

# Package ‘colourvision’

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**Type** Package

**Title** Colour Vision Models

**Version** 2.0.2

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**Description** Colour vision models, colour spaces and colour thresholds. Provides flexibility to build user-defined colour vision models for n number of photoreceptor types. Also includes Vorobyev & Osorio (1998) Receptor Noise Limited models, Chitka (1992) colour hexagon, and Endler & Mielke (2005) model. Models have been extended to accept any number of photoreceptor types.

**License** GPL-2

**Imports** graphics, stats, utils, rgl, Matrix

**Suggests** testthat, knitr, rmarkdown, corplot

**VignetteBuilder** knitr

**NeedsCompilation** no

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colourvision-package    *Colour Vision Models*

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## Description

Colour vision models, colour spaces and colour thresholds. Provides flexibility to build user-defined colour vision models for n number of photoreceptor types. Also includes Vorobyev & Osorio (1998) Receptor Noise Limited models, Chittka (1992) colour hexagon, and Endler & Mielke (2005) model. Models have been extended to accept any number of photoreceptor types.

## Details

The DESCRIPTION file:

```

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Title:       Colour Vision Models
Version:     2.0.2
Date:       2018-08-01
Author:      Felipe M. Gawryszewski
Maintainer:  Felipe Malheiros Gawrysewski <f.gawry@gmail.com>
Description: Colour vision models, colour spaces and colour thresholds. Provides flexibility to build user-defined colour
License:     GPL-2
Imports:     graphics, stats, utils, rgl, Matrix
Suggests:   testthat, knitr, rmarkdown, corrplot

```

VignetteBuilder: knitr

Index of help topics:

CTTKhexagon	Chittka (1992) colour hexagon
CTTKhexagon3D	Chittka (1992) colour space for tetrachromatic animals.
CTTKmodel	Chittka (1992) colour vision model
D65	CIE Standard Illuminant D65 in quantum flux (umol/m2/s)
EMline	Endler and Mielke (2005) 1-D colour space
EMmodel	Endler and Mielke (2005) colour vision model
EMtetrahedron	Endler and Mielke (2005) tetrahedron colour space
EMtriangle	Endler and Mielke (2005) triangle colour space
GENmodel	N-dimensional generic colour vision model
GENplot	Generic model colour space 2D and 1D plot
GENplot3d	Generic model colour space 3D plot
Q	Total photon capture
Qr	Photoreceptor relative quantum catch
RNLmodel	Receptor Noise Limited Models (Vorobyev & Osorio 1998)
RNLplot	Receptor noise limited model 2D and 1D plot
RNLplot3d	Receptor noise limited model 3D plot
RNLthres	Colour thresholds based on the Receptor Noise Limited Model (Vorobyev & Osorio 1998).
Rb	Brazilian savannah background reflectance spectrum.
bee	Honeybee photoreceptors
colour_space	N-dimensional colour spaces
colourvision-package	Colour Vision Models
deltaS	Chromaticity distances
energytoflux	Irradiance from energy to quantum units.
logistic	Logistic curve
noise_e	Receptor noise
photor	Photoreceptor sensitivity spectra.
plot.colourvision	Plot colour vision models into chromaticity diagrams
plot3d.colourvision	Plot colour vision models into 3D chromaticity diagrams.
radarplot	Radar plot
spec.denoise	Smooth function for reflectance spectra.

**Author(s)**

Felipe M. Gawryszewski

Maintainer: Felipe Malheiros Gawrysewski <f.gawry@gmail.com>

## References

Gawryszewski, F.M. 2018. Colour vision models: Some simulations, a general n-dimensional model, and the colourvision R package. *Ecology and Evolution*, 10.1002/ece3.4288.

## Examples

```
##Honeybee photoreceptor sensitivity curves
data("bee")

##Grey background:
## with 10 percent. reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(10, length(300:700)))

## Read CIE D65 standard illuminant already converted to quantum flux:
data("D65")

##Reflectance data
## with a sigmoid spectrum and midpoint at 500nm and 550 nm
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1, R2[,2])

## Run colour vision model:
model<-CTTKmodel(photo="tri", R=R, I=D65, Rb=Rb,
C=bee)

##plot data in the colour space
plot(model)
```

---

bee

*Honeybee photoreceptors*

---

## Description

Honeybee (*Apis mellifera*) photoreceptor sensitivity curves.

## Usage

```
data("bee")
```

## Format

A data frame with 401 observations on the following 4 variables.

Wavelength a numeric vector

UV a numeric vector

Blue a numeric vector

Green a numeric vector

**Details**

Original data were interpolated to 1nm intervals from 300 to 700nm.

**Source**

Chittka, L., and P. Kevan. 2005. Flower colour as advertisement. Pp. 157-196 in Practical pollination biology.

**Examples**

```
data("bee")
plot(bee[,2]~bee[,1], col = "violet", type="l", xlab="Wavelength(nm)", ylab= "Absorbance")
lines(bee[,3]~bee[,1], col = "blue", type="l")
lines(bee[,4]~bee[,1], col = "green", type="l")
```

---

 colour\_space

*N-dimensional colour spaces*


---

**Description**

Generates a colour space based on any number of photoreceptor types and finds a colour locus for a given photoreceptor output.

**Usage**

```
colour_space(n, type="length", length=NA, edge=NA,
             q=rep(1,n), recep.noise=FALSE, e=NA)
```

**Arguments**

n	Number of photoreceptor types. Function accepts any number of photoreceptor types $\geq 2$ . For instance, trichromatic: $n=3$ ; tetrachromatic: $n=4$ , etc.
type	Whether the colour space should be built with a fixed vector length ( <code>type="length"</code> ), or a fixed distance between vertices ( <code>type="edge"</code> ; e.g. Pike 2012 and Renoult et al. 2015).
length	Vector length used to construct the colour space. Used when <code>type="length"</code> . Typically <code>length=1</code> .
edge	Edge length used to construct the colour space. Used when <code>type="edge"</code> .
q	Photoreceptor output values
recep.noise	Whether receptor noise should be used to calculate colour locus coordinates.
e	Vector representing photoreceptor noises. Used when <code>recep.noise=TRUE</code>

**Details**

This function is used internally in colour vision models.

**Value**

A list with the following dimensions:

coordinates      Colour locus of photoreceptor output values  $q$  in the colour space  
vector\_matrix    Matrix of column vectors, each representing one photoreceptor type

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

Pike, T.W. 2012. Generalised chromaticity diagrams for animals with n-chromatic colour vision. *Journal of Insect Behavior* 255: 277-286.

Renoult, J. P., A. Kelber, and H. M. Schaefer. 2015. Colour spaces in ecology and evolutionary biology. *Biol Rev Camb Philos Soc*, doi: 10.1111/brv.12230.

**See Also**

[Q](#), [Qr](#), [CTTKmodel](#), [EMmodel](#), [RNLmodel](#), [GENmodel](#)

**Examples**

```
#A trichromatic colour space based on Endler and Mielke (2005)
tri<-colour_space(n=3, length=0.75, q=c(0.5,0.2,0.3))

#showing:
#(1) Limits of the colour space (triangle)
plot(0, ylim=c(-1,1), xlim=c(-1,1), asp=1, ylab="X2", xlab="X1", type="n")
polygon(x=tri$vector_matrix[1,], y=tri$vector_matrix[2,], lty=2)

#(2) Vectors (length=0.75) used to build the colour space (arrows)
arrows(x0=0,y0=0, x1=tri$vector_matrix[1,1], y1=tri$vector_matrix[2,1], col="red")
arrows(x0=0,y0=0, x1=tri$vector_matrix[1,2], y1=tri$vector_matrix[2,2], col="red")
arrows(x0=0,y0=0, x1=tri$vector_matrix[1,3], y1=tri$vector_matrix[2,3], col="red")

#(3) Colour loci of given photoreceptor outputs
points(x=tri$coordinates[[1]], y=tri$coordinates[[2]], pch=21, col="blue", bg="blue")
```

---

CTTKhexagon

*Chittka (1992) colour hexagon*

---

**Description**

Plots Chittka (1992) colour hexagon for trichromatic animals and a line plot for dichromatic animals.

