Package ‘visualFields’

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Type Package

Title Statistical Methods for Visual Fields

Description A collection of tools for analyzing the field of vision. It provides a framework for development and use of innovative methods for visualization, statistical analysis, and clinical interpretation of visual-field loss and its change over time. It is intended to be a tool for collaborative research.

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`visualFields-package` *Statistical methods for visual fields*

Description

This is a collection of tools for analyzing the field of vision. It provides a framework for the development and use of innovative methods for visualization, statistical analysis, and clinical interpretation of visual-field loss and its change over time. `visualFields` is intended to be a tool for collaborative research

Author(s)

Ivan Marin-Franch

References

[1] Marín-Franch I & Swanson WH. The visualFields package: A tool for analysis and visualization of visual fields. Journal of Vision, 2013, 13(4):10, 1-12

[2] Turpin A, Artes PH, & McKendrick AM. The Open Perimetry Interface: An enabling tool for clinical visual psychophysics. Journal of Vision, 2012, 12(11):22, 21–25

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See Also

`OPI`, the Open Perimetry Initiative http://people.eng.unimelb.edu.au/aturpin/opi/index.html

---

agecalc *Calculates age*

Description

Tool to calculate ages from date of birth and date of test, etc

Usage

```
agecalc( from, to, daysyear = NULL )
```

Arguments

`from`	date from
`to`	date to
`daysyear`	if `NULL`, calculates real age. If informed, then calculates year based on the number of days per year (e.g. 362.25)

Value

returns age in years

Author(s)

Ivan Marin-Franch

Examples

```
agecalc( "1977-01-31", "2014-01-30" )
```

ageLinearModel *linear model for age effect on visual sensitivity*

Description

calculates the linear model to account for mean age effect on visual sensitivity at each location from a sample of controls subjects

Usage

```
ageLinearModel( vf, smooth = TRUE, smoothFunction = quad2Dfit )
```

Arguments

`vf`	a `vf` object. It needs to be in a specific format
`smooth`	whether to use a function to smooth the results or not. Default is `TRUE`
`smoothFunction`	If `smooth` is `TRUE`, the function to use for smoothing. Default is `quad2Dfit`, a 2D quadratic fit to resulting data. This function is not really a smoothing procedure, but a parametric fit

Details

The function obtains for each location a regression line of sensitivity threshold on age. The `vf` object may contain data for many visits of many subjects. The number of visits per subject can be variable and hence, to account for that, weighted least-squares linear regression is performed in which the weights for is the inverse of the number of visits for the subject. By default, the slopes and intercepts are "smoothed" by fitting a 2-dimensional quadratic fit, as in [1]. Other `smoothFunctions` can be defined instead using other type of parametric or non-parametric fits. The 2-dimensional quadratic fit has been found to be innapropriate for the stimulus used in frequency-doubling perimetry (FDP) [2].

All the data passed to the function must belong to the same perimeter `tperimetry`, the same pattern of locations `talgorithm`, and the same presentation algorithm `tpattern`.

Value

returns a table with intercepts and slopes modelling age-related mean sensitivity change.

Author(s)

Ivan Marin-Franch

References

[1] A. Heijl, G. Lindgren, and J. Olsson. *A package for the statistical analysis of visual fields*. Documenta Ophthalmologica Proceedings Series, 49, 1987

[2] A. J. Anderson, C. A. Johnson, M. Fingeret, J. L. Keltner, P. G. D. Spry, M. Wall, and J. S. Werner. *Characteristics of the normative database for the humphrey matrix perimeter*. Investigative Ophthalmology and Visual Science, 46, 2005

See Also

sdnv, locperc, quad2Dfit

---

bebie *Bebie curve*

Description

Plots Bebie rank TD curve

Usage

```
bebie( tdr, type = "conventional", diff = TRUE, percentiles = TRUE,
       correction = TRUE, txtfont = "serif", pointsize = 12, cex = 1 )
```

