

# Package ‘ggspectra’

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**Type** Package

**Title** Extensions to 'ggplot2' for Radiation Spectra

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**Maintainer** Pedro J. Aphalo <pedro.aphalo@helsinki.fi>

**Description** Additional annotations, and stats for plotting ``light" spectra with 'ggplot2', together with specializations of ggplot() and plot() methods for spectral data stored in objects of the classes defined in package 'photobiology' and a plot() method for objects of class ``waveband", also defined in package 'photobiology'. Part of the 'r4photobiology' suite, Aphalo P. J. (2015) <doi:10.19232/uv4pb.2015.1.14>.

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<https://bitbucket.org/aphalo/ggspectra>

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**Author** Pedro J. Aphalo [aut, cre] (<<https://orcid.org/0000-0003-3385-972X>>),  
Titta K. Kotilainen [ctb] (<<https://orcid.org/0000-0002-2822-9734>>)

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ggspectra-package	<i>ggspectra: Extensions to 'ggplot2' for Radiation Spectra</i>
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## Description

Additional annotations, and stats for plotting "light" spectra with 'ggplot2', together with specializations of ggplot() and plot() methods for spectral data stored in objects of the classes defined in package 'photobiology' and a plot() method for objects of class "waveband", also defined in package 'photobiology'. Part of the 'r4photobiology' suite, Aphalo P. J. (2015) <doi:10.19232/uv4pb.2015.1.14>.

## Details

Package 'ggspectra' provides a set of stats, geoms and methods extending packages 'ggplot2' and 'photobiology'. They ease the task of plotting radiation-related spectra and of annotating the resulting plots with labels and summary quantities derived from the spectral data.

Plot methods automate in many respects the plotting of spectral data. 'ggplot2' compatible statistics make the addition of labels or plotting of subject-area specific summaries possible as well as the addition of labels and wavelength-based colour to plots easy. Available summaries are most of those relevant to photobiology. However, many of the functions in the package are more generally useful for plotting UV, VIS and NIR spectra of light emission, transmittance, reflectance, absorptance, and responses.

The available summary quantities are both simple statistical summaries and response-weighted summaries. Simple derived quantities represent summaries of a given range of wavelengths, and can be expressed either in energy or photon based units. Derived `_biologically_effective_` quantities are used to quantify the effect of radiation on different organisms or processes within organisms. These effects can range from damage to perception of informational light signals. Additional features of spectra may be important and worthwhile annotating in plots. Of these, local maxima (peaks) and minima (valleys) present in spectral data can also be annotated with statistics made available by the 'ggspectra' package.

Package 'ggspectra' is useful solely for plotting spectral data as most functions depend on the x aesthetic being mapped to a variable containing wavelength values expressed in nanometres. It works well together with some other extensions to package 'ggplot2' such as packages 'ggrepel' and 'cowplot'.

This package is part of a suite of R packages for photobiological calculations described at the [r4photobiology](<https://www.r4photobiology.info>) web site.

## Note

This package makes use of the new features of 'ggplot2' 2.0.0 that make writing this kind of extensions really easy and is consequently not compatible with earlier versions of 'ggplot2'.

## Author(s)

**Maintainer:** Pedro J. Aphalo <pedro.aphalo@helsinki.fi> (0000-0003-3385-972X)

Other contributors:

- Titta K. Kotilainen (0000-0002-2822-9734) [contributor]

## References

Aphalo, Pedro J. (2015) The r4photobiology suite. UV4Plants Bulletin, 2015:1, 21-29. <https://doi.org/10.19232/uv4pb.2015.1.14>.

ggplot2 web site at <http://ggplot2.org/>

ggplot2 source code at <https://github.com/hadley/ggplot2>

Function multiplot from <http://www.cookbook-r.com/>

## See Also

Useful links:

- <https://www.r4photobiology.info>
- <https://bitbucket.org/aphalo/ggspectra>
- Report bugs at <https://bitbucket.org/aphalo/ggspectra>

## Examples

```
library(ggplot2)
library(photobiology)
library(photobiologyWavebands)

ggplot(sun.spct) + geom_line() + stat_peaks(span = NULL)

ggplot(sun.spct, aes(w.length, s.e.irrad)) + geom_line() +
  stat_peaks(span = 21, geom = "point", colour = "red") +
  stat_peaks(span = 51, geom = "text", colour = "red", vjust = -0.3,
            label.fmt = "%3.0f nm")

ggplot(polyester.spct, range = UV()) + geom_line()

plot(sun.spct)

plot(polyester.spct, UV_bands(), range = UV(),
      annotations = c("=", "segments", "labels"))
```

---

A_internal_label	<i>Absorbance axis labels</i>
------------------	-------------------------------

---

### Description

Generate cps axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

### Usage

```
A_internal_label(unit.exponent = 0, format = getOption("photobiology.math",  
  default = "R.expression"))
```

```
A_total_label(unit.exponent = 0, format = getOption("photobiology.math",  
  default = "R.expression"))
```

### Arguments

unit.exponent integer

format character string, "R", "R.expression", "R.character", or "LaTeX".

### Value

a character string or an R expression.

### Examples

```
A_internal_label()  
A_internal_label(-3)  
A_internal_label(format = "R.expression")  
A_internal_label(format = "LaTeX")  
A_internal_label(-3, format = "LaTeX")
```

```
A_total_label()  
A_total_label(-3)  
A_total_label(format = "R.expression")  
A_total_label(format = "LaTeX")  
A_total_label(-3, format = "LaTeX")
```

---

black_or_white	<i>Chose black vs. white color based on weighted mean of RGB channels</i>
----------------	---

---

**Description**

Chose black or white color based on a color to be used as background. Usefull when using `geom_text` on top of tiles or bars, or `geom_label` with a variable fill.

**Usage**

```
black_or_white(colors, threshold = 0.45)
```

**Arguments**

colors	character A vector of color definitions.
threshold	numeric in range 0 to 1.

**Examples**

```
black_or_white("red")
black_or_white(colors()[1:10])
```

---

color_chart	<i>Create a color checker chart</i>
-------------	-------------------------------------

---

**Description**

Color-checker-chart ggplot labelled with color names or with indexes of the colors in the vector passed as first argument.

**Usage**

```
color_chart(colors = grDevices::colors(), ncol = NULL, use.names = NULL,
  text.size = 2, text.color = NULL, grid.color = "white")
```

**Arguments**

colors	character A vector of color definitions.
ncol	integer Number of column in the checker grid.
use.names	logical Force use of names or indexes.
text.size	numeric Size of the text labels drawn on each color tile.
text.color	character Color definition, used for text on tiles.
grid.color	character Color definition, used for grid lines between tiles.

**Note**

Default `text.color` uses `black_or_white()` to ensure enough contrast. Default for `use.names` depends on number of columns in the grid, indexes are used when columns are seven or more.

**Examples**

```
color_chart()
color_chart(grep("dark", colors(), value = TRUE), text.size = 3.5)
```

---

counts_label	<i>Raw-counts axis labels</i>
--------------	-------------------------------

---

**Description**

Generate axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

**Usage**

```
counts_label(unit.exponent = 3, format = getOption("photobiology.math",
  default = "R.expression"))
```

**Arguments**

`unit.exponent` integer  
`format` character string, "R", "R.expression", "R.character", or "LaTeX".

**Value**

a character string or an R expression.

**Examples**

```
counts_label()
counts_label("R.expression")
counts_label("LaTeX")
```

---

cps_label	<i>Counts-per-second axis labels</i>
-----------	--------------------------------------

---

**Description**

Generate cps axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

**Usage**

```
cps_label(unit.exponent = 0, format = getOption("photobiology.math", default
= "R.expression"))
```

**Arguments**

unit.exponent integer  
format character string, "R", "R.expresion", "R.character", or "LaTeX".

**Value**

a character string or an R expression.

**Examples**

```
cps_label()  
cps_label(3)  
cps_label(format = "R.expression")  
cps_label(format = "LaTeX")  
cps_label(3, format = "LaTeX")
```

---

exponent2prefix	<i>SI unit prefixes</i>
-----------------	-------------------------

---

**Description**

Convert SI unit prefixes into exponents of ten of multipliers and vice-versa.



**Usage**

```
exponent2prefix(exponent, char.set = getOption("photobiology.fancy.chars",
  default = "utf8"))

exponent2factor(exponent = 0, if.zero.exponent = "1")

exponent2prefix_name(exponent)

prefix_name2exponent(name)

prefix2exponent(prefix, char.set = getOption("photobiology.fancy.chars",
  default = "utf8"))

has_SI_prefix(exponent)

nearest_SI_exponent(exponent)
```

**Arguments**

exponent	numeric	The power of 10 of the unit multiplier.
char.set	character	How to encode Greek letters and other fancy characters in prefixes: "utf8", "ascii", "LaTeX".
if.zero.exponent	character	string to return when exponent is equal to zero.
name	character	Long SI name of multiplier.
prefix	character	Unit prefix used for multiplier.

**Note**

To change the default `char.set`, set R option `"photobiology.fancy.chars"`. Implementation is based on a table of data and extensible to any alphabet supported by R character objects by expanding the table.

**Examples**

```
exponent2prefix(3)
exponent2prefix(0)
exponent2prefix(-6)
```

```
exponent2factor(3)
exponent2factor(0)
exponent2factor(0, NULL)
exponent2factor(0, "")
exponent2factor(-6)
```

---

 geom\_spect

*Spectral data plots.*


---

### Description

For each continuous x value, `geom_spect` displays a y interval. `geom_spect` is a special case of `geom_area`, where the minimum of the range is fixed to 0, but stacking is not enabled.

### Usage

```
geom_spect(mapping = NULL, data = NULL, stat = "identity",
           position = "identity", na.rm = FALSE, show.legend = NA,
           inherit.aes = TRUE, ...)
```

### Arguments

<code>mapping</code>	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
<code>data</code>	A data frame. If specified, overrides the default data frame defined at the top level of the plot.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>na.rm</code>	If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Details

An spectrum plot is the analog of a line plot (see [geom\\_path](#)), and can be used to show y varies over the range of x. The difference is that the area under the line is filled.

### Aesthetics

See [geom\\_ribbon](#)

### See Also

[geom\\_ribbon](#) for stacked areas, [geom\\_path](#) for lines (lines), [geom\\_point](#) for scatter plots.

## Examples

```
library(ggplot2)
library(photobiology)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) + geom_spct()
```

---

ggplot

*Create a new ggplot plot from spectral data.*

---

## Description

`ggplot()` initializes a ggplot object. It can be used to declare the input spectral object for a graphic and to optionally specify the set of plot aesthetics intended to be common throughout all subsequent layers unless specifically overridden.

