Package 'colorSpec'

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Type Package

Title Color Calculations with Emphasis on Spectral Data

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Description Calculate with spectral properties of light sources, materials, cameras, eyes, and scanners. Build complex systems from simpler parts using a spectral product algebra. For light sources, compute CCT, CRI, and SSI. For object colors, compute optimal colors and Logvinenko coordinates. Work with the standard CIE illuminants and color matching functions, and read spectra from text files, including CGATS files. Estimate a spectrum from its response. A user guide and 9 vignettes are included.

License GPL (>= 3)

LazyLoad yes

LazyData yes

Depends R (>= 3.5.0)

Suggests spacesXYZ, rootSolve, MASS, quadprog, rgl, knitr, rmarkdown, spacesRGB, microbenchmark, arrangements

Enhances plyr

NeedsCompilation no

Repository CRAN

VignetteBuilder knitr

BuildVignettes yes

ByteCompile no

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R **topics documented:**

colorSpec-package	*Package colorSpec - Color Calculations with Emphasis on Spectral Data*

Description

Package **colorSpec** is for working with spectral color data in R.

Details

Features:

1. a clear classification of the commonly seen spectra into 4 types - depending on the vector space to which they belong

2. flexible organization for the spectra in memory, using an S3 class - **colorSpec**

3. a product algebra for the **colorSpec** objects

4. uniform handling of biological eyes, electronic cameras, and general action spectra

5. a few advanced calculations, such as computing optimal colors (aka Macadam Limits)

6. inverse colorimetry, e.g. reflectance recovery from response

7. built-in essential tables, such as the CIE illuminants and color matching functions

8. a package logging system with log levels taken from the popular **Log4J**

9. support for reading a few spectrum file types, including CGATS

10. bonus files containing some other interesting spectra

11. minimal dependencies on other R packages

Non-features:

1. there is no support for many common 3D color spaces, such as CIELAB, HSL, etc.. For these spaces see packages **colorspace**, **colorscience**, **spacesRGB**, and **spacesXYZ**.

2. there are few non-linear operations

3. there is little support for scientific units; for these see package **colorscience**

4. photons are parameterized by wavelength in nanometers; other wavelength units (such as Angstrom and micron) and alternative parameterizations (such as wavenumber and electronvolt) are not available

Regarding the non-linear operations in 2, the only such operations are conversion of linear RGB to display RGB, conversion of absorbance to transmittance, and the reparameterized wavelength in `computeADL`. The electronic camera model is purely linear with no dark current offset or other deviations.

Many ideas are taken from packages **hyperSpec**, **hsdar**, **pavo**, and **zoo**.

Author(s)

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See Also

`colorSpec` for the S3 class provided by this package.

colorSpec User Guide

ABC   *Standard Illuminants A, B, and C (1931)*

Description

A.1nm	standard Illuminant A, 360 to 780 nm at 1 nm intervals
B.5nm	standard Illuminant B, 320 to 780 nm at 5 nm intervals
C.5nm	standard Illuminant C, 320 to 780 nm at 5 nm intervals

Format

Each is a **colorSpec** object organized as a vector, with `quantity` equal to "energy".

Details

All of these have been divided by 100, to make the values at 560nm near 1 instead of 100.

Source

<http://www.cvrl.org>

References

Günther Wyszecki and W. S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982.

A	Table I(3.3.4) pp. 754-758.
B	Table II(3.3.4) pp. 759.
C	Table II(3.3.4) pp. 759.

See Also

[D50](#) [D65](#)

Examples

```
summary(xyz1931.1nm)
white.point = product( D65.1nm, xyz1931.1nm, wave='auto' )
```

---

actinometric	*convert a colorSpec object to be actinometric*

Description

Convert a radiometric **colorSpec** object to have quantity that is actinometric (number of photons). Test an object for whether it is actinometric.

Usage

```
## S3 method for class 'colorSpec'
actinometric( x, multiplier=1, warn=FALSE )

## S3 method for class 'colorSpec'
is.actinometric( x )
```

Arguments

x	a **colorSpec** object
multiplier	a scalar which is multiplied by the output, and intended for unit conversion
warn	if TRUE and a conversion actually takes place, the a WARN message is issued. This makes the user aware of the conversion, so units can be verified. This can be useful when actinometric() is called from another **colorSpec** function.

Details

If the [quantity](#) of x does not start with `'energy'` then the quantity is not radiometric and so x is returned unchanged. Otherwise x is radiometric (energy-based), and must be converted.

If [type](#)(x) is `'light'` then the most common radiometric energy unit is joule.
The conversion equation is:

$$Q = E * \lambda * 10^6 / (N_A * h * c)$$

wher Q is the photon count, E is the energy of the photons, N_A is Avogadro's constant, h is Planck's constant, c is the speed of light, and λ is the wavelength. The output unit of photon count is (μmole of photons) = $(6.02214 * 10^{17}$ photons). If a different unit for Q is desired, then the output should be scaled appropriately. For example, if the desired unit of photon count is exaphotons, then set `multiplier=0.602214`.

If the [quantity](#)(x) is `'energy->electrical'`, then the most common radiometric unit of responsivity to light is coulombs/joule (C/J) or amps/watt (A/W). The conversion equation is:

$$QE = R_e * ((h * c)/e)/\lambda$$

where QE is the quantum efficiency, R_e is the energy-based responsivity, and e is the charge of an electron (in C).
If the unit of x is not C/J, then `multiplier` should be set appropriately.

If the [quantity](#)(x) is `'energy->neural'` or `'energy->action'`, the most common radiometric unit of energy is joule (J).

The conversion equation is:

$$R_p = R_e * 10^{-6} * (N_A * h * c)/\lambda$$

where R_p is the photon-based responsivity, and R_e is the energy-based responsivity, The output unit of photon count is (μmole of photons) = $(6.02214 * 10^{17}$ photons). This essentially the reciprocal of the first conversion equation.

The argument `multiplier` is applied to the right side of all the above conversion equations.

Value

actinometric() returns a **colorSpec** object with [quantity](#) that is actinometric (photon-based) and not radiometric (energy-based). If type(x) is a material type (`'material'` or `'responsivity.material'`) then x is returned unchanged.

If quantity(x) starts with `'photons'`, then is.actinometric() returns TRUE, and otherwise FALSE.

Note

To log the executed conversion equation, execute cs.options(loglevel=`'INFO'`).

Source

Wikipedia. **Photon counting**. https://en.wikipedia.org/wiki/Photon_counting

See Also

quantity, type, cs.options, radiometric

Examples

```
colSums( solar.irradiance ) # step size is 1nm, from 280 to 1000 nm. organized as a matrix
# AirMass.0  GlobalTilt AirMass.1.5
#  944.5458    740.3220    649.7749  # irradiance, watts*m^{-2}


colSums( actinometric(solar.irradiance) )
# AirMass.0  GlobalTilt AirMass.1.5
# 4886.920   3947.761   3522.149 # photon irradiance, (umoles of photons)*sec^{-1}*m^{-2}

colSums( actinometric(solar.irradiance,multiplier=0.602214) )
# AirMass.0  GlobalTilt AirMass.1.5
#  2942.972    2377.397    2121.088  # photon irradiance, exaphotons*sec^{-1}*m^{-2}
```

---

applyspec	*apply a function to each spectrum in a colorSpec object*

Description

apply a function to each spectrum in a **colorSpec** object

Usage

```
## S3 method for class 'colorSpec'
applyspec( x, FUN, ... )
```

Arguments

x	a **colorSpec** object with N wavelengths
FUN	a function that takes an N-vector as argument and returns an N-vector
...	additional arguments passed to FUN

Details

applyspec() simply calls apply() with the right MARGIN.

Value

a **colorSpec** object with the same dimensions, wavelength, quantity, and organization. If FUN does not return an N-vector, it is an ERROR and applyspec() returns NULL.

See Also

quantity, wavelength, linearize, organization, apply

Examples

```
#  convert absorbance to transmittance
path = system.file( "extdata/stains/Hematoxylin.txt", package='colorSpec' )
x = readSpectra( path )
x = applyspec( x, function(y) {10^(-y)} ) # this is what linearize(x) does
```

---

as.data.frame   *Convert a colorSpec Object to a data.frame*

Description

convert a **colorSpec** object to a data.frame

Usage

```
## S3 method for class 'colorSpec'
as.data.frame( x, row.names=NULL, optional=FALSE, organization='auto', ... )
```

Arguments

x	a **colorSpec** object
organization	The organization of the returned data.frame, which can be 'row', 'col', or 'auto'. If 'auto', then 'row' or 'col' is selected automatically, see **Details**
row.names	ignored
optional	ignored
...	extra arguments ignored

Details

If organization is 'auto', and the organization of x is 'df.row', then organization is set to 'row' and the returned data.frame has the spectra in the rows. Otherwise the returned data.frame has the spectra in the columns.

Value

If the returned data.frame has the spectra in the rows, then the spectra are in a matrix in the last column (with name spectra), and any existing extradata are also returned in the other columns. The wavelengths are only present in character form, as the colnames of the matrix.

If the returned data.frame has the spectra in the columns, then the wavelengths are in the first column, and the spectra are in the other columns.

See Also

as.matrix, extradata

---

atmosphere   *atmospheric transmittance along a horizontal path*

Description

Calculate transmittance along a horizontal optical path in the atmosphere, as a function of length (distance) and the molecular and aerosol properties. Because the path is horizontal, the atmospheric properties are assumed to be constant on the path. Only molecular scattering is considered. There is no modeling of molecular absorption; for visible wavelengths this is reasonable.

Usage

```
atmosTransmittance( distance, wavelength=380:720,
                    molecules=list(N=2.547305e25,n0=1.000293),
                    aerosols=list(metrange=25000,alpha=0.8,beta=0.0001) )
```

Arguments

distance
: the length of the optical path, in meters. It can also be a numeric vector of lengths.

wavelength
: a vector of wavelengths, in nm, for the transmittance calculations

molecules
: a list of molecular properties, see **Details**. If this is NULL, then the molecular transmittance is identically 1.

aerosols
: a list of aerosol properties, see **Details**. If this is NULL, then the aerosol transmittance is identically 1.

Details

The list `molecules` has 2 parameters that describe the molecules in the atmosphere. `N` is the molecular density of the atmosphere at sea level, in $molecules/meter^3$. The given default is the density at sea level. `n0` is the refractive index of pure molecular air (with no aerosols). For the molecular attenuation, the standard model for Rayleigh scattering is used, and there is no modeling of molecular absorption.

The list `aerosols` has 3 parameters that describe the aerosols in the atmosphere. The standard Angstrom aerosol attenuation model is:

$$attenuation(\lambda) = \beta * (\lambda/\lambda_0)^{-\alpha}$$

α is the Angstrom exponent, and is dimensionless. $attenuation$ and β have unit m^{-1}. And λ_0=550nm.

`metrange` is the *Meteorological Range* of the atmosphere in meters, as defined by *Koschmieder*. This is the distance at which the transmittance=0.02 at λ_0. If `metrange` is not NULL (the default is 25000) then both α and β are calculated to achieve this desired `metrange`, and the supplied α and β are ignored. α is calculated from `metrange` using the *Kruse* model, see **Note**. β is calculated so that the product of molecular and aerosol transmittance yields the desired `metrange`. In fact:

$$\beta = -\mu_0 - log(0.02)/V_r$$

where μ_0 is the molecular attenuation at λ_0, and V_r is the meteorological range. For a log message with the calculated values, execute `cs.options(loglevel='INFO')` before calling `atmosTransmittance()`.

Value

`atmosTransmittance()` returns a **colorSpec** object with quantity equal to `'transmittance'`. There is a spectrum in the object for each value in the vector `distance`. The specnames are set to `sprintf("dist=%gm",distance)`.

The final transmittance is the product of the molecular transmittance and the aerosol transmittance. If both `molecules` and `aerosols` are `NULL`, then the final transmittance is identically 1; the atmosphere has become a vacuum.

Note

The Kruse model for α as a function of V_r is defined in 3 pieces. For $0 \leq V_r < 6000$, $\alpha = 0.585 * (V_r/1000)^{1/3}$. For $6000 \leq V_r < 50000$, $\alpha = 1.3$. And for $V_r \geq 50000$, $\alpha = 1.6$. So α is increasing, but not strictly, and not continuously. V_r is in meters. See *Kruse* and *Kaushal*.

The built-in object atmosphere2003 is transmittance along an optical path that is **NOT** horizontal, and extends to outer space. This is *much* more complicated to calculate.

References

Angstrom, Anders. On the atmospheric transmission of sun radiation and on dust in the air. *Geogr. Ann.*, no. 2. 1929.

Kaushal, H. and Jain, V.K. and Kar, S. **Free Space Optical Communication**. Springer. 2017.

Koschmieder, Harald. Theorie der horizontalen Sichtweite. *Beitrage zur Physik der Atmosphare*. 1924. **12**. pages 33-53.

P. W. Kruse, L. D. McGlauchlin, and R. B. McQuistan. **Elements of Infrared Technology: Generation, Transmission, and Detection**. J. Wiley & Sons, New York, 1962.

See Also

solar.irradiance, specnames

Examples

```
trans = atmosTransmittance( c(5,10,15,20,25)*1000 ) # 5 distances with atmospheric defaults

# verify that transmittance[550]=0.02 at dist=25000
plot( trans, legend='bottomright', log='y' )

# repeat, but this time assign alpha and beta explicitly
trans = atmosTransmittance( c(5,10,15,20,25)*1000, aero=list(alpha=1,beta=0.0001) )
```

---

bandSpectra	*Compute Band-based Material Spectra, and Bands for Existing Material Spectra*

Description

A band-based material spectrum is a superimposition of bandpass filters, and (optionally) a band-stop filter. The 2 functions in this topic convert a vector of numbers between 0 and 1 to a band representation, and back again.

Usage

```
bandMaterial( lambda, wavelength=380:780 )

## S3 method for class 'colorSpec'
bandRepresentation( x )
```

Arguments

lambda	a numeric Mx2 matrix with wavelength pairs in the rows, or a vector that can be converted to such a matrix, by row. The two wavelengths in a row (the *transition wavelengths*) define either a bandpass or bandstop filter, and all the rows are superimposed to define the transmittance spectrum of the final material. If the 2 wavelengths are denoted by λ_1 and λ_2, and $\lambda_1 < \lambda_2$ then the filter is a bandpass filter. If the 2 wavelengths are swapped, then the spectrum is "flipped" and is a bandstop filter, and the band "wraps around" from long wavelengths to short. There can be at most 1 bandstop filter in the matrix, otherwise it is an error. The bands must be pairwise disjoint, otherwise it is an error. To get a material with transmittance identically 0, set lambda to a 0x2 matrix. To get a material with transmittance identically 1, set lambda to a 1x2 matrix with $\lambda_1 = \beta_0$ and $\lambda_2 = \beta_N$, where N is the number of wavelengths. See vignette **Convexity and Transitions** for the definition of β_0 and β_N and other mathematical details. lambda can also be a list of such matrices, which are processed separately, see **Value**.
wavelength	a vector of wavelengths for the returned object
x	a **colorSpec** object with type equal to 'material'

Details

bandRepresentation() is a right-inverse of bandMaterial(), see **Examples** and the test script test-bands.R. For more mathematical details, see the vignette **Convexity and Transitions**.

Value

bandMaterial() returns a **colorSpec** object with quantity equal to 'transmitance'. If lambda is a matrix, then the object has 1 spectrum. If lambda is a list of matrices with length N, then the object has N spectra.

bandRepresentation() returns a list of matrices with 2 columns. There is a matrix in the list for each spectrum in x.

See Also

rectangularMaterial(), vignette **Convexity and Transitions**

Examples

```
# make a vector superimposing a bandpass and a bandstop filter, and of the proper length 401
vec = c( rep(1,100), 0.5, rep(0,40), .25, rep(1,50), 0.9, rep(0,100), 0.4, rep(1,107) )

#  convert that vector to a colorSpec object, with a single spectrum
spec = colorSpec( vec, wavelength=380:780, quantity='transmittance', specnames='sample' )

#  extract and print the 2 bands
lambda = bandRepresentation( spec ) ;  print(lambda)

##  $sample
##      lambda1 lambda2
##  BS   673.10   480.0
##  BP1  521.25   572.4

#  convert the 2 bands  (the transition wavelengths) back to a vector of length 401
#  and compare with the original vector
delta = vec - coredata( bandMaterial(lambda) )

range(delta)
## [1] -9.092727e-14  2.275957e-14
```

---

bind	*Combine colorSpec Objects*

Description

Take a sequence of **colorSpec** objects and combine their spectra

Usage

```
## S3 method for class 'colorSpec'
bind( ... )
```

Arguments

...	**colorSpec** objects with the same wavelength and quantity, and with distinct specnames (no duplicates)

Details

The organization of the returned object is the most complex of those in the inputs, where the order of complexity is:

`'matrix' < 'df.col' < 'df.row'`

If the selected `organization` is `'df.row'`, the extradata is combined in a way that preserves all the columns. Missing data is filled with NAs, analogous to rbind.fill().

The metadata of the returned object is copied from the first object in the input list.

Value

bind() returns a **colorSpec** object, or NULL in case of ERROR. If the bind is successful, the number of spectra in the output object is the sum of the number of spectra in the input objects.

See Also

wavelength, quantity, specnames, organization, extradata, metadata, rbind.fill()

Examples

```
Rosco = readSpectra( system.file( 'extdata/objects/Rosco.txt', package='colorSpec' ) )
Rosco = resample( Rosco, wave=wavelength(Hoya) )
numSpectra(Hoya)        # prints 4
numSpectra(Rosco)       # prints 42

filters = bind( Hoya, Rosco )
numSpectra(filters)     # prints 46

colnames( extradata(Hoya) )
## [1] "SAMPLE_NAME"  "FresnelReflectance"  "Thickness"

colnames( extradata(Rosco) )
## [1] "Model"  "SampleID"  "SAMPLE_NAME"  "Substrate"  "RefractiveIndex"  "Thickness"

##  The columns in common are "SAMPLE_NAME" and "Thickness"


colnames( extradata(filters) )
## [1] "FresnelReflectance" "Model" "RefractiveIndex" "SAMPLE_NAME"
## [5] "SampleID" "Substrate" "Thickness"
##
## "SAMPLE_NAME" and "Thickness" are combined in the usual way
## The other columns are present, and missing data is filled with NAs
```

---

calibrate *make a linear modification to a colorSpec responder*

Description

make a linear modification to a **colorSpec** responder with M spectra, so a specific stimulus (a single spectrum) creates a specific response (an M-vector). It is generalized form of *white balance*.

The options are complicated, but in all cases the returned object is [multiply](x,gmat) where gmat is an internally calculated MxM matrix - called the *gain matrix*. Stated another way, the spectra in the output are linear combinations of spectra in the input x.

In case of ERROR, a message is logged and the original x is returned.

Usage

```
## S3 method for class 'colorSpec'
calibrate( x, stimulus=NULL, response=NULL, method=NULL )
```

Arguments

x	a **colorSpec** responder with M spectra. The type must be 'responsivity.light' or 'responsivity.material'.
stimulus	a **colorSpec** object with a single spectrum, with type either 'light' or 'material' to match x. The wavelength sequence of stimulus must be equal to that of x. If stimulus is NULL, then an appropriate default is chosen, see **Details**.
response	an M-vector, or a scalar which is then replicated to length M. Normally all entries are not NA, but it is OK to have exactly one that is not NA. In this special case, a single scaling factor is computed from that non-NA coordinate, and then applied to *all* M coordinates; the method must be 'scaling'. This is useful for the recommended method for calibration in ASTM E308-01 section 7.1.2. The same type of scaling is also recommended method in CIE 15: Technical Report section 7.1. In this case response=c(NA,100,NA) so the special coordinate is the luminance Y. See the **Examples** below and the vignettes **Viewing Object Colors in a Gallery** and **The Effect of the Aging Human Lens on Color Vision**. All entries in response, that are not NA, must be positive. If response is NULL, then an appropriate default *may be* chosen, see **Details**.
method	an MxM *adaptation matrix*. method can also be 'scaling' and it is then set to the MxM identity matrix, which scales each responsivity spectrum in x independently. If M=3, method can also be 'Bradford', 'Von Kries', 'MCAT02', or 'Bianco+Schettini', and it is then set to the popular corresponding *chromatic adaptation matrix*. For these special matrices, the spectra in x are **not** scaled independently; there is "cross-talk". If method is NULL, then an appropriate default is chosen, see **Details**.

Details

If `stimulus` is NULL, it is set to [illuminantE]()`()` or [neutralMaterial](`()`) to match `x`.

If `response` is NULL and the response of `x` is `electrical` or `action`, then `response` is set to an M-vector of all 1s. If `response` is NULL and the response of `x` is `neural`, then this is an ERROR and the user is prompted to supply a specific `response`.

If `method` is NULL, its assignment is complicated.
If M=3 and the response of `x` is `neural`, and the specnames of `x` partially match `c('x','y','z')` (case-insensitive), and none of the components of `response` are NA, then the neural response is assumed to be human, and the `method` is set to `'Bradford'`.
Otherwise `method` is set to `'scaling'`.

Value

a **colorSpec** object equal to [multiply](`(x,gmat)` where gmat is an internally calculated MxM matrix. The [quantity](`()` and [wavelength](`()` are preserved.
Note that gmat is not the same as the the MxM *adaptation matrix*. To inspect gmat execute [summary](`()` on the returned object. If `method` is `'scaling'` then gmat is diagonal and the diagonal entries are the M gain factors needed to achieve the calibration.
Useful data is attached as attribute `"calibrate"`.

Note

Chromatic adaptation transforms, such as `'Bradford'`, do not belong in the realm of spectra, for this is not really a spectral calculation. For more about this subject see the explanation in *Digital Color Management*, Chapter 15 - Myths and Misconceptions. These sophisticated adaptation transforms are provided in `calibrate()` because it is possible and convenient.

References

ASTM E308-01. Standard Practice for Computing the Colors of Objects by Using the CIE System. 2001.

CIE 15: Technical Report: Colorimetry, 3rd edition. CIE 15:2004.

