# Package ‘Luminescence’

**Type**: Package  

**Title**: Comprehensive Luminescence Dating Data Analysis  

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**Description**: A collection of various R functions for the purpose of Luminescence dating data analysis. This includes, amongst others, data import, export, application of age models, curve deconvolution, sequence analysis and plotting of equivalent dose distributions.  

**Contact**: Package Developer Team <team@r-luminescence.de>  

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Description

A collection of various R functions for the purpose of Luminescence dating data analysis. This includes, amongst others, data import, export, application of age models, curve deconvolution, sequence analysis and plotting of equivalent dose distributions.

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References

analyse_IRSAR.RF Analyse IRSAR RF measurements

Description
Function to analyse IRSAR RF measurements on K-feldspar samples, performed using the protocol according to Erfurt et al. (2003)

Usage
```R
analyse_IRSAR.RF(object, sequence.structure = c("NATURAL", "REGENERATED"),
method = "FIT", rejection.criteria, fit.range.min, fit.range.max,
fit.trace = FALSE, fit.MC.runs = 10, slide.MC.runs = 10,
slide.outlier.rm = FALSE, slide.trend.corr = FALSE, slide.show.density = TRUE,
plot = TRUE, xlab.unit = "s", legend.pos, ...)
```
Arguments

- **object** `RLum.Analysis` *(required)*: input object containing data for protocol analysis
- **sequence.structure** `vector character` *(with default)*: specifies the general sequence structure. Allowed steps are NATURAL, REGENERATED. In addition any other character is allowed in the sequence structure; such curves will be ignored.
- **method** `character` *(with default)*: setting method applied for the data analysis. Possible options are "FIT" or "SLIDE".
- **rejection.criteria** `list` *(with default)*: set rejection criteria for, see details for more information *Currently without usage!*
- **fit.range.min** `integer` *(optional)*: set the minimum channel range for signal fitting and sliding. Usually the entire data set is used for curve fitting, but there might be reasons to limit the channels used for fitting. Note: This option also limits the values used for natural signal calculation.
- **fit.range.max** `integer` *(optional)*: set maximum channel range for signal fitting and sliding. Usually the entire data set is used for curve fitting, but there might be reasons to limit the channels used for fitting.
- **fit.trace** `logical` *(with default)*: trace fitting (for debugging use)
- **fit.MC.runs** `numeric` *(with default)*: set number of Monte Carlo runs for start parameter estimation. Note: Large values will significantly increase the calculation time.
- **slide.MC.runs** `integer` *(with default)*: set number of Monte Carlo runs error calculation Note: Large values will significantly increase the calculation time.
- **slide.outlier.rm** `logical` *(with default)*: enable or disable outlier removal. Outliers are removed from the natural signal curve only.
- **slide.trend.corr** `logical` *(with default)*: enable or disable trend correction. If TRUE, the sliding is applied to a previously trend corrected data set.
- **slide.show.density** `logical` *(with default)*: enable or disable KDE for MC runs. If FALSE, the final values are indicated with triangles.
- **plot** `logical` *(with default)*: plot output (TRUE or FALSE)
- **xlab.unit** `character` *(with default)*: set unit for x-axis
- **legend.pos** `character` *(with default)*: useful keywords are bottomright, bottom, bottomleft, left, topleft, top, topright, right and center. For further details see `legend`.

... further arguments that will be passed to the plot output. Currently supported arguments are main, xlab, ylab, xlim, ylim, log

Details

The function performs an IRSAR analysis described for K-feldspar samples by Erfurt et al. (2003) assuming a negligible sensitivity change of the RF signal.

**General Sequence Structure** *(according to Erfurt et al. (2003))**
1. Measuring IR-RF intensity of the natural dose for a few seconds ($D_{natural}$)
2. Bleach the samples under solar conditions for at least 30 min without changing the geometry
3. Waiting for at least one hour
4. Regeneration of the IR-RF signal to at least the natural level
5. Fitting data with a stretched exponential function
6. Calculate the palaeodose $D_e$ using the parameters from the fitting

**Function Used For The Fitting** (according to Erfurt et al. (2003))

$$\phi(D) = \phi_0 - \Delta\phi(1 - \exp(-\lambda \ast D))^{\beta}$$

with $\phi(D)$ the dose dependent IR-RF flux, $\phi_0$ the initial IR-RF flux, $\Delta\phi$ the dose dependent change of the IR-RF flux, $\lambda$ the exponential parameter, $D$ the dose and $\beta$ the dispersive factor.

To obtain the palaeodose $D_e$ the function is changed to:

$$D_e = \ln\left(-\frac{(\phi(D) - \phi_0)}{(-\lambda \ast \phi)^{1/\beta} + 1}\right) - \lambda$$

The fitting is done using the port algorithm of the nls function.

Two methods are supported to obtain the $D_e$:

method = "FIT"

The principle is described above and follows the original suggestions from Erfurt et al., 2003.

method = "SLIDE"

For this method the natural curve is slided along the x-axis until congruence with the regenerated curve is reached. Instead of fitting this allows to work with the original data without the need of any physical model. This approach was introduced for RF curves by Buylaert et al., 2012 and Lapp et al., 2012.

Here the sliding is done by searching for the minimum of the residual squares.

$$min(\Sigma(RF.reg_{k,i} - RF.nat_{k,i})^2)$$

for

$$k = t.0 + i, ..., t.max + i$$

**Correction for outliers** (slide.outlier.rm = TRUE)

By using method = "SLIDE" and setting the argument slide.outlier.rm = TRUE an automatic outlier removal can be applied to the natural curve. Outliers may be observed also on the regeneration curve, but here the impact of single outliers on the curve adjustment (sliding) is considered as negligible.
The applied outlier removal algorithm consists of three steps:

(a) Input data are smoothed using the function `rollmedian`. Value $k$ for the rolling window is fixed to 11. Therefore, the natural curve needs to comprise at least of 33 values, otherwise outlier removal is rejected.

(b) To subsequently remove outliers, code blocks from the function `apply_CosmicRayRemoval` were recycled, therefore in general the outlier correction works as described by Pych (2003). In contrast, here no sigma clipping before constructing the histograms is applied.

(c) Outliers are marked in the data set and visualised in the graphical output. The subsequent adjustment of both curves (natural and regenerative) is done without outliers, whereas the sliding itself is done with the entire data set.

**Trend correction** (slide.trend.corr = TRUE)

This option allows for correcting any linear trend in the natural curve in comparison to the regenerative curve. The trend correction is based on regression analysis of the residuals from the slided curve. The corrected De is obtained by sliding the trend corrected values (again) along the regenerative data curve. This correction is driven by the idea that the residuals from the regenerative and the natural curve should be free of any trend, as long as they are comparable.

**Error estimation**

For `method = "FIT"` the asymmetric error range is taken from the standard deviation of the natural signal.

For `method = "SLIDE"` an beta-version of an error estimation based on boostrapping is implemented, however, this needs further documentation.

**Value**

A plot (optional) and an `RLum.Results` object is returned containing the following elements:

- `De.values` `data.frame` containing De-values with error (gray dashed lines in the plot) and further parameters. Corrected De values are only provided for the method "SLIDE", provided the trend correction is applied.

- `fit` `nls nlsModel` object

**Note:** The output (`De.values`) should be accessed using the function `get_RLum.Results`

**Function version**

0.3.1 (2015-03-23 13:07:08)
Note

This function assumes that there is no sensitivity change during the measurements (natural vs. re-generated signal), which is in contrast to the findings from Buylaert et al. (2012).

Please note that method = "FIT" has beta status and was not properly tested yet!

Author(s)

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References


See Also

RLum.Analysis,RLum.Results,get_RLum.Results,nls
analyse_pIRIRSequence

Examples

```r
# load data
data(ExampleData.RLum.Analysis, envir = environment())

# perform analysis
temp <- analyse_IRSAR.RF(object = IRSAR.RF.Data)
```

Description

The function performs an analysis of post-IR IRSL sequences including curve fitting on `RLum.Analysis` objects.

Usage

```r
analyse_pIRIRSequence(object, signal.integral.min, signal.integral.max,
background.integral.min, background.integral.max, dose.points,
sequence.structure = c("TL", "IR50", "pIRIR225"), plot = TRUE,
plot.single = FALSE, ...)
```

Arguments

- **object**: `RLum.Analysis` *(required)*: input object containing data for analysis
- **signal.integral.min**: integer *(required)*: lower bound of the signal integral. Provide this value as vector for different integration limits for the different IRSL curves.
- **signal.integral.max**: integer *(required)*: upper bound of the signal integral. Provide this value as vector for different integration limits for the different IRSL curves.
- **background.integral.min**: integer *(required)*: lower bound of the background integral. Provide this value as vector for different integration limits for the different IRSL curves.
- **background.integral.max**: integer *(required)*: upper bound of the background integral. Provide this value as vector for different integration limits for the different IRSL curves.
- **dose.points**: numeric *(optional)*: a numeric vector containing the dose points values. Using this argument overwrites dose point values in the signal curves.
- **sequence.structure**: vector character *(with default)*: specifies the general sequence structure. Allowed values are "TL" and any "IR" combination (e.g., "IR50", "pIRIR225"). Additionally a parameter "EXCLUDE" is allowed to exclude curves from the analysis (Note: If a preheat without PMT measurement is used, i.e. preheat as non TL, remove the TL step.)
analyse_pIRIRSequence

plot logical (with default): enables or disables plot output.
plot.single logical (with default): single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. Requires plot = TRUE.
...

Details

To allow post-IR IRSL protocol (Thomsen et al., 2008) measurement analysis this function has been written as extended wrapper function for the function `analyse_SAR.CWOSL`, facilitating an entire sequence analysis in one run. With this, its functionality is strictly limited by the functionality of the function `analyse_SAR.CWOSL`.

Value

Plots (optional) and an `RLum.Results` object is returned containing the following elements:

De.values data.frame containing De-values, De-error and further parameters

LnLxTx.values data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.

rejection.criteria data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

The output should be accessed using the function `get_RLum.Results`.

Function version

0.1.4 (2015-03-04 12:43:39)

Note

Best graphical output can be achieved by using the function `pdf` with the following options:
`pdf(file = "...", height = 15, width = 15)`

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
R Luminescence Package Team
References


See Also

analyse_sarNcwosl, calc_OSLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results
get_RLum.Results

Examples

```r
### NOTE: For this example existing example data are used. These data are non pIRIR data.
###
###(1) Compile example data set based on existing example data (SAR quartz measurement)
###(a) Load example data
data(ExampleData.BINfileData, envir = environment())

###(b) Transform the values from the first position in a RLum.Analysis object
object <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)

###(c) Grep curves and exclude the last two (one TL and one IRSL)
object <- get_RLum.Analysis(object, record.id = c(-29,-30))

###(d) Define new sequence structure and set new RLum.Analysis object
sequence.structure <- c(1,2,3,4)

# set random seed for reproducibility
set.seed(1)
# object <- sapply(1:length(sequence.structure), function(x){
#
#   object[[[sequence.structure[x]]]]
#
# })

object <- set_RLum.Analysis(records = object, protocol = "pIRIR")

###(2) Perform pIRIR analysis (for this example with quartz OSL data!)
### Note: output as single plots to avoid problems with this example
results <- analyse_pIRIRSequence(object,
signal.integral.min = 1,
signal.integral.max = 2,
background.integral.min = 900,
background.integral.max = 1000,
fit.method = "EXP",
sequence.structure = c("TL", "pseudoIRSL1", "pseudoIRSL2"),
main = "Pseudo pIRIR data set based on quartz OSL")
```
plot.single = TRUE)

##(3) Perform pIRIR analysis (for this example with quartz OSL data!)
## Alternative for PDF output, uncomment and complete for usage
#
# pdf(file = "...", height = 15, width = 15)
# results <- analyse_pIRIRSequence(object,
# signal.integral.min = 1,
# signal.integral.max = 2,
# background.integral.min = 900,
# background.integral.max = 1000,
# fit.method = "EXP",
# main = "Pseudo pIRIR data set based on quartz OSL")
#
# dev.off()

---

**analyse_SAR.CWOSL**  
*Analyse SAR CW-OSL measurements*

**Description**

The function performs a SAR CW-OSL analysis on an R Lum.Analysis object including growth curve fitting.

**Usage**

```r
analyse_SAR.CWOSL(object, signal.integral.min, signal.integral.max,
background.integral.min, background.integral.max, rejection.criteria,
dose.points, mtext.outer, plot = TRUE, plot.single = FALSE,
...)
```

**Arguments**

- `object` (*R Lum.Analysis* (**required**)): input object containing data for analysis
- `signal.integral.min`  
  - integer (**required**): lower bound of the signal integral
- `signal.integral.max`  
  - integer (**required**): upper bound of the signal integral
- `background.integral.min`  
  - integer (**required**): lower bound of the background integral
- `background.integral.max`  
  - integer (**required**): upper bound of the background integral
rejection.criteria

list (with default): provide list and set rejection criteria in percentage for further calculation. Allowed arguments are recycling.ratio, recuperation.rate, palaeodose.error and exceed.max.regpoint = TRUE/FALSE e.g. rejection.criteria = list(recycling.ratio = 0.1, recuperation.rate = 0.2, palaeodose.error = 0.05, exceed.max.regpoint = FALSE). Per default all values are set to 10.

dose.points numeric (optional): a numeric vector containing the dose points values. Using this argument overwrites dose point values in the signal curves.

mtext.outer character (optional): option to provide an outer margin mtext.

plot logical (with default): enables or disables plot output.

plot.single logical (with default) or numeric (optional): single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. If a numeric vector is provided the plots can be selected individually, i.e., plot.single = c(1, 2, 3, 4) will plot the TL and Lx, Tx curves but not the legend (5) or the growth curve (6), (7) and (8) belong to rejection criteria plots. Requires plot = TRUE.

... further arguments that will be passed to the function plot_GrowthCurve

Details

The function performs an analysis for a standard SAR protocol measurements introduced by Murray and Wintle (2000) with CW-OSL curves. For the calculation of the Lx/Tx value the function calc_OSL_LxTxRatio is used.

Working with IRSL data

The function was originally designed to work just for ‘OSL’ curves, following the principles of the SAR protocol. An IRSL measurement protocol may follow this procedure, e.g., post-IR IRSL protocol (Thomsen et al., 2008). Therefore this functions has been enhanced to work with IRSL data, however, the function is only capable of analysing curves that follow the SAR protocol structure, i.e., to analyse a post-IR IRSL protocol, curve data have to be pre-selected by the user to fit the standards of the SAR protocol, i.e., Lx,Tx,Lx,Tx and so on.

Example: Imagine the measurement contains pIRIR50 and pIRIR225 IRSL curves. Only one curve type can be analysed at the same time: The pIRIR50 curves or the pIRIR225 curves.

Supported rejection criteria

‘recycling.ratio’: calculated for every repeated regeneration dose point.

‘recuperation.rate’: recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988).

‘palaeodose.error’: set the allowed error for the De value, which per default should not exceed 10%. 

...
**Value**

A plot (optional) and an `RLum.Results` object is returned containing the following elements:

- `De.values` data.frame containing De-values, De-error and further parameters
- `LnLxTx.values` data.frame of all calculated Lx/Tx values including signal, background counts and the dose points
- `rejection.criteria` data.frame with values that might be used as rejection criteria. NA is produced if no R0 dose point exists.

**Formula**

Formula used for the growth curve fitting

The output should be accessed using the function `get_RLum.Results`.

**Function version**

0.5.1 (2015-03-09 15:43:53)

**Note**

This function must not be mixed up with the function `Analyse_SAR.OSLdata`, which works with `Risoe.BINfileData-class` objects.

The function currently does only support 'OSL' or 'IRSL' data!

**Author(s)**

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R Luminescence Package Team

**References**


**See Also**

calc_OSLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results get_RLum.Results
Examples

# load data
## ExampleData.BINfileData contains two BINfileData objects
## CWOSL.SAR.Data and TL.SAR.Data
data(ExampleData.BINfileData, envir = environment())

## transform the values from the first position in a RLum.Analysis object
object <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)

## perform SAR analysis
results <- analyse_sarCWOSL(object,
                            signal.integral.min = 1,
                            signal.integral.max = 2,
                            background.integral.min = 000,
                            background.integral.max = 1000,
                            log = "x",
                            fit.method = "EXP")

## show De results
get_RLum.Results(results)

## show LnTnLxTx table
get_RLum.Results(results, data.object = "LnLxTnLxTx.table")

---

Analyse_SAR.OSLdata  Analyse SAR CW-OSL measurements.

Description

The function analyses SAR CW-OSL curve data and provides a summary of the measured data for every position. The output of the function is optimised for SAR OSL measurements on quartz.

Usage

Analyse_SAR.OSLdata(input.data, signal.integral, background.integral,
                    position, run, set, dtype, keep.SEL = FALSE, info.measurement = "unknown measurement",
                    log = "", output.plot = FALSE, output.plot.single = FALSE,
                    cex.global = 1)

Arguments

  input.data  Risoe.BINfileData-class (required): input data from a Risoe BIN file, produced by the function readBIN2R.
  signal.integral  vector (required): channels used for the signal integral, e.g. signal.integral=c(1:2)
  background.integral  vector (required): channels used for the background integral, e.g. background.integral=c(85:100)
position vector (optional): reader positions that want to be analysed (e.g. position=c(1:48). Empty positions are automatically omitted. If no value is given all positions are analysed by default.

run vector (optional): range of runs used for the analysis. If no value is given the range of the runs in the sequence is deduced from the Risoe.BINfileData object.

set vector (optional): range of sets used for the analysis. If no value is given the range of the sets in the sequence is deduced from the Risoe.BINfileData object.

dtype character (optional): allows to further limit the curves by their data type (DTYPE), e.g., dtype = c("Natural", "Dose") limits the curves to this two data types. By default all values are allowed. See Risoe.BINfileData-class for allowed data types.

keep.SEL logical (default): option allowing to use the SEL element of the Risoe.BINfileData-class manually. NOTE: In this case any limitation provided by run, set and dtype are ignored!

info.measurement character (with default): option to provide information about the measurement on the plot output (e.g. name of the BIN or BINX file).

log character (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. See plot.default.

output.plot logical (with default): plot output (TRUE/FALSE)

output.plot.single logical (with default): single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. Requires output.plot = TRUE.

cex.global numeric (with default): global scaling factor.

Details

The function works only for standard SAR protocol measurements introduced by Murray and Wintle (2000) with CW-OSL curves. For the calculation of the Lx/Tx value the function calc_OSLLxTxRatio is used.

Provided rejection criteria

‘recycling ratio’: calculated for every repeated regeneration dose point.
‘recuperation’: recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988)

‘IRSL/BOSL’: the integrated counts (signal.integral) of an IRSL curve are compared to the integrated counts of the first regenerated dose point. It is assumed that IRSL curves got the same dose as the first regenerated dose point. **Note:** This is not the IR depletation ratio described by Duller (2003).
Analyse_SAR.OSLdata

Value
A plot (optional) and list is returned containing the following elements:

data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.

RejectionCriteria
data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

SARParameters data.frame of additional measurement parameters obtained from the BIN file, e.g. preheat or read temperature (not valid for all types of measurements).

Function version
0.2.15 (2015-03-04 00:19:53)

Note
Rejection criteria are calculated but not considered during the analysis to discard values.

The development of this function will not be continued. We recommend to use the function analyse_SAR.CWOSL instead.

Author(s)
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Margret C. Fuchs, AWI Potsdam (Germany), TU Bergakademie Freiberg (Germany)
R Luminescence Package Team

References


See Also
calc_OSLLxTxRatio, Risoe.BINfileData-class, readBIN2R
and for further analysis plot_GrowthCurve
Examples

```r
# load data
data(ExampleData.BINfileData, envir = environment())

# analyse data
output <- analyse_SAR.OSLdata(input.data = CWOSL.SAR.Data, 
                               signal.integral = c(1:5), 
                               background.integral = c(900:1000), 
                               position = c(1:1), 
                               output.plot = TRUE)

# combine results relevant for further analysis
output.SAR <- data.frame(Dose = output$LnLxTx[[1]]$Dose, 
                          LxTx = output$LnLxTx[[1]]$LxTx, 
                          LxTx.Error = output$LnLxTx[[1]]$LxTx.Error)
output.SAR
```

---

**analyse_SAR.TL**  
*Analyze SAR TL measurements*

**Description**

The function performs a SAR TL analysis on a `RLum.Analysis` object including growth curve fitting.

**Usage**

```r
analyse_SAR.TL(object, object.background, signal.integral.min, 
                signal.integral.max, sequence.structure = c("PREHEAT", "SIGNAL", 
                                                            "BACKGROUND"), 
                rejection.criteria = list(recycling.ratio = 10, 
                                         recuperation.rate = 10), log = "", ...)```

**Arguments**

- `object` *RLum.Analysis*(required): input object containing data for analysis
- `object.background` currently not used
- `signal.integral.min` *integer*(required): requires the channel number for the lower signal integral bound (e.g. `signal.integral.min = 100`)
- `signal.integral.max` *integer*(required): requires the channel number for the upper signal integral bound (e.g. `signal.integral.max = 200`)
sequence.structure

vector character (with default): specifies the general sequence structure. Three steps are allowed ("PREHEAT", "SIGNAL", "BACKGROUND"), in addition a parameter "EXCLUDE". This allows excluding TL curves which are not relevant for the protocol analysis. (Note: None TL are removed by default)

rejection.criteria

list (with default): list containing rejection criteria in percentage for the calculation.

log

character (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. See plot.default).

... further arguments that will be passed to the function plot_GrowthCurve

Details

This function performs a SAR TL analysis on a set of curves. The SAR procedure in general is given by Murray and Wintle (2000). For the calculation of the Lx/Tx value the function calc_TLLxTxRatio is used.

Provided rejection criteria

‘recycling.ratio’: calculated for every repeated regeneration dose point.
‘recuperation.rate’: recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988)

Value

A plot (optional) and an RLum.Results object is returned containing the following elements:

De.values data.frame containing De-values and further parameters
LnLxTnTx.values data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.
rejection.criteria data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

note: the output should be accessed using the function get_RLum.Results

Function version

0.1.4 (2015-03-04 00:19:53)
Note

**THIS IS A BETA VERSION**

None TL curves will be removed from the input object without further warning.

**Author(s)**

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany)
R Luminescence Package Team

**References**


**See Also**

calc_TLLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results get_RLum.Results

**Examples**

```r
# load data
data(ExampleData.BINfileData, envir = environment())

# transform the values from the first position in a RLum.Analysis object object <- Risoe.BINfileData2RLum.Analysis(TL.SAR.Data, pos=3)

# perform analysis
analyse_SAR.TL(object,
                   signal.integral.min = 210,
                   signal.integral.max = 220,
                   log = "y",
                   fit.method = "EXP OR LIN",
                   sequence.structure = c("SIGNAL", "BACKGROUND"))
```

---

**apply_CosmicRayRemoval**

*Function to remove cosmic rays from an RLum.Data.Spectrum S4 class object*

**Description**

The function provides several methods for cosmic ray removal and spectrum smoothing for an RLum.Data.Spectrum S4 class object.
Usage

```r
apply_CosmicRayRemoval(object, method = "Pych", method.Pych.smoothing = 2,
          silent = FALSE, plot = FALSE, ...)
```

Arguments

- `method`: character (with default): Defines method that is applied for cosmic ray removal. Allowed methods are `smooth`, `smooth.spline` and `Pych` (default). See details for further information.
- `method.Pych.smoothing`: integer (with default): Smoothing parameter for cosmic ray removal according to Pych (2003). The value defines how many neighboring values in each frame are used for smoothing (e.g., 2 means that the two previous and two following values are used).
- `silent`: logical (with default): Option to suppress terminal output.
- `plot`: logical (with default): If `TRUE` the histograms used for the cosmic-ray removal are returned as plot including the used threshold. Note: A separate plot is returned for each frame! Currently only for `method = "Pych"` a graphical output is provided.
- `...`: further arguments and graphical parameters that will be passed to the `smooth` function.

Details

- `method = "Pych"`

This method applies the cosmic-ray removal algorithm described by Pych (2003). Some aspects that are different to the publication:

- For interpolation between neighbouring values the median and not the mean is used.
- The number of breaks to construct the histogram is set to: \(\text{length(number.of.input.values)}/2\)

For further details see references below.

- `method = "smooth"

Method uses the function `smooth` to remove cosmic rays.

Arguments that can be passed are: `kind, twiceit`

- `method = "smooth.spline"

Method uses the function `smooth.spline` to remove cosmic rays.

Arguments that can be passed are: `spar`

**How to combine methods?**

Different methods can be combined by applying the method repeatedly to the dataset (see example).
apply_EfficiencyCorrection

Value
Returns same object as input (RLum.Data.Spectrum)

Function version
0.1.3 (2015-03-21 10:34:18)

Note
-

Author(s)
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France) R Luminescence Package Team

References

See Also
RLum.Data.Spectrum, smooth, smooth.spline, apply_CosmicRayRemoval

Examples

```r
##(1) - use with your own data and combine (uncomment for usage)
## run two times the default method and smooth with another method
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "Pych"
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "Pych"
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "smooth"
```

-------------------------------------------------------------------
apply_EfficiencyCorrection

Function to apply spectral efficiency correction to RLum.Data.Spectrum S4 class objects

-------------------------------------------------------------------

Description
The function allows spectral efficiency corrections for RLum.Data.Spectrum S4 class objects

Usage
apply_EfficiencyCorrection(object, spectral.efficiency)
Arguments

object \textbf{RLum.Data.Spectrum} (\textbf{required}): S4 object of class \texttt{RLum.Data.Spectrum}

\texttt{spectral.efficiency}

\texttt{data.frame} (\textbf{required}): Data set containing wavelengths (x-column) and relative spectral response values (y-column) in percentage

Details

The efficiency correction is based on a spectral response dataset provided by the user. Usually the data set for the quantum efficiency is of lower resolution and values are interpolated for the required spectral resolution.

Value

Returns same object as input (\texttt{RLum.Data.Spectrum})

Function version

0.1 (2015-03-04 00:19:53)

Note

Please note that the spectral efficiency data from the camera may not sufficiently correct for spectral efficiency of the entire optical system (e.g., spectrometer, camera ...).

This function has BETA status.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Johannes Friedrich, University of Bayreuth (Germany)
R Luminescence Package Team

References

-

See Also

\texttt{RLum.Data.Spectrum}

Examples