## Usage

```
## S3 method for class 'source_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        unit.out = getOption("photobiology.radiation.unit", default = "energy"),
        environment = parent.frame())

## S3 method for class 'response_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        unit.out = getOption("photobiology.radiation.unit", default = "energy"),
        environment = parent.frame())

## S3 method for class 'filter_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        plot.qty = getOption("photobiology.filter.qty", default = "transmittance"),
        environment = parent.frame())

## S3 method for class 'reflector_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        plot.qty = NULL, environment = parent.frame())

## S3 method for class 'cps_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        environment = parent.frame())

## S3 method for class 'calibration_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
        environment = parent.frame())

## S3 method for class 'raw_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
```

```

environment = parent.frame())

## S3 method for class 'object_spct'
ggplot(data, mapping = NULL, ..., range = NULL,
       plot.qty = getOption("photobiology.object.qty", default = "all"),
       environment = parent.frame())

## S3 method for class 'generic_mspct'
ggplot(data, mapping = NULL, ..., range = NULL,
       environment = parent.frame())

```

### Arguments

<code>data</code>	Default spectrum dataset to use for plot. If not a spectrum, the methods used will be those defined in package <code>ggplot2</code> . See <a href="#">ggplot</a> . If not specified, must be supplied in each layer added to the plot.
<code>mapping</code>	Default list of aesthetic mappings to use for plot. If not specified, in the case of spectral objects, a default mapping will be used.
<code>...</code>	Other arguments passed on to methods.
<code>range</code>	an R object on which <code>range()</code> returns a vector of length 2, with min and max wavelengths (nm).
<code>unit.out</code>	character string indicating type of units to use for plotting.
<code>environment</code>	If a variable defined in the aesthetic mapping is not found in the data, <code>ggplot</code> will look for it in this environment. It defaults to using the environment in which <code>ggplot()</code> is called.
<code>plot.qty</code>	character string one of "transmittance" or "absorbance" for <code>filter_spct</code> , and one of "transmittance", "reflectance" or "all" for <code>object_spct</code> .

### Details

`ggplot()` is typically used to construct a plot incrementally, using the `+` operator to add layers to the existing `ggplot` object. This is advantageous in that the code is explicit about which layers are added and the order in which they are added. For complex graphics with multiple layers, initialization with `ggplot` is recommended.

We show seven common ways to invoke `ggplot` for spectra and collections of spectra:

- `ggplot(spct)`
- `ggplot(spct, unit.out = <unit.to.use>)`
- `ggplot(spct, plot.qty = <quantity.to.plot>)`
- `ggplot(spct, range = <wavelength.range>)`
- `ggplot(spct) + aes(<other aesthetics>)`
- `ggplot(spct, aes(x, y, <other aesthetics>))`
- `ggplot(spct, aes())`

The first method is recommended if all layers use the same data and the same set of automatic default x and y aesthetics. The second, third and fourth use automatic default x and y aesthetics but first transform or trim the spectral data to be plotted. The fifth uses automatic default x and y aesthetics and adds mappings for other aesthetics. These patterns can be combined as needed. The sixth disables the use of a default automatic mapping, while the seventh delays the mapping of aesthetics and can be convenient when using different mappings for different geoms.

### Collections of spectra

The method for collections of spectra accepts arguments for the same parameters as the corresponding methods for single spectra. Heterogeneous generic collections of spectra are not supported. When plotting collections of spectra the factor `spct.idx` contains as levels the names of the individual members of the collection, and can be mapped to aesthetics or used for faceting.

### Note

Current implementation does not merge the default mapping with user supplied mapping. If user supplies a mapping, it is used as is, and variables should be present in the spectral object. In contrast, when using the default mapping, unit conversion is done on the fly when needed. To add to the default mapping, `aes()` can be used by itself to compose the ggplot.

`plot.qty` is ignored for reflectors.

### Examples

```
library(photobiology)
library(ggplot2)
ggplot(sun.spct) + geom_line()
ggplot(sun.spct, unit.out = "photon") + geom_line()

ggplot(yellow_gel.spct) + geom_line()
ggplot(yellow_gel.spct, plot.qty = "absorbance") + geom_line()

ggplot(Ler_leaf.spct) + facet_grid(~variable) + geom_line()
ggplot(Ler_leaf.spct) + aes(linetype = variable) + geom_line()
```

---

ggtitle\_spct

*Add title to a spectral plot*

---

### Description

Add a title to a spectral plot based on metadata stored in an spectral object.

### Usage

```
ggtitle_spct(x, x.name = deparse(substitute(x)), annotations = "title",
  time.format = "", tz = lubridate::tz(getWhenMeasured(x)),
  default.title = "title:objt")
```

**Arguments**

<code>x</code>	generic_spect	The spectral object plotted.
<code>x.name</code>	character	The name of the object being plotted.
<code>annotations</code>	character vector	Annotations as described for <code>plot()</code> methods, values unrelated to title are ignored.
<code>time.format</code>	character	Format as accepted by <code>strptime</code> .
<code>tz</code>	character	time zone used in labels.
<code>default.title</code>	character vector	The default used for annotations = "title".

**Details**

`ggtitle_spect()` retrieves from object `x` metadata and passes it to `ggplot2::ggtitle()` as arguments for `title` and `subtitle`. The specification for the title is passed as argument to `annotations`, and consists in the keyword `title` with optional modifiers selecting the kind of metadata to use, separated by colons. "objt", "class", "what", "when", "where", "inst.name", "inst.sn" and "none" are recognized as modifiers to "title".

**Value**

The return value of `ggplot2::ggtitle()`.

**Examples**

```
library(ggplot2)
library(photobiology)

p <- ggplot(sun.spct) +
  geom_line()

p + ggtitle_spect(sun.spct)
p + ggtitle_spect(sun.spct, annotations = "title:where:when")
```

---

multiplot

*Multiple plot function*


---

**Description**

Grid based; allows multiple plots arranged in a matrix and printed to any R device. `ggplot` objects can be passed in ..., or to `plotlist` (as a list of `ggplot` objects)

**Usage**

```
multiplot(..., plotlist = NULL, cols = 1, layout = NULL)
```

**Arguments**

...	one or more ggplot objects
plotlist	list of ggplot objects
cols	numerical Number of columns in layout
layout	A numeric matrix specifying the layout. If present, 'cols' is ignored.

**Details**

ggplot objects can be passed in ..., or to plotlist (as a list of ggplot objects) If the layout is something like matrix(c(1,2,3,3), nrow=2, byrow=TRUE), then plot 1 will go in the upper left, 2 will go in the upper right, and 3 will go all the way across the bottom.

**Note**

Modified from example by Winston Chang found in the Cookbook for R Licenced under CC BY-SA

**References**

from <http://www.cookbook-r.com/>

**Examples**

```
library(photobiology)
multiplot(plot(sun.spct), plot(yellow_gel.spct), cols = 1)
```

---

plot.calibration\_spct *Plot methods for spectral irradiation calibrations.*

---

**Description**

These methods return a ggplot object with an annotated plot of a calibration\_spct object or of the spectra contained in a calibration\_mspct object.

**Usage**

```
## S3 method for class 'calibration_spct'
plot(x, ...,
     w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
     UVA(), PAR())), range = NULL, unit.out = "counts", pc.out = FALSE,
     label.qty = "mean", span = NULL, annotations = NULL, time.format = "",
     tz = "UTC", norm = NULL, text.size = 2.5, na.rm = TRUE)

## S3 method for class 'calibration_mspct'
plot(x, ..., range = NULL)
```

**Arguments**

x	a calibration_spct object or a calibration_mspct object.
...	other arguments passed along, such as label.qty.
w.band	a single waveband object or a list of waveband objects.
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm).
unit.out	character IGNORED.
pc.out	logical, if TRUE use percents instead of fraction of one.
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector ("summaries" is ignored).
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
norm	numeric normalization wavelength (nm) or character string "max" for normalization at the wavelength of highest peak.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated.

**See Also**

Other plot functions: [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

---

plot.cps\_spct

*Plot method for spectra expressed as detector counts per second.*

---

**Description**

This function returns a ggplot object with an annotated plot of a response\_spct object.



**Usage**

```
## S3 method for class 'cps_spct'
plot(x, ..., w.band = getOption("photobiology.plot.bands",
  default = list(UVC(), UVB(), UVA(), PAR())), range = NULL,
  unit.out = "cps", pc.out = FALSE, label.qty = "mean", span = NULL,
  annotations = NULL, time.format = "", tz = "UTC", norm = NULL,
  text.size = 2.5, na.rm = TRUE)
```

**Arguments**

x	a cps_spct object
...	other arguments passed along, such as label.qty
w.band	a single waveband object or a list of waveband objects
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)
unit.out	character IGNORED
pc.out	logical, if TRUE use percents instead of fraction of one
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector ("summaries" is ignored)
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
norm	numeric normalization wavelength (nm) or character string "max" for normalization at the wavelength of highest peak.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

---

plot.filter\_spect      *Plot methods for filter spectra.*

---

### Description

These methods return a ggplot object with an annotated plot of a filter\_spect object or of the spectra contained in a filter\_mspct object.

### Usage

```
## S3 method for class 'filter_spect'
plot(x, ...,
     w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
     UVA(), PAR())), range = NULL,
     plot.qty = getOption("photobiology.filter.qty", default = "transmittance"),
     pc.out = FALSE, label.qty = NULL, span = NULL, annotations = NULL,
     time.format = "", tz = "UTC", text.size = 2.5, na.rm = TRUE)

## S3 method for class 'filter_mspct'
plot(x, ..., range = NULL)
```

### Arguments

x	a filter_spect object or a filter_mspct object.
...	other arguments passed along, such as label.qty.
w.band	a single waveband object or a list of waveband objects.
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm).
plot.qty	character string one of "transmittance" or "absorbance".
pc.out	logical, if TRUE use percents instead of fraction of one.
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector.
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

### Value

a ggplot object.

**Note**

The ggplot object returned can be further manipulated and added to. Except when no annotations are added, limits are set for the x-axis and y-axis scales. The y scale limits are expanded to include all data, or at least to the range of expected values. The plotting of absorbance is an exception as the y-axis is not extended past 6 a.u. In the case of absorbance, values larger than 6 a.u. are rarely meaningful due to stray light during measurement. However, when transmittance values below the detection limit are rounded to zero, and later converted into absorbance, values Inf a.u. result, disrupting the plot. Scales are further expanded so as to make space for the annotations.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

**Examples**

```
library(photobiology)
plot(yellow_gel.spct)
plot(yellow_gel.spct, pc.out = TRUE)
```

---

plot.object_spct	<i>Plot method for object spectra.</i>
------------------	--

---

**Description**

This function returns a ggplot object with an annotated plot of an object\_spct object.