Arguments

tdr	a vf object with the rank TD curve
type	whether to use a conventional way to plot the rank TD curve or ghrank type where the vf object passed is the reconstructed within-normal TD rank curve. Default is conventional
diff	add absolute td values or differences from mean normal. Default is TRUE
percentiles	add percentile lines. Default is TRUE
correction	add ranked TD line after correcting for general height difference. Default is TRUE
txtfont	font of the text with visual-sensitivity values. Default is serif
pointsize	size of the text with visual-sensitivity values. Default is 12
cex	a numerical value giving the amount by which plotting text and symbols should be magnified relative to the default, which is 1

Value

returns a graph with the Bebie rank TD curve (also known as the cumulative defect curve [1]) if the option diff is set to FALSE. If the option diff is set to true, then it returns the difference between the subject's rank curve and the mean normal curve. To use this option (and the options with percentile = TRUE), the tables nvtdrank, perctdrank, and perctdrankadj must exist in the nv-object, for the perimeter tperimetry, the pattern of locations talgorithm, and thepresentation algorithm tpattern. See nvsapdefault to see the structure the tables must have

Author(s)

Ivan Marin-Franch

References

[1] H. Bebie, J. Flammer, and T. Bebie. *The cumulative defect curve: separation of local and diffuse components of visual field damage*. Graefe's Archive Clinical Experimental Ophthalmology, 227, 1989

Examples

```
# conventional "Bebie" rank TD curve
td <- tdval( vf91016right[15,] )
tdr <- tdrank( td )
bebie( tdr )

# "ghrank" type of "Bebie" rank TD curve
td  <- tdval( vf91016right[15,] )
tdr <- tdrank( td )
ghr <- ghranktd( td )
bebie( ghr, type = "ghrank" )
```

`cart2jpolar` *convert from Cartesian coordinate to polar coordinates for use with the Jansonius map*

Description

converts from `(x,y)` in degrees to polar coordinates. This is a necessary step to compute average fiber paths as a function of their angle of incidence in the optic nerve head with the Jansonius map

Usage

```
cart2jpolar( xy )
```

Arguments

`xy`	Visual field location in Cartesian coordinates

Details

Input xy needs to be a data frame. It returns a data frame with the radial and angular coordinates

Value

Data frame with the radial and angular coordinates

Author(s)

Ivan Marin-Franch

See Also

`jpolar2cart`

Examples

```
cart2jpolar( data.frame( x = c( 0, 10 ), y = c( 0, 10 ) ) )
```

`colormapgraph` *color legend for p-values in td and pd probability plots*

Description

It geneartes color legend for p-values in td and pd probability plots

Usage

```
colormapgraph( ncol = 3, mapval = NULL, notSeenAsBlack = TRUE,
                      txtfont = "sans", pointsize = 10,
                      symbol = "circle", size = 1, inch = 0.18  )
```

Arguments

`ncol`	number of columns in where to show the color symbols. Default is `3`
`notSeenAsBlack`	Add a black color-code representing non-seen to the color scheme of the probability maps for td and pd
`mapval`	map and cutoff values to be used for the generation of the color map. If `NULL`, then go to current `nv$pmapsettings`. Default is `NULL`
`txtfont`	font of the text with visual-sensitivity values. Default is `sans`
`pointsize`	size of the text with visual-sensitivity values. Default is `10`
`symbol`	The outer symbol at all locations. Can be any of circles, squares, rectangles, stars. Default is `circle`
`size`	Size of the outer symbol. Default is `1`
`inch`	Maximum size of the outer symbol in inches. Default is `0.35`

Details

it generates a graph with the color legend for p-values in td and pd probability plots given the actual normative values version set for `visualFields`

Author(s)

Ivan Marin-Franch

See Also

`vfcolormap`

Examples

```
colormapgraph()
```

---

createviewport *Wrapup for createviewport in package* grid

Description

create regions in where to print graphs. Used for the generation of printouts

Usage

```
createviewport( name, left, top, width, height, pwidth = 8.27,
                pheight = 11.69 )
```

Arguments

name	name of he viewport
left	a numeric vector or unit object specifying left location (in inches)
top	a numeric vector or unit object specifying topvflocation (in inches)
width	a numeric vector or unit object specifying width (in inches)
height	a numeric vector or unit object specifying height (in inches)
pwidth	width of the page (in inches). Default is `8.27`
pheight	height of the page (in inches). Default is `11.69`

Details

create regions in where to print graphs. Used for the generation of printouts

Value

returns a viewport object

Author(s)

Ivan Marin-Franch

See Also

vflayout

`csplocmap` *xy-position mapping between CSP-custom-device convention (William H Swanson perimeter) and visualFields convention for patterns of location*

Description

A table with relevant information about test location data for each pattern of locations.