```r
###(1) - use with your own data (uncomment for usage)
### spectral.efficiency <- read.csv("your data")
###
### your.spectrum <- apply.EfficiencyCorrection(your.spectrum, )
```
BaseDataSet.CosmicDoseRate

Base data set for cosmic dose rate calculation

Description
Collection of data from various sources needed for cosmic dose rate calculation

Usage
BaseDataSet.CosmicDoseRate

Format
values.cosmic.Softcomp: data frame containing cosmic dose rates for shallow depths (< 167 g cm^-2) obtained using the „AGE“ program by Rainer Gruen (cf. Gruen 2009). These data essentially reproduce the graph shown in Fig. 1 of Prescott & Hutton (1988).

values.factor.Altitude: data frame containing altitude factors for adjusting geomagnetic field-change factors. Values were read from Fig. 1 in Prescott & Hutton (1994).

values.par.FJH: data frame containing values for parameters F, J and H (read from Fig. 2 in Prescott & Hutton 1994) used in the expression

\[ Dc = D0 \times (F + J \times \exp((\text{altitude}/1000)/H)) \]

Version
0.1

Source
The following data were carefully read from figures in mentioned sources and used for fitting procedures. The derived expressions are used in the function calc.CosmicDoseRate.

values.cosmic.Softcomp

Program: "AGE"
Reference: Gruen (2009)
Fit: Polynomials in the form of

For depths between 40-167 g cm^-2:

\[ y = 2 \times 10^{-6} \times x^2 - 0.0008 \times x + 0.2535 \]

(For depths <40 g cm^-2)

\[ y = -6 \times 10^{-8} \times x^3 + 2 \times 10^{-5} \times x^2 - 0.0025 \times x + 0.2969 \]

values.factor.Altitude
Fit: 2-degree polynomial in the form of

\[ y = -0.026 \times x^2 + 0.6628 \times x + 1.0435 \]

values.par.FJH

F (non-linear part, \( \lambda < 36.5 \) deg.):

\[ y = -7 \times 10^{-7} \times x^3 - 8 \times 10^{-5} \times x^2 - 0.0009 \times x + 0.3988 \]

F (linear part, \( \lambda > 36.5 \) deg.):

\[ y = -0.0001 \times x + 0.2347 \]

J (non-linear part, \( \lambda < 34 \) deg.):

\[ y = 5 \times 10^{-6} \times x^3 - 5 \times 10^{-5} \times x^2 + 0.0026 \times x + 0.5177 \]

J (linear part, \( \lambda > 34 \) deg.):

\[ y = 0.0005 \times x + 0.7388 \]

H (non-linear part, \( \lambda < 36 \) deg.):

\[ y = -3 \times 10^{-6} \times x^3 - 5 \times 10^{-5} \times x^2 - 0.0031 \times x + 4.398 \]

H (linear part, \( \lambda > 36 \) deg.):

\[ y = 0.0002 \times x + 4.0914 \]

References


**Description**

Estimate the number of grains on an aliquot. Alternatively, the packing density of an aliquot is computed.

**Usage**

```r
calc_AliquotSize(grain.size, sample.diameter, packing.density = 0.65,
                  MC = TRUE, grains.counted, plot = TRUE, ...)
```

**Arguments**

- **grain.size**: numeric (required): mean grain size (microns) or a range of grain sizes from which the mean grain size is computed (e.g. c(100, 200)).
- **sample.diameter**: numeric (required): diameter (mm) of the targeted area on the sample carrier.
- **packing.density**: numeric (with default) empirical value for mean packing density. If packing.density = "inf" a hexagonal structure on an infinite plane with a packing density of 0.906... is assumed.
- **MC**: logical (optional): if TRUE the function performs a monte carlo simulation for estimating the amount of grains on the sample carrier and assumes random errors in grain size distribution and packing density. Requires a vector with min and max grain size for grain.size. For more information see details.
- **grains.counted**: numeric (optional) grains counted on a sample carrier. If a non-zero positive integer is provided this function will calculate the packing density of the aliquot. If more than one value is provided the mean packing density and its standard deviation is calculated. Note that this overrides packing.density.
- **plot**: logical (with default): plot output (TRUE/FALSE)
- **...**: further arguments to pass (main, xlab, MC.iter).

**Details**

This function can be used to either estimate the number of grains on an aliquot or to compute the packing density depending on the the arguments provided. The following function is used to estimate the number of grains $n$:

$$n = \frac{\pi \times x^2}{\pi \times y^2} \times d$$
where \( x \) is the radius of the aliquot size (microns), \( y \) is the mean radius of the mineral grains (mm) and \( d \) is the packing density (value between 0 and 1).

**Packing density**

The default value for packing\_density is 0.65, which is the mean of empirical values determined by Heer et al. (2012) and unpublished data from the Cologne luminescence laboratory. If packing\_density = "inf" a maximum density of \( \pi/\sqrt{12} = 0.9068 \ldots \) is used. However, note that this value is not appropriate as the standard preparation procedure of aliquots resembles a PECC ("Packing Equal Circles in a Circle") problem where the maximum packing density is asymptotic to about 0.87.

**Monte Carlo simulation**

The number of grains on an aliquot can be estimated by Monte Carlo simulation when setting \( \text{MC} = \text{TRUE} \). Each of the parameters necessary to calculate \( n(x, y, d) \) are assumed to be normally distributed with means \( \mu_x, \mu_y, \mu_d \) and standard deviations \( \sigma_x, \sigma_y, \sigma_d \).

For the mean grain size random samples are taken first from \( N(\mu_y, \sigma_y) \), where \( \mu_y = \text{mean.grain.size} \) and \( \sigma_y = (\text{max.grain.size} - \text{min.grain.size})/4 \) so that 95% of all grains are within the provided the grain size range. This effectively takes into account that after sieving the sample there is still a small chance of having grains smaller or larger than the used mesh sizes. For each random sample the mean grain size is calculated, from which random subsamples are drawn for the Monte Carlo simulation.

The packing density is assumed to be normally distributed with an empirically determined \( \mu = 0.65 \) (or provided value) and \( \sigma = 0.18 \). The normal distribution is truncated at \( d = 0.87 \) as this is approximately the maximum packing density that can be achieved in PECC problem.

The sample diameter has \( \mu = \text{sample.diameter} \) and \( \sigma = 0.2 \) to take into account variations in sample disc preparation (i.e. applying silicon spray to the disc). A lower truncation point at \( x = 0.5 \) is used, which assumes that aliquots with smaller sample diameters of 0.5 mm are discarded. Likewise, the normal distribution is truncated at 9.8 mm, which is the diameter of the sample disc.

For each random sample drawn from the normal distributions the amount of grains on the aliquot is calculated. By default, \( 10^5 \) iterations are used, but can be reduced/increased with \( \text{MC.iter} \) (see \ldots). The results are visualised in a bar- and boxplot together with a statistical summary.

**Value**

Returns a terminal output. In addition an \texttt{RLum.Results} object is returned containing the following element:

- \texttt{summary} \texttt{data.frame} summary of all relevant calculation results.
- \texttt{args} \texttt{list} used arguments
- \texttt{call} \texttt{call} the function call
- \texttt{MC} \texttt{list} results of the Monte Carlo simulation
calc_CentralDose

The output should be accessed using the function `get_RLum.Results`

Function version

0.31 (2015-03-04 00:19:53)

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References


Further reading


Examples

```r
## Estimate the amount of grains on a small aliquot
calc_AliquotSize(grain.size = c(100,150), sample.diameter = 1)

## Calculate the mean packing density of large aliquots
calc_AliquotSize(grain.size = c(100,200), sample.diameter = 8,
grains.counted = c(2525,2312,2880))
```

calc_CentralDose  

Apply the central age model (CAM) after Galbraith et al. (1999) to a given De distribution

Description

This function calculates the central dose and dispersion of the De distribution, their standard errors and the profile log likelihood function for sigma.
Usage

calc_CentralDose(data, sigmab, plot = TRUE, ...)

Arguments

data R Lum.Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab numeric (with default): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
plot logical (with default): plot output
... further arguments (trace, verbose).

Details

This function uses the equations of Galbraith et al. (1999, 358-359). The parameter sigma is estimated using the maximum likelihood approach. A detailed explanation on maximum likelihood estimation can be found in the appendix of Galbraith & Laslett (1993, 468-470)

Value

Returns a plot (optional) and terminal output. In addition an R Lum.Results object is returned containing the following element:

summary data.frame summary of all relevant model results.
data data.frame original input data
args list used arguments
call call the function call
profile data.frame the log likelihood profile for sigma

The output should be accessed using the function get_RLum.Results

Function version

1.3 (2015-03-04 13:35:16)

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010

R Luminescence Package Team
References


Further reading


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

See Also

plot, calc_CommonDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```r
# load example data
data(ExampleData.DeValues, envir = environment())

# apply the central dose model
calc_CentralDose(ExampleData.DeValues$CA1)
```

(calc_CommonDose) **Apply the (un-)logged common age model after Galbraith et al. (1999) to a given De distribution**
Description

Function to calculate the common dose of a De distribution.

Usage

calc_CommonDose(data, sigmab, log = TRUE, ...)

Arguments

data \text{RLum.Results or data.frame (required)}: for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab numeric (with default): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
log logical (with default): fit the (un-)logged common age model to De data
... currently not used.

Details

(Un-)logged model

When \text{log} = \text{TRUE} this function calculates the weighted mean of logarithmic De values. Each of the estimates is weighted by the inverse square of its relative standard error. The weighted mean is then transformed back to the dose scale (Galbraith & Roberts 2012, p. 14).

The log transformation is not applicable if the De estimates are close to zero or negative. In this case the un-logged model can be applied instead (log = \text{FALSE}). The weighted mean is then calculated using the un-logged estimates of De and their absolute standard error (Galbraith & Roberts 2012, p. 14).

Value

Returns a terminal output. In addition an \text{RLum.Results} object is returned containing the following element:

summary data.frame summary of all relevant model results.
data data.frame original input data
args list used arguments
call call the function call

The output should be accessed using the function \text{get_RLum.Results}

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team
calc_CosmicDoseRate

References


Further reading


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

See Also

calc_CentralDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```r
## load example data
data(ExampleData.DeValues, envir = environment())

## apply the common dose model
calc_CommonDose(ExampleData.DeValues$CA1)
```

calc_CosmicDoseRate Calculate the cosmic dose rate
Description

This function calculates the cosmic dose rate taking into account the soft- and hard-component of the cosmic ray flux and allows corrections for geomagnetic latitude, altitude above sea-level and geomagnetic field changes.

Usage

calc_CosmicDoseRate(depth, density, latitude, longitude, altitude, 
corr.fieldChanges = FALSE, est.age = NA, half.depth = FALSE, 
error = 10)

Arguments

- **depth** numeric (required): depth of overburden (m). For more than one absorber use c(depth_1, depth_2, ..., depth_n)
- **density** numeric (required): average overburden density (g/cm^3). For more than one absorber use c(density_1, density_2, ..., density_n)
- **latitude** numeric (required): latitude (decimal degree), N positive
- **longitude** numeric (required): longitude (decimal degree), E positive
- **altitude** numeric (required): altitude (m above sea-level)
- **corr.fieldChanges** logical (with default): correct for geomagnetic field changes after Prescott & Hutton (1994). Apply only when justified by the data.
- **est.age** numeric (with default): estimated age range (ka) for geomagnetic field change correction (0-80 ka allowed)
- **half.depth** logical (with default): How to overcome with varying overburden thickness. If TRUE only half the depth is used for calculation. Apply only when justified, i.e. when a constant sedimentation rate can safely be assumed.
- **error** numeric (with default): general error (percentage) to be implemented on corrected cosmic dose rate estimate

Details

This function calculates the total cosmic dose rate considering both the soft- and hard-component of the cosmic ray flux.

Internal calculation steps

1. Calculate total depth of all absorber in hg/cm^2 (1 hg/cm^2 = 100 g/cm^2)

   \[ absorber = depth_1 \times density_1 + depth_2 \times density_2 + ... + depth_n \times density_n \]

2. If half.depth = TRUE

   \[ absorber = absorber/2 \]
(3) Calculate cosmic dose rate at sea-level and 55 deg. latitude
a) If absorber is > 167 g/cm² (only hard-component; Allkofer et al. 1975): apply equation given by Prescott & Hutton (1994) (c.f. Barbouti & Rastin 1983)

\[ D_0 = C' / \left( (\text{absorber} + d)^a + a \right) \times (\text{absorber} + H) \times \exp(-B \times \text{absorber}) \]

b) If absorber is < 167 g/cm² (soft- and hard-component): derive D0 from Fig. 1 in Prescott & Hutton (1988).


\[ \lambda = \arcsin(0.203 \times \cos(\text{latitude}) \times \cos(\text{longitude} - 291) + 0.979 \times \sin(\text{latitude})) \]

(5) Apply correction for geomagnetic latitude and altitude above sea-level. Values for F, J and H were read from Fig. 3 shown in Prescott & Stephan (1982) and fitted with 3-degree polynomials for lambda < 35 degree and a linear fit for lambda > 35 degree.

\[ D_c = D_0 \times (F + J \times \exp((\text{altitude}/1000)/H)) \]

(6) Optional: Apply correction for geomagnetic field changes in the last 0-80 ka (Prescott & Hutton 1994). Correction and altitude factors are given in Table 1 and Fig. 1 in Prescott & Hutton (1994). Values for altitude factor were fitted with a 2-degree polynomial. The altitude factor is operated on the decimal part of the correction factor.

\[ D_c' = D_c \times \text{correctionFactor} \]

Usage of depth and density

(1) If only one value for depth and density is provided, the cosmic dose rate is calculated for exactly one sample and one absorber as overburden (i.e. depth×density).

(2) In some cases it might be useful to calculate the cosmic dose rate for a sample that is overlain by more than one absorber, e.g. in a profile with soil layers of different thickness and a distinct difference in density. This can be calculated by providing a matching number of values for depth and density (e.g. depth = c(1, 2), density = c(1.7, 2.4))

(3) Another possibility is to calculate the cosmic dose rate for more than one sample of the same profile. This is done by providing more than one values for depth and only one for density. For example, depth = c(1, 2, 3), density = 1.7 will calculate the cosmic dose rate for three samples in 1, 2 and 3 m depth in a sediment of density 1.7 g/cm³.

Value

Returns a terminal output. In addition an RLum.Results object is returned containing the following element:

- summary data.frame summary of all relevant calculation results.
- args list used arguments
- call call the function call

The output should be accessed using the function get_R Lum.Results
Function version

0.5.2 (2015-03-04 00:19:53)

Note

Despite its universal use the equation to calculate the cosmic dose rate provided by Prescott & Hutton (1994) is falsely stated to be valid from the surface to $10^4$ hg/cm$^2$ of standard rock. The original expression by Barbouti & Rastin (1983) only considers the muon flux (i.e. hard-component) and is by their own definition only valid for depths between $10$-$10^4$ hg/cm$^2$.

Thus, for near-surface samples (i.e. for depths $< 167$ g/cm$^2$) the equation of Prescott & Hutton (1994) underestimates the total cosmic dose rate, as it neglects the influence of the soft-component of the cosmic ray flux. For samples at zero depth and at sea-level the underestimation can be as large as ~0.1 Gy/ka. In a previous article, Prescott & Hutton (1988) give another approximation of Barbouti & Rastins equation in the form of

$$ D = 0.21 * \exp(-0.070 * \text{absorber} + 0.0005 * \text{absorber}^2) $$

which is valid for depths between 150-5000 g/cm$^2$. For shallower depths ($< 150$ g/cm$^2$) they provided a graph (Fig. 1) from which the dose rate can be read.

As a result, this function employs the equation of Prescott & Hutton (1994) only for depths $> 167$ g/cm$^2$, i.e. only for the hard-component of the cosmic ray flux. Cosmic dose rate values for depths $< 167$ g/cm$^2$ were obtained from the "AGE" program (Gruen 2009) and fitted with a 6-degree polynomial curve (and hence reproduces the graph shown in Prescott & Hutton 1988). However, these values assume an average overburden density of 2 g/cm$^3$.

It is currently not possible to obtain more precise cosmic dose rate values for near-surface samples as there is no equation known to the author of this function at the time of writing.

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References


calc_CosmicDoseRate


See Also

BaseDataSet.CosmicDoseRate

Examples

```r
##(1) calculate cosmic dose rate (one absorber)
calc_CosmicDoseRate(depth = 2.78, density = 1.7, 
                      latitude = 38.06451, longitude = 1.49646, 
                      altitude = 364, error = 10)

##(2a) calculate cosmic dose rate (two absorber)
calc_CosmicDoseRate(depth = c(5.0, 2.78), density = c(2.65, 1.7), 
                      latitude = 38.06451, longitude = 1.49646, 
                      altitude = 364, error = 10)

##(2b) calculate cosmic dose rate (two absorber) and 
##correct for geomagnetic field changes
calc_CosmicDoseRate(depth = c(5.0, 2.78), density = c(2.65, 1.7), 
                      latitude = 12.04332, longitude = 4.43243, 
                      altitude = 364, corr.fieldChanges = TRUE, 
                      est.age = 67, error = 15)

##(3) calculate cosmic dose rate and export results to .csv file
#calculate cosmic dose rate and save to variable
results<- calc_CosmicDoseRate(depth = 2.78, density = 1.7, 
                             latitude = 38.06451, longitude = 1.49646, 
                             altitude = 364, error = 10)

# the results can be accessed by
get_RLum.Results(results, "summary")

#export results to .csv file - uncomment for usage
#write.csv(results, file = "c:/users/public/results.csv")

##(4) calculate cosmic dose rate for 6 samples from the same profile
## and save to .csv file
#calculate cosmic dose rate and save to variable
results<- calc_CosmicDoseRate(depth = c(0.1, 0.5, 2.1, 2.7, 4.2, 6.3), 
                             density = 1.7, latitude = 38.06451, 
                             longitude = 1.49646, altitude = 364,
```

fun() error = 10)

#export results to .csv file - uncomment for usage
#write.csv(results, file = "c:/users/public/results_profile.csv")

calc_FadingCorr  Apply a fading correction according to Huntley & Lamothe (2001) for a given g-value.

Description
This function runs the iterations that are needed to calculate the corrected age including the error for a given g-value according to Huntley & Lamothe (2001).

Usage
calc_FadingCorr(g_value, tc, age.faded, n.MCruns = 10000)

Arguments
- **g_value**: vector (required): g-value and error obtained from separate fading measurements (see example)
- **tc**: numeric (required): time in seconds (time between irradiation and the prompt measurement, cf. Huntely & Lamothe 2001)
- **age.faded**: numeric vector (required): uncorrected age with error in ka (see example)
- **n.MCruns**: integer (with default): number of Monte Carlo simulation runs for error estimation

Details
The error of the fading-corrected age is determined using a Monte Carlo simulation approach. Solving of the equation is realised using `uniroot`. Large values for **n.MCruns** will significantly increase the computation time.

Value
Returns an S4 object of type `RLum.Results`. Slot data contains a list with the following structure:
- $age.corr (data.frame) .. $ age
  .. $ age.error
  $ age.corr.MC (numeric)

$age.corr.MC contain all possible ages from the Monte Carlo (error) simulation.
Function version
0.2 (2015-03-21 01:18:50)

Note
The upper age limit is set to 500 ka!

Author(s)
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne R Luminescence Package Team

References

See Also
RLum.Results, get_RLum.Results, uniroot

Examples

```r
calc_FiniteMixture(data, sigmab, n.components, grain.proportion = FALSE, 
dose.scale, pdf.weight = TRUE, pdf.sigma = "sigmab", pdf.colors = "gray", 
pdf.scale, plot.proportions = TRUE, plot = TRUE, ...)
```

Description
This function fits a k-component mixture to a De distribution with differing known standard errors. Parameters (doses and mixing proportions) are estimated by maximum likelihood assuming that the log dose estimates are from a mixture of normal distributions.

Usage

```r
calc_FiniteMixture(data, sigmab, n.components, grain.proportion = FALSE, 
dose.scale, pdf.weight = TRUE, pdf.sigma = "sigmab", pdf.colors = "gray", 
pdf.scale, plot.proportions = TRUE, plot = TRUE, ...)
```
Arguments

- **data**: RLuc.Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
- **sigmab**: numeric (required): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Wallinga 2012, p. 100).
- **n.components**: numeric (required): number of components to be fitted. If a vector is provided (e.g. c(2:8)) the finite mixtures for 2, 3 ... 8 components are calculated and a plot and a statistical evaluation of the model performance (BIC score and maximum log-likelihood) is provided.
- **grain.probability**: logical (with default): prints the estimated probabilities of which component each grain is in
- **dose.scale**: numeric: manually set the scaling of the y-axis of the first plot with a vector in the form of c(min, max)
- **pdf.weight**: logical (with default): weight the probability density functions by the components proportion (applies only when a vector is provided for n.components)
- **pdf.sigma**: character (with default): if "sigmab" the components normal distributions are plotted with a common standard deviation (i.e. sigmab) as assumed by the FFM. Alternatively, "se" takes the standard error of each component for the sigma parameter of the normal distribution
- **pdf.colors**: character (with default): color coding of the components in the the plot. Possible options are "gray", "colors" and "none"
- **pdf.scale**: numeric: manually set the max density value for proper scaling of the x-axis of the first plot
- **plot.proportions**: logical (with default): plot barplot showing the proportions of components
- **plot**: logical (with default): plot output
- **...**: further arguments to pass. See details for their usage.

Details

This model uses the maximum likelihood and Bayesian Information Criterion (BIC) approaches.

Indications of overfitting are:

- increasing BIC
- repeated dose estimates
- covariance matrix not positive definite
- covariance matrix produces NaNs
- convergence problems

Plot

If a vector (c(k.min:k.max)) is provided for n.components a plot is generated showing the the k
components equivalent doses as normal distributions. By default pdf.weight is set to FALSE, so
that the area under each normal distribution is always 1. If TRUE, the probability density functions
are weighted by the components proportion for each iteration of k components, so the sum of areas
of each component equals 1. While the density values are on the same scale when no weights are
used, the y-axis are individually scaled if the probability density are weighted by the components
proportion.
The standard deviation (sigma) of the normal distributions is by default determined by a common
sigmab (see pdf.sigma). For pdf.sigma = "se" the standard error of each component is taken
instead.
The stacked barplot shows the proportion of each component (in per cent) calculated by the FFM.
The last plot shows the achieved BIC scores and maximum log-likelihood estimates for each itera-
tion of k.

Value

Returns a plot (optional) and terminal output. In addition an RLuc.Results object is returned
containing the following elements:

summary data.frame summary of all relevant model results.
data data.frame original input data
args list used arguments
call call the function call
mle covariance matrices of the log likelihoods
BIC BIC score
llik maximum log likelihood
grain.probability probabilities of a grain belonging to a component
components matrix estimates of the de, de error and proportion for each component
single.comp data.frame single componente FFM estimate

If a vector for n.components is provided (e.g. c(2:8)), mle and grain.probability are lists
containing matrices of the results for each iteration of the model.
The output should be accessed using the function get_RLum.Results

Function version

0.4 (2015-03-04 13:33:56)

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2006.

RLuminescence Package Team
References


Further reading


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

See Also

calc_CentralDose, calc_CommonDose, calc_FuchsLang2001, calc_MinDose

Examples

```r
## load example data
data(ExampleData.DeValues, envir = environment())

## (1) apply the finite mixture model
## NOTE: the data set is not suitable for the finite mixture model,
## which is why a very small sigmab is necessary
calc_FiniteMixture(ExampleData.DeValues$CA1,
sigmab = 0.2, n.components = 2,
grain.probability = TRUE)

## (2) repeat the finite mixture model for 2, 3 and 4 maximum number of fitted
## components and save results
```
calc_FuchsLang2001

Apply the model after Fuchs & Lang (2001) to a given De distribution.

Description

This function applies the method according to Fuchs & Lang (2001) for heterogeneously bleached samples with a given coefficient of variation threshold.

Usage

calc_FuchsLang2001(data, cvThreshold = 5, startDeValue = 1, plot = TRUE, ...)

Arguments

data R Lum.Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
cvThreshold numeric (with default): coefficient of variation in percent, as threshold for the method, e.g. cvThreshold = 3. See details.
startDeValue numeric (with default): number of the first aliquot that is used for the calculations
plot logical (with default): plot output TRUE/FALSE
...

Details

Used values
If the coefficient of variation (c[v]) of the first two values is larger than the threshold cv_threshold, the first value is skipped. Use the startDeValue argument to define a start value for calculation (e.g. 2nd or 3rd value).

Basic steps of the approach

```r
## NOTE: The following example is computationally intensive. Please un-comment
## the following lines to make the example work.
FMM <- calc_FiniteMixture(ExampleData.DeValues$CA1,
                        sigmab = 0.2, n.components = c(2:4),
                        pdf.weight = TRUE, dose.scale = c(0, 100))

## show structure of the results
FMM

## show the results on equivalent dose, standard error and proportion of
## fitted components
get_RLum.Results(object = FMM, data.object = "components")
```
(1) Estimate natural relative variation of the sample using a dose recovery test
(2) Sort the input values ascendingly
(3) Calculate a running mean, starting with the lowermost two values and add values iteratively.
(4) Stop if the calculated c[v] exceeds the specified cvThreshold

Value

Returns a plot (optional) and terminal output. In addition an RLum.Results object is returned containing the following elements:

- summary: data.frame summary of all relevant model results.
- data: data.frame original input data
- args: list used arguments
- call: call the function call
- usedDeValues: data.frame containing the used values for the calculation

Function version

0.4.1 (2015-03-04 13:31:55)

Note

Please consider the requirements and the constraints of this method (see Fuchs & Lang, 2001)

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France) Christoph Burow, University of Cologne (Germany) R Luminescence Package Team

References


See Also

plot, calc_MinDose, calc_FiniteMixture, calc_CentralDose, calc_CommonDose, RLum.Results

Examples

```r
# load example data
data(ExampleData.DeValues, envir = environment())