**Usage**

```
## S3 method for class 'object_spct'
plot(x, ...,
      w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
        UVA(), PAR())), range = NULL, plot.qty = "all", pc.out = FALSE,
      label.qty = NULL, span = 61, annotations = NULL, time.format = "",
      tz = "UTC", stacked = TRUE, text.size = 2.5, na.rm = TRUE)

## S3 method for class 'object_mspct'
plot(x, ..., range = NULL)
```

**Arguments**

x	an object_spct object
...	other arguments passed along, such as label.qty
w.band	a single waveband object or a list of waveband objects
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)

plot.qty	character string, one of "all", "transmittance", "absorbance", "absorptance", or "reflectance".
pc.out	logical, if TRUE use percents instead of fraction of one
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
stacked	logical
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

The ggplot object returned can be further manipulated and added to. Except when no annotations are added, limits are set for the x-axis and y-axis scales. The y scale limits are expanded to include all data, or at least to the range of expected values. Scales are further expanded so as to make space for the annotations.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

**Examples**

```
library(photobiology)
plot(Ler_leaf.spct)
```

---

plot.raw\_spct

*Plot method for spectra expressed as raw detector counts.*

---

**Description**

This function returns a ggplot object with an annotated plot of a response\_spct object.

**Usage**

```
## S3 method for class 'raw_spct'
plot(x, ..., w.band = getOption("photobiology.plot.bands",
  default = list(UVC(), UVB(), UVA(), PAR())), range = NULL,
  unit.out = "counts", pc.out = FALSE, label.qty = "mean", span = NULL,
  annotations = NULL, time.format = "", tz = "UTC", norm = NULL,
  text.size = 2.5, na.rm = TRUE)
```

**Arguments**

x	a raw_spct object
...	other arguments passed along, such as label.qty
w.band	a single waveband object or a list of waveband objects
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)
unit.out	character IGNORED
pc.out	logical, if TRUE use percents instead of fraction of one
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector ("summaries" is ignored)
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
norm	numeric normalization wavelength (nm) or character string "max" for normalization at the wavelength of highest peak.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

---

plot.reflector\_spct *Plot methods for reflector spectra.*

---

## Description

These methods return a ggplot object with an annotated plot of a reflector\_spct object or of the spectra contained in a reflector\_mspct object.

## Usage

```
## S3 method for class 'reflector_spct'
plot(x, ...,
     w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
     UVA(), PAR())), range = NULL,
     plot.qty = getOption("photobiology.reflector.qty", default = "reflectance"),
     pc.out = FALSE, label.qty = NULL, span = NULL, annotations = NULL,
     time.format = "", tz = "UTC", text.size = 2.5, na.rm = TRUE)

## S3 method for class 'reflector_mspct'
plot(x, ..., range = NULL)
```

## Arguments

x	a reflector_spct object or a reflector_mspct object.
...	other arguments passed along, such as label.qty
w.band	a single waveband object or a list of waveband objects
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)
plot.qty	character string (currently ignored)
pc.out	logical, if TRUE use percents instead of fraction of one
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

## Value

a ggplot object.

**Note**

The ggplot object returned can be further manipulated and added to. Except when no annotations are added, limits are set for the x-axis and y-axis scales. The y scale limits are expanded to include all data, or at least to the range of expected values. Scales are further expanded so as to make space for the annotations.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

**Examples**

```
library(photobiology)
plot(Ler_leaf_rflt.spct)
```

---

plot.response\_spct      *Plot methods for response spectra.*

---

**Description**

These methods return a ggplot object with an annotated plot of a response\_spct object or of the spectra contained in a response\_mspct object.

**Usage**

```
## S3 method for class 'response_spct'
plot(x, ...,
     w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
     UVA(), PAR())), range = NULL,
     unit.out = getOption("photobiology.radiation.unit", default = "energy"),
     pc.out = FALSE, label.qty = NULL, span = NULL, annotations = NULL,
     time.format = "", tz = "UTC", norm = "max", text.size = 2.5,
     na.rm = TRUE)

## S3 method for class 'response_mspct'
plot(x, ..., range = NULL)
```

**Arguments**

x	a response_spct object or a response_mspct object.
...	other arguments passed along, such as label.qty
w.band	a single waveband object or a list of waveband objects
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)

unit.out	character string indicating type of radiation units to use for plotting: "photon" or its synonym "quantum", or "energy"
pc.out	logical, if TRUE use percents instead of fraction of one
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
norm	numeric normalization wavelength (nm) or character string "max" for normalization at the wavelength of highest peak.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated and added to.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.source\\_spct](#), [plot.waveband](#)

**Examples**

```
library(photobiology)
plot(photodiode.spct)
plot(photodiode.spct, unit.out = "photon")
```

---

plot.source\_spct

*Plot methods for light-source spectra.*

---

**Description**

These methods return a ggplot object with an annotated plot of a source\_spct object or of the spectra contained in a source\_mspect object.



**Usage**

```
## S3 method for class 'source_spct'
plot(x, ...,
     w.band = getOption("photobiology.plot.bands", default = list(UVC(), UVB(),
     UVA(), PAR())), range = NULL,
     unit.out = getOption("photobiology.radiation.unit", default = "energy"),
     label.qty = NULL, span = NULL, annotations = NULL, time.format = "",
     tz = "UTC", text.size = 2.5, na.rm = TRUE)

## S3 method for class 'source_mspct'
plot(x, ..., range = NULL)
```

**Arguments**

x	a source_spct or a source_mspct object.
...	other arguments passed along, such as label.qty.
w.band	a single waveband object or a list of waveband objects.
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm).
unit.out	character string indicating type of radiation units to use for plotting: "photon" or its synonym "quantum", or "energy".
label.qty	character string giving the type of summary quantity to use for labels, one of "mean", "total", "contribution", and "relative".
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
annotations	a character vector.
time.format	character Format as accepted by <a href="#">strptime</a> .
tz	character Time zone to use for title and/or subtitle.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated and added to.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.waveband](#)

**Examples**

```
library(photobiology)
plot(sun.spct)
plot(sun.spct, unit.out = "photon")
```

---

plot.waveband	<i>Plot method for waveband objects.</i>
---------------	--

---

**Description**

This function returns a ggplot object with an annotated plot of a waveband object.

**Usage**

```
## S3 method for class 'waveband'
plot(x, ..., w.length = NULL, range = c(280, 800),
      fill = 0, span = NULL,
      unit.in = getOption("photobiology.radiation.unit", default = "energy"),
      annotations = NULL, wb.trim = TRUE, norm = NULL, text.size = 2.5,
      na.rm = TRUE)
```

**Arguments**

x	a waveband object
...	other arguments passed to plot.response_spct()
w.length	numeric vector of wavelengths (nm)
range	an R object on which range() returns a vector of length 2, with min and max wavelengths (nm)
fill	value to use as response for wavelengths outside the waveband range
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element.
unit.in	the type of unit we assume as reference "energy" or "photon" based
annotations	a character vector.
wb.trim	logical
norm	numeric normalization wavelength (nm) or character string "max" for normalization at the wavelength of highest peak.
text.size	numeric size of text in the plot decorations.
na.rm	logical.

**Value**

a ggplot object.

**Note**

Note that scales are expanded so as to make space for the annotations. The object returned is a ggplot object, and can be further manipulated.

Effectiveness spectra are plotted expressing the spectral effectiveness either as  $1 \text{ mol}^{-1} \text{ nm}$  photons of  $1 \text{ J}^{-1} \text{ nm}$  which can be selected through formal argument `unit.out`. The value of `unit.in` has no effect on the result when using BSWFs, as BSWFs are defined based on a certain base of expression, which is enforced. In contrast, for wavebands which only define a wavelength range, changing the assumed reference irradiance, changes the responsivity according to Planck's law.

This function creates a `response_spct` object from the waveband object and plots it. Unused arguments are passed along, which means that other plot aspects can be controlled by providing arguments for the plot method of the `response_spct` class.

**See Also**

Other plot functions: [plot.calibration\\_spct](#), [plot.cps\\_spct](#), [plot.filter\\_spct](#), [plot.object\\_spct](#), [plot.raw\\_spct](#), [plot.reflector\\_spct](#), [plot.response\\_spct](#), [plot.source\\_spct](#)

**Examples**

```
library(photobiology)
plot(waveband(c(400, 500)))
```

---

Rfr_specular_label	<i>Reflectance axis labels</i>
--------------------	--------------------------------

---

**Description**

Generate spectral reflectance labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

**Usage**

```
Rfr_specular_label(unit.exponent = 0,
  format = getOption("photobiology.math", default = "R.expression"))
```

```
Rfr_total_label(unit.exponent = 0, format = getOption("photobiology.math",
  default = "R.expression"))
```

**Arguments**

`unit.exponent` integer  
`format` character string, "R", "R.expression", "R.character", or "LaTeX".

**Value**

a character string or an R expression.

**Examples**

```

Rfr_specular_label()
Rfr_specular_label(3)
Rfr_specular_label(format = "R.expression")
Rfr_specular_label(format = "LaTeX")
Rfr_specular_label(3, format = "LaTeX")

Rfr_total_label()
Rfr_total_label(-2)
Rfr_total_label(-3)
Rfr_total_label(format = "R.expression")
Rfr_total_label(format = "LaTeX")
Rfr_total_label(-2, format = "LaTeX")
Rfr_total_label(-3, format = "LaTeX")

```

---

s.e.irrad_label	<i>spectral irradiance axis labels</i>
-----------------	--

---

**Description**

Generate axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

**Usage**

```

s.e.irrad_label(unit.exponent = 0, format = getOption("photobiology.math",
  default = "R.expression"))

s.q.irrad_label(unit.exponent = -6, format = getOption("photobiology.math",
  default = "R.expression"))

```

**Arguments**

```

unit.exponent  integer
format         character string, "R", "R.expression", "R.character", or "LaTeX".

```

**Value**

a character string or an R expression.