Usage

```
data( csplocmap )
```

Format

The structure saplocmap has 1 table for the test pattern `sgrnfl`. The table has six columns:

- `xod` stimulus x position
- `yod` stimulus y position
- `loc` sequential location number in the original device
- `size` size of the stimulus presentation
- `jmangle` angle of incidence in blind spot from Jansonious map
- `jmslope` orientation of an average bundle at that position of the visual field as calculated from the Jansonious map
- `region` region of the visual fields in comparison with ONH sector.

Author(s)

Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. *A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research*, 49, 2009.

See Also

`saplocmap`,`fdplocmap`

fdplocmap *xy-position mapping between FDP device convention and visualFields convention for patterns of location*

Description

A table with relevant information about test location data for the pattern of locations 24-2. The convention for visualFields is to use always a right-eye format. That is, a left eye would be "flipped" left-right and location number are counted row-wise from top-left to bottom-right. Information about the size of the stimulus and the corresponding angle of incidence and slope with Jansonious map [1] are included.

Usage

```
data( fdplocmap )
```

Format

The structure fdplocmap has 3 tables, one for each test pattern: `p24d2`, `p10d2`, `p30d2`. Each table has six columns:

`xod` stimulus x position

`yod` stimulus y position

`loc` sequential location number in the original device

`size` size of the stimulus presentation

`jmangle` angle of incidence in blind spot from Jansonious map

`jmslope` orientation of an average bundle at that position of the visual field as calculated from the Jansonious map

`region` region of the visual fields in comparison with ONH sector. Garway-Heath map

Author(s)

Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. *A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research*, 49, 2009.

See Also

`saplocmap`

fiberpathpsi *Average path of a nerve fiber bundle function generator*

Description

Generates a function that renders the average path of a nerve fiber bundle that exits through the optic nerve head with a particular angle

Usage

```
fiberpathpsi( psi0, r0 = 4 )
```

Arguments

psi0	Angle of incidence of the average bundle path on the optic nerve head
r0	Radius of the optic head nerve. It is a necessity of the model and changing it, changes the calculated average bundle paths. Default value is 4

Details

The function generated works in polar coordinates. The input is the radial coordinate r and output is the angular coordinate. The path in the cartesian `(x,y)` space is easily obtained with the function `jpolar2cart`

Value

A function that returns angular coordinates for each radial coordinate.

Author(s)

Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research, 49(17):2157-2163, 2009.

[2] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. Erratum to "a mathematical description of nerve fiber bundle trajectories and their variability in the human retina" [vision research 49(17) (2009) 2157-2163]. Vision Research, 50:1501, 2010.

[3] N. M. Jansonius, J. Schiefer, J. Nevalainen, J. Paetzold, and U. Schiefer. A mathematical model for describing the retinal nerve fiber bundle trajectories in the human eye: Average course, variability, and influence of refraction, optic disc size and optic disc position. Experimental Eye Research, 105:70-78, 2012.

See Also

gcloc2psi

Examples

```
fiberpathpsi( 90 + 45 )
```

`filterReliability` *identify visual fields that did not pass filter for reliability*

Description

identify visual fields that did not pass filter for reliability

Usage

```
filterReliability( vf, relCriteria = c( 0.2, 0.2, 0.2 ) )
```

Arguments

`vf`	visual field, should have columns perc of false positives, false negatives, and fixation losses
`relCriteria`	reliability limits for false positives, false negatives, and fixation losses

Value

returns a list of visual fields that did not pass the reliability criteria

Author(s)

Ivan Marin-Franch

See Also

lidLensArtifact

gcdisp *average GC displacement from [1]*

Description

average GC displacement from [1] in degrees of visual angle (0.3 mm per degree of visual angle [2])

Usage

```
data( gcdisp )
```

Format

Displacement is a function of eccentricity of the GC soma position.

