

# Package ‘gamma’

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**Title** Dose Rate Estimation from in-Situ Gamma-Ray Spectrometry Measurements

**Version** 1.0.0

**Maintainer** Brice Lebrun

<brice.lebrun@u-bordeaux-montaigne.fr>

**Description** Process in-situ Gamma-Ray Spectrometry for Luminescence Dating. This package allows to import, inspect and correct the energy shifts of Gamma-ray spectra. It provides methods for estimating the gamma dose rate by the use of a calibration curve. The package only supports Canberra CNF and TKA files.

**License** GPL-3

**URL** <https://crp2a.github.io/gamma/>, <https://github.com/crp2a/gamma>

**BugReports** <https://github.com/crp2a/gamma/issues>

**Depends** R (>= 3.5)

**Imports** ggplot2, graphics, IsoplotR, methods, rlang, rxylib, stats, tools, utils

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'baseline\_rubberband.R' 'baseline\_snip.R' 'coerce.R' 'data.R'  
'dose\_fit.R' 'dose\_predict.R' 'energy\_calibrate.R'  
'gamma-package.R' 'initialize.R' 'mutators.R' 'operators.R'  
'peaks\_find.R' 'plot.R' 'read.R' 'show.R' 'signal\_integrate.R'  
'signal\_slice.R' 'signal\_stabilize.R' 'smooth.R'  
'smooth\_rectangular.R' 'smooth\_savitzky.R'  
'smooth\_triangular.R' 'subset.R' 'summarize.R' 'utilities.R'  
'validate.R'

**NeedsCompilation** no

**Author** Nicolas Frerebeau [aut] (<<https://orcid.org/0000-0001-5759-4944>>),  
 Brice Lebrun [aut, cre] (<<https://orcid.org/0000-0001-7503-8685>>),  
 Guilhem Paradol [aut],  
 Magali Rizza [ctb] (<<https://orcid.org/0000-0003-2364-5621>>),  
 Christelle Lahaye [ctb] (<<https://orcid.org/0000-0003-2215-9015>>),  
 Université Bordeaux Montaigne [cph, fnd],  
 CNRS [fnd],  
 LabEx Sciences archéologiques de Bordeaux [fnd],  
 Idex Aix-Marseille [fnd]

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`AIX_NaI_1`*CEREGE Calibration Curve (NaI)*

---

**Description**

CEREGE Calibration Curve (NaI)

**Usage**`data(AIX_NaI_1)`**Format**An object of class `CalibrationCurve`.

<b>Laboratory</b>	CEREGE
<b>Instrument</b>	Canberra Inspector 1000
<b>Detector</b>	NaI
<b>Authors</b>	CEREGE Luminescence Team

**See Also**Other datasets: `BDX_LaBr_1`, `clermont`**Examples**

```
## Load the curve
utils::data(AIX_NaI_1, package = "gamma")
plot(AIX_NaI_1)
```

---

`baseline`*Baseline Estimation and Removal*

---

**Description**

Baseline Estimation and Removal

**Usage**`signal_baseline(object, ...)``signal_correct(object, ...)``baseline_snip(object, ...)``baseline_rubberband(object, ...)`

```
## S4 method for signature 'GammaSpectrum'
signal_baseline(object, method = c("SNIP", "rubberband"), ...)

## S4 method for signature 'GammaSpectra'
signal_baseline(object, method = c("SNIP", "rubberband"), ...)

## S4 method for signature 'GammaSpectrum'
signal_correct(object, method = c("SNIP", "rubberband"), ...)

## S4 method for signature 'GammaSpectra'
signal_correct(object, method = c("SNIP", "rubberband"), ...)

## S4 method for signature 'GammaSpectrum'
baseline_rubberband(object, noise = 0, spline = TRUE, ...)

## S4 method for signature 'GammaSpectra'
baseline_rubberband(object, noise = 0, spline = TRUE, ...)

## S4 method for signature 'GammaSpectrum'
baseline_snip(object, LLS = FALSE, decreasing = FALSE, n = 100, ...)

## S4 method for signature 'GammaSpectra'
baseline_snip(object, LLS = FALSE, decreasing = FALSE, n = 100, ...)
```

### Arguments

object	A <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object.
...	Extra parameters to be passed to further methods.
method	A <a href="#">character</a> string specifying the method to be used for baseline estimation (see details). Any unambiguous substring can be given.
noise	A length-one <a href="#">numeric</a> vector giving the noise level. Only used if method is "rubberband".
spline	A <a href="#">logical</a> scalar: should spline interpolation through the support points be used instead of linear interpolation? Only used if method is "rubberband".
LLS	A <a href="#">logical</a> scalar: should the LLS operator be applied on x before employing SNIP algorithm? Only used if method is "SNIP".
decreasing	A <a href="#">logical</a> scalar: should a decreasing clipping window be used? Only used if method is "SNIP".
n	An <a href="#">integer</a> value giving the number of iterations. Only used if method is "SNIP".

### Details

The following methods are available for baseline estimation:

**SNIP** Sensitive Nonlinear Iterative Peak clipping algorithm.

**rubberband**

**Value**

baseline\_\* returns a [BaseLine](#) object.

signal\_correct returns a corrected [GammaSpectrum](#) or [GammaSpectra](#) object (same as object).

**Note**

baseline\_rubberband is slightly modified from C. Beleites' [spc.rubberband](#).

**Author(s)**

N. Frerebeau

**References**

Liland, K. H. (2015). 4S Peak Filling - baseline estimation by iterative mean suppression. *MethodsX*, 2, 135-140. DOI: [10.1016/j.mex.2015.02.009](#).