# calculate De according to Fuchs & Lang (2001)
temp<- calc_Fuchslang2001(ExampleData.DeValues$BT998, cvThreshold = 5)
```
calc_HomogeneityTest

Apply a simple homogeneity test after Galbraith (2003)

Description
A simple homogeneity test for De estimates

Usage
calc_HomogeneityTest(data, log = TRUE, ...)

Arguments
- data: Rlum.Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
- log: logical (with default): perform the homogeneity test with (un-)logged data
- ...: further arguments (for internal compatibility only).

Details
For details see Galbraith (2003).

Value
Returns a terminal output. In addition an Rlum.Results object is returned containing the following element:

- summary: data.frame summary of all relevant model results.
- data: data.frame original input data
- args: list used arguments
- call: call the function call

The output should be accessed using the function get_Rlum.Results

Function version
0.2 (2015-03-04 13:31:44)

Author(s)
Christoph Burow, University of Cologne (Germany),
R Luminescence Package Team

References
calc_IEU

See Also

pchisq

Examples

## load example data
data(ExampleData.DeValues, envir = environment())

## apply the homogeneity test
calc_HomogeneityTest(ExampleData.DeValues$BT998)

calc_IEU

Apply the internal-external-uncertainty (IEU) model after Thomsen et al. (2007) to a given De distribution

Description

Function to calculate the IEU De for a De data set.

Usage

calc_IEU(data, a, b, interval, decimal.point = 2, plot = TRUE, ...)

Arguments

data            RLuc.Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
a              numeric: slope
b              numeric: intercept
interval            numeric: fixed interval (e.g. 5 Gy) used for iteration of Dbar, from the mean to Lowest.De used to create Graph.IEU [Dbar.Fixed vs Z]
decimal.point numeric (with default): number of decimal points for rounding calculations (e.g. 2)
plot            logical (with default): plot output
...            further arguments (trace, verbose).

Details

This function uses the equations of Thomsen et al. (2007). The parameters a and b are estimated from dose-recovery experiments.
calc_IEU

Value

Returns a plot (optional) and terminal output. In addition an R Lum. Results object is returned containing the following element:

- **summary**: data.frame summary of all relevant model results.
- **data**: data.frame original input data
- **args**: list used arguments
- **call**: call the function call
- **tables**: list a list of data frames containing all calculation tables

The output should be accessed using the function `get_RLum.Results`.

Function version

0.1 (2015-03-04 13:18:38)

Author(s)

Rachel Smedley, Geography & Earth Sciences, Aberystwyth University (United Kingdom)
Based on an excel spreadsheet and accompanying macro written by Kristina Thomsen. R Luminescence Package Team

References


See Also

- `plot`
- `calc_CommonDose`
- `calc_CentralDose`
- `calc_FiniteMixture`
- `calc_FuchslangRPPQ`
- `calc_MinDose`

Examples

```r
## load data
data(ExampleData.DeValues, envir = environment())

## apply the IEU model
ieu <- calc_IEU(ExampleData.DeValues$CA1, a = 0.2, b = 1.9, interval = 1)
```
calc_MaxDose

Apply the maximum age model to a given De distribution

Description

Function to fit the maximum age model to De data. This is a wrapper function that calls calc_MinDose() and applies a similar approach as described in Olley et al. (2006).

Usage

calc_MaxDose(data, sigmab, log = TRUE, par = 3, bootstrap = FALSE, init.values, plot = TRUE, ...)

Arguments

data R Lum. Results or data.frame (required): for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab numeric (required): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
log logical (with default): fit the (un-)logged three parameter minimum dose model to De data
par numeric (with default): apply the 3- or 4-parametric minimum age model (par=3 or par=4).
bootstrap
init.values numeric (with default): starting values for gamma, sigma, p0 and mu. Custom values need to be provided in a vector of length three in the form of c(gamma, sigma, p0).
plot logical (with default): plot output (TRUE/FALSE)
...

Details

Data transformation

To estimate the maximum dose population and its standard error, the three parameter minimum age model of Galbraith et al. (1999) is adapted. The measured De values are transformed as follows:

1. convert De values to natural logs
2. multiply the logged data to creat a mirror image of the De distribution
3. shift De values along x-axis by the smallest x-value found to obtain only positive values
4. combine in quadrature the measurement error associated with each De value with a relative error specified by sigmab
5. apply the MAM to these data
When all calculations are done the results are then converted as follows

1. subtract the x-offset
2. multiply the natural logs by -1
3. take the exponent to obtain the maximum dose estimate in Gy

**Further documentation**

Please see calc_MinDose.

**Value**

Please see calc_MinDose.

**Function version**

0.3 (2015-03-04 13:31:23)

**Author(s)**

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010

R Luminescence Package Team

**References**


Further reading


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

See Also

calc_CentralDose, calc_CommonDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```r
## load example data
data(ExampleData.DeValues, envir = environment())

# apply the maximum dose model
calc_MaxDose(ExampleData.DeValues$CA1, sigmab = 0.2, par = 3)
```

**calc_MinDose**

*Apply the (un-)logged minimum age model (MAM) after Galbraith et al. (1999) to a given De distribution*

**Description**

Function to fit the (un-)logged three or four parameter minimum dose model (MAM-3/4) to De data.

**Usage**

calc_MinDose(data, sigmab, log = TRUE, par = 3, bootstrap = FALSE, init.values, plot = TRUE, multicore = FALSE, ...)
**calc_MinDose**

**Arguments**
- **data** \(\text{RLum.Results} \text{ or data.frame (required)}\): for data.frame: two columns with De (data[,1]) and De error (values[,2]).
- **sigmab** \(\text{numeric (required)}\): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
- **log** \(\text{logical (with default)}\): fit the (un-)logged minimum dose model to De data
- **par** \(\text{numeric (with default)}\): apply the 3- or 4-parametric minimum age model (par=3 or par=4). The MAM-3 is used by default.
- **bootstrap** \(\text{logical (with default)}\): apply the recycled bootstrap approach of Cunningham & Wallinga (2012).
- **init.values** \(\text{numeric (optional)}\): a named list with starting values for gamma, sigma, p0 and mu (e.g. list(gamma=100, sigma=1.5, p0=0.1, mu=100)). If no values are provided reasonable values are tried to be estimated from the data.
- **plot** \(\text{logical (with default)}\): plot output (TRUE/FALSE)
- **multicore** \(\text{logical (with default)}\): enable parallel computation of the bootstrap by creating a multicore SNOW cluster. Depending on the number of available logical CPU cores this will drastically reduce the computation time. Note that this option is highly experimental and not work for all machines. (TRUE/FALSE)
- **...** \(\text{(optional) further arguments for bootstrapping (bs.M, bs.N, bs.h, sigmab.sd)}\). See details for their usage. Further arguments are verbose to de-/activate console output (logical), debug for extended console output (logical) and cores (integer) to manually specify the number of cores to be used when multicore=TRUE.

**Details**

**Parameters**

This model has four parameters:

- **gamma**: minimum dose on the log scale
- **mu**: mean of the non-truncated normal distribution
- **sigma**: spread in ages above the minimum
- **p0**: proportion of grains at gamma

If par=3 (default) the 3-parametric minimum age model is applied, where gamma=mu. For par=4 the 4-parametric model is applied instead.

**(Un-)logged model**

In the original version of the three-parameter minimum dose model, the basic data are the natural logarithms of the De estimates and relative standard errors of the De estimates. This model will
be applied if \(\text{log} = \text{TRUE}\).

If \(\text{log} = \text{FALSE}\), the modified un-logged model will be applied instead. This has essentially the same form as the original version. \(\gamma\) and \(\sigma\) are in Gy and \(\gamma\) becomes the minimum true dose in the population.

While the original (logged) version of the minimum dose model may be appropriate for most samples (i.e. \(\text{De}\) distributions), the modified (un-logged) version is specially designed for modern-age and young samples containing negative, zero or near-zero \(\text{De}\) estimates (Arnold et al. 2009, p. 323).

**Initial values & boundaries**

The log likelihood calculations use the \texttt{nlminb} function for box-constrained optimisation using PORT routines. Accordingly, initial values for the four parameters can be specified via \texttt{init.values}. If no values are provided for \texttt{init.values} reasonable starting values are estimated from the input data. If the final estimates of \(\gamma\), \(\mu\), \(\sigma\) and \(p0\) are totally off target, consider providing custom starting values via \texttt{init.values}.

In contrast to previous versions of this function the boundaries for the individual model parameters can no longer be specified. Appropriate boundary are now hard-coded and are valid for all input data sets.

**Bootstrap**

When \(\text{bootstrap} = \text{TRUE}\) the function applies the bootstrapping method as described in Wallinga & Cunningham (2012). By default, the minimum age model produces 1000 first level and 3000 second level bootstrap replicates (actually, the number of second level bootstrap replicates is three times the number of first level replicates unless specified otherwise). The uncertainty on \(\sigma_{\text{mab}}\) is 0.04 by default. These values can be changed by using the arguments \texttt{bs.M} (first level replicates), \texttt{bs.N} (second level replicates) and \texttt{sigmab.sd} (error on \(\sigma_{\text{mab}}\)). With \texttt{bs.h} the bandwidth of the kernel density estimate can be specified. By default, \(h\) is calculated as

\[
h = (2 \times \sigma_{\text{DE}}) / \sqrt{n}
\]

**Multicore support**

This function supports parallel computing and can be activated by \texttt{multicore=TRUE}. By default, the number of available logical CPU cores is determined automatically, but can be changed with cores. The multicore support is only available when \(\text{bootstrap} = \text{TRUE}\) and spawns \(n\) \(\text{R}\) instances for each core to get MAM estimates for each of the \(N\) and \(M\) bootstrap replicates. Note that this option is highly experimental and may or may not work for your machine. Also the performance gain increases for larger number of bootstrap replicates. Also note that with each additional core and hence \(\text{R}\) instance and depending on the number of bootstrap replicates the memory usage can significantly increase. Make sure that memory is always availabe, otherwise there will be a massive perfomance hit.
calc_MinDose

Value

Returns a plot (optional) and terminal output. In addition an RLum.Results object is returned containing the following elements:

summary  data.frame summary of all relevant model results.
data  data.frame original input data
args  list used arguments
call  call the function call
mle  mle2 object containing the maximum log likelihood functions for all parameters
BIC  numeric BIC score
confint  data.frame confidence intervals for all parameters
profile  profile.mle2 the log likelihood profiles
bootstrap  list bootstrap results

The output should be accessed using the function get_RLum.Results

Function version

0.4.1 (2015-03-18 13:29:54)

Note

The default starting values for gamma, mu, sigma and p0 may only be appropriate for some De data sets and may need to be changed for other data. This is especially true when the un-logged version is applied.

Also note that all R warning messages are suppressed when running this function. If the results seem odd consider re-running the model with debug=TRUE which provides extended console output and forwards all internal warning messages.

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010
The bootstrap approach is based on a rewritten MATLAB script of Alastair Cunningham.
Alastair Cunningham is thanked for his help in implementing and cross-checking the code.
R Luminescence Package Team

References


Further reading


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

See Also

calc_CentralDose, calc_CommonDose, calc_FiniteMixture, calc_FuchslangRPPQ, calc_MaxDose

Examples

```r
## Load example data
data(ExampleData.DValues, envir = environment())

# (1) Apply the minimum age model with minimum required parameters.
# By default, this will apply the un-logged 3-parametric MAM.
calc_MinDose(data = ExampleData.DValues$CA1, sigmab = 0.1)

# (2) Re-run the model, but save results to a variable and turn
# plotting of the log-likelihood profiles off.
mam <- calc_MinDose(data = ExampleData.DValues$CA1,
sigmab = 0.1,
plot = FALSE)

# Show structure of the RLum.Results object
```
calc_MinDose

mam

# Show summary table that contains the most relevant results
res <- get_RLum.Results(mam, "summary")
res

# Plot the log likelihood profiles retroactively, because before
# we set plot = FALSE
plot_RLum.Results(mam)

# Plot the dose distribution in an abanico plot and draw a line
# at the minimum dose estimate
plot_AbanicoPlot(data = ExampleData.DeValues$CA1,
   main = "3-parameter Minimum Age Model",
   line = mam,polygon.col = "none",
   hist = TRUE,
   rug = TRUE,
   summary = c("n", "mean", "mean.weighted", "median", "in.cl"),
   centrality = res$de,
   line.col = "red",
   grid.col = "none",
   line.label = paste0(round(res$de, 1), "\000B1",
      round(res$de.err, 1), " Gy"),
   bw = 0.1,
   ylim = c(-25, 18),
   summary.pos = "topleft",
   mtext = bquote("Parameters: " ~
      sigma[b] == .(get_RLum(mam, "args")$sigmab) ~ " ~
      gamma == .(round(log(res$de), 1)) ~ " ~
      sigma == .(round(res$sig, 1)) ~ " ~
      rho == .(round(res$p0, 2))))

# (3) Run the minimum age model with bootstrap
# NOTE: Bootstrapping is computationally intensive, which is why the
# following example is commented out. To run the examples just
# uncomment the code.
# (3.1) Run the minimum age model with default values for bootstrapping
#calc_MinDose(data = ExampleData.DeValues$CA1,
#   sigmab = 0.15,
#   bootstrap = TRUE)

# (3.2) Bootstrap control parameters
#mam <- calc_MinDose(data = ExampleData.DeValues$CA1,
#   sigmab = 0.15,
#   bootstrap = TRUE,
#   bs.M = 300,
#   bs.N = 500,
#   bs.h = 4,
#   sigmab.sd = 0.06,
#   plot = FALSE)

# Plot the results
#plot_RLum(mam)
# save bootstrap results in a separate variable
bs <- get.RLum.Results(mam, "bootstrap")

# show structure of the bootstrap results
str(bs, max.level = 2, give.attr = FALSE)

# print summary of minimum dose and likelihood pairs
summary(bs$pairs$gamma)

# Show polynomial fits of the bootstrap pairs
bs$poly.fits$poly.three

# Plot various statistics of the fit using the generic plot() function
par(mfcol=c(2,2))
plot(bs$poly.fits$poly.three, ask = FALSE)

# Show the fitted values of the polynomials
summary(bs$poly.fits$poly.three$fitted.values)

calc_OSLxTxRatio

---

**Description**

Calculate Lx/Tx ratios from a given set of CW-OSL curves.

**Usage**

```
calc_OSLxTxRatio(Lx.data, Tx.data, signal.integral, background.integral, background.count.distribution = "non-poisson", sigmab)
```

**Arguments**

- **Lx.data** 
  - `data.frame` *(required)*: requires a CW-OSL shine down curve (x = time, y = counts)

- **Tx.data** 
  - `data.frame` *(optional)*: requires a CW-OSL shine down curve (x = time, y = counts). If no input is given the Tx.data will be treated as NA and no Lx/Tx ratio is calculated.

- **signal.integral** 
  - `vector` *(required)*: vector with the limits for the signal integral.

- **background.integral** 
  - `vector` *(required)*: vector with the bounds for the background integral.

- **background.count.distribution** 
  - `character` *(with default)*: Sets the count distribution assumed for the error calculation. Possible arguments poisson or non-poisson. See details for further information.
calc_OSLLxTxRatio

**sigmab** numeric (optional): Option to set a manual value for the overdispersion (for LnTx and TnTx), used for the Lx/Tx error calculation. The value should be provided as absolute squared count values, e.g. sigmab = c(300, 300). Note: If only one value is provided this value is taken for both (LnTx and TnTx) signals.

**Details**

The integrity of the chosen values for the signal and background integral is checked by the function; the signal integral limits have to be lower than the background integral limits. If a vector is given as input instead of a data.frame, an artificial data.frame is produced. The error calculation is done according to Galbraith (2002).

**background.count.distribution**

This argument allows selecting the distribution assumption that is used for the error calculation. According to Galbraith (2002, 2014) the background counts may be overdispersed (i.e. do not follow a poisson distribution, which is assumed for the photomultiplier counts). In that case (might be the normal case) it has to be accounted for the overdispersion by estimating $\sigma^2$ (i.e. the overdispersion value). Therefore the relative standard error is calculated as:

(a) poisson

$$rse(\mu_s) \approx \sqrt{(Y_0 + Y_1/k^2)} / Y_0 - Y_1/k$$

(b) non-poisson

$$rse(\mu_s) \approx \sqrt{(Y_0 + Y_1/k^2 + \sigma^2(1 + 1/k))} / Y_0 - Y_1/k$$

**Value**

Returns an S4 object of type RLum.Results. Slot data contains a list with the following structure:

- $LxTx.table (data.frame)$
  - $LnLx$
  - $TnTx$
  - $Net_LnLx$
  - $Net_TnTx$
  - $LxTx$
  - $LxTx.Error$

- $calc.parameters (list)$
  - $sigmab.LnTx$
  - $sigmab.TnTx$
  - $k$

**Function version**

0.4.5 (2015-03-04 00:19:53)
Note
The results of this function have been cross-checked with the Analyst (vers. 3.24b). Access to the results object via `get_RLum.Results`.

Author(s)
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
R Luminescence Package Team

References


See Also
`analyse_sar.OSLdata`, `plot_GrowthCurve`, `analyse_sar.CWOSL`

Examples
```r
# load data
data(ExampleData.LxTxOSLData, envir = environment())

# calculate Lx/Tx ratio
results <- calc_OSLxTxRatio(Lx.data, Tx.data, signal.integral = c(1:2),
                               background.integral = c(85:100))

# get results object
get_RLum.Results(results)
```

calc_SourceDoseRate Calculation of the source dose rate via the date of measurement

Description
Calculating the dose rate of the irradiation source via the date of measurement based on: source calibration date, source dose rate, dose rate error. The function returns a data.frame that provides the input argument dose_rate for the function `Second2Gray`. 
Usage

calc_SourceDoseRate(measurement.date, calib.date, calib.dose.rate, calib.error, source.type = "Sr-90", dose.rate.unit = "Gy/s")

Arguments

measurement.date  character (required): date of measurement in "YYYY-MM-DD"
calib.date  character (required): date of source calibration in "YYYY-MM-DD"
calib.dose.rate  numeric (required): dose rate at date of calibration in Gy/s or Gy/min
calib.error  numeric (required): error of dose rate at date of calibration Gy/s or Gy/min
source.type  character (with default): specify irradiation source (Sr-90 or Co-60 or Am-214), see details for further information
dose.rate.unit  character (with default): specify dose rate unit for input (Gy/min or Gy/s), the output is given in Gy/s as valid for the function Second2Gray

Details

Calculation of the source dose rate based on the time elapsed since the last calibration of the irradiation source. Decay parameters assume a Sr-90 beta source.

\[
dose.rate = D_0 \times \exp(-\log(2) / T_{1/2} \times t)
\]

with: \(D_0\) <- calibration dose rate \(T_{1/2}\) <- half-life of the source nuclide (here in days) \(t\) <- time since source calibration (in days) \(\log(2) / T_{1/2}\) equals the decay constant lambda

Information on the date of measurements may be taken from the data’s original .BIN file (using e.g., BINfile <- readBIN2R() and the slot BINfile@METADATA$DATE)

Allowed source types and related values

<table>
<thead>
<tr>
<th>#</th>
<th>Source type</th>
<th>T.1/2</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>Sr-90</td>
<td>28.90 y</td>
<td>NNDC, Brookhaven National Laboratory</td>
</tr>
<tr>
<td>[3]</td>
<td>Co-60</td>
<td>5.274 y</td>
<td>NNDC, Brookhaven National Laboratory</td>
</tr>
</tbody>
</table>

Value

Returns an S4 object of type RLum.Results. Slot data contains a list with the following structure:

$ dose.rate (data.frame)
  .. $ dose.rate
  .. $ dose.rate.error
$ parameters (list)
  .. $ source.type
  .. $ halflife
  .. $ dose.rate.unit
calc_SourceDoseRate

Function version

0.1 (2015-03-04 14:33:28)

Note

#

Author(s)

Margret C. Fuchs, AWI Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

NNDC, Brookhaven National Laboratory (http://www.nndc.gov/)

See Also

Second2Gray

Examples

```r
##(1) Simple function usage
##Basic calculation of the dose rate for a specific date
dose.rate <- calc_SourceDoseRate(measurement.date = "2012-01-27",
calib.date = "2014-12-19",
calib.dose.rate = 0.8438,
calib.error = 0.0019)

##show results
get_RLum.Results(dose.rate)

##(2) Usage in combination with another function (e.g., Second2Gray() )
## load example data
data(ExampleData.DeValues, envir = environment())

## use the calculated variable dose.rate as input argument
## to convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, dose.rate)
```
Function to calculate statistic measures

Description

This function calculates a number of descriptive statistics for De-data, most fundamentally using error-weighted approaches.

Usage

calc_statistics(data, weight.calc = "reciprocal", na.rm = TRUE)

Arguments

data: data.frame or RLum.Results object (required): for data.frame two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot the data sets must be provided as list, e.g. list(data.1, data.2).

weight.calc: character: type of weight calculation. One out of "reciprocal" (weight is 1/error), "square" (weight is 1/error^2).

na.rm: logical (with default): indicating whether NA values should be stripped before the computation proceeds.

Value

Returns a list with weighted and unweighted statistic measures.

Function version

0.1.1 (2015-03-04 17:27:01)

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
R Luminescence Package Team

Examples

```r
## load example data
data(ExampleData.DeValues, envir = environment())

## show a rough plot of the data to illustrate the non-normal distribution
plot_KDE(ExampleData.DeValues$BT998)

## calculate statistics and show output
str(calc_statistics(ExampleData.DeValues$BT998))

## now the same for 10000 normal distributed random numbers with equal errors
x <- as.data.frame(cbind(rnorm(n = 10^5, mean = 0, sd = 1),
```
## Description

Calculate Lx/Tx ratio for a given set of TL curves.

## Usage

```r
calc_TLLxTxRatio(Lx.data.signal, Lx.data.background, Tx.data.signal, Tx.data.background, signal.integral.min, signal.integral.max)
```

## Arguments

- **Lx.data.signal**: data.frame (required): TL data (x = temperature, y = counts) (TL signal)
- **Lx.data.background**: data.frame (optional): TL data (x = temperature, y = counts). If no data are provided no background subtraction is performed.
- **Tx.data.signal**: data.frame (required): TL data (x = temperature, y = counts) (TL test signal)
- **Tx.data.background**: data.frame (optional): TL data (x = temperature, y = counts). If no data are provided no background subtraction is performed.
- **signal.integral.min**: integer (required): channel number for the lower signal integral bound (e.g. `signal.integral.min = 100`)
- **signal.integral.max**: integer (required): channel number for the upper signal integral bound (e.g. `signal.integral.max = 200`)

## Value

Returns an S4 object of type `RLum.Results`. Slot `data` contains a list with the following structure:

- `$ LxTx.table`
  - `.$ LnLx`
  - `.$ LnLx.BG`
- `$ TnTx`
  - `.$ TnTx.BG`
calc_TLLxTxRatio

.. $ Net_LnLx
.. $ Net_LnLx.Error

Function version

0.3 (2015-03-04 00:19:53)

Note

This function has still BETA status!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Christoph Schmidt, University of Bayreuth (Germany),
R Luminescence Package Team

References

-

See Also

RLum.Results, analyse_SAR.TL

Examples

```r
## load package example data
data(ExampleData.BINfileData, envir = environment())

## convert Risoe.BINfileData into a curve object
temp <- Risoe.BINfileData2RLum.Analysis(TL.SAR.Data, pos = 3)

Lx.data.signal <- get_RLum.Analysis(temp, record.id=1)
Lx.data.background <- get_RLum.Analysis(temp, record.id=2)
Tx.data.signal <- get_RLum.Analysis(temp, record.id=3)
Tx.data.background <- get_RLum.Analysis(temp, record.id=4)
signal.integral.min <- 210
signal.integral.max <- 230

output <- calc_TLLxTxRatio(Lx.data.signal,
                            Lx.data.background,
                            Tx.data.signal, Tx.data.background,
                            signal.integral.min, signal.integral.max)

get_RLum.Results(output)
```
Transform a CW-OSL curve into a pHM-OSL curve via interpolation under hyperbolic modulation conditions

Description

This function transforms a conventionally measured continuous-wave (CW) OSL-curve to a pseudo hyperbolic modulated (pHM) curve under hyperbolic modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).

Usage

`cw2pHMi(values, delta)`

Arguments

- `values`: `RLum.Data.Curve` or `data.frame` (required): `RLum.Data.Curve` or `data.frame` with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2]).
- `delta`: `vector` (optional): stimulation rate parameter, if no value is given, the optimal value is estimated automatically (see details). Smaller values of delta produce more points in the rising tail of the curve.

Details

The complete procedure of the transformation is described in Bos & Wallinga (2012). The input `data.frame` consists of two columns: time (t) and count values (CW(t))

Internal transformation steps

1. `log(CW-OSL)` values
2. Calculate t’ which is the transformed time:
   \[ t' = t - \frac{1}{\delta} \times \log(1 + \delta \times t) \]
3. Interpolate CW(t’), i.e. use the `log(CW(t))` to obtain the count values for the transformed time (t’). Values beyond `min(t)` and `max(t)` produce NA values.
4. Select all values for t’ < `min(t)`, i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no NA values and use these values for a linear fit using `lm`.
5. Extrapolate values for t’ < `min(t)` based on the previously obtained fit parameters.
(6) Transform values using

\[ pHM(t) = \left( \frac{\delta \ast t}{1 + \delta \ast t} \right) \ast c \ast CW(t') \]

\[ c = \frac{1 + \delta \ast P}{\delta \ast P} \]

\[ P = length(stimulation \_ period) \]

(7) Combine all values and truncate all values for \( t' > \max(t) \)

*The number of values for \( t' < \min(t) \) depends on the stimulation rate parameter delta. To avoid the production of too many artificial data at the raising tail of the determined pHM curve, it is recommended to use the automatic estimation routine for delta, i.e. provide no value for delta.*

**Value**

The function returns the same data type as the input data type with the transformed curve values.

RLum.Data.Curve

package RLum object with two additional info elements:

- $CW2pHMi.x.t : transformed time values
- $CW2pHMi.method : used method for the production of the new data points

**data.frame** with four columns:

- $x : time
- $y.t : transformed count values
- $x.t : transformed time values
- $method : used method for the production of the new data points

**Function version**

0.2.2 (2015-03-04 18:42:57)

**Note**

According to Bos & Wallinga (2012), the number of extrapolated points should be limited to avoid artificial intensity data. If delta is provided manually and more than two points are extrapolated, a warning message is returned.

The function **approx** may produce some Inf and NaN data. The function tries to manually interpolate these values by calculating the mean using the adjacent channels. If two invalid values are succeeding, the values are removed and no further interpolation is attempted. In every case a warning message is shown.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

References


Further Reading


See Also

CW2pLM, CW2pLMi, CW2pPMi, fit_LMCurve, lm, RLum.Data.Curve

Examples

```r
##(1) - simple transformation

# load CW-OSL curve data
data(ExampleData.CW_OSL_Curve, envir = environment())

# transform values
values.transformed <- CW2pHMi(ExampleData.CW_OSL_Curve)

# plot
plot(values.transformed$x, values.transformed$y, log = "x")

##(2) - load CW-OSL curve from BIN-file and plot transformed values

data(BINfileData)
data(ExampleData.BINfileData) # load BINfile

# sum first CW-OSL curve
curve.ID <- CWOSL.SAR.Data@METADATA["LTYPE"] == "OSL" & curve.ID["ID"]

curve.HIGH <- CWOSL.SAR.Data@METADATA["ID"] == curve.ID["HIGH"]

curve.NPOINTS <- CWOSL.SAR.Data@METADATA["ID"] == curve.ID["NPOINTS"]
```
## Combine curve to data set

```r
curve <- data.frame(x = seq(curve_HIGH/curve_NPOINT, curve_HIGH, by = curve_HIGH/curve_NPOINT),
                     y = unlist(CWOSL.SAR.Data@DATA[curve.ID[1]]))
```

## Transform values

```r
curve.transformed <- CW2pHMi(curve)
```

## Plot curve

```r
plot(curve.transformed$x, curve.transformed$y, log = "x")
```

## Load data

```r
data(ExampleData.CW_OSL_Curve, envir = environment())
values <- CW_Curve.BosWallinga2012
```

## Open plot area

```r
plot(NA, NA,
     xlim = c(0.001, 10),
     ylim = c(0.0000, 1e6),
     ylab = "pseudo OSL (cts/0.01 s)",
     xlab = "t [s]",
     log = "x",
     main = "Fig. 4 - Bos & Wallinga (2012)"
)
```

```r
values.t <- CW2pLMi(values, P = 1/20)
lines(values[1:length(values.t[,1]),1], CW2pLMi(values, P = 1/20)[,2],
      col = "red", lwd = 1.3)
text(0.03, 4500, "LM", col = "red", cex = .8)
```

```r
values.t <- CW2pHMi(values, delta = 40)
lines(values[1:length(values.t[,1]),1], CW2pHMi(values, delta = 40)[,2],
      col = "black", lwd = 1.3)
text(0.005, 3000, "HM", cex = .8)
```

```r
values.t <- CW2pPMi(values, P = 1/10)
lines(values[1:length(values.t[,1]),1], CW2pPMi(values, P = 1/10)[,2],
      col = "blue", lwd = 1.3)
text(0.5, 6500, "PM", col = "blue", cex = .8)
```
Description

Transforms a conventionally measured continuous-wave (CW) curve into a pseudo linearly modulated (pLM) curve using the equations given in Bulur (2000).

Usage

CW2pLM(values)

Arguments

<table>
<thead>
<tr>
<th>values</th>
</tr>
</thead>
<tbody>
<tr>
<td>RLuc.Data.Curve or data.frame (required): RLuc.Data.Curve data object. Alternatively, a data.frame of the measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2]) can be provided.</td>
</tr>
</tbody>
</table>

Details

According to Bulur (2000) the curve data are transformed by introducing two new parameters $P$ (stimulation period) and $u$ (transformed time):

$$P = 2 \times \text{max}(t)$$

$$u = \sqrt{(2 \times t \times P)}$$

The new count values are then calculated by

$$cts^{NEW} = cts(u/P)$$

and the returned data.frame is produced by: `data.frame(u, ctsNEW)`

Value

The function returns the same data type as the input data type with the transformed curve values.

data.frame generic R data structure
RLuc.Data.Curve package RLuc object

Function version

0.4.1 (2015-03-04 18:47:17)

Note

The transformation is recommended for curves recorded with a channel resolution of at least 0.05 s/channel.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team
References


Further Reading


See Also

`CW2pLMi, CW2pLMi, CW2pPMi, fit_LMCurve, lm, RLum.Data.Curve`

The output of the function can be further used for LM-OSL fitting: `CW2pLMi, CW2pHMi, CW2pPMi, fit_LMCurve, RLum.Data.Curve, plot_RLum`

Examples

```r
# read curve from CWOSL.SAR.Data transform curve and plot values
data(ExampleData.BINfileData, envir = environment())

# read id for the 1st OSL curve
id.OSL <- CWOSL.SAR.Data@METADATA[CWOSL.SAR.Data@METADATA[,"LTYPE"] == "OSL","ID"]

# produce x and y (time and count data for the data set)
x <- seq(CWOSL.SAR.Data@METADATA[id.OSL[1],"HIGH"])/CWOSL.SAR.Data@METADATA[id.OSL[1],"NPOINTS"],
     by = CWOSL.SAR.Data@METADATA[id.OSL[1],"HIGH"]/CWOSL.SAR.Data@METADATA[id.OSL[1],"NPOINTS"])
y <- unlist(CWOSL.SAR.Data@DATA[id.OSL[1]]))
values <- data.frame(x,y)

# transform values
values.transformed <- CW2pLM(values)

# plot
plot(values.transformed)
```

---

**CW2pLMi**

Transform a CW-OSL curve into a pLM-OSL curve via interpolation under linear modulation conditions

**Description**

Transforms a conventionally measured continuous-wave (CW) OSL-curve into a pseudo linearly modulated (pLM) curve under linear modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).
Usage

`CW2pLMi(values, P)`

Arguments

- **values** \( \text{RLum.Data.Curve or data.frame (required): RLum.Data.Curve or data.frame with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2])} \)
- **P** \( \text{vector (optional): stimulation time in seconds. If no value is given the optimal value is estimated automatically (see details). Greater values of P produce more points in the rising tail of the curve.} \)

Details

The complete procedure of the transformation is given in Bos & Wallinga (2012). The input data.frame consists of two columns: time (t) and count values (CW(t))

Nomenclature

- \( P = \text{stimulation time (s)} \)
- \( 1/P = \text{stimulation rate (1/s)} \)

Internal transformation steps

1. log(CW-OSL) values
2. Calculate \( t' = 1/2 * 1/P * t^2 \)
3. Interpolate CW(t'), i.e. use the log(CW(t)) to obtain the count values for the transformed time \( t' \). Values beyond \( \min(t) \) and \( \max(t) \) produce NA values.
4. Select all values for \( t' < \min(t) \), i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no NA values and use these values for a linear fit using `lm`.
5. Extrapolate values for \( t' < \min(t) \) based on the previously obtained fit parameters.
6. Transform values using \( pLM(t) = t/P * CW(t') \)
7. Combine values and truncate all values for \( t' > \max(t) \)

The number of values for \( t' < \min(t) \) depends on the stimulation period (P) and therefore on the stimulation rate \( 1/P \). To avoid the production of too many artificial data at the raising tail of the determined pLM curves it is recommended to use the automatic estimation routine for P, i.e. provide no own value for P.
**Value**

The function returns the same data type as the input data type with the transformed curve values.

RLum.Data.Curve

package RLum object with two additional info elements:

$CW2pLMi.x.t : transformed time values
$CW2pLMi.method : used method for the production of the new data points

**Function version**

0.3.1 (2015-03-04 18:48:02)

**Note**

According to Bos & Wallinga (2012) the number of extrapolated points should be limited to avoid artificial intensity data. If $P$ is provided manually and more than two points are extrapolated, a warning message is returned.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

**References**


**Further Reading**


**See Also**

CW2pLM, CW2pHMi, CW2pPMi, fit_LMCurve, RLum.Data.Curve

**Examples**

```r
#(1)
#load CW-OSL curve data
```
Transform a CW-OSL curve into a pPM-OSL curve via interpolation under parabolic modulation conditions

**Description**

Transforms a conventionally measured continuous-wave (CW) OSL-curve into a pseudo parabolic modulated (pPM) curve under parabolic modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).
Usage

\texttt{CW2pPMi(values, P)}

Arguments

\begin{itemize}
  \item \texttt{values} \texttt{RLum.Data.Curve} or \texttt{data.frame} \texttt{(required): RLum.Data.Curve} or \texttt{data.frame} with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2])
  \item \texttt{P} \texttt{vector} \texttt{(optional):} stimulation period in seconds. If no value is given, the optimal value is estimated automatically (see details). Greater values of P produce more points in the rising tail of the curve.
\end{itemize}

Details

The complete procedure of the transformation is given in Bos & Wallinga (2012). The input \texttt{data.frame} consists of two columns: time (t) and count values (CW(t))

Nomenclature

\begin{align*}
P &= \text{stimulation time (s)} \\
1/P &= \text{stimulation rate (1/s)}
\end{align*}

Internal transformation steps

1. \text{log}(\text{CW-OSL}) \text{ values}

2. Calculate \( t' \) which is the transformed time:

\[ t' = (1/3) \times (1/P^2) t^3 \]

3. Interpolate \( CW(t') \), i.e. use the \text{log}(CW(t)) to obtain the count values for the transformed time \( (t') \). Values beyond \text{min}(t) and \text{max}(t) produce \text{NA} values.

4. Select all values for \( t' < \text{min}(t) \), i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no \text{NA} values and use these values for a linear fit using \texttt{lm}.

5. Extrapolate values for \( t' < \text{min}(t) \) based on the previously obtained fit parameters. The extrapolation is limited to two values. Other values at the beginning of the transformed curve are set to 0.

6. Transform values using:

\[ pLM(t) = t^2/P^2 \times CW(t') \]

7. Combine all values and truncate all values for \( t' > \text{max}(t) \)
The number of values for $t' < \min(t)$ depends on the stimulation period $p$. To avoid the production of too many artificial data at the raising tail of the determined $p$PM curve, it is recommended to use the automatic estimation routine for $p$, i.e. provide no value for $p$.

Value

The function returns the same data type as the input data type with the transformed curve values.

RLum.Data.Curve

package RLum object with two additional info elements:

$CW2pPMi.x.t$ : transformed time values
$CW2pPMi.method$ : used method for the production of the new data points

Data.frame with four columns:

$x$ : time
$y.t$ : transformed count values
$x.t$ : transformed time values
$method$ : used method for the production of the new data points

Function version

0.2.1 (2015-03-04 18:48:47)

Note

According to Bos & Wallinga (2012), the number of extrapolated points should be limited to avoid artificial intensity data. If $p$ is provided manually, not more than two points are extrapolated.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

References


Further Reading


See Also


Examples

```r
###(1)
# load CW-OSL curve data
data(ExampleData.CW_OSL_Curve, envir = environment())

# transform values
values.transformed <- CW2pPMi(ExampleData.CW_OSL_Curve)

# plot
plot(values.transformed$x, values.transformed$y, log = "x")

###(2) - produce Fig. 4 from Bos & Wallinga (2012)

# load data
data(ExampleData.CW_OSL_Curve, envir = environment())
values <- CW_Curve.BosWallinga2012

# open plot area
plot(NA, NA,
    xlim = c(0.001, 10),
    ylim = c(0, 8000),
    ylab = "pseudo OSL (cts/0.01 s)",
    xlab = "t [s]",
    log = "x",
    main = "Fig. 4 - Bos & Wallinga (2012)"
)

values.t <- CW2pLMi(values, P = 1/20)
lines(values[1:length(values.t[,1]),2], CW2pLMi(values, P = 1/20)[,2],
      col = "red", lwd = 1.3)
text(0.03, 4500, "LM", col = "red", cex = .8)

values.t <- CW2pHMi(values, delta = 40)
lines(values[1:length(values.t[,1]),1], CW2pHMi(values, delta = 40)[,2],
      col = "black", lwd = 1.3)
text(0.005, 3000, "HM", cex = .8)

values.t <- CW2pPMi(values, P = 1/10)
lines(values[1:length(values.t[,1]),1], CW2pPMi(values, P = 1/10)[,2],
      col = "blue", lwd = 1.3)
text(0.5, 6500, "PM", col = "blue", cex = .8)
```
ExampleData.BINfileData

Example data from a SAR OSL and SAR TL measurement for the package Luminescence

Description
Example data from a SAR OSL and TL measurement for package Luminescence directly extracted from a Risoe BIN-file and provided in an object of type 

Usage
ExampleData.BINfileData

Format
CWOSL.SAR.Data: SAR OSL measurement data
TL.SAR.Data: SAR TL measurement data

Each class object contains two slots: (a) METADATA is a data.frame with all metadata stored in the BIN file of the measurements and (b) DATA contains a list of vectors of the measured data (usually count values).

Version
0.1

Source
CWOSL.SAR.Data

Lab: Luminescence Laboratory Bayreuth
Lab-Code: BT607
Location: Saxony/Germany
Material: Middle grain quartz measured on aluminum cups on a Risoe TL/OSL DA-15 reader
Reference: unpublished

TL.SAR.Data

Lab: Luminescence Laboratory of Cologne
Lab-Code: LP1_5
Location: Spain
Material: Flint
Setup: Risoe TL/OSL DA-20 reader
(Filter: Semrock Brightline, HC475/50, N2, unpolished steel discs)
Reference: unpublished
Remarks: dataset limited to one position

References

**CWOSL.SAR.Data**: unpublished data

**TL.SAR.Data**: unpublished data

Examples

```r
# show first 5 elements of the METADATA and DATA elements in the terminal
data(ExampleData.BINfileData, envir = environment())
CWOSL.SAR.Data@METADATA[1:5,]
CWOSL.SAR.Data@DATA[1:5]
```

Data frame containing CW-OSL curve data (time, counts)

Usage

```r
data(ExampleData.CW_OSL_Curve)
```

Format

- Data frame with 1000 observations on the following 2 variables:
  - `x`: a numeric vector, time
  - `y`: a numeric vector, counts

Details

see source

Source

**ExampleData.CW_OSL_Curve**

- **Lab**: Luminescence Laboratory Bayreuth
- **Lab-Code**: BT607
- **Location**: Saxony/Germany
- **Material**: Middle grain quartz measured on aluminum cups on a Risoe TL/OSL DA-15 reader.
- **Reference**: unpublished data
**CW_Curve.BosWallinga2012**

Lab: Netherlands Centre for Luminescence Dating (NCL)
Lab-Code: NCL-2108077
Location: Guadalentin Basin, Spain
Material: Coarse grain quartz
Reference: Bos & Wallinga (2012) and Baartman et al. (2011)

**References**


**Examples**

```r
data(ExampleData.CW_OSL_Curve, envir = environment())
plot(ExampleData.CW_OSL_Curve)
```

---

**ExampleData.DeValues**  
*Example De data sets for the package Luminescence*

**Description**

Equivalent dose (De) values measured for a fine grain quartz sample from a loess section in Rottewitz (Saxony/Germany) and for a coarse grain quartz sample from a fluvial deposit in the rock shelter of Cueva Anton (Murcia/Spain).

**Usage**

ExampleData.DeValues

**Format**

A list with two elements, each containing a two column data.frame:

$BT998: De and De error values for a fine grain quartz sample from a loess section in Rottewitz.

$CA1: Single grain De and De error values for a coarse grain quartz sample from a fluvial deposit in the rock shelter of Cueva Anton

**Source**

BT998
Lab: Luminescence Laboratory Bayreuth
Lab-Code: BT998
Location: Rottewitz (Saxony/Germany)
Material: Fine grain quartz measured on aluminum discs on a Risoe TL/OSL DA-15 reader
Units: Values are given in seconds
Dose Rate: Dose rate of the beta-source at measurement ca. 0.0438 Gy/s +/- 0.0019 Gy/s
Measurement Date: 2012-01-27

CA1
Lab: Cologne Luminescence Laboratory (CLL)
Lab-Code: C-L2941
Location: Cueva Anton (Murcia/Spain)
Material: Coarse grain quartz (200-250 microns) measured on single grain discs on a Risoe TL/OSL DA-20 reader
Units: Values are given in Gray
Measurement Date: 2012

References

BT998
Unpublished data

CA1

Examples

```r
##(1) plot values as histogram
data(ExampleData.DeValues, envir = environment())
plot_Histogram(ExampleData.DeValues$BT998, xlab = "De [s]")

##(2) plot value as histogram (with Second to Gray conversion)
data(ExampleData.DeValues, envir = environment())
De.values <- Second2Gray(ExampleData.DeValues$BT998,
dose.rate = c(0.0438, 0.0019),
method = "gaussian")
plot_Histogram(De.values, xlab = "De [Gy]")
```
ExampleData.FittingLM  Example data for fit_LMCurve() in the package Luminescence

Description

Linearly modulated (LM) measurement data from a quartz sample from Norway including background measurement. Measurements carried out in the luminescence laboratory at the University of Bayreuth.

Usage

ExampleData.FittingLM

Format

Two objects (data.frames) with two columns (time and counts).

Source

Lab: Luminescence Laboratory Bayreuth
Lab-Code: BT900
Location: Norway
Material: Beach deposit, coarse grain quartz measured on aluminum discs on a Risoe TL/OSL DA-15 reader

References


Examples

```r
# show LM data
data(ExampleData.FittingLM, envir = environment())
plot(values.curve, log="x")
```

ExampleData.LxTxData  Example Lx/Tx data from CW-OSL SAR measurement

Description

LxTx data from a SAR measurement for the package Luminescence.
Usage

ExampleData.LxTxData

Format

A data.frame with 4 columns (Dose, LxTx, LxTx.Error, TnTx).

Source

Lab: Luminescence Laboratory Bayreuth
Lab-Code: BT607
Location: Ostrau (Saxony-Anhalt/Germany)
Material: Middle grain (38-63 \(\mu\)m) quartz measured on a Risoe TL/OSL DA-15 reader.

References

unpublished data

Examples

```r
# plot Lx/Tx data vs dose [s]
data(ExampleData.LxTxData, envir = environment())
plot(LxTxData$Dose,LxTxData$LxTx)
```

ExampleData.LxTxOSLData

---

Example Lx and Tx curve data from an artificial OSL measurement

---

Description

Lx and Tx data of continuous wave (CW-) OSL signal curves.

Usage

ExampleData.LxTxOSLData.RData

Format

Two data.frames containing time and count values.

Source

Arbitrary OSL measurement.
ExampleData.RLum.Analysis

References

unpublished data

Examples

```r
# load data
data(ExampleData.LxTxOSLData, envir = environment())

# plot data
plot(Lx.data)
plot(Tx.data)
```

ExampleData.RLum.Analysis

*Example data as RLum.Analysis objects*

Description

Collection of different RLum.Analysis objects for protocol analysis.

Usage

ExampleData.RLum.Analysis

Format

IRSAR.RF.Data: IRSAR.RF.Data on coarse grain feldspar

Each object contains data needed for the given protocol analysis.

Version

0.1

Source

IRSAR.RF.Data

These data were kindly provided by Tobias Lauer and Matthias Krbetschek.

<table>
<thead>
<tr>
<th>Lab:</th>
<th>Luminescence Laboratory TU Bergakademie Freiberg</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lab-Code:</td>
<td>ZEU/SA1</td>
</tr>
<tr>
<td>Location:</td>
<td>Zeuchfeld (Zeuchfeld Sandur; Saxony-Anhalt/Germany)</td>
</tr>
<tr>
<td>Material:</td>
<td>K-feldspar (130-200 ( \mu )m)</td>
</tr>
<tr>
<td>Reference:</td>
<td>Kreutzer et al. (2014)</td>
</tr>
</tbody>
</table>
References

IRSAR.RF.Data


Examples

```r
# load data
data(ExampleData.RLum.Analysis, envir = environment())

# plot data
plot_RLum(IRSAR.RF.Data)
```

ExampleData.RLum.Data.Image

*Example data as RLum.Data.Image objects*

Description

Measurement of Princeton Instruments camera imported with the function `readSPE2R` to R to produce an `RLum.Data.Image` object.

Usage

ExampleData.RLum.Data.Image

Format

Object of class `RLum.Data.Image`

Version

0.1

Source

ExampleData.RLum.Data.Image

These data were kindly provided by Regina DeWitt.

Lab.: Department of Physics, East-Carolina University, NC, USA
Lab-Code: -
Location: -
Material: -
Reference: -
Image data is a measurement of fluorescent ceiling lights with a cooled Princeton Instruments (TM) camera fitted on Risoe DA-20 TL/OSL reader.

References

Examples

```r
# load data
data(ExampleData.RLum.Data.Image, envir = environment())

# plot data
plot_RLum(ExampleData.RLum.Data.Image)
```

Example data for a SAR OSL measurement and a TL spectrum using a lexsg reader

Description

Example data from a SAR OSL measurement and a TL spectrum for package Luminescence imported from a Freiberg Instruments XSYG file using the function `readXSYG2R`.

Usage

ExampleData.XSYG

Format

**OSL.SARMeasurement**: SAR OSL measurement data

The data contain two elements: (a) `Sequence.Header` is a data.frame with metadata from the measurement,(b) `Sequence.Object` contains an `RLum.Analysis` object for further analysis.

**TL.Spectrum**: TL spectrum data

`RLum.Data.Spectrum` object for further analysis. The spectrum was cleaned from cosmic-rays using the function `apply_CosmicRayRemoval`. Note that no quantum efficiency calibration was performed.

Version

0.1
### Source

**OSL.SARMeasurement**

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<td>no code</td>
</tr>
<tr>
<td>Location:</td>
<td>not specified</td>
</tr>
<tr>
<td>Material:</td>
<td>Coarse grain quartz</td>
</tr>
<tr>
<td></td>
<td>on steel cups on lexsyg research reader</td>
</tr>
<tr>
<td>Reference:</td>
<td>unpublished</td>
</tr>
</tbody>
</table>

**TL.Spectrum**

<table>
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<tr>
<td>Lab-Code:</td>
<td>BT753</td>
</tr>
<tr>
<td>Location:</td>
<td>Dolni Vestonice/Czech Republic</td>
</tr>
<tr>
<td>Material:</td>
<td>Fine grain polymineral</td>
</tr>
<tr>
<td></td>
<td>on steel cups on lexsyg research reader</td>
</tr>
<tr>
<td>Reference:</td>
<td>Fuchs et al., 2013</td>
</tr>
<tr>
<td>Spectrum:</td>
<td>Integration time 19 s, channel time 20 s</td>
</tr>
<tr>
<td>Heating:</td>
<td>1 K/s, up to 500 deg. C</td>
</tr>
</tbody>
</table>

### References

Unpublished data measured to serve as example data for that package. Location origin of sample BT753 is given here:


### See Also

readXSYG2R, RLum.Analysis.


plot_RLum.Analysis, plot_RLum.Data.Spectrum

### Examples

```r
## show data
data(ExampleData.XSYG, envir = environment())

## show $Sequence.Object
OSL.SARMasurement$Sequence.Object

## grep OSL curves and plot the first curve
OSLcurve <- get_RLum.Analysis(OSL.SARMasurement$Sequence.Object,
                               curr=1)
```
extract_IrradiationTimes

Extract irradiation times from an XSYG file

Description

Extracts irradiation times, dose and times since last irradiation, from a Freiberg Instruments XSYG-file. These information can be further used to update an existing BINX-file.

Usage

extract_IrradiationTimes(file.XSYG, file.BINX, recordType = c("irradiation (NA)", "IRSL (UVVIS)", "OSL (UVVIS)", "TL (UVVIS)"), txtProgressbar = TRUE)

Arguments

file.XSYG character (required): path and file name of the XSYG file.
file.BINX character (optional): path and file name of an existing BINX-file. If a file name is provided the file will be updated with the information from the XSYG file in the same folder as the original BINX-file. Note: The XSYG and the BINX-file have to be originate from the same measurement!
recordType character (with default): select relevant curves types from the XSYG file. As the XSYG-file format comprises much more information than usually needed for routine data analysis and allowed in the BINX-file format, only the relevant
curves are selected by using the function `get_RLum.Analysis`. The argument
recordType works as described for this function.

Note: A wrong selection will causes a function error. Please change this argu-
ment only if you have reasons to do so.

txtProgressBar logical (with default): enables TRUE or disables FALSE the progression bars
during import and export

Details

The function was written to compensate missing information in the BINX-file output of Freiberg
Instruments lexsyg readers. As all information are available within the XSYG-file anyway, these in-
formation can be extracted and used for further analysis or/and to stored in a new BINX-file, which
can be further used by other software, e.g. Analyst (Geoff Duller).

Typical application example: g-value estimation from fading measurements using the Analyst or
any other self written script.

Beside the some simple data transformation steps the function applies the functions `readXSYG2R`,
`readBIN2R`, `writeR2BIN` for data import and export.

Value

An `RLum.Results` object is returned with the following structure:

.. $irr.times (data.frame)

If a BINX-file path and name is set, the output will be additionally transferred to a new BINX-file
with the function name as suffix. For the output the path of the input BINX-file itself is used.

Function version

0.1 (2015-03-23 12:56:18)

Note

The produced output object contains still the irradiation steps to keep the output transparent. How-
ever, for the BINX-file export this steps are removed as the BINX-file format description does not
allow irradiations as separat sequences steps.

Know issue: The 'fading correction' menu in the Analyst will not work appear with the produced
BIN/BINX-file due to hidden bits, which are not reproduced by the function `writeR2BIN()`.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team
References


See Also

RLum.Results, Risoe.BINfileData, readXSYG2R, readBIN2R, writeR2BIN

Examples

```r
## (1) - example for your own data
##
## set files and run function
##
## file.XSYG <- file.choose()
## file.BINX <- file.choose()
##
## output <- extract_IrradiationTimes(file.XSYG = file.XSYG, file.BINX = file.BINX)
## get_RLum.Results(output)
##
## export results additionally to a CSV.file in the same directory as the XSYG-file
##
## write.table(x = get_RLum.Results(output),
##
## file = paste0(file.BINX,"_extract_IrradiationTimes.csv"),
##
## sep = ",",
##
## row.names = FALSE)
```

---

**fit CWCurve**  

*Nonlinear Least Squares Fit for CW-OSL curves [beta version]*

**Description**

The function determines the weighted least-squares estimates of the component parameters of a CW-OSL signal for a given maximum number of components and returns various component parameters. The fitting procedure uses the `nls` function with the `port` algorithm.