`ecc` eccentricity of the GC soma position

`displ` displacement

Author(s)

Ivan Marin-Franch

References

[1] N. Drasdo, C. L. Millican, C. R. Katholi, and C. A. Curcio. The length of Henle fibers in the human retina and a model of ganglion receptive field density in the visual field. Vision Research, 47:2901-2911, 2007.

[2] B. A. Wandell. Foundations of vision. Sinauer Associates, Sunderland, Massachusets, 1995.

gcloc2psi *Angle of incidence in the optic nerve head for vf locations*

Description

This is the inverse of the model: it obtains the angle of incidence psi of the average path that passes through position `(x,y)`

Usage

```
gcloc2psi( xy, r0 = 4 )
```

Arguments

`xy` Visual field location in Cartesian coordinates

`r0` Radius of the optic head nerve. It is a necessity of the model and changing it, changes the calculated average bundle paths. Default value is `4`

Value

The angle of incidence psi of the average path that passes through position `(x,y)`

Author(s)

Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research, 49(17):2157-2163, 2009.

[2] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. Erratum to "a mathematical description of nerve fiber bundle trajectories and their variability in the human retina" [vision research 49(17) (2009) 2157-2163]. Vision Research, 50:1501, 2010.

[3] N. M. Jansonius, J. Schiefer, J. Nevalainen, J. Paetzold, and U. Schiefer. A mathematical model for describing the retinal nerve fiber bundle trajectories in the human eye: Average course, variability, and influence of refraction, optic disc size and optic disc position. Experimental Eye Research, 105:70-78, 2012.

See Also

`fiberpathpsi`

Examples

```
gcloc2psi( data.frame( x = c( 0, 10 ), y = c( 0, 10 ) ) )
```

---

getnv *get normative values and location map*

Description

get normative values and stimuli location map to be used with visualFields

Usage

```
getnv()
```

Details

gets normative values and stimuli location map to be used with visualFields

Value

returns the names of the variables containing the normative values and the stimuli location map

Author(s)

Ivan Marin-Franch

See Also

`setnv`

Examples

```
getnv()
```

---

ghpostd — *general height estimated as the rankRef-th ranked TD location*

Description

gets the general height estimated as the rankRef-th ranked TD location

Usage

```
ghpostd( td, correction = FALSE )
```

Arguments

`td`	vf-object with total-deviation values
`correction`	obtain general height as difference from mean normal "85th" percentile TD value? Default is `FALSE`

Details

calculates the general height estimated as the pos-th ranked TD location

Value

returns the subject's estimated general height

Author(s)

Ivan Marin-Franch

See Also

`pdval`

Examples

```
td <- tdval( vf91016right[15,] )
ghseventh <- ghpostd( td )
```

ghranktd *general height estimated from rank TD curve*

Description

estimates the general height by comparison of the rank TD curve of the subject compared with mean normal rank TD curve

Usage

```
ghranktd( td, minPts = 2, strategy = "isospaced", withinNormal = 95, pCentral = 1,
          link = make.link( "logit" ), scaleFactor = 52.4 )
```

Arguments

`td`	total-deviation values
`minPts`	minimum number of TD values within normal limits necessary to estimate the general height. Default is 2. If there are less than 2 TD values within normal limits, then NA is returned
`strategy`	strategy for the comparison of the reconstructed within normal part of the rank TD curve with the mean normal rank TD curve. There are two posibilities at the moment `isospaced` and `parallel`. In the option `isospaced`, the TD values identified as within-normal limits are equally spaced and compared with the corresponding rank location of the mean normal TD curve. In the slightly more computationally complicated option `parallel`, the rank positions are obtained so that the all differences between subject's TD values and mean normal TD values in the corresponding rank position are equal. In both strategies, the mean rank position of the reconstructed rank TD curve corresponds with the mean rank position of the mean normal TD rank curve (for the pattern of locations 24-2 that is location 26.5). This way uniqueness is ensured on both strategies. Default is `parallel`. For more details see [1]
`withinNormal`	value or label used to identify the locations that are within normal limits. Default is `95`
`pCentral`	proportion of the TD rank curve to be used for the estimation of the general height. Default is `1`
`link`	link function to use with `glm` fit. See `family`. Defaulut is `logit`
`scaleFactor`	scale to use for ranks to make them be between 0 and 1. Default is `52.4`

Value

returns the estimated general height for the test, or NA if the number of TD values within normal limits was less than `numPts`

Author(s)

Ivan Marin-Franch

References

[1] I. Marin-Franch, W. H. Swanson, and V. E. Malinovsky. A novel strategy for the estimation of the general height of the visual field in patients with glaucoma. Graefe's Archive Clinical Experimental Ophthalmology, 252(5):801-809, 2014.