Morháč, M., Kliman, J., Matoušek, V., Veselský, M. & Turzo, I. (1997). Background elimination methods for multidimensional gamma-ray spectra. *Nuclear Instruments and Methods in Physics Research Section A: Accelerators, Spectrometers, Detectors and Associated Equipment*, 401(1), p. 113-132. DOI: [10.1016/S0168-9002\(97\)01023-1](#)

Morháč, M. & Matoušek, V. (2008). Peak Clipping Algorithms for Background Estimation in Spectroscopic Data. *Applied Spectroscopy*, 62(1), p. 91-106. DOI: [10.1366/000370208783412762](#)

Ryan, C. G., Clayton, E., Griffin, W. L., Sie, S. H. & Cousens, D. R. (1988). SNIP, a statistics-sensitive background treatment for the quantitative analysis of PIXE spectra in geoscience applications. *Nuclear Instruments and Methods in Physics Research Section B: Beam Interactions with Materials and Atoms*, 34(3), p. 396-402. DOI: [10.1016/0168-583X\(88\)90063-8](#)

**See Also**

Other signal processing: [peaks\\_find\(\)](#), [signal\\_integrate\(\)](#), [signal\\_slice\(\)](#), [signal\\_stabilize\(\)](#), [smooth\(\)](#)

**Examples**

```
## Import a CNF file
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(spc_file)

## Remove the first 35 channels
spc <- signal_slice(spc, -c(1:35))

## SNIP baseline
bsl_snip <- baseline_snip(spc, LLS = FALSE, decreasing = FALSE, n = 100)
plot(spc, bsl_snip)

## Rubberband baseline
bsl_rubber <- baseline_rubberband(spc)
plot(spc, bsl_rubber)
```

```
## Remove baseline
spc_clean1 <- signal_correct(spc)
spc_clean2 <- spc - bsl_snip
all(spc_clean1 == spc_clean2)

plot(spc_clean1)
```

---

Baseline-class      *An S4 Class to Represent a Spectrum Baseline*

---

## Description

An S4 Class to Represent a Spectrum Baseline

## Note

This class extends the [GammaSpectrum](#) class.

## Author(s)

N. Frerebeau

## See Also

Other class: [CalibrationCurve-class](#), [GammaSpectra-class](#), [GammaSpectrum-class](#), [PeakPosition-class](#), [coerce\(\)](#)

## Examples

```
## Import a CNF file
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(spc_file)

## Remove the first 35 channels
spc <- signal_slice(spc, -c(1:35))

## SNIP baseline
bsl_snip <- baseline_snip(spc, LLS = FALSE, decreasing = FALSE, n = 100)
plot(spc, bsl_snip)

## Rubberband baseline
bsl_rubber <- baseline_rubberband(spc)
plot(spc, bsl_rubber)

## Remove baseline
spc_clean1 <- signal_correct(spc)
spc_clean2 <- spc - bsl_snip
all(spc_clean1 == spc_clean2)

plot(spc_clean1)
```

---

`BDX_LaBr_1`*CRP2A Calibration Curve (LaBr)*

---

**Description**

CRP2A Calibration Curve (LaBr)

**Usage**`data(BDX_LaBr_1)`**Format**An object of class [CalibrationCurve](#).

<b>Laboratory</b>	IRAMAT-CRP2A (UMR 5060)
<b>Instrument</b>	Canberra Inspector 1000
<b>Detector</b>	LaBr
<b>Authors</b>	CRP2A Luminescence Team

**See Also**Other datasets: [AIX\\_NaI\\_1](#), [clermont](#)**Examples**

```
## Load the curve
utils::data(BDX_LaBr_1, package = "gamma")
plot(BDX_LaBr_1)
```

---

`CalibrationCurve-class`*An S4 class to Represent a Dose Rate Calibration Curve*

---

**Description**

An S4 class to Represent a Dose Rate Calibration Curve

**Slots**`Ni` A [DoseRateModel](#) object.`NiEi` A [DoseRateModel](#) object.`details` A [list](#) of length-one vector giving the curve metadata.`slope` A [numeric](#) vector.`intercept` A [numeric](#) vector.

covariance A [numeric](#) vector.  
MSWD A [numeric](#) vector.  
df A [numeric](#) vector.  
p\_value A [numeric](#) vector.  
data A [data.frame](#).  
range A [numeric](#) vector.  
background A [numeric](#) vector.

### Subset

In the code snippets below, x is a CalibrationCurve object.

`x[[i]]` Extracts informations from a slot selected by subscript i. i is a character vector of length one.

### Author(s)

N. Frerebeau

### See Also

Other class: [Baseline-class](#), [GammaSpectra-class](#), [GammaSpectrum-class](#), [PeakPosition-class](#), [coerce\(\)](#)

---

clermont

*Clermont Reference Data*

---

### Description

Clermont Reference Data

### Usage

```
data("clermont")
```

### Format

TODO

### Source

Guérin, G., Mercier, N. & Adamiec, G. (2011). Dose-Rate Conversion Factors: Update. *Ancient TL*, 29(1), p. 5-8.

Miallier, D., Guérin, G., Mercier, N., Pilleyre, T. & Sanzelle, S. (2009). The Clermont Radiometric Reference Rocks: A Convenient Tool for Dosimetric Purposes. *Ancient TL*, 27(2), p. 37-44.

### See Also

Other datasets: [AIX\\_NaI\\_1](#), [BDX\\_LaBr\\_1](#)

---

coerce	<i>Coerce</i>
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---

## Description

Coerce

## Usage

```
## S3 method for class 'GammaSpectrum'  
as.matrix(x, ...)
```

## Arguments

x	An object to be coerced.
...	Currently not used.

## Value

A coerced object.

## Author(s)

N. Frerebeau

## See Also

Other class: [Baseline-class](#), [CalibrationCurve-class](#), [GammaSpectra-class](#), [GammaSpectrum-class](#), [PeakPosition-class](#)

## Examples

```
## Import a Canberra CNF file  
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")  
spc <- read(spc_file)  
  
## Coerce  
mtx <- as.matrix(spc)  
df <- as.data.frame(spc)  
head(df)
```

---

`dose_rate`*Dose Rate Estimation*

---

**Description**

`dose_fit` builds a calibration curve for gamma dose rate estimation.