**Usage**

```r
fit_CWCurve(values, n.components.max, fit.failure_threshold = 3,
            fit.trace = FALSE, fit.calcError = FALSE, LED.power = 36,
            LED.wavelength = 470, cex.global = 0.6, sample_code = "Default",
            output.path, output.terminal = TRUE, output.terminalAdvanced = TRUE,
            output.plot = TRUE, ...)
```
Arguments

values  
RLum.Data.Curve or data.frame (required): x, y data of measured values (time and counts). See examples.

n.components.max  
vector (optional): maximum number of components that are to be used for fitting. The upper limit is 7.

fit.failure_threshold  
vector (with default): limits the failed fitting attempts.

fit.trace  
logical (with default): traces the fitting process on the terminal.

fit.calcError  
logical (with default): calculate 1-sigma error range of components using confint

LED.power  
numeric (with default): LED power (max.) used for intensity ramping in mW/cm^2. 
Note: The value is used for the calculation of the absolute photoionisation cross section.

LED.wavelength  
numeric (with default): LED wavelength used for stimulation in nm. 
Note: The value is used for the calculation of the absolute photoionisation cross section.

cex.global  
numeric (with default): global scaling factor.

sample_code  
character (optional): sample code used for the plot and the optional output table (mtext).

output.path  
character (optional): output path for table output containing the results of the fit. The file name is set automatically. If the file already exists in the directory, the values are appended.

output.terminal  
logical (with default): terminal output with fitting results.

output.terminalAdvanced  
logical (with default): enhanced terminal output. Requires output.terminal = TRUE. If output.terminal = FALSE no advanced output is possible.

output.plot  
logical (with default): returns a plot of the fitted curves.

...  
further arguments and graphical parameters passed to plot.

Details

Fitting function

The function for the CW-OSL fitting has the general form:

\[ y = I_0_1 \times \lambda_1 \times exp(-\lambda_1 \times x) + \ldots + I_0_i \times \lambda_i \times exp(-\lambda_i \times x) \]

where \( 1 < i < 8 \)

and \( \lambda \) is the decay constant and \( N_0 \) the initial number of trapped electrons.
(for the used equation cf. Boetter-Jensen et al., 2003)

Start values
Start values are estimated automatically by fitting a linear function to the logarithmized input data set. Currently, there is no option to manually provide start parameters.

**Goodness of fit**

The goodness of the fit is given as pseudoR^2 value (pseudo coefficient of determination). According to Lave (1970), the value is calculated as:

\[ pseudoR^2 = 1 - \frac{RSS}{TSS} \]

where \( RSS \) = Residual Sum of Squares
and \( TSS \) = Total Sum of Squares

**Error of fitted component parameters**

The 1-sigma error for the components is calculated using the function `confint`. Due to considerable calculation time, this option is deactivated by default. In addition, the error for the components can be estimated by using internal R functions like `summary`. See the `nls` help page for more information.

*For details on the nonlinear regression in R, see Ritz & Streibig (2008).*

**Value**

- plot: (optional) the fitted CW-OSL curves are returned as plot.
- table: (optional) an output table (*.csv) with parameters of the fitted components is provided if the `output.path` is set.
- `RLum.Results` object: beside the plot and table output options, an `RLum.Results` object is returned.
- `fit`: an `nls` object (\$fit) for which generic R functions are provided, e.g. `summary`, `confint`, `profile`. For more details, see `nls`.
- output.table: a `data.frame` containing the summarised parameters including the error component.contribution.matrix: matrix containing the values for the component to sum contribution plot (\$component.contribution.matrix).

Matrix structure:
Column 1 and 2: time and \texttt{rev(time)} values
Additional columns are used for the components, two for each component, containing I0 and n0. The last columns \texttt{cont.} provide information on the relative component contribution for each time interval including the row sum for this values.

**Function version**

0.4.4 (2015-03-04 00:19:53)
Note

Beta version - This function has not been properly tested yet and should therefore not be used for publication purposes!

The pseudo-R^2 may not be the best parameter to describe the goodness of the fit. The trade off between the n.components and the pseudo-R^2 value is currently not considered.

The function **does not** ensure that the fitting procedure has reached a global minimum rather than a local minimum!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

R Luminescence Package Team

References


See Also

`fit_LMCurve, plot.nls, RLum.Data.Curve, RLum.Results, get_RLum.Results`

Examples

```r
# load data
data(ExampleData.CW_OSL_Curve, envir = environment())

# fit data
fit <- fit_CWCurve(values = ExampleData.CW_OSL_Curve,
                   main = "CW Curve Fit",
                   n.components.max = 4,
                   log = "x")
```

---

**fit_LMCurve**  
*Nonlinear Least Squares Fit for LM-OSL curves*
Description

The function determines weighted nonlinear least-squares estimates of the component parameters of an LM-OSL curve (Bulur 1996) for a given number of components and returns various component parameters. The fitting procedure uses the function \texttt{nls} with the \texttt{port} algorithm.

Usage

\begin{verbatim}
fit_LMCurve(values, values.bg, n.components = 3, start_values, 
input.dataType = "LM", sample_code = "", sample_ID = "", 
LED.power = 36, LED.wavelength = 470, cex.global = 0.8, fit.trace = FALSE, 
fit.advanced = FALSE, fit.calcError = FALSE, bg.subtraction = "polynomial", 
output.path, output.terminal = TRUE, output.terminaladvanced = TRUE, 
output.plot = TRUE, output.plotBG = FALSE, ...)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{values} \hspace{1cm} \texttt{RLum.Data.Curve} or \texttt{data.frame} (required): x,y data of measured values (time and counts). See examples.
\item \texttt{values.bg} \hspace{1cm} \texttt{RLum.Data.Curve} or \texttt{data.frame} (optional): x,y data of measured values (time and counts) for background subtraction.
\item \texttt{n.components} \hspace{1cm} \texttt{integer} (with default): fixed number of components that are to be recognised during fitting (min = 1, max = 7).
\item \texttt{start_values} \hspace{1cm} \texttt{data.frame} (optional): start parameters for lm and xm data for the fit. If no start values are given, an automatic start value estimation is attempted (see details).
\item \texttt{input.dataType} \hspace{1cm} \texttt{character} (with default): alter the plot output depending on the input data: "LM" or "pLM" (pseudo-LM). See: \texttt{CW2pLM}
\item \texttt{sample_code} \hspace{1cm} \texttt{character} (optional): sample code used for the plot and the optional output table (mtext).
\item \texttt{sample_ID} \hspace{1cm} \texttt{character} (optional): additional identifier used as column header for the table output.
\item \texttt{LED.power} \hspace{1cm} \texttt{numeric} (with default): LED power (max.) used for intensity ramping in mW/cm^2. \textbf{Note:} This value is used for the calculation of the absolute photoionisation cross section.
\item \texttt{LED.wavelength} \hspace{1cm} \texttt{numeric} (with default): LED wavelength in nm used for stimulation. \textbf{Note:} This value is used for the calculation of the absolute photoionisation cross section.
\item \texttt{cex.global} \hspace{1cm} \texttt{numeric} (with default): global scaling factor.
\item \texttt{fit.trace} \hspace{1cm} \texttt{logical} (with default): traces the fitting process on the terminal.
\item \texttt{fit.advanced} \hspace{1cm} \texttt{logical} (with default): enables advanced fitting attempt for automatic start parameter recognition. Works only if no start parameters are provided. \textbf{Note:} It may take a while.
\item \texttt{fit.calcError} \hspace{1cm} \texttt{logical} (with default): calculate 1-sigma error range of components using \texttt{confint}.
\item \texttt{bg.subtraction} \hspace{1cm} \texttt{character} (with default): specifies method for background subtraction (polynomial, linear, channel, see Details). \textbf{Note:} requires input for \texttt{values.bg}.
\end{itemize}
output.path character (optional): output path for table output containing the results of the fit. The file name is set automatically. If the file already exists in the directory, the values are appended.

output.terminal logical (with default): terminal output with fitting results.

output.terminaladvanced logical (with default): enhanced terminal output. Requires output.terminal = TRUE. If output.terminal = FALSE no advanced output is possible.

output.plot logical (with default): returns a plot of the fitted curves.

output.plotBG logical (with default): returns a plot of the background values with the fit used for the background subtraction.

... Further arguments that may be passed to the plot output, e.g. xlab, xlab, main, log.

Details

Fitting function

The function for the fitting has the general form:

$$y = (\exp(0.5) \cdot Im_1 \cdot x / xm_1) \cdot \exp(-x^2 / (2 \cdot xm_1^2)) + \ldots + (\exp(0.5) \cdot Im_i \cdot x / xm_i) \cdot \exp(-x^2 / (2 \cdot xm_i^2))$$

where $1 < i < 8$

This function and the equations for the conversion to $b$ (detrapping probability) and $n_0$ (proportional to initially trapped charge) have been taken from Kitis et al. (2008):

$$xm_i = \sqrt{\text{max}(t) / b_i}$$

$$Im_i = \exp(-0.5) n_0 / Xm_i$$

Background subtraction

Three methods for background subtraction are provided for a given background signal (values.bg). polynomial: default method. A polynomial function is fitted using glm and the resulting function is used for background subtraction:

$$y = a \cdot x^4 + b \cdot x^3 + c \cdot x^2 + d \cdot x + e$$

linear: a linear function is fitted using glm and the resulting function is used for background subtraction:

$$y = a \cdot x + b$$

channel: the measured background signal is subtracted channelwise from the measured signal.

Start values
The choice of the initial parameters for the nls-fitting is a crucial point and the fitting procedure may mainly fail due to ill chosen start parameters. Here, three options are provided:

(a) If no start values (start_values) are provided by the user, a cheap guess is made by using the detrapping values found by Jain et al. (2003) for quartz for a maximum of 7 components. Based on these values, the pseudo start parameters \( x_m \) and \( I_m \) are recalculated for the given data set. In all cases, the fitting starts with the ultra-fast component and (depending on \( n \) components) steps through the following values. If no fit could be achieved, an error plot (for output.plot = TRUE) with the pseudo curve (based on the pseudo start parameters) is provided. This may give the opportunity to identify appropriate start parameters visually.

(b) If start values are provided, the function works like a simple nls fitting approach.

(c) If no start parameters are provided and the option fit.advanced = TRUE is chosen, an advanced start parameter estimation is applied using a stochastical attempt. Therefore, the recalculated start parameters (a) are used to construct a normal distribution. The start parameters are then sampled randomly from this distribution. A maximum of 100 attempts will be made. **Note:** This process may be time consuming.

**Goodness of fit**

The goodness of the fit is given by a pseudoR^2 value (pseudo coefficient of determination). According to Lave (1970), the value is calculated as:

\[
\text{pseudoR}^2 = 1 - \frac{RSS}{TSS}
\]

where \( RSS = \text{Residual}^\text{Sum}^\text{of}^\text{Squares} \)
and \( TSS = \text{Total}^\text{Sum}^\text{of}^\text{Squares} \)

**Error of fitted component parameters**

The 1-sigma error for the components is calculated using the function confint. Due to considerable calculation time, this option is deactived by default. In addition, the error for the components can be estimated by using internal R functions like summary. See the nls help page for more information.

*For more details on the nonlinear regression in R, see Ritz & Streibig (2008).*

**Value**

- **plot** (optional) various types of plots are returned. For details see above.
- **table** (optional) an output table (*.csv) with the fitted components is provided if the output.path is set.
- **list object** beside the plot and table output, a list is returned. The list contains:
  (a) an nls object ($fit) for which generic R functions are provided, e.g. summary, confint, profile. For more details, see nls.
  (b) a data.frame containing the summarised parameters including the error ($output.table).
  (c) a matrix containing the values for the component to sum contribution plot ($component.contribution.matrix).
Matrix structure:
Column 1 and 2: time and \text{rev(time)} values
Additional columns are used for the components, two for each component, containing I_0 and n_0. The last columns contain information on the relative component contribution for each time interval including the row sum for this values.

**Function version**

0.2.16 (2015-03-10 16:11:27)

**Note**

The pseudo-R^2 may not be the best parameter to describe the goodness of the fit. The trade off between the \(n\) components and the pseudo-R^2 value currently remains unconsidered.

The function **does not** ensure that the fitting procedure has reached a global minimum rather than a local minimum! In any case of doubt, the use of manual start values is highly recommended.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

**References**


**See Also**

`fit_CWCurve`, `plot`, `nls`

**Examples**

```r
#(1) fit LM data without background subtraction
data(ExampleData.FittingLM, envir = environment())
fit_LMCurve(values = values.curve, n.components = 3, log = "x")
```
get_layout

Collection of layout definitions

Description

This helper function returns a list with layout definitions for homogeneous plotting.

Usage

get_layout(layout)

Arguments

- **layout**: character or list object (required): name of the layout definition to be returned. If name is provided the respective definition is returned. One of the following supported layout definitions is possible: "default", "journal.1", "small", "empty". User-specific layout definitions must be provided as a list object of predefined structure, see details.

Details

The easiest way to create a user-specific layout definition is perhaps to create either an empty or a default layout object and fill/modify the definitions (user.layout <- get_layout(data = "empty")).

Value

A list object with layout definitions for plot functions.

Function version

0.1 (2015-03-04 00:19:53)
get_RLum

Author(s)
Michael Dietze, GFZ Potsdam (Germany)
R Luminescence Package Team

Examples

```r
## read example data set
data(ExampleData.DeValues, envir = environment())

## show structure of the default layout definition
layout.default <- get_layout(layout = "default")
str(layout.default)

## show colour definitions for Abanico plot, only
layout.default$abanico$colour

## set Abanico plot title colour to orange
layout.default$abanico$colour$main <- "orange"

## create Abanico plot with modified layout definition
plot_AbanicoPlot(data = ExampleData.DeValues, 
                 layout = layout.default)

## create Abanico plot with predefined layout "journal"
plot_AbanicoPlot(data = ExampleData.DeValues, 
                 layout = "journal")
```

get_RLum  General accessor function for RLum S4 class objects

Description

Function calls object-specific get functions for RLum S4 class objects.

Usage

get_RLum(object, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>RLum (required): S4 object of class RLum</td>
</tr>
<tr>
<td>...</td>
<td>further arguments that one might want to pass to the specific get function</td>
</tr>
</tbody>
</table>

Details

The function provides a generalised access point for specific RLum objects. Depending on the input object, the corresponding get function will be selected. Allowed arguments can be found in the documentations of each get function.
get_RLum

<table>
<thead>
<tr>
<th>object</th>
<th>corresponding get function</th>
</tr>
</thead>
<tbody>
<tr>
<td>RLum.Analysis</td>
<td>get_RLum.Analysis</td>
</tr>
<tr>
<td>RLum.Results</td>
<td>get_RLum.Results</td>
</tr>
</tbody>
</table>

**Value**

Return is the same as input objects as provided in the list.

**Function version**

0.1 (2015-03-04 14:39:52)

**Note**

-

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

**References**

-

**See Also**


**Examples**

```r
##Example based using data and from the calc_CentralDose() function

##load example data
data(ExampleData.DeValues, envir = environment())

##apply the central dose model 1st time
temp1 <- calc_CentralDose(ExampleData.DeValues$CA1)

##get results and store them in a new object
temp.get<- get_RLum(object = temp1)
```
merge_Risoe.BINfileData

merge_Risoe.BINfileData

Merge Risoe.BINfileData objects or Risoe BIN-files

Description

Function allows merging Risoe BIN/BINX files or Risoe.BINfileData objects.

Usage

```r
merge_Risoe.BINfileData(input.objects, output.file, keep.position.number = FALSE, position.number.append.gap = 0)
```

Arguments

- `input.objects` character or `Risoe.BINfileData` (required): Character vector with path and files names (e.g. `input.objects = c("path/file1.bin", "path/file2.bin")`) or `Risoe.BINfileData` objects (e.g. `input.objects = c(object1, object2)`) 
- `output.file` character (optional): File output path and name. If no value is given, a `Risoe.BINfileData` is returned instead of a file.
- `keep.position.number` logical (with default): Allows keeping the original position numbers of the input objects. Otherwise the position numbers are recalculated.
- `position.number.append.gap` integer (with default): Set the position number gap between merged BIN-file sets, if the option `keep.position.number = FALSE` is used. See details for further information.

Details

The function allows merging different measurements to one file or one object. The record IDs are recalculated for the new object. Other values are kept for each object. The number of input objects is not limited.

- `position.number.append.gap` option

If the option `keep.position.number = FALSE` is used, the position numbers of the new data set are recalculated by adding the highest position number of the previous data set to the each position number of the next data set. For example: The highest position number is 48, then this number will be added to all other position numbers of the next data set (e.g. 1 + 48 = 49)

However, there might be cases where an additional addend (summand) is needed before the next position starts. Example:
merge_Risoe.BINfileData

Position number set (A): 1, 3, 5, 7
Position number set (B): 1, 3, 5, 7

With no additional summand the new position numbers would be: 1, 3, 5, 7, 8, 9, 10, 11. That might be unwanted. Using the argument position.number.append.gap = 1 it will become: 1, 3, 5, 7, 9, 11, 13, 15, 17.

Value

Returns a file or a Risoe.BINfileData object.

Function version

0.2.2 (2015-03-04 12:43:39)

Note

The validity of the output objects is not further checked.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References


See Also

Risoe.BINfileData, readBIN2R, writeR2BIN

Examples

```r
## merge two objects
data(ExampleData.BINfileData, envir = environment())

object1 <- CWOSL.SAR.Data
object2 <- CWOSL.SAR.Data

object.new <- merge_Risoe.BINfileData(c(object1, object2))
```
merge_RLum

---

**merge_RLum**  
*General merge function for RLum S4 class objects*

---

**Description**

Function calls object-specific merge functions for RLum S4 class objects.

**Usage**

`merge_RLum(objects, ...)`

**Arguments**

- `objects`  
  *list of RLum (required)*: list of S4 object of class RLum
- `...`  
  further arguments that one might want to pass to the specific merge function

**Details**

The function provides a generalised access point for merge specific RLum objects. Depending on the input object, the corresponding merge function will be selected. Allowed arguments can be found in the documentations of each merge function.

<table>
<thead>
<tr>
<th>object</th>
<th>corresponding merge function</th>
</tr>
</thead>
<tbody>
<tr>
<td>RLum.Results</td>
<td>merge_RLum.Results</td>
</tr>
</tbody>
</table>

**Value**

Return is the same as input objects as provided in the list.

**Function version**

0.1 (2015-03-04 14:47:38)

**Note**

So far not for every RLum object a merging function exists.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),  
R Luminescence Package Team

**References**

#
merge_RLum.Analysis

Merge function for RLum.Analysis S4 class objects

Description
Function allows merging of RLum.Analysis objects and adding of allowed objects to an RLum.Analysis.

Usage
merge_RLum.Analysis(objects)

Arguments
objects list of RLum.Analysis (required): list of S4 objects of class RLum.Analysis. Furthermore other objects of class RLum can be added, see details.

Details
This function simply allowing to merge RLum.Analysis objects. Additionally other RLum objects can be added to an existing RLum.Analysis object. Supported objects to be added are: RLum.Data.Curve, RLum.Data.Spectrum and RLum.Data.Image.

The order in the new RLum.Analysis object is the object order provided with the input list.

Value
Return an RLum.Analysis object.

Examples

```r
###Example based using data and from the calc_CentralDose() function

####load example data
data(ExampleData.DeValues, envir = environment())

####apply the central dose model 1st time
temp1 <- calc_CentralDose(ExampleData.DeValues$CA1)

####apply the central dose model 2nd time
temp2 <- calc_CentralDose(ExampleData.DeValues$CA1)

####merge the results and store them in a new object
temp.merged <- get_RLum.Results(merge_RLum(objects = list(temp1, temp2)))
```
Function version
0.1 (2015-03-04 00:19:53)

Note
The information for the slot 'protocol' is taken from the first `RLum.Analysis` object in the input list. Therefore at least one object of type `RLum.Analysis` has to be provided.

Author(s)
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References
-

See Also

Examples

```r
# merge different RLum objects from the example data
data(ExampleData.RLum.Analysis, envir = environment())
data(ExampleData.BINfileData, envir = environment())

object <- Risoe.BINfileData$RLum.Analysis(CWOSL.SAR.Data, pos=1)
curve <- get_RLum(object)[[2]]

temp.merged <- merge_RLum.Analysis(list(curve, IRSAR.RF.Data, IRSAR.RF.Data))
```


Description
Function allows merging of `RLum.Data.Curve` objects in different ways

Usage
```
merge_RLum.Data.Curve(object, merge.method = "mean", method.info)
```
merge_RLum.Data.Curve

Arguments

merge.method character (required): method for combining of the objects, e.g. 'mean', 'sum', see details for further information and allowed methods. Note: Elements in slot info will be taken from the first curve in the list.
method.info numeric (optional): allows to specify how info elements of the input objects are combined, e.g. 1 means that just the elements from the first object are kept, 2 keeps only the info elements from the 2 object etc. If nothing is provided all elements are combined.

Details

This function simply allowing to merge RLum.Data.Curve objects without touching the objects itself. Merging is always applied on the 2nd column of the data matrix of the object.

Supported merge operations are RLum.Data.Curve

"sum"

All count values will be summed up using the function rowSums.

"mean"

The mean over the count values is calculated using the function rowMeans.

"-" 

The row sums of the last objects are subtracted from the first object.

"*"

The row sums of the last objects are multiplied with the first object.

"/"

Values of the first object are divided by row sums of the last objects.

Value


Function version

0.1 (2015-03-04 00:19:53)

Note

The information from the slot 'recordType' is taken from the first RLum.Data.Curve object in the input list. The slot 'curveType' is filled with the name merged.
**plot_AbanicoPlot**

*Function to create an Abanico Plot.*

**Description**

A plot is produced which allows comprehensive presentation of data precision and its dispersion around a central value as well as illustration of a kernel density estimate of the dose values.

**Usage**

```r
plot_AbanicoPlot(data, na.exclude = TRUE, log.z = TRUE, central.value, centrality = "mean.weighted", dispersion = "sd", plot.ratio = 0.75, rotate = FALSE, mtext, summary, summary.pos, legend, legend.pos, stats, rug = FALSE, kde = TRUE, hist = FALSE, dots = FALSE, y.axis = TRUE, error.bars = FALSE, polygon.col, bar.col, line, line.col, line.label, grid.col, bw = "SJ", output = FALSE, ...)
```

**Examples**

```r
# Load example data
data(ExampleData.XSYG, envir = environment())

# Grep first and 3d TL curves
tl.curves <- get_RLum.Analysis(OSL.SARMeasurement$Sequence.Object, recordType = "TL (UVVIS)"
TL.curve.1 <- tl.curves[[1]]
TL.curve.3 <- tl.curves[[3]]

# Plot single curves
plot_RLum(TL.curve.1)
plot_RLum(TL.curve.3)

# Subtract the 1st curve from the 2nd and plot
TL.curve.merged <- merge_RLum.Data.Curve(list(TL.curve.3, TL.curve.1), merge.method = "/")
plot_RLum(TL.curve.merged)
```
Arguments

data  data.frame or RLum.Results object (required): for data.frame two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot the data sets must be provided as list, e.g. list(data.1, data.2).

na.exclude  logical (with default): exclude NA values from the data set prior to any further operations.

log.z  logical (with default): Option to display the z-axis in logarithmic scale. Default is TRUE.

central.value  numeric: User-defined central value, primarily used for horizontal centering of the z-axis.

centrality  character or numeric (with default): measure of centrality, used for automatically centering the plot and drawing the central line. Can either be one out of "mean", "median", "mean.weighted" and "median.weighted" or one or more numeric values used for the standardisation. If more than one value is specified, more than one 2-sigma bar will be plotted and the dataset is centered using the median. Default is "mean.weighted".

dispersion  character (with default): measure of dispersion, used for drawing the polygon that depicts the dose distribution. One out of "sd" (standard deviation), "2sd" (2 standard deviations), "qr" (quartile range) or "cin" (confidence interval with n\text{n}\text{ specifying the level, e.g. "ci95" meaning the 95 % confidence interval, i.e. data between the quantiles 0.025 and 0.975), default is "sd".

plot.ratio  numeric: Relative space, given to the radial versus the cartesian plot part, default is 0.75.

rotate  logical: Option to turn the plot by 90 degrees.

mtext  character: additional text below the plot title.

summary  character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "sdr1" (relative standard deviation in percent), "sdrabs" (absolute standard deviation), "ser1" (relative standard error), "seabs" (absolute standard error) and "in.ci" (percent of samples in confidence interval, e.g. 2-sigma).

summary.pos  numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used.

legend  character vector (optional): legend content to be added to the plot.

legend.pos  numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the legend to be plotted.

stats  character: additional labels of statistically important values in the plot. One or more out of the following: "min", "max", "median".

rug  logical: Option to add a rug to the KDE part, to indicate the location of individual values.

kde  logical: Option to add a KDE plot to the dispersion part, default is TRUE.
The Abanico Plot is a combination of the classic Radial Plot and a kernel density estimate plot. It allows straightforward visualisation of data precision, error scatter around a user-defined central value and the combined distribution of the values, on the actual scale of the measured data (e.g. seconds, equivalent dose, years). The principle of the plot is shown in Galbraith & Green (1990). The function authors are thankful for the thoughtprovocing figure in this article.

The semi circle (z-axis) of the classic Radial Plot is bent to a straight line here, which actually is the basis for combining this polar (radial) part of the plot with any other cartesian visualisation method (KDE, histogram, PDF and so on). Note that the plot allows displaying two measures of distribution. One is the 2-sigma bar, which illustrates the spread in value errors, and the other is the polygon, which stretches over both parts of the Abanico Plot (polar and cartesian) and illustrates the actual spread in the values themselfes.

Since the 2-sigma-bar is a polygon, it can be (and is) filled with shaded lines. To change density (lines per inch, default is 15) and angle (default is 45 degrees) of the shading lines, specify these parameters. See ?polygon() for further help.

The Abanico Plot supports other than the weighted mean as measure of centrality. When it is obvious that the data is not (log-)normally distributed, the mean (weighted or not) cannot be a valid measure of centrality and hence central dose. Accordingly, the median and the weighted median can be
chosen as well to represent a proper measure of centrality (e.g. centrality = "median.weighted"). Also user-defined numeric values (e.g. from the central age model) can be used if this appears appropriate.