**Usage**

```
CTTKhexagon(x, y, photo=3,  
            vnames=c(expression(E[1]),expression(E[2]),expression(E[3])),  
            pch=16, bty="n", yaxt="n", xaxt="n", col="black",  
            xlim="auto", ylim="auto", asp=1, ann=FALSE,  
            axes=FALSE, vectors=FALSE, ...)
```

**Arguments**

x	x-coordinate
y	y-coordinate. $y=0$ when <code>photo=2</code>
photo	Number of photoreceptor types. <code>photo=3</code> for a trichromatic animal, and <code>photo=2</code> for a dichromatic animal.
vnames	Vector names.
pch	see <a href="#">par</a> function.
bty	see <a href="#">par</a> function.
yaxt	see <a href="#">par</a> function.
xaxt	see <a href="#">par</a> function.
col	see <a href="#">par</a> function.
xlim	see <a href="#">plot</a> function. Default calculates <code>xlim</code> automatically.
ylim	see <a href="#">plot</a> function. Default calculates <code>ylim</code> automatically.
asp	see <a href="#">plot</a> function.
ann	see <a href="#">par</a> function.
axes	see <a href="#">plot.default</a> function.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
...	Other arguments passed to <a href="#">plot</a> function.

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**References**

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.

**See Also**

[CTTKmodel](#), [CTTKhexagon3D](#)

**Examples**

```
##Honeybee photoreceptor sensitivity curves
data("bee")

##Grey background:
## with 7 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant already converted to quantum flux:
data("D65")

##Reflectance data
## with a sigmoid spectrum and midpoint at 500nm and 550 nm
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1, R2[,2])

## Run colour vision model:
model<-CTTKmodel(photo="tri", R=R, I=D65, Rb=Rb,
C=bee)

##plot data in the colour space
CTTKhexagon(x=model[, "X1"], y=model[, "X2"])
```

---

CTTKhexagon3D

*Chittka (1992) colour space for tetrachromatic animals.*


---

**Description**

Plots a hexagonal trapezohedron representing Chittka (1992) colour space for tetrachromatic animals (They and Casas, 2002).

**Usage**

```
CTTKhexagon3D(x, y, z, s.col = "red", f.col = "black",
              vnames = c("E1", "E2", "E3", "E4"), type = "p",
              radius = 0.01, add = F, xlab = "", ylab = "", zlab = "",
              box = F, axes = F, ylim = c(-1, 1), xlim = c(-1, 1),
              zlim = c(-1,1), aspect = T, vectors=F, ...)
```

**Arguments**

x	x coordinate of points to be plotted
y	y coordinate of points to be plotted
z	z coordinate of points to be plotted
s.col	Colour to be used for plotted items. See <a href="#">plot3d</a> .
f.col	Colour of tetrahedron lines. See <a href="#">plot3d</a> .



vnames	Vector names.
type	see <a href="#">plot3d</a> function.
radius	see <a href="#">plot3d</a> function.
add	see <a href="#">plot3d</a> function.
xlab	see <a href="#">plot3d</a> function.
ylab	see <a href="#">plot3d</a> function.
zlab	see <a href="#">plot3d</a> function.
box	see <a href="#">plot3d</a> function.
axes	see <a href="#">plot3d</a> function.
ylim	see <a href="#">plot3d</a> function.
xlim	see <a href="#">plot3d</a> function.
zlim	see <a href="#">plot3d</a> function.
aspect	see <a href="#">plot3d</a> function.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
...	Other arguments passed to function <a href="#">plot3d</a> .

**Author(s)**

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**References**

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170, 533-543.

Thery, M., and J. Casas. 2002. Predator and prey views of spider camouflage. *Nature* 415, 133-133.

**See Also**

[CTTKmodel](#), [CTTKhexagon](#)

**Examples**

```
## Not run:  
library(rgl)  
CTTKhexagon3D(x=0,y=0,z=0)  
  
## End(Not run)
```

CTTKmodel

*Chittka (1992) colour vision model***Description**

Chittka (1992) colour hexagon extended to animals with any number of photoreceptor types.

**Usage**

```
CTTKmodel(photo=ncol(C)-1, R, I, Rb, C,
           interpolate=TRUE, nm=seq(300,700,1))
```

**Arguments**

photo	Number of photoreceptor types. Model accepts any number of photoreceptor types (>=2). For instance, dichromatic: photo=2; trichromatic: photo=3; tetrachromatic: photo=4, etc. Default gets number of photoreceptor types from C argument.
R	Reflectance of observed objects. A data frame with first column corresponding to wavelength values and following columns with reflectance values. R must be in the same scale as Rb (percentage or proportion).
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. Rb must be in the same scale as R (percentage or proportion).
C	Photoreceptor sensitivity curves, from lowest to longest lambda-max. A data frame: first column corresponding to wavelength values and following columns with photoreceptor sensitivity values (see function <a href="#">photor</a> ).
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .

**Details**

The original model is available for trichromatic animals only. They and Casas (2002) derived a version for tetrachromatic animals which is implemented here. In `colourvision`, this model was extended to any number of photoreceptor types (Gawryszewski 2018; see also Pike 2012). The colour hexagon in Chittka (1992) has a vector of length = 1.0 The chromaticity coordinates in `colourvision` preserve the same vector length.

Photoreceptor outputs ( $E_i$ ) are calculated by:

$$E_i = \frac{q_i}{q_i + 1}$$

where  $q_i$  is given by  $Qr$ .

Then, for trichromatic vision, coordinates in the colour space are found by (Chittka 1992):

$$X_1 = \frac{\sqrt{3}}{2}(E_3 - E_1)$$

$$X_2 = E_2 - \frac{1}{2}(E_1 + E_3)$$

For tetrachromatic vision (They and Casas 2002):

$$X_1 = \frac{\sqrt{3}\sqrt{2}}{3}(E_3 - E_4)$$

$$X_2 = E_1 - \frac{1}{3}(E_2 + E_3 + E_4)$$

$$X_3 = \frac{2\sqrt{2}}{3}\left(\frac{1}{2}(E_3 + E_4) - E_2\right)$$

For a pentachromatic animal following the same vector length:

$$X_1 = \frac{5}{2\sqrt{2}\sqrt{5}}(E_2 - E_1)$$

$$X_2 = \frac{5\sqrt{2}}{2\sqrt{3}\sqrt{5}}\left(E_3 - \frac{E_1 + E_2}{2}\right)$$

$$X_3 = \frac{5\sqrt{3}}{4\sqrt{5}}\left(E_4 - \frac{E_1 + E_2 + E_3}{3}\right)$$

$$X_4 = E_5 - \frac{E_1 + E_2 + E_3 + E_4}{4}$$

## Value

$Qr_i$	Photoreceptor photon catch values after the von Kries transformation (see function $Qr$ ).
$E_i$	Photoreceptor output values. Values can vary from 0 to 1.
$X_i$	Coordinates in the colour space.
$\delta$	Euclidean distance to the origin of the colour space. It represents the conspicuousness of the stimulus (R) in relation to the background (Rb).

## Author(s)

Felipe M. Gawryszewski <f.gawry@gmail.com>

## References

- Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.
- Gawryszewski, F.M. 2018. Colour vision models: Some simulations, a general n-dimensional model, and the colourvision R package. *Ecology and Evolution*, 10.1002/ece3.4288.
- Pike, T.W. 2012. Generalised chromaticity diagrams for animals with n-chromatic colour vision. *Journal of Insect Behavior* 255: 277-286.
- They, M., and J. Casas. 2002. Predator and prey views of spider camouflage. *Nature* 415:133-133.

**See Also**

[CTTKhexagon](#), [CTTKhexagon3D](#), [photor](#), [RNLmodel](#), [EMmodel](#), [deltaS](#)

**Examples**

```
##Photoreceptor sensitivity curves
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

## Grey background
## with 10 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(10, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

## Reflectance data
## with a sigmoid spectrum and midpoint at 500nm
R<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)

## Run model
model<-CTTKmodel(photo=3, R=R, I=D65,
  Rb=Rb, C=C)

#plot
plot(model)
```

---

D65

*CIE Standard Illuminant D65 in quantum flux (umol/m2/s)*


---

**Description**

CIE Standard Illuminant D65. Datum has already been converted to quantum flux (umol/m2/s) and therefore can be used in colour vision models directly.

**Usage**

```
data("D65")
```

**Format**

A data frame with 107 observations on the following 2 variables.

l.nm a numeric vector

Standard.Illuminant.D65 a numeric vector

**Source**

<http://www.cie.co.at/>

**Examples**

```
data("D65")
plot(D65, type="l")
```

---

deltaS

*Chromaticity distances*

---

**Description**

Calculates a matrix with all possible pairwise comparison between stimulus reflectance spectra based on a given colour vision model output.

**Usage**

```
deltaS(model)
```

**Arguments**

model                      Output of a colour vision model.

**Value**

A matrix with pairwise chromaticity distances.

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**See Also**

[CTTKmodel](#), [RNLmodel](#), [EMmodel](#), [GENmodel](#)

**Examples**

```
##Photoreceptor sensitivity curves
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

## Grey background
## with 10 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(10, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

## Reflectance data
## with a sigmoid spectrum and midpoint at 500nm
R1<-logistic(x=seq(300,700,1), x0=450, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
```

```

R3<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1,R2[,2],R3[,2])

## Run model
model<-CTTKmodel(photo=3, R=R, I=D65,
  Rb=Rb, C=C)

#Chromaticity distances between R1, R2 and R3
deltaS(model)

```

---

EMline

*Endler and Mielke (2005) 1-D colour space*


---

### Description

Plots a colour space for dichromatic Endler and Mielke (2005) colour vision model.

### Usage

```

EMline(x,y=rep(0, length(x)), type="length",
  vnames=c("E1", "E2"),
  ylim="auto", xlim="auto",
  ann=FALSE, axes = FALSE, ...)

```

### Arguments

x	x-coordinate
y	y-coordinate
type	Whether the colour space should be built with a fixed vector length, or a fixed edge length (distance between vertices).
vnames	Vector names
ylim	see <a href="#">plot</a> function.
xlim	see <a href="#">plot</a> function.
ann	see <a href="#">par</a> function.
axes	see <a href="#">plot.default</a> function.
...	Other arguments passed to <a href="#">plot</a> .

### Details

The original model is available for tetrachromatic animals only. Colour space is built either with a vector length = 0.75 or a edge length =  $\sqrt{3/2}$ , to match the tetrahedron proposed by Endler and Mielke (2005).

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**References**

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

**See Also**

[EMtriangle](#), [EMtetrahedron](#), [EMmodel](#)

**Examples**

```
EMline(x=0.1, pch=16, col="red")
```

---

EMmodel

*Endler and Mielke (2005) colour vision model*

---

**Description**

Endler and Mielke (2005) colour vision model extended to animals with any number of photoreceptor types.

**Usage**

```
EMmodel(photo = ncol(C)-1, type="length", R, I, Rb, C,
         interpolate=TRUE, nm=seq(300,700,1))
```

**Arguments**

photo	Number of photoreceptor types. Model accepts any number of photoreceptor types ( $\geq 2$ ). For instance, dichromatic: photo=2; trichromatic: photo=3; tetrachromatic: photo=4, etc. Default gets number of photoreceptor types from C argument.
type	Whether the colour space should be built with a fixed vector length (type="length"), or a fixed edge length (distance between vertices; type="edge").
R	Reflectance of observed objects. A data frame with first column corresponding to wavelength values and following columns with reflectance values. R must be in the same scale as Rb (percentage or proportion).
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. Rb must be in the same scale as R (percentage or proportion).
C	Photoreceptor sensitivity curves, from lowest to longest lambda-max. A data frame: first column corresponding to wavelength values and following columns with photoreceptor sensitivity values (see function <a href="#">photor</a> ).

interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx.</a>
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx.</a>

### Details

The original model is available for tetrachromatic animals only. In colourvision, the model was extended to any number of photoreceptors types (see also Pike 2012 formula).

First, relative quantum catches are log-transformed:

$$f_i = \ln q_i$$

where  $q_i$  is the relative quantum catch of photoreceptor type  $i$ , given by [Qr](#). The model uses only relative output values, so that photoreceptor outputs are given by:

$$E_i = \frac{f_i}{\sum_{i=1}^n f_i}$$

For tetrachromatic vision (Endler and Mielke 2005):

$$X1 = \sqrt{\frac{3}{2}} \left( \frac{1 - 2E_2 - E_3 - E_1}{2} \right)$$

$$X2 = \frac{-1 + 3E_3 + E_1}{2\sqrt{2}}$$

$$X3 = E_1 - \frac{1}{4}$$

Tetrachromatic chromaticity diagram (tetrahedron) in Endler and Mielke (2005) has a vector of length = 0.75 and and edge length = sqrt(3/2). The chromaticity coordinates for other colour spaces may preserve either the same vector length or edge length.

For instance, for dichromatic vision coordinate (X1) in the colour space preserving the same vector length is found by:

$$X1 = \frac{3}{4}(E_2 - E_1)$$

Whereas for trichromatic vision coordinates (X1 and X2) are found by:

$$X1 = \frac{3\sqrt{3}}{8}(E_2 - E_1)$$

$$X2 = \frac{3}{4}\left(E_3 - \frac{E_2 + E_1}{2}\right)$$

### Value

Qr <sub>i</sub>	Photoreceptor photon catch values after the von Kries transformation (see function <a href="#">Qr</a> ).
E <sub>i</sub>	Photoreceptor outputs after conversion to relative values.
X <sub>i</sub>	Coordinates in the colour space.
deltaS	Euclidean distance to the origin of the colour space. It represents the conspicousness of the stimulus (R) in relation to the background (Rb).



**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

- Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.
- Pike, T.W. 2012. Generalised chromaticity diagrams for animals with n-chromatic colour vision. *Journal of Insect Behavior* 255: 277-286.

**See Also**

[EMline](#), [EMtriangle](#), [EMtetrahedron](#), [photor](#), [CTTKmodel](#), [RNLmodel](#), [GENmodel](#)

**Examples**

```
##Photoreceptor sensitivity curves
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

##Gray background
##with 7 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

##Reflectance data
## with a sigmoid spectrum and midpoint at 500nm and 550 nm
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1, R2[,2])
R[,2]<-R[,2]+10
R[,3]<-R[,3]+10

## Run model
model<-EMmodel(photo=3, type="edge",
               R=R, I=D65, Rb=Rb, C=C)

plot(model)
```

---

EMtetrahedron

*Endler and Mielke (2005) tetrahedron colour space*

---

**Description**

Plots Endler and Mielke (2005) tetrahedron colour space for tetrachromatic animals.

**Usage**

```
EMtetrahedron(x, y, z, s.col = "red", f.col = "black",
              vnames = c("u", "s", "m", "l"), type = "p",
              radius = 0.01, add = F, xlab = "",
              ylab = "", zlab = "", box = F, axes = F,
              ylim = c(-0.75, 0.75), xlim = c(-0.75, 0.75),
              zlim = c(-0.75, 0.75), aspect = T,
              mar = c(1, 1, 1, 1), vectors=FALSE, ...)
```

**Arguments**

x	x coordinate of points to be plotted
y	y coordinate of points to be plotted
z	z coordinate of points to be plotted
s.col	Colour to be used for plotted items. See <a href="#">plot3d</a> .
f.col	Colour of tetrahedron lines. See <a href="#">plot3d</a> .
vnames	Vector names.
type	see <a href="#">plot3d</a> function.
radius	see <a href="#">plot3d</a> function.
add	see <a href="#">plot3d</a> function.
xlab	see <a href="#">plot3d</a> function.
ylab	see <a href="#">plot3d</a> function.
zlab	see <a href="#">plot3d</a> function.
box	see <a href="#">plot3d</a> function.
axes	see <a href="#">plot3d</a> function.
ylim	see <a href="#">plot3d</a> function.
xlim	see <a href="#">plot3d</a> function.
zlim	see <a href="#">plot3d</a> function.
aspect	see <a href="#">plot3d</a> function.
mar	see <a href="#">plot3d</a> function.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
...	Other arguments passed to function <a href="#">plot3d</a> .

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**References**

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

**See Also**

[EMtriangle](#), [EMmodel](#)

**Examples**

```
## Not run:
library(rgl)
EMtetrahedron(x=0,y=0,z=0)

## End(Not run)
```

---

EMtriangle

*Endler and Mielke (2005) triangle colour space*


---

**Description**

Plots a triangle colour space for trichromatic Endler and Mielke (2005) colour vision model.

**Usage**

```
EMtriangle(x, y, type=c("length", "edge"), vnames=c("u", "s", "m"),
           ylim=c(-0.9, 0.9), xlim=c(-0.9, 0.9),
           pch=16, bty="n", yaxt="n", xaxt="n",
           col="black", asp=1, ann=FALSE, vectors=FALSE, ...)
```

**Arguments**

x	x-coordinate
y	y-coordinate
type	Whether the colour space should be built with a fixed vector length, or a fixed edge length (distance between vertices).
vnames	Vector names
ylim	see <a href="#">plot</a> function.
xlim	see <a href="#">plot</a> function.
pch	see <a href="#">par</a> function.
bty	see <a href="#">par</a> function.
yaxt	see <a href="#">par</a> function.
xaxt	see <a href="#">par</a> function.
col	see <a href="#">par</a> function.
asp	see <a href="#">plot</a> function.
ann	see <a href="#">par</a> function.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
...	Other arguments passed to <a href="#">plot</a> .

**Details**

The original model is available for tetrachromatic animals only. Trichromatic version is implemented in `colourvision` based on Pike (2012) formula. The triangle is built either with a vector length = 0.75 or a edge length =  $\sqrt{3}/2$ , to match the tetrahedron proposed by Endler and Mielke (2005). Doris Gomez derived a trichromatic version which is available in software AVICOL (Gomez, 2006) and was previously implemented here (`colouvision v0.1`).

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

- Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.
- Pike, T.W. 2012. Generalised chromaticity diagrams for animals with n-chromatic colour vision. *Journal of Insect Behavior* 255: 277-286.
- Gomez, D. 2006. AVICOL, a program to analyse spectrometric data. Last update october 2011. Free executable available at:  
<http://sites.google.com/site/avicolprogram/> or from the author at <dodogomez@yahoo.fr>

**See Also**

[EMtetrahedron](#), [EMmodel](#)

**Examples**

```
EMtriangle(x=0,y=0, type="length", pch=16, col="red")
```

---

energytoflux

*Irradiance from energy to quantum units.*

---

**Description**

Convert Irradiance datum from energy units (uW/cm2/nm) to quantum flux units (umol/m2/s)

**Usage**

```
energytoflux(datum)
```

**Arguments**

`datum` A data frame with first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in energy units (uW/cm2/nm).

**Value**

A data frame with first column corresponding to wavelength values and second column with irradiance values in  $\mu\text{mol}/\text{m}^2/\text{s}$ .

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

---

 GENmodel

*N-dimensional generic colour vision model*


---

**Description**

A flexible function to build colour vision models based on any number of photoreceptor types (Gawryszewski 2018).

**Usage**

```
GENmodel(photo=ncol(C)-1, type="length", length=NA, edge=NA,
          R, I, Rb=NA, C, vonKries = TRUE, func, unity=FALSE,
          recep.noise=FALSE, noise.given=TRUE, e=NA, v=NA, n=NA,
          interpolate=TRUE, nm=seq(300,700,1))
```

**Arguments**

photo	Number of photoreceptor types. Model accepts any number of photoreceptor types ( $\geq 2$ ). For instance, dichromatic: photo=2; trichromatic: photo=3; tetrachromatic: photo=4, etc. Default gets number of photoreceptor types from C argument.
type	Whether the colour space should be built with a fixed vector length (type="length"), or a fixed distance between vertices (type="edge"; e.g. Pike 2012 and Renoult et al. 2015).
length	Vector length used to construct the colour space. Used when type="length". Typically length=1.
edge	Edge length used to construct the colour space. Used when type="edge".
R	Reflectance of observed objects. A data frame with first column corresponding to wavelength values and following columns with reflectance values. R must be in the same scale as Rb.
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. Rb must be in the same scale as in R.

C	Photoreceptor sensitivity curves, from lowest to longest lambda-max. A data frame: first column corresponding to wavelength values and following columns with photoreceptor sensitivity values (see function <a href="#">photor</a> ).
vonKries	Whether the von Kries transformation should be applied to photoreceptor photon catches. Calculates the ratio between stimulus and background photoreceptor photon catches
func	Transformation of photoreceptors inputs. For instance, func=log for a ln-transformation.
unity	Whether sum of photoreceptor output should be normalized to 1, as in <a href="#">EMmodel</a>
recep.noise	Logical. Whether chromaticity distances should be calculated based on receptor noises.
noise.given	Logical. Whether receptor noise is provided (noise.given = TRUE) or calculated from photoreceptor relative abundances (noise.given = FALSE). Used when recep.noise=TRUE.
e	Receptor noise of each photoreceptor type. Used when recep.noise = TRUE and noise.given = TRUE
n	Relative number of each photoreceptor type in the retina. Used to calculate e when recep.noise = TRUE and noise.given = TRUE.
v	Noise-to-signal ratio of a single photoreceptor. Used to calculate e when recep.noise = TRUE and noise.given = TRUE.
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .

### Value

ei	Noise of photoreceptor channels. Calculated only when recep.noise=TRUE
Qri	Photoreceptor photon catch values from R. Relative Photoreceptor photon catches when vonKries=TRUE. See functions <a href="#">Q</a> and <a href="#">Qr</a> .
Ei	Photoreceptor outputs.
Xi	Stimulus colour locus coordinates in the colour space
deltaS	Euclidean distance to the origin of the colour space. It represents the conspicuousness of the stimulus (R) in relation to the background (Rb)

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

### References

- Gawryszewski, F.M. 2018. Colour vision models: Some simulations, a general n-dimensional model, and the colourvision R package. *Ecology and Evolution*, 10.1002/ece3.4288.
- Pike, T.W. 2012. Generalised chromaticity diagrams for animals with n-chromatic colour vision. *Journal of Insect Behavior* 255: 277-286.
- Renoult, J. P., A. Kelber, and H. M. Schaefer. 2015. Colour spaces in ecology and evolutionary biology. *Biol Rev Camb Philos Soc*, doi: 10.1111/brv.12230.

**See Also**

[Q](#), [Qr](#), [CTTKmodel](#), [EMmodel](#), [RNLmodel](#), [colour\\_space](#)

**Examples**

```
#A trichromatic colour vision model based on Endler and Mielke (2005)

##Photoreceptor sensitivity curves
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

##Gray background
##with 7 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

##Reflectance data
## with a sigmoid spectrum and midpoint at 500nm and 550 nm
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1, R2[,2])
R[,2]<-R[,2]+10
R[,3]<-R[,3]+10

## Run model
model<-GENmodel(length=0.75, R=R, I=D65, Rb=Rb, C=C,
                func=log, unity=TRUE)

plot(model)
```

---

GENplot

*Generic model colour space 2D and 1D plot*

---

**Description**

Plots models based on the GENmodel() function for trichromatic and dichromatic animals.

**Usage**

```
GENplot(model, photo, col.names=c("X1","X2"),
        vectors=TRUE, vnames=TRUE, vsize="auto",
        ylab="y", xlab="x", xlim="auto", ylim="auto", asp=1, ...)
```

**Arguments**

model	Output of a colour vision model.
photo	Number of photoreceptor types.
col.names	Column names to be plotted.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
vnames	Whether vector names should be plotted.
vsize	Length of vectors to be plotted. Default calculates length automatically.
ylab	y-axis range. Default calculates range automatically. See <a href="#">par</a> function.
xlab	x-axis range. Default calculates range automatically. See <a href="#">par</a> function.
xlim	see <a href="#">par</a> function.
ylim	see <a href="#">par</a> function.
asp	see <a href="#">plot</a> function.
...	Other arguments passed to <a href="#">plot</a> function.

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**See Also**

[CTTKhexagon](#), [CTTKhexagon3D](#), [EMtriangle](#), [EMtetrahedron](#), [RNLplot](#), [RNLplot3d](#), [GENplot3d](#), [plot.colourvision](#), [plot3d.colourvision](#)

---

GENplot3d

*Generic model colour space 3D plot*

---

**Description**

Plots models based on the `GENmodel()` function for tetrachromatic animals.

**Usage**

```
GENplot3d(model, col.names=c("X1","X2","X3"),
          vectors=TRUE, vnames=TRUE, vsize="auto",
          xlab="x", ylab="y", zlab="z",
          xlim="auto", ylim="auto", zlim="auto", asp=1, ...)
```



**Arguments**

model	Output of a colour vision model.
col.names	Column names to be plotted.
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
vnames	Whether vector names should be plotted.
vsize	Length of vectors to be plotted. Default calculates length automatically.
xlab	see <a href="#">par3d</a> function.
ylab	see <a href="#">par3d</a> function.
zlab	see <a href="#">par3d</a> function.
xlim	x-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
ylim	y-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
zlim	z-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
asp	see <a href="#">plot3d</a> function.
...	Other arguments passed to <a href="#">plot3d</a> function.

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**See Also**

[CTTKhexagon](#), [CTTKhexagon3D](#), [EMtriangle](#), [EMtetrahedron](#), [RNLplot](#), [RNLplot3d](#), [GENplot](#), [plot.colourvision](#), [plot3d.colourvision](#)

---

logistic

*Logistic curve*

---

**Description**

Generates a logistic curve.

**Usage**

```
logistic(x = seq(300, 700, 1), x0, L, k)
```

**Arguments**

x	Range.
x0	Midpoint value.
L	Maximum value.
k	Steepness of the curve

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

[https://en.wikipedia.org/wiki/Logistic\\_function](https://en.wikipedia.org/wiki/Logistic_function)

**Examples**

```
l<-logistic(x=seq(300,700,1), x0=650, L=50, k=0.04)
plot(l, type="l")
```

---

noise\_e

*Receptor noise*

---

**Description**

Receptor noise either provided by the user or based on noise-to-signal ratio of a single photoreceptor and the relative abundance of photoreceptor types in the retina. This function is used internally in Receptor Noise Limited models.

**Usage**

```
noise_e(noise, e, v, n)
```

**Arguments**

noise	Logical. Whether receptor noise is provided (noise = TRUE) or calculated from photoreceptor relative abundances (noise = FALSE)
e	Receptor noise of each photoreceptor type. It is used when noise = TRUE
v	Noise-to-signal ratio of a single photoreceptor.
n	Relative abundance of the photoreceptor in the retina.

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

Vorobyev, M., and D. Osorio. 1998. Receptor noise as a determinant of colour thresholds. *Proceedings of the Royal Society B* 265:351-358.

**See Also**

[RNLmodel](#), [RNLthres](#), [GENmodel](#), [colour\\_space](#)

---

photor	<i>Photoreceptor sensitivity spectra.</i>
--------	---

---

### Description

Generates photoreceptor sensitivity spectra based on lambda-max values.

### Usage

```
photor(lambda.max, lambda = seq(300, 700, 1), beta.band = FALSE)
```

### Arguments

lambda.max	Vector with photoreceptor wavelength at maximum sensitivity values, in increasing order.
lambda	Range and interval to calculate the sensitivity curves.
beta.band	Logical. Whether or not to include a beta-band in the sensitivity curve.

### Value

A data frame with first column corresponding to wavelength values and following columns with photoreceptor sensitivity values

### Author(s)

Felipe M. Gawryszewski <f.gawry@gmail.com>

### References

Govardovskii, V. I., N. Fyhrquist, T. Reuter, D. G. Kuzmin, and K. Donner. 2000. In search of the visual pigment template. *Vis. Neurosci.* 17:509-528.

### See Also

[CTTKmodel](#), [EMmodel](#), [RNLmodel](#), [RNLthres](#)

### Examples

```
## Generates photoreceptor sensitivity
## values with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

plot(C[,2]~C[,1], type="l", col="violet")
lines(C[,3]~C[,1], type="l", col="blue")
lines(C[,4]~C[,1], type="l", col="green")
```

---

plot.colourvision      *Plot colour vision models into chromaticity diagrams*

---

### Description

Plotting method for objects of class colourvision. Plotting method for animals with two or three photoreceptor types.

### Usage

```
## S3 method for class 'colourvision'
plot(x, ...)
```

### Arguments

x                      Object of class "colourvision".

...                    Additional arguments passed to the plot function. See [CTTKhexagon](#) for Chittka (1992) model ([CTTKmodel](#)) plotting arguments; [EMtriangle](#) and [EMline](#) for Endler and Mielke (2005) model ([EMmodel](#)) plotting arguments; [RNLplot](#) for RNL plotting arguments; and [GENplot](#) for generic model ([GENmodel](#)) plotting arguments.

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

### References

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

### See Also

[plot3d.colourvision](#), [EMtriangle](#), [CTTKhexagon](#), [EMmodel](#), [CTTKmodel](#), [RNLmodel](#), [RNLthres](#)

### Examples

```
#trichromatic
##Photoreceptor sensitivity curves
C<-photor(lambda.max=c(350,450,550))

##Gray background
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")
```

```

##Reflectance data
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1[,2]<-R1[,2]+10

##Run models
model<-EMmodel(photo=3,
               R=R1, I=D65, Rb=Rb, C=C)
plot(model)

model<-CTTKmodel(photo=3,
                 R=R1, I=D65, Rb=Rb, C=C)
plot(model)

model<-RNLMmodel(model="log", photo=3,
                 R1=R1, I=D65, Rb=Rb, C=C, noise=TRUE, e=c(0.13, 0.06, 0.12))
plot(model)

#colour threshold
model<-RNLMthres(photo=3, I=D65, Rb=Rb, C=C,
                 noise=TRUE, e=c(0.13, 0.06, 0.12))
plot(model)

#dichromatic
##Photoreceptor sensitivity curves
C<-photor(lambda.max=c(400,550))

##Run models
model<-EMmodel(photo=2,
               R=R1, I=D65, Rb=Rb, C=C)
plot(model)

model<-EMmodel(photo=2, type="edge",
               R=R1, I=D65, Rb=Rb, C=C)
plot(model)

model<-CTTKmodel(photo=2,
                 R=R1, I=D65, Rb=Rb, C=C)
plot(model)

model<-RNLMmodel(model="log", photo=2,
                 R1=R1, I=D65, Rb=Rb, C=C, noise=TRUE, e=c(0.13, 0.06))
plot(model)

#colour threshold
model<-RNLMthres(photo=2, I=D65, Rb=Rb, C=C,
                 noise=TRUE, e=c(0.13, 0.06))
plot(model)

```

**Description**

'plot3d' method for objects of class colourvision. Plotting method for animals with four photoreceptor types.

**Usage**

```
## S3 method for class 'colourvision'
plot3d(x, ...)
```

**Arguments**

x                    Object of class "colourvision".

...                   Additional arguments passed to the plot3d function. See [CTTKhexagon3D](#) for Chittka (1992) model ([CTTKmodel](#)) plotting arguments; [EMtetrahedron](#) for Endler and Mielke (2005) model ([EMmodel](#)) plotting arguments; [RNLplot3d](#) for RNL plotting arguments; and [GENplot3d](#) for generic model ([GENmodel](#)) plotting arguments.

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

Thery, M., and J. Casas. 2002. Predator and prey views of spider camouflage. *Nature* 415:133-133.

**See Also**

[plot.colourvision](#), [EMtetrahedron](#), [CTTKhexagon3D](#), [EMmodel](#), [CTTKmodel](#), [RNLmodel](#)

**Examples**

```
## Not run:
##Photoreceptor sensitivity curves
C<-photor(lambda.max=c(350,420,490,560))

##Gray background
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

##Reflectance data
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1[,2]<-R1[,2]+10
```

```
##Run models
model<-EMmodel(photo=4,
               R=R1, I=D65, Rb=Rb, C=C)
plot3d(model)

model<-CTTKmodel(photo=4,
                 R=R1, I=D65, Rb=Rb, C=C)
plot3d(model)

model<-RNLmodel(photo=4, model="log",
                 R1=R1, I=D65, Rb=Rb, C=C, noise=TRUE, e=c(0.13, 0.06, 0.12, 0.07))
plot3d(model, ylim=c(-6,6), xlim=c(-6,6))

## End(Not run)
```

---

Q *Total photon capture*

---

### Description

Total photoreceptor photon capture for a given irradiance, reflectance and photoreceptor sensitivity curve. This function is used internally in colour vision models.

### Usage

```
Q(R,I,C,interpolate,nm)
```

### Arguments

R	Reflectance of observed object. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values.
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
C	Photoreceptor sensitivity curve. A data frame with two columns only: first column corresponding to wavelength values and second column with photoreceptor absorbance values.
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .

### Value

Gives the total photoreceptor photon capture.

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

Backhaus, W., and R. Menzel. 1987. Color distance derived from a receptor model of color vision in the honeybee. *Biological Cybernetics* 55:321-331.

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

Vorobyev, M., and D. Osorio. 1998. Receptor noise as a determinant of colour thresholds. *Proceedings of the Royal Society B* 265:351-358.

**See Also**

[Qr](#), [CTTKmodel](#), [EMmodel](#), [RNLmodel](#), [RNLthres](#), [GENmodel](#)

---

Qr *Photoreceptor relative quantum catch*

---

**Description**

von Kries transformation. Photoreceptors are assumed to be adapted to the background. This function is used internally in colour vision models.

**Usage**

Qr(R, I, Rb, C, interpolate, nm)

**Arguments**

R	Reflectance of observed object. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values.
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. Photoreceptors are assumed to be adapted to the background reflectance.
C	Photoreceptor sensitivity curve. A data frame with two columns only: first column corresponding to wavelength values and second column with photoreceptor absorbance values.
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .



**Details**

For the von Kries transformation, first the quantum catches of the observed reflectance and the environmental background are calculated (see [Q](#)). Then:

$$qi = \frac{Q_i}{Q_{bi}}$$

where  $Q_i$  is the quantum catch arising from the observed object and  $Q_{bi}$  is the quantum catch from the background, for each one of the photoreceptor types (i).

**Value**

Photoreceptor relative quantum catch.

**Author(s)**

Felipe M. Gawryszewski <f.gawry@gmail.com>

**References**

Backhaus, W. 1991. Color opponent coding in the visual system of the honeybee. *Vision Res* 31:1381-1397.

Chittka, L. 1992. The colour hexagon: a chromaticity diagram based on photoreceptor excitations as a generalized representation of colour opponency. *J Comp Physiol A* 170:533-543.

Endler, J. A., and P. Mielke. 2005. Comparing entire colour patterns as birds see them. *Biol J Linn Soc* 86:405-431.

Vorobyev, M., and D. Osorio. 1998. Receptor noise as a determinant of colour thresholds. *Proceedings of the Royal Society B* 265:351-358.

**See Also**

[CTTKmodel](#), [EMmodel](#), [RNLmodel](#), [RNLthres](#), [GENmodel](#)

---

radarplot

*Radar plot*

---

**Description**

Plots quantum catches or E-values (photoreceptor outputs) into a radar plot.

**Usage**

```
radarplot(model, item=c("Qr", "E"), item.labels=FALSE, item.lwd=1,
           border=NULL, radar.lwd=1, radar.col="grey",
           length="auto", xlim="auto", ylim="auto",
           xlab="", ylab="", asp=1, add = FALSE, ...)
```

**Arguments**

<code>model</code>	Output of a colour vision model.
<code>item</code>	Whether photoreceptor inputs (Qr) or outputs (E) should be plotted.
<code>item.labels</code>	Logical. Whether vector names should be plotted.
<code>item.lwd</code>	Width of lines connecting item values.
<code>border</code>	Colour of lines connecting item values. See <a href="#">polygon</a> .
<code>radar.lwd</code>	Width of lines representing item vectors.
<code>radar.col</code>	Colour of lines representing item vectors.
<code>length</code>	Length of item vectors. Default calculates length automatically.
<code>xlim</code>	x-axis range. Default calculates range automatically. See <a href="#">plot</a> function.
<code>ylim</code>	y-axis range. Default calculates range automatically. See <a href="#">plot</a> function.
<code>xlab</code>	see <a href="#">par</a> function.
<code>ylab</code>	see <a href="#">par</a> function.
<code>asp</code>	see <a href="#">par</a> function.
<code>add</code>	Logical. Whether data should be added to an existing plot.
<code>...</code>	Other arguments passed to <a href="#">plot</a> .

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**Examples**

```
##Photoreceptor sensitivity curves
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

## Grey background
## with 10 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(10, length(300:700)))

## Read CIE D65 standard illuminant
data("D65")

## Reflectance data
## with a sigmoid spectrum and midpoint at 500nm
R1<-logistic(x=seq(300,700,1), x0=450, L=50, k=0.04)
R2<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R3<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R<-cbind(R1,R2[,2],R3[,2])

## Run model
model<-CTTKmodel(photo=3, R=R, I=D65,
  Rb=Rb, C=C)

#Radarplot
radarplot(model, border=c("violet", "red", "blue"), item="E", item.labels=TRUE)
```

---

Rb *Brazilian savannah background reflectance spectrum.*

---

### Description

Brazilian savannah background reflectance spectrum calculated by the average reflectance of leaf, leaf litter, tree bark and twigs.

### Usage

```
data("Rb")
```

### Format

A data frame with 401 observations on the following 2 variables.

X300.700 a numeric vector

cerrado a numeric vector

### Source

Gawryszewski, F. M., and P. C. Motta. 2012. Colouration of the orb-web spider *Gasteracantha cancriformis* does not increase its foraging success. *Ethol Ecol Evol* 24:23-38.

---

RNLmodel *Receptor Noise Limited Models (Vorobyev & Osorio 1998)*

---

### Description

Receptor noise limited colour vision models (Vorobyev & Osorio 1998; Vorobyev et al. 1998) extended to any number of photoreceptor types.

### Usage

```
RNLmodel(model = c("linear", "log"), photo=ncol(C)-1,
          R1, R2=Rb, Rb, I, C,
          noise = FALSE, v=NA, n=NA, e=NA,
          interpolate = TRUE, nm = seq(300, 700, 1),
          coord="colourvision")
```

**Arguments**

model	Linear ("linear"; Vorobyev & Osorio, 1998), or log-linear ("log"; Vorobyev et al. 1998) RNLmodel version. model="log" is preferred. model="linear" can be used only if comparison is to be made between two very similar colours.
photo	Number of photoreceptor types. Model accepts any number of photoreceptor types ( $\geq 2$ ). For instance, dichromatic: photo=2; trichromatic: photo=3; tetrachromatic: photo=4, etc. Default gets number of photoreceptor types from C argument.
R1	Reflectance of observed objects. A data frame with first column corresponding to wavelength values and following columns with reflectance values. R1 must be in the same scale as R2 and Rb(percentage or proportion).
R2	Reflectance to be compared against R1. R2=Rb if comparison is to be made against the background. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. R2 must be in the same scale as R1 and Rb(percentage or proportion).
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values. Rb must be in the same scale as R1 and R2 (percentage or proportion).
I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
C	Photoreceptor sensitivity curves, from lowest to longest lambda-max. A data frame: first column corresponding to wavelength values and following columns with photoreceptor sensitivity values (see function <a href="#">photor</a> ).
noise	Logical. Whether receptor noise is provided (noise = TRUE) or calculated from photoreceptor relative abundances (noise = FALSE).
e	Receptor noise of each photoreceptor type. Used when noise = TRUE
n	Relative number of each photoreceptor type in the retina. Usually increases with lambda-max. Used to calculate e when noise = FALSE.
v	Noise-to-signal ratio of a single photoreceptor. Used to calculate e when noise = FALSE.
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .
coord	Whether colour locus coordinates should be calculated by the method (coord="colourvision") by Gawryszewski (under review), or by alternative (coord="alternative"; available for 2-4 photoreceptor types only) methods (Hempel de Ibarra et al. 2001; Renoult et al. 2017).

**Details**

The receptor noise limited model was originally developed to calculate  $\Delta S$  between two reflectance curves directly, without finding colour locus coordinates (e.g.  $x, y$ ; Vorobyev and Osorio 1998).

This function uses later formulae to find colour loci in a chromaticity diagram (similarly to Hempel de Ibarra et al. 2001; Renoult et al. 2015).

In lack of a direct measurement, receptor noise ( $e_i$ ) can be estimated by the relative abundance of photoreceptor types in the retina, and a measurement of a single photoreceptor noise-to-signal ratio:

$$e_i = \frac{\nu}{\sqrt{\eta_i}}$$

where  $\nu$  is the noise-to-signal ratio of a single photoreceptor, and  $\eta$  is the relative abundance of photoreceptor  $i$  in the retina. Alternatively, noise may be dependent of the intensity, but this possibility is not implement in colourvision yet. Noise dependent of intensity usually holds for low light conditions only (Vorobyev et al. 1998).

### Value

<code>ei</code>	Noise of photoreceptor channels.
<code>Qri_R1</code>	Photoreceptor photon catch values from R1, after the von Kries transformation (see function <a href="#">Qr</a> ).
<code>Qri_R2</code>	Photoreceptor photon catch values from R2, after the von Kries transformation (see function <a href="#">Qr</a> ).
<code>Ei_R1</code>	Photoreceptor outputs from the stimulus (R1)
<code>Ei_R2</code>	Photoreceptor outputs from R2
<code>Xi_R1</code>	Coordinates in the colour space for R1
<code>Xi_R2</code>	Coordinates in the colour space for R2. Equals zero when R1=Rb
<code>deltaS</code>	Euclidean distance from R1 to R2. It represents the conspicuousness of the stimulus (R1) in relation to the background when R1=Rb.

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

### References

- Hempel de Ibarra, N., M. Giurfa, and M. Vorobyev. 2001. Detection of coloured patterns by honeybees through chromatic and achromatic cues. *J Comp Physiol A* 187:215-224.
- Renoult, J. P., A. Kelber, and H. M. Schaefer. 2017. Colour spaces in ecology and evolutionary biology. *Biol Rev Camb Philos Soc*, doi: 10.1111/brv.12230
- Vorobyev, M., and D. Osorio. 1998. Receptor noise as a determinant of colour thresholds. *Proceedings of the Royal Society B* 265:351-358.
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### See Also

[photor](#), [RNLthres](#), [CTTKmodel](#), [EMmodel](#), [GENmodel](#)

**Examples**

```

#1
## Photoreceptor sensitivity spectra
##with lambda max at 350nm, 450nm and 550nm:
C<-photor(lambda.max=c(350,450,550))

##Grey background
##with 7 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant:
data("D65")

##Reflectance data of R1 and R2
R1.1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1.2<-logistic(x=seq(300,700,1), x0=400, L=50, k=0.04)
w<-R1.1[,1]
R1.1<-R1.1[,2]+10
R1.2<-R1.2[,2]+10
R1<-data.frame(w=w, R1.1=R1.1, R1.2=R1.2)

R2<-logistic(x=seq(300,700,1), x0=550, L=50, k=0.04)
R2[,2]<-R2[,2]+10

## Run model
model<-RNLmodel(photo=3, model="log",
                R1=R1, R2=R2, Rb=Rb, I=D65, C=C,
                noise=TRUE, e = c(0.13, 0.06, 0.12))

#plot
plot(model)

#2
##Pentachromatic animal
## Photoreceptor sensitivity spectra
##with lambda max at 350,400,450,500,and 550nm:
C<-photor(lambda.max=c(350,400,450,500,550))

##Grey background
##with 7 percent reflectance from 300 to 700nm:
Rb <- data.frame(300:700, rep(7, length(300:700)))

## Read CIE D65 standard illuminant:
data("D65")

##Reflectance data of R1
R1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1[,2]<-R1[,2]+10

#RNL model
RNLmodel(photo=5, model="log",
          R1=R1, R2=Rb, Rb=Rb, I=D65, C=C,

```

```
noise=TRUE, e = c(0.13, 0.06, 0.12, 0.07, 0.08))
```

---

RNLplot

*Receptor noise limited model 2D and 1D plot*


---

### Description

Plots receptor noise limited model (RNL) for trichromatic and dichromatic animals.

### Usage

```
RNLplot(model, photo, item="R1",
         vectors=TRUE, vnames=TRUE, vsize="auto",
         xlab="x", ylab="y", xlim="auto", ylim="auto", asp=1, ...)
```

### Arguments

model	Output of a colour vision model.
photo	Number of photoreceptor types.
item	Model output item to be plotted. Default plots stimulus data. See <a href="#">RNLmodel</a> .
vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
vnames	Whether vector names should be plotted.
vsize	Length of vectors to be plotted. Default calculates length automatically.
xlab	x-axis range. Default calculates range automatically. See <a href="#">par</a> function.
ylab	y-axis range. Default calculates range automatically. See <a href="#">par</a> function.
xlim	see <a href="#">par</a> function. Default calculates xlim automatically.
ylim	see <a href="#">par</a> function. Default calculates ylim automatically.
asp	see <a href="#">plot</a> function.
...	Other arguments passed to <a href="#">plot</a> function.

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

### See Also

[CTTKhexagon](#), [CTTKhexagon3D](#), [EMtriangle](#), [EMtetrahedron](#), [RNLplot3d](#), [plot.colourvision](#), [plot3d.colourvision](#)

**Examples**

```

#dichromat
C<-photor(lambda.max=c(450,550))
Rb <- data.frame(300:700, rep(7, length(300:700)))
data("D65")
R1.1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1.2<-logistic(x=seq(300,700,1), x0=400, L=50, k=0.04)
w<-R1.1[,1]
R1.1<-R1.1[,2]+10
R1.2<-R1.2[,2]+10
R1<-data.frame(w=w, R1.1=R1.1, R1.2=R1.2)
model<-RNLmodel(model="log",
                R1=R1, Rb=Rb, I=D65, C=C,
                noise=TRUE, e = c(0.13, 0.06))
plot(model)

#trichromat
C<-photor(lambda.max=c(350,450,550))
Rb <- data.frame(300:700, rep(7, length(300:700)))
data("D65")
R1.1<-logistic(x=seq(300,700,1), x0=500, L=50, k=0.04)
R1.2<-logistic(x=seq(300,700,1), x0=400, L=50, k=0.04)
w<-R1.1[,1]
R1.1<-R1.1[,2]+10
R1.2<-R1.2[,2]+10
R1<-data.frame(w=w, R1.1=R1.1, R1.2=R1.2)
model<-RNLmodel(model="log",
                R1=R1, Rb=Rb, I=D65, C=C,
                noise=TRUE, e = c(0.13, 0.06, 0.12))
plot(model)

```

---

RNLplot3d

*Receptor noise limited model 3D plot*


---

**Description**

Plots receptor noise limited model (RNL) for tetrachromatic animals.

**Usage**

```

RNLplot3d(model, item="R1",
          vectors=TRUE, vnames=TRUE, vsize="auto",
          xlab="x", ylab="y", zlab="z",
          xlim="auto", ylim="auto", zlim="auto", asp=1, ...)

```

**Arguments**

**model**                    Output of a colour vision model.

**item**                    Model output item to be plotted. Default plots stimulus data. See [RNLmodel](#).



vectors	Whether vectors representing direction of photoreceptor outputs should be plotted.
vnames	Whether vector names should be plotted.
vsize	Length of vectors to be plotted. Default calculates length automatically.
xlab	see <a href="#">par3d</a> function.
ylab	see <a href="#">par3d</a> function.
zlab	see <a href="#">par3d</a> function.
xlim	x-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
ylim	y-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
zlim	z-axis range. Default calculates range automatically. See <a href="#">par3d</a> function.
asp	see <a href="#">plot3d</a> function.
...	Other arguments passed to <a href="#">plot3d</a> function.

**Author(s)**

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

**See Also**

[CTTKhexagon](#), [CTTKhexagon3D](#), [EMtriangle](#), [EMtetrahedron](#), [RNLplot](#), [plot.colourvision](#), [plot3d.colourvision](#)

---

RNLthres	<i>Colour thresholds based on the Receptor Noise Limited Model (Vorobyev &amp; Osorio 1998).</i>
----------	--

---

**Description**

Colour thresholds based on receptor noise for any number of photoreceptor types (Vorobyev & Osorio 1998).

**Usage**

```
RNLthres(photo=ncol(C)-1, Rb, I, C, noise=TRUE, v=NA, n=NA, e=NA,
          interpolate=TRUE, nm=seq(300,700,1))
```

**Arguments**

photo	Number of photoreceptor types. Model accepts any number of photoreceptor types ( $\geq 2$ ). For instance, dichromatic: photo=2; trichromatic: photo=3; tetrachromatic: photo=4, etc. Default gets number of photoreceptor types from C argument.
Rb	Background reflectance. A data frame with two columns only: first column corresponding to wavelength values and second column with reflectance values.

I	Irradiance spectrum. A data frame with two columns only: first column corresponding to wavelength values and second column with irradiance values. Irradiance values must be in quantum flux units.
C	Photoreceptor sensitivity curves, from lowest to longest lambda-max. A data frame: first column corresponding to wavelength values and following columns with photoreceptor sensitivity values (see function <a href="#">photor</a> ).
noise	Logical. Whether receptor noise is provided (noise = TRUE) or calculated from photoreceptor relative abundances (noise = FALSE).
e	Receptor noise of each photoreceptor type. Used when noise = TRUE
n	Relative number of each photoreceptor type in the retina. Usually increases with lambda-max. Used to calculate e when noise = FALSE.
v	Noise-to-signal ratio of a single photoreceptor. Used to calculate e when noise = FALSE.
interpolate	Whether data files should be interpolated before further calculations. See <a href="#">approx</a> .
nm	A sequence of numeric values specifying where interpolation is to take place. See <a href="#">approx</a> .

### Details

Colour thresholds based on receptor noise limited model as in Vorobyev and Osorio (1998). In lack of a direct measurement, receptor noise ( $e_i$ ) can be estimated by the relative abundance of photoreceptor types in the retina, and a measurement of a single photoreceptor noise-to-signal ratio:

$$e_i = \frac{\nu}{\sqrt{\eta_i}}$$

where  $\nu$  is the noise-to-signal ratio of a single photoreceptor, and  $\eta$  is the relative abundance of photoreceptor  $i$  in the retina. Alternatively, noise may be dependent of the intensity, but this possibility is not implement in `colourvision` yet. Noise dependent of intensity usually holds for low light conditions only (Vorobyev et al. 1998).

### Value

A data.frame with the following columns:

nm	Wavelength in nm.
T	Colour threshold value.
S	Log of sensitivity value (inverse of threshold).

### Author(s)

Felipe M. Gawryszewski <[f.gawry@gmail.com](mailto:f.gawry@gmail.com)>

### References

Vorobyev, M., and D. Osorio. 1998. Receptor noise as a determinant of colour thresholds. *Proceedings of the Royal Society B* 265:351-358.

**See Also**

[photor](#), [RNLmodel](#)

**Examples**

```
###Bee photoreceptors normalized to max=1.
data("bee")
C<-bee
C[,2]<-C[,2]/max(C[,2])
C[,3]<-C[,3]/max(C[,3])
C[,4]<-C[,4]/max(C[,4])

##Grey background:
Rb <- data.frame(300:700, rep(0.1, length(300:700)))

## CIE D65 illuminant:
data("D65")

#Thresholds
thres<-RNLthres(photo=3, Rb=Rb, I=D65, C=C,
               noise=TRUE, e = c(0.13, 0.06, 0.12))

plot(thres)
```

---

spec.denoise

*Smooth function for reflectance spectra.*

---

**Description**

Applies a [smooth.spline](#) for data frame containing spectrometric data.

**Usage**

```
spec.denoise(specfiles, spar = 0.7, ...)
```

**Arguments**

specfiles	A data frame with first column representing wavelength values and following columns with reflectance data.
spar	see <a href="#">smooth.spline</a> . Smoothing parameter, typically (but not necessarily) in (0,1].
...	Other arguments passed to function <a href="#">smooth.spline</a> .

**Value**

A data frame with first column representing wavelength values and following columns with reflectance data.

**Author(s)**

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