

# Package ‘spectrolab’

June 1, 2021

**Type** Package

**Title** Class and Methods for Hyperspectral Data

**Version** 0.0.12

**Date** 2021-05-18

**Description** Input/Output, processing and visualization of spectra taken with different spectrometers, including SVC (Spectra Vista), ASD and PSR (Spectral Evolution). Implements an S3 class 'spectra' that other packages can build on. Provides methods to access, plot, manipulate, splice sensor overlap, vector normalize and smooth spectra.

**License** GPL-3

**URL** <https://CRAN.R-project.org/package=spectrolab>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Depends** R (>= 3.4), stats

**Suggests** knitr (>= 1.16), rmarkdown (>= 1.5), testthat (>= 1.0.2)

**VignetteBuilder** knitr

**Imports** grDevices, parallel, RColorBrewer, shiny, shinyjs

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-06-01 18:10:02 UTC

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---

*aggregate.spectra*      *Aggregate spectra*

---

### Description

Applies FUN (and FUN\_meta) over spectra aggregating by factor 'by'.

### Usage

```
## S3 method for class 'spectra'  
aggregate(x, by, FUN, FUN_meta = NULL, ...)
```

### Arguments

x	spectra object
by	vector of factors to guide the aggregation
FUN	function to be applied to refl (and meta if FUN_meta is NULL)
FUN_meta	function to be applied to metadata. If NULL (default), same FUN applied to value is used.
...	extra args to FUN

### Details

Argument FUN\_meta is useful if you want to apply a different function to metadata and value. If you want to aggregate spectra and metadata using 'mean', 'sd', 'median' etc. but try to keep the text values, wrap your function in try\_keep\_txt(f).

### Value

spectra object

### Author(s)

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec_mean = aggregate(spec, by = names(spec), mean, try_keep_txt(mean))
```

---

apply_by_band	<i>Apply numeric function by band</i>
---------------	---------------------------------------

---

**Description**

apply\_by\_band is conceptually similar to `apply(as.matrix(x), 2, fun)`, but returns a spectra object while dealing with metadata and attributes. Applying a function that does not act on numeric values may crash the function or render all values NA.

**Usage**

```
apply_by_band(x, fun, na.rm = TRUE, keep_txt_meta = TRUE, name = NULL, ...)

## S3 method for class 'spectra'
apply_by_band(x, fun, na.rm = TRUE, keep_txt_meta = TRUE, name = NULL, ...)
```

**Arguments**

x	spectra
fun	numeric function to be applied to each band.
na.rm	boolean. remove NAs?
keep_txt_meta	boolean. try to keep text in the metadata?
name	name for each sample in the output spectra. The default (NULL) will give samples sequential numeric names. Recycled if necessary.
...	extra arguments passed to fun

**Value**

spectra

**Methods (by class)**

- spectra: Apply a numeric function by band

**Author(s)**

Jose Eduardo Meireles  
Jose Eduardo Meireles

## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec_mean = apply_by_band(spec, mean)
```

---

as.data.frame.spectra *Convert spectra to data.frame*

---

## Description

Returns a data.frame that includes sample names, metadata (if present) and value data. One advantage over as.matrix, is that the metadata are returned.

## Usage

```
## S3 method for class 'spectra'
as.data.frame(
  x,
  row.names = NULL,
  optional = FALSE,
  fix_names = "none",
  metadata = TRUE,
  ...
)
```

## Arguments

x	spectra object
row.names	does nothing. Here for compatibility with S3 generics
optional	does nothing. Here for compatibility with S3 generics
fix_names	Use make.names to normalize names? Pick one: "none" "row" "col" "both".
metadata	boolean. Include spectral metadata? Defaults to TRUE
...	extra parameters passed to the generic as_spectra

## Value

data.frame with: sample\_name, metadata (if any) and value.

## Author(s)

Jose Eduardo Meireles

## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
df = as.data.frame(spec, fix_names = "none")
```

---

as.matrix.spectra      *Convert spectra to matrix*

---

**Description**

Convert spectra to matrix

**Usage**

```
## S3 method for class 'spectra'  
as.matrix(x, fix_names = "none", ...)
```

**Arguments**

x	spectra object
fix_names	Use make.names to normalize names? Pick one: "none" "row" "col" "both".
...	does nothing. Here for compatibility with S3 generics

**Value**

matrix of spectral value. columns are bands and rows are samples

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
mat = as.matrix(spec)
```

---

as\_spectra      *Convert matrix or data frame to spectra*

---

**Description**

Convert matrix or data frame to spectra

**Usage**

```
as_spectra(x, name_idx = NULL, meta_idx = NULL)
```

**Arguments**

x	matrix or dataframe. Samples are in rows and bands in columns. Any data that are not the spectra themselves (labels or metadata) must have their column index included in 'name_idx' or 'meta_idx's'.
name_idx	column index with sample names. Defaults to NULL. If NULL or 0, row-names(x) or a sequence of integers will be assigned as names.
meta_idx's	column indices with metadata (not name and not value). Defaults to NULL