Edward J. Giorgianni and Thomas E. Madden. **Digital Color Management: Encoding Solutions.** 2nd Edition John Wiley. 2009. Chapter 15 - Myths and Misconceptions.

See Also

[is.regular](`()`, [multiply](`()`, [quantity](`()`, [wavelength](`()`, [colorSpec](), [summary](`()`, [illuminantE](`()`, [neutralMaterial](`()`, [product](`()`)

Examples

```
wave = 380:780

# make an art gallery illuminated by illuminant A, and with tristimulus XYZ as output
gallery = product( A.1nm, 'artwork', xyz1931.1nm, wave=wave )

#  calibrate simplistically,
```

```
#  so the perfect reflecting diffuser has the standard XYZ coordinates for Illuminant A
#  using the convention that Y=100 (instead of Y=1)
A = 100 * spacesXYZ::standardXYZ('A')
A
##        X   Y      Z
##  A 109.85 100 35.585


gallery.cal1 = calibrate( gallery, response=A, method='scaling' )

#  calibrate following the ASTM and CIE recommendation
gallery.cal2 = calibrate( gallery, response=c(NA,100,NA), method='scaling' )

#   make the Perfect Reflecting Diffuser for testing
prd = neutralMaterial( 1, wave=wave ) ; specnames(prd) = 'PRD'

#   compare responses to the PRD for gallery.cal1 and gallery.cal2
white.1 = product( prd, gallery.cal1 )
white.2 = product( prd, gallery.cal2 )
white.1 ; white.2 ; white.1 - white.2

##          X   Y      Z
##  PRD 109.85 100 35.585
##            X   Y        Z
##  PRD 109.8488 100 35.58151
##              X            Y           Z
##  PRD 0.001210456 -2.842171e-14 0.003489313


# make an RGB flatbead scanner from illuminant F11 and a Flea2 camera
scanner = product( subset(Fs.5nm,'F11'), 'paper', Flea2.RGB, wave='auto')
# adjust RGB gain factors (white balance) so the perfect reflecting diffuser yields RGB=(1,1,1)
scanner = calibrate( scanner )

# same flatbead scanner, but this time with some "white headroom"
scanner = product( subset(Fs.5nm,'F11'), 'paper', Flea2.RGB, wave='auto' )
scanner = calibrate( scanner, response=0.95 )
scanner
```

---

canonicalOptimalColors
compute the Canonical Optimal Colors

Description

Consider a **colorSpec** object x with type equal to 'responsivity.material'. The set of all possible material reflectance functions (or transmittance functions) is convex, closed, and bounded (in any reasonable function space), and this implies that the set of all possible output responses from x is also convex, closed, and bounded. The latter set is called the *object-color solid* or *Rösch Farbkörper* for x. A color on the boundary of the *object-color solid* is called an *optimal color*

for x. The corresponding transmittance spectrum is called an *optimal spectrum* for x. The special points **W** (the response to the perfect reflecting diffuser) and **0** (the response to the perfect absorbing diffuser) are optimal.

Currently the function only works if the number of spectra in x is 3 (e.g. RGB or XYZ). In this case the *object-color solid* is a zonohedron whose boundary is the union of parallelograms, which may be coplanar. These parallelograms are indexed by distinct pairs of the wavelengths of x; if x has N wavelengths, then there are N*(N-1) parallelograms. The center of each parallelogram is called a *canonical optimal color*. Interestingly, the special points **W** and **0** are not canonical.

Usage

```
## S3 method for class 'colorSpec'
canonicalOptimalColors( x, lambda, spectral=FALSE )
```

Arguments

x   a **colorSpec** object with type equal to 'responsivity.material' and 3 spec-
            tra

lambda   a numeric Mx2 matrix whose rows contain distinct pairs of wavelengths of x, or
            a numeric vector that can be converted to such a matrix, by row. If any entry in
            lambda is not a wavelength of x, it is an error.

spectral   if TRUE, the function returns a **colorSpec** object with the optimal spectra, see
            Value.

Details

The 3 responsivities are regarded not as continuous functions, but as step functions. This implies that the color solid is a zonohedron. In the preprocessing phase the zonohedral representation is calculated. The faces of the zonohedron are either parallelograms, or *compound faces* that can be partitioned into parallelograms. The centers of all these parallelograms are the canonical optimal colors.

The optimal spectra take value 1/2 at the 2 given wavelengths, and 0 or 1 elsewhere. If the 2 wavelengths are λ_1 and λ_2, and $\lambda_1 < \lambda_2$ then the spectrum is approximately a bandpass filter. If the 2 wavelengths are swapped, then the spectrum is "flipped" and is approximately a bandstop filter.

Value

If argument spectral=FALSE, canonicalOptimalColors() returns a data.frame with a row for each row in lambda. The columns in the output are:

lambda   the given matrix argument lambda

optimal   the computed optimal colors - an Mx3 matrix

transitions   the number of transitions in the optimal spectrum, this is a positive even number

If rownames(lambda) is not NULL, they are copied to the row names of the output.

If argument spectral=TRUE, it returns a **colorSpec** object with quantity 'transmittance'. This object contains the optimal spectra, and the above-mentioned data.frame can then be obtained by applying [extradata](), to the returned object.

In case of global error, the function returns NULL.

References

Centore, Paul. *A zonohedral approach to optimal colours*. **Color Research & Application**. Vol. 38. No. 2. pp. 110-119. April 2013.

Logvinenko, A. D. An object-color space. **Journal of Vision**. 9(11):5, 1-23, (2009). https://jov.arvojournals.org/article.aspx?articleid=2203976 doi:10.1167/9.11.5.

Schrödinger, E. (1920). Theorie der Pigmente von grösster Leuchtkraft. **Annalen der Physik**. 62, 603-622.

West, G. and M. H. Brill. Conditions under which Schrödinger object colors are optimal. **Journal of the Optical Society of America**. 73. pp. 1223-1225. 1983.

See Also

probeOptimalColors(), bandRepresentation(), scanner.ACES, extradata(), type, vignette **Convexity and Transitions**

Examples

```
wave    = seq(400,700,by=5)
D50.eye = product( D50.5nm, 'material', xyz1931.1nm, wavelength=wave )
canonicalOptimalColors( D50.eye, c(500,600, 550,560, 580,585) )
##   lambda.1 lambda.2   optimal.x   optimal.y   optimal.z transitions
## 1      500      600 47.02281830 80.07281030  4.33181530           2
## 2      550      560  5.18490614 10.09045773  0.06121505           2
## 3      580      585 26.91247649 21.49031008  0.03457904           6
```

---

chop	*chop spectra into low and high parts*

Description

chop all spectra in a **colorSpec** object into low and high parts at a blending interval

Usage

```
## S3 method for class 'colorSpec'
chop( x, interval, adj=0.5 )
```

Arguments

x	a **colorSpec** object
interval	a numeric vector with length 2 giving the endpoints of the interval, in nm
adj	a number in [0,1] defining weights of low and high parts over the interval

Details

For each spectrum, the low and high parts sum to the original spectrum. The low part vanishes on the right of the interval, and the high part vanishes on the left.

Value

chop(x) returns a **colorSpec** object with twice the number of spectra in x and with organization equal to 'matrix'. The names of the new spectra are formed by appending ".lo" and ".hi" to the original spectrum names.

See Also

organization,

Examples

```
# chop blue butane flame into diatomic carbon and hydrocarbon parts
path = system.file( "extdata/sources/BlueFlame.txt", package="colorSpec" )
blueflame = readSpectra( path, seq(375,650,0.5) )
plot( chop( blueflame, interval=c(432,435), adj=0.8 ) )

# chop 'white' LED into blue and yellow parts
path = system.file( "extdata/sources/Gepe-G-2001-LED.sp", package="colorSpec" )
LED = readSpectra( path )
plot( chop( LED, c(470,495) ) )
```

---

colorSpec   *constructing and testing colorSpec Objects*

Description

The function colorSpec() is the constructor for **colorSpec** objects.

is.colorSpec() tests whether an object is a valid **colorSpec** object.
as.colorSpec() converts other variables to a **colorSpec** object, and is designed to be overridden by other packages.

Usage

```
colorSpec( data, wavelength, quantity='auto', organization='auto', specnames=NULL )

is.colorSpec(x)

## Default S3 method:
as.colorSpec( ... )
```

Arguments

data	a vector or matrix of the spectrum values. In case data is a vector, there is a single spectrum and the number of points in that spectrum is the length of the vector. In case data is a matrix, the spectra are stored in the columns, so the number of points in each spectrum is the number of rows in data, and the number of spectra is the number of columns in data. It is OK for the matrix to have only 0 or 1 column.
wavelength	a numeric vector of wavelengths for all the spectra, in nm. The length of this vector must be equal to NROW(data). The sequence must be increasing. The wavelength vector can be changed after construction.
quantity	a character string giving the quantity of all spectra in data; see quantity for a list of possible values. In case of 'auto', a guess is made from the specnames. The quantity can be changed after construction.
organization	a character string giving the desired organization of the returned **colorSpec** object. In case of 'auto', the organization is 'vector' or 'matrix' depending on data. Other possible organizations are 'df.col' or 'df.row'; see organization for discussion of all 4 possible organizations. The organization can be changed after construction.
specnames	a character vector with length equal to the number of spectra, and with no duplicates. If specnames is NULL and data is a vector, then specnames is set to deparse(substitute(data)). If specnames is NULL and data is a matrix, then specnames is set to colnames(data). If specnames is *still* not a character vector with the right length, or if there are duplicate names, then specnames is set to 'S1', 'S2', ... with a warning message. The specnames vector can be changed after construction.
x	an R object to test for being a valid **colorSpec** object.
...	arguments for use in other packages.

Details

Under the hood, a **colorSpec** object is either a vector, matrix, or data.frame. It is of S3 class 'colorSpec' with these extra attributes:

wavelength a numeric vector of wavelengths for all the spectra. If the organization of the object is 'df.col', then this is absent.

quantity a character string that gives the physical quantity of all spectra, see quantity() for a list of possible values.

metadata a named list for user-defined data. The names 'path', 'header' and 'date' are already reserved; see metadata().

step.wl step between adjacent wavelengths in nm. This is assigned only when the wavelengths are regular; see is.regular().

specname only assigned when the organization is 'vector', in which case it is equal to the single character string name of the single spectrum. Note that the word specname is singular. Also see specnames().

And there are a few more attributes that exist only in special cases; see the **colorSpec User Guide**.

Value

colorSpec() returns a **colorSpec** object, or NULL in case of ERROR. Compare this function with stats::ts().

is.colorSpec() returns TRUE or FALSE. It does more than check the class, and also checks wavelength, quantity, and organization. If FALSE, it logs (at loglevel='DEBUG') the reason that x is invalid.

as.colorSpec.default() issues an ERROR message and returns NULL

See Also

[wavelength](), [quantity](), [organization](), [metadata](), [step.wl](), [specnames](), [is.regular](), [coredata]()

Examples

```
#  make a synthetic Gaussian bandpass filter

center = 600
wave   = 400:700
trans  = exp( -(wave-center)^2 / 20^2 )

filter.bp  = colorSpec( trans, wave, quantity='transmittance', specnames='myfilter' )

organization( filter.bp )  # returns:  "vector"

# and now plot it
plot( filter.bp )
```

---

computeADL   *compute ADL coordinates by ray tracing*

Description

Consider a **colorSpec** object x with type equal to responsivity.material. The set of all possible material reflectance functions (or transmittance functions) is convex, closed, and bounded (in any reasonable function space), and this implies that the set of all possible output responses from x is also convex, closed, and bounded. The latter set is called the *object-color solid* or *Rösch Farbkörper* for x. A color on the boundary of the *object-color solid* is called an *optimal color*. The special points **W** (the response to the perfect reflecting diffuser) and **0** are on the boundary of this set. The interior of the line segment of neutrals joining **0** to **W** is in the interior of the *object-color solid*. It is natural to parameterize this segment from 0 to 1 (from **0** to **W**). The solid is symmetrical about the neutral gray midpoint **G=W/2**.

Now suppose that x has 3 spectra (3 responses) and consider a color response **R** not equal to **G**. There is a ray based at **G** and passing through **R** that intersects the boundary of the *object-color solid* at an *optimal color* **B** on the boundary with Logvinenko coordinates (δ, ω). If these 2 coordinates are combined with α, where $\mathbf{R} = (1 - \alpha)\mathbf{G} + \alpha\mathbf{B}$, it yields the *Logvinenko coordinates* (α, δ, ω) of **R**. These coordinates are also denoted by ADL; see **References**. A response is in the *object-color solid* iff $\alpha \leq 1$. A response is *optimal* iff $\alpha = 1$.

The coordinates of **0** are (α, δ, ω)=(1,0,0). The coordinates of **W** are (α, δ, ω)=(1,1,0). The coordinates of **G** are undefined.

Usage

```
## S3 method for class 'colorSpec'
computeADL( x, response )
```

Arguments

x	a **colorSpec** object with type equal to `responsivity.material` and 3 spectra
response	a numeric Nx3 matrix with responses in the rows, or a numeric vector that can be converted to such a matrix, by row.

Details

For each response, a ray is computed and the ray tracing is done by [probeOptimalColors]().

Value

`computeADL()` returns a `data.frame` with a row for each response. The columns in the data frame are:

response	the input response vector
ADL	the computed ADL coordinates of the response vector
omega	the reparameterized λ in the interval [0,1]; see **References**
lambda	lambda.1 and lambda.2 at the 2 transitions, in nm. lambda.1 < lambda.2 => bandpass, and lambda.1 > lambda.2 => bandstop.

If an individual ray could not be traced, or if the optimal spectrum has more than 2 transitions, the row contains NA in appropriate columns.
In case of global error, the function returns NULL.

WARNING

Since this function is really a simple wrapper around [probeOptimalColors](), please see the performance warnings there.

References

Logvinenko, A. D. An object-color space. **Journal of Vision**. 9(11):5, 1-23, (2009). https://jov.arvojournals.org/article.aspx?articleid=2203976. doi:10.1167/9.11.5.

Godau, Christoph and Brian Funt. XYZ to ADL: Calculating Logvinenko's Object Color Coordinates. Proceedings Eighteenth IS&T Color Imaging Conference. San Antonio. Nov 2009.

See Also

[type](), [probeOptimalColors](), vignette **Plotting Chromaticity Loci of Optimal Colors**

Examples

```
D50.eye = product( D50.5nm, 'varmat', xyz1931.1nm, wave=seq(360,830,by=5) )
computeADL( D50.eye, c(30,50,70) )
##    response.X response.Y response.Z  ADL.alpha  ADL.delta  ADL.lambda     omega
## 1          30         50         70  0.7371475  0.5384104 473.3594572 0.3008817

##  lambda.1 lambda.2
##  427.2011 555.5261

## since alpha < 1, XYZ=c(30,50,70) is *inside* the object-color solid of D50.eye
```

---

computeCCT   *Compute Correlated Color Temperature (CCT) of Light Spectra*

Description

Compute the CCT, in K, of a **colorSpec** object with type equal to 'light'

Usage

```
## S3 method for class 'colorSpec'
computeCCT( x, isotherms='robertson', locus='robertson', strict=FALSE )
```

Arguments

x   an **colorSpec** R object with type equal to 'light', and M spectra

isotherms A character vector whose elements match one of the available isotherm fam-
           ilies: 'robertson', 'mccamy', and 'native'. Matching is partial and case-
           insensitive. When more than one family is given, a matrix is returned, see **Value**.
           When isotherms='native' the isotherms are defined implicitly as lines per-
           pendicular to the locus, see **Details** in [spacesXYZ::CCTfromXYZ](). The char-
           acter NA (NA_character_) is taken as a synonym for 'native'.

locus   valid values are 'robertson' and 'precision', see above. Matching is partial
           and case-insensitive.

strict   The CIE considers the CCT of a chromaticity uv to be meaningful only if the
           distance from uv to the Planckian locus is less than or equal to 0.05 [in CIE
           UCS 1960]. If strict=FALSE, then this condition is ignored. Otherwise, the
           distance is computed along the corresponding isotherm, and if it exceeds 0.05
           the returned CCT is set to NA.

Details

In computeCCT(), for each spectrum, XYZ is computed using [xyz1931.1nm](), and the result passed
to spacesXYZ::CCTfromXYZ(). If the quantity of x is 'photons' (actinometric) each spectrum
is converted to 'energy' (radiometric) on the fly.

Value

computeCCT() returns a numeric vector of length M, where M is the number of spectra in x. The vector's names is set to specnames(x).
If the type of x is not 'light', then a warning is issued and all values are NA_real_.

References

McCamy, C. S. *Correlated color temperature as an explicit function of chromaticity coordinates*. Color Research & Application. Volume 17. Issue 2. pages 142-144. April 1992.

Robertson, A. R. Computation of correlated color temperature and distribution temperature. Journal of the Optical Society of America. 58. pp. 1528-1535 (1968).

Wyszecki, Günther and W. S. Stiles. **Color Science: Concepts and Methods, Quantitative Data and Formulae, Second Edition.** John Wiley & Sons, 1982. Table 1(3.11). pp. 227-228.

See Also

[type](), [quantity](), [xyz1931](), [planckSpectra](), [specnames](), [spacesXYZ::CCTfromXYZ]()

Examples

```
computeCCT( D65.1nm )                    # returns 6502.068
computeCCT( D65.1nm, isotherms='native' )   # returns 6503.323
computeCCT( A.1nm )                       # returns 2855.656
computeCCT( A.1nm, isotherms='native' )   # returns 2855.662
computeCCT( A.1nm, isotherms='mccamy' )   # returns 2857.188

moon = readSpectra( system.file( "extdata/sources/moonlight.txt", package='colorSpec' ) )
computeCCT( moon )                 # returns 4482.371
```

---

computeCRI   *Compute Color Rendering Index (CRI) of Light Spectra*

Description

Compute the CIE 1974 color rendering index (CRI) of a light spectrum, called the *the test illuminant*.
From the given spectrum a *reference illuminant* is selected with the same CCT (Correlated Color Temperature). A selected set of 8 color samples is rendered in XYZ (1931) with both illuminants and 8 color differences are computed in a special **CIEUVW** color space. For each color difference a CRI is computed, where 100 is a perfect color match. The final CRI is the average of these 8 CRI values.

Usage

```
## S3 method for class 'colorSpec'
computeCRI( x, adapt=TRUE, attach=FALSE, tol=5.4e-3 )
```

Arguments

x	an **colorSpec** R object with type equal to `'light'`, and exactly 1 spectrum
adapt	if TRUE, then a special chromatic adaption is performed, see **Details**
attach	if TRUE, then a large list of intermediate calculations is attached to the returned number, as attribute `data`. This attached list includes data for all special 14 color samples, although the last 6 do not affect the returned CRI.
tol	for the CRI to be meaningful the chromaticities of the test and reference illuminants must be sufficiently close in the CIE 1960 uniform chromaticity space. If the tolerance is exceeded, the function returns NA. The default `tol=5.4e-3` is the one recommended by the CIE, but the argument allows the user to override it.

Details

The CCT of `x` is computed by `computeCCT()` with default options.

If `adapt` is TRUE the 8 test uv points are chromatically adapted from the test illuminant to the reference illuminant using a special von Kries type transformation; see *Oleari* and *Wikipedia*. The test UVW values are computed relative to the reference illuminant.

If `adapt` is FALSE the 8 test uv points are *not* chromatically adapted, and the test UVW values are computed relative to the test illuminant.

Value

`computeCRI()` returns a single number ≤ 100. In case of ERROR it returns NA. If `attach` is TRUE a large list of intermediate calculations is attached to the returned number.

Source

The test color reflectance spectra are taken from:
http://www.lrc.rpi.edu/programs/nlpip/lightinganswers/lightsources/scripts/NLPIP_LightSourceColor_Script.m

References

Oleari, Claudio, Gabriele Simone. **Standard Colorimetry: Definitions, Algorithms and Software**. John Wiley. 2016. pp. 465-470.

Günther Wyszecki and W. S. Stiles. **Color Science: Concepts and Methods, Quantitative Data and Formulae, Second Edition**. John Wiley & Sons, 1982. Table 1(3.11). p. 828.

Wikipedia. **Color rendering index**. https://en.wikipedia.org/wiki/Color_rendering_index

Hunt, R. W. G. and M. R. Pointer. **Measuring Colour**. 4th edition. John Wiley & Sons. 2011. Appendix 7.

See Also

type, xyz1931, computeCCT

Examples

```
computeCRI( subset(Fs.5nm,'F2') )        # returns 64.15195
computeCRI( subset(Fs.5nm,'F4') )        # returns 51.36348
```

---

computeSSI   *Compute the Spectrum Similarity Index of light spectra*

Description

Compute the Spectrum Similarity Index (SSI), an index between 0 and 100, of a **colorSpec** object
with type equal to 'light'. It compares a test spectrum with a reference spectrum (an ideal). The
value 100 means a perfect match to the reference, and a smaller value mean a poorer match (similar
to CRI). Only values in the interval [375,675] nm are used; for details see *Holm*.

Usage

```
## S3 method for class 'colorSpec'
computeSSI( x, reference=NULL, digits=0, isotherms='mccamy', locus='robertson' )
```

Arguments

x	a **colorSpec** object with type equal to 'light', and M test spectra
reference	a **colorSpec** object with type equal to 'light', and either 1 or M reference spectra. reference can also be NULL (the default), which means to generate each reference spectrum from the corresponding test spectrum.
digits	the number of digits after the decimal point in the returned vector. According to *Holm* the output should be rounded to the nearest integer, which corresponds to digits=0. To return full precision, set digits=Inf.
isotherms	this is only used when reference=NULL. It is passed to [computeCCT](){.link}() in order to compute the CCT of each test spectrum.
locus	this is only used when reference=NULL. It is passed to [computeCCT](){.link}() in order to compute the CCT of each test spectrum.

Details

If reference contains a single spectrum, then each test spectrum is compared to that one reference
spectrum. If reference contains M spectra, then the i'th test spectrum is compared to the i'th
reference spectrum.