See Also

`pdval`,`ghpostd`

`gloperc` *percentiles for global indices*

Description

gets the percentiles for global indices

Usage

```
gloperc( vals, percentiles = c( 0.5, 1, 2, 5, 95 ),
         type = c( "quantile", "(i-1)/(n-1)", "i/(n+1)", "i/n" ) )
```

Arguments

`vals`	table with global indices for control subjects
`percentiles`	percentiles at which to calculate cutoff values
`type`	see `wtd.quantile` for a list of different options

Details

gets the percentiles for global indices. This function works in conjunction with `vfstats`. In `vfstats` all global indices refering to mean must start with `m` and all refereing to standard deviation must start with `s`, otherwise `gloperc` won't calculate the cutoff values correctly

Value

percentiles for global indices

Author(s)

Ivan Marin-Franch

See Also

`vfindex`, `vfstats`, `vfiperc`, `locperc` `hist_poplr` *histogram for PoPLR analysis*

Description

plots an histogram of Fisher S statistic combining all location p-values

Usage

```
hist_poplr( s, pval, sp, nLoc = 52, showLabels = TRUE,
                   txtfont = "sans", pointsize = 10,
                   plt = c( 0, 1.0, 0.3, 1 ), mpg = c( 1.85, 0.5, 0 ),
                   coltxt  = rgb( red = 1.0, green = 0.0, blue = 0.0 ),
                colhist = rgb( red = 1.0, green = 0.0, blue = 0.0, alpha = 0.5 ))
```

Arguments

`s`	observed S-statistic for the pointwise significance tests that slopes are lower than (or greater than) a specified reference (typically zero)
`pval`	p-value for the pointwise significance tests that slopes are lower than (or greater than) a specified reference (typically zero)
`sp`	S-statistics calculated for the permutation of visual fields
`nLoc`	number of locations in the visual field to be analyzed. For 24-2, it is 52 (54 minus the locations in the blind spot). Default is 52.
`showLabels`	Whether or not to show histogram x-labels. Default is `TRUE`.
`plt`	Graphics parameter plt. Default is `c( 0, 1.0, 0.3, 1 )`
`mpg`	Graphics parameter mpg. Default is `c( 1.85, 0.5, 0 )`
`txtfont`	font of the text with visual-sensitivity values. Default is `sans`
`pointsize`	size of the text with visual-sensitivity values. Default is `10`
`colhist`	Histogram color. Default is `rgb( red = 1.0, green = 0.0, blue = 0.0 )`
`coltxt`	Text color. Default is `rgb( red = 1.0, green = 0.0, blue = 0.0 )`

Author(s)

Ivan Marin-Franch

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

`poplr`, `poplr_cstat`, `poplr_pstat`, `vflayout_poplr`, `vfplot_plr`

jpolar2cart *converts to* `(x,y)` *in degrees from polar coordinates*

Description

converts to `(x,y)` in degrees from polar coordinates. It is the inverse of `( cart2jpolar)`

Usage

```
jpolar2cart( rpsi )
```

Arguments

`rpsi`	Visual field location in polar coordinates

Details

Input rpsi needs to be a data frame. It returns a data frame with the Cartesian coordinates

Value

Data frame with the (x,y) Cartesian coordinates

Author(s)

Ivan Marin-Franch

See Also

`cart2jpolar`

Examples

```
jpolar2cart( cart2jpolar( data.frame( x = c( 0, 10 ), y = c( 0, 10 ) ) ) )
```

lidLensArtifact *visual fields with lid or lens artifacts*

Description

identifies in a very coarse way visual fields that may have been affected by lid or lens artifacts. This function is to be used only with control data. It is probably better not to use it and look to the visual-fields printouts directly to identify those with lid and lens artifacts