**Usage**

```
dose_fit(object, background, doses, ...)
```

```
dose_predict(object, spectrum, ...)
```

```
## S4 method for signature 'GammaSpectra,GammaSpectrum,matrix'
```

```
dose_fit(  
  object,  
  background,  
  doses,  
  range_Ni,  
  range_NiEi,  
  alpha = 0.05,  
  details = list(authors = "", date = Sys.time())  
)
```

```
## S4 method for signature 'GammaSpectra,GammaSpectrum,data.frame'
```

```
dose_fit(  
  object,  
  background,  
  doses,  
  range_Ni,  
  range_NiEi,  
  alpha = 0.05,  
  details = list(authors = "", date = Sys.time())  
)
```

```
## S4 method for signature 'CalibrationCurve,missing'
```

```
dose_predict(object, sigma = 1, epsilon = 0)
```

```
## S4 method for signature 'CalibrationCurve,GammaSpectrum'
```

```
dose_predict(object, spectrum, sigma = 1, epsilon = 0)
```

```
## S4 method for signature 'CalibrationCurve,GammaSpectra'
```

```
dose_predict(object, spectrum, sigma = 1, epsilon = 0)
```

**Arguments**

`object` A [GammaSpectra](#) or [CalibrationCurve](#) object.

background	A <a href="#">GammaSpectrum</a> object of a length-two <a href="#">numeric</a> vector giving the background noise integration value and error, respectively.
doses	A <a href="#">matrix</a> or <a href="#">data.frame</a> TODO.
...	Currently not used.
spectrum	An optional <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object in which to look for variables with which to predict. If omitted, the fitted values are used.
range_Ni, range_NiEi	A length-two <a href="#">numeric</a> vector giving the energy range to integrate within (in keV).
alpha	A <a href="#">numeric</a> value giving the cutoff value for confidence intervals (see <a href="#">york</a> ).
details	A <a href="#">list</a> of length-one vector specifying additional informations about the instrument for which the curve is built.
sigma	A <a href="#">numeric</a> value giving TODO.
epsilon	A <a href="#">numeric</a> value giving an extra error term introduced by the calibration of the energy scale of the spectrum.

### Details

`dose_predict` predicts in situ gamma dose rate.

To estimate the gamma dose rate, one of the calibration curves distributed with this package can be used (fig. [\@ref\(fig:curve\)](#)). These built-in curves are in use in several luminescence dating laboratories and can be used to replicate published results. As these curves are instrument specific, the user may have to build its own curve.

The construction of a calibration curve requires a set of reference spectra for which the gamma dose rate is known and a background noise measurement. First, each reference spectrum is integrated over a given interval, then normalized to active time and corrected for background noise. The dose rate is finally modelled by the integrated signal value used as a linear predictor (York *et al.*, 2004).

See `vignette(doserate)` for a reproducible example.

### Value

`dose_fit` returns a [CalibrationCurve](#) object.

`dose_predict` returns a [data.frame](#) with the following columns:

**name** ([character](#)) the name of the spectra.

**\*\_signal** ([numeric](#)) the integrated signal value (according to the value of threshold; see [signal\\_integrate](#)).

**\*\_error** ([numeric](#)) the integrated signal error value (according to the value of threshold; see [signal\\_integrate](#)).

**gamma\_signal** ([numeric](#)) the predicted gamma dose rate.

**gamma\_error** ([numeric](#)) the predicted gamma dose rate error.

### Author(s)

N. Frerebeau

## References

Mercier, N. & Falguères, C. (2007). Field Gamma Dose-Rate Measurement with a NaI(Tl) Detector: Re-Evaluation of the "Threshold" Technique. *Ancient TL*, 25(1), p. 1-4.

York, D., Evensen, N. M., Martínez, M. L. & De Basabe Delgado, J. (2004). Unified Equations for the Slope, Intercept, and Standard Errors of the Best Straight Line. *American Journal of Physics*, 72(3), p. 367-75. DOI: [10.1119/1.1632486](https://doi.org/10.1119/1.1632486).

## See Also

[signal\\_integrate](#)

## Examples

```
## Import CNF files
## Spectra
spc_dir <- system.file("extdata/BDX_LaBr_1/calibration", package = "gamma")
spc <- read(spc_dir)

## Background
bkg_dir <- system.file("extdata/BDX_LaBr_1/background", package = "gamma")
bkg <- read(bkg_dir)

## Get dose rate values
data("clermont")
(doses <- clermont[, c("gamma_dose", "gamma_error")])

## Build the calibration curve
calib_curve <- dose_fit(spc, bkg, doses,
                      range_Ni = c(300, 2800),
                      range_NiEi = c(165, 2800))

## Plot the curve
plot(calib_curve, threshold = "Ni")

## Estimate gamma dose rates
dose_predict(calib_curve, spc)
```

---

energy

*Energy Scale Calibration*

---

## Description

Calibrates the energy scale of a gamma spectrum.

**Usage**

```
energy_calibrate(object, lines, ...)  
  
has_energy(object)  
  
## S4 method for signature 'GammaSpectrum,list'  
energy_calibrate(object, lines, ...)  
  
## S4 method for signature 'GammaSpectrum,PeakPosition'  
energy_calibrate(object, lines, ...)  
  
## S4 method for signature 'GammaSpectrum'  
has_energy(object)  
  
## S4 method for signature 'GammaSpectra'  
has_energy(object)
```

**Arguments**

object	A <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object.
lines	A <a href="#">PeakPosition</a> object or a <a href="#">list</a> of length two. If a <a href="#">list</a> is provided, each element must be a named numeric vector giving the observed peak position ("channel") and the corresponding expected "energy" value (in keV).
...	Currently not used.

**Details**

The energy calibration of a spectrum is the most tricky part. To do this, the user must specify the position of at least three observed peaks and the corresponding energy value (in keV). A second order polynomial model is fitted on these energy *vs* channel values, then used to predict the new energy scale of the spectrum.

The package allows to provide the channel-energy pairs to be use. However, the spectrum can be noisy so it is difficult to properly determine the peak channel. In this case, a better approach may be to pre-process the spectrum (variance-stabilization, smoothing and baseline correction) and perform a peak detection. Once the identified peaks are satisfactory, you can set the corresponding energy values (in keV) and use these lines to calibrate the energy scale of the spectrum.

Regardless of the approach you choose, it is strongly recommended to check the result before proceeding.

**Value**

energy\_calibrate returns a [GammaSpectrum](#) object.  
has\_energy returns a [logical](#) vector.

**Author(s)**

N. Frerebeau

**Examples**

```

## Import a CNF file
spc_file <- system.file("extdata/LaBr.TKA", package = "gamma")
(spc <- read(spc_file))

## Set peak positions (channel) and expected energy values
calib_lines <- list(
  channel = c(86, 495, 879),
  energy = c(238, 1461, 2615)
)

## Adjust the energy scale
(spc1 <- energy_calibrate(spc, lines = calib_lines))

## Inspect results
plot(spc1, xaxis = "energy", yaxis = "count") +
  ggplot2::geom_vline(xintercept = c(238, 1461, 2614.5), linetype = 3)

```

---

GammaSpectra-class      *An S4 Class to Represent a Collection of Gamma Spectra*

---

**Description**

Represents a collection of spectra of gamma ray spectrometry measurements.

**Details**

This class extends the base `list` and can only contains `GammaSpectrum` objects.

**Access**

In the code snippets below, `x` is a `GammaSpectra` object.

`length(x)` Get the number of elements in `x`.

`lengths(x)` Get the number of channels in each element of `x`.

`get_names(x), set_names(x) <- value` Retrieves or sets the names of `x` according to value.

`get_hash(x)` Get the MD5 hash of the raw data files.

`get_channels(x)` Get the number of channels in each element of `x`.

`get_counts(x)` Get the counts of each element of `x`.

`get_energy(x)` Get the energy range of each element of `x`.

`get_rates(x)` Get the count rates of each element of `x`.

**Subset**

In the code snippets below, `x` is a `GammaSpectra` object.

`x[i]` Extracts the elements selected by subscript `i`. `i` can be missing or `NULL`, numeric or character vector or a factor. Returns a new `GammaSpectra` object.

`x[i, j]` Like the above but allows to select a slot thru `j` (see examples). `j` is a character vector of length one. Returns a list.

`x[[i]]` Extracts the elements selected by subscript `i`. `i` can be a numeric or character vector of length one. Returns the corresponding `GammaSpectrum` object.

**Author(s)**

N. Frerebeau

**See Also**

Other class: [Baseline-class](#), [CalibrationCurve-class](#), [GammaSpectrum-class](#), [PeakPosition-class](#), [coerce\(\)](#)

**Examples**

```
## Import all CNF files in a given directory
spc_dir <- system.file("extdata/BDX_LaBr_1/calibration", package = "gamma")
(spc <- read(spc_dir))

## Access
get_hash(spc)
get_names(spc)
get_livetime(spc)
get_realtime(spc)

lengths(spc)
range_energy(spc)

## Subset
spc[] # All spectra
spc[NULL] # All spectra
spc[1] # The first spectrum
spc[-6] # Delete the sixth spectrum
spc[1:3] # The first three spectra
spc[c(1, 3)] # The first and third spectra
spc["BRIQUE"] # The spectrum named 'BRIQUE'
spc[c("BRIQUE", "C347")] # The spectra named 'BRIQUE' and 'C347'
spc[1:3, "energy"] # The slot 'energy' of the first three spectra
spc[[1]]
spc[["BRIQUE"]]
```

---

GammaSpectrum-class    *An S4 Class to Represent a Gamma Spectrum*

---

### Description

Represents a single spectrum of a gamma ray spectrometry measurement.

### Slots

hash A [character](#) string giving the 32-byte MD5 hash of the imported file.  
 name A [character](#) string the measurement reference.  
 date A [POSIXct](#) element giving the measurement date and time.  
 instrument A [character](#) string giving the instrument name.  
 file\_format A [character](#) string giving the format of the imported file.  
 live\_time A [numeric](#) value.  
 real\_time A [numeric](#) value.  
 channel A [integer](#) vector giving the channel number. Numeric values are coerced to integer as by [as.integer](#) (and hence truncated towards zero).  
 energy A [numeric](#) vector giving the gamma ray's energy (in keV).  
 count A [numeric](#) vector giving the counts number for each channel. Numeric values are coerced to integer as by [as.integer](#) (and hence truncated towards zero).  
 rate A [numeric](#) vector the count rate (in 1/s) for each channel.  
 calibration A [linear model](#) used for energy scale calibration (see [energy\\_calibrate](#)).

### Access

In the code snippets below, x is a GammaSpectrum object.

length(x) Get number of channel in x.  
 get\_hash(x) Get the MD5 hash of the raw data file.  
 get\_names(x), set\_names(x) <- value Retrieves or sets the name of x according to value.  
 get\_channels(x) Get the number of channels in x.  
 get\_counts(x) Get the counts of x.  
 get\_energy(x) Get the energy range of x.  
 get\_rates(x) Get the count rates of x.

### Coerce

In the code snippets below, x is a GammaSpectrum object.

as.matrix) Coerces x to a [matrix](#).  
 as.data.frame) Coerces x to a [data.frame](#).

**Subset**

In the code snippets below, x is a GammaSpectrum object.

`x[[i]]` Extracts informations from a slot selected by subscript i. i is a character vector of length one and will be matched to the name of the slots.

**Note**

This class retains copy construction.

**Author(s)**

N. Frerebeau

**See Also**

Other class: [Baseline-class](#), [CalibrationCurve-class](#), [GammaSpectra-class](#), [PeakPosition-class](#), [coerce\(\)](#)

**Examples**

```
## Import a Canberra CNF file
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
(spc <- read(spc_file))

## Access
get_hash(spc)
get_names(spc)
get_livetime(spc)
get_realtime(spc)

length(spc)
range_energy(spc)

## Subset
spc[["date"]]
spc[["instrument"]]
spc[["file_format"]]
```

---

mutator

*Get or Set Parts of an Object*

---

**Description**

Getters and setters to extract or replace parts of an object.

**Usage**

```
get_hash(x)
get_names(x)
set_names(x) <- value
get_livetime(x)
get_realtime(x)
get_channels(x)
get_counts(x)
get_rates(x)
get_energy(x)
set_energy(x) <- value
get_method(x)
set_method(x) <- value
get_residuals(x)
range_channels(x, ...)
range_energy(x, ...)

## S4 method for signature 'GammaSpectrum'
length(x)

## S4 method for signature 'GammaSpectrum'
get_hash(x)

## S4 method for signature 'GammaSpectrum'
get_names(x)

## S4 method for signature 'GammaSpectrum'
get_livetime(x)

## S4 method for signature 'GammaSpectrum'
get_realtime(x)

## S4 method for signature 'GammaSpectrum'
get_channels(x)
```

```
## S4 method for signature 'GammaSpectrum'  
get_counts(x)  
  
## S4 method for signature 'GammaSpectrum'  
get_rates(x)  
  
## S4 method for signature 'GammaSpectrum'  
get_energy(x)  
  
## S4 method for signature 'GammaSpectrum'  
range_energy(x, na.rm = FALSE)  
  
## S4 method for signature 'GammaSpectrum'  
range_channels(x, na.rm = FALSE)  
  
## S4 method for signature 'Baseline'  
get_method(x)  
  
## S4 method for signature 'GammaSpectra'  
get_hash(x)  
  
## S4 method for signature 'GammaSpectra'  
get_names(x)  
  
## S4 method for signature 'GammaSpectra'  
get_livetime(x)  
  
## S4 method for signature 'GammaSpectra'  
get_realtime(x)  
  
## S4 method for signature 'GammaSpectra'  
get_channels(x)  
  
## S4 method for signature 'GammaSpectra'  
get_counts(x)  
  
## S4 method for signature 'GammaSpectra'  
get_rates(x)  
  
## S4 method for signature 'GammaSpectra'  
get_energy(x)  
  
## S4 method for signature 'GammaSpectra'  
range_energy(x, na.rm = FALSE)  
  
## S4 method for signature 'GammaSpectra'  
range_channels(x, na.rm = FALSE)
```

```
## S4 method for signature 'DoseRateModel'  
get_residuals(x)  
  
## S4 method for signature 'PeakPosition'  
get_hash(x)  
  
## S4 method for signature 'PeakPosition'  
get_channels(x)  
  
## S4 method for signature 'PeakPosition'  
get_energy(x)  
  
## S4 replacement method for signature 'GammaSpectrum'  
set_names(x) <- value  
  
## S4 replacement method for signature 'Baseline'  
set_method(x) <- value  
  
## S4 replacement method for signature 'GammaSpectra'  
set_names(x) <- value  
  
## S4 replacement method for signature 'PeakPosition,numeric'  
set_energy(x) <- value
```

### Arguments

x	An object from which to get or set element(s).
value	A possible value for the element(s) of x.
...	Currently not used.
na.rm	A <a href="#">logical</a> scalar: should NA be omitted?

### Value

An object of the same sort as x with the new values assigned.

### Author(s)

N. Frerebeau

### See Also

Other mutator: [subset\(\)](#)

---

operator	<i>Common Operations on GammaSpectrum Objects</i>
----------	---

---

**Description**

Performs common operations on GammaSpectrum objects.

**Usage**

```
## S4 method for signature 'GammaSpectrum,GammaSpectrum'  
Arith(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,numeric'  
Arith(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,GammaSpectrum'  
Compare(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,numeric'  
Compare(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,GammaSpectrum'  
Logic(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,numeric'  
Logic(e1, e2)  
  
## S4 method for signature 'GammaSpectrum,logical'  
Logic(e1, e2)  
  
## S4 method for signature 'GammaSpectrum'  
Math(x)  
  
## S4 method for signature 'GammaSpectrum'  
Math2(x, digits)  
  
## S4 method for signature 'GammaSpectrum'  
Summary(x, ..., na.rm = FALSE)
```

**Arguments**

x, e1, e2	An object (typically a <a href="#">GammaSpectrum</a> object).
digits	A length-one <a href="#">numeric</a> vector giving the number of digits to be used in <a href="#">round</a> or <a href="#">signif</a> .
...	Further arguments passed to or from methods.
na.rm	A <a href="#">logical</a> scalar: should missing values (including NaN) be omitted from the calculations?

**Group Generics**

**GammaSpectrum** objects have support for S4 group generic functionality to operate within elements across objects:

Arith "+", "-", "\*", "^", "%%", "%/%", "/"

Compare "==" ">" "<" "!=" "<=" ">="

Logic "&", "|"

Math "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "cummax", "cummin", "cumprod", "cumsum",  
 "log", "log10", "log2", "log1p", "acos", "acosh", "asin", "asinh", "atan", "atanh", "exp",  
 "expm1", "cos", "cosh", "cospi", "sin", "sinh", "sinpi", "tan", "tanh", "tanpi", "gamma",  
 "lgamma", "digamma", "trigamma"

Math2 "round", "signif"

Ops "Arith", "Compare", "Logic"

Summary "min", "max", "range", "prod", "sum", "any", "all"

**Author(s)**

N. Frerebeau

**Examples**

```
## No examples
```

---

PeakPosition-class      *An S4 Class to Represent a Set of Peaks*

---

**Description**

An S4 Class to Represent a Set of Peaks

**Slots**

hash A **character** string giving the 32-byte MD5 hash of the imported spectrum file.

noise\_method A **character** string specifying the method used for peak detection.

noise\_threshold A length one **numeric** vector giving the noise threshold.

window A length one **numeric** vector giving the half-window size.

channel A **integer** vector giving the channel number. Numeric values are coerced to integer as by **as.integer** (and hence truncated towards zero).

energy A **numeric** vector giving the gamma ray's energy (in keV).

**Access**

In the code snippets below, `x` is a `PeakPosition` object.

`get_hash(x)` Get the MD5 hash of the raw data file.

`get_channels(x)` Get the channels of `x`.

`get_energy(x)`, `set_energy(x) <- value` Retrieves or sets the energy scale of `x` according to `value`.

**Coerce**

In the code snippets below, `x` is a `PeakPosition` object.

`matrix()` Coerces `x` to a [matrix](#).

`as.data.frame()` Coerces `x` to a [data.frame](#).

**Subset**

In the code snippets below, `x` is a `PeakPosition` object.

`x[[i]]` Extracts informations from a slot selected by subscript `i`. `i` is a character vector of length one and will be matched to the name of the slots.

**Note**

This class retains copy construction.

**Author(s)**

N. Frerebeau

**See Also**

Other class: [Baseline-class](#), [CalibrationCurve-class](#), [GammaSpectra-class](#), [GammaSpectrum-class](#), [coerce\(\)](#)

---

peaks\_find

*Peaks*

---

**Description**

Finds local maxima in sequential data.

**Usage**

```
peaks_find(object, ...)
```

```
## S4 method for signature 'GammaSpectrum'
```

```
peaks_find(object, method = c("MAD"), SNR = 2, span = NULL, ...)
```

### Arguments

object	A <a href="#">GammaSpectrum</a> or <a href="#">PeakPosition</a> object.
...	Extra parameters to be passed to internal methods.
method	A <a href="#">character</a> string specifying the method to be used for background noise estimation (see below).
SNR	An <a href="#">integer</a> giving the signal-to-noise-ratio for peak detection (see below).
span	An <a href="#">integer</a> giving the half window size (in number of channels). If NULL, 5% of the number of channels is used as the half window size.

### Details

A local maximum has to be the highest one in the given window and has to be higher than  $SNR \times noise$  to be recognized as peak.

The following methods are available for noise estimation:

**MAD** Median Absolute Deviation.

### Value

An object of class [PeakPosition](#).

### Author(s)

N. Frerebeau

### See Also

Other signal processing: [baseline](#), [signal\\_integrate\(\)](#), [signal\\_slice\(\)](#), [signal\\_stabilize\(\)](#), [smooth\(\)](#)

### Examples

```
## Import a Canberra CNF file
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(spc_file)

## Find peaks
(pks <- peaks_find(spc))
plot(spc, pks)
```

plot

*Plot***Description**

Plot

**Usage**

```
## S4 method for signature 'GammaSpectrum,missing'
plot(x, xaxis = c("channel", "energy"), yaxis = c("count", "rate"), ...)

## S4 method for signature 'GammaSpectrum,Baseline'
plot(x, y, xaxis = c("channel", "energy"), yaxis = c("count", "rate"), ...)

## S4 method for signature 'GammaSpectra,missing'
plot(
  x,
  xaxis = c("channel", "energy"),
  yaxis = c("count", "rate"),
  select = NULL,
  facet = FALSE,
  ...
)

## S4 method for signature 'GammaSpectrum,PeakPosition'
plot(x, y, ...)

## S4 method for signature 'CalibrationCurve,missing'
plot(
  x,
  error_ellipse = TRUE,
  error_bar = FALSE,
  energy = FALSE,
  level = 0.95,
  n = 50,
  ...
)
```

**Arguments**

x, y	Objects to be plotted.
xaxis, yaxis	A <a href="#">character</a> string specifying the data to be plotted along each axis. It must be one of "energy" or "channel" (x axis) and "counts" or "rate" (y axis). Any unambiguous substring can be given.
...	Currently not used.

select	A <a href="#">numeric</a> or <a href="#">character</a> vector giving the selection of the spectrum that are drawn.
facet	A <a href="#">logical</a> scalar: should a matrix of panels defined by spectrum be drawn?
error_ellipse	A <a href="#">logical</a> scalar: should error ellipses be plotted?
error_bar	A <a href="#">logical</a> scalar: should error bars be plotted?
energy	A <a href="#">logical</a> scalar: TODO.
level	length-one <a href="#">numeric</a> vector giving the the probability cutoff for the error ellipses.
n	A length-one <a href="#">numeric</a> vector giving the resolution of the error ellipses.

### Value

A [ggplot](#) object.

### Author(s)

N. Frerebeau

### See Also

[ellipse](#), [isochron](#)

### Examples

```
# Import CNF files
spc_dir <- system.file("extdata/BDX_LaBr_1/calibration", package = "gamma")
spc <- read(spc_dir)

# Plot all spectra
plot(spc, yaxis = "rate", facet = FALSE) +
  ggplot2::theme_bw()

# Plot the spectrum named 'BRIQUE'
plot(spc, xaxis = "energy", yaxis = "count", select = "BRIQUE") +
  ggplot2::theme_bw()

# Plot the first three spectra
plot(spc, xaxis = "channel", yaxis = "rate", select = 1:3, facet = TRUE) +
  ggplot2::theme_bw()
```

---

read

*Data Input*

---

### Description

Reads a gamma ray spectrum file.

**Usage**

```
read(file, ...)

## S4 method for signature 'character'
read(file, extensions = c("cnf", "tka"), ...)
```

**Arguments**

file	A <a href="#">character</a> string giving the path of files to be imported.
...	Extra parameters to be passed to <a href="#">read_xyData</a> .
extensions	A <a href="#">character</a> vector specifying the possible file extensions. It must be one or more of "cnf", "tka".

**Value**

A [GammaSpectra](#) object if more than one spectrum are imported at once, else a [GammaSpectrum](#) object.

**Note**

*Only supports Canberra CNF and TKA files.*

**Author(s)**

N. Frerebeau

**See Also**

[read\\_xyData](#)

Other IO: [summarise\(\)](#)

**Examples**

```
## Import a Canberra CNF file
cnf_file <- system.file("extdata/LaBr.CNF", package = "gamma")
(cnf_spc <- read(cnf_file))

## Import a TKA file
tka_file <- system.file("extdata/LaBr.TKA", package = "gamma")
(tka_spc <- read(tka_file))

## Import all files in a given directory
spc_dir <- system.file("extdata/BDX_LaBr_1/calibration", package = "gamma")
(spc <- read(spc_dir))
```

---

signal\_integrate      *Signal Integration*

---

## Description

Signal Integration

## Usage

```

signal_integrate(object, background, ...)

## S4 method for signature 'GammaSpectrum,missing'
signal_integrate(object, range, energy = FALSE)

## S4 method for signature 'GammaSpectrum,GammaSpectrum'
signal_integrate(object, background, range, energy = FALSE)

## S4 method for signature 'GammaSpectrum,numeric'
signal_integrate(object, background, range, energy = FALSE)

## S4 method for signature 'GammaSpectra,missing'
signal_integrate(object, range, energy = FALSE, simplify = TRUE)

## S4 method for signature 'GammaSpectra,GammaSpectrum'
signal_integrate(object, background, range, energy = FALSE, simplify = TRUE)

## S4 method for signature 'GammaSpectra,numeric'
signal_integrate(object, background, range, energy = FALSE, simplify = TRUE)

```

## Arguments

object	A <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object.
background	A <a href="#">GammaSpectrum</a> object.
...	Currently not used.
range	A length-two <a href="#">numeric</a> vector giving the energy range to integrate within (in keV).
energy	A <a href="#">logical</a> scalar: TODO?
simplify	A <a href="#">logical</a> scalar: should the result be simplified to a matrix? The default value, FALSE, returns a list.

## Details

It assumes that each spectrum has an energy scale.

**Value**

If `simplify` is `FALSE` (the default) returns a [list](#) of numeric vectors (the signal value and its error), else returns a [matrix](#).

**Author(s)**

N. Frerebeau

**References**

Guérin, G. & Mercier, M. (2011). Determining Gamma Dose Rates by Field Gamma Spectroscopy in Sedimentary Media: Results of Monte Carlo Simulations. *Radiation Measurements*, 46(2), p. 190-195. DOI: [10.1016/j.radmeas.2010.10.003](https://doi.org/10.1016/j.radmeas.2010.10.003).

Mercier, N. & Falguères, C. (2007). Field Gamma Dose-Rate Measurement with a NaI(Tl) Detector: Re-Evaluation of the "Threshold" Technique. *Ancient TL*, 25(1), p. 1-4.

**See Also**

Other signal processing: [baseline](#), [peaks\\_find\(\)](#), [signal\\_slice\(\)](#), [signal\\_stabilize\(\)](#), [smooth\(\)](#)

---

signal\_slice

*Choose channels by Position*

---

**Description**

Choose channels by position.

**Usage**

```
signal_slice(object, ...)

## S4 method for signature 'GammaSpectrum'
signal_slice(object, ...)

## S4 method for signature 'GammaSpectra'
signal_slice(object, ...)
```

**Arguments**

`object` A [GammaSpectrum](#) or [GammaSpectra](#) object.

`...` [integer](#) values giving the channels of the spectrum to be kept/dropped (see below). Numeric values are coerced to integer as by [as.integer](#) (and hence truncated towards zero).

**Details**

Either positive values to keep, or negative values to drop, should be provided. The values provided must be either all positive or all negative.

If no value is provided, an attempt is made to define the number of channels to skip at the beginning of the spectrum. This drops all channels before the highest count maximum. This is intended to deal with the artefact produced by the rapid growth of random background noise towards low energies.

**Value**

A [GammaSpectrum](#) or [GammaSpectra](#) object.

**Author(s)**

N. Frerebeau

**See Also**

Other signal processing: [baseline](#), [peaks\\_find\(\)](#), [signal\\_integrate\(\)](#), [signal\\_stabilize\(\)](#), [smooth\(\)](#)

**Examples**

```
## Import CNF files
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(spc_file)

## Plot spectrum
plot(spc)

## Slice
sliced <- signal_slice(spc)
plot(sliced)

sliced <- signal_slice(spc, -c(1:35))
plot(sliced)

sliced <- signal_slice(spc, 450:550)
plot(sliced)
```

---

signal\_stabilize

*Transform Intensities*

---

**Description**

Transform Intensities

**Usage**

```
signal_stabilize(object, ...)  
  
## S4 method for signature 'GammaSpectrum'  
signal_stabilize(object, f, ...)  
  
## S4 method for signature 'GammaSpectra'  
signal_stabilize(object, f, ...)
```

**Arguments**

object	A <a href="#">GammaSpectrum</a> object.
...	Extra arguments to be passed to transformation.
f	A <a href="#">function</a> that takes a numeric vector as argument and returns a numeric vector.

**Details**

The stabilization step aims at improving the identification of peaks with a low signal-to-noise ratio. This particularly targets higher energy peaks.

**Value**

A new [GammaSpectrum](#) or [GammaSpectra](#) object with transformed intensities.

**Author(s)**

N. Frerebeau

**See Also**

Other signal processing: [baseline](#), [peaks\\_find\(\)](#), [signal\\_integrate\(\)](#), [signal\\_slice\(\)](#), [smooth\(\)](#)

---

smooth

*Smooth*

---

**Description**

Smooths intensities.

**Usage**

```

signal_smooth(object, ...)

smooth_rectangular(object, ...)

smooth_triangular(object, ...)

smooth_savitzky(object, ...)

## S4 method for signature 'GammaSpectrum'
signal_smooth(object, method = c("rectangular", "triangular", "savitzky"), ...)

## S4 method for signature 'GammaSpectra'
signal_smooth(object, method = c("rectangular", "triangular", "savitzky"), ...)

## S4 method for signature 'GammaSpectrum'
smooth_rectangular(object, m = 3, ...)

## S4 method for signature 'GammaSpectra'
smooth_rectangular(object, m = 3, ...)

## S4 method for signature 'GammaSpectrum'
smooth_savitzky(object, m = 3, p = 2, ...)

## S4 method for signature 'GammaSpectra'
smooth_savitzky(object, m = 3, p = 2, ...)

## S4 method for signature 'GammaSpectrum'
smooth_triangular(object, m = 3, ...)

## S4 method for signature 'GammaSpectra'
smooth_triangular(object, m = 3, ...)

```

**Arguments**

object	A <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object.
...	Extra parameters to be passed to further methods.
method	A <a href="#">character</a> string specifying the smoothing method to be used. It must be one of "unweighted" (default), "weighted" or "savitzky" (see details). Any unambiguous substring can be given.
m	An odd <a href="#">integer</a> giving the number of adjacent points to be used.
p	An <a href="#">integer</a> giving the polynomial degree. Only used if method is "savitzky".

**Details**

The following smoothing methods are available:

**rectangular** Unweighted sliding-average or rectangular smooth. It replaces each point in the signal with the average of  $m$  adjacent points.

**triangular** Weighted sliding-average or triangular smooth. It replaces each point in the signal with the weighted mean of  $m$  adjacent points.

**savitzky** Savitzky-Golay filter. This method is based on the least-squares fitting of polynomials to segments of  $m$  adjacent points.

There will be  $(m - 1)/2$  points both at the beginning and at the end of the spectrum for which a complete  $m$ -width smooth cannot be calculated. To prevent data loss, progressively smaller smooths are used at the ends of the spectrum if method is unweighted or weighted. If the Savitzky-Golay filter is used, the original  $(m - 1)/2$  points at the ends of the spectrum are preserved.

### Value

A [GammaSpectrum](#) or [GammaSpectra](#) object.

### Author(s)

N. Frerebeau

### References

Gorry, P. A. (1990). General Least-Squares Smoothing and Differentiation by the Convolution (Savitzky-Golay) Method. *Analytical Chemistry*, 62(6), p. 570-573. DOI: [10.1021/ac00205a007](#).

Savitzky, A. & Golay, M. J. E. (1964). Smoothing and Differentiation of Data by Simplified Least Squares Procedures. *Analytical Chemistry*, 36(8), p. 1627-1639. DOI: [10.1021/ac60214a047](#).

### See Also

Other signal processing: [baseline](#), [peaks\\_find\(\)](#), [signal\\_integrate\(\)](#), [signal\\_slice\(\)](#), [signal\\_stabilize\(\)](#)

### Examples

```
# Import CNF files
spc_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(spc_file)
spc <- signal_slice(spc, -c(1:35))

# Plot raw spectrum
spc_clean <- signal_correct(spc)
plot(spc_clean)

# Rectangular smooth
spc_unweighted <- smooth_rectangular(spc, m = 3)
spc_unweighted_clean <- signal_correct(spc_unweighted)
plot(spc_unweighted_clean)

# Triangular smooth
spc_weighted <- smooth_triangular(spc, m = 5)
spc_weighted_clean <- signal_correct(spc_weighted)
plot(spc_weighted_clean)
```

```
# SavitzkyGolay
spc_savitzky <- smooth_savitzky(spc, m = 21, p = 2)
spc_savitzky_clean <- signal_correct(spc_savitzky)
plot(spc_savitzky_clean)
```

---

subset

*Extract or Replace Parts of an Object*

---

## Description

Operators acting on objects to extract or replace parts.

## Usage

```
## S4 method for signature 'GammaSpectrum'
x[[i]]

## S4 method for signature 'GammaSpectra'
x[i, j]

## S4 method for signature 'DoseRateModel'
x[[i]]

## S4 method for signature 'DoseRateModel'
x[[i]]

## S4 method for signature 'CalibrationCurve'
x[[i]]

## S4 method for signature 'PeakPosition'
x[[i]]
```

## Arguments

x	An object from which to extract element(s) or in which to replace element(s).
i, j	Indices specifying elements to extract or replace. Indices are <a href="#">numeric</a> , <a href="#">integer</a> or <a href="#">character</a> vectors or empty (missing) or NULL. Numeric values are coerced to <a href="#">integer</a> as by <a href="#">as.integer</a> (and hence truncated towards zero). Character vectors will be matched to the name of the elements. An empty index (a comma separated blank) indicates that all entries in that dimension are selected.

## Value

A subsetted object.

**Author(s)**

N. Frerebeau

**See Also**Other mutator: [mutator](#)

---

`summarise`*Summarize*

---

**Description**

Summarize

**Usage**

```
summarise(object, ...)  
  
## S4 method for signature 'GammaSpectrum'  
summarise(object)  
  
## S4 method for signature 'GammaSpectra'  
summarise(object)  
  
## S4 method for signature 'DoseRateModel'  
summarise(object)  
  
## S4 method for signature 'CalibrationCurve'  
summarise(object)
```

**Arguments**

<code>object</code>	A <a href="#">GammaSpectrum</a> or <a href="#">GammaSpectra</a> object.
<code>...</code>	Currently not used.

**Value**A [data.frame](#).**Author(s)**

N. Frerebeau

**See Also**Other IO: [read\(\)](#)

**Examples**

```
## Import a Canberra CNF file
cnf_file <- system.file("extdata/LaBr.CNF", package = "gamma")
spc <- read(cnf_file)
summarise(spc)

## Import all CNF files in a given directory
spc_dir <- system.file("extdata/BDX_LaBr_1/calibration", package = "gamma")
spc <- read(spc_dir)
summarise(spc)
```

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