**Examples**

```

counts_label()
counts_label("R.expression")
counts_label("LaTeX")

```

---

s.e.response\_label     *spectral response axis labels*

---

### Description

Generate axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

### Usage

```
s.e.response_label(unit.exponent = 0,
  format = getOption("photobiology.math", default = "R.expression"))
```

```
s.q.response_label(unit.exponent = -6,
  format = getOption("photobiology.math", default = "R.expression"))
```

### Arguments

unit.exponent     integer  
format             character string, "R", "R.expression", "R.character", or "LaTeX".

### Value

a character string or an R expression.

### Examples

```
counts_label()
counts_label("R.expression")
counts_label("LaTeX")
```

---

scale\_x\_wl\_continuous     *Wavelength x-scale*

---

### Description

Scale x continuous with defaults suitable for wavelengths in nanometres.

### Usage

```
scale_x_wl_continuous(unit.exponent = -9,
  name = w_length_label(unit.exponent = unit.exponent),
  breaks = scales::pretty_breaks(n = 7), labels = SI_pl_format(exponent =
  unit.exponent + 9), ...)
```

**Arguments**

<code>unit.exponent</code>	integer
<code>name</code>	The name of the scale, used for the axis-label.
<code>breaks</code>	The positions of ticks or a function to generate them.
<code>labels</code>	The tick labels or a function to generate them from the tick positions.
<code>...</code>	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)
library(photobiology)

ggplot(sun.spct) +
  geom_line() +
  scale_x_wl_continuous()

ggplot(sun.spct) +
  geom_line() +
  scale_x_wl_continuous(-6)

ggplot(sun.spct) +
  geom_line() +
  scale_x_wl_continuous(sec.axis = sec_axis_w_number())

ggplot(sun.spct) +
  geom_line() +
  scale_x_wl_continuous(unit.exponent = -6,
                        sec.axis = sec_axis_w_number())
```

---

`scale_y_A_internal_continuous`

*Absorbance y-scale*

---

**Description**

Scale y continuous with defaults suitable for spectral absorbance.

**Usage**

```
scale_y_A_internal_continuous(unit.exponent = 0,  
  name = A_internal_label(unit.exponent = unit.exponent),  
  labels = SI_pl_format(exponent = unit.exponent), ...)  
  
scale_y_A_total_continuous(unit.exponent = 0,  
  name = A_total_label(unit.exponent = unit.exponent),  
  labels = SI_pl_format(exponent = unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)  
library(photobiology)  
  
ggplot(yellow_gel.spct, plot.qty = "absorbance") +  
  geom_line() +  
  scale_y_A_internal_continuous() +  
  scale_x_wl_continuous()  
  
ggplot(yellow_gel.spct, plot.qty = "absorbance") +  
  geom_line() +  
  scale_y_A_total_continuous() +  
  scale_x_wl_continuous()
```

---

scale\_y\_counts\_continuous

*Raw-counts y-scale*

---

**Description**

Scale y continuous with defaults suitable for raw detector counts.

**Usage**

```
scale_y_counts_continuous(unit.exponent = 3,  
  name = counts_label(unit.exponent = unit.exponent),  
  labels = SI_pl_format(exponent = unit.exponent), ...)  
  
scale_y_counts_tg_continuous(unit.exponent = 3,  
  name = counts_label(unit.exponent = 0), labels = SI_tg_format(exponent =  
  unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)  
library(photobiology)  
  
ggplot(white_led.raw_spct) +  
  geom_line() +  
  scale_y_counts_continuous() +  
  scale_x_wl_continuous()  
  
ggplot(white_led.raw_spct) +  
  geom_line() +  
  scale_y_counts_continuous(0) +  
  scale_x_wl_continuous()  
  
ggplot(white_led.raw_spct) +  
  geom_line() +  
  scale_y_counts_tg_continuous() +  
  scale_x_wl_continuous()
```

---

scale\_y\_cps\_continuous

*Counts-per-second y-scale*

---

**Description**

Scale y continuous with defaults suitable for raw detector counts.



**Usage**

```
scale_y_cps_continuous(unit.exponent = 0, name = cps_label(unit.exponent =
  unit.exponent), labels = SI_pl_format(exponent = unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to scale_y_continuous

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)
library(photobiology)

ggplot(white_led.cps_spct) +
  geom_line() +
  scale_y_cps_continuous() +
  scale_x_wl_continuous()

ggplot(white_led.cps_spct) +
  geom_line() +
  scale_y_cps_continuous(3) +
  scale_x_wl_continuous()
```

---

scale\_y\_Rfr\_specular\_continuous  
*Reflectance y-scale*

---

**Description**

Scale y continuous with defaults suitable for spectral transmittance.

**Usage**

```
scale_y_Rfr_specular_continuous(unit.exponent = 0,
  name = Rfr_specular_label(unit.exponent = unit.exponent),
  labels = SI_pl_format(exponent = unit.exponent), ...)

scale_y_Rfr_total_continuous(unit.exponent = 0,
  name = Rfr_total_label(unit.exponent = unit.exponent),
  labels = SI_pl_format(exponent = unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)
library(photobiology)

ggplot(yellow_gel.spct) +
  geom_line() +
  scale_y_Rfr_total_continuous() +
  scale_x_wl_continuous()

ggplot(yellow_gel.spct) +
  geom_line() +
  scale_y_Rfr_total_continuous(-2) +
  scale_x_wl_continuous()

ggplot(yellow_gel.spct) +
  geom_line() +
  scale_y_Rfr_total_continuous(-3) +
  scale_x_wl_continuous()

ggplot(yellow_gel.spct) +
  geom_line() +
  scale_y_Rfr_total_continuous() +
  scale_x_wl_continuous()
```

---

scale\_y\_s.e.irrad\_continuous  
*Spectral irradiance y-scale*

---

**Description**

Scale y continuous with defaults suitable for raw detector counts.

**Usage**

```
scale_y_s.e.irrad_continuous(unit.exponent = 0,
  name = s.e.irrad_label(unit.exponent), labels = SI_pl_format(exponent =
  unit.exponent), ...)

scale_y_s.q.irrad_continuous(unit.exponent = -6,
  name = s.q.irrad_label(unit.exponent = unit.exponent),
  labels = SI_pl_format(exponent = unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to scale_y_continuous

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)
library(photobiology)

ggplot(sun.spct) +
  geom_line() +
  scale_y_s.e.irrad_continuous() +
  scale_x_wl_continuous()

ggplot(sun.spct) +
  geom_line() +
  scale_y_s.e.irrad_continuous(-1) +
  scale_x_wl_continuous()

ggplot(sun.spct, unit.out = "photon") +
  geom_line() +
  scale_y_s.q.irrad_continuous() +
  scale_x_wl_continuous()
```

---

scale\_y\_s.e.response\_continuous  
*Spectral response y-scale*

---

**Description**

Scale y continuous with defaults suitable for raw detector counts.

**Usage**

```
scale_y_s.e.response_continuous(unit.exponent = 0,
  name = s.e.response_label(unit.exponent), labels = SI_pl_format(exponent =
  -unit.exponent), ...)

scale_y_s.q.response_continuous(unit.exponent = 0,
  name = s.q.response_label(unit.exponent = unit.exponent),
  labels = SI_pl_format(exponent = -unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)
library(photobiology)

ggplot(ccd.spct) +
  geom_line() +
  scale_y_s.e.response_continuous(unit.exponent = 6) +
  scale_x_wl_continuous()

ggplot(ccd.spct, unit.out = "photon") +
  geom_line() +
  scale_y_s.q.response_continuous() +
  scale_x_wl_continuous()
```

---

scale\_y\_Tfr\_internal\_continuous  
*Transmittance y-scale*

---

**Description**

Scale y continuous with defaults suitable for spectral transmittance.

**Usage**

```
scale_y_Tfr_internal_continuous(unit.exponent = 0,  
  name = Tfr_internal_label(unit.exponent = unit.exponent),  
  labels = SI_pl_format(exponent = unit.exponent), ...)  
  
scale_y_Tfr_total_continuous(unit.exponent = 0,  
  name = Tfr_total_label(unit.exponent = unit.exponent),  
  labels = SI_pl_format(exponent = unit.exponent), ...)
```

**Arguments**

unit.exponent	integer
name	The name of the scale, used for the axis-label.
labels	The tick labels or a function to generate them.
...	other named arguments passed to <code>scale_y_continuous</code>

**Note**

This function only alters two default arguments, please, see documentation for [scale\\_continuous](#)

**Examples**

```
library(ggplot2)  
library(photobiology)  
  
ggplot(yellow_gel.spct) +  
  geom_line() +  
  scale_y_Tfr_internal_continuous() +  
  scale_x_wl_continuous()  
  
ggplot(yellow_gel.spct) +  
  geom_line() +  
  scale_y_Tfr_internal_continuous(-2) +  
  scale_x_wl_continuous()  
  
ggplot(yellow_gel.spct) +  
  geom_line() +  
  scale_y_Tfr_internal_continuous(-3) +  
  scale_x_wl_continuous()  
  
ggplot(yellow_gel.spct) +  
  geom_line() +  
  scale_y_Tfr_total_continuous() +  
  scale_x_wl_continuous()
```

---

sec_axis_w_number	<i>Secondary axes for wavelengths</i>
-------------------	---------------------------------------

---

### Description

Secondary axes for wavelength data in nanometres. With suitable scaling and name (axis label) for frequency and wavenumber.

### Usage

```
sec_axis_w_number(unit.exponent = -6)

sec_axis_w_frequency(unit.exponent = 12)
```

### Arguments

unit.exponent integer

### Examples

```
library(ggplot2)
library(photobiology)

ggplot(sun.spct) +
  geom_line() +
  scale_x_continuous(name = w_length_label(),
                    sec.axis = sec_axis_w_number())

ggplot(sun.spct) +
  geom_line() +
  scale_x_continuous(name = w_length_label(),
                    sec.axis = sec_axis_w_number(-4))

ggplot(sun.spct) +
  geom_line() +
  scale_x_continuous(name = w_length_label(),
                    sec.axis = sec_axis_w_number(nearest_SI_exponent(-4)))

ggplot(sun.spct) +
  geom_line() +
  scale_x_continuous(name = w_length_label(),
                    sec.axis = sec_axis_w_number(-3))

ggplot(sun.spct) +
  geom_line() +
  scale_x_continuous(name = w_length_label(),
                    sec.axis = sec_axis_w_frequency())
```

---

SI_pl_format	<i>Formatter for plain labels discounting for SI multipliers</i>
--------------	--

---

**Description**

The labels generated represent numbers rescaled to compensate for a change in unit's by a factor of ten or by a power of ten.

**Usage**

```
SI_pl_format(exponent = 0, digits = 3, ...)
```

```
SI_plain(x, exponent = 0, digits = 3, ...)
```

**Arguments**

exponent	numeric Power of 10 to use as multiplier
digits	number of significant digits to show
...	other arguments passed on to <a href="#">format</a>
x	a numeric vector to format

**Value**

a function with single parameter x, a numeric vector, that returns a character vector

**Examples**

```
SI_pl_format()(1:10)
SI_pl_format()(runif(10))
SI_pl_format(exponent = 2)(runif(10))
SI_plain(1:10)
SI_plain(runif(10))
SI_plain(runif(10), digits = 2)
```

---

SI_tg_format	<i>Formatter for tagged labels using SI multipliers</i>
--------------	---

---

**Description**

The labels generated represent the same numbers, but with trailing zeros removed/added and compensated by attaching to each label an SI multiplier "prefix".

**Usage**

```
SI_tg_format(exponent = 0, digits = 3, ...)
```

```
SI_tagged(x, exponent = 0, digits = 3, ...)
```

**Arguments**

exponent	numeric Power of 10 to use as multiplier
digits	number of significant digits to show
...	other arguments passed on to <a href="#">format</a>
x	a numeric vector to format

**Value**

a function with single parameter x, a numeric vector, that returns a character vector

**Note**

If the exponent passed has no SI prefix defined, the exponent will be adjusted to match one.

**Examples**

```
SI_tg_format()(1:10)
SI_tg_format()(runif(10))
SI_tg_format(exponent = 2)(runif(10))
SI_tagged(1:10)
SI_tagged(runif(10))
SI_tagged(runif(10), digits = 2)
```

---

stat_color	<i>Calculate colours from wavelength.</i>
------------	---

---

**Description**

stat\_color computes color definitions according to human vision.

**Usage**

```
stat_color(mapping = NULL, data = NULL, geom = "point", type = "CMF",
  position = "identity", na.rm = FALSE, show.legend = FALSE,
  inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
type	character one of "CMF" (color matching function) or "CC" (color coordinates).
position	The position adjustment to use for overlapping points on this layer



<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

**Value**

The original data frame with a variable with color definitions added.

**Computed variable**

**color** color corresponding to x-value giving wavelength in nanometres.

**Default aesthetics**

Set by the statistic and available to geoms.

**color** `..color..`

**fill** `..color..`

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

`color_of`, which is used internally.

Other stats functions: `stat_label_peaks`, `stat_peaks`, `stat_wb_box`, `stat_wb_column`, `stat_wb_contribution`, `stat_wb_hbar`, `stat_wb_irrad`, `stat_wb_label`, `stat_wb_mean`, `stat_wb_relative`, `stat_wb_sirrad`, `stat_wb_total`, `stat_wl_strip`, `stat_wl_summary`

**Examples**

```
library(photobiology)
library(ggplot2)
ggplot(sun.spct) + geom_line() +
  stat_color() + scale_color_identity()
```

---

stat\_label\_peaks      *Label peaks and valleys.*

---

### Description

stat\_labels\_peaks finds at which x positions local maxima are located, and adds labels and colors to the data without subsetting. To find local minima, you can use stat\_labels\_valleys instead.

### Usage

```
stat_label_peaks(mapping = NULL, data = NULL, geom = "text", span = 5,
  ignore_threshold = 0, strict = FALSE, label.fmt = "%.3g",
  x.label.fmt = label.fmt, y.label.fmt = label.fmt, position = "identity",
  na.rm = TRUE, show.legend = FALSE, inherit.aes = TRUE, ...)
```

```
stat_label_valleys(mapping = NULL, data = NULL, geom = "text", span = 5,
  ignore_threshold = 0, strict = FALSE, label.fmt = "%.3g",
  x.label.fmt = label.fmt, y.label.fmt = label.fmt, position = "identity",
  na.rm = TRUE, show.legend = FALSE, inherit.aes = TRUE, ...)
```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element. The default value is 5, meaning that a peak is bigger than two consecutive neighbors on each side. Default: 5.
ignore_threshold	numeric value between 0.0 and 1.0 indicating the size threshold below which peaks will be ignored.
strict	logical flag: if TRUE, an element must be strictly greater than all other values in its window to be considered a peak. Default: FALSE.
label.fmt	character string giving a format definition for converting values into character strings by means of function <a href="#">sprintf</a> .
x.label.fmt	character string giving a format definition for converting $x$ -values into character strings by means of function <a href="#">sprintf</a> .
y.label.fmt	character string giving a format definition for converting $y$ -values into character strings by means of function <a href="#">sprintf</a> .
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.

<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

These stats use `geom_text` by default as it is the geom most likely to work well in almost any situation without need of tweaking. These statistics work best with `geom_text_repel` and `geom_label_repel` from package 'ggrepel' as they are designed so that peak or valley labels will not overlap any observation in the whole data set. Default aesthetics set by these stats allow their direct use with `geom_text`, `geom_label`, `geom_line`, `geom_rug`, `geom_hline` and `geom_vline`. The formatting of the labels returned can be controlled by the user.

## Value

The original data with additional computed variables added.

## Computed variables

**x.label** x-value at a peak (or valley) formatted as character or an empty string ("") otherwise

**y.label** y-value at the peak (or valley) formatted as character or an empty string ("") otherwise

**color** At peaks and valleys, color definition calculated by assuming that x-values are wavelengths expressed in nanometres, otherwise, "white".

## Default aesthetics

Set by the statistic and available to geoms.

**label** ..x.label..

**xintercept** ..x..

**yintercept** ..y..

**color** ifelse(..color.. == "white", "black", ..color..)

**fill** ..color..

## Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**Note**

These stats work nicely together with geoms `geom_text_repel` and `geom_label_repel` from package `ggrepel` to solve the problem of overlapping labels by displacing them. To discard overlapping labels use `check_overlap = TRUE` as argument to `geom_text`. By default the labels are character values suitable to be plotted as is, but with a suitable `label.fmt` labels suitable for parsing by the geoms (e.g. into expressions containing greek letters or super or subscripts) can be also easily obtained.

**See Also**

[stat\\_peaks](#), [stat\\_valleys](#) and [find\\_peaks](#), which is used internally.

Other stats functions: [stat\\_color](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) + geom_line() +
  stat_label_peaks(hjust = "left", span = 31, angle = 90, color = "red")
ggplot(sun.spct) + geom_line() +
  stat_label_valleys(hjust = "right", span = 21, angle = 90, color = "blue")

# using 'ggrepel' to avoid overlaps
# too slow for CRAN checks
## Not run:
library(ggrepel)
ggplot(sun.spct) + geom_line() +
  stat_peaks(span = 41, shape = 21, size = 3) +
  stat_label_peaks(span = 41, geom = "label_repel", segment.colour = "red",
                  nudge_y = 0.12, label.fmt = "%3.0f nm") +
  scale_fill_identity() +
  scale_color_identity() +
  expand_limits(y = c(NA, 1))

## End(Not run)
```

---

stat\_peaks

*Find peaks and valleys.*

---

**Description**

`stat_peaks` finds at which x positions local maxima are located. If you want find local minima, you can use `stat_valleys` instead.

**Usage**

```
stat_peaks(mapping = NULL, data = NULL, geom = "point", span = 5,
  ignore_threshold = 0, strict = FALSE, label.fmt = "%.3g",
  x.label.fmt = label.fmt, y.label.fmt = label.fmt, position = "identity",
  na.rm = FALSE, show.legend = FALSE, inherit.aes = TRUE, ...)

stat_valleys(mapping = NULL, data = NULL, geom = "point", span = 5,
  ignore_threshold = 0, strict = FALSE, label.fmt = "%.3g",
  x.label.fmt = label.fmt, y.label.fmt = label.fmt, position = "identity",
  na.rm = FALSE, show.legend = FALSE, inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
span	a peak is defined as an element in a sequence which is greater than all other elements within a window of width span centered at that element. The default value is 5, meaning that a peak is bigger than two consecutive neighbors on each side. Default: 5.
ignore_threshold	numeric value between 0.0 and 1.0 indicating the size threshold below which peaks will be ignored.
strict	logical flag: if TRUE, an element must be strictly greater than all other values in its window to be considered a peak. Default: FALSE.
label.fmt	character string giving a format definition for converting values into character strings by means of function <a href="#">sprintf</a> .
x.label.fmt	character string giving a format definition for converting $\$x$ -values into character strings by means of function <a href="#">sprintf</a> .
y.label.fmt	character string giving a format definition for converting $\$y$ -values into character strings by means of function <a href="#">sprintf</a> .
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Details

These stats use `geom_point` by default as it is the geom most likely to work well in almost any situation without need of tweaking. The default aesthetics set by these stats allow their direct use with `geom_text`, `geom_label`, `geom_line`, `geom_rug`, `geom_hline` and `geom_vline`. The formatting of the labels returned can be controlled by the user.

## Value

A data frame with one row for each peak (or valley) found in the data.

## Computed variables

**x** x-value at the peak (or valley) as numeric

**y** y-value at the peak (or valley) as numeric

**x.label** x-value at the peak (or valley) formatted as character

**y.label** y-value at the peak (or valley) formatted as character

**color** color definition calculated by assuming that x-values are wavelengths expressed in nanometres.

## Default aesthetics

Set by the statistic and available to geoms.

**label** `..x.label..`

**xintercept** `..x..`

**yintercept** `..y..`

**fill** `..color..`

## Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

## Note

These stats work nicely together with geoms `geom_text_repel` and `geom_label_repel` from package `ggrepel` to solve the problem of overlapping labels by displacing them. To discard overlapping labels use `check_overlap = TRUE` as argument to `geom_text`. By default the labels are character values suitable to be plotted as is, but with a suitable `label.fmt` labels suitable for parsing by the geoms (e.g. into expressions containing greek letters or super or subscripts) can be also easily obtained.

**See Also**

[find\\_peaks](#), which is used internally.

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) + geom_line() + stat_peaks()
ggplot(sun.spct) + geom_line() + stat_valleys()
ggplot(sun.spct) + geom_line() +
  stat_peaks(span = 21, geom = "point", colour = "red") +
  stat_peaks(span = 51, geom = "text", colour = "red",
            vjust = -0.3, label.fmt = "%3.0f nm")
ggplot(sun.spct, unit.out = "photon") + geom_point() +
  stat_peaks(span = 5, geom = "line", colour = "red")
```

---

stat\_wb\_box

*Draw colour boxes for wavebands*


---

**Description**

stat\_wb\_box plots boxes corresponding to wavebands, by default located slightly above the peak of the spectrum. Sets suitable default aesthetics for "rect" geom.

**Usage**

```
stat_wb_box(mapping = NULL, data = NULL, geom = "rect", w.band = NULL,
            ypos.mult = 1.07, ypos.fixed = NULL, position = "identity",
            na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
ypos.mult	numeric Multiplier constant used to scale returned y values.
ypos.fixed	numeric If not NULL used a constant value returned in y.
position	The position adjustment to use for overlapping points on this layer

<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named `integral` below is the result of applying `integral.fun` to the data, with default `integrate_xy`.

**x** `w.band-midpoint`  
**xmin** `w.band` minimum  
**xmax** `w.band` maximum  
**ymin** `data$y` minimum  
**ymax** `data$y` maximum  
**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`  
**wb.color** color of the `w.band`  
**wb.name** label of `w.band`  
**BW.color** `black_or_white(wb.color)`

### Default aesthetics

Set by the statistic and available to geoms.

**xmin** `..xmin..`  
**xmax** `..xmax..`  
**ymin** `..y.. - (..ymax.. - ..ymin..) * 0.03`  
**ymax** `..y.. + (..ymax.. - ..ymin..) * 0.03`  
**fill** `..wb.color..`

### Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres  
**y** numeric, a spectral quantity



**Note**

The value returned as default value for `y` is based on the `y`-range of spectral values for the whole data set.

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  stat_wb_box(w.band = VIS_bands()) +
  geom_line() +
  scale_fill_identity()
ggplot(sun.spct) +
  stat_wb_box(w.band = VIS_bands(), color = "white") +
  geom_line() +
  scale_fill_identity()
```

---

stat\_wb\_column

*Integrate ranges under curve.*


---

**Description**

`stat_wb_column` computes means under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for "rect" geom.

**Usage**

```
stat_wb_column(mapping = NULL, data = NULL, geom = "rect",
  w.band = NULL, integral.fun = integrate_xy, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

**Arguments**

<code>mapping</code>	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
<code>data</code>	A layer specific dataset - only needed if you want to override the plot defaults.
<code>geom</code>	The geometric object to use display the data

<code>w.band</code>	a waveband object or a list of waveband objects or numeric vector of at least length two.
<code>integral.fun</code>	function on <code>\$x\$</code> and <code>\$y\$</code> .
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named `integral` below is the result of applying `integral.fun`, with default `integrate_xy`.

**x** `w.band-midpoint`  
**xmin** `w.band` minimum  
**xmax** `w.band` maximum  
**ymin** `data$y` minimum  
**ymax** `data$y` maximum  
**ymean** `yint` divided by `wl_expanse(w.band)`  
**y** `ymean`  
**wb.color** color of the `w.band`  
**wb.name** label of `w.band`  
**BW.color** `black_or_white(wb.color)`

### Default aesthetics

Set by the statistic and available to geoms.

**xmin** `..xmin..`  
**xmax** `..xmax..`  
**ymin** `0`  
**ymax** `..ymean..`  
**fill** `..wb.color..`

### Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

### Note

If the argument passed to `w.band` is a BSWF it is silently converted to a wavelength range and the average of spectral values without weighting is returned as default value for `ymin` while the default value for `ymax` is zero.

### See Also

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

### Examples

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  stat_wb_column(w.band = VIS_bands()) +
  geom_line() +
  scale_fill_identity()

ggplot(sun.spct) +
  stat_wb_column(w.band = VIS_bands(), alpha = 0.5) +
  geom_line() +
  scale_fill_identity()
```

---

`stat_wb_contribution` *Integrate ranges under spectral curve.*

---

### Description

`stat_wb_contribution` computes means under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for "rect", "hline", "vline", "text" and "label" geoms displaying "contributions" per waveband to the total of the spectral integral.

**Usage**

```
stat_wb_contribution(mapping = NULL, data = NULL, geom = "text",
  w.band = NULL, integral.fun = integrate_xy, label.mult = 1,
  label.fmt = "%1.2f", ypos.mult = 1.07, ypos.fixed = NULL,
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
integral.fun	function on $\$x\$$ and $\$y\$$ .
label.mult	numeric Scaling factor applied to y-integral values before conversion into character strings.
label.fmt	character string giving a format definition for converting y-integral values into character strings by means of function <a href="#">sprintf</a> .
ypos.mult	numeric Multiplier constant used to scale returned y values.
ypos.fixed	numeric If not NULL used a constant value returned in y.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

**Value**

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

**Computed variables**

What it is named `integral` below is the result of applying `integral.fun` to the data, with default `integrate_xy`.

**y.label** `yint` multiplied by `label.mult` and formatted according to `label.fmt`

**x** `w.band-midpoint`

**xmin** w.band minimum  
**xmax** w.band maximum  
**ymin** data\$y minimum  
**ymax** data\$y maximum  
**yint** data\$y integral for w.band / data\$y integral for whole range of data\$x  
**xmean** yint divided by wl\_expance(w.band)  
**y** ypos.fixed or top of data, adjusted by ypos.mult  
**wb.color** color of the w.band  
**wb.name** label of w.band

### Default aesthetics

Set by the statistic and available to geoms.

**label** ..y.label..  
**x** ..x..  
**xmin** ..xmin..  
**xmax** ..xmax..  
**ymin** ..y.. - (..ymax.. - ..ymin..) \* 0.03  
**ymax** ..y.. + (..ymax.. - ..ymin..) \* 0.03  
**yintercept** ..ymean..  
**fill** ..wb.color..

### Required aesthetics

Required by the statistic and need to be set with aes().

**x** numeric, wavelength in nanometres  
**y** numeric, a spectral quantity

### See Also

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

### Examples

```

library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS()) +
  stat_wb_contribution(w.band = VIS()) +

```

```

scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS_bands()) +
  stat_wb_contribution(w.band = VIS_bands(), angle = 90, size = 2.5) +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS_bands()) +
  stat_wb_contribution(w.band = VIS_bands(), angle = 90, size = 2.5,
                      label.mult = 100, label.fmt = "%3.0f%%") +
  scale_fill_identity() + scale_color_identity()

```

---

stat\_wb\_hbar

*Integrate ranges under curve.*


---

## Description

stat\_wb\_hbar computes means under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for geoms "errorbarh" and "hline" from 'ggplot', and "linrangeh", and "errorbarh" from 'ggstance'.

## Usage

```

stat_wb_hbar(mapping = NULL, data = NULL, geom = "errorbarh",
             w.band = NULL, integral.fun = integrate_xy, ypos.fixed = NULL,
             position = "identity", na.rm = FALSE, show.legend = NA,
             inherit.aes = TRUE, ...)

```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
integral.fun	function on $x$ and $y$ .
ypos.fixed	numeric If not NULL used a constant value returned in $y$ .
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.

<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named `integral` below is the result of applying `integral.fun`, with default `integrate_xy`.

**x** w.band-midpoint  
**xmin** w.band minimum  
**xmax** w.band maximum  
**ymin** data\$y minimum  
**ymax** data\$y maximum  
**yint** data\$y integral for the range of w.band  
**ymean** yint divided by `wl_expance(w.band)`  
**y** `ypos.fixed` or mean of data  
**wb.color** color of the w.band  
**wb.name** label of w.band

### Default aesthetics

Set by the statistic and available to geoms.

**xmin** `..xmin..`  
**xmax** `..xmax..`  
**yintercept** `..ymean..`  
**height** `(..ymax.. - ..ymin..) * 2e-2`  
**color** `..wb.color..`

### Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres  
**y** numeric, a spectral quantity

**Note**

If the argument passed to `w.band` is a BSWF it is silently converted to a wavelength range and the average of spectral values without any weighting is returned as default value for `y`.

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = VIS_bands(), size = 1) +
  scale_color_identity() +
  theme_bw()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = PAR(), size = 1) +
  scale_color_identity() +
  theme_bw()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = PAR(), size = 1, ypos.fixed = 0) +
  scale_color_identity() +
  theme_bw()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = CIE(), size = 1) +
  scale_color_identity() +
  theme_bw()
```

---

`stat_wb_irrad`*Integrate irradiance for wavebands.*

---

**Description**

`stat_wb_irrad` computes areas under a curve.



**Usage**

```
stat_wb_irrad(mapping = NULL, data = NULL, geom = "text", w.band = NULL,
  time.unit, unit.in, label.qty = "total", label.mult = 1,
  label.fmt = "%.3g", ypos.mult = 1.07, ypos.fixed = NULL,
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

```
stat_wb_e_irrad(mapping = NULL, data = NULL, geom = "text",
  w.band = NULL, time.unit = "second", unit.in = "energy",
  label.qty = "total", label.mult = 1, label.fmt = "%.3g",
  ypos.mult = 1.07, ypos.fixed = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

```
stat_wb_q_irrad(mapping = NULL, data = NULL, geom = "text",
  w.band = NULL, time.unit = "second", unit.in = "photon",
  label.qty = "total", label.mult = 1, label.fmt = "%.3g",
  ypos.mult = 1.07, ypos.fixed = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
time.unit	character or lubridate::duration
unit.in	character One of "photon","quantum" or "energy"
label.qty	character
label.mult	numeric Scaling factor applied to y-integral values before conversion into character strings.
label.fmt	character string giving a format definition for converting y-integral values into character strings by means of function <a href="#">sprintf</a> .
ypos.mult	numeric Multiplier constant used to scale returned y values.
ypos.fixed	numeric If not NULL used a constant value returned in y.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .

... other arguments passed on to `layer`. This can include aesthetics whose values you want to set, not map. See `layer` for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named integral below is the result of applying `irrad`, `e_irrad` or `q_irrad` to the data.

**y.label** `yeff` multiplied by `label.mult` and formatted according to `label.fmt`

**x** `w.band`-midpoint

**xmin** `w.band` minimum

**xmax** `w.band` maximum

**ymin** `data$y` minimum

**ymax** `data$y` maximum

**yeff** weighted irradiance if `w.band` describes a BSWF

**yint** not weighted irradiance for the range of `w.band`

**xmean** `yint` divided by `wl_expance(w.band)`

**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`

**wb.color** color of the `w.band`

**wb.name** label of `w.band`

**BW.color** `black_or_white(wb.color)`

### Default aesthetics

Set by the statistic and available to geoms.

**label** `..y.label..`

**x** `..x..`

**xmin** `..xmin..`

**xmax** `..xmax..`

**ymin** `..y.. - (..ymax.. - ..ymin..) * 0.03`

**ymax** `..y.. + (..ymax.. - ..ymin..) * 0.03`

**yintercept** `..y.mean..`

**fill** `..wb.color..`

### Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  stat_wb_column(w.band = VIS_bands()) +
  stat_wb_e_irrad(w.band = VIS_bands(),
                 angle = 90, size = 4,
                 label.fmt = "%2.0f", ypos.fixed = 0.1) +
  geom_line() +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  stat_wb_box(w.band = VIS_bands()) +
  stat_wb_e_irrad(w.band = VIS_bands(),
                 angle = 90, size = 4,
                 label.fmt = "%2.0f") +
  geom_line() +
  scale_fill_identity() + scale_color_identity()
```

---

stat_wb_label	<i>Label ranges under spectral curve.</i>
---------------	---

---

**Description**

stat\_wb\_label computes the center of a waveband. Sets suitable default aesthetics for "text" and "label" geoms displaying "boundaries" and "names" of wavebands.

**Usage**

```
stat_wb_label(mapping = NULL, data = NULL, geom = "text", w.band = NULL,
              label.fmt = "%s", ypos.fixed = 0, position = "identity",
              na.rm = TRUE, show.legend = NA, inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data

<code>w.band</code>	a waveband object or a list of waveband objects or numeric vector of at least length two.
<code>label.fmt</code>	character string giving a format definition for formatting the name of the waveband. <a href="#">sprintf</a> .
<code>ypos.fixed</code>	numeric If not NULL used a constant value returned in <code>y</code> .
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
<code>...</code>	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

**x** `w.band-midpoint`  
**xmin** `w.band` minimum  
**xmax** `w.band` maximum  
**y** `ypos.fixed` or zero  
**wb.color** color of the `w.band`  
**wb.name** label of `w.band`  
**wb.label** formatted `wb.name`

### Default aesthetics

Set by the statistic and available to geoms.

**label** `..wb.label..`  
**x** `..x..`  
**xmin** `..xmin..`  
**xmax** `..xmax..`  
**fill** `..wb.color..`

### Required aesthetics

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS(), ymin = -0.04, ymax = 0,
             color = "black", fill = "white") +
  stat_wb_label(w.band = VIS(), ypos.fixed = -0.02, color = "black")

ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = PAR(), ypos.fixed = 0, size = 1) +
  stat_wb_label(aes(color = ..wb.color..),
               w.band = PAR(), ypos.fixed = +0.025) +
  scale_color_identity()
```

---

stat_wb_mean	<i>Integrate ranges under curve.</i>
--------------	--------------------------------------

---

**Description**

stat\_wb\_mean computes means under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for "rect", "hline", "vline", "text" and "label" geoms.

**Usage**

```
stat_wb_mean(mapping = NULL, data = NULL, geom = "text", w.band = NULL,
             integral.fun = integrate_xy, label.mult = 1, label.fmt = "%.3g",
             ypos.mult = 1.07, xpos.fixed = NULL, ypos.fixed = NULL,
             position = "identity", na.rm = FALSE, show.legend = NA,
             inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data

<code>w.band</code>	a waveband object or a list of waveband objects or numeric vector of at least length two.
<code>integral.fun</code>	function on <code>\$x</code> and <code>\$y</code> .
<code>label.mult</code>	numeric Scaling factor applied to y-integral values before conversion into character strings.
<code>label.fmt</code>	character string giving a format definition for converting y-integral values into character strings by means of function <code>sprintf</code> .
<code>ypos.mult</code>	numeric Multiplier constant used to scale returned y values.
<code>xpos.fixed</code> , <code>ypos.fixed</code>	numeric If not NULL used as constant value returned in x or y.
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named `integral` below is the result of applying `integral.fun`, with default `integrate_xy`.

**y.label** ymean multiplied by `label.mult` and formatted according to `label.fmt`

**x** `w.band`-midpoint

**xmin** `w.band` minimum

**xmax** `w.band` maximum

**ymin** `data$y` minimum

**ymax** `data$y` maximum

**yint** `data$y` integral for the range of `w.band`

**xmean** `yint` divided by `wl_expance(w.band)`

**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`

**wb.color** color of the `w.band`

**wb.name** label of `w.band`

**BW.color** `black_or_white(wb.color)`

**Default aesthetics**

Set by the statistic and available to geoms.

**label** ..y.label..  
**x** ..x..  
**xmin** ..xmin..  
**xmax** ..xmax..  
**ymin** 0  
**ymax** ..y.mean..  
**yintercept** ..y.mean..  
**fill** ..wb.color..

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres  
**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  stat_wb_column(w.band = VIS_bands()) +
  stat_wb_mean(w.band = VIS_bands(), angle = 90, color = "black") +
  geom_line() +
  scale_fill_identity() + scale_color_identity()

## Not run:
# example takes long to run
library(ggrepel)
ggplot(sun.spct) +
  geom_line() +
  stat_wb_hbar(w.band = VIS_bands(), size = 1.5) +
  stat_wb_mean(w.band = VIS_bands(),
              geom = "label_repel", nudge_y = +0.03,
              segment.colour = NA) +
  scale_fill_identity() + scale_color_identity()

## End(Not run)
```

---

stat\_wb\_relative      *Integrate ranges under spectral curve.*

---

### Description

stat\_wb\_relative computes means under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for "rect", "hline", "vline", "text" and "label" geoms displaying values per waveband "relative" to the sum of the wavebands.

### Usage

```
stat_wb_relative(mapping = NULL, data = NULL, geom = "text",
  w.band = NULL, integral.fun = integrate_xy, label.mult = 1,
  label.fmt = "%1.2f", ypos.mult = 1.07, ypos.fixed = NULL,
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
integral.fun	function on $\$x\$$ and $\$y\$$ .
label.mult	numeric Scaling factor applied to y-integral values before conversion into character strings.
label.fmt	character string giving a format definition for converting y-integral values into character strings by means of function <a href="#">sprintf</a> .
ypos.mult	numeric Multiplier constant used to scale returned y values.
ypos.fixed	numeric If not NULL used a constant value returned in y.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.



**Value**

A data frame with one row for each waveband object in the argument to `w.band`. Wavebands outside the range of the spectral data are trimmed or discarded.

**Computed variables**

What it is named `integral` below is the result of applying `integral.fun` to the data, with default `integrate_xy`.

**y.label** `yint` multiplied by `label.mult` and formatted according to `label.fmt`

**x** `w.band`-midpoint

**xmin** `w.band` minimum

**xmax** `w.band` maximum

**ymin** `data$y` minimum

**ymax** `data$y` maximum

**yint** `data$y` integral for each member of `w.band` / sum of `data$y` integrals for all wavebands in `w.band`

**xmean** `yint` divided by `wl_expance(w.band)`

**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`

**wb.color** color of the `w.band`

**wb.name** label of `w.band`

**BW.color** `black_or_white(wb.color)`

**Default aesthetics**

Set by the statistic and available to geoms.

**label** `..y.label..`

**x** `..x..`

**xmin** `..xmin..`

**xmax** `..xmax..`

**ymin** `..y.. - (..ymax.. - ..ymin..) * 0.03`

**ymax** `..y.. + (..ymax.. - ..ymin..) * 0.03`

**yintercept** `..ymean..`

**fill** `..wb.color..`

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS()) +
  stat_wb_relative(w.band = VIS()) +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS_bands()) +
  stat_wb_relative(w.band = VIS_bands(), angle = 90, size = 2.5) +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS_bands()) +
  stat_wb_relative(w.band = VIS_bands(), angle = 90, size = 2.5,
                  label.mult = 100, label.fmt = "%3.0f%") +
  scale_fill_identity() + scale_color_identity()
```

---

stat\_wb\_sirrad

*Integrate spectral irradiance for wavebands.*


---

**Description**

stat\_wb\_sirrad computes areas under a curve.

**Usage**

```
stat_wb_sirrad(mapping = NULL, data = NULL, geom = "text",
              w.band = NULL, time.unit, unit.in, label.qty = "mean", label.mult = 1,
              label.fmt = "%.3g", ypos.mult = 0.55, xpos.fixed = NULL,
              ypos.fixed = NULL, position = "identity", na.rm = FALSE,
              show.legend = NA, inherit.aes = TRUE, ...)

stat_wb_e_sirrad(mapping = NULL, data = NULL, geom = "text",
                w.band = NULL, time.unit = "second", unit.in = "energy",
                label.qty = "mean", label.mult = 1, label.fmt = "%.3g",
```

```
ypos.mult = 0.55, xpos.fixed = NULL, ypos.fixed = NULL,
position = "identity", na.rm = FALSE, show.legend = NA,
inherit.aes = TRUE, ...)
```

```
stat_wb_q_sirrad(mapping = NULL, data = NULL, geom = "text",
w.band = NULL, time.unit = "second", unit.in = "photon",
label.qty = "mean", label.mult = 1, label.fmt = "%.3g",
ypos.mult = 1.07, xpos.fixed = NULL, ypos.fixed = NULL,
position = "identity", na.rm = FALSE, show.legend = NA,
inherit.aes = TRUE, ...)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
time.unit	character or lubridate::duration
unit.in	character One of "photon", "quantum" or "energy"
label.qty	character
label.mult	numeric Scaling factor applied to y-integral values before conversion into character strings.
label.fmt	character string giving a format definition for converting y-integral values into character strings by means of function <a href="#">sprintf</a> .
ypos.mult	numeric Multiplier constant used to scale returned y values.
xpos.fixed, ypos.fixed	numeric If not NULL used a constant value returned in x or y.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

## Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

**Computed variables**

What it is named integral below is the result of applying `irrad`, `e_irrad` or `q_irrad` to the data.

**y.label** `yeff` multiplied by `label.mult` and formatted according to `label.fmt`

**x** `w.band-midpoint`

**xmin** `w.band` minimum

**xmax** `w.band` maximum

**ymin** `data$y` minimum

**ymax** `data$y` maximum

**yeff** weighted irradiance if `w.band` describes a BSWF

**yint** not weighted irradiance for the range of `w.band`

**xmean** `yint` divided by `wl_expance(w.band)`

**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`

**wb.color** color of the `w.band`

**wb.name** label of `w.band`

**BW.color** `black_or_white(wb.color)`

**Default aesthetics**

Set by the statistic and available to geoms.

**label** `..y.label..`

**x** `..x..`

**xmin** `..xmin..`

**xmax** `..xmax..`

**ymin** 0

**ymax** `..ymean..`

**yintercept** `..ymean..`

**fill** `..wb.color..`

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

## Examples

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  stat_wb_column(w.band = VIS_bands()) +
  stat_wb_e_sirrad(w.band = VIS_bands(), angle = 90, size = 4,
                  label.fmt = "%1.2f", ypos.fixed = 0.1) +
  geom_line() +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct, unit.out = "photon") +
  geom_line() +
  stat_wb_hbar(w.band = PAR(), size = 1) +
  stat_wb_q_sirrad(aes(color = ..wb.color..),
                  w.band = PAR(), label.fmt = "mean = %.3g",
                  ypos.mult = 1, xpos.fixed = 390, hjust = 1) +
  scale_color_identity()
```

---

stat\_wb\_total

*Integrate ranges under spectral curve.*


---

## Description

stat\_wb\_total computes integral under a curve. It first integrates the area under a spectral curve and also the mean expressed per nanometre of wavelength for each waveband in the input. Sets suitable default aesthetics for "rect", "hline", "vline", "text" and "label" geoms displaying "totals" per waveband.

## Usage

```
stat_wb_total(mapping = NULL, data = NULL, geom = "text", w.band = NULL,
              integral.fun = integrate_xy, label.mult = 1, label.fmt = "%.3g",
              ypos.mult = 1.07, ypos.fixed = NULL, position = "identity",
              na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

## Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
w.band	a waveband object or a list of waveband objects or numeric vector of at least length two.
integral.fun	function on $x$ and $y$ .

<code>label.mult</code>	numeric Scaling factor applied to y-integral values before conversion into character strings.
<code>label.fmt</code>	character string giving a format definition for converting y-integral values into character strings by means of function <code>sprintf</code> .
<code>ypos.mult</code>	numeric Multiplier constant used to scale returned y values.
<code>ypos.fixed</code>	numeric If not NULL used a constant value returned in y.
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>show.legend</code>	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>inherit.aes</code>	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders</code> .
<code>...</code>	other arguments passed on to <code>layer</code> . This can include aesthetics whose values you want to set, not map. See <code>layer</code> for more details.

### Value

A data frame with one row for each waveband object in the argument to `w.band`. Waveband outside the range of the spectral data are trimmed or discarded.

### Computed variables

What it is named integral below is the result of applying `integral.fun`, with default `integrate_xy`.

**y.label** ymean multiplied by `label.mult` and formatted according to `label.fmt`

**x** w.band-midpoint

**xmin** w.band minimum

**xmax** w.band maximum

**ymin** data\$y minimum

**ymax** data\$y maximum

**yint** data\$y integral for the range of w.band

**xmean** yint divided by `wl_expanse(w.band)`

**y** `ypos.fixed` or top of data, adjusted by `ypos.mult`

**wb.color** color of the w.band

**wb.name** label of w.band

**BW.color** `black_or_white(wb.color)`

**Default aesthetics**

Set by the statistic and available to geoms.

**label** ..y.label..

**x** ..x..

**xmin** ..xmin..

**xmax** ..xmax..

**ymin** ..y.. - (..ymax.. - ..ymin..) \* 0.03

**ymax** ..y.. + (..ymax.. - ..ymin..) \* 0.03

**yintercept** ..ymean..

**fill** ..wb.color..

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wl\\_strip](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(photobiologyWavebands)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = VIS()) +
  stat_wb_total(w.band = VIS()) +
  scale_fill_identity() + scale_color_identity()

ggplot(sun.spct) +
  geom_line() +
  stat_wb_box(w.band = UV_bands(), color = "white") +
  stat_wb_total(w.band = UV_bands()) +
  scale_fill_identity() + scale_color_identity()
```

stat\_wl\_strip

*Calculate colours from wavelength.***Description**

stat\_wl\_strip computes color definitions according to human vision.

**Usage**

```
stat_wl_strip(mapping = NULL, data = NULL, geom = "rect", type = "CMF",
  w.band = NULL, length.out = 150, position = "identity", na.rm = TRUE,
  show.legend = FALSE, inherit.aes = TRUE, ...)
```

```
wl_guide(mapping = NULL, data = NULL, type = "CMF", w.band = NULL,
  length.out = 150, ymin = -Inf, ymax = Inf, position = "identity",
  na.rm = FALSE, show.legend = FALSE, inherit.aes = TRUE, ...)
```

**Arguments**

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
type	character one of "CMF" (color matching function) or "CC" (color coordinates).
w.band	waveband object or a list of such objects or NULL.
length.out	The number of steps to use to simulate a continuous range of colours when w.band == NULL.
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.
ymin, ymax	numeric used as aesthetics for plotting the guide.

**Value**

generic\_spect object with new x values plus other computed variables described below.



**Computed variables**

**x**  $(w.low + w.high) / 2$   
**wl.low** boundary of waveband  
**wl.high** boundary of waveband  
**wl.color** color corresponding to wavelength  
**wb.color** color corresponding to waveband  
**wb.name** label of w.band

**Default aesthetics**

Set by the statistic and available to geoms.

**x** ..x..  
**label** as.character(..wb.f..  
**xmin** ..wl.low..  
**xmax** ..wl.high..  
**fill** ..wb.color..

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**See Also**

[color\\_of](#), which is used internally.

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_summary](#)

**Examples**

```
library(photobiology)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) + geom_line() +
  stat_wl_strip(ymax = -0.02, ymin = -0.04) +
  scale_fill_identity()

# on some graphic devices the output may show spurious vertical lines
ggplot(sun.spct) + wl_guide(alpha = 0.33, color = NA) + geom_line()
```

---

stat_wl_summary	<i>Average area under curve for regions.</i>
-----------------	--

---

### Description

stat\_wl\_summary computes the area under a curve.

### Usage

```
stat_wl_summary(mapping = NULL, data = NULL, geom = "text",
  range = NULL, integral.fun = integrate_xy, label.fmt = "%.3g",
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

### Arguments

mapping	The aesthetic mapping, usually constructed with <a href="#">aes</a> or <a href="#">aes_</a> . Only needs to be set at the layer level if you are overriding the plot defaults.
data	A layer specific dataset - only needed if you want to override the plot defaults.
geom	The geometric object to use display the data
range	a numeric vector of at least length two.
integral.fun	function on $x$ and $y$ .
label.fmt	character string giving a format definition for converting y-integral values into character strings by means of function <a href="#">sprintf</a> .
position	The position adjustment to use for overlapping points on this layer
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders</a> .
...	other arguments passed on to <a href="#">layer</a> . This can include aesthetics whose values you want to set, not map. See <a href="#">layer</a> for more details.

### Value

A data frame with one row.

**Computed variables**

What it is named `integral` below is the result of applying `integral.fun`, with default `integrate_xy`.

**y.label** `y` formatted according to `label.fmt`

**x** `w.band-midpoint`

**xmin** range minimum

**xmax** range maximum

**y** `data$y` integral for the range by the expanse of the range

**Default aesthetics**

Set by the statistic and available to geoms.

**label** `..label..`

**x** `..x..`

**xmin** `..xmin..`

**xmax** `..xmax..`

**y** `..y..`

**ymin** `0`

**ymax** `..y..`

**yintercept** `..y..`

**Required aesthetics**

Required by the statistic and need to be set with `aes()`.

**x** numeric, wavelength in nanometres

**y** numeric, a spectral quantity

**See Also**

Other stats functions: [stat\\_color](#), [stat\\_label\\_peaks](#), [stat\\_peaks](#), [stat\\_wb\\_box](#), [stat\\_wb\\_column](#), [stat\\_wb\\_contribution](#), [stat\\_wb\\_hbar](#), [stat\\_wb\\_irrad](#), [stat\\_wb\\_label](#), [stat\\_wb\\_mean](#), [stat\\_wb\\_relative](#), [stat\\_wb\\_sirrad](#), [stat\\_wb\\_total](#), [stat\\_wl\\_strip](#)

**Examples**

```
library(photobiology)
library(ggplot2)
# ggplot() methods for spectral objects set a default mapping for x and y.
ggplot(sun.spct) + geom_line() +
  stat_wl_summary(geom = "hline")
ggplot(sun.spct) + geom_line() +
  stat_wl_summary(label.fmt = "mean = %.3f", color = "red", vjust = -0.3) +
  stat_wl_summary(geom = "hline", color = "red")
```

---

Tfr\_internal\_label      *Transmittance axis labels*

---

### Description

Generate cps axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

### Usage

```
Tfr_internal_label(unit.exponent = 0,  
  format = getOption("photobiology.math", default = "R.expression"))
```

```
Tfr_total_label(unit.exponent = 0, format = getOption("photobiology.math",  
  default = "R.expression"))
```

### Arguments

unit.exponent    integer

format            character string, "R", "R.expression", "R.character", or "LaTeX".

### Value

a character string or an R expression.

### Examples

```
Tfr_internal_label()  
Tfr_internal_label(3)  
Tfr_internal_label(format = "R.expression")  
Tfr_internal_label(format = "LaTeX")  
Tfr_internal_label(3, format = "LaTeX")  
  
Tfr_total_label()  
Tfr_total_label(-2)  
Tfr_total_label(-3)  
Tfr_total_label(format = "R.expression")  
Tfr_total_label(format = "LaTeX")  
Tfr_total_label(-2, format = "LaTeX")  
Tfr_total_label(-3, format = "LaTeX")
```

---

w_length_label	<i>Wave- axis labels</i>
----------------	--------------------------

---

### Description

Generate wavelength, wavenumber and wave frequency axis labels in SI units, using SI scale factors. Output can be selected as character, expression (R default devices) or LaTeX (for tikz device).

### Usage

```
w_length_label(unit.exponent = -9, format = getOption("photobiology.math",  
  default = "R.expression"))
```

```
w_number_label(unit.exponent = 0, format = getOption("photobiology.math",  
  default = "R.expression"))
```

```
w_frequency_label(unit.exponent = 9, format = getOption("photobiology.math",  
  default = "R.expression"))
```

### Arguments

unit.exponent integer

format character string, "R", "R.expression", "R.character", or "LaTeX".

### Value

a character string or an R expression.

### Examples

```
w_length_label()  
w_length_label("R.expression")  
w_length_label("LaTeX")  
w_number_label()  
w_number_label("R.expression")  
w_frequency_label()  
w_frequency_label("R.expression")
```

---

`w_number`*Wavelength conversions*

---

**Description**

Convert wavelength into wavenumber or into frequency.

**Usage**

```
w_number(w.length, unit.exponent = 0)
```

```
w_frequency(w.length, unit.exponent = 0)
```

**Arguments**

`w.length`        numeric wavelength (nm)

`unit.exponent`   integer

**Examples**

```
w_number(600)
```

```
w_frequency(600)
```

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