Usage

```
lidLensArtifact( vf, min_dB = c( 12 ) )
```

Arguments

vf	visual-field object
min_dB	lowest dB value considered normal

Value

it returns a list of indices of visual fields in `vf` that may have been affected by lid or lens artifact

Author(s)

Ivan Marin-Franch

See Also

`filterReliability`

`loadvfcsv` *load visual fields from a CSV file*

Description

loads visual fields from a CSV file

Usage

```
loadvfcsv( filename, patternMap )
```

Arguments

filename	filename
patternMap	pattern of stimulus locations

Details

The columns in the CSV file must follow the format of `vf`. Make sure that all dates have the format `MM/DD/YYYY` and all times have the format `HH:MM:SS`. Excel tends to change the format, and any edits in Excel that are safe may cause problems when loading the data as `vf`-object

Value

returns a `vf`-object with all the data in the CSV file `filename`

Author(s)

Ivan Marin-Franch

See Also

`loadvfxml`, `loadvfxmlbatch`

loadvfEyesuite *Import visual field data from Haag-Streit Eyesuite*

Description

`loadvfEyesuite` imports visual field data from the Eyesuite software by Haag-Streit. These data are converted into a vf object.

Usage

```
loadvfEyesuite(filename, date_format = "%d.%m.%Y")
```

Arguments

`filename`	the filename of the csv-file
`date_format`	the order of the dates used in the specific locale

Value

a vf object

loadvfxml *loads visual fields from a XML file*

Description

loads visual fields from a XML file

Usage

```
loadvfxml( filename, patternMap, typeData = "vf", typeSubject = "pwg",
           extractionType = c( "average" ), daysyear = NULL )
```

Arguments

`filename`	filename
`patternMap`	pattern of stimulus locations. Default is `saplocmap$p24d2`
`typeData`	Type of data to load; visual field (`vf`), total deviations (`td`), pattern deviations (`pd`), global indices (`gi`), visual-field index (`vfi`), total-deviation p-values (`tdp`), pattern-deviation p-values (`pdp`), global indices probability maps (`gip`), visual-field-index probability map (`vfip`). Default is `vf`
`typeSubject`	Type of subject, control (`ctr`) or patient (`pwg`). Default is (`pwg`)
`extractionType`	When typeData is (`vf`) what type of extraction we want: all re-tested sensitivities `"all"` or just the mean `"average"` over re-tested values? Default is `"average"`
`daysyear`	if `NULL`, calculates real age. If informed, then calculates year based on the number of days per year (e.g. 362.25)

Details

The XML files format must be as from the extraction of the HFA device

Value

returns a `vf`-object with one row containing the information for the subject loaded in the XML

Author(s)

Ivan Marin-Franch

See Also

`loadvfcsv`, `loadvfxmlbatch`

`loadvfxmlbatch` *loads visual fields from a set of XML files*

Description

loads visual fields from a set of XML files

Usage

```
loadvfxmlbatch( filename, patternMap, typeData = "vf" )
```

Arguments

`filename`	filename in CSV format with the list of XML files to upload and whether the subject whose data is in the XML file is a patient with glaucoma pwg or a control `ctr`
`patternMap`	pattern of stimulus locations. Default is `saplocmap$p24d2`
`typeData`	Type of data to load; visual field (`vf`), total deviations (`td`), pattern deviations (pd), global indices (`gi`), visual-field index (`vfi`), total-deviation p-values (`tdp`), pattern-deviation p-values (pdp), global indices probability maps (`gip`), visual-field-index probability map (`vfip`). Default is `vf`

Value

returns a `vf`-object with as many rows as XML files exists in `filename`

Author(s)

Ivan Marin-Franch

See Also

`loadvfcsv`, `loadvfxml`

`locperc` *percentiles for each location*

Description

gets the percentiles for each location

Usage

```
locperc( vals, stds, percentiles = c( 0.5, 1, 2, 5, 95 ),
         type = c( "quantile", "(i-1)/(n-1)", "i/(n+1)", "i/n" ),
         poolLocations = FALSE )
```

Arguments

`vals`	table with sensitivity values, total-deviation values, or pattern-deviation values
`stds`	standard deviations per location for sensitivity values, total-deviation values, