OSL decay curves:

**cw** a number of CW-OSL decay curves of a sand sample from the Tengger Desert in northern china (Peng and Han, 2013)

**lm** a LM-OSL decay curve from Li and Li (2006)

**References**

Li SH, Li B, 2006. Dose measurement using the fast component of LM-OSL signals from quartz. *Radiation Measurements*, 41(5): 534-541.

Peng J, Han FQ, 2013. Selections of fast-component OSL signal using sediments from the south edge of Tengger Desert. *Acta Geoscientica Sinica*, 34(6): 757-762.

**See Also**

[decomp](#); [fastED](#)

**Examples**

```
# Not run.  
# data(Signaldata)  
# names(Signaldata)
```

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