**Value**

spectra object

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
as_spectra(spec_matrix_example, name_idx = 1)
```

---

as\_spectra.data.frame *Convert data.frame to spectra*

---

**Description**

Convert data.frame to spectra

**Usage**

```
## S3 method for class 'data.frame'
as_spectra(x, name_idx = NULL, meta_idx's = NULL)
```

**Arguments**

x	data.frame
name_idx	column index with sample names. Defaults to NULL.
meta_idx's	column indices with metadata (not name and not value). Defaults to NULL

**Value**

spectra object

**Author(s)**

Jose Eduardo Meireles

---

as\_spectra.matrix      *Convert matrix to spectra*

---

### Description

Convert matrix to spectra

### Usage

```
## S3 method for class 'matrix'
as_spectra(x, name_idx = NULL, meta_idx = NULL)
```

### Arguments

x	matrix
name_idx	column index with sample names. Defaults to NULL
meta_idx	column indices with metadata (not name and not value). Defaults to NULL

### Value

spectra object

### Author(s)

Jose Eduardo Meireles

---

bands      *Get spectra band labels*

---

### Description

bands returns a vector of band labels from spectra

### Usage

```
bands(x, min = NULL, max = NULL, return_num = TRUE)
```

```
## S3 method for class 'spectra'
bands(x, min = NULL, max = NULL, return_num = TRUE)
```

### Arguments

x	spectra object
min	= NULL
max	= NULL
return_num	boolean. return vector of numeric values (default). otherwise, a vector of strings is returned



`bands<-`

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### Value

vector of bands. numeric if `'return_num' = TRUE` (default).

### Methods (by class)

- `spectra`: Get spectra band labels

### Author(s)

Jose Eduardo Meireles

### Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
head(bands(spec))
```

---

`bands<-` *Set band labels*

---

### Description

`bands` sets band labels of lhs to the rhs values

### Usage

```
bands(x) <- value
```

### Arguments

<code>x</code>	spectra object (lhs)
<code>value</code>	rhs

### Value

nothing. called for its side effect.

### Author(s)

Jose Eduardo Meireles

### Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
bands(spec) = bands(spec) / 1000
```

---

`combine`*Combine spectral datasets*

---

**Description**

`combine` binds two spectral datasets. Both spectra must have the very same band labels, but different metadata are acceptable

**Usage**

```
combine(s1, s2)
```

```
## S3 method for class 'spectra'  
combine(s1, s2)
```

**Arguments**

```
s1          spectra object 1  
s2          spectra object 2
```

**Value**

combined spectra object

**Methods (by class)**

- `spectra`: Combines two spectral datasets

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)  
  
# Create dummy spectra datasets. Pretend that these are all different...  
s1 = as_spectra(spec_matrix_example, name_idx = 1)  
s2 = as_spectra(spec_matrix_example, name_idx = 1)  
s3 = as_spectra(spec_matrix_example, name_idx = 1)  
  
# combine 2 spectra objects  
s_1and2 = combine(s1, s2)  
  
# combine n spectra objects using the `Reduce` function  
s_n = Reduce(combine, list(s1, s2, s3))
```

---

default\_spec\_regions *Return default spectral regions matrix*

---

**Description**

Return default spectral regions matrix

**Usage**

```
default_spec_regions()
```

**Value**

matrix with default\_spec\_regions

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
# matrix that defines regions on the spectra
# Useful for plotting w/ plot_regions()
```

---

dim.spectra *Get dimension of spectra*

---

**Description**

dim returns a vector with number of samples and bands (bands)

**Usage**

```
## S3 method for class 'spectra'
dim(x)
```

**Arguments**

x                    spectra object

**Value**

tuple of integers: c("n\_samples", "n\_bands")

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
dim(spec)
```

---

guess_splice_at	<i>Guess splice bands (bounds between sensors)</i>
-----------------	--

---

**Description**

Guess splice bands (bounds between sensors)

**Usage**

```
guess_splice_at(x)

## S3 method for class 'spectra'
guess_splice_at(x)
```

**Arguments**

x                    spectra object

**Value**

vector of band values

**Methods (by class)**

- spectra: Guess splice bands (bounds between sensors)

**Author(s)**

Jose Eduardo Meireles

---

is_spectra	<i>Is it a spectra object?</i>
------------	--------------------------------