If reference=NULL then for each test spectrum the CCT is computed and used to compute a refer-
ence spectrum with the same CCT. It is either a Planckian (black-body) or daylight illuminant, see
Holm for details. The test spectrum and auto-computed reference spectrum are then compared.

Value

computeSSI() returns a numeric vector of length M, where M is the number of spectra in x. The vector's names is set from specnames(x) and a compact code for the corresponding reference spectrum.

If the type of x is not 'light', or reference is not valid, then the function returns NULL.

References

J. Holm and T. Maier and P. Debevec and C. LeGendre and J. Pines and J. Erland and G. Joblove and S. Dyer and B. Sloan and J. di Gennaro and D. Sherlock. *A Cinematographic Spectral Similarity Index*. SMPTE 2016 Annual Technical Conference and Exhibition. pp. 1-36. (2016).

See Also

type(), computeCCT(), planckSpectra(), daylightSpectra(), specnames()

Examples

```
computeSSI( planckSpectra( 1000*(2:6) )  )
##  P2000_SSI[2027K] P3000_SSI[3057K] P4000_SSI[D4063] P5000_SSI[D5061] P6000_SSI[D6063]
##               99               98               93               92               92
```

---

convolvewith	*Convolve each spectrum in a colorSpec object with a kernel*

Description

This function convolves each spectrum in a colorSpec object with a kernel of odd length. Its primary purpose is to correct raw spectrometer data (with positive instrumental bandwidth) to have bandwidth=0. Two popular correction kernels for this, with lengths 3 and 5, are built-in options, see **Details**.

Usage

```
## S3 method for class 'colorSpec'
convolvewith( x, coeff )
```

Arguments

x	a **colorSpec** object with N wavelengths
coeff	a convolution kernel of odd length. The center entry of this vector is taken as index 0 in the convolution. coeff can also be the string 'SS3' which means to apply the Stearns&Stearns bandwidth correction kernel coeff=c(-1,14,-1)/12, see **Details**. coeff can also be the string 'SS5' which means to apply the Stearns&Stearns bandwidth correction kernel coeff=c(1,-12,120,-12,1)/98, see **Details**.

Details

The built-in kernels, `'SS3'` and `'SS5'`, were derived by *Stearns & Stearns* under specific hypotheses on the spectrometer profile, bandpass, and pitch; see **References**.
Missing values at both ends are filled by copying from the nearest valid value.
The function creates a function calling `stats::filter()` and passes that function to `applyspec()`.

Value

a **colorSpec** object with the same dimensions, wavelength, quantity, and organization. If `coeff` is invalid it is an ERROR and `convolvewith()` returns NULL.

References

Stearns, E.I., Stearns R.E. An example of a method for correction radiance data for bandpass error. *Color Research and Application*. 13-4. 257-259. 1988.

Schanda, Janos. CIE Colorimetry, in *Colorimetry: Understanding the CIE System*. Wiley Interscience. 2007. p. 124.

Oleari, Claudio, Gabriele Simone. *Standard Colorimetry: Definitions, Algorithms and Software*. John Wiley. 2016. p. 309.

See Also

quantity, wavelength, linearize, applyspec, organization

---

coredata   *Extract the Core Data of a colorSpec Object*

Description

functions for extracting the core data contained in a **colorSpec** object.

Usage

```
## S3 method for class 'colorSpec'
coredata( x, forcemat=FALSE )

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

Arguments

x	a **colorSpec** object
forcemat	if x has only 1 spectrum, return a matrix with 1 column instead of a vector
...	extra arguments ignored

Value

coredata	If x has organization equal to 'vector' then it returns x, unless forcemat is TRUE when it returns x as a matrix with 1 column.
	If x has any other organization then it returns a matrix with spectra in the columns. All of the **colorSpec** attributes are stripped except the column names, and the row names are set to as.character(wavelength(x)).
as.matrix	a wrapper for coredata with forcemat=TRUE

See Also

[organization](#)

---

cs.options   *Functions to set and retrieve colorSpec package options*

Description

colorSpec has a few options. The options are stored in the **R** global list and they are:

colorSpec.loglevel, colorSpec.logformat, and colorSpec.stoponerror

For details on what they do see [logging](#).

They can be set using the built-in function [options](#)(). When R starts up, an option can be set using a call to options() in the file **Rprofile.site**. If **colorSpec** is later loaded, the value of the option will not be changed. If an option has not been assigned, then it is created with a default value.

The function cs.options() makes setting the options a little easier in a few ways:

- it automatically prepends the string 'colorSpec.'
- partial matching of the option name is enabled
- a warning is issued when the option value has the wrong type

Usage

```
cs.options( ... )
```

Arguments

...	named arguments are set; unnamed arguments are ignored with a warning. See **Examples**.

Value

returns a list with all the **colorSpec** options.

See Also

[logging](#), [options](#)

Examples

```
cs.options( loglevel="DEBUG", stop=FALSE )  # 'stop' partially matches 'stoponerror'
cs.options( stop='TRUE' )                   # warns that value has the wrong type
cs.options( stop=FALSE, "DEBUG" )           # warns that the 2nd argument has no name
cs.options( loglevel="WARN" )               # back to default
```

D50   *Standard Illuminant D50 (1964)*

Description

D50.5nm   standard Illuminant D50, from 300 to 830 nm at 5 nm intervals.

Format

A **colorSpec** object organized as a vector, with 107 data points and [specnames](#) equal to 'D50'.

Details

This spectrum is not copied from a table from a CIE publication, though it does match such a table. It is computed using the function [daylightSpectra](#)() by following the special CIE recipe given in the **References**. The temperature is set to (14388/14380) * 5000 = 5002.781 Kelvin. The coefficients of the daylight components S_0, S_1, and S_2 are rounded to 3 decimal places. This linear combination is computed at 10nm intervals and then linearly interpolated to 5nm intervals. The result is normalized to value 1 at 560nm (instead of the usual 100), and finally rounded to 5 decimal places. See **Examples**.

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. Table I(3.3.4) pp. 754-758

CIE 15: Technical Report: Colorimetry, 3rd edition. CIE 15:2004. Table T.1, pp 30-32, and Note 5 on page 69.

Schanda, Janos. CIE Colorimetry, in *Colorimetry: Understanding the CIE System*. Wiley Interscience. 2007. p. 42.

See Also

[ABC](#) , [D65](#) , [daylightSpectra](#)

Examples

```
#   the CIE recipe for computing D50.5nm
correction  = 14388 / 14380    # note 5, page 69 in CIE 15:2004
```

```
D50.10nm   = daylightSpectra( correction*5000, wavelength=seq(300,830,by=10), roundMs=TRUE )
D50.5nm    = resample( D50.10nm, seq(300,830,by=5), method='linear' )
D50.5nm    = round( D50.5nm, 5 )

summary( D50.5nm )
white.point = product( D50.5nm, xyz1931.1nm, wave='auto' )
```

D65   *Standard Illuminant D65 (1964)*

Description

D65.1nm	standard Illuminant D65, 300 to 830 nm at 1 nm intervals
D65.5nm	standard Illuminant D65, 380 to 780 nm at 5 nm intervals

Format

Each is a **colorSpec** object organized as a vector, with [specnames](#) equal to `'D65'`.

Details

Both of these have been divided by 100, to make the values at 560nm equal to 1 instead of 100.

Source

<http://www.cvrl.org>

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. Table I(3.3.4) pp. 754-758

ASTM E 308-01. Standard Practice for Computing the Colors of Objects by Using the CIE System. Table 3. pages 3-4.

See Also

[ABC](#), [D50](#), [daylightSpectra](#) , [daylight](#)

Examples

```
summary( D65.1nm )
white.point = product( D65.1nm, xyz1931.1nm, wave='auto' )
```

---

daylight   *Standard Daylight Components*

Description

daylight1964   spectral components S_0, S_1, S_2; from 300 to 830 nm at 5 nm intervals
daylight2013   smoothed spectral components S_0, S_1, S_2; from 300 to 830 nm at 1 nm intervals

Format

Each is a **colorSpec** object organized as a matrix with 3 columns

S0   component 0, the mean power spectrum
S1   component 1, the 1st characteristic spectrum
S2   component 2, the 2nd characteristic spectrum

Source

http://www.cie.co.at/publ/abst/datatables15_2004/CIE_sel_colorimetric_tables.xls

http://vision.vein.hu/~schanda/CIE%20TC1-74/

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. Table V(3.3.4) p. 762.

Smoothing spectral power distribution of daylights. Zsolt Kosztyan and Janos Schanda. Color Research & Application. Volume 38, Issue 5, pages 316-321, October 2013.

CIE 15: Technical Report: Colorimetry, 3rd edition. CIE 15:2004. Table T.2, pp 33-34

JUDD, D.B., MACADAM, D.L. and WYSZECKI, G., with the collaboration of BUDDE, H.W, CONDIT, H.R, HENDERSON, S.T, and SIMONDS, J.L. Spectral distribution of typical daylight as a function of correlated color temperature. J Opt. Soc. Am. 54, 1031-1040, 1964.

Zsolt Kosztyan and Janos Schanda. Smoothing spectral power distribution of daylights. Color Research & Application. Volume 38, Issue 5, pages 316-321, October 2013.

See Also

D65, D50, daylightSpectra

Examples

```
summary( daylight1964 )
day1964 = daylightSpectra( c(5000,6500), comp=daylight1964 )
day2013 = daylightSpectra( c(5000,6500), comp=daylight2013 )

plot( day1964, col='black' )
plot( day2013, col='black', add=TRUE )
```

DisplayRGB   *Compute Display RGB from Linear RGB*

Description

All RGB displays have a non-linear "gamma function" of some sort. This function converts from linear RGB to an RGB appropriate for the gamma function of the display; which is also called the *electro-optical conversion function* (EOCF).

Usage

```
DisplayRGBfromLinearRGB( RGB, gamma='sRGB' )
```

Arguments

RGB   linear RGB values organized as a vector or matrix of any size; all 3 channels are treated the same way so size does not matter

gamma   either the string 'sRGB' or a positive number giving the gamma of the display.

Value

The function first clamps the input RGB to the interval [0,1]. If gamma='sRGB' (not case-sensitive) it then maps [0,1] to [0,1] using the special piecewise-defined sRGB function, see *Wikipedia*. In case gamma is a positive number, the function raises all values to the power 1/gamma. The dimensions and names of the input are copied to the output.
In case of error, the function returns the clamped input values.

WARNING

This function is deprecated. New software should use spacesRGB::SignalRGBfromLinearRGB() instead.

Source

Wikipedia. **sRGB**. <https://en.wikipedia.org/wiki/SRGB>

See Also

RGBfromXYZ

Examples

```
DisplayRGBfromLinearRGB( c(0.2, 0.5) )
# [1] 0.4845292 0.7353570     #  this is display sRGB, in [0,1]

DisplayRGBfromLinearRGB( c(-0.1, 0.2, 0.5, 1), 2.2 )
# [1] 0.0000000 0.4811565 0.7297401 1.0000000    #  gamma=2.2

x = seq( 0, 1, len=101)
plot( x, DisplayRGBfromLinearRGB(x), type='l' )
```

| emulate | *modify a colorSpec responder to emulate (approximate) another responder* |

Description

The two possible modifications are:

- pre-multiplication by a transmitting filter
- post-multiplication by a matrix

Both of these are optional. If neither of these modifications is enabled, the original x is returned.

Usage

```
## S3 method for class 'colorSpec'
emulate( x, y, filter=FALSE, matrix=TRUE )
```

Arguments

x	a **colorSpec** responder with M spectra, to be modified. The type must be 'responsivity.light' or 'responsivity.material'
y	a **colorSpec** responder with N spectra, to be emulated by a modified x. It must have the same type and wavelength vector as x
filter	enable filter pre-multiplication.
matrix	enable matrix post-multiplication. If matrix=TRUE then the computed matrix A is MxN.

Details

If `filter=FALSE` and `matrix=TRUE` then the returned value is `multiply(x,A)`, where the matrix `A` is computed to minimize the difference with y, in the least squares sense (Frobenius matrix norm). The function [`ginv`](`)` is used here.

If `filter=TRUE` and `matrix=FALSE` then the returned value is `product(filter,x)`, where the object `filter` is computed to minimize the difference with y, in the least squares sense (Frobenius matrix norm). This calculation is fairly straightforward, but requires that the responsivity of x does not vanish at any wavelength. It also requires that M=N. The computed filter may be unrealistic, i.e. the transmittance may be > 1. If this happens a `WARN` message is issued.

If `filter=TRUE` and `matrix=TRUE` then the returned value is `product(filter,multiply(x,A))`, where `(filter,A)` are chosen with the above minimization criterion. If N=1 then we must have M=1 as well; the calculation is trivial and the emulation is exact. If $N \geq 2$, the calculation is iterative - solving alternatively for `filter` and A until convergence. The function [`ginv`](`)` is used on each iteration. This is a bilinear optimization. If convergence fails, it is an error and the function returns `NULL`. If convergence succeeds, there is 1 degree of freedom in the `(filter,A)` pair. If one is scaled by a positive constant, the other can be scaled by the inverse, and the returned object is the same. The filter is scaled so the maximum transmittance is 1.

If `filter=FALSE` and `matrix=FALSE` then the original x is returned, with a `WARN` message.

Value

a **colorSpec** object close to y, as in **Details**. The `quantity` is the same as y. The `specnames()` are the same as those of y, except that `".em"` is appended to each one. The function attaches attribute `"emulate"`, whose value is a list containing `filter` and/or A as appropriate.

Examples

see the vignette [Emulation of one Camera by another Camera](#)

See Also

[wavelength](#), [type](#), [quantity](#), [multiply](#), [product](#), [specnames](#)

---

extradata	*extradata of a colorSpec object*

Description

Retrieve or set the extradata of a **colorSpec** object.

Usage

```
## S3 method for class 'colorSpec'
extradata(x)

## S3 replacement method for class 'colorSpec'
extradata(x,add=FALSE) <- value
```

Arguments

x	a **colorSpec** object with M spectra
value	a data.frame with M rows. It is OK for value to have 0 columns, and value can also be NULL; see add.
add	If add is FALSE, then any existing extradata is discarded and replaced by value, except when value is NULL when x is left with no extradata. If add is TRUE, then value is appended to the existing extradata, except when value is NULL when x is left unchanged.

Details

If the organization of x is not 'df.row', then extradata cannot be stored in x and the assignment is ignored, with a warning. First change the [organization](#) to 'df.row', and *then* assign the extradata.

If the organization of x is 'df.row', but value does not have the right number of rows, the assignment is ignored, with a warning.

Value

extradata(x) returns a data.frame with M rows, where M is the number of spectra in x. The rownames are set to the specnames of x. If there is no extra data then the number of columns in this data.frame is 0.

Note

Do not confuse extradata and metadata.
metadata is unstructured data that is attached to the entire **colorSpec** object. extradata is structured data, with a row of data for each spectrum in the object.

See Also

[metadata](#), [organization](#)

F96T12	*Photon Irradiance of F96T12 Fluorescent Bulb*

Description

F96T12
Sylvania F96T12 CW/VHO 215-Watt fluorescent bulb photon irradiance, measured with a LI-COR LI-1800 spectroradiometer, from 300 to 900 nm at 1 nm intervals.

Format

A **colorSpec** object organized as a vector, with 601 data points and [specnames](#) equal to 'F96T12'.

Details

The unit is (μmole of photons)$*sec^{-1} * m^{-2} * nm^{-1}$.

Source

Pedro J. Aphalo. <https://www.mv.helsinki.fi/home/aphalo/photobio/lamps.html>

See Also

ABC , D65 , daylightSpectra

Examples

```
sum( F96T12 )
# [1] 320.1132  photon irradiance, (micromoles of photons)*m^{-2}

sum( radiometric(F96T12) )
# [1] 68.91819  irradiance, watts*m^{-2}
```

Flea2.RGB   *Flea2 Camera FL2-14S3C from Point Grey*

Description

Flea2.RGB   an RGB responder to light, from 360 to 800 nm at 10 nm intervals

Format

A **colorSpec** object with quantity equal to 'energy->electrical' and 3 spectra: Red, Green, and Blue.

Details

This data is read from the file **Flea2-spectral.txt** which was digitized from the plot in **Flea2-spectral.png**.

Source

<https://ptgreycamera.com/product/camera/flir/flea2/firewireb-flea2/fl2-14s3c-c/>

See Also

quantity, vignette **Blue Flame and Green Comet**

Examples

```
#  Make a scanner from a tungsten source and a Flea2 camera
Flea2.scanner = product( A.1nm, "VARMATERIAL", Flea2.RGB, wavelength=420:680 )
Flea2.scanner = calibrate( Flea2.scanner )
```

Fluorescents   *Standard series F Illuminants F1, F2, F3, F4, F5, F6, F7, F8, F9, F10, F11, and F12*

Description

Fs.5nm contains 12 CIE Fluorescent Illuminants, from 380 to 780 nm, at 5nm intervals.

Format

Fs.5nm is a **colorSpec** object with 12 spectra. It is organized as a data frame with quantity equal to "energy".

Note

The series F illuminants do not seem to be normalized in a consistent way.

Source

http://www.rit-mcsl.org/UsefulData/Fluorescents.htm

See Also

ABC, D50, D65

Examples

```
#   plot only F4
plot( subset(Fs.5nm,"F4") )
```

HigherPasserines   *Cone Fundamentals for the Higher Passerines*

Description

HigherPasserines   Tetrachromatic Cone Fundamentals of Higher Passerine Birds

Format

A **colorSpec** object organized as a matrix with the 4 spectra:

UV	the UV wavelength responsivity
Short	the short wavelength responsivity
Medium	the medium wavelength responsivity
Long	the long wavelength responsivity

The wavelength is from 300 to 700 nm, at 1nm intervals.

Source

https://onlinelibrary.wiley.com/doi/full/10.1111/j.1095-8312.2005.00540.x

References

Endler & Mielke. Comparing entire colour patterns as birds see them. Biological Journal of the Linnean Society. Volume 86, Issue 4, pages 405-431, December 2005. Original Name of File: BIJ_540_Endler_Mielke_OnlineAppendix.txt.

See Also

[lms2000](#)

Examples

```
summary(HigherPasserines)
```

Hoya   *standard Hoya filters*

Description

Hoya   4 standard Hoya filters; from 300 to 750 nm at 10nm intervals.

Format

A **colorSpec** object with [quantity](#) equal to 'transmittance' and 4 spectra:

R-60   long-pass red filter with cutoff about 600nm

G-533	band-pass green filter with peak about 533nm
B-440	band-pass blue filter with peak about 440nm
LB-120	Light-balancing Blue filter with mired shift equal to -120

Source

https://hoyaoptics.com/

See Also

quantity

Examples

```
#   compute response of ACES scanner to the Hoya filters
product( Hoya, scanner.ACES, wave='auto' )
```

---

interpolate	*interpolate spectra*

Description

interpolate along a 1-parameter path of spectra

Usage

```
## S3 method for class 'colorSpec'
interpolate( x, p, pout, pname=deparse(substitute(p)) )
```

Arguments

x	a **colorSpec** object, typically with multiple spectra
p	a numeric vector with length(p)==numSpectra(x). The value p[i] is associated with the i'th spectrum in x.
pout	a numeric vector of parameter values at which interpolation of the spectra in x take place
pname	the name of the parameter p

Details

Each spectrum in x can be thought of as a point in a high-dimensional space, and each point has a real-valued parameter associated with it. The function performs natural spline interpolation on these points, one coordinate at a time. For each wavelength value it calls spline with method='natural'.

Value

interpolate(x) returns a **colorSpec** object y with a spectrum for each value in pout. The organization of y is 'df.row', and extradata(y) has a single column which is a copy of pout. The name of the column is pname. The names in specnames(y) are <pname>=<pout>. Other properties of y, e.g. wavelength, quantity, ..., are the same as x.

In case of ERROR, the function returns NULL.

See Also

organization, wavelength, extradata, spline

Examples

```
path = system.file( "extdata/stains/PhenolRed-Fig7.txt", package="colorSpec" )
wave = 350:650
phenolred = readSpectra( path, wavelength=wave )
pH = as.numeric( sub( '[^0-9]+([0-9]+)$', '\\1', specnames(phenolred) ) )
pHvec = seq(min(pH),max(pH),by=0.05)
phenolinterp = interpolate( phenolred, pH, pHvec )
```

---

invert	*estimate spectra from responses, effectively inverting the operator from spectrum to response*

Description

Given a light responder (e.g. an eye or a camera), two light spectra that produce the same response from the responder are called *metamers* for that responder. Similarly, given a material responder (e.g. a scanner), two reflectance spectra that produce the same response from the responder are called *metamers* for that responder.

For a given responder and response, there are typically infinitely many *metamers*. The set of all of them is often called the *metameric suite*. The goal of the function invert() is to calculate a "good" metamer in the "suite". *Koenderink* calls this topic *inverse colorimetry*. In the case that the estimated spectrum is a reflectance spectrum, the topic is often called *reflectance estimation* or *reflectance recovery*, see *Bianco*.

The *centroid method*, which is the default and the featured method in this package, computes the centroid of the set of all the metamers (if any). The centroid is computed in an infinite-dimensional context and is expounded further in *Davis*.

The *Hawkyard method*, see *Hawkyard* and *Bianco*, has been around a long time. The centroid and Hawkyard methods have similarities, e.g. both are low-dimensional with the number of variables equal to the number of responses (usually 3). The Hawkyard method is very fast, but has a key problem, see below.

The *Transformed Least Slope Squared* (TLSS) method was developed by Scott Burns, see **References**. This is my name for it, not his. What I call TLLS is actually is a combination of Burns' LHTSS and LLSS methods; the one that invert() chooses depends on type(x), see below. Both of these are high-dimensional, with the number of variables equal to #(responses) + #(wavelengths).

The first argument to `invert()` is the responder `x`, and the second is the matrix `response` of responses (e.g. XYZs or RGBs).

The goal is to return a "good" spectrum for each response so that:

$$\text{product(invert(x,response), x)} \cong \text{response}$$

The error is returned as column `estim.precis`, see below.

First consider the case where `x` has type `type='responsivity.material'`. The goal is to compute a reflectance spectra. All the methods will fail if the response is on the object-color boundary (an *optimal color*) or outside the boundary. They *may* also fail if the response is inside the object-color solid (the *Rösch Farbkörper*) and very close to the boundary.

The centroid method solves a non-linear system that contains a *Langevin-function-based* squashing function, see *Davis* for details. When successful it always returns a feasible spectrum with small `estim.precis`.

The Hawkyard method is linear and very fast, but in raw form it may return a non-feasible reflectance spectrum. In this case `invert()` simply clamps to the interval [0,1] and so `estim.precis` can be large.

The TLSS method solves a non-linear system that contains the squashing function $(\tanh(z) + 1)/2$, see *Burns* for details. When successful it always returns a feasible spectrum with small `estim.precis`.

Now consider the case where `x` has `type='responsivity.light'`. The goal is to compute the spectrum of a light source. All the methods will fail if chromaticity of the response is on the boundary of the inverted-U (assuming `x` models the human eye) or outside the boundary. They *may* also fail if the response is inside the inverted-U and very close to the boundary.

The centroid method works on a relatively small range of chromaticities; it will fail if the response is too far from the response to Illuminant E. See *Davis* for the details. When successful it always returns an everywhere positive spectrum with small `estim.precis`. This method has the desirable property that if the response is multiplied by a positive number, the computed spectrum is multiplied by that same number.

The Hawkyard method does not work in this case.

The TLSS method solves a non-linear system that contains the squashing function $\exp(z)$, see *Burns* for the details. When successful it always returns an everywhere positive spectrum with small `estim.precis`. This method succeeds on a larger set of chromaticities than the centroid method. It also has the desirable scaling multiplication property mentioned above.

The centroid and Hawkyard methods have an equalization option, which is controlled by the argument `alpha` and is enabled by default, see below. When enabled, if the response comes from a constant spectrum (a perfectly neutral gray material, or a multiple of Illuminant E), then the computed spectrum is that same constant spectrum (up to numerical precision). I call this the *neutral-exact property*. Equalization is a complicated mechanism, for details see *Davis*. For the TLSS method, the neutral-exact property is intrinsic, and `alpha` is ignored.

NOTE: If the responder has only one output channel (e.g. a monochrome camera) and equalization is enabled, then *all* responses are inverted to a constant spectrum. This may or may not be desirable.

Usage

```
## S3 method for class 'colorSpec'
invert( x, response, method='centroid', alpha=1 )
```

Arguments

x	a **colorSpec** object with type(x) = 'responsivity.material' or 'responsivity.light' and M responsivities. The wavelengths must be regular (equidistant).
response	a numeric NxM matrix, or a numeric vector that can be converted to such matrix, by row. The N responses are contained in the rows. The rownames(response) are copied to the output specnames.
method	either 'centroid' or 'Hawkyard' or 'TLSS'. 'Hawkyard' is only valid when type(x) is 'responsivity.material'. Matching is partial and case-insensitive.
alpha	a vector of M weighting coefficients, or a single number that is replicated to length M. When method='centroid', alpha is used for *equalizing* the responsivities, which is recommended. For alpha to be valid, the linear combination of the M responsivities, with coefficients alpha, must be positive. To disable equalization (not recommended) and use the original responsivities, set alpha=NULL. Similarly, when method='Hawkyard', alpha is used for equalizing the responsivities, which is also recommended. When method='TLSS', alpha is ignored.

Details

For method='centroid' the function calls the non-linear root-finder [rootSolve::multiroot](), which is general purpose and "full Newton".

For method='Hawkyard' the function solves a linear system by inverting a small matrix (#[responses] x #[responses]). The spectra are then clamped to [0,1].

For method='TLSS' the function solves a constrained least-squares problem using Lagrange multipliers. A critical point is found using a "full Newton" iteration. The original MATLAB code is posted at *Burns*, and was ported from MATLAB to R with only trivial changes. When computing a reflectance spectrum, the Hawkyard method is used for the initial guess, after little extra clamping. This improved guess cuts the number of iterations substantially, and the extra computation time is negligible.

Value

If type(x)='responsivity.material' it returns a **colorSpec** object with type = 'material' (quantity = 'reflectance').

If type(x)='responsivity.light' it returns a **colorSpec** object with type = 'light' (quantity='energy' or quantity='photons' depending on quantity(x)).

In either case, the returned object has organization = 'df.row' and the extradata is a data.frame with these columns:

response	the input matrix of desired responses
estim.precis	the difference between the desired response and actual response. It is the mean of the absolute value of the differences. See [rootSolve::multiroot]()
time.msec	the time to compute the spectrum, in msec. When method='Hawkyard', all N spectra are computed at once, so all N spectra are assigned the same mean time.
iters	the number of iterations that were required to find the relevant root. This is not present when method='Hawkyard'.

clamped   a logical indicating whether the reflectance was clamped to [0,1]. This is present only when `method='Hawkyard'`.

If a response could not be estimated, the row contains NA in appropriate columns, and a warning is issued.

In case of global error, the function returns NULL.

Known Issues

If `type(x)='responsivity.light'` the centroid method may fail (not converge) if the response is too far from that of Illuminant E.

References

Davis, Glenn. A Centroid for Sections of a Cube in a Function Space, with Application to Colorimetry. https://arxiv.org/abs/1811.00990. [math.FA]. 2018.

Bianco, Simone. Reflectance spectra recovery from tristimulus values by adaptive estimation with metameric shape correction. vol. 27, no 8. *Journal of the Optical Society of America A*. pages 1868-1877. 2010 https://opg.optica.org/josaa/abstract.cfm?uri=josaa-27-8-1868.

Burns, Scott A. Generating Reflectance Curves from sRGB Triplets. http://scottburns.us/reflectance-curves-from-srgb/.

Hawkyard, C. J. Synthetic reflectance curves by additive mixing. *Journal of the Society of Dyers and Colourists*. vol. 109. no. 10. Blackwell Publishing Ltd. pp. 323-329. 1993.

Koenderink, J.J. Color for the Sciences. MIT Press. 2010.

See Also

type(), quantity(), organization(), specnames(), product(), extradata(), rootSolve::multiroot(), vignette **Estimating a Spectrum from its Response**

Examples

```
wave = 400:700
E.eye = product( illuminantE(1,wave), ”material”, xyz1931.1nm, wavelength=wave )
path = system.file( 'extdata/targets/CC_Avg30_spectrum_CGATS.txt', package='colorSpec' )
MacbethCC = readSpectra( path, wavelength=wave )
XYZ = product( MacbethCC, E.eye, wavelength=wave )
est.eq   = invert( E.eye, XYZ, method='centroid', alpha=1 )
extra    = extradata(est.eq)
range(extra$estim.precis)       # prints   0.000000e+00 3.191741e-08
```

`lightResponsivitySpectra`

compute standard light responsivity spectra

Description

Some action spectra standards are defined by simple equations; the erythemal spectrum for human sunburn is one of them.

Usage

```
erythemalSpectrum( wavelength=250:400 )
```

Arguments

wavelength   a vector of wavelengths, in nm

Details

This erythemal spectrum is defined in 4 pieces: $\lambda \leq 298$, $298 \leq \lambda \leq 328$, $328 \leq \lambda \leq 400$, and $400 < \lambda$. The unit is nm. The spectrum is used in the definition of the international standard **UV Index**.

Value

For `erythemalSpectrum()`
A **colorSpec** object with [quantity](#) equal to 'energy->action'. The responsivity is 0 for $\lambda > 400$ nm, so this putting this spectrum in the category of human vision is a bit of a stretch.

Source

https://en.wikipedia.org/wiki/Ultraviolet_index

References

McKinlay, A.F., and B.L. Diffey. A reference action spectrum for ultraviolet induced erythema in human skin. CIE Res. Note, 6(1), 17-22. (1987)

See Also

[daylight](#), [quantity](#), [materialSpectra](#), [lightSpectra](#)

LightSpectra   *compute standard light spectra*

Description

Two families of standard illuminants that are parameterized by temperature are the Planckian spectra (black-body spectra), and daylight spectra. For the daylight spectra, a smoothed version is available. Illuminant E, a third and trivial spectrum, is also available.

Usage

```
planckSpectra( temperature, wavelength=300:830, normalize=TRUE, c2=1.4388e-2 )

daylightSpectra( temperature, wavelength=NULL,
                    components=colorSpec::daylight1964, roundMs=FALSE )

illuminantE( energy=1, wavelength=380:780 )
```

Arguments

temperature	a vector of temperatures, in Kelvin
wavelength	a vector of wavelengths. For `planckSpectra()` and `illuminantE()` this is required. For `daylightSpectra()` this is optional. The default `wavelength=NULL` means to use the wavelengths in `components`, and otherwise `components` is resampled at the given `wavelength` vector.
normalize	a logical value. If `TRUE` the Planck spectra are normalized to have value 1 at 560nm. If `FALSE` then the quantity returned is radiant exitance with unit $W * m^{-2} * nm^{-1}$.
c2	the value of hc/k in Planck's law. h is the Planck constant; c is the speed of light in m/sec; and k is the Boltzmann constant. The default value of 1.4388e-2 $m * K$ was recommended by the CIE in 2005; in 1986 the CIE recommended `c2=1.438e-2`. If `c2='calc'` then c2 is calculated directly from the 3 physical constants, as recommended by CODATA 2014.
components	a **colorSpec** object with the daylight components S_0, S_1, and S_2. The default is daylight1964 and a smoothed version daylight2013 is also available.
roundMs	a logical value. The original CIE method for the daylight spectra requires rounding intermediate coefficients M1 and M2 to 3 decimal places. This rounding is necessary to reproduce the tabulated values in Table T.1 of the CIE publication in **References**.
energy	a vector of energy levels

Details

For `planckSpectra()` the valid range of temperatures is 0 to `Inf` (∞) K, but with exceptions at the endpoints. For a negative temperature the spectrum is set to all `NA`s.

If `temperature=0` and `normalize=TRUE`, the spectrum is set to all NAs. If `temperature=0` and `normalize=FALSE`, the spectrum is set to all 0s.

Conversely, if `temperature=Inf` and `normalize=FALSE`, the spectrum is set to all NAs. If `temperature=Inf` and `normalize=TRUE`, the spectrum is set to the pointwise limit $(560/\lambda)^4$ (which appears blue).

For `daylightSpectra()` the valid range of temperatures is 4000 to 25000 K. For a temperature outside this range the spectrum is set to all NAs.

The equations for `daylightSpectra()` and `planckSpectra()` are complex and can be found in the **References**.

`IlluminantE()` is trivial - all constant energy.

Value

For `planckSpectra()` and `daylightSpectra()` :
A **colorSpec** object with quantity equal to `'energy'`, and organization equal to `'matrix'` or `'vector'`. The specnames are PNNNN or DNNNN for `planckSpectra()` and `daylightSpectra()` respectively.
The number of spectra in the object is the number of temperatures = `length(temperature)`.

For `illuminantE()` :
A **colorSpec** object with quantity equal to `'energy'`.
The number of spectra in the object is the number of energy levels = `length(energy)`.

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. page 146.

CIE 15: Technical Report: Colorimetry, 3rd edition. CIE 15:2004. Table T.1, pp 30-32, and Note 5 on page 69.

Schanda, Janos. CIE Colorimetry, in *Colorimetry: Understanding the CIE System*. Wiley Interscience. 2007. p. 42.

See Also

daylight, resample, organization, quantity, materialSpectra

---

linearize	*linearize a colorSpec object - to make it ready for colorimetric calculations*

Description

linearize spectra and return modified object

Usage

```
## S3 method for class 'colorSpec'
linearize( x )
```

Arguments

x   a **colorSpec** object

Details

If the [quantity](x) is not `'absorbance'` then x is returned unchanged.

If the [quantity](x) is `'absorbance'` then absorbance is converted to transmittance using

$$transmittance = 10^{-absorbance}$$

Surprisingly, there does not seem to be a similar logarithmic version of reflectance. Plots with log(responsivity) is somewhat common, but does not seem to have a separate name. I have not seen log(radiometric power).

Value

linearize returns a **colorSpec** object with linear quantities.

See Also

quantity

---

lms1971   *Cone Fundamentals - 2-degree (1971)*

Description

lms1971.5nm   the Vos & Walraven (1971) 2° cone fundamentals from 380 to 780 nm, at 5nm intervals

Format

A **colorSpec** object organized as a matrix with 3 columns:

long	the long wavelength responsivity
medium	the medium wavelength responsivity
short	the short wavelength responsivity

Source

http://www.cvrl.org/database/text/cones/vw.htm

References

Vos, J. J. & Walraven, P. L. On the derivation of the foveal receptor primaries. **Vision Research**. 11 (1971) pp. 799-818.

See Also

[lms2000](lms2000)

Examples

```
summary(lms1971.5nm)
white.point = product( D65.1nm, lms1971.5nm, wave='auto' )
```

---

lms2000   *Cone Fundamentals - 2-degree (2000)*

Description

lms2000.1nm   the Stockman and Sharpe (2000) 2° cone fundamentals from 390 to 830 nm, at 1nm intervals

Format

A **colorSpec** object organized as a matrix with 3 columns:

long	the long wavelength responsivity
medium	the medium wavelength responsivity
short	the short wavelength responsivity

Source

<http://www.cvrl.org/cones.htm>

References

Stockman, A., Sharpe, L. T., & Fach, C. C. (1999). The spectral sensitivity of the human short-wavelength cones. **Vision Research**. 39, 2901-2927.

Stockman, A., & Sharpe, L. T. (2000). Spectral sensitivities of the middle- and long-wavelength sensitive cones derived from measurements in observers of known genotype. **Vision Research**. 40, 1711-1737.

See Also

[lms1971](#)

Examples

```
summary(lms2000.1nm)
white.point = product( D65.1nm, lms2000.1nm, wave='auto' )
```

| logging | *Logging in colorSpec package* |

Description

There is some flexibility in the **colorSpec** logging level and format. Logging output goes to stderr(), just like the message stream; but see [sink](#)() (and the pitfalls of using it).

Logging Options

colorSpec.loglevel The levels are: "FATAL", "ERROR", "WARN", "INFO", "DEBUG", and "TRACE" - the usual ones from **Log4j**. The initial level is "WARN". A "FATAL" event usually means an internal package error. When setting colorSpec.loglevel an initial letter is sufficient.

colorSpec.logformat The format is given by a string with standard **Log4j** *conversion specifications*:

%t	the date/time of the logging event.	%t can be followed by standard strftime specs in braces; see example.
%l	the level of the logging event	
%n	namespace where event occurred	
%f	function where event occurred	
%m	the message itself	

colorSpec.stoponerror If the this option is TRUE (the default), a log event with level "ERROR" stops execution; otherwise, execution keeps going. For interactive use, TRUE is probably better. For long batch jobs, FALSE might be appropriate, since then a single error may not force a complete repeat.
A "FATAL" event always stops execution.

References

Wikipedia. **Log4j**. <https://en.wikipedia.org/wiki/Log4j>

See Also

[options](#), [cs.options](#), [sink](#), [stderr](#)

Examples

```
options( colorSpec.logformat="%t{%H:%M:%OS3} %l %n::%f(). %m", colorSpec.stoponerror=TRUE )

# or equivalently
cs.options( logformat="%t{%H:%M:%OS3} %l %n::%f(). %m", stop=TRUE )
```

---

luminsivity   *Luminous Efficiency Functions (photopic and scotopic)*

Description

luminsivity.1nm   Four luminous efficiency functions, from 360 to 830 nm, at 1nm step

Format

A **colorSpec** object, with quantity `'energy->neural'`, and with 4 spectra:

photopic1924 The luminous efficiency function adopted by the CIE in 1924, and defining the *standard photopic observer*. It is only to be used when light levels are high enough that the sensitivity of the eye is mediated by cones, and not rods. It is the same as the *y-bar* function in xyz1931.1nm. It is used to define the *candela* in the *International System* (SI) and is the only one of these functions to appear in the SI. It was downloaded from http://www.cvrl.org/database/data/lum/vl1924e_1.csv where it is defined from 360 to 830 nm.

scotopic1951 The luminous efficiency function adopted by the CIE in 1951, and defining the *standard scotopic observer*. It is only to be used when light levels are low enough to exclude the activation of cones. It has no effective role in colorimetry. It was downloaded from http://www.cvrl.org/database/data/lum/scvle_1.csv where it is defined from 380 to 780 nm. It has been padded with 0s to 360 to 830 nm.

photopic1978 The luminous efficiency function for photopic vision, with adjustments in the blue region by Judd (1951) and Vos (1978). It was published by the CIE in 1988. It was downloaded from http://www.cvrl.org/database/data/lum/vme_1.csv where it is defined from 380 to 780 nm. It has been padded with 0s to 360 to 830 nm.

photopic2008 The CIE (2008) *physiologically-relevant* luminous efficiency function for photopic vision, by Stockman, Jagle, Pirzer, & Sharpe. It was downloaded from http://www.cvrl.org/database/data/lum/linCIE2008v2e_1.csv where it is defined from 390 to 830 nm. It has been padded with 0s to 360 to 830 nm.

Note

Luminsivity is a self-coined *portmanteau word*: luminsivity = luminous * responsivity. The word is unrelated to *emissivity*. The term *luminous responsivity* is not common, but appears on page 15 of *Grum*. The term *luminous efficiency function* is standard, but too long. The term *luminosity*

function is common, but *luminosity* is ambiguous and also appears in astronomy and scattering theory.

The object `luminsivity.1nm` is used by the function [`photometric`](#)`()`.

Source

Colour & Vision Research Laboratory. Institute of Opthalmology. University College London. UK.
http://www.cvrl.org/

References

Grum, Franc and Richard J. Becherer. **Radiometry**. Optical Radiation Measurements, Volume 1. Academic Press. 1979.

Stockman, A., Jagle, H., Pirzer, M., & Sharpe, L. T. (2008). The dependence of luminous efficiency on chromatic adaptation. Journal of Vision, 8, 16:1, 1-26.

See Also

[`xyz1931.1nm`](#), [`photometric`](#)

Examples

```
summary(luminsivity.1nm)
product( D65.1nm, luminsivity.1nm, wave='auto' )
```

| materialSpectra | *compute standard material spectra* |

Description

Compute neutral gray material constant reflectance/transmittance, and rectangular spectra. Also compute absorbance of the human lens, as a function of age.

Usage

```
neutralMaterial( gray=1, wavelength=380:780 )
rectangularMaterial( lambda, alpha=1, wavelength=380:780 )

lensAbsorbance( age=32, wavelength=400:700 )
```

Arguments

gray   a numeric N-vector of gray levels, in the interval [0,1]. `gray=1` represents the
                Perfect Reflecting Diffuser.

lambda   a numeric Nx2 matrix with wavelength pairs in the rows, or a vector that can be
                converted to such a matrix, by row. The two wavelengths are the two *transition
                wavelengths* of the returned spectrum, see **Details**.

alpha	a numeric N-vector of *chromatic amplitudes* in the interval [-1,1]. N must be equal to nrow(lambda). alpha can also be a single number, which is then replicated to length nrow(lambda). The *chromatic amplitude* is defined by *Logvinenko* and controls the size of both transitions, see **Details**.
age	a numeric N-vector of ages in years; all ages must be ≥ 20.
wavelength	a vector of wavelengths for the returned object

Details

A *rectangular spectrum*, or *rectangular metamer*, is easiest to define when $\alpha = 1$ and $\lambda_1 < \lambda_2$. In this case it is a band-pass filter with transmittance=1 for $\lambda \in [\lambda_1, \lambda_2]$ and transmittance=0 otherwise. To create a long-pass filter, just set λ_2 to Inf, or any large wavelength outside the spectrum range; and similarly for a short-pass filter.

When $0 < \alpha < 1$ the spectrum is a weighted mixture of this band-pass filter with a perfect neutral gray filter with transmittance=0.5 at all λ, using α and $1 - \alpha$ as the two weights. The minimum transmittance is $(1 - \alpha)/2$ and the maximum is $(1 + \alpha)/2$, and their difference, the *chromatic amplitude*, is α. It is still a band-pass filter.

If $\alpha = 0$ the spectrum is a perfect neutral with transmittance=0.5.

To "flip" the spectrum to its complement (change band-pass to band-stop, etc.), change α to a negative number, or swap λ_1 and λ_2. If $\lambda_1 == \lambda_2$ then the spectrum is undefined and a warning is issued (unless $\alpha = 0$).

Value

neutralMaterial() returns a **colorSpec** object with quantity equal to 'reflectance'. The reflectance of each spectrum is constant and taken from gray. There are N spectra in the object - one for each gray level.

rectangularMaterial() returns a **colorSpec** object with quantity equal to 'transmitance'. The transmitance of each spectrum is a step function with 0, 1 or 2 transitions (jumps) defined by the corresponding row in lambda. If rownames(lambda) is not NULL, they are copied to specnames of the output. Otherwise the specnames are computed from the shape of the spectrum using these acronyms: LP (long-pass), SP (short-pass), BP (band-pass), BS (band-stop), and N (neutral, in case alpha==0).

lensAbsorbance() returns a **colorSpec** object with quantity equal to 'absorbance'. The absorbance model for the human lens is taken from *Pokorny*. There are N spectra in the object - one for each age (N=length(age)).

Logvinenko

It is clear that there are 3 degrees-of-freedom in the spectra returned by rectangularMaterial(). *Logvinenko* shows that these spectra in fact form a 3D ball, which he calls the *rectangle color atlas*. He also shows that if a material responder satisfies the 2-transition condition, then these spectra uniquely generate *all* colors in the corresponding object color solid. For more on this, see the vignette **Estimating a Spectrum from its Response**.

Ostwald

Every spectrum returned by rectangularMaterial() is an Ostwald ideal spectrum. In Ostwald's terminology, the *color content = chromatic amplitude = α*. And the *black content = white content*

$= (1 - \alpha)/2$. Note that the sum of these 3 contents is 1. However, Ostwald allows *black content*
and *white content* to be unequal, as long as the sum of the 3 contents is 1, and all are non-negative.
Thus there is one extra degree-of-freedom for Ostwald's ideal spectra, for a total of 4 degrees-of-
freedom. If an additional argument (or arguments) were added to `rectangularMaterial()`, then
it could return all Ostwald ideal spectra.

References

Foss, Carl E. and Dorothy Nickerson and Walter C. Granville. Analysis of the Ostwald Color
System. *J. Opt. Soc. Am.*. vol. 34. no. 7. pp. 361-381. July, 1944.

Logvinenko, A. D. An object-color space. **Journal of Vision**. 9(11):5, 1-23, (2009).
https://jov.arvojournals.org/article.aspx?articleid=2203976. doi:10.1167/9.11.5.

Pokorny, Joel, Vivianne C. Smith, and Margaret Lutze. Aging of the Human Lens. **Applied Optics**.
Vol. 26, No. 8. 15 April 1987. Table I. Page 1439.

See Also

lightSpectra, quantity(), specnames(), computeADL(), vignette **Estimating a Spectrum from
its Response**

Examples

```
#   make a perfect reflecting diffuser (PRD)
prd = neutralMaterial( 1 )

#   make a perfect transmitting filter (PTF)
ptf = prd
quantity(ptf) = 'transmittance'

#   make a band-stop filter (for interval [500,550])
#   with 1% transmittance in the band, and 99% outside the band
bs = rectangularMaterial( c(500,550), -0.98, 400:700 )
bs = rectangularMaterial( c(550,500),  0.98, 400:700 )  # equivalent to previous line

#   compare transmittance at 3 ages: 20, 32, and 80 years
plot( linearize(lensAbsorbance( c(20,32,80) )), col='black', lty=1:3 )
```

---

mean   *calculate mean of multiple spectra*

Description

compute mean of all spectra in a **colorSpec** object

Usage

```
## S3 method for class 'colorSpec'
mean( x, ... )
```

Arguments

x	a colorSpec object
...	further arguments ignored

Details

This function might be useful when capturing many spectra on a spectrometer and averaging them to reduce noise.

Value

a **colorSpec** object with single spectrum = average of all spectra in **colorSpec**.

---

metadata	*metadata of a colorSpec object*

Description

Retrieve or set the metadata of a **colorSpec** object.

Usage

```
## S3 method for class 'colorSpec'
metadata(x, ...)

## S3 replacement method for class 'colorSpec'
metadata(x, add=FALSE ) <- value
```

Arguments

x	a **colorSpec** R object
...	optional names of metadata to return
value	a named list. If add is FALSE, value replaces any existing metadata. If add is TRUE, value is appended to the existing list of metadata. If a name already exists, its value is updated using [modifyList](). Unnamed items in value are ignored.
add	if add=FALSE, any existing metadata is discarded. If add=TRUE then existing metadata is preserved, using modifyList().

Details

The metadata list is stored as attr(x,'metadata'). After construction this list is empty.

Value

metadata(x) with no additional arguments returns the complete named list of metadata. If arguments are present, then only those metadata items are returned.

Note

Do not confuse `extradata` and `metadata`.

`metadata` is unstructured data that is attached to the entire **colorSpec** object. `extradata` is structured data, with a row of data for each spectrum in the object.

See Also

[extradata](), [modifyList]()

Examples

```
## Not run:
# get list of *all* metadata
metadata(x)

# get just the file 'path'
metadata( x, 'path' )

# set the 'date'
metadata( x ) = list( date="2016-04-01" )

## End(Not run)
```

---

multiply   *multiply a colorSpec object by scalar, vector, or matrix*

Description

multiply spectra by coefficients and return modified object

Usage

```
## S3 method for class 'colorSpec'
multiply( x, s )

## S3 method for class 'colorSpec'
normalize( x, norm='L1' )
```

Arguments

x	a **colorSpec** object with M spectra
s	a scalar, an M-vector, or an MxP matrix. In the case of a matrix, assigning `colnames(s)` is recommended; see **Details**.
norm	one of `'L1'`, `'L2'`, or `'Linf'`, specifying one of the standard vector norms $L^1, L^2, or L^{inf}$.
	norm can also be a numeric wavelength (e.g. 560 nm), and then the spectrum is scaled to have value 1 at this wavelength. Of course, this is not a true vector norm.

Details

For `multiply()`:

If `s` is an MxP matrix, say **S**, and one thinks of the spectra as organized in an NxM matrix **X**, then the new spectra are defined by the matrix **XS**, which is NxP. If the P column names of `s` are set, then they are copied to the `specnames` of the output. Otherwise, default spectrum names are assigned as in [colorSpec](), with a warning.

If `s` is an M-vector, then **S**=diag(s) is computed and used in the previous sentence. This has the effect of multiplying spectrum i by s[i].

If `s` is a scalar then every spectrum is multiplied by `s`.

The multiplication may produce negative entries, but no check is made for this.

WARNING: An M-vector and an Mx1 matrix may yield quite different results.

For `normalize()`:

`normalize()` calls `multiply()` with `s` = an M-vector. If the norm of a spectrum is 0, then it is left unchanged.

Value

`multiply` returns a **colorSpec** object with the matrix of spectra of `x` multiplied by `s`.

`normalize` returns a **colorSpec** object with each spectrum of `x` scaled to have given norm equal to 1.

In both functions, the [quantity]() and [wavelength]() are preserved.

Note

If `x` is organized as a matrix, and `s` is a scalar, the one can use the simpler and equivalent `s*x`.

See Also

[product](), [quantity](), [wavelength](), [specnames](), [colorSpec]()

---

officialXYZ   *Query the Official XYZ values for Standard Illuminants*

Description

In careful calcuations with standard illuminants, it is often helpful to have the 'official' values of XYZ, i.e. with the right number of decimal places.

Usage

```
officialXYZ( name )
```

Arguments

name   a subvector of c('A','B','C','D50','D50.ICC','D55','D65','D75', 'E','F2','F7','F11'), which are the names of some standard illuminants

Details

All XYZ values are taken from the ASTM publication in **References**, except B which is taken from *Wyszecki & Stiles* and D50.ICC which is taken from ICC publications. The latter is different than that of ASTM.

Value

An Mx3 matrix where M is the length of name. Each row filled with the official XYZ, but if the illuminant name is not recognized the row is all NAs. The matrix rownames are set to name, and colnames to c('X','Y','Z').

WARNING

This function is deprecated. New software should use spacesRGB::standardXYZ() instead.

Note

The input names are case-sensitive. The output XYZ is normalized so that Y=1.

References

ASTM E 308 - 01. Standard Practice for Computing the Colors of Objects by Using the CIE System. (2001).

Günther Wyszecki and W. S. Stiles. Color Science: Concepts and Methods, Quantitative Data and Formulae, Second Edition. John Wiley & Sons, 1982. Table I(3.3.8) p. 769.

See Also

[ABC](#), [D50](#), [D65](#), [Fluorescents](#), [illuminantE](#)

Examples

```
officialXYZ( c('A','D50','D50.ICC','D65') )
#               X Y         Z
# A       1.0985000 1 0.3558500
# D50     0.9642200 1 0.8252100
# D50.ICC 0.9642029 1 0.8249054
# D65     0.9504700 1 1.0888300
```

---

organization   *organization of a colorSpec object*

Description

Retrieve or set the organization of a **colorSpec** object.

Usage

```
## S3 method for class 'colorSpec'
organization(x)

## S3 replacement method for class 'colorSpec'
organization(x) <- value
```

Arguments

x	a **colorSpec** R object
value	a valid organization: `'vector'`, `'matrix'`, `'df.col'`, or `'df.row'`.

Details

If `organization(x)` is "vector", then x is a vector representing a single spectrum. Compare this with `stats::ts()`.

If `organization(x)` is "matrix", then x is a matrix and the spectra are stored in the columns.

If `organization(x)` is "df.col", then x is a data.frame with M+1 columns, where M is the number of spectra. The wavelengths are stored in column 1, and the spectra in columns 2:(M+1). This organization is good for printing to the console, and writing to files.

If the `organization` of x is "df.row", then x is a data.frame with N rows, where N is the number of spectra. The spectra are stored in the last column, which is a matrix with the name "spectra". The other columns preceding spectra (if present) contain extra data associated with the spectra; see extradata.

Value

`organization(x)` returns a valid organization: `'vector'`, `'matrix'`, `'df.col'`, or `'df.row'`.

Note

In `organization(x) <- value`
if x has more than 1 spectrum, then value equal to `'vector'` is invalid and ignored.
If `organization(x)` is equal to `'df.row'` and also has extradata, then changing the organization silently discards the extradata.

See Also

colorSpec; extradata

Examples

```
organization(Hoya)              # returns 'df.row'
organization(Hoya) = 'matrix'   # extradata in Hoya is silently discarded
```

---

photometric   *convert illuminant spectra to photometric units*

Description

Convert radiometric units of power or energy to photometric units, using 4 standard photometric
weighting curves. Actinometric units (number of photons) are converted to radiometric units (en-
ergy of photons) on-the-fly.

Usage

```
## S3 method for class 'colorSpec'
photometric( x, photopic=683, scotopic=1700, multiplier=1 )
```

Arguments

x	a **colorSpec** object with type equal to 'light', and with M spectra
photopic	the conversion factor for photopic vision, in lumen/watt. The CIE standard is 683, and another common value is 683.002.
scotopic	the conversion factor for scotopic vision, in lumen/watt. The CIE standard is 1700, and another common value is 1700.06.
multiplier	an conversion factor intended for conversion of units, and applied to both pho- topic and scotopic vision. For example if the input unit of x is $watt * sr^{-1}$, and the desired output unit is $candlepower$, then set multiplier=1/0.981.

Details

The function computes the product of x with luminsivity.1nm. This product is an Mx4 matrix,
where M is the number of spectra in x. There are 3 columns for photopic vision, and 1 column
for scotopic vision. These columns are multiplied by the appropriate conversion factors and the
resulting Mx4 matrix is returned.

The 5 power-based input quantities and corresponding photometric outputs are:

radiant power $[watt]$	$\longrightarrow$	**luminous flux** $[lumen]$
irradiance $[watt * m^{-2}]$	$\longrightarrow$	**illuminance** $[lumen * m^{-2} = lux]$
radiant exitance $[watt * m^{-2}]$	$\longrightarrow$	**luminous exitance** $[lumen * m^{-2} = lux]$
radiant intensity $[watt * sr^{-1}]$	$\longrightarrow$	**luminous intensity** $[lumen * sr^{-1} = candela]$
radiance $[watt * sr^-1 * m^{-2}]$	$\longrightarrow$	**luminance** $[candela * m^{-2} = nit]$

The 2 *common* energy-based input quantities and corresponding photometric outputs are:

radiant energy $[joule]$	$\longrightarrow$	**luminous energy** $[talbot = lumen - second]$
radiant exposure $[joule * m^{-2}]$	$\longrightarrow$	**luminous exposure** $[talbot * m^{-2} = lux - second]$

and there are 3 more obtained by integrating over time. For example "time-integrated radiance" —>
"time integrated luminance". But I have not been able to find names for these 3. The *talbot* is the
unofficial name for a lumen-second.

Value

photometric() returns an Mx4 matrix, where M is the number of spectra in x. The rownames are
specnames(x), and the colnames are specnames(luminsivity.1nm).
In case of ERROR it returns NULL.

Note

To get the right output quantity and units, the user must know the input quantity and units. If the
units are different than those in the above list, then set multiplier appropriately.
It is up to the user to determine whether *photopic* or *scotopic* vision (or neither) is appropriate. The
intermediate *mesopic* vision is currently a subject of research by the CIE, and might be added to
this function in the future.

References

Poynton, Charles. **Digital Video and HD - Algorithms and Interfaces**. Morgan Kaufmann. Sec-
ond Edition. 2012. Appendix B, pp. 573-580.

See Also

quantity, type, luminsivity.1nm, radiometric

Examples

```
photometric( solar.irradiance )  # unit is watt*m^{-2}

#              photopic1924 scotopic1951 photopic1978 photopic2008  # units are lux
# AirMass.0       133100.41     313883.2     133843.65     140740.3
# GlobalTilt      109494.88     250051.5     110030.31     115650.0
# AirMass.1.5      97142.25     215837.1      97571.57     102513.7
```

---

plot	*plot spectra*

Description

plot the spectra in a **colorSpec** object as lines or points

Usage

```
## S3 method for class 'colorSpec'
plot( x, color=NULL, subset=NULL, main=TRUE, legend=TRUE, CCT=FALSE, add=FALSE, ... )
```

Arguments

x	a colorSpec object
color	If color=NULL then colors are computed from the spectra themselves. If type(x) is 'material' the color is computed using illuminant D65.1nm and responder BT.709.RGB with no further normalization. Otherwise the spectrum color is faked by changing its quantity to 'energy' and taking the product with BT.709.RGB. The resulting RGBs are normalized to have a maximum of 1. This RGB normalization is done *before* processing the subset argument. If color='auto' then a suitable set of colors is generated using colorRamp(). Otherwise color is passed on to lines.default() as the col argument, e.g. col='black'.
subset	specifies a subset of x to plot; see subset() for acceptable arguments.
main	If main=TRUE then a main title is generated from the file 'path' in the metadata list, or from deparse(substitute(x)). If main=FALSE then no main title is displayed. And if main is a string then that string is used as the main title.
legend	If legend=TRUE then a pretty legend using specnames(x) is placed in the 'topright' corner of the plot. If legend is a string it is interpreted as naming a corner of the plot and passed as such to the function legend. If legend=FALSE then no legend is drawn.
CCT	If CCT=TRUE and the type of x is 'light' then the CCT of each spectrum is added to the legend; see computeCCT().
add	If add=TRUE then the lines are added to an existing plot, and these arguments are ignored: main, ylab, xlim, ylim, and log; see **Details**.
...	other graphical parameters, see **Details**

Details

Commonly used graphical parameters are:

type passed to lines.default(), with default type='l'. Other valid values are 'p' (points), 'b', 'c', 'o', 'h', 'S', 's', and 'n', see plot() for their meanings.

An additional type='step' is available. This option draws each spectrum as a *step function*, similar to 'S' and 's', except that the jumps are *between* the wavelengths (with appropriate extensions at min and max wavelengths). The function segments() is used for the drawing. For type='step', lwd and lty should be vectors of length 1 or 2. If the length of lwd is 1, then horizontal segments are draw with that width, but vertical segments are not drawn. If the length of lwd is 2, then vertical segments are draw with width lwd[2]. If the length of lty is 2, then the styles are applied to the horizontal and vertical segments in that order. If the length of lty is 1, then that style is applied to both horizontal and vertical segments. For examples of this plotting option, see the vignette **Convexity and Transitions**.

lwd, lty passed to lines.default(), except when type='step' when they are passed to segments(). In the former case these can be vectors, and components are passed sequentially to each spectrum, similar to matplot(). In the latter case, see the description in type. The default value for both is 1.

pch passed to lines.default(), but it only has meaning when type='p', 'b', or 'o'. This can be a vector, and components are passed sequentially to each spectrum.

ylab If ylab is a string then it is passed on to `plot.default`(), otherwise suitable default string is generated.

xlim, ylim If xlim and ylim are 2-vectors, they are passed to `plot.default`. If one of the components is NA then a suitable default is supplied.

log passed on to `plot.default`(). Care must be taken for y because many spectra are 0 at some wavelengths, and even negative. Use ylim in such cases.

Value

TRUE or FALSE

See Also

computeCCT(), subset(), lines(), segments(), plot(), matplot(), colorRamp()

Examples

```
plot( 100 * BT.709.RGB )
plot( xyz1931.1nm, add=TRUE, lty=2, legend=FALSE )
```

---

plotOptimals   *Plot Optimal Colors*

Description

Consider a **colorSpec** object x with type equal to 'responsivity.material' and 3 responsivity spectra. The function plotOptimals3D() makes a plot of the *object-color solid* for x. This solid is a *zonohedron* in 3D. The 3D drawing package **rgl** is required.

Consider a **colorSpec** object x with type equal to 'responsivity.material' and 2 responsivity spectra. The function plotOptimals2D() makes a plot of the *object-color solid* for x. This solid is a *zonogon* in 2D. The 3D drawing package **rgl** is *not* required.

The set of all possible material reflectance functions (or transmittance functions) is convex, closed, and bounded (in any reasonable function space), and this implies that the set of all possible output responses from x is also convex, closed, and bounded. The latter set is called the *object-color solid*, or *Rösch Farbkörper*, for x. A color on the boundary of the *object-color solid* is called an *optimal color*. For more discussion see sectionOptimalColors().

Usage

```
## S3 method for class 'colorSpec'
plotOptimals3D( x, size=50, type='w', both=TRUE )

## S3 method for class 'colorSpec'
plotOptimals2D( x )
```

Arguments

x	a **colorSpec** object with type equal to `'responsivity.material'` and 2 or 3 spectra, as appropriate.
size	an integer giving the number of wavelengths at which to resample x. To skip resampling, set `size=NA`.
type	`type='w'` for a wireframe plot of the parallelogram faces. `type='p'` for a point plot with points at the centers of the parallelograms.
both	the color solid is symmetric about its center, so only half of it must be computed. If `both=TRUE` it plots one half in black and the other half in red. If `both=FALSE` it only plots one half in black.

Value

The functions return `TRUE` or `FALSE`.

Details for 3D

If n is the number of wavelengths, the number of parallelogram faces of the zonohedron is `n*(n-1)`. The time to compute these faces increase with n even faster, so that is why the default `size=50` is a fairly small number. It was chosen to be a reasonable compromise between detail and performance. In addition to the wireframe or points, it draws the box with opposite vertices at the "poles" **0** and **W** and the diagonal segment of neutral grays that connects **0** and **W**.

Details for 2D

If n is the number of wavelengths, the number of edges in the zonogon is `2*n`. Computing these edges is fast and visualization is easy, so there are no plotting options at this time.

Note

If all responsivity functions of x are non-negative, the *object-color solid* of x is inside the box. If the responsivity functions of x have negative lobes, the *object-color solid* of x extends outside the box. Indeed, the box may actually be *inside* the optimals.

References

Centore, Paul. *A Zonohedral Approach to Optimal Colours*. **Color Research & Application**. Vol. 38. No. 2. pp. 110-119. April 2013.

Logvinenko, A. D. An object-color space. Journal of Vision. 9(11):5, 1-23, (2009). `https://jov.arvojournals.org/article.aspx?articleid=2203976`. doi:10.1167/9.11.5.

West, G. and M. H. Brill. Conditions under which Schrödinger object colors are optimal. **Journal of the Optical Society of America**. 73. pp. 1223-1225. 1983.

See Also

[type](), [probeOptimalColors](), [sectionOptimalColors](), vignette **Plotting Chromaticity Loci of Optimal Colors**

Examples

```
human = product( D50.5nm, 'slot', xyz1931.5nm, wave=seq(400,770,by=5) )
plotOptimals3D( human )

plotOptimals2D( subset(human,2:3) )     # y and z only

scanner = product( D50.5nm, 'slot', BT.709.RGB, wave=seq(400,770,by=5) )
plotOptimals3D( scanner )
```

---

print   *Convert colorSpec object to readable text*

Description

display a **colorSpec** object as readable text. Output goes to stdout().

Usage

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

## S3 method for class 'colorSpec'
summary( object, long=TRUE, ... )
```

Arguments

x	a colorSpec object
object	a colorSpec object
long	logical indicating whether to print metadata, calibrate, sequence, and emulate data
...	further arguments ignored

Details

If long=FALSE, summary() prints a summary of the wavelength vector, and names of all spectra.
For each spectrum it prints the range of values, LambdaMax, and extradata if any. If long=TRUE it
also prints data listed above (if any).
The function print() simply calls summary() with long=FALSE.

Value

Both functions return (invisibly) the character vector that was just printed to stdout().

See Also

[extradata](), [print](), [summary](), [stdout]()

Examples

```
print( xyz1931.1nm )

xyz1931.1nm     # same thing, just calls print()
```

---

probeOptimalColors   *compute optimal colors by ray tracing*

Description

Consider a **colorSpec** object x with type equal to 'responsivity.material'. The set of all possible material reflectance functions (or transmittance functions) is convex, closed, and bounded (in any reasonable function space), and this implies that the set of all possible output responses from x is also convex, closed, and bounded. The latter set is called the *object-color solid* or *Rösch Farbkörper* for x. A color on the boundary of the *object-color solid* is called an *optimal color*. The special points **W** (the response to the perfect reflecting diffuser) and **0** are on the boundary of this set. The interior of the line segment of neutrals joining **0** to **W** is in the interior of the *object-color solid*. It is natural to parameterize this segment from 0 to 1 (from **0** to **W**).

A ray r that is based at a point on the interior of the neutral line segment must intersect the boundary of the *object-color solid* in a unique optimal color. The purpose of the function probeOptimalColors() is to compute that intersection point.

Currently the function only works if the number of spectra in x is 3 (e.g. RGB or XYZ).

Before **colorSpec** v 0.8-1 this function used a 2D root-finding method that could only find optimal colors whose spectra contain 0, 1, or 2 transitions. But starting with v0.8-1, we have switched to zonohedral representation of the object-color solid, which makes it possible to discover more than 2 transitions. The inspiration for this change is the article by *Centore*. To *inspect* these computed spectra, the argument spectral must be set to TRUE.

Usage

```
## S3 method for class 'colorSpec'
probeOptimalColors( x, gray, direction, aux=FALSE, spectral=FALSE, tol=1.e-6 )
```

Arguments

x	a **colorSpec** object with type equal to 'responsivity.material' and 3 spectra
gray	vector of numbers in the open interval (0,1) that define neutral grays on the line segment from black to white; this neutral gray point is the basepoint of a probe ray
direction	a numeric Nx3 matrix with directions of the probe rays in the rows, or a numeric vector that can be converted to such a matrix, by row.
aux	a logical that specifies whether to return extra performance and diagnostic data; see **Details**

spectral	if TRUE, the function returns a **colorSpec** object with the optimal spectra, see **Value**.
tol	error tolerance for the intersection of probe and object-color boundary

Details

Each gray level and each direction defines a ray. So the total number of rays traced is length(gray) * nrow(direction). The 3 responsivies are regarded not as continuous functions, but as step functions. This implies that the color solid is a zonohedron. In the preprocessing phase the zonohedral representation is calculated. The faces of the zonohedron are either parallelograms, or *compound faces* that can be partitioned into parallelograms. The centers of all these parallelograms are computed, along with their normals and plane constants.

This representation of the color solid is very strict regarding the 2-transition assumption. During use, one can count on there being some spectra with more than two transitions. Forcing the best 2-transition spectrum is a possible topic for the future.

Value

If argument spectral=FALSE, probeOptimalColors() returns a data.frame with a row for each traced ray. There are length(gray) * nrow(direction) rays. The columns in the output are:

gray	the graylevel defining the $basepoint$ of the ray. $basepoint = gray * W$
direction	the $direction$ of the ray
s	computed scalar so that $basepoint + s * direction$ is optimal
optimal	the optimal color on the boundary; $optimal = basepoint + s * direction$
lambda	lambda.1 and lambda.2 at the 2 transitions, in nm. lambda.1 < lambda.2 => bandpass, and lambda.1 > lambda.2 => bandstop. It will happen that the optimal spectrum has more than 2 transitions; in this case both lambdas are set to NA.
dol	delta and omega - the Logvinenko parameters (δ, ω) for optimal colors, plus lambda (λ) in nm. ω is the reparameterization of λ ; see *Logvinenko*. If there are more than 2 transistions, these are set to NA.

If aux is TRUE, these auxiliary columns related to performance and diagnostics are added:

timetrace	time to trace the ray, in seconds
parallelograms	# of parallelograms in the (possibly compound) face. 1 means just a single parallelogram.
tested	# of parallelograms actually tested for ray intersection. This only has meaning for compound faces.
alpha	the 2 coordinates of the intersection point inside the parallelogram

If argument spectral=TRUE, probeOptimalColors() returns a **colorSpec** object with quantity 'reflectance'. This object contains the optimal spectra, and can be used to inspect the spectra with more than 2 transitions, which will happen. The above-mentioned data.frame can then be obtained by applying [extradata](()) to the returned object.

If an individual ray could not be traced (which should be rare), the row contains NA in appropriate columns.

In case of global error, the function returns NULL.

WARNING

The preprocessing calculation of the zonohedron dominates the total time. And this time goes up rapidly with the number of wavelengths. We recommend using a wavelength step of 5nm, as in the **Examples**. For best results, batch a lot of rays into a single function call and then process the output.

Moreover, the preprocessing time is dominated by the partitioning of the compound faces into parallelograms. This is made worse by spectral responses with little overlap, as in `scanner.ACES`. In these cases, try a larger step size, and then reduce. Optimizing these compound faces is a possible topic for the future.

References

Centore, Paul. *A zonohedral approach to optimal colours*. **Color Research & Application**. Vol. 38. No. 2. pp. 110-119. April 2013.

Logvinenko, A. D. An object-color space. **Journal of Vision**. 9(11):5, 1-23, (2009). `https://jov.arvojournals.org/article.aspx?articleid=2203976`. doi:10.1167/9.11.5.

Schrödinger, E. (1920). Theorie der Pigmente von grösster Leuchtkraft. **Annalen der Physik**. 62, 603-622.

West, G. and M. H. Brill. Conditions under which Schrödinger object colors are optimal. **Journal of the Optical Society of America**. 73. pp. 1223-1225. 1983.

See Also

`type`, vignette **Plotting Chromaticity Loci of Optimal Colors**, `scanner.ACES`, `extradata()`

Examples

```
wave    = seq(400,700,by=5)
D50.eye = product( D50.5nm, 'material', xyz1931.1nm, wavelength=wave )
probeOptimalColors( D50.eye, c(0.2,0.5,0.9), c(1,2,1, -1,-2,-1) )

##    gray direction.1 direction.2 direction.3         s optimal.1  optimal.2
## 1  0.2           1           2           1 32.306207 52.533143  85.612065
## 2  0.2          -1          -2          -1  8.608798 11.618138   3.782055
## 3  0.5           1           2           1 20.993144 71.560483  94.485416
## 4  0.5          -1          -2          -1 20.993144 29.574196  10.512842
## 5  0.9           1           2           1  4.333700 95.354911 103.165832
## 6  0.9          -1          -2          -1 35.621938 55.399273  23.254556


##    optimal.3 lambda.1 lambda.2  dol.delta   dol.omega  dol.lambda
## 1  49.616046 451.8013 598.9589 0.63409966  0.48287469 536.97618091
## 2   8.701041 636.3031 429.4659 0.08458527  0.99624955 674.30015903
## 3  64.267740 441.9105 615.0822 0.78101041  0.49048222 538.73234859
## 4  22.281453 615.0822 441.9105 0.21898959  0.99048222 662.20606601
## 5  82.227974 422.9191 648.7404 0.95800430  0.49825407 540.49590064
## 6  42.272337 593.2415 455.2425 0.42035428  0.97962398 650.57382749


# create a 0-1 spectrum with 2 transitions
rectspec = rectangularMaterial( lambda=c(579.8697,613.7544), alpha=1, wave=wave )
```

```
# compute the corresponding color XYZ
XYZ = product( rectspec, D50.eye )
XYZ
##                                X        Y         Z
##  BP_[579.87,613.754] 33.42026 21.96895 0.02979764

# trace a ray from middle gray through XYZ
white.XYZ   = product( neutralMaterial(1,wave=wave), D50.eye )
direction   = XYZ - white.XYZ/2

res = probeOptimalColors( D50.eye, 0.5, direction, aux=FALSE )
res$s
##  1.00004    the ray has gone past the original color to the boundary

res$optimal
##              X        Y         Z
##  [1,] 33.41958 21.96774 0.02808178

res$lambda
##  NA NA     because there are more than 2 transitions in the true optimal

# since s=1.00004 > 1,
# XYZ is actually in the interior of the color solid, and not on the boundary.
# The boundary is a little-bit further along the ray,
# and the corresponding spectrum has more than 2 transitions.
```

---

product   *Compute the product of colorSpec objects*

Description

Take a sequence of **colorSpec** objects and compute their product. Only certain types of sequences are allowed. The return value can be a new **colorSpec** object or a matrix; see **Details**.

Usage

```
## S3 method for class 'colorSpec'
product( ... )
```

Arguments

...   unnamed arguments are **colorSpec** objects, and possibly a single character string, see **Details**. Possible named arguments are:

           wavelength The default wavelength='identical' means that all the **color-Spec** objects must have the same wavelength sequence; if they do not it is an ERROR. wavelength can be a new wavelength sequence, and all the objects are then [resample](#)d at these new wavelengths. wavelength can

also be `'auto'` or `NULL` which means to compute a suitable wavelength sequence from those of the objects, see **Details**. It is OK to abbreviate the string `wavelength` (e.g. to wave); see **Examples**. It is OK for the wavelength sequence to be irregular; when the return value is a matrix the integration weights the spectrum values appropriately.

method, span, extrapolation, clamp   passed to resample() with no checking or changes

integration   only applies when the return type is matrix. The default option is `'rectangular'`, which means to weight the spectrum value equally at all wavelengths; this is the ASTM E308-01 recommendation. The other option is `'trapezoidal'`, which means to give the 2 endpoint wavelength values 1/2 the weight of the others. Trapezoidal integration is provided mostly for compatibility with other software.

Details

To explain the allowable product sequences it is helpful to introduce some simple notation for the objects:

notation	**colorSpec** type	description of the object
L	light	a light source
M	material	a material
R_L	responsivity.light	a light responder (aka detector)
R_M	responsivity.material	a material responder (e.g. a scanner)

It is also helpful to define a sequence of positive integers to be *conformable* iff it has at most one value greater than 1. For example, a sequence of all 1s is conformable. A sequence of all q's is conformable. The sequences `c(1,3)` and `c(1,1,4,1,1,4,1)` are conformable, but `c(1,1,4,1,3,4,1)` is not.

There are 6 types of sequences for which the product is defined:

1. $M_1 * M_2 * ... * M_m \mapsto M'$
The product of m materials is another material. Think of a stack of m transmitting filters effectively forming a new filter. If we think of each object as a matrix (with the spectra in the columns), then the product is element-by-element using R's `*` - the Hadamard product. The numbers of spectra in the terms must be conformable. If some objects have 1 spectrum and all the others have q, then the column-vector spectrums are repeated q times to form a matrix with q columns. If the numbers of spectra are not conformable, it is an ERROR and the function returns `NULL`.
As an example, suppose M_1 has 1 spectrum and M_2 has q spectra, and $m = 2$. Then the product is a material with q spectra. Think of an IR-blocking filter followed by the RGB filters in a 3-CCD camera.

2. $L * M_1 * M_2 * ... * M_m \mapsto L'$

The product of a light source followed by m materials is a light source. Think of a light source followed by a stack of m transmitting filters, effectively forming a new light source. The numbers of spectra in the terms must be conformable as in sequence 1, and the matrices are multiplied element by element.

As an example, suppose L has 1 spectrum and M_1 has q spectra, and $m = 1$. Then the product is a light source with q spectra. Think of a light source followed by a filter wheel with q filters.

3. $M_1 * M_2 * ... * M_m * R_L \mapsto R'_L$

The product of m materials followed by a light responder, is a light responder. Think of a stack of m transmitting filters in front of a camera, effectively forming a new camera. The numbers of spectra in the terms must be conformable as in sequence 1, and the matrices are multiplied element by element.

As an example, suppose R_L has 1 spectrum and M_1 has q spectra, and $m = 1$. Then the product is a light responder with q spectra. Think of a 3-CCD camera in which all 3 CCDs have exactly the same responsivity and so can be modeled with a single object R_L.

4. $L * M_1 * ...* \bullet *... * M_m * R_L \mapsto R'_M$

This is the strangest product. The bullet symbol $\bullet$ means that a variable material is inserted at that slot in the sequence (or light path). For each material spectrum inserted there is a response from R_L. Therefore the product of this sequence is a material responder R_M. Think of a light source L going through a transparent object $\bullet$ on a flatbed scanner and into a camera R_L. For more about the mathematics of this product, see the **colorSpec-guide.pdf** in the doc directory. These material responder spectra are the same as the *effective spectral responsivities* in *Digital Color Management*. The numbers of spectra in the terms must be conformable as in sequence 1, and the product is a material responder with q spectra.

In the function `product()` the location of the $\bullet$ is marked by any character string whatsoever - it's up to the user who might choose something that describes the typical material (between the light source and camera). For example one might choose:

`scanner = product( A.1nm, 'photo', Flea2.RGB, wave='auto')`

to model a scanner that is most commonly used to scan photographs. Other possible strings could be `'artwork'`, `'crystal'`, `'varmaterial'`, or even `'slot'`. See the vignette **Viewing Object Colors in a Gallery** for a worked-out example.

5. $L * M_1 * M_2 * ... * M_m * R_L \mapsto matrix$

The product of a light source, followed by m materials, followed by a light responder, is a matrix! The numbers of spectra in the terms must be splittable into a conformable left part (L' from sequence 2.) and a conformable right part (R'_L from sequence 3.). There is a row for each spectrum in L', and a column for each spectrum in R'_L. Suppose the element-by-element product of the left part is $n{\times}p$ and the element-by-element product of the right part is and $n{\times}q$, where n is the number of wavelengths. Then the output matrix is the usual matrix product `%*%` of the transpose of the left part times and right part, which is $p{\times}q$.

As an example, think of a light source followed by a reflective color target with 24 patches followed by an RGB camera. The sequence of spectra counts is `c(1,24,3)` which is splittable into `c(1,24)` and `c(3)`. The product matrix is 24$\times$3. See the vignette **Viewing Object Colors in a Gallery** for a worked-out example.

Note that is OK for there to be no materials in this product; it is OK if $m = 0$. See the vignette **Blue Flame and Green Comet** for a worked-out example.

6. $M_1 * M_2 * ... * M_m * R_M \mapsto matrix$
The product of m materials followed by a material responder, is a matrix ! The sequence of numbers of spectra must be splittable into left and right parts as in sequence 4, and the product matrix is formed the same way. One reason for computing this matrix in 2 steps is that one can `calibrate` the material responder separately in a customizable way. See the vignette **Viewing Object Colors in a Gallery** for a worked-out example with a flatbed scanner.

Note that sequences 5. and 6. are the only ones that use the usual matrix product `%*%`. They may also use the Hadamard matrix product `*`, as in sequences 1 to 4.

The argument `wavelength` can also be `'auto'` or `NULL`. In this case the intersection of all the wavelength ranges of the objects is computed. If the intersection is empty, it is an ERROR and the function returns `NULL`. The wavelength step `step.wl` is taken to be the smallest over all the object wavelength sequences. If the minimum `step.wl` is less than 1 nanometer, it is rounded off to the nearest power of 2 (e.g 1, 0.5, 0.25, ...).

Value

`product()` returns either a **colorSpec** object or a matrix, see **Details**.

If `product()` returns a **colorSpec** object, the `organization` of the object is `'matrix'` or `'vector'`; any `extradata` is lost. However, all terms in the product are saved in `attr(*,'sequence')`. One can use `str()` to inspect this attribute.

If `product()` returns a matrix, this matrix can sometimes be ambiguous, see **Note**.

All actinometric terms are converted to radiometric on-the-fly and the returned **colorSpec** object is also radiometric.

In case of ERROR it returns `NULL`.

Note

The product for sequences 1, 2, and 3 is associative. After all matrices are filled out to have q columns, the result is essentially a Hadamard product of matrices, which is associative. Also note that a subsequence of sequences 2 and 3 might be sequence 1.

The product for sequence 4 is never associative, since subproducts that contain the variable ● are undefined. However the result is essentially a Hadamard product of matrices, and is unambiguous.

The product for sequence 5 is associative in special cases, but not in general. The problem is that the left and right splitting point is not unique. If all objects have only a single spectrum, then it *is* associative, and therefore unambiguous. If the left part has a different number of multiple spectra than the right part, then it is not associative in general since some ways of grouping the product may be undefined.
Moreover, in some cases the product can be ambiguous. Suppose that the vector of spectrum counts is `c(1,3,1)`; this could come from a single light source, followed by 3 filters (e.g. RGB), followed by a graylevel camera. There are 2 ways to split this: `"1|3,1"` and `"1,3|1"`. The first split is

interpreted as the light source into a camera with 3 channels. The second split is interpreted as 3 colored light sources into a graylevel camera. In the first split the returned matrix is a 1x3 row vector. In the second split the returned matrix is a 3x1 column vector. For the vector "1,3,1", one can show that the computed components in the 2 vectors are equal, so the ambiguity is benign. But consider the longer sequence "1,3,3,1". There are 3 ways to split this, and the returned matrices are 1x3, 3x3, and 3x1. So this ambiguity is obviously a problem. Whenever there is an ambiguity, the function chooses a splitting in which the left part is as long as possible, and issues a warning message. The user should inspect the result carefully. To avoid the ambiguity, the user should break the product into smaller pieces and call product() multiple times.

The product for sequence 6 is essentially the same as sequence 5, and the function issues a warning message when appropriate. Note that a subproduct is defined only if it avoids the final multiplication with R_M.

References

Edward J. Giorgianni and Thomas E. Madden. **Digital Color Management: Encoding Solutions.** 2nd Edition John Wiley. 2009. Figure 10.11a. page 141.

Wikipedia. **Hadamard product (matrices)**. https://en.wikipedia.org/wiki/Hadamard_product_(matrices)

ASTM E308-01. Standard Practice for Computing the Colors of Objects by Using the CIE System. (2001).

See Also

wavelength, type, resample, calibrate, radiometric, step.wl

Examples

```
#  sequence 1.
path = system.file( "extdata/objects/Midwest-SP700-2014.txt", package='colorSpec' )
blocker.IR = readSpectra( path )
product( blocker.IR, Hoya, wave='auto' )


#  sequence 2.
product( subset(solar.irradiance,1), atmosphere2003, blocker.IR, Hoya, wave='auto' )


#  sequence 3.
plumbicon = readSpectra( system.file( "extdata/cameras/plumbicon30mm.txt", package='colorSpec' ) )
product( blocker.IR, subset(Hoya,1:3), plumbicon, wave='auto' )


#   sequence 4.
#   make an RGB scanner
bluebalancer = subset(Hoya,'LB')
# combine tungsten light source A.1nm with blue light-balance filter
# use the string 'artwork' to mark the variable material slot
scanner = product( A.1nm, bluebalancer, 'artwork', Flea2.RGB, wave='auto' )
```

```
# sequence 5.
product( D65.1nm, Flea2.RGB, wave='auto' )  # a 1x3 matrix, no materials
product( D65.1nm, neutralMaterial(0.01), Flea2.RGB, wave='auto' ) # a 1x3 matrix, 1 material
path = system.file( "extdata/sources/Lumencor-SpectraX.txt", package='colorSpec' )
lumencor = readSpectra( path, wave=340:660 )
product( lumencor, Flea2.RGB, wave='auto' )   # a 7x3 matrix, no materials


# sequence 6.
scanner = calibrate( scanner )
target = readSpectra( system.file( "extdata/targets/N130501.txt", package='colorSpec') )
product( target, scanner, wave='auto' )  #  a 288x3 matrix
```

---

ptransform   *make a linear transformation to a colorSpec responder*

Description

apply a linear transformation to a **colorSpec** responder with M spectra, so that multiples of M given *primary* vectors are transformed to the standard basis of R^M. And a given *white* vector is transformed to the M-vector of all 1s.

The returned object is always multiply(x,A) where A is an internally calculated MxM matrix. The name ptransform is short for *projective transformation*.

In case of ERROR, a message is logged and NULL returned.

Usage

```
## S3 method for class 'colorSpec'
ptransform( x, primary, white, digits=Inf )
```

Arguments

x	a **colorSpec** responder with M spectra. type(x) must be 'responsivity.light' or 'responsivity.material'.
primary	an MxM matrix whose rows define the M primary vectors in the response space of x. It is OK for each row to have a single value that is NA. In this case the NA value is changed so that the sum of the row is 1. This is done because typically the rows represent chromaticities in the response space of x. After this change, the rows of primary must form a basis of R^M. rownames(primary) must be defined; when M=3 they are typically c('R','G','B').
white	an M-vector in the response space of x, that is typically the ideal white point of a color display. When white is expressed in the basis defined by primary, the coordinates must all be non-zero. white can also be a **colorSpec** object with a single spectrum suitable as stimulus for x; in this case the vector white is set to product(white, x, wavelength='auto').

digits   if a positive integer, then white is rounded to this number of decimal digits, but in a non-standard way, see **Details**. This is typically done so the internally calculated MxM matrix A agrees with that from a color standard, see **Examples**.

Details

The formal mathematical requirements for primary and white are:

- The rows of primary must form a basis of R^M. Equivalently, if P denotes the matrix primary, then P is invertible.

- The coordinates of white in this basis are all non-zero. Equivalently, if x is the solution of $xP = white$, then every component of x is non-zero.

Assuming both of these are true, then there is a unique matrix A so that

- A transforms a multiple of the i'th row of P to the i'th standard basis vector of R^M.

- A transforms white to the M-vector of all 1s.

This statement is essentially the fundamental theorem of (analytic) projective geometry; see *Bumcrot* page 87, and *Semple* page 398. The rows of P plus $white$ define a *projective frame*; the former are the *fundamental points* and the latter is the *unit point*.

If digits is a positive integer, the chromaticity of white is computed by dividing white by sum(white). The latter must be non-zero, or else it is an ERROR. This chromaticity is rounded to digits decimal digits, while preserving the sum of 1. This *rounded chromaticity* is non-zero, and defines a line through 0. The vector white is projected onto this line to get the new and rounded white, with the rounded chromaticity. See **Examples**.

Value

a **colorSpec** object equal to multiply(x,A) where A is an internally calculated MxM matrix. The quantity and wavelength are preserved. The specnames of the returned object are set to tolower(rownames(primary)).
The user may want to change the quantity of the returned object; see **Examples**.

References

Bumcrot, Robert J. **Modern Projective Geometry**. Holt, Rinehart, and Winston. 1969.

IEC 61966-2-1:1999. Multimedia systems and equipment - Colour measurement and management. Part 2-1: Colour management - Default RGB colour space - sRGB. https://webstore.iec.ch/publication/6169

Semple, J. G. and G. T. Kneebone. **Algebraic Projective Geometry**. Oxford. 1952.

See Also

quantity, wavelength, colorSpec, multiply, product

Examples

```
############ Example for sRGB   ###########

# assign the standard sRGB primaries
P = matrix( c(0.64,0.33,NA,  0.3,0.6,NA, 0.15,0.06,NA ), 3, 3, byrow=TRUE )
rownames(P) = c('R','G','B')
P
#   [,1] [,2] [,3]
# R 0.64 0.33   NA
# G 0.30 0.60   NA
# B 0.15 0.06   NA

white = product( D65.1nm, xyz1931.1nm, wave='auto' )
white
#           X       Y        Z
# D65 100.437 105.6708 115.0574

white/sum(white)
#           X         Y         Z
# D65 0.3127269 0.3290232 0.3582499

# But the sRGB standard D65 is xy=(0.3127,0.3290)
# so when the next line is executed,
# the calculated 3x3 matrix will *NOT* agree with the sRGB standard
y = ptransform( xyz1931.1nm, P, white, digits=Inf )

product( D65.1nm, y, wave='auto' )
#     R G B
# D65 1 1 1     # this is exactly what we want, but the internal 3x3 matrix is a little off

# now repeat, but this time round the white chromaticity to
# xy=(0.3127,0.3290) in order to get the matrix right
y = ptransform( xyz1931.1nm, P, white, digits=4 )

rgb = product( D65.1nm, y, wave='auto' )
rgb
#            R        G        B
# D65 1.000238 1.000053 0.999835   # off in the 4'th digit  (WARN: this is linear RGB)

255 * rgb
#            R        G        B
# D65 255.0607 255.0134 254.9579   # good enough for 8-bit RGB

65535 * rgb
#            R        G        B
# D65 65550.59 65538.44 65524.18   # NOT good enough for 16-bit RGB

# So for 16-bit RGB, one can get the white RGB right, or the 3x3 matrix right, but not both !


############ Example for ProPhoto RGB   ###########
```

```
# assign the standard ProPhoto RGB primaries
P = matrix( c(0.7347,0.2653,NA,  0.1596,0.8404,NA, 0.0366,0.0001,NA ), 3, 3, byrow=TRUE )
rownames(P) = c('R','G','B')
P
#     [,1]   [,2] [,3]
# R 0.7347 0.2653   NA
# G 0.1596 0.8404   NA
# B 0.0366 0.0001   NA

white = product( D50.5nm, xyz1931.5nm, wave='auto' )
white
#          X       Y        Z
# D50 101.2815 105.042 86.67237

white / sum(white)
#            X         Y         Z
# D50 0.3456755 0.3585101 0.2958144

# but the ProPhoto RGB standard is xy=(0.3457,0.3585);  proceed anyway
y = ptransform( xyz1931.5nm, P, white, digits=Inf )

product( D50.5nm, y, wave='auto' )
#     R G B
# D50 1 1 1    #  this is exactly what we want, but the internal 3x3 matrix is a little off

# the following line is an equivalent way to compute y.
# pass D50.5nm directly as the 'white' argument
y = ptransform( xyz1931.5nm, P, D50.5nm )
```

---

quantity	*quantity of a colorSpec object*

Description

Retrieve or set the quantity of a **colorSpec** object.

Usage

```
## S3 method for class 'colorSpec'
quantity(x)

## S3 replacement method for class 'colorSpec'
quantity(x) <- value

## S3 method for class 'colorSpec'
type(x)
```

Arguments

x   a **colorSpec** R object

value   a valid quantity string; see Details.

Details

There are 4 valid types, which are further divided into 14 valid quantities. All of these are strings:

For type='light'
quantity = 'energy' (radiometric), or 'photons' (actinometric)

For type='responsivity.light'
quantity = 'energy->electrical', 'energy->neural', 'energy->action',
'photons->electrical', 'photons->neural', or 'photons->action'

For type='material'
quantity = 'reflectance', 'transmittance', or 'absorbance'

For type='responsivity.material'
quantity = 'material->electrical', 'material->neural', or 'material->action'

Also see the **colorSpec User Guide**.

Value

quantity() returns the quantity of x

type() returns the type of x, which depends only on the quantity.

Note

The **colorSpec** quantity is more general than the physical SI quantity; for example quantity='energy'
really includes 10 distinct SI quantities and maybe more. The unit is left arbitrary in most cases.
Exceptions are reflectance, transmittance, and absorbance which are dimensionless.

Changing the quantity should only be done if one knows what one is doing. It does not change the
underlying numbers. For example, changing photons to energy does not do numerical conversion.
For this specific conversion, see radiometric().

Similarly, see linearize() for conversion from absorbance to transmittance.

See Also

colorSpec, radiometric, linearize

---

radiometric	*convert a colorSpec object from actinometric to radiometric*

Description

Convert a **colorSpec** object to have quantity that is radiometric (energy of photons) - to prepare it for colorimetric calculations. Test an object for whether it is radiometric.

Usage

```
## S3 method for class 'colorSpec'
radiometric( x, multiplier=1, warn=FALSE )

## S3 method for class 'colorSpec'
is.radiometric( x )
```

Arguments

x	a **colorSpec** object
multiplier	a scalar which is multiplied by the output, and intended for unit conversion
warn	if TRUE and a conversion actually takes place, the a WARN message is issued. This makes the user aware of the conversion, so units can be verified. This can be useful when radiometric() is called from another **colorSpec** function.

Details

If the quantity of x does not start with 'photons' then the quantity is not actinometric and so x is returned unchanged. Otherwise x is actinometric (photon-based).

If type(x) is 'light' then the most common actinometric unit of photon count is (μmole of photons) = $(6.02214x10^{17}$ photons). The conversion equation is:

$$E = Q * 10^{-6} * N_A * h * c/\lambda$$

where E is the energy of the photons, Q is the photon count, N_A is Avogadro's constant, h is Planck's constant, c is the speed of light, and λ is the wavelength in meters. The output energy unit is joule.
If the unit of Q is not (μmole of photons), then the output should be scaled appropriately. For example, if the unit of photon count is exaphotons, then set multiplier=1/0.602214.

If the quantity(x) is 'photons->electrical', then the most common actinometric unit of responsivity to light is quantum efficiency (QE). The conversion equation is:

$$R_e = QE * \lambda * e/(h * c)$$

where R_e is the energy-based responsivity, QE is the quantum efficiency, and e is the charge of an electron (in C). The output responsivity unit is coulombs/joule (C/J) or amps/watt (A/W).
If the unit of x is not quantum efficiency, then multiplier should be set appropriately.

If the [quantity](x) is 'photons->neural' or 'photons->action', the most common actinometric unit of photon count is (μmole of photons) = $(6.02214 x 10^{17}$ photons). The conversion equation is:

$$R_e = R_p * \lambda * 10^6 / (N_A * h * c)$$

where R_e is the energy-based responsivity, R_p is the photon-based responsivity. This essentially the reciprocal of the first conversion equation.

The argument multiplier is applied to the right side of all the above conversion equations.

Value

radiometric() returns a **colorSpec** object with quantity that is radiometric (energy-based) and not actinometric (photon-based). If type(x) is a material type ('material' or 'responsivity.material') then x is returned unchanged.

If quantity(x) starts with 'energy', then is.radiometric() returns TRUE, and otherwise FALSE.

Note

To log the executed conversion equation, execute cs.options(loglevel='INFO').

Source

Wikipedia. **Photon counting**. https://en.wikipedia.org/wiki/Photon_counting

See Also

quantity, type, [F96T12](F96T12), cs.options, actinometric

Examples

```
sum( F96T12 )     # the step size is 1nm, from 300 to 900nm
# [1] 320.1132  photon irradiance, (micromoles of photons)*m^{-2}*sec^{-1}

sum( radiometric(F96T12) )
# [1] 68.91819  irradiance, watts*m^{-2}
```

---

readCGATS   *read tables from files in ANSI/CGATS.17 format*

Description

The CGATS text format supports a preamble followed by N tables, where N $\geq$ 1. Each table can have a separate header. A table may or may not contain spectral data, see **Note**. The function converts each table to a data.frame with attributes; see **Details**.

Usage

```
readCGATS( path, collapsesingle=FALSE )
```

Arguments

path   the path name of a single file, in CGATS format

collapsesingle If path has only one table (N=1) and collapsesingle is TRUE, then return the
                single data.frame (instead of a list with 1 data.frame). If path has multiple
                tables (N ≥ 2), then collapsesingle is ignored.

Details

The returned list is given attributes: "path", "preamble", and (if present) "date", "created",
"originator", and "file_descriptor". The attribute values are all character vectors. The value
of attribute "path" is the argument path, and the other values are extracted from "preamble". The
length of "preamble" is (typically) greater than 1, and the others have length 1. Each line of the
preamble is a keyword-value pair. The keyword ORIGINATOR is converted to attribute "originator".
The keyword FILE_DESCRIPTOR is converted to attribute "file_descriptor". The keyword CREATED
is converted to attributes "created" and "date". The list is also given names. If the keyword
TABLE_NAME is present in the table header, then its value is used. Otherwise the names are "TABLE_1",
"TABLE_2", ...

Each data.frame in the list is assigned attributes: "header", and (if present) "descriptor". The
length of "header" is (typically) greater than 1, and "descriptor" has length 1. Each line of
the table header is a keyword-value pair. The keywords DESCRIPTOR and TABLE_DESCRIPTOR are
converted to attribute "descriptor".

For the lines between BEGIN_DATA and END_DATA, two conventions for separating the values are
supported:

- In the standard convention, fields are separated by contiguous spaces or tabs, and character
  strings (which may have embedded spaces or even tabs) are enclosed by double-quotes. This
  is is the convention in the CGATS standard. The function [scan]() is used here.

- In the non-standard convention, fields are separated by a *single* tab, and character strings
  (which may have embedded spaces but not tabs) are *not* enclosed by double-quotes. This
  convention is often easier to work with in spreadsheet software. The function [strsplit]() is
  used here.

The function readCGATS() selects the separation convention by examining the line after BEGIN_DATA_FORMAT.
If this line is split by a single tab and the number of fields matches that given on the NUMBER_OF_FIELDS
line, then the non-standard convention is selected; otherwise, the standard convention is selected.

Value

readCGATS() returns a list of data.frames - one data.frame for each table found in path. The
list and each individual data.frame have attributes, see **Details**.

If path has only a single table (the majority of files have only 1) and collapsesingle is TRUE,
then the attributes of the list are copied to those of the data.frame, and the data.frame is then
returned. The name of the table is lost.

If there is an error in any table, then the function returns NULL.

Note

In the BEGIN_DATA_FORMAT line(s), field names may not be quoted and may not have embedded spaces.

The CGATS standard allows duplicated field names, and readCGATS() returns them as they appear, with no attempt to append numbers in order to make them unique. Examples of field names which may be duplicated are: SPECTRAL_NM, SPECTRAL_DEC, and SPECTRAL_PCT; for more on these see readSpectraCGATS().

No attempt is made to recognize those tables that contain spectral data. For conversion of spectral data to **colorSpec** objects, see readSpectraCGATS().

References

ANSI/CGATS.17. Graphic technology - Exchange format for colour and process control data using XML or ASCII text. https://webstore.ansi.org/ 2009.

ISO/28178. Graphic technology - Exchange format for colour and process control data using XML or ASCII text. https://www.iso.org/standard/44527.html. 2009.

CGATS.17 Text File Format. http://www.colorwiki.com/wiki/CGATS.17_Text_File_Format.

See Also

readSpectraCGATS, scan, strsplit, names

Examples

```
#   read file with 2 tables of non-spectral data
A70 = readSpectra( system.file( "tests/A70.ti3", package='colorSpec' ) )
length(A70)        # [1] 2  # the file has 2 tables
ncol( A70[[1]] )   # [1] 7  # the 1st table has 7 columns
ncol( A70[[2]] )   # [1] 4  # the 2nd table has 4 columns
```

---

readSpectra *read colorSpec objects from files*

Description

These functions read **colorSpec** objects from files. In case of ERROR, they return NULL. There are 5 different file formats supported; see **Details**.

Usage

```
readSpectra( pathvec, ... )

readSpectraXYY( path )
readSpectraSpreadsheet( path )
readSpectrumScope( path )

readSpectraCGATS( path )
```

```
readSpectraControl( path )
```

Arguments

pathvec   a character vector to (possibly) multiple files. The file extension and a few lines from each file are read and a guess is made regarding the file format.

...   optional arguments passed on to [resample](). The most important is wavelength. If these are missing then [resample]() is not called.

path   a path to a single file with the corresponding format: XYY, Spreadsheet, Scope, CGATS, or Control. See Details. If the function cannot recognize the format, it returns NULL.

Details

readSpectra() reads the first few lines of the file in order to determine the format, and then calls the corresponding format-specific function. If readSpectra() cannot determine the format, it returns NULL. The 5 file formats are:

XYY
There is a column header line matching ^(wave|wv?l) (not case sensitive) followed by the the names of the spectra. All lines above this one are taken to be metadata. The separarator on this header line can be space, tab, or comma; the line is examined and the separator found there is used in the lines with data below. The organization of the returned object is 'df.col'. This is probably the most common file format; see the sample file ciexyz31_1.csv.

Spreadsheet
There is a line matching "^(ID|SAMPLE|Time)". This line and lines below must be tab-separated. Fields matching '^[A-Z]+([0-9.]+)nm$' are taken to be spectral data and other fields are taken to be extradata. All lines above this one are taken to be metadata. The organization of the returned object is 'df.row'. This is a good format for automated acquisition, using a spectrometer, of many spectra. See the sample file N130501.txt from **Wolf Faust**.

Scope
This is a file format used by **Ocean Optics** spectrometer software. There is a line
>>>>>Begin Processed Spectral Data<<<<<
followed by wavelength and energy separated by a tab. There is only 1 spectrum per file. The organization of the returned object is 'vector'. See the sample file pos1-20x.scope.

CGATS
This is a complex format that is best understood by looking at some samples, such as extdata/objects/Rosco.txt; see also the **References**. The function [readCGATS]() is first called to get all the tables, and then for each table the column names are examined. There are 2 conventions for presenting the spectral data:

- In the standard convention the fields SPECTRAL_DEC or SPECTRAL_PCT have the spectral values. The former is the true value, and the latter is the true value x 100. Each value column is preceded a corresponding wavelength column, which has the field name SPECTRAL_NM. Note

that these field names are highly duplicated. In principle, this convention allows each record in a CGATS table to have a different wavelength vector. However, this complication is rejected by readSpectraCGATS(), which treats it as an ERROR.

- In the non-standard convention the field names that match the pattern "^(nm|SPEC_|SPECTRAL_)[_A-Z]*([0-9.]+)$" are considered to be spectral value data, and other fields are considered extradata. The wavelength is the numerical value of the 2nd parenthesized expression ([0-9.]+) in nanometers. Note that every record in this CGATS table has the same wavelength vector. Although this convention is non-standard, it appears in files from many companies, including X-Rite.

If a data.frame has spectral data, it is converted to a **colorSpec** object and placed in the returned list. The organization of the resulting **colorSpec** object is 'df.row'. If the data.frame of extradata contains a column SAMPLE_NAME, SAMPLE_ID, SampleID, or Name, (examined in that order), then that column is taken to be the specnames of the object. If a table has no spectral data, then it is ignored. If the CGATS file has no tables with spectral data, then it is an ERROR and the function returns NULL.

Control
This is a personal format used for digitizing images of plots from manufacturer datasheets and academic papers. It is structured like a .INI file. There is a [Control] section establishing a simple linear map from pixels to the wavelength and spectrum quantities. Only 3 points are really necessary. It is OK for there to be a little rotation of the plot axes relative to the image. This is followed by a section for each spectrum, in XY pixel units only. Conversion to wavelength and spectral quantities is done on-the-fly after they are read. Extrapolation can be a problem, especially when the value is near 0. To force constant extrapolation (see [resample](), repeat the control point (knot) at the endpoint. See the sample file Lumencor-SpectraX.txt. The organization of the returned objects is 'vector'.

Value

readSpectra() returns a single **colorSpec** object or NULL in case of ERROR. If there are multiple files in pathvec and they cannot be combined using bind() because their wavelengths are different, it is an ERROR. To avoid this ERROR, the wavelength argument can be used for resampling to common wavelengths. If there are multiple files, the [organization]() of the returned object is 'df.row' and the first column is the path from which the spectrum was read.

The functions readSpectraXYY(), readSpectraSpreadsheet(), and readSpectraScope(), return a single **colorSpec** object, or NULL in case of ERROR.

The functions readSpectraCGATS() and readSpectraControl() are more complicated. These 2 file formats can contain multiple spectra with different wavelength sequences, so both functions return a *list* of **colorSpec** objects, even when that list has length 1. If no spectral objects are found, they return NULL.

If readSpectra() calls readSpectraCGATS() or readSpectraControl() and receives a list of **colorSpec** objects, readSpectra() attempts to [bind]() them into a single object. If they all have the same wavelength vector, then the bind() succeeds and the single **colorSpec** object is returned. Otherwise the bind() fails, and it is an ERROR. To avoid this error readSpectra() can be called with a wavelength argument. The multiple spectra are resampled using [resample]() and *then* combined using bind(), which makes it much more convenient to read such files.

Note

During import, each read function tries to guess the quantity from spectrum names or other cues. For example the first line in **N130501.txt** is IT8.7/1, which indicates that the quantity is 'transmittance' (a reflective target is denoted by IT8.7/2). If a confident guess cannot be made, it makes a wild guess and issues a warning. If the quantity is incorrect, one can assign the correct value after import. Alternatively one can add a line to the header part of the file with the keyword 'quantity' followed by some white-space and the correct value. It is OK to put the value in quotes. See example files under folder **extdata**.

References

CGATS.17 Text File Format. http://www.colorwiki.com/wiki/CGATS.17_Text_File_Format.

ANSI/CGATS.17. Graphic technology - Exchange format for colour and process control data using XML or ASCII text. https://webstore.ansi.org/ 2009.

ISO/28178. Graphic technology - Exchange format for colour and process control data using XML or ASCII text. https://www.iso.org/standard/44527.html. 2009.

See Also

[wavelength](), [quantity](), [metadata](), [resample](), [bind](), [readCGATS]()

Examples

```
#   read file with header declaring the quantity to be "photons->neural"
bird = readSpectra( system.file( "extdata/eyes/BirdEyes.txt", package='colorSpec' ) )
quantity(bird)   # [1] "photons->neural"
```

| resample | *resample a colorSpec Object to new wavelengths* |

Description

interpolate or smooth to new wavelengths. Simple extrapolation and clamping is also performed.

Usage

```
## S3 method for class 'colorSpec'
resample( x, wavelength, method='auto', span=0.02, extrapolation='const', clamp='auto' )
```

Arguments

x	a **colorSpec** object
wavelength	vector of new wavelengths, in nanometers
method	interpolation methods available are `'sprague'`, `'spline'`, and `'linear'`. Also available is `'auto'` which means to use `'sprague'` if x is regular, and `'spline'` otherwise. An available smoothing method is `'loess'`. See **Details**.
span	smoothing argument passed to [loess](#)() during interpolation, and not used by other methods. The default value `span=0.02` is suitable for `.scope` spectra but may be too small in many other cases.
extrapolation	extrapolation methods available are `'const'` and `'linear'`. These can be abbreviated to the initial letter. Also available is a numeric value, which is used for simple padding. See **Details**. Also available is a vector or list of length 2 that combines 2 of the above. The first item is used on the low side (shorter wavelengths), and the second item is used on the high side (longer wavelengths).
clamp	clamp methods available are `'auto'`, `TRUE`, and `FALSE`. Also available is a numeric vector of length 2, which defines the clamping interval. See **Details**.

Details

If method is `'sprague'`, the quintic polynomial in *De Kerf* is used. Six weights are applied to nearby data values: 3 on each side. The `'sprague'` method is only supported when x is regular.

If method is `'spline'`, the function `stats::`[spline](#)() is called with `method='natural'`.

The `'spline'` method is supported even when x is irregular.

If method is `'linear'`, the function `stats::`[approx](#)() is called. Two weights are applied to nearby data values: 1 on each side. The `'linear'` method is supported even when x is irregular.

If method is `'loess'`, the function `stats::`[loess](#)() is called with the given span parameter. Smoothing is most useful for noisy data, e.g. raw data from a spectrometer. I have found that `span=0.02` works well for Ocean Optics `.scope` files, but this may be too small in other cases, which triggers an error in `stats::loess()`. The `'loess'` method is supported even when x is irregular.

If extrapolation is `'const'`, the extreme values at each end are simply extended. If extrapolation is `'linear'`, the line defined by the 2 extreme values at each end is used for extrapolation. If the ultimate and penultimate wavelengths are equal, then this line is undefined and the function reverts to `'const'`.

If clamp is `'auto'`, output values are clamped to the physically realizable interval appropriate for x. This is the interval [0,1] when `quantity(x)` is `'reflectance'` or `'transmittance'`, and the interval [0,∞) otherwise. Exception: If an input spectrum in x violates a limit, then clamping the output spectrum to this limit is *NOT* enforced. This happens most frequenty for theoretical (or matrixed) cameras, such as [BT.709.RGB](#).

If clamp is `TRUE`, the result is the same as `'auto'`, but with no exceptions. If clamp is `FALSE`, then no clamping is done.

If clamp is a numerical interval, then clamping is done to that interval, with no exceptions. The two standard intervals mentioned above can be expressed in **R** as `c(0,1)` and `c(0,Inf)` respectively.

Value

resample(x) returns a **colorSpec** object with the new wavelength. Other properties, e.g. organization, quantity, ..., are preserved.
In case of ERROR, the function returns NULL.

References

De Kerf, Joseph L. F. **The interpolation method of Sprague-Karup**. *Journal of Computational and Applied Mathematics*. volume I, no 2, 1975. equation (S).

See Also

organization(), quantity(), wavelength(), is.regular(), theoreticalRGB, spline(), approx(), loess

Examples

```
path = system.file( "extdata/sources/pos1-20x.scope", package='colorSpec' )
y = readSpectra( path )
# plot noisy data in gray
plot( y, col='gray' )
# plot smoothed plot in black on top of the noisy one to check quality
plot( resample( y, 200:880, meth='loess', span=0.02 ), col='black', add=TRUE )
```

---

responsivityMetrics   *Compute Metrics for a Light Responder (e.g. a camera) or a Material Responder (e.g. a scanner)*

Description

This function computes a few technical metrics regarding some geometric objects related to a responder: the spherical chromaticity polygon, cone, convex cone, and color-solid.

Currently the function only works if the number of spectra in x is 3 (e.g. RGB or XYZ). In this case the rows of as.matrix(x) (after weighting by step size) are called the *generators*; they are vectors in R^3 and we require that they are all in some open linear halfspace (unless a generator is 0). The 0-based rays through the generators intersect a plane inside the halfspace to form the vertices of the *chromaticity polygon* P. The 0-based rays through points of the interior of P form a cone, and the convex hull of this cone is a convex cone. The central projection of P onto the unit sphere is the *spherical chromaticity polygon* P_S. If type is 'responsivity.material', then x has an *object-color solid* or *Rösch Farbkörper*, which is a zonohedron Z. See *Centore* and vignette **Convexity and Transitions** for details.

Some simplification of the generators is performed during pre-processing. Generators that are 0 (in all channels) are removed, and a group of generators that are all positive multiples of each other is replaced by their sum. The 3-vectors are called the *condensed generators*. These simplifications do not change any of the geometric objects defined above.