The proportion of the polar part and the cartesian part of the Abanico Plot can be modified for display reasons (plot.ratio = 0.75). By default, the polar part spreads over 75 % and leaves 25 % for the part that shows the KDE graph.

The optional parameter layout allows to modify the entire plot more sophisticated. Each element of the plot can be addressed and its properties can be defined. This includes font type, size and decoration, colours and sizes of all plot items. To infer the definition of a specific layout style cf. get.Layout() or type eg. for the layout type "journal" get.Layout("journal"). A layout type can be modified by the user by assigning new values to the list object.

It is possible for the z-scale to specify where ticks are to be drawn by using the parameter at, e.g. at = seq(80, 200, 20), cf. function documentation of axis. Specifying tick positions manually overrides a zlim-definition.

Value
returns a plot object and, optionally, a list with plot calculus data.

Function version
0.1.2 (2015-03-04 14:53:26)

Author(s)
Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
Inspired by a plot introduced by Galbraith & Green (1990)
R Luminescence Package Team

References

See Also
plot.RadialPlot, plot_KDE, plot_Histogram

Examples
```r
## store original graphics parameters
par.old <- par(no.readonly = TRUE)

## load example data and recalculate to Gray
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <- Second2Gray(ExampleData.DeValues$BT998, c(0.0438, 0.0019))
```
## plot the example data straightforward
```r
plot_AbanicoPlot(data = ExampleData.DeValues)
```

## now with linear z-scale
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  log.z = FALSE)
```

## now with output of the plot parameters
```r
plot1 <- plot_AbanicoPlot(data = ExampleData.DeValues,
                          output = TRUE)
str(plot1)
plot1$zlim
```

## now with adjusted z-scale limits
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  zlim = c(100, 200))
```

## now with adjusted x-scale limits
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  xlim = c(0, 60))
```

## now with rug to indicate individual values in KDE part
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  rug = TRUE)
```

## now with a smaller bandwidth for the KDE plot
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  bw = 0.01)
```

## now with a histogram instead of the KDE plot
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  hist = TRUE,
                  kde = FALSE)
```

## now with a KDE plot and histogram with manual number of bins
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  hist = TRUE,
                  breaks = 20)
```

## now with a KDE plot and a dot plot
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  dots = TRUE)
```

## now with user-defined plot ratio
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  plot.ratio = 0.5)
```

## now with user-defined central value
```r
plot_AbanicoPlot(data = ExampleData.DeValues,
                  central.value = 120)
```

## now with weighted median as measure of centrality
plot_AbanicoPlot(data = ExampleData.DeValues,
        centrality = "median.weighted")

## now with median/quartile range as measure of centrality/dispersion
plot_AbanicoPlot(data = ExampleData.DeValues,
        centrality = "median",
        dispersion = "qr")

## now with user-defined green line for minimum age model
CAM <- calc_CentralDose(ExampleData.DeValues,
          plot = FALSE)

plot_AbanicoPlot(data = ExampleData.DeValues,
        line = CAM,
        line.col = "darkgreen",
        line.label = "CAM")

## now create plot with legend, colour, different points and smaller scale
plot_AbanicoPlot(data = ExampleData.DeValues,
        legend = "Sample 1",
        col = "tomato4",
        bar.col = "peachpuff",
        pch = "R",
        cex = 0.8)

## now without 2-sigma bar, polygon, grid lines and central value line
plot_AbanicoPlot(data = ExampleData.DeValues,
        bar.col = "none",
        polygon.col = "none",
        grid.col = "none",
        y.axis = FALSE,
        lwd = 0)

## now with direct display of De errors, without 2-sigma bar
plot_AbanicoPlot(data = ExampleData.DeValues,
        bar.col = "none",
        ylab = "",
        y.axis = FALSE,
        error.bars = TRUE)

## now with user-defined axes labels
plot_AbanicoPlot(data = ExampleData.DeValues,
        xlab = c("Data error [%]",
               "Data precision",
               "Kernel density"),
        ylab = "Scatter",
        zlab = "Equivalent dose [Gy]")

## now with minimum, maximum and median value indicated
plot_AbanicoPlot(data = ExampleData.DeValues,
        central.value = 150,
        stats = c("min", "max", "median"))
## now with a brief statistical summary
```r
plot_AbanicoPlot(data = ExampleData.DeValues, summary = c("n", "in.ci"))
```

## now with another statistical summary as subheader
```r
plot_AbanicoPlot(data = ExampleData.DeValues, summary = c("mean.weighted", "median"), summary.pos = "sub")
```

## now a plot with two 2-sigma bars for one data set
```r
plot_AbanicoPlot(data = ExampleData.DeValues, centrality = c(120, 160), mtext = "n = 25")
```

## now the data set is split into sub-groups, one is manipulated
```r
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3
```

## now a common dataset is created from the two subgroups
```r
data.3 <- list(data.1, data.2)
```

## now the two data sets are plotted in one plot
```r
plot_AbanicoPlot(data = data.3)
```

## now with some graphical modification
```r
plot_AbanicoPlot(data = data.3, 
col = c("steelblue4", "orange4"),
bar.col = c("steelblue3", "orange3"),
polygon.col = c("steelblue1", "orange1"),
pch = c(2, 6),
density = c(10, 20),
age = c(30, 50),
summary = c("n", "in.ci"))
```

## create Abanico plot with predefined layout definition
```r
plot_AbanicoPlot(data = ExampleData.DeValues, layout = "journal")
```

## now with predefined layout definition and further modifications
```r
plot_AbanicoPlot(data = data.3, 
layout = "journal",
col = c("steelblue4", "orange4"),
bar.col = adjustcolor(c("steelblue3", "orange3"), alpha.f = 0.5),
polygon.col = c("steelblue3", "orange3"))
```

## for further information on layout definitions see documentation
## of function get_layout()

## restore original graphical parameters
```r
par(par.old)
```
plot_DRTResults  Visualise dose recovery test results

Description

The function provides a standardised plot output for dose recovery test measurements.

Usage

plot_DRTResults(values, given.dose, error.range = 10, preheat,
    boxplot = FALSE, mtext, summary, summary.pos, legend, legend.pos,
    par.local = TRUE, na.rm = FALSE, ...)

Arguments

values  RLum.Results or data.frame, (required): input values containing at least De
and De error. To plot more than one data set in one figure, a list of the individ-
ual data sets must be provided (e.g. list(dataset.1, dataset.2)).
given.dose numeric (optional): given dose used for the dose recovery test to normalise data.
If only one given dose is provided this given dose is valid for all input data sets
(i.e., values is a list). Otherwise a given dose for each input data set has to
be provided (e.g., given.dose = c(100, 200)). If no given.dose values are
plotted without normalisation (might be useful for preheat plateau tests). Note:
Unit has to be the same as from the input values (e.g., Seconds or Gray).
error.range numeric: symmetric error range in percent will be shown as dashed lines in the
plot. Set error.range to 0 to void plotting of error ranges.
preheat numeric: optional vector of preheat temperatures to be used for grouping the
De values. If specified, the temperatures are assigned to the x-axis.
boxplot logical: optionally plot values, that are grouped by preheat temperature as
boxplots. Only possible when preheat vector is specified.
mtext character: additional text below the plot title.
summary character (optional): adds numerical output to the plot. Can be one or more
out of: "n" (number of samples), "mean" (mean De value), "mean.weighted"
(error-weighted mean), "median" (median of the De values), "sdrel" (relative
standard deviation in percent), "sdabs" (absolute standard deviation), "serel"
(relative standard error) and "seabs" (absolute standard error).
summary.pos numeric or character (with default): optional position coordinates or keyword
(e.g. "topright") for the statistical summary. Alternatively, the keyword "sub"
may be specified to place the summary below the plot header. However, this
latter option in only possible if mtext is not used.
legend character vector (optional): legend content to be added to the plot.
legend.pos numeric or character (with default): optional position coordinates or keyword
(e.g. "topright") for the legend to be plotted.
**plot_DRTResults**

**par.local** logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If `par.local = FALSE`, global parameters are inherited.

**na.rm** logical: indicating whether NA values are removed before plotting from the input data set

... further arguments and graphical parameters passed to `plot`.

**Details**

Procedure to test the accuracy of a measurement protocol to reliably determine the dose of a specific sample. Here, the natural signal is erased and a known laboratory dose administered which is treated as unknown. Then the De measurement is carried out and the degree of congruence between administered and recovered dose is a measure of the protocol’s accuracy for this sample. In the plot the normalised De is shown on the y-axis, i.e. obtained De/Given Dose.

**Value**

A plot is returned.

**Function version**

0.1.6 (2015-03-04 13:27:28)

**Note**

Further data and plot arguments can be added by using the appropriate R commands.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Michael Dietze, GFZ Potsdam (Germany), R Luminescence Package Team

**References**


**See Also**

`plot`

**Examples**

```r
## read example data set and misapply them for this plot type
data(ExampleData.DeValues, envir = environment())

## plot values
```
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800, mtext = "Example data")

## plot values with legend
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800,
legend = "Test data set")

## create and plot two subsets with randomised values
x.1 <- ExampleData.DeValues$BT998[7:11,]
x.2 <- ExampleData.DeValues$BT998[7:11,] * c(runif(5, 0.9, 1.1), 1)

plot_DRTResults(values = list(x.1, x.2),
given.dose = 2800)

## some more user-defined plot parameters
plot_DRTResults(values = list(x.1, x.2),
given.dose = 2800,
pch = c(2, 5),
col = c("orange", "blue"),
xlim = c(0, 8),
ylim = c(0.85, 1.15),
lab = "Sample aliquot")

## plot the data with user-defined statistical measures as legend
plot_DRTResults(values = list(x.1, x.2),
given.dose = 2800,
summary = c("n", "mean.weighted", "sd"))

## plot the data with user-defined statistical measures as sub-header
plot_DRTResults(values = list(x.1, x.2),
given.dose = 2800,
summary = c("n", "mean.weighted", "sd"),
summary.pos = "sub")

## plot the data grouped by preheat temperatures
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800,
preheat = c(200, 200, 200, 240, 240))

## read example data set and misapply them for this plot type
data(ExampleData.DeValues, envir = environment())

## plot values
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800, mtext = "Example data")

## plot two data sets grouped by preheat temperatures
plot_DRTResults(values = list(x.1, x.2),
given.dose = 2800,
preheat = c(200, 200, 200, 240, 240))

## plot the data grouped by preheat temperatures as boxplots
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800,
preheat = c(200, 200, 200, 240, 240),
boxplot = TRUE)

plot_GrowthCurve

Description

A dose response curve is produced for luminescence measurements using a regenerative protocol.

Usage

plot_GrowthCurve(sample, na.rm = TRUE, fit.method = "EXP", fit.weights = TRUE,
fit.includingRepeatedRegPoints = TRUE, fit.NumberRegPoints,
fit.NumberRegPointsReal, fit.bounds = TRUE, NumberIterations.MC = 100,
output.plot = TRUE, output.plotExtended = TRUE, output.plotExtended.single = FALSE,
cex.global = 1, ...)

Arguments

sample [data.frame (required]): data frame with three columns for x=Dose,y=LxTx,z=LxTx.Error,
y1=TnTx. The column for the test dose response is optional, but requires 'TnTx' as column name if used.
na.rm [logical (with default): excludes NA values from the data set prior to any further operations.
fit.method [character (with default): function used for fitting. Possible options are: LIN, EXP, EXP OR LIN, EXP+LIN or EXP+EXP. See details.
fit.weights [logical (with default): option whether the fitting is done with or without weights. See details.
fit.includingRepeatedRegPoints [logical (with default): includes repeated points for fitting (TRUE/FALSE).
fit.NumberRegPoints [integer (optional): set number of regeneration points manually. By default the number of all (!) regeneration points is used automatically.
fit.NumberRegPointsReal [integer (optional): if the number of regeneration points is provided manually, the value of the real, regeneration points = all points (repeated points) including reg 0, has to be inserted.
fit.bounds [logical (with default): set lower fit bounds for all fitting parameters to 0. Limited for the use with the fit methods EXP, EXP+LIN and EXP OR LIN. Argument to be inserted for experimental application only!
NumberIterations.MC [integer (with default): number of Monte Carlo simulations for error estimation. See details.
output.plot [logical (with default): plot output (TRUE/FALSE).
output.plotExtended

Logical (with default): If TRUE, 3 plots on one plot area are provided: (1) growth curve, (2) histogram from Monte Carlo error simulation and (3) a test dose response plot. If FALSE, just the growth curve will be plotted. Requires output.plot = TRUE.

details

output.plotExtended. single

Logical (with default): Single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. Requires output.plot = TRUE and output.plotextended = TRUE.

cex.global

Numeric (with default): Global scaling factor.

Further arguments and graphical parameters to be passed. Note: Standard arguments will only be passed to the growth curve plot. Supported: xlim, ylim, main, xlab, ylab

Details

Fitting methods

For all options (except for the LIN and the EXP OR LIN), the nls function with the port algorithm is used.

LIN: fits a linear function to the data using lm:

\[ y = m \times x + n \]

EXP: try to fit a function of the form

\[ y = a \times (1 - \exp(-(x + c)/b)) \]

Parameters b and c are approximated by a linear fit using lm. Note: b = D0

EXP OR LIN: works for some cases where an EXP fit fails. If the EXP fit fails, a LIN fit is done instead.

EXP+LIN: tries to fit an exponential plus linear function of the form:

\[ y = a \times (1 - \exp(-(x + c)/b) + (g \times x)) \]

The De is calculated by iteration.

Note: In the context of luminescence dating, this function has no physical meaning. Therefore, no D0 value is returned.

EXP+EXP: tries to fit a double exponential function of the form

\[ y = (a1 \times (1 - \exp(-(x)/b1))) + (a2 \times (1 - \exp(-(x)/b2))) \]

This fitting procedure is not robust against wrong start parameters and should be further improved.

Fit weighting

If the option fit.weights = TRUE is chosen, weights are calculated using provided signal errors (Lx/Tx error):

\[ fit.weights = 1/error/(sum(1/error)) \]
Error estimation using Monte Carlo simulation

Error estimation is done using a Monte Carlo (MC) simulation approach. A set of $L_x/T_x$ values is constructed by randomly drawing curve data from sampled from normal distributions. The normal distribution is defined by the input values (mean = value, sd = value.error). Then, a growth curve fit is attempted for each dataset resulting in a new distribution of single $D_e$ values. The sd of this distribution becomes then the error of the $D_e$. With increasing iterations, the error value becomes more stable. Note: It may take some calculation time with increasing MC runs, especially for the composed functions (EXP+LIN and EXP+EXP).

Each error estimation is done with the function of the chosen fitting method.

Subtitle information

To avoid plotting the subtitle information, provide an empty user mtext mtext = "". To plot any other subtitle text, use mtext.

Value

RLum.Results object containing the $D_e$ ($D_e$, $D_e$ Error, $D_01$ value, $D_02$ value, $D_e$.MC and Fit type) and the fit object nls object for EXP, EXP+LIN and EXP+EXP. In case of a resulting linear fit when using EXP OR LIN, a lm object is returned.

The formula Formula is returned as R expression for further evaluation. Additionally a plot is returned.

Function version

1.5 (2015-03-04 12:43:39)

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany),
R Luminescence Package Team

Examples

```r
##(1) plot growth curve for a dummy data.set and show De value
data(ExampleData.LxTxData, envir = environment())
temp <- plot_GrowthCurve(LxTxData)
get_RLum.Results(temp)

##(1a) to access the fitting value try
get_RLum.Results(temp, data.object = "Fit")

##(2) plot the growth curve only - uncomment to use
#pdf(file = "~/Desktop/Growth_Curve_Dummy.pdf", paper = "special")
plot_GrowthCurve(LxTxData)
#dev.off()

##(3) plot growth curve with pdf output - uncomment to use, single output
#pdf(file = "~/Desktop/Growth_Curve_Dummy.pdf", paper = "special")
plot_GrowthCurve(LxTxData, output.plotExtended.single = TRUE)
#dev.off()
```
plot_Histogram

Plot a histogram with separate error plot

Description

Function plots a predefined histogram with an accompanying error plot as suggested by Rex Galbraith at the UK LED in Oxford 2010.

Usage

plot_Histogram(data, na.exclude = TRUE, mtext, cex.global, breaks, se, rug, normal_curve, summary, summary.pos, colour, ...)

Arguments

data data.frame or RLum.Results object (required): for data.frame: two columns: De (data[,1]) and De error (data[,2])

na.exclude logical (with default): excludes NA values from the data set prior to any further operations.

mtext character (optional): further sample information (mtext).

cex.global numeric (with default): global scaling factor.

breaks (with default): sets breakpoints for histogram. Works as in hist.

se logical (optional): plots standard error points over the histogram, default is FALSE.

rug logical (optional): adds rugs to the histogram, default is TRUE.

normal_curve logical (with default): adds a normal curve to the histogram. Mean and sd are calculated from the input data. More see details section.

summary character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "kdemax" (maximum of the KDE), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error), "seabs" (absolute standard error), "skewness" (skewness) and "kurtosis" (kurtosis). Note: Keywords "kdemax" is implemented for consistency reasons, however, no KDE is shown. The bandwidth is calculated according to plot_KDE

summary.pos numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used. In case of coordinate specification, y-coordinate refers to the right y-axis.

colour numeric or character (with default): optional vector of length 4 which specifies the colours of the following plot items in exactly this order: histogram bars, rug lines, normal distribution curve and standard error points (e.g., c("grey", "black", "red", "grey")).
... further arguments and graphical parameters passed to `plot`. If y-axis labels are provided, these must be specified as a vector of length 2 since the plot features two axes (e.g. `ylab = c("axis label 1", "axis label 2")`). Y-axes limits (`ylim`) must be provided as vector of length four, with the first two elements specifying the left axes limits and the latter two elements giving the right axis limits.

Details

If the normal curve is added, the y-axis in the histogram will show the probability density.

Function version

0.4.3 (2015-03-04 13:26:15)

Note

The input data is not restricted to a special type.

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

See Also

`hist`, `plot`

Examples

```r
## load data
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <-
  Second2Gray(ExampleData.DeValues$BT998, dose.rate = c(0.0438, 0.0019))

## plot histogram the easiest way
plot_Histogram(ExampleData.DeValues)

## plot histogram with some more modifications
plot_Histogram(ExampleData.DeValues, 
               rug = TRUE, 
               normal_curve = TRUE, 
               cex.global = 0.9, 
               pch = 2, 
               colour = c("grey", "black", "blue", "green"), 
               summary = c("n", "mean", "sdrel"), 
               summary.pos = "topleft", 
               main = "Histogram of De-values", 
               mtext = "Example data set", 
               ylab = c(expression(paste(D[e], " distribution")), 
                        "Error"), 
               ```
plot_KDE

Plot kernel density estimate with statistics

Description

Plot a kernel density estimate of measurement values in combination with the actual values and associated error bars in ascending order. Optionally, statistical measures such as mean, median, standard deviation, standard error and quartile range can be provided visually and numerically.

Usage

plot_KDE(data, na.exclude = TRUE, weights = FALSE, values.cumulative = TRUE, centrality, dispersion, summary, summary.pos, polygon.col, order = TRUE, bw = "nrd0", output = FALSE, ...)

Arguments

data: data.frame or RLum.Results object (required): for data.frame: two columns: De (values[,1]) and De error (values[,2]). For plotting multiple data sets, these must be provided as list (e.g. list(dataset1, dataset2)).

na.exclude: logical (with default): exclude NA values from the data set prior to any further operations.

weights: logical (with default): calculate the KDE with De-errors as weights. Attention, using errors as weights will result in a plot similar to a probability density plot, with all ambiguities related to this plot type!

values.cumulative: logical (with default): show cumulative individual data.

centrality: character: measure(s) of centrality, used for plotting vertical lines of the respective measure. Can be one out of "mean", "median", "mean.weighted", "median.weighted" and "kdemax".

dispersion: character: measure of dispersion, used for drawing the polygon that depicts the dose distribution. One out of "sd" (standard deviation),"2sd" (2 standard deviations) "qr" (quartile range).

summary: character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error), "seabs" (absolute standard error), "kdemax" (maximum of the KDE), "skewness" (skewness) and "kurtosis" (kurtosis).
summary.pos numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used. In case of coordinate specification, y-coordinate refers to the right y-axis.

polygon.col character or numeric (with default): colour of the polygon showing the dose dispersion around the central value. Only relevant if dispersion is specified.

order logical: Order data in ascending order.

bw character (with default): bin-width, chose a numeric value for manual setting.

output logical: Optional output of numerical plot parameters. These can be useful to reproduce similar plots. Default is FALSE.

... further arguments and graphical parameters passed to plot.

Details

The function allow passing several plot arguments, such as main, xlab, cex. However, as the figure is an overlay of two separate plots, ylim must be specified in the order: c(ymin_axis1, ymax_axis1, ymin_axis2, ymax_axis2) when using the cumulative values plot option. Similarly, if other than the default colours are desired, the argument col must be provided with colours in the following order: probability density function, De values, De error bars, sd or qr polygon. The line type (lty) for additional measures of centrality will cycle through the default values (1, 2, ...) by default, i.e. KDE line solid, further vertical lines dashed, dotted, dash-dotted and so on. To change this behaviour specify the desired order of line types (e.g. lty = c(1, 3, 2, 5)). See examples for some further explanations. For details on the calculation of the bin-width (parameter bw) see density.

Function version

3.5 (2015-03-04 13:25:51)

Note

The plot output is no 'PD' plot (cf. the discussion of Berger and Galbraith in Ancient TL; see references)!

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne,
R Luminescence Package Team

See Also

density, plot
Examples

```r
## read example data set
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <-
  Second2Gray(ExampleData.DeValues$BT998, c(0.0438, 0.0019))

## create plot straightforward
plot_KDE(data = ExampleData.DeValues)

## create plot with logarithmic x-axis
plot_KDE(data = ExampleData.DeValues,
          log = "x")

## create plot with user-defined labels and axes limits
plot_KDE(data = ExampleData.DeValues,
          main = "Dose distribution",
          xlab = "Dose [s]",
          ylab = c("KDE estimate", "Cumulative dose value"),
          xlim = c(100, 250),
          ylim = c(0, 0.08, 0, 30))

## create plot with centrality lines and distribution polygons
plot_KDE(data = ExampleData.DeValues,
          ylim = c(0, 0.08, 0, 35),
          centrality = c("median", "mean"),
          dispersion = "sd",
          polygon.col = "lightblue")

## create plot with statistical summary below header
plot_KDE(data = ExampleData.DeValues,
          summary = c("n", "median", "skewness", "qr"))

## create plot with statistical summary as legend
plot_KDE(data = ExampleData.DeValues,
          summary = c("n", "mean", "sdrel", "seabs"),
          summary.pos = "topleft")

## split data set into sub-groups, one is manipulated, and merge again
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3
data.3 <- list(data.1, data.2)

## create plot with two subsets straightforward
plot_KDE(data = data.3)

## create plot with two subsets and summary legend at user coordinates
plot_KDE(data = data.3,
          summary = c("n", "median", "skewness"),
          summary.pos = c(110, 0.07),
          col = c("blue", "orange"))

## example of how to use the numerical output of the function
```
## Description

A Galbraith’s radial plot is produced on a logarithmic or a linear scale.

## Usage

```r
plot_RadialPlot(data, na.exclude = TRUE, negatives = "remove", 
                 log.z = TRUE, central.value, centrality = "mean.weighted", 
                 mtext, summary, summary.pos, legend, legend.pos, stats, rug = FALSE, 
                 plot.ratio, bar.col, y.ticks = TRUE, grid.col, line, line.col, 
                 line.label, output = FALSE, ...)
```

## Arguments

- **data**: `data.frame` or `RLum.Results` object (required): for `data.frame` two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot, the data sets must be provided as list, e.g. `list(data.1, data.2)`.
- **na.exclude**: logical (with default): excludes NA values from the data set prior to any further operations.
- **negatives**: character (with default): rule for negative values. Default is "remove" (i.e. negative values are removed from the data set).
- **log.z**: logical (with default): Option to display the z-axis in logarithmic scale. Default is TRUE.
- **central.value**: numeric: User-defined central value, primarily used for horizontal centering of the z-axis.
- **centrality**: character or numeric (with default): measure of centrality, used for automatically centering the plot and drawing the central line. Can either be one out of "mean", "median", "mean.weighted" and "median.weighted" or a numeric value used for the standardisation.
Details and the theoretical background of the radial plot are given in the cited literature. This function is based on an S script of Rex Galbraith. To reduce the manual adjustments, the function has
been rewritten. Thanks to Rex Galbraith for useful comments on this function.
Plotting can be disabled by adding the argument `plot = "FALSE"`, e.g. to return only numeric plot output.

Earlier versions of the Radial Plot in this package had the 2-sigma-bar drawn onto the z-axis. However, this might have caused misunderstanding in that the 2-sigma range may also refer to the z-scale, which it does not! Rather it applies only to the x-y-coordinate system (standardised error vs. precision). A spread in doses or ages must be drawn as lines originating at zero precision (x0) and zero standardised estimate (y0). Such a range may be drawn by adding lines to the radial plot (`line`, `line.col`, `line.label`, cf. examples).

Value

Returns a plot object.

Function version

0.5.3 (2015-03-04 13:25:19)

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
Based on a rewritten S script of Rex Galbraith, 2010
R Luminescence Package Team

References


See Also

`plot, plot_KDE, plot_Histogram`
Examples

```r
# load example data
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <- Second2Gray(ExampleData.DeValues$BT998, c(0.0438, 0.0019))

# plot the example data straightforward
plot_RadialPlot(data = ExampleData.DeValues)

# now with linear z-scale
plot_RadialPlot(data = ExampleData.DeValues,
                 log.z = FALSE)

# now with output of the plot parameters
plot1 <- plot_RadialPlot(data = ExampleData.DeValues,
                          log.z = FALSE,
                          output = TRUE)

plot1
plot1$zlim

# now with adjusted z-scale limits
plot_RadialPlot(data = ExampleData.DeValues,
                 log.z = FALSE,
                 zlim = c(100, 200))

# now the two plots with serious but seasonally changing fun
#plot_RadialPlot(data = data.3, fun = TRUE)

# now with user-defined central value, in log-scale again
plot_RadialPlot(data = ExampleData.DeValues,
                 central.value = 150)

# now with a rug, indicating individual De values at the z-scale
plot_RadialPlot(data = ExampleData.DeValues,
                 rug = TRUE)

# now with legend, colour, different points and smaller scale
plot_RadialPlot(data = ExampleData.DeValues,
                 legend.text = "Sample 1",
                 col = "tomato4",
                 bar.col = "peachpuff",
                 pch = "R",
                 cex = 0.8)

# now without 2-sigma bar, y-axis, grid lines and central value line
plot_RadialPlot(data = ExampleData.DeValues,
                 bar.col = "none",
                 grid.col = "none",
                 y.ticks = FALSE,
                 lwd = 0)

# now with user-defined axes labels
plot_RadialPlot(data = ExampleData.DeValues,
                 x.axis = "Depth",
                 y.axis = "Age",
                 x.text = "Depth",
                 y.text = "Age")
```
plot_Risoe.BINfileData

Plot single luminescence curves from a BIN file object

Description

Plots single luminescence curves from an object returned by the readBIN2R function.

Usage

plot_Risoe.BINfileData(BINfileData, position, run, set, sorter = "POSITION", ltype = c("IRSL", "OSL", "TL", "RIR", "RBR", "RL"), curve.transformation, dose_rate, temp.lab, cex.global = 1, ...)

```r
lab = c("Data error [%]",
       "Data precision"),
ylab = "Scatter",
zlab = "Equivalent dose [Gy]"
```

```r
## now with minimum, maximum and median value indicated
plot_RadialPlot(data = ExampleData.DeValues,
               central.value = 150,
               stats = c("min", "max", "median"))
```

```r
## now with a brief statistical summary
plot_RadialPlot(data = ExampleData.DeValues,
              summary = c("n", "in.ci"))
```

```r
## now with another statistical summary as subheader
plot_RadialPlot(data = ExampleData.DeValues,
               summary = c("mean.weighted", "median"),
               summary.pos = "sub")
```

```r
## now the data set is split into sub-groups, one is manipulated
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3
```

```r
## now a common dataset is created from the two subgroups
data.3 <- list(data.1, data.2)
```

```r
## now the two data sets are plotted in one plot
plot_RadialPlot(data = data.3)
```

```r
## now with some graphical modification
plot_RadialPlot(data = data.3,
         col = c("darkblue", "darkgreen"),
         bar.col = c("lightblue", "lightgreen"),
         pch = c(2, 6),
         summary = c("n", "in.ci"),
         summary.pos = "sub",
         legend = c("Sample 1", "Sample 2"))
```
Arguments

BINfileData  Risoe.BINfileData-class (required): requires an S4 object returned by the read-BIN2R function.
position  vector (optional): option to limit the plotted curves by position (e.g. position = 1, position = c(1,3,5)).
run  vector (optional): option to limit the plotted curves by run (e.g., run = 1, run = c(1,3,5)).
set  vector (optional): option to limit the plotted curves by set (e.g., set = 1, set = c(1,3,5)).
sorter  character (with default): the plot output can be ordered by "POSITION" or "RUN". POSITION, SET and RUN are options defined in the Risoe Sequence Editor.
ltype  character (with default): option to limit the plotted curves by the type of luminescence stimulation. Allowed values: "IRSL", "OSL","TL", "RIR", "RBR" (corresponds to LM-OSL), "RL". All type of curves are plotted by default.

dose_rate  numeric (optional): dose rate of the irradiation source at the measurement date. If set, the given irradiation dose will be shown in Gy. See details.
temp.lab  character (optional): option to allow for different temperature units. If no value is set deg. C is chosen.
cex.global  numeric (with default): global scaling factor.
...  further undocumented plot arguments.

Details

Nomenclature

See Risoe.BINfileData-class

curve.transformation

This argument allows transforming continuous wave (CW) curves to pseudo (linear) modulated curves. For the transformation, the functions of the package are used. Currently, it is not possible to pass further arguments to the transformation functions. The argument works only for ltype OSL and IRSL.

Irradiation time

Plotting the irradiation time (s) or the given dose (Gy) requires that the variable IRR_TIME has been set within the BIN-file. This is normally done by using the 'Run Info’ option within the Sequence Editor or by editing in R.


**plot_Risoe.BINfileData**

**Value**

Returns a plot.

**Function version**

0.4.1 (2015-03-04 00:19:53)

**Note**

The function has been successfully tested for the Sequence Editor file output version 3 and 4.

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany)
R Luminescence Package Team

**References**


**See Also**

* Risoe.BINfileData-class.readBIN2R, CW2pLM, CW2pLMi, CW2pPMi, CW2pPHMi

**Examples**

```r
# load data
data(ExampleData.BINfileData, envir = environment())

# plot all curves from the first position to the desktop
#pdf(file = "~/Desktop/CurveOutput.pdf", paper = "a4", height = 11, onefile = TRUE)

# example - load from *.bin file
#BINfile<- file.choose()
#BINfileData<-readBIN2R(BINfile)

#par(mfrow = c(4,3), oma = c(0.5,1,0.5,1))
#plot_Risoe.BINfileData(CWOSL.SAR.Data,position = 1)
#mtext(side = 4, BINfile, outer = TRUE, col = "blue", cex = .7)
#dev.off()
```
plot_RLum

General plot function for RLum S4 class objects

Description

Function calls object specific plot functions for RLum S4 class objects.

Usage

plot_RLum(object, ...)

Arguments

- **object**: S4 object of class RLum (required)
- **...**: further arguments and graphical parameters that will be passed to the specific plot functions

Details

The function provides a generalised access point for plotting specific RLum objects. Depending on the input object, the corresponding plot function will be selected. Allowed arguments can be found in the documentations of each plot function.

<table>
<thead>
<tr>
<th>object</th>
<th>corresponding plot function</th>
</tr>
</thead>
<tbody>
<tr>
<td>RLum.Analysis</td>
<td>plot_RLum.Analysis</td>
</tr>
<tr>
<td>RLum.Results</td>
<td>plot_RLum.Results</td>
</tr>
</tbody>
</table>

Value

Returns a plot.

Function version

0.3 (2015-03-04 00:19:53)

Note

The provided plot output depends on the input object.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Université Bordeaux Montaigne (France), R Luminescence Package Team
References

#

See Also

RLum.Results

Examples

# load Example data
data(ExampleData.CW_OSL_Curve, envir = environment())

# transform data.frame to RLum.Data.Curve object
temp <- as(ExampleData.CW_OSL_Curve, "RLum.Data.Curve")

# plot RLum object
plot_RLum(temp)

plot_RLum.Analysis "Plot function for an RLum.Analysis S4 class object"

Description

The function provides a standardised plot output for curve data of an RLum.Analysis S4 class object

Usage

plot_RLum.Analysis(object, nrows = 3, ncols = 2, abline, combine = FALSE, 
curve.transformation, plot.single = FALSE, ...)

Arguments

object RLum.Analysis (required): S4 object of class RLum.Analysis
nrows integer (with default): sets number of rows for plot output
ncols integer (with default): sets number of columns for plot output
abline list (optional): allows to set similar ablines in each plot. This option uses the 
function do.call, meaning that every argument in the list has to be provided 
as list, e.g. abline = list(list(v = 120), list(v = 350)) produces 
two vertical ablines: One at 150 and another one at 350. Within the call all 
arguments supported by abline are fully supported.
combine logical (with default): allows to combine all codeRLum.Data.Curve objects in 
one single plot. Works only for RLum.Analysis that comprises a single curve 
object (option is currently only roughly implemented),
curve.transformation


plot.single logical (with default): each curve is plotted in a single window, overwrites the settings of nrows and ncols.

... further arguments and graphical parameters will be passed to the plot function. Supported arguments: main, mtext, log, lwd, lty type, pch, col ...

and for combine = TRUE also: ylim, xlab, ylab, sub, legend.text, legend.pos

Details

The function produces a multiple plot output. A file output is recommended (e.g., pdf).

curve.transformation

This argument allows transforming continuous wave (CW) curves to pseudo (linear) modulated curves. For the transformation, the functions of the package are used. Currently, it is not possible to pass further arguments to the transformation functions. The argument works only for ltype osl and irsl.

Please note: The curve transformation within this functions works roughly, i.e. every IRSL or OSL curve is transformed, without considerung whether it is measured with the PMT or not! However, for a fast look it might be helpful.

Value

Returns multiple plots.

Function version

0.2.0 (2015-03-04 19:15:10)

Note

Not all arguments available for plot will be passed! Only plotting of RLum.Data.Curve and RLum.Data.Spectrum objects are currently supported.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#
**plot_RLum.Data.Curve**

**See Also**

`plot.plot_RLum, plot_RLum.Data.Curve`

**Examples**

```r
### load data
data(ExampleData.BINfileData, envir = environment())

### convert values for position 1
temp <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)

### plot all values
plot_RLum.Analysis(temp)

### plot (combine) TL curves in one plot
temp.sel <- get_RLum.Analysis(temp, recordType = "TL", keep.object = TRUE)
plot_RLum.Analysis(temp.sel, combine = TRUE, norm = TRUE, main = "TL combined")
```

---

**plot_RLum.Data.Curve**  *Plot function for an RLum.Data.Curve S4 class object*

**Description**

The function provides a standardised plot output for curve data of an RLum.Data.Curve S4 class object.

**Usage**

```r
plot_RLum.Data.Curve(object, par.local = TRUE, norm = FALSE, ...)
```

**Arguments**

- `par.local`  *logical* (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If `par.local` = FALSE, global parameters are inherited.
- `norm`  *logical* (with default): allows curve normalisation to the highest count value
- `...` further arguments and graphical parameters that will be passed to the plot function

**Details**

Only single curve data can be plotted with this function. Arguments according to `plot`.
Value

Returns a plot.

Function version

0.1.5 (2015-03-04 00:19:53)

Note

Not all arguments of `plot` will be passed!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References

#

See Also

`plot`, `plot_RLum`

Examples

```r
# plot curve data

# load Example data
data(ExampleData.CW_OSL_Curve, envir = environment())

# transform data.frame to RLum.Data.Curve object
temp <- as(ExampleData.CW_OSL_Curve, "RLum.Data.Curve")

# plot RLum.Data.Curve object
plot_RLum.Data.Curve(temp)
```

Description

The function provides a standardised plot output for image data of an `RLum.Data.Image` S4 class object, mainly using the plot functions provided by the `raster` package.
plot_RLum.Data.Image

Usage

plot_RLum.Data.Image(object, par.local = TRUE, plot.type = "plot.raster", ...)

Arguments

  par.local       logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE global parameters are inherited.
  plot.type       character (with default): plot types. Supported types are plot.raster, plotRGB or contour
  ...             further arguments and graphical parameters that will be passed to the specific plot functions.

Details

  Details on the plot functions

  Image is visualised as 2D plot using generic plot types provided by other packages. Supported plot types:

  plot.type = "plot.raster"

  Uses the standard plot function for raster data from the package raster: plot. For each raster layer in a raster brick one plot is produced.
  Arguments that are passed through the function call:

  main, axes, xlab, ylab, xlim, ylim, col

  plot.type = "plotRGB"

  Uses the function plotRGB from the raster package. Only one image plot is produced as all layers in a brick a combined. This plot type is useful to see whether any signal is recorded by the camera.
  Arguments that are passed through the function call:

  main, axes, xlab, ylab, ext, interpolate, maxpixels, alpha, colNA, stretch

  plot.type = "contour"

  Uses the function contour plot function from the raster function (contour). For each raster layer one contour plot is produced. Arguments that are passed through the function call:

  main, axes, xlab, ylab, xlim, ylim, col
Value

Returns a plot.

Function version

0.1 (2015-03-04 00:19:53)

Note

This function has been created to facilitate the plotting of image data imported by the function `readSPE2R`. However, so far the function is not optimized to handle image data > ca. 200 MByte and thus plotting of such data is extremely slow.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References

-

See Also


Examples

```r
# load data
data(ExampleData.RLum.Data.Image, envir = environment())

# plot data
```

---

**plot_RLum.Data.Spectrum**

*Plot function for an RLum.Data.Spectrum S4 class object*

Description

The function provides a standardised plot output for spectrum data of an RLum.Data.Spectrum S4 class object
Usage

plot_RLum.Data.Spectrum(object, par.local = TRUE, plot.type = "contour",
    optical.wavelength.colours = TRUE, bg.channels, bin.rows = 1,
    bin.cols = 1, rug = TRUE, xaxis.energy = FALSE, legend.text,
    ...
)

Arguments

par.local logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE global parameters are inherited.
plot.type character (with default): plot type, for 3D-plot use persp, or persp3d, for a 2D-plot contour, single or multiple.lines (along the time or temperature axis) or transect (along the wavelength axis)

Note: The use of persp3d will produce a dynamic 3D surface plot on the screen.
optical.wavelength.colours logical (with default): use optical wavelength colour palette. Note: For this, the spectrum range is limited: c(HSUPLWUI). Own colours can be set with the argument col.
bg.channels vector (optional): defines channel for background subtraction. If a vector is provided the mean of the channels is used for subtraction. Note: Background subtraction is applied prior to channel binning.
bin.rows integer (with default): allow summing-up wavelength channels (horizontal binning), e.g. bin.rows = 2 two channels are summed up
bin.cols integer (with default): allow summing-up channel counts (vertical binning) for plotting, e.g. bin.cols = 2 two channels are summed up
rug logical (with default): enables or disables colour rug. Currently only implemented for plot type multiple.lines.
xaxis.energy logical (with default): enables or disables energy instead of wavelength axis. Axis labelling are changed accordingly, so far no manual axis labelling is choosen.
legend.text character (with default): possibility to provide own legend text. This argument is only considered for plot types providing a legend, e.g. plot.type="transect"
...

further arguments and graphical parameters that will be passed to the plot function.

Details

Matrix structure
(cf. RLum.Data.Spectrum)

- rows (x-values): wavelengths/channels (xlim, xlab)
- columns (y-values): time/temperature (ylim, ylab)
- cells (z-values): count values (zlim, zlab)

**Note:** This nomenclature is valid for all plot types of this function!

**Nomenclature for value limiting**

- `xlim`: Limits values along the wavelength axis
- `ylim`: Limits values along the time/temperature axis
- `zlim`: Limits values along the count value axis

**Details on the plot functions**

Spectrum is visualised as 3D or 2D plot. Both plot types are based on internal R plot functions.

```r
plot.type = "persp"
```

Arguments that will be passed to `persp`:

- `shade`: default is 0.4
- `phi`: default is 30
- `theta`: default is 30
- `expand`: default is 1
- `ticktype`: default is detailed

**Note:** Further parameters can be adjusted via `par`. For example to set the background transparent and reduce the thickness of the lines use: `par(bg = NA, lwd = 0.7)` previous the function call.

```r
plot.type = "single"
```

Per frame a single curve is returned. Frames are time or temperature steps.

```r
plot.type = "multiple.lines"
```

All frames drawn in one frame.

```r
plot.type = "transect"
```

Depending on the selected wavelength/channel range a transect over the time/temperature (y-axis) will be plotted along the wavelength/channels (x-axis). If the range contains more than one channel, values (z-values) are summed up. To select a transect use the `xlim` argument, e.g. `xlim = c(300, 310)` plot along the summed up count values of channel 300 to 310.

**Further arguments that will be passed (depending on the plot type)**

- `xlab`, `ylab`, `zlab`, `xlim`, `ylim`, `zlim`, `main`, `mtext`, `pch`, `type`, `border`, `box`, `lwd`, `bty`

**Value**

Returns a plot.

**Function version**

0.3.5 (2015-03-21 10:14:55)
plot_RLum.Data.Spectrum

Note

Not all additional arguments (…) will be passed similarly!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

RLum.Data.Spectrum, plot, plot_RLum, persp, persp3d, contour

Examples

```r
# load example data
data(ExampleData.XSYG, envir = environment())

#(1) plot simple spectrum (2D) - contour
plot_RLum.Data.Spectrum(TL.Spectrum,
    plot.type="contour",
    xlim = c(310,750),
    ylim = c(0,300),
    bin.rows=10,
    bin.cols = 1)

#(2) plot simple spectrum (2D) - multiple.lines (with ylim)
plot_RLum.Data.Spectrum(TL.Spectrum,
    plot.type="multiple.lines",
    xlim = c(310,750),
    ylim = c(0,100),
    bin.rows=10,
    bin.cols = 1)

#(3) plot 3d spectrum (uncomment for usage)
# plot_RLum.Data.Spectrum(TL.Spectrum, plot.type="persp",
# xlim = c(310,750), ylim = c(0,300), bin.rows=10,
# bin.cols = 1)
```
plot_RLum.Results

Plot function for an RLum.Results S4 class object

Description

The function provides a standardised plot output for data of an RLum.Results S4 class object

Usage

plot_RLum.Results(data, single = TRUE, ...)

Arguments

data RLum.Results (required): S4 object of class RLum.Results
single logical (with default): single plot output (TRUE/FALSE) to allow for plotting the results in as few plot windows as possible.
...

Details

The function produces a multiple plot output. A file output is recommended (e.g., pdf).

Value

Returns multiple plots.

Function version

0.1 (2015-03-10 09:43:59)

Note

Not all arguments available for plot will be passed! Only plotting of RLum.Results objects are supported.

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References

#

See Also

plot, plot_RLum,
Examples

```r
### load data
data(ExampleData.DeValues, envir = environment())

# apply the un-logged minimum age model
mam <- calc_Mindose(data = ExampleData.DeValues$CA1, sigmab = 0.2, log = TRUE, plot = FALSE)

# plot
plot_RLum.Results(mam)

# estimate the number of grains on an aliquot
gains <- calc_AliquotSize(grain.size = c(100, 150), sample.diameter = 1, plot = FALSE)

# plot
plot_RLum.Results(gains)
```

---

**readBIN2R**

Import Risoe BIN-file into R

Description

Import a *.bin or a *.binx file produced by a Risoe DA15 and DA20 TL/OSL reader into R.

Usage

`readBIN2R(file, show.raw.values = FALSE, n.records, show.record.number = FALSE, txtProgressBar = TRUE, forced.VersionNumber)`

Arguments

- `file` character (required): bin-file name (including path), e.g. 
  [WIN]: `readBIN2R("C:/Desktop/test.bin")`
  [MAC/LINUX]: `readBIN2R("/User/test/Desktop/test.bin")`
- `show.raw.values` logical (with default): shows raw values from BIN file for LTYPE, DTYPE and LIGHTSOURCE without translation in characters.
- `n.records` raw (optional): limits the number of imported records. Can be used in combination with `show.record.number` for debugging purposes, e.g. corrupt BIN files.
- `show.record.number` logical (with default): shows record number of the imported record, for debugging usage only.
- `txtProgressBar` logical (with default): enables or disables `txtProgressBar`.
readBIN2R

forced.VersionNumber

integer (optional): allows to cheat the version number check in the function by own values for cases where the BIN-file version is not supported.

Note: The usage is at own risk, only supported BIN-file versions have been tested.

Details

The binary data file is parsed byte by byte following the data structure published in the Appendices of the Analyst manual p. 42.

For the general BIN-file structure, the reader is referred to the Risoe website: http://www.nutech.dtu.dk/

Value

Returns an S4 Risoe.BINfileData-class object containing two slots:

- **METADATA**
  A data.frame containing all variables stored in the bin-file.

- **DATA**
  A list containing a numeric vector of the measured data. The ID corresponds to the record ID in METADATA.

Function version

0.8.1 (2015-03-04 12:43:39)

Note

The function has been successfully tested for BIN format versions 03, 04 and 06. The version number depends on the used Sequence Editor.

Other BIN format versions are currently not supported.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Margret C. Fuchs, AWI Potsdam (Germany),
R Luminescence Package Team

References


See Also

writeR2BIN, Risoe.BINfileData, readBin, merge_Risoe.BINfileData, txtProgressBar
Examples

```r
#(1) import Risoe BIN-file to R (uncomment for usage)

#FILE <- file.choose()
#temp <- readBIN2R(FILE)
#temp
```

**readSPE2R**

*Import Princeton Intruments (TM) SPE-file into R*

**Description**

Function imports Princeton Instruments (TM) SPE-files into R environment and provides RLum objects as output.

**Usage**

```r
readSPE2R(file, output.object = "RLum.Data.Image", frame.range, 
txtProgressBar = TRUE)
```

**Arguments**

- **file** character (required): spe-file name (including path), e.g. [WIN]: readSPE2R("C:/Desktop/test.spe"), [MAC/LINUX]: readSPE2R("/User/test/Desktop/test.spe")
- **output.object** character (with default): set RLum output object. Allowed types are "RLum.Data.Spectrum", "RLum.Data.Image" or "matrix"
- **frame.range** vector (optional): limit frame range, e.g. select first 100 frames by frame.range = c(1,100)
- **txtProgressBBar** logical (with default): enables or disables txtProgressBBar.

**Details**

Function provides an import routine for the Princton Instruments SPE format. Import functionality is based on the file format description provided by Princton Instruments and a MatLab script written by Carl Hall (s. references).

**Value**

Depending on the chosen option the functions returns three different type of objects:

- **output.object**.
- **RLum.Data.Spectrum**
An object of type `RLum.Data.Spectrum` is returned. Row sums are used to integrate all counts over one channel.

`RLum.Data.Image`

An object of type `RLum.Data.Image` is returned. Due to performance reasons the import is aborted for files containing more than 100 frames. This limitation can be overwritten manually by using the argument `frame.range`.

`matrix`

Returns a matrix of the form: Rows = Channels, columns = Frames For the transformation the function `get_RLum.Data.Spectrum` is used, meaning that the same results can be obtained by using the function `get_RLum.Data.Spectrum` on an `RLum.Data.Spectrum` object or `get_RLum.Data.Image` on an `RLum.Data.Image` object.

**Function version**

0.1 (2015-03-04 12:43:39)

**Note**

The function does not test whether the input data are spectra or pictures for spatial resolved analysis!

The function has been successfully tested for SPE format versions 2.x.

*Currently not all information provided by the SPE format are supported.*

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

**References**


Hall, C., 2012: readSPE.m. http://www.mathworks.com/matlabcentral/fileexchange/35940-readspe/content/readSPE.m

**See Also**

`readBin`, `RLum.Data.Spectrum`, `raster`
Examples

```r
temp <- readXSygRr(file)
```

### Usage

```r
readXSyg2R(file, recalculate.TL.curves = TRUE, import = TRUE, txtProgressBar = TRUE)
```

#### Arguments

- **file** character (required): path and file name of the XSYG file.
- **recalculate.TL.curves** logical (with default): if set to TRUE, TL curves are returned as temperature against count values (see details for more information) Note: The option overwrites the time vs. count TL curve. Select FALSE to import the raw data delivered by the lexsyg. Works for TL curves and spectra.
- **import** logical (with default): if set to FALSE, only the XSYG file structure is shown.
- **txtProgressBar** logical (with default): enables TRUE or disables FALSE the progression bar during import

---

**Description**

Imports XSYG files produced by a Freiberg Instrument lexsyg reader into R.
Details

**How does the import function work?**

The function uses the `xml` package to parse the file structure. Each sequence is subsequently translated into an `RLum.Analysis` object.

**General structure XSYG format**

```xml
<?xml?
<Sample>
<Sequence>
<Record>
<Curve name="first curve" />
<Curve name="curve with data"/>
 x0 , y0 ; x1 , y1 ; x2 , y2 ; x3 , y3
</Curve>
</Record>
</Sequence>
</Sample>
```

So far, each XSYG file can only contain one `<Sample></Sample>`, but multiple sequences.

Each record may comprise several curves.

**TL curve recalculation**

On the FI lexsysyg device TL curves are recorded as time against count values. Temperature values are monitored on the heating plate and stored in a separate curve (time vs. temperature). If the option `recalculate.TL.curves = TRUE` is chosen, the time values for each TL curve are replaced by temperature values.

Practically, this means combining two matrices (Time vs. Counts and Time vs. Temperature) with different row numbers by their time values. Three cases are considered:

- **HE**: Heating element
- **PMT**: Photomultiplier tube

Interpolation is done using the function `approx`

**CASE (1):** $\text{nrow(matrix(PMT))} > \text{nrow(matrix(HE))}$

Missing temperature values from the heating element are calculated using time values from the PMT measurement.

**CASE (2):** $\text{nrow(matrix(PMT))} < \text{nrow(matrix(HE))}$
Missing count values from the PMT are calculated using time values from the heating element measurement.

CASE (3): nrow(matrix(PMT)) == nrow(matrix(HE))

A new matrix is produced using temperature values from the heating element and count values from the PMT.

Note: Please note that due to the recalculation of the temperature values based on values delivered by the heating element, it may happen that multiple count values exist for each temperature value and temperature values may also decrease during heating, not only increase.

Value

Using the option import = FALSE

A list consisting of two elements is shown:

Sample data.frame with information on file.
Sequences data.frame with information on the sequences stored in the XSYG file.

Using the option import = TRUE (default)

A list is provided, the list elements contain:

Sequence.Header data.frame with information on the sequence.
Sequence.Object RLum.Analysis containing the curves.

Function version

0.4.1 (2015-03-21 03:09:47)

Note

This function is a beta version as the XSYG file format is not yet fully specified. Thus, further file operations (merge, export, write) should be done using the functions provided with the package xml.

So far, no image data import is provided!
Corresponding values in the XSXG file are skipped.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team
Risoe.BINfileData-class

References


Further reading


See Also

xml.RLum.Analysis, RLum.Data.Curve, approx

Examples

```r
##(1) import XSYG file to R (uncomment for usage)

#FILE <- file.choose()
#temp <- readXSYG2R(FILE)

##(2) additional examples for pure XML import using the package XML
## (uncomment for usage)

##import entire XML file
FILE <- file.choose()
#temp <- xmlRoot(xmlTreeParse(FILE))

##search for specific subnodes with curves containing 'OSL'
getNodeSet(temp, "//Sample/Sequence/Record[@recordType = 'OSL']/Curve")

##(2) How to extract single curves ... after import
data(ExampleData.XSYG, envir = environment())

##grep one OSL curves and plot the first curve
OSLCurve <- get_RLum.Analysis(OSL.SARMeasurement$Sequence.Object, recordType="OSL")[[1]]

##(3) How to see the structure of an object?
get_structure.RLum.Analysis(OSL.SARMeasurement$Sequence.Object)
```

Risoe.BINfileData-class

Class "Risoe.BINfileData"

Description

S4 class object for luminescence data in R. The object is produced as output of the function readBIN2R.
Objects from the Class

Objects can be created by calls of the form `new("Risoe.BINfileData", ...).`

Slots

`METADATA`: Object of class "data.frame" containing the meta information for each curve.

`DATA`: Object of class "list" containing numeric vector with count data.

`.RESERVED`: Object of class "list" containing list of undocumented raw values for internal use only.

`.S3Class`: Object of class "character"

Methods

`show` signature(object = "Risoe.BINfileData"): ...

`set_Risoe.BINfileData` signature(METADATA = "data.frame", DATA = "list", .RESERVED = "list"): The `Risoe.BINfileData` is normally produced as output of the function `readBIN2R`. This construction method is intended for internal usage only.

`get_Risoe.BINfileData` signature(object = "Risoe.BINfileData"): Formal get-method for `Risoe.BINfileData` object. It does not allow accessing the object directly, it is just showing a terminal message.

Version

0.4 (2014-02-27)

Note

Internal METADATA - object structure

<table>
<thead>
<tr>
<th>#</th>
<th>Name</th>
<th>Data Type</th>
<th>V</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>ID</td>
<td>numeric</td>
<td>RLum</td>
<td>Unique record ID (same ID as in slot DATA)</td>
</tr>
<tr>
<td>[2]</td>
<td>SEL</td>
<td>logic</td>
<td>RLum</td>
<td>Record selection, not part official BIN-format, triggered by TAG</td>
</tr>
<tr>
<td>[3]</td>
<td>VERSION</td>
<td>raw</td>
<td>03-06</td>
<td>BIN-file version number</td>
</tr>
<tr>
<td>[4]</td>
<td>LENGTH</td>
<td>integer</td>
<td>03-06</td>
<td>Length of this record</td>
</tr>
<tr>
<td>[5]</td>
<td>PREVIOUS</td>
<td>integer</td>
<td>03-06</td>
<td>Length of previous record</td>
</tr>
<tr>
<td>[6]</td>
<td>NPOINTS</td>
<td>integer</td>
<td>03-06</td>
<td>Number of data points in the record</td>
</tr>
<tr>
<td>[7]</td>
<td>RUN</td>
<td>integer</td>
<td>03-06</td>
<td>Run number</td>
</tr>
<tr>
<td>[8]</td>
<td>SET</td>
<td>integer</td>
<td>03-06</td>
<td>Set number</td>
</tr>
<tr>
<td>[9]</td>
<td>POSITION</td>
<td>integer</td>
<td>03-06</td>
<td>Position number</td>
</tr>
<tr>
<td>[10]</td>
<td>GRAIN</td>
<td>integer</td>
<td>03-04</td>
<td>Grain number</td>
</tr>
<tr>
<td>[11]</td>
<td>GRAINNUMBER</td>
<td>integer</td>
<td>06</td>
<td>Grain number</td>
</tr>
<tr>
<td>[12]</td>
<td>CURVENO</td>
<td>integer</td>
<td>06</td>
<td>Curve number</td>
</tr>
<tr>
<td>[13]</td>
<td>XCOORD</td>
<td>integer</td>
<td>03-06</td>
<td>X position of a single grain</td>
</tr>
<tr>
<td>[14]</td>
<td>YCOORD</td>
<td>integer</td>
<td>03-06</td>
<td>Y position of a single grain</td>
</tr>
<tr>
<td>[15]</td>
<td>SAMPLE</td>
<td>factor</td>
<td>03-06</td>
<td>Sample name</td>
</tr>
<tr>
<td>[16]</td>
<td>COMMENT</td>
<td>factor</td>
<td>03-06</td>
<td>Comment name</td>
</tr>
<tr>
<td>[17]</td>
<td>SYSTEMID</td>
<td>integer</td>
<td>03-06</td>
<td>Risoe system id</td>
</tr>
<tr>
<td>Field</td>
<td>Type</td>
<td>Description</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-------</td>
<td>------</td>
<td>-------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FNAME</td>
<td>factor</td>
<td>File name (<em>.bin/</em>.binx)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>USER</td>
<td>factor</td>
<td>User name</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TIME</td>
<td>character</td>
<td>Data collection time (hh-mm-ss)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DATE</td>
<td>factor</td>
<td>Data collection date (ddmmyy)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DTYPE</td>
<td>character</td>
<td>Data type</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BL_TIME</td>
<td>numeric</td>
<td>Bleaching time</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BL_UNIT</td>
<td>integer</td>
<td>Bleaching unit (mJ, J, secs, mins, hrs)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NORM1</td>
<td>numeric</td>
<td>Normalisation factor (1)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NORM2</td>
<td>numeric</td>
<td>Normalisation factor (2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NORM3</td>
<td>numeric</td>
<td>Normalisation factor (3)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>BG</td>
<td>numeric</td>
<td>Background level</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SHIFT</td>
<td>integer</td>
<td>Number of channels to shift data</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TAG</td>
<td>integer</td>
<td>Tag, triggers SEL</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LTYPE</td>
<td>character</td>
<td>Luminescence type</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LIGHTSOURCE</td>
<td>character</td>
<td>Light source</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LPOWER</td>
<td>numeric</td>
<td>Optical stimulation power</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LIGHTPOWER</td>
<td>numeric</td>
<td>Optical stimulation power</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LOW</td>
<td>numeric</td>
<td>Low (temperature, time, wavelength)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HIGH</td>
<td>numeric</td>
<td>High (temperature, time, wavelength)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RATE</td>
<td>numeric</td>
<td>Rate (heating rate, scan rate)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TEMPERATURE</td>
<td>integer</td>
<td>Sample temperature</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MEASTEMP</td>
<td>integer</td>
<td>Measured temperature</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AN_TEMP</td>
<td>numeric</td>
<td>Annealing temperature</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AN_TIME</td>
<td>numeric</td>
<td>Annealing time</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOLDELAY</td>
<td>integer</td>
<td>TOL 'delay' channels</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOLON</td>
<td>integer</td>
<td>TOL 'on' channels</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOLOFF</td>
<td>integer</td>
<td>TOL 'off' channels</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRR_TIME</td>
<td>numeric</td>
<td>Irradiation time</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRR_TYPE</td>
<td>integer</td>
<td>Irradiation type (alpha, beta or gamma)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRR_UNIT</td>
<td>integer</td>
<td>Irradiation unit (Gy, Rads, secs, mins, hrs)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRR_DOSE_RATE</td>
<td>numeric</td>
<td>Irradiation dose rate (Gy/s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRR_DOSE_RATE_ERR</td>
<td>numeric</td>
<td>Irradiation dose rate error (Gy/s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TIMESINCEIRR</td>
<td>integer</td>
<td>Time since irradiation (s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>TIMETICK</td>
<td>numeric</td>
<td>Time tick for pulsing (s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ONTIME</td>
<td>integer</td>
<td>On-time for pulsing (in time ticks)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>STIMPERIOD</td>
<td>integer</td>
<td>Stimulation period (on+off in time ticks)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GATE_ENABLED</td>
<td>raw</td>
<td>PMT signal gating enabled</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ENABLE_FLAGS</td>
<td>raw</td>
<td>PMT signal gating enabled</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GATE_START</td>
<td>integer</td>
<td>Start gating (in time ticks)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GATE_STOP</td>
<td>integer</td>
<td>Stop gating (in time ticks), 'Gateend' for version 04, here only GATE_STOP is used</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PTIME_ENABLED</td>
<td>raw</td>
<td>Photon time enabled</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DTENABLED</td>
<td>raw</td>
<td>PMT dead time correction enabled</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DEADM TIME</td>
<td>numeric</td>
<td>PMT dead time (s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAXLPOWER</td>
<td>numeric</td>
<td>Stimulation power to 100 percent (mW/cm^2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>XRF_ACQ_TIME</td>
<td>numeric</td>
<td>XRF acquisition time (s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>XRF_HV</td>
<td>numeric</td>
<td>XRF X-ray high voltage (V)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>XRF_CURR</td>
<td>integer</td>
<td>XRF X-ray current (uA)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>XRF_DEAD_TIME</td>
<td>numeric</td>
<td>XRF dead time fraction</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
**Risoe.BINfileData-class**

| V = BIN-file version (RLum means that it does not depend on a specific BIN version) |

- **Note** that the `Risoe.BINfileData` object combines all values from different versions from the BIN-file, reserved bits are skipped, however, the function `writeR2BIN` reset arbitrary reserved bits. Invalid values for a specific version are set to `NA`. Furthermore, the internal R data types do not necessarily match the required data types for the BIN-file data import! Data types are converted during data import.

**LTYPES**

| [0] TL | : Thermoluminescence |
| [1] OSL | : Optically stimulated luminescence |
| [5] TOL | : Thermo-optical luminescence |
| [7] RIR | : Ramped IRSL |
| [8] RBR | : Ramped (Blue) LEDs |
| [9] USER | : User defined |
| [10] POSL | : Pulsed OSL |

**LTYPES**

| [0] 0 | Natural |
| [1] 1 | N+dose |
| [2] 2 | Bleach |
| [3] 3 | Bleach+dose |
| [4] 4 | Natural (Bleach) |
| [5] 5 | N+dose (Bleach) |
| [6] 6 | Dose |
| [7] 7 | Background |

(information on the LTYPE and Dtype kindly provided by Risoe, DTU Nutech)

**Author(s)**

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

**References**

Risoe DTU, 2013. The Sequence Editor User Manual - Feb 2013
Risoe.BINfileData2RLum.Analysis

http://www.nutech.dtu.dk/

See Also

Examples
showClass("Risoe.BINfileData")

Risoe.BINfileData2RLum.Analysis

Convert Risoe.BINfileData object to an RLum.Analysis object

Description
Converts values from one specific position of a Risoe.BINfileData S4-class object to an RLum.Analysis object.

Usage
Risoe.BINfileData2RLum.Analysis(object, pos, run, set, ltype, protocol = "unknown")

Arguments

object Risoe.BINfileData (required): Risoe.BINfileData object
pos integer (required): position number of the Risoe.BINfileData object for which the curves are stored in the RLum.Analysis object. If the position is not valid NA is returned.
run vector, numeric (optional): run number from the measurement to limit the converted data set (e.g., run = c(1:48)).
set vector, numeric (optional): set number from the measurement to limit the converted data set (e.g., set = c(1:48)).
ltype vector, character (optional): curve type to limit the converted data. Allowed values are: IRSL, OSL, TL, RIR, RBR and USER
protocol character (optional): sets protocol type for analysis object. Value may be used by subsequent analysis functions.

Details
The RLum.Analysis object requires a set of curves for specific further protocol analyses. However, the Risoe.BINfileData usually contains a set of curves for different aliquots and different protocol types that may be mixed up. Therefore, a conversion is needed.
Value

Returns an \texttt{RLum.Analysis} object.

Function version

0.1.2 (2015-03-04 00:19:53)

Note

The protocol argument of the \texttt{RLum.Analysis} object is set to 'unknown' if not stated otherwise.

Author(s)

Sebastian Kreutzer, JLU Giessen (Germany), R Luminescence Package Team

References

#

See Also

\texttt{Risoe.BINfileData}, \texttt{RLum.Analysis}, \texttt{readBIN2R}

Examples

```
# load data
data(ExampleData.BINfileData, envir = environment())

# convert values for position 1
Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos = 1)
```

---

\texttt{Risoe.BINfileData2RLum.Data.Curve}

\textit{Convert an element from a \texttt{Risoe.BINfileData} object to an \texttt{RLum.Data.Curve} object}

---

Description

The function converts one specified single record from a \texttt{Risoe.BINfileData} object to an \texttt{RLum.Data.Curve} object.

Usage

\texttt{Risoe.BINfileData2RLum.Data.Curve(object, id, pos, run, set)}
Arguments

object  Risoe.BINfileData (required): Risoe.BINfileData object

id  integer (required): record id in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If no value for id is provided, the record has to be specified by pos, set and run.

pos  integer (optional): record position number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.

run  integer (optional): record run number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.

set  integer (optional): record set number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.

Details

The function extracts all METADATA from the Risoe.BINfileData object and stores them in the RLum.Data.Curve object.

Value


Function version

0.1 (2015-03-04 00:19:53)

Note

The function is intended for experimental usage. Normally, the function Risoe.BINfileData2RLum.Analysis should be used for the conversion.

Author(s)

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany),
R Luminescence Package Team

References

#

See Also

**Examples**

```r
## get package example data
data(ExampleData.BINfileData, envir = environment())
```

```r
## convert one record
Risoe.BINfileData2RLum.Data.Curve(CWOSL.SAR.Data, id = 1)
```

---

**Description**

Abstract class for data in the package Luminescence

**Objects from the Class**

A virtual Class: No objects can be created from it.

**Slots**

- `.S3Class`: Object of class "character"

**Methods**

No methods defined with class "RLum" in the signature.

**Version**

0.1 (2013-01-18)

**Note**

RLum is a virtual class.

**Author(s)**

Sebastian Kreutzer, 2013 (Freiberg Instruments/JLU Giessen, Germany)

**References**

#

**See Also**

RLum.Data, RLum.Analysis
Examples

showClass("RLum")

---

**Description**

Object class containing analysis data for protocol analysis.

**Objects from the Class**

Objects can be created by calls of the form `new("RLum.Analysis", ...)`.

**Slots**

- records: Object of class "list" containing objects of class `RLum.Data`
- protocol: Object of class "character" describing the applied measurement protocol
- .S3Class: Object of class "character"

**Methods**

- **show** signature(object = "RLum.Analysis"): ...
- **set_RLum.Analysis** signature(records = "list", protocol = "character"): Construction method for `RLum.Analysis` object. The slot protocol is optional and predefined as UNKNOWN by default.
  The slots record.id, record.type, curve.type and rlum.type are optional to allow for records limited by their id (list index number), their record type (e.g. record.type = "OSL") or object type.
  Example: curve type (e.g. curve.type = "predefined" or curve.type = "measured")
  
  **The selection of a specific RLum.type object superimposes the default selection.** Currently supported objects are: RLum.Data.Curve and RLum.Data.Spectrum

  The argument get.index = TRUE just returns a numeric vector with the index of each element in the RLum.Analysis object.
  The argument keep.object allowing returns an RLum.Analysis object instead of the single elements. Default is keep.object = FALSE.

- **get_structure.RLum.Analysis** signature(object = "RLum.Analysis"): get meta structure of object as data.frame
- **length_RLum.Analysis** signature(object = "RLum.Analysis"): returns length of the object, i.e., number of records in the object
**Version**

0.1.4 (2014-02-26)

**Note**

The method `get_structure.RLum.Analysis` is currently just available for objects containing `RLum.Data.Curve`.

**Author(s)**

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany)

**References**

#

**See Also**

`Riso2BNfile2RLum.BAnalysis`, `Riso2BNfile2RLum.BRLum`

**Examples**

```r
showClass("RLum.BAnalysis")

## usage of get_RLum.Analysis() with returning an RLum.Analysis object
# get_RLum.Analysis(object, keep.object = TRUE)
```

---

**Description**

Generalized virtual data class for luminescence data.

**Objects from the Class**

A virtual Class: No objects can be created from it.

**Slots**

`.S3Class`: Object of class "character"

**Methods**

No methods defined with class "RLum.Data" in the signature.
Version
0.1 (2013-01-18)

Note
Just a virtual class.

Author(s)
Sebastian Kreutzer, 2013 (Freiberg Instruments/JLU Giessen, Germany)

References
#

See Also

Examples
showClass("RLum.Data")

---

**Description**

Class for luminescence curve data.

**Objects from the Class**

Objects can be created by calls of the form `new("RLum.Data.Curve", ...).`

**Slots**

- `recordType`: Object of class "character" containing the type of the curve (e.g. "TL" or "OSL")
- `curveType`: Object of class "character" containing curve type, allowed values are measured or predefined
- `data`: Object of class "matrix" containing curve x and y data
- `info`: Object of class "list" containing further meta information objects
- `.S3Class`: Object of class "character"

**Extends**

Class "RLum.Data".
Methods

**coerce** signature(from = "data.frame", to = "RLum.Data.Curve")
signature(from = "matrix", to = "RLum.Data.Curve")
Furthermore, lossy coercing is possible from RLum.Data.Curve to:

```
data.frame, matrix
```

**show** signature(object = "RLum.Data.Curve"): ...

**set_RLum.Data.Curve** signature(recordType = "character", curveType = "character", data = "matrix", info = "character"): Construction method for RLum.Data.Curve object. The slot info is optional and predefined as empty list by default.

**get_RLum.Data.Curve** signature(object = "RLum.Data.Curve", info.object = "character"): Accessor method for RLum.Data.Curve object. The argument info.object is optional to directly access the info elements. If no info element name is provided, the raw curve data (matrix) will be returned.

Version

0.1.2 (2013-11-22)

Note

The class should only contain data for a single curve. For additional elements the slot info can be used (e.g. providing additional heating ramp curve).

Author(s)

Sebastian Kreutzer Freiberg Instruments/JLU Giessen (Germany)

References

#

See Also

`RLum, RLum.Data, plot_RLum`

Examples

```
showClass("RLum.Data.Curve")
```
RLum.Data.Image-class  

Description

Class for luminescence image data (TL/OSL/RF).

Objects from the Class

Objects can be created by calls of the form `new("RLum.Data.Image", ...)`. 

Slots

- **recordType**: Object of class "character" containing the type of the curve (e.g. "OSL image", "TL image")
- **curveType**: Object of class "character" containing curve type, allowed values are measured or predefined
- **data**: Object of class "RasterBrick" containing images (raster data).
- **info**: Object of class "list" containing further meta information objects
- **S3Class**: Object of class "character"

Extends

Class "RLum.Data", directly.

Methods

- **coerce** signature(from = "data.frame", to = "RLum.Data.Image")
  signature(from = "matrix", to = "RLum.Data.Image")
  Furthermore, lossy coercing is possible from RLuc.Dat.Image to:

  - **data.frame**, **matrix**

- **show** signature(object = "RLum.Data.Image"): ... 

- **set_RLum.Data.Image** signature(recordType = "character", curveType = "character", data = "RasterBrick")
  Construction method for RLuc.Data.Image object. The slot **info** is optional and predefined as empty list by default.

- **get_RLum.Data.Image** signature(object = "RLum.Data.Image", info.object = "character")
  Accessor method for RLuc.Data.Image object. The argument info.object is optional to directly access the info elements. If no info element name is provided, the raw image data (RasterBrick) will be returned.

Version

0.1 (2014-07-22)
Note
The class should only contain data for a set of images. For additional elements the slot `info` can be used.

Author(s)
Sebastian Kreutzer, Universite Bordeaux Montaigne (France)

References
#

See Also
`RLum`, `RLum.Data`, `plot_RLum`

Examples

```r
showClass("RLum.Data.Image")
```

## so far no further example available

---

**RLum.Data.Spectrum-class**

Class "RLum.Data.Spectrum"

---

Description
Class for luminescence spectra data (TL/OSL/RF).

Objects from the Class
Objects can be created by calls of the form `new("RLum.Data.Spectrum", ...)`.  

Slots
- `recordType`: Object of class "character" containing the type of the curve (e.g. "TL" or "OSL")
- `curveType`: Object of class "character" containing curve type, allowed values are measured or predefined
- `data`: Object of class "matrix" containing spectrum (count) values.
  - **Row labels** indicating wavelength/pixel values
  - **Column labels** temperature or time values.
- `info`: Object of class "list" containing further meta information objects
- `.S3Class`: Object of class "character"
**Extends**

Class "RLum.Data", directly.

**Methods**

- **coerce** signature(from = "data.frame", to = "RLum.Data.Spectrum")
- signature(from = "matrix", to = "RLum.Data.Spectrum")

Furthermore, lossy coercing is possible from RLum.Data.Spectrum to:

- `data.frame`
- `matrix`

- **show** signature(object = "RLum.Data.Spectrum"): ...  

- **set_RLum.Data.Spectrum** signature(recordType = "character", curveType = "character", data = "matrix", info = "list"):  

  Construction method for RLum.Data.Spectrum object. The slot info is optional and predefined as empty list by default.


  Accessor method for RLum.Data.Spectrum object. The argument info.object is optional to directly access the info elements. If no info element name is provided, the raw curve data (matrix) will be returned.

**Version**

0.1 (2013-11-23)

**Note**

The class should only contain data for a single spectra data set. For additional elements the slot info can be used.

**Author(s)**

Sebastian Kreutzer, JLU Giessen (Germany)

**References**

#

**See Also**

RLum, RLum.Data, plot_RLum

**Examples**

```r
showClass("RLum.Data.Spectrum")
```

```
# show example data (uncomment for usage)
# data(ExampleData.XSYG, envir = environment())
# TL.Spectrum
```
Description

Object class contains results data from functions.

Objects from the Class

Objects can be created by calls of the form `new("RLum.Results", ...)`.

Slots

- `originator`: Object of class "character" containing name of the producing function
- `data`: Object of class "list" containing output data
- `.S3Class`: Object of class "character"

Methods

- `validObject` signature(object = "RLum.Results"): validates object depending on the `originator` argument
- `show` signature(object = "RLum.Results"): ...
- `set_RLum.Results` signature(originator = "character", data = "list"): Construction method for `RLum.Results` object. The slot `originator` is optional and pre-defined as the function that calls the function `set_RLum.Results`.
- `get_RLum.Results` signature(object = "RLum.Results", data.object = "character"): accessor method for `RLum.Results` object. The argument `data.object` allows directly accessing objects delivered within the slot data. If no `data.object` is specified, a pre-selected object is returned. The default return object depends on the object `originator` (e.g. `fit_LMCurve`).
- `merge_RLum.Results` signature(object.list = "list"): merge method for `RLum.Results` objects. The argument `object.list` requires a list of `RLum.Results` objects. Merging is done by appending similar elements to the first object of the input list.

Version

0.2.3 (2014-12-16)

Note

The class is intended to store results from functions to be used by other functions. The data in the object should always be accessed by the method `get_RLum.Results`.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
Conversion of absorbed radiation dose in seconds (s) to the SI unit gray (Gy) including error propagation. Normally used for equivalent dose data.

Usage

Second2Gray(data, dose.rate, method = "gaussian")

Arguments

data data.frame (required): input values, structure: data (values[,1]) and data error (values[,2]) are required
dose.rate RLUm.Results or vector (required): RLUm.Results needs to be originated from the function calc_SourceDoseRate, for vector dose rate in Gy/s and dose rate error in Gy/s
method character (with default): method used for error calculation (gaussian or absolute), see details for further information

Details

Calculation of De values from seconds (s) to gray (Gy)

\[
De[Gy] = De[s] \times DoseRate[Gy/s]
\]

Provided calculation methods for error calculation: \textbf{gaussian} error propagation

\[
De.error.gray = \sqrt{(dose.rate \times De.error.seconds)^2 + (De.seconds \times dose.rate.error)^2})
\]

\textbf{absolute} error propagation

\[
De.error.gray = abs(dose.rate \times De.error.seconds) + abs(De.seconds \times dose.rate.error)
\]
Value

Returns a data.frame with converted values.

Function version

0.4 (2015-03-04 13:42:29)

Note

If no or a wrong method is given, the execution of the function is stopped.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany),
Margret C. Fuchs, AWI Potsdam (Germany),
R Luminescence Package Team

References

#

See Also

#

Examples

###(A) for known source dose rate at date of measurement
## - load De data from the example data help file
data(ExampleData.DeValues, envir = environment())
## - convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, c(0.0438,0.0019))

###(B) for source dose rate calibration data
## - calculate source dose rate first
dose.rate <- calc_SourceDoseRate(measurement.date = "2012-01-27",
  calib.date <- "2014-12-19",
  calib.dose.rate <- 0.0438,
  calib.error <- 0.0019)

# read example data
data(ExampleData.DeValues, envir = environment())

# apply dose.rate to convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, dose.rate)
Description

This function provides a sophisticated routine for comprehensive luminescence dating data analysis.

Usage

steve (n_frames = 10, t_animation = 2, n.tree = 7, type)

Arguments

- n_frames: integer (with default): n frames
- t_animation: integer (with default): t animation
- n.tree: integer (with default): How many trees do you want to cut?
- type: integer (optional): Make a decision: 1, 2 or 3

Details

This amazing sophisticated function validates your data seriously.

Value

Validates your data.

Note

This function should not be taken too seriously.

Author(s)

R Luminescence Team, 2012-2013

References

#

See Also

plot_KDE

Examples

##No example available
writeR2BIN  

Export Risoe.BINfileData into Risoe BIN-file

Description

Exports a Risoe.BINfileData object in a *.bin or *.binx file that can be opened by the Analyst software or other Risoe software.

Usage

writeR2BIN(object, file, version, txtProgressBar = TRUE)

Arguments

- **object**  
  *Risoe.BINfileData* *(required)*: input object to be stored in a bin file.

- **file**  
  *character* *(required)*: file name and path of the output file  
  [WIN]: writeR2BIN(object, "C:/Desktop/test.bin").  
  [MAC/LINUX]: writeR2BIN("/User/test/Desktop/test.bin")

- **version**  
  *character* *(optional)*: version number for the output file. If no value is provided the highest version number from the *Risoe.BINfileData* is taken automatically.

  Note: This argument can be used to convert BIN-file versions.

- **txtProgressBar**  
  *logical* *(with default)*: enables or disables *txtProgressBar*.

Details

The structure of the exported binary data follows the data structure published in the Appendices of the Analyst manual p. 42.

If LTYPE, DTYPE and LIGHTSOURCE are not of type *character*, no transformation into numeric values is done.

Value

Write a binary file.

Function version

0.2.5 (2015-03-23 12:57:25)
Note

The function just roughly checks the data structures. The validity of the output data depends on the user.

The validity of the file path is not further checked. BIN-file conversions using the argument version may be a lossy conversion, depending on the chosen input and output data (e.g., conversion from version 06 to 04 or 03).

Warning

Although the coding was done carefully it seems that the BIN/BINX-files produced by Risoe DA 15/20 TL/OSL readers slightly differ on the byte level. No obvious differences are observed in the METADATA, however, the BIN/BINX-file may not fully compatible, at least not similar to the once directly produced by the Risoe readers!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References


See Also

readBIN2R, Risoe.BINfileData, writeBin

Examples

```r
# uncomment for usage

data(ExampleData.BINfileData, envir = environment())
writeR2BIN(CWOSL.SAR.Data, file="[your path]/output.bin")
```
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