---

**Description**

is\_spectra tests if the argument is a spectra class object

**Usage**

```
is_spectra(x)
```

**Arguments**

x                    any object

**Value**

boolean

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec1 = unclass(spec)
is_spectra(spec)
is_spectra(spec1)
```

---

match_sensors	<i>Match spectra at sensor transitions</i>
---------------	--

---

**Description**

match\_sensors scales values of sensors 1 (vis) and 3 (swir2)

**Usage**

```
match_sensors(x, splice_at, fixed_sensor = 2, interpolate_wvl = c(5, 1))
```

```
## S3 method for class 'spectra'
```

```
match_sensors(x, splice_at, fixed_sensor = 2, interpolate_wvl = c(5, 2))
```

**Arguments**

x	spectra object
splice_at	bands that serve as splice points, i.e the beginnings of the rightmost sensor. Must be length 1 or 2 (max 3 sensors)
fixed_sensor	sensor to keep fixed. Can be 1 or 2 if matching 2 sensors. If matching 3 sensors, 'fixed_sensor' must be 2 (default).
interpolate_wvl	extent around splice_at values over which the splicing factors will be calculated. Defaults to 5

**Details**

Splice\_at has no default because sensor transition points vary between vendors and individual instruments. The function guess\_splice\_at can help you guess what those values could be. However, splice\_at is an important parameter though, so you should visually inspect your spectra before assigning it. Typical values in our own individual instruments were: SVC ~ c(990, 1900), ASD ~ c(1001, 1801).

If the factors used to match spectra are unreasonable, match\_sensors will throw. Unreasonable factors (f) are defined as  $0.5 > f > 3$  or NaN, which happens when the value for the right sensor is 0.

**Value**

spectra object

**Methods (by class)**

- spectra: Match sensor overlap regions

**Author(s)**

Jose Eduardo Meireles and Anna Schweiger

---

max.spectra

*Maximum value*

---

**Description**

max Returns the maximum value in a spectra object

**Usage**

```
## S3 method for class 'spectra'
max(..., na.rm = FALSE)
```

**Arguments**

... spectra object  
 na.rm boolean. remove NAs? Defaults to FALSE

**Value**

single numeric value

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
max(spec)
```

---

mean.spectra	<i>Mean spectrum</i>
--------------	----------------------

---

**Description**

mean computes the arithmetic mean spectrum.

**Usage**

```
## S3 method for class 'spectra'
mean(x, na.rm = TRUE, keep_txt_meta = TRUE, ...)
```

**Arguments**

x spectra  
 na.rm boolean. remove NAs? Defaults to TRUE  
 keep\_txt\_meta try to keep text in the metadata  
 ... nothing

**Value**

single spectrum

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
mean(spec)
```

---

median.spectra	<i>Median spectrum</i>
----------------	------------------------

---

**Description**

median computes the median spectrum

**Usage**

```
## S3 method for class 'spectra'
median(x, na.rm = TRUE, keep_txt_meta = TRUE, ...)
```

**Arguments**

x	spectra
na.rm	boolean. remove NAs? Defaults to TRUE
keep_txt_meta	try to keep text in the metadata
...	nothing

**Value**

single spectrum

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
median(spec)
```



---

meta	<i>Get metadata</i>
------	---------------------

---

## Description

meta returns metadata of spectra

## Usage

```
meta(x, label, sample, simplify = FALSE, quiet = TRUE)
```

```
## S3 method for class 'spectra'
```

```
meta(x, label = NULL, sample = NULL, simplify = FALSE, quiet = TRUE)
```

## Arguments

x	spectra object
label	metadata column index or label
sample	sample index or name
simplify	boolean. defaults to FALSE
quiet	boolean. warn about non-existent metadata? defaults to TRUE

## Value

data frame or vector

## Methods (by class)

- spectra: get metadata

## Author(s)

Jose Eduardo Meireles

## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec = normalize(spec)
meta(spec, "normalization_magnitude")
```

---

meta<-	<i>Set metadata</i>
--------	---------------------

---

**Description**

meta sets metadata

**Usage**

```
meta(x, label, sample) <- value
```

**Arguments**

x	spectra object (lhs)
label	metadata column label
sample	sample name
value	rhs. TODO

**Value**

nothing. called for its side effect

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
meta(spec, "random") = rnorm(nrow(spec), mean(10), sd = 2)
```

---

min.spectra	<i>Minimum value</i>
-------------	----------------------

---

**Description**

min Returns the minimum value in a spectra object

**Usage**

```
## S3 method for class 'spectra'
min(..., na.rm = FALSE)
```

**Arguments**

... spectra object  
na.rm boolean. remove NAs? Defaults to FALSE

**Value**

single numeric value

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
min(spec)
```

---

names.spectra      *Get spectra sample names*

---

**Description**

names returns a vector of sample names

**Usage**

```
## S3 method for class 'spectra'
names(x)
```

**Arguments**

x spectra object

**Value**

vector of sample names

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
names(spec)
```

---

names<-.spectra	<i>Set spectra sample names</i>
-----------------	---------------------------------

---

## Description

names assigns sample names to lhs

## Usage

```
## S3 replacement method for class 'spectra'  
names(x) <- value
```

## Arguments

x	spectra object (lhs)
value	values to be assigned (rhs)

## Details

Sample names must not be coercible to numeric. That is, names such as "1" and "153.44" are invalid even if they are encoded as character. names will add the prefix "spec\_" to any element of value that is coercible to numeric.

## Value

nothing. called for its side effect.

## Author(s)

Jose Eduardo Meireles

## Examples

```
library(spectrolab)  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
names(spec) = toupper(names(spec))
```

---

normalize	<i>Vector normalize spectra</i>
-----------	---------------------------------

---

### Description

normalize returns a spectra obj with vector normalized values. Normalization value for each spectrum computed as  $\sqrt{\sum(x^2)}$

### Usage

```
normalize(x, quiet = FALSE, ...)
```

```
## S3 method for class 'spectra'  
normalize(x, quiet = FALSE, ...)
```

### Arguments

x	spectra object. bands must be strictly increasing
quiet	boolean. Warn about change in y value units? Defaults to FALSE
...	nothing

### Value

spectra object with normalized spectra

### Methods (by class)

- spectra: Vector normalize spectra

### Author(s)

Jose Eduardo Meireles

### Examples

```
library(spectrolab)  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
spec = normalize(spec)
```

---

 Ops.spectra

*Arithmetic operators for spectra*


---

**Description**

Overloads arithmetic operators for spectra using ‘Ops.’

**Usage**

```
## S3 method for class 'spectra'
Ops(e1, e2)
```

**Arguments**

e1	lhs
e2	rhs

**Value**

Depends on the operator. math operators will return spectra and logical or comparison operators will return boolean matrices

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec1 = spec * 2
spec2 = spec + spec
all(spec1 == spec2)
```

---

 plot.spectra

*Plot spectra*


---

**Description**

plot plots spectra.

**Usage**

```
## S3 method for class 'spectra'
plot(x, ylab = "value", xlab = "band", col = "black", lty = 1, type = "l", ...)
```

**Arguments**

x	spectra object
ylab	label for y axis. Defaults to "value".
xlab	label for x axis. Defaults to "band".
col	line color. Defaults to "black".
lty	line type. Defaults to 1.
type	type of plot. Meant to take either line "l" or no plotting "n".
...	other arguments passed to matplot.

**Value**

nothing. Called for side effect.

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
plot(spec, lwd = 1.2)
```

---

plot\_interactive      *Plot spectra interactively*

---

**Description**

Interactively plots spectra with a shiny app. Useful to inspect large datasets.

**Usage**

```
plot_interactive(
  spec,
  colpalette = function(n) RColorBrewer::brewer.pal(n, "Dark2"),
  ...
)
```

**Arguments**

spec	spectra object
colpalette	a color palette function, e.g. rainbow, terrain.colors, or a function returned by colorRampPalette() or colorRamps package
...	Other arguments passed to plot

**Details**

plot\_interact limits the number of spectra displayed at once to 600 for performance reasons. As of now, the function does not return anything and does not have side effects. This means that spectra can be selected and highlighted but not yet deleted or subset from the shiny app.

**Value**

interactive plot

**Author(s)**

Anna K. Schweiger and Jose Eduardo Meireles

**Examples**

```
## Not run:  
# Create a spectra object  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
  
# Start interactive plot  
plot_interactive(spec)  
  
## End(Not run)
```

---

plot\_quantile

*Plot spectra quantiles*

---

**Description**

plot\_quantile plots polygons for the quantiles of spectra per band.

**Usage**

```
plot_quantile(  
  spec,  
  total_prob = 0.95,  
  col = rgb(0, 0, 0, 0.1),  
  border = TRUE,  
  add = FALSE,  
  na.rm = TRUE,  
  ...  
)
```



**Arguments**

spec	spectra object
total_prob	total probability mass to encompass. Single number between 0.0 and 1.0. Defaults to 0.95.
col	polygon color
border	boolean. Draw border?
add	if add = FALSE (default), a new plot is created. Otherwise (add = TRUE), the quantile is added to the current plot.
na.rm	boolean. remove NAs to compute quantiles? Defaults to TRUE
...	other parameters passed to polygon() or to plot.

**Value**

nothing. Called for its side effect.

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
plot_quantile(spec, total_prob = 0.5)
```

---

plot\_regions      *Plot polygons for spectral regions*

---

**Description**

plot\_regions plots polygons for default (VIS, NIR, SWIR 1, SWIR 2) or customized regions of the spectrum.

**Usage**

```
plot_regions(  
  spec,  
  regions = default_spec_regions(),  
  col = grDevices::rgb(0.7, 0.7, 0.7, 0.3),  
  border = FALSE,  
  add = TRUE,  
  add_label = TRUE,  
  cex_label = 1,  
  ...  
)
```

**Arguments**

spec	spectra object
regions	matrix with spectral regions in columns and only two rows named "begin" and "end". Values are the bands where a spectral regions begins and ends. See details for how the default regions are defined.
col	color for regions. Single value or vector of length ncol (regions).
border	color for region borders. Defaults to FALSE (no border).
add	boolean. If TRUE (default) adds polygons to current plot (if a plot exists) or throws an error if a plot does not exist. If FALSE, a new plot is created <b>**without**</b> any spectra.
add_label	boolean. Add region column names on top of the polygons?
cex_label	label scale
...	additional parameters passed to polygon().

**Details**

Default regions: `spec_regions = cbind("VIS" = c(begin = 400, end = 700), "NIR" = c(begin = 800, end = 1300), "SWIR1" = c(begin = 1550, end = 1800), "SWIR2" = c(begin = 2000, end = 2400))`.

**Value**

nothing. Called for its side effect.

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
plot_regions(spec, default_spec_regions())
plot(spec, add = TRUE)

# Alternatively, if you want to get fancy...
## Not run:
col_fun = colorRampPalette(c(rgb(1, 1, 0, 0.7), rgb(1, 0, 0, 0.7)), alpha = TRUE)
colors = col_fun(4)

plot_regions(spec, default_spec_regions(), col = colors)
plot(spec, add = TRUE)

## End(Not run)
```

---

print.spectra	<i>Print spectra</i>
---------------	----------------------

---

**Description**

print prints basic information about the spectra obj to the console

**Usage**

```
## S3 method for class 'spectra'  
print(x, ...)
```

**Arguments**

x	spectra object
...	other arguments passed to print. not implemented for spectra

**Value**

nothing. called for side effect

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
print(spec)  
## or simply  
spec
```

---

quantile.spectra	<i>Compute spectra quantiles</i>
------------------	----------------------------------

---

**Description**

quantile computes quantiles by band and returns them as 'spectra'.

**Usage**

```
## S3 method for class 'spectra'
quantile(
  x,
  probs = c(0.025, 0.25, 0.5, 0.75, 0.975),
  na.rm = TRUE,
  names = NULL,
  ...
)
```

**Arguments**

x	spectra object. Must have at least the same number of sample that length(probs) has.
probs	Probabilities to compute quantiles. Must be a vector of numerics between 0.0 and 1.0. Defaults to c(0.025, 0.25, 0.5, 0.75, 0.975). Duplicated probs will be removed.
na.rm	remove NAs before computing quantiles? Defaults to TRUE
names	names for each quantile spectrum. If NULL (default), names are set to probs. A char vector should otherwise be given. Recycled.
...	other arguments passed to quantile.

**Value**

spectra object with one spectrum for each prob

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
quantile(spec, probs = c(0.25, 0.75))
```

---

range.spectra	<i>Range of spectral values</i>
---------------	---------------------------------

---

**Description**

range Returns the range of (min, max) values in spectra

**Usage**

```
## S3 method for class 'spectra'
range(..., na.rm = FALSE)
```

**Arguments**

... spectra object  
 na.rm boolean. remove NAs? Defaults to FALSE

**Value**

tuple of numeric values (min, max)

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
range(spec)
```

---

read_spectra	<i>Read files from various formats into 'spectra'</i>
--------------	---

---

**Description**

Read files from various formats into 'spectra'

**Usage**

```
read_spectra(
  path,
  format,
  type = "target_reflectance",
  recursive = FALSE,
  exclude_if_matches = NULL,
  ignore_extension = FALSE,
  ...
)
```

**Arguments**

path Path to directory or input files  
 format file formats. "asd" (for ASD); "sig" or "svc" (for SVC); "sed" or "psr" (for SpecEvo PSR).  
 type Data type to read. "target\_reflectance", "target\_radiance", or "reference\_radiance". Defaults to "target\_reflectance".  
 recursive read files recursively

```

exclude_if_matches
    excludes files that match this regular expression. Example: "BAD"
ignore_extension
    boolean. If TRUE, the parser will try to read every file in path regardless of the
    expected extension.
...
    nothing yet

```

**Value**

a single 'spectra' or a list of 'spectra' (in case files have incompatible band number or bands values)

**Author(s)**

Jose Eduardo Meireles

**Examples**

```

library(spectrolab)
dir_path = system.file("extdata", "Acer_example", package = "spectrolab")

# Relative reflectance is re
spec     = read_spectra(path = dir_path, format = "sig")

```

---

resample

*Resample spectra*

---

**Description**

resample returns spectra resampled to new bands using spline smoothing. Possible to increase or decrease the spectral resolution.

**Usage**

```

resample(x, new_wvls, ...)

## S3 method for class 'spectra'
resample(x, new_wvls, ...)

```

**Arguments**

```

x           spectra object. bands must be strictly increasing
new_wvls   numeric vector of bands to sample from spectra
...        additional parameters passed to the smooth.spline function.

```

**Details**

resample doesn't predict values for bands outside of the original range.

**Value**

spectra object with resampled spectra

**Methods (by class)**

- spectra: Resample spectra

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec = resample(spec, new_wvls = seq(400, 2400, 0.5), parallel = FALSE)
```

---

sd	<i>Standard deviation</i>
----	---------------------------

---

**Description**

sd computes the standard deviation spectrum. Note that values will not reflect value anymore, but the sd of the value instead.

**Usage**

```
sd(x, na.rm = FALSE)
```

**Arguments**

x	a numeric vector or an R object which is coercible to one by <code>as.double(x)</code>
na.rm	logical. Should missing values be removed?

**Value**

standard deviation

---

sd.default	<i>Default variance</i>
------------	-------------------------

---

### Description

This function computes the standard deviation of the values in `x`. If `na.rm` is `TRUE` then missing values are removed before computation proceeds.

### Usage

```
## Default S3 method:
sd(x, na.rm = FALSE)
```

### Arguments

<code>x</code>	a numeric vector or an R object but not a <a href="#">factor</a> coercible to numeric by <code>as.double(x)</code> .
<code>na.rm</code>	logical. Should missing values be removed?

### Details

Like [var](#) this uses denominator  $n - 1$ .

The standard deviation of a length-one or zero-length vector is `NA`.

### See Also

[var](#) for its square, and [mad](#), the most robust alternative.

### Examples

```
sd(1:2) ^ 2
```

---

sd.spectra	<i>Standard deviation spectrum</i>
------------	------------------------------------

---

### Description

Forces `keep_txt_meta = TRUE`

### Usage

```
## S3 method for class 'spectra'
sd(x, na.rm = TRUE)
```



**Arguments**

x	spectra
na.rm	boolean. remove NAs?

**Value**

single spectrum

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
sd(spec)
```

---

smooth

*Generic Smoothing function*

---

**Description**

Generic Smoothing function

**Usage**

```
smooth(x, ...)
```

**Arguments**

x	data to smooth over
...	additional arguments

**Value**

smoothed data

---

smooth.default	<i>Default smoothing function</i>
----------------	-----------------------------------

---

**Description**

Default smoothing function

**Usage**

```
## Default S3 method:
smooth(x, ...)
```

**Arguments**

x	data to smooth over
...	additional arguments

**Value**

smoothed data

---

smooth.spectra	<i>Smooth spectra</i>
----------------	-----------------------

---

**Description**

smooth runs each spectrum by a smoothing and returns the spectra

**Usage**

```
## S3 method for class 'spectra'
smooth(x, method = "spline", ...)
```

**Arguments**

x	spectra object. bands must be strictly increasing
method	Choose smoothing method: "spline" (default) or "moving_average"
...	additional parameters passed to smooth.spline or parameters 'n' and 'save_wvls_to_meta' for the moving average smoothing.

**Value**

a spectra object of with smoothed spectra

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)

spec = as_spectra(spec_matrix_example, name_idx = 1)
spec = smooth(spec, parallel = FALSE)
```

---

*smooth\_moving\_avg*      *Smooth moving average for spectra*

---

**Description**

Smooth moving average for spectra

**Usage**

```
smooth_moving_avg(x, n = NULL, save_wvls_to_meta = TRUE)
```

**Arguments**

x                    spectra object  
n                    = NULL  
save\_wvls\_to\_meta    boolean. keep lost ends of original wvls in metadata

**Value**

spectra object

**Author(s)**

Jose Eduardo Meireles

---

smooth_spline	<i>Smooth spline functions for spectra</i>
---------------	--

---

**Description**

Gets spline functions for each spectrum in a spectra object.

**Usage**

```
smooth_spline(x, parallel = TRUE, ...)
```

**Arguments**

x	spectra object. bands must be strictly increasing
parallel	boolean. Do computation in parallel? Defaults to TRUE. Unfortunately, the parallelization does not work on Windows.
...	additional parameters passed to smooth.spline except nknots, which is computed internally

**Value**

a list of spline functions

**Author(s)**

Jose Eduardo Meireles

---

spectra	<i>Spectra object constructor</i>
---------	-----------------------------------

---

**Description**

spectra "manually" creates a spectra object

**Usage**

```
spectra(value, bands, names, meta = NULL, ...)
```

**Arguments**

value	N by M numeric matrix. N samples in rows and M bands in columns
bands	band names in vector of length M
names	sample names in vector of length N
meta	spectra metadata. defaults to NULL. Must be either of length or nrow equals to the number of samples (nrow(value) or length(names))
...	additional arguments to metadata creation. not implemented yet

**Value**

spectra object

**Note**

This function resorts to an ugly hack to deal with metadata assignment. Need to think a little harder to find a solution.

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
# 1. Create a value matrix.
# In this case, by removing the first column that holds the species name
rf = spec_matrix_example[ , -1]

# (2) Create a vector with band labels that match
# the value matrix columns.
wl = colnames(rf)

# (3) Create a vector with sample labels that match
# the value matrix rows.
# In this case, use the first column of spec_matrix_example
sn = spec_matrix_example[ , 1]

# Finally, construct the spectra object using the `spectra` constructor
spec = spectra(value = rf, bands = wl, names = sn)
```

---

spectrolab

*Spectrolab*

---

**Description**

Class and methods for hyperspectral data.

---

spec\_matrix\_example    *Example spectral dataset*

---

**Description**

Simulated spectral dataset as a matrix. First column hold species names and the remaining ones store the spectra values. band labels are given as column names

**Usage**

```
spec_matrix_example
```

**Format**

An object of class `matrix` (inherits from `array`) with 50 rows and 2102 columns.

**Author(s)**

Jose Eduardo Meireles

---

split.spectra    *Split spectra*

---

**Description**

split a spectra object into a list of spectra according to grouping f.

**Usage**

```
## S3 method for class 'spectra'  
split(x, f, drop = FALSE, ...)
```

**Arguments**

x	spectra object
f	factor vector defining the grouping. Must have length <code>nrow(x)</code>
drop	NOT used
...	NOT used

**Value**

list of spectra

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
spec_list = split(spec, names(spec))
```

---

str.spectra	<i>Structure of the spectra object</i>
-------------	--

---

**Description**

Structure of the spectra object

**Usage**

```
## S3 method for class 'spectra'
str(object, ...)
```

**Arguments**

object	spectra object
...	additional args. not implemented

**Value**

prints to console

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
str(spec)
```

---

subset\_by                      *Subset spectra by factor*

---

### Description

subset\_by subsets spectra by a factor 'by' ensuring that it appears at most 'n\_max' times **and** at least 'n\_min' times in the dataset.

### Usage

```
subset_by(x, by, n_min, n_max, random = TRUE)
```

```
## S3 method for class 'spectra'  
subset_by(x, by, n_min, n_max, random = TRUE)
```

### Arguments

x	spectra object
by	vector coercible to factor and of same length as nrow(x)
n_min	int. only keep spectra with at least (inclusive) 'n_min' number of samples per unique 'by'.
n_max	int. keep at most (incl) this number of spectra per unique 'by'
random	boolean. Sample randomly or keep first n_max? Defaults to TRUE

### Details

Note that subset\_by forces you to provide both a minimum and a maximum number of spectra to be kept for each unique value of 'by'. In case you're interested in subsetting *only* based on 'n\_min', set 'n\_max' to 'Inf'.

### Value

spectra

### Methods (by class)

- spectra: Subset spectra by factor

### Author(s)

Jose Eduardo Meireles



## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)

# remove spec of species with less than 4 samples
spec = subset_by(spec, by = names(spec), n_min = 4, n_max = Inf)
```

---

summary.spectra	<i>Summarize spectra</i>
-----------------	--------------------------

---

## Description

Summarize spectra

## Usage

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

## Arguments

object	spectra object
...	additional params to summary. not used yet

## Value

nothing yet (just prints to console)

## Author(s)

Jose Eduardo Meireles

## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
summary(spec)
```

---

t.spectra	<i>Spectra Transpose</i>
-----------	--------------------------

---

**Description**

spectra are not transposable. Transpose the value instead

**Usage**

```
## S3 method for class 'spectra'  
t(x)
```

**Arguments**

x                    spectra

**Value**

nothing. operation not allowed

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)  
s = as_spectra(spec_matrix_example, name_idx = 1)  
  
# This will throw an error  
## Not run:  
t(s)  
  
## End(Not run)  
# But these options should work  
t(value(s))  
t(as.matrix(s))
```

---

try_keep_txt	<i>Wrap function to try to keep text</i>
--------------	--

---

**Description**

Function operator returning a function f that tries to keep text.

**Usage**

```
try_keep_txt(f)
```

**Arguments**

f                    function to be applied

**Details**

try\_keep\_txt takes a function f as argument, typically a mathematical operation such as mean, median, etc. and returns a modified version of it that will try return a string of unique values in case function f emits a warning. Useful when aggregating over spectral metadata that has both numeric values (which you want to aggregate) and text values, which you want to keep.

**Value**

modified function f (f').

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
g = try_keep_txt(mean)
g(c(1, 2))
g(c("a", "b"))
```

---

value	<i>Get spectra value</i>
-------	--------------------------

---

**Description**

value returns the value matrix from spectra

**Usage**

```
value(x)

## S3 method for class 'spectra'
value(x)
```

**Arguments**

x                    spectra object

**Value**

matrix with samples in rows and bands in columns

**Methods (by class)**

- spectra: Get spectra value

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
is.matrix(value(spec))
```

---

value<-                      *Set spectra value*

---

**Description**

value Assigns the rhs to the value of the lhs spectra obj

**Usage**

```
value(x) <- value
```

**Arguments**

x	spectra object
value	value to be assigned to the lhs

**Value**

nothing. called for its side effect

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
# scale all reflectance values by 2
value(spec) = value(spec) * 2
```

---

var	<i>Variance</i>
-----	-----------------

---

**Description**

var computes the variance spectrum. Note that values will not reflect value anymore, but the variance of the value instead.

**Usage**

```
var(x, y = NULL, na.rm = FALSE, use)
```

**Arguments**

x	a numeric vector, matrix or data frame
y	NULL (default) or a vector, matrix or data frame with compatible dimensions to x.
na.rm	logical. Should missing values be removed?
use	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs"

**Value**

variance

---

var.default	<i>Variance</i>
-------------	-----------------

---

**Description**

var computes the variance spectrum. Note that values will not reflect value anymore, but the variance of the value instead.

**Usage**

```
## Default S3 method:
var(x, y = NULL, na.rm = FALSE, use)
```

**Arguments**

x	a numeric vector, matrix or data frame
y	NULL (default) or a vector, matrix or data frame with compatible dimensions to x.
na.rm	logical. Should missing values be removed?
use	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs"

**Value**

variance

---

var.spectra	<i>Variance spectrum</i>
-------------	--------------------------

---

**Description**

Forces keep\_txt\_meta = TRUE

**Usage**

```
## S3 method for class 'spectra'
var(x, y = NULL, na.rm = TRUE, use)
```

**Arguments**

x	spectra
y	nothing
na.rm	boolean. remove NAs?
use	nothing

**Value**

single spectrum

**Author(s)**

Jose Eduardo Meireles

**Examples**

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
var(spec)
```

---

[.spectra                      *Subset spectra*

---

## Description

`[` Subsets spectra by sample names (rows) or (and) bands (columns)

## Usage

```
## S3 method for class 'spectra'
x[i, j, simplify = TRUE]
```

## Arguments

x	spectra object
i	Sample names (preferred), index, or a logical vector of length nrow(x)
j	band labels, as numeric or character or a logical vector of length ncol(x). Do not use indexes!
simplify	Boolean. If TRUE (default), single band selections are returned as a named vector of values

## Details

Subset operations based on samples (first argument) will match sample names or indexes, in that order. The spectra constructor ensures that names are not numeric nor are coercible to numeric, such that `x[1:2, ]` will return the first and second samples in the 'spectra' object. Subsetting based on bands (second argument) matches the band labels, not indices! That is, `x[, 600]` will give you the value data for the 600nm band and not the 600th band. Boolean vectors of the appropriate length can be used to subset samples and bands.

## Value

usually a spectra object, but see param 'simplify'

## Author(s)

Jose Eduardo Meireles

## Examples

```
library(spectrolab)
spec = as_spectra(spec_matrix_example, name_idx = 1)
head(names(spec), n = 3)
# by name
spec1 = spec[ "species_7" , ]
spec1
# by band
spec2 = spec[ , 400:700 ]
spec2
```

---

[<-.spectra                      *Assign values to spectra*

---

### Description

`[<-`` assigns the rhs values to spectra

### Usage

```
## S3 replacement method for class 'spectra'  
x[i, j] <- value
```

### Arguments

<code>x</code>	spectra object (lhs)
<code>i</code>	Sample names (preferred), index, or a logical vector of length <code>nrow(x)</code>
<code>j</code>	band labels, as numeric or character or a logical vector of length <code>ncol(x)</code> . Do not use indexes!
<code>value</code>	value to be assigned (rhs). Must either data coercible to numeric or another 'spectra' obj

### Value

nothing. modifies spectra as side effect

### Author(s)

Jose Eduardo Meireles

### Examples

```
library(spectrolab)  
spec = as_spectra(spec_matrix_example, name_idx = 1)  
spec[ , 400:500] = spec[ , 400:500] * 1.2  
spec
```



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