Usage

```
## S3 method for class 'colorSpec'
responsivityMetrics( x )
```

Arguments

x	a **colorSpec** object with type equal to `'responsivity.light'` or `'responsivity.material'`, and 3 spectra

Value

`responsivityMetrics()` returns a list with these items:

generators	a pair of integers, the 1st is the number of original generators, and the 2nd is the number of condensed generators
zeros	vector of wavelengths at which the responsivity is 0 (in all 3 channels)
multiples	a list of vectors of wavelengths; the responsivities in each vector (group) are positive multiples of each other
salient	a logical where TRUE means that there is some open linear halfspace that contains all the non-zero generators. If all the responsivities are non-negative, which is the usual case, then `salient=TRUE`.
normal	If `salient=TRUE`, then the inward pointing unit normal for the previous halfspace. Otherwise, `normal=NA`.

If `salient=TRUE`, then the list also contains:

concavities	a `data.frame` with 2 columns: `wavelength` and `extangle`, where `extangle` is the external angle at the wavelength (for the spherical chromaticity polygon P_S), and is negative. A negative angle means that P_S is concave at that vertex.
coneangle	the solid angle of the cone generated by the generators. This is identical to the area of the spherical chromaticity polygon, with concavities preserved.
cxconeangle	the solid angle of the convex cone generated by the generators, with no concavities. This is identical to the area of the convex hull of the spherical chromaticity polygon. If all responsivities are non-negative, which is the usual case, then this solid angle is less than the solid angle of an octant, which is $\pi/2$.

If the type of x is `'responsivity.material'` then the list also contains:

area	the surface area of the object-color solid of x
volume	the volume of the object-color solid of x

In case of global error, the function returns `NULL`.

Note

To determine the value of `salient`, the package **quadprog** might be required.

References

Centore, Paul. *A zonohedral approach to optimal colours*. **Color Research & Application**. Vol. 38. No. 2. pp. 110-119. April 2013.

See Also

[type](#), vignette **Convexity and Transitions**

---

scanner	*standard RGB scanners*

Description

scanner.ACES is an RGB responder to material; an ACES/SMPTE standard for scanning RGB film. The 3 spectra are defined from 368 to 728 nm, at 2nm intervals.

Format

A **colorSpec** object with [quantity](#) equal to 'material->electrical' and 3 spectra: r, g, and b.

Details

The responsivities have been scaled (by [calibrate](#)) so the response to the *perfect transmitting filter* (PTF) is RGB=(1,1,1).

References

Technical Bulletin TB-2014-005. Informative Notes on SMPTE ST 2065-2 - Academy Printing Density (APD). Spectral Responsivities, Reference Measurement Device and Spectral Calculation.

SMPTE ST 2065-3 Academy Density Exchange Encoding (ADX). Encoding Academy Printing Density (APD) Values.

The Academy of Motion Picture Arts and Sciences. Science and Technology Council. Academy Color Encoding System (ACES) Project Committee. Version 1.0 December 19, 2014. Annex A Spectral Responsivities.

See Also

[quantity](#), [calibrate](#)

Examples

```
#   compute response of ACES scanner to the Hoya filters
product( Hoya, scanner.ACES, wave='auto' )

##                 R            G          B
## R-60   0.902447043 2.022522e-05 0.00000000
## G-533  0.038450857 4.900983e-01 0.05431134
## B-440  0.008466317 1.686241e-02 0.42863320
## LB-120 0.184408941 3.264111e-01 0.53492533
```

---

sectionOptimalColors   *compute sections of an optimal color surface by hyperplanes*

Description

Consider a **colorSpec** object x with type equal to 'responsivity.material'. The set of all possible material reflectance functions (or transmittance functions) is convex, closed, and bounded (in fact they form a cube), and this implies that the set of all possible output responses from x is also convex, closed, and bounded. The latter set is called the *object-color solid* or *Rösch Farbkörper* for x. If the dimension of the response of x is 2, this solid is a convex polygon that is centrally symmetric - a *zonogon*. If the dimension of the response of x is 3 (e.g. RGB or XYZ), this solid is a special type of centrally symmetric convex polyhedron called a *zonohedron*, see *Centore*. This function only supports dimensions 2 and 3. Denote this object-color solid by **Z**.

A color on the boundary of **Z** is called an *optimal color*. Consider the intersection of a hyperplane with the boundary of **Z**. Let the equation of the hyperplane be given by:

$$< v, normal >= \beta$$

where $normal$ is orthogonal to the hyperplane, and β is the plane constant, and v is a variable vector. The purpose of the function sectionOptimalColors() is to compute the intersection set.

In dimension 2 this hyperplane is a line, and the intersection is generically 2 points, and 1 point if the line only intersects the boundary (we ignore the special case when the intersection is an edge of the polygon).

In dimension 3 this hyperplane is a 2D plane, and the intersection is generically a polygon, and 1 point if the line only intersects the boundary (we ignore the special case when the intersection is a face of the zonohedron).

Of course, the intersection can also be empty.

Usage

```
## S3 method for class 'colorSpec'
sectionOptimalColors( x, normal, beta )
```

Arguments

x	a **colorSpec** object with type equal to 'responsivity.material' and M spectra, where M=2 or 3.
normal	a nonzero vector of dimension M, that is the normal to a hyperplane
beta	a vector of numbers of positive length. The number beta[k] defines the plane <v,normal> = beta[k]. .

Details

Consider first the case that the dimension of x is 3, so that **Z** is a zonohedron. In the preprocessing phase the zonohedral representation is calculated. The faces of **Z** are either parallelograms, or *compound faces* that are partitioned into parallelograms. The centers of all these parallelograms are

computed, along with their extent in direction $normal$. For a given plane $< v, normal >= \beta$, the parallelograms that intersect the plane are extracted. The boundary of each parallelogram intersects the plane in 2 points (in general) and one of those points is computed. The set of all these points is then sorted into proper order around the boundary.

In the case that the dimension of x is 2, so that **Z** is a zonogon, the parallelograms are replaced by line segments (edges), and the processing is much easier.

Value

The function returns a list with an item for each value in vector `beta`. Each item in the output is a list with these items:

beta   the value of the plane constant β

section   an NxM matrix, where N is the number of points in the section, and M is the dimension of `normal`. If the intersection is empty, then N=0.

In case of global error, the function returns `NULL`.

WARNING

The preprocessing calculation of the zonohedron dominates the total time. And this time goes up rapidly with the number of wavelengths. We recommend using a wavelength step of 5nm, as in the **Examples**. For best results, batch a lot of `beta`s into a single function call and then process the output.

Moreover, the preprocessing time is dominated by the partitioning of the compound faces into parallelograms. This is made worse by an x whose spectral responses have little overlap, as in `scanner.ACES`. In these cases, try a larger step size, and then reduce. Optimizing these compound faces is a possible topic for the future.

References

Centore, Paul. *A Zonohedral Approach to Optimal Colours*. **Color Research & Application**. Vol. 38. No. 2. pp. 110-119. April 2013.

Logvinenko, A. D. An object-color space. **Journal of Vision**. 9(11):5, 1-23, (2009). `https://jov.arvojournals.org/article.aspx?articleid=2203976`. doi:10.1167/9.11.5.

See Also

vignette **Plotting Chromaticity Loci of Optimal Colors**, `probeOptimalColors()`

Examples

```
wave = seq(420,680,by=5)
Flea2.scanner = product( A.1nm, "material", Flea2.RGB, wavelength=wave )
seclist = sectionOptimalColors( Flea2.scanner, normal=c(0,1,0), beta=10 )
length( seclist[[1]]$section )
seclist[[1]]$section[ 1:5, ]
## [1] 207   # the polygon has 207 vertices, and the first 5 are:
##           Red Green     Blue
## [1,] 109.2756    10 3.5391342
```

```
## [2,] 109.5729    10 2.5403628
## [3,] 109.8078    10 1.7020526
## [4,] 109.9942    10 1.0111585
## [5,] 110.1428    10 0.4513051
```

---

solar.irradiance   *Standard Solar Irradiance - Extraterrestrial and Terrestrial*

Description

solar.irradiance Three power spectra; from 280 to 1000 nm at 1 nm intervals. The unit is $W * m^{-2} * nm^{-1}$.

atmosphere2003 a transmittance spectrum = the quotient of 2 spectra from solar.irradiance

Format

solar.irradiance is a **colorSpec** object with quantity equal to 'energy' and with 3 spectra:

AirMass.0 Extraterrestrial Radiation (solar spectrum at top of atmosphere) at mean Earth-Sun distance

GlobalTilt spectral radiation from solar disk plus sky diffuse and diffuse reflected from ground on south facing surface tilted 37 deg from horizontal

AirMass.1.5 the sum of Direct and Circumsolar irradiance, when the optical path is 1.5 times that of the sun at zenith, see **Details**

atmosphere2003 is a **colorSpec** object with quantity equal to 'transmittance' and with 1 spectrum:

AirMass.1.5 the quotient AirMass.1.5 / AirMass.0 from solar.irradiance

Details

Direct is Direct Normal Irradiance Nearly parallel (0.5 deg divergent cone) radiation on surface with surface normal tracking (pointing to) the sun, excluding scattered sky and reflected ground radiation.

Circumsolar is Spectral irradiance within +/- 2.5 degree (5 degree diameter) field of view centered on the 0.5 deg diameter solar disk, but excluding the radiation from the disk.

Note

The reference spectra in ASTM G173-03 are designed for Photovoltaic Performance Evaluation.

The original wavelength sequence in ASTM G173-03 is irregular. The interval is 0.5 nanometer from 280 to 400 nm, 1 nm from 400 to 1700 nm, an intermediate wavelength at 1702 nm, and 5 nm from 1705 to 4000 nm. To create the object solar.irradiance with a regular step size, the original was resampled from 280 to 1000 nm at 1nm intervals.

Source

Reference Solar Spectral Irradiance: ASTM G-173. http://rredc.nrel.gov/solar/spectra/am1.5/astmg173/astmg173.html

References

ASTM G173-03 Reference Spectra Derived from SMARTS v. 2.9.2.
Standard Tables for Reference Solar Spectral Irradiances: Direct Normal and Hemispherical on 37-deg Tilted Surface (2003)

See Also

D65, D50, daylightSpectra, resample, vignette **Blue Flame and Green Comet**

---

specnames   *specnames of a colorSpec object*

Description

Retrieve or set the specnames of a **colorSpec** object. Retrieve the number of spectra.

Usage

```
## S3 method for class 'colorSpec'
specnames(x)

## S3 replacement method for class 'colorSpec'
specnames(x) <- value

## S3 method for class 'colorSpec'
numSpectra(x)
```

Arguments

x   a **colorSpec** R object
value   a character vector with length equal to the number of spectra in x.

Details

If the organization of x is ″vector″ then x is a vector and value is a single string, which is stored as attr(x,'specname').

If the organization of x is ″matrix″, then x is a matrix and value is stored as colnames(x).

If the organization of x is ″df.col″, then x is a data.frame with N+1 columns, where N is the number of spectra. value is stored as colnames(x)[2:(N+1)].

If the organization of x is ″df.row″, then x is a data.frame and value is stored as row.names(x).

Value

specnames() returns a character vector with the names of the spectra.

numSpectra(x) is equal to length(specnames(x)) but much more efficient.

See Also

[rownames](), [colnames]()

---

standardRGB   *Convert from XYZ to some standard RGB spaces*

Description

To display an XYZ value, it typically must be converted to a standard RGB space. This is the function to do it.

Usage

```
RGBfromXYZ( XYZ, space )
```

Arguments

XYZ	a 3-vector, or a matrix with 3 columns with XYZs in the rows
space	the name of the RGB space - either 'sRGB' or 'Adobe RGB'. The match is case-insensitive, and spaces in the string are ignored.

Details

The input XYZ is multiplied by the appropriate 3x3 conversion matrix (for **sRGB** or **Adobe RGB**). These matrices are taken from *Lindbloom* and not from the corresponding *Wikipedia* articles; for the reason why see **Note**.

Value

An Mx3 matrix where M is the number of rows in XYZ, or M=1 if XYZ is a 3-vector. Each row of the returned matrix is filled with linear RGB in the appropriate RGB space. Values outside the unit cube are not clamped. To compute non-linear display RGB, see [DisplayRGBfromLinearRGB](). In case of error the function returns NULL.

WARNING

This function is deprecated. New software should use spacesRGB::RGBfromXYZ() instead. The new function returns "signal RGB" instead of linear RGB.

Note

An RGB space is normally defined by the xy chromaticities of the 3 primaries and the white point. We follow *Lindbloom* in using the 'official' XYZ of the white point from ASTM E308. Using this XYZ of the white point makes the color space a little more consistent with other areas of color. For example, from IEC 61966-2-1 we have D65 xyY=(0.3127,0.3290,1) -> XYZ=(0.9504559,1,1.0890578). But from ASTM E308, D65 XYZ=(0.95047,1,1.08883), which is a little different.

Source

IEC 61966-2-1:1999. Multimedia systems and equipment - Colour measurement and management. Part 2-1: Colour management - Default RGB colour space - sRGB. `https://webstore.iec.ch/publication/6169`

Lindbloom, Bruce. RGB/XYZ Matrices. `http://brucelindbloom.com/index.html?Eqn_RGB_XYZ_Matrix.html`

Wikipedia. **sRGB**. `https://en.wikipedia.org/wiki/SRGB`

Wikipedia. **Adobe RGB**. `https://en.wikipedia.org/wiki/Adobe_RGB_color_space`

See Also

`D65`, `officialXYZ`, `DisplayRGBfromLinearRGB`

Examples

```
RGBfromXYZ( officialXYZ('D65'), 'sRGB' )
#      R G B
# [1,] 1 1 1    # not really 1s, but difference < 1.e-7

RGBfromXYZ( c(.3127,0.3290,0.3583)/0.3290, 'sRGB' )
#              R         G        B
# [1,] 0.9998409 1.000023 1.00024    difference > 1.e-5
```

---

subset   *extract a subset of a colorSpec Object*

Description

extract a subset of the spectra in a **colorSpec** object.
The subset can be specified by indexes, by a logical vector, or by a regular expression matching the `specnames`

Usage

```
## S3 method for class 'colorSpec'
subset( x, subset, ... )
```

Arguments

x	a **colorSpec** object
subset	an integer vector, a logical vector, or a regular expression
...	additional arguments ignored

Details

If subset is an integer vector, each integer must be between 1 and M, where M the number of spectra in x. No duplicates are allowed. The number of spectra returned is equal to length(subset). It is OK for the length to be 0, in which case the function returns the empty subset.

If subset is a logical vector, its length must be equal to M. The number of spectra returned is equal to the number of TRUEs in subset.

If subset is a regular expression, the number of spectra returned is equal to the number of specnames(x) matched by the expression.

Value

subset(x) returns a **colorSpec** object with the same [organization](#) as x. Exception: if the organization of x is 'vector' and the subset is empty, then the returned object is a matrix with 0 columns.

Note

subset() can also be used for re-ordering the spectra; just set argument subset to the desired permutation vector.

See Also

[organization](#)

Examples

```
tritanope = subset( lms2000.1nm, 1:2 ) # keep long and medium cone fundamentals, but drop the short

sml2000.1nm = subset( lms2000.1nm, 3:1 ) #   reorder from short to long
```

---

theoreticalRGB   *Theoretical   RGB   Cameras   -   BT.709.RGB,   Adobe.RGB,   and*
                         ACES.RGB

Description

These are 3 built-in **colorSpec** objects, with [quantity](#) equal to `'energy->electrical'`.

BT.709.RGB a theoretical RGB responder to light. The 3 responsivity spectra are constructed so that the RGBs from this theoretical camera, when displayed on an sRGB display after correct EOTF adjustment, would emit light with the same XYZs as the captured scene (up to a constant multiple). All three responsivities have negative lobes.

Adobe.RGB a theoretical RGB responder to light. The 3 responsivity spectra are constructed so that the RGBs from this theoretical camera, when displayed on an Adobe RGB display after correct EOTF adjustment, would emit light with the same XYZs as the captured scene (up to a constant multiple). All three responsivities have negative lobes.

ACES.RGB a theoretical RGB responder to light. Unlike the two above cameras, the responsivities are non-negative and so this camera could be built, in principle. These are the ACES RICD (Reference Input Capture Device) spectral sensitivities.

Format

All are **colorSpec** objects with [quantity](#) equal to `'energy->electrical'` and 3 spectra: r, g, and b. The wavelengths are 360 to 830 nm at 1 nm intervals.

Details

All responsivity spectra are linear combinations of the spectra in [xyz1931.1nm](#). These 3 theoretical cameras satisfy the *Maxwell-Ives criterion* by construction.
For BT.709.RGB and Adobe.RGB, the responsivities are scaled so the response to [D65.1nm](#) is RGB=(1,1,1). These responsivities have negative lobes.
The BT.709 primaries and white point are the same as those of sRGB (though the EOTF functions are different).
Adobe RGB and sRGB share the same Red, Blue, and White chromaticities, and only differ in the Green. This implies that for both cameras the Green output is 0 at Red and Blue, and 1 at White. This in turn implies that the Green output is identical for both cameras for all input spectra, and so the Green responsivity spectra are identical for both cameras.
For ACES.RGB the responsivities are area normalized as in Annex C of S-2008-001. They are scaled so that the response to Illuminant E is RGB=(1,1,1). For an example of white-balancing, as in Annex B, see the examples below.

References

Poynton, Charles. **Digital Video and HD - Algorithms and Interfaces**. Morgan Kaufmann. Second Edition. 2012. Figure 26.5 on page 302.

Academy Color Encoding Specification (ACES). S-2008-001. 2011. Annex B, pp. 23-25. Annex C, pp. 26-33.

See Also

[quantity](#)(), [D65.1nm](#), [xyz1931.1nm](#), [ptransform](#)(), [calibrate](#)(), vignette **[Blue Flame and Green Comet](#)**

Examples

```
#######    BT.709.RGB is created using the following recipe  ########
P = matrix( c(0.64,0.33,NA,  0.3,0.6,NA, 0.15,0.06,NA ), 3, 3, byrow=TRUE )
rownames(P) = c('R','G','B')
BT.709.RGB  = ptransform( xyz1931.1nm, P, D65.1nm )
quantity(BT.709.RGB) = "energy->electrical"

#######    Adobe.RGB recipe is the same, except for the matrix P  ########
P = matrix( c(0.64,0.33,NA,  0.21,0.71,NA, 0.15,0.06,NA ), 3, 3, byrow=TRUE )
rownames(P) = c('R','G','B')
Adobe.RGB  = ptransform( xyz1931.1nm, P, D65.1nm )
quantity(Adobe.RGB) = "energy->electrical"

#######  white-balancing ACES.RGB for CIE Standard Illuminant D60 ########
# in a scene illuminated by daylight illuminant D6003,
# and with a perfect-reflecting-diffuser in that scene,
# object 'camera1' would have response RGB=(1,1,1) for that diffuser.
D6003 = daylightSpectra( 6000*1.4388/1.4380, wavelength=wavelength(ACES.RGB) )
camera1 = calibrate( ACES.RGB, D6003, 1, method='scaling' )
```

---

wavelength	*wavelength vector of a colorSpec object*

Description

Retrieve or set the wavelengths of a **colorSpec** object. Retrieve the number of wavelengths, and whether the wavelength sequence is regular.

Usage

```
## S3 method for class 'colorSpec'
wavelength(x)

## S3 replacement method for class 'colorSpec'
wavelength(x) <- value

## S3 method for class 'colorSpec'
numWavelengths(x)

## S3 method for class 'colorSpec'
is.regular(x)
step.wl(x)
```

Arguments

x	a **colorSpec** R object
value	a numeric vector with length equal to the number of wavelengths in x. The wavelengths must be increasing. The unit must be nanometers.

Details

If the `organization` of x is `'df.col'`, then x is a `data.frame` and the wavelength vector is stored in the first column of x.
Otherwise, the wavelength vector is stored as `attr(x,'wavelength')`.

Value

`wavelength()` returns a numeric vector with the wavelengths of the spectra, in nanometers.

`numWavelengths(x)` is equal to `length(wavelength(x))` but much more efficient.

`is.regular()` returns `TRUE` or `FALSE`, depending on whether the step between consecutive wavelengths is a constant. A truncation error of 1.e-6 nm is tolerated here. For example, the X-Rite ColorMunki spectrometer in hi-res mode has a step of 3.33333nm, and it is considered regular.

`step.wl()` returns the *mean* step in nm, whether the wavelengths are regular or not.

See Also

[colorSpec](#)

| xyz1931 | *CIE Color Matching Functions - 2-degree (1931)* |

Description

xyz1931.1nm	the 1931 2° functions from 360 to 830 nm, at 1nm intervals
xyz1931.5nm	the 1931 2° functions from 380 to 780 nm, at 5nm intervals

Format

Each is a **colorSpec** object organized as a matrix with 3 variables.

x	the x-bar responsivity function
y	the y-bar responsivity function
z	the z-bar responsivity function

Source

<http://www.cvrl.org>

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. Table I(3.3.1). pp. 723-735.

ASTM E 308 - 01. Standard Practice for Computing the Colors of Objects by Using the CIE System. Table 1

See Also

xyz1964

Examples

```
summary(xyz1931.1nm)
white.point = product( D65.1nm, xyz1931.1nm, wave='auto' )
```

---

xyz1964   *CIE Color Matching Functions - 10-degree (1964)*

Description

xyz1964.1nm	the 10° 1964 functions from 360 to 830 nm, at 1nm intervals
xyz1964.5nm	the 10° 1964 functions from 380 to 780 nm, at 5nm intervals

Format

Each is a **colorSpec** object organized as a matrix with 3 columns.

x	the x-bar responsivity function
y	the y-bar responsivity function
z	the z-bar responsivity function

Source

http://www.cvrl.org

References

Günther Wyszecki and W.S. Stiles. **Color Science : Concepts and Methods, Quantitative Data and Formulae**. Second Edition. Wiley-Interscience. 1982. Table I(3.3.1). pp. 723-735.

ASTM E 308 - 01. Standard Practice for Computing the Colors of Objects by Using the CIE System. Table 1

See Also

[xyz1931](xyz1931)

Examples

```
summary(xyz1964.1nm)
white.point = product( D65.1nm, xyz1964.1nm, wave='auto' )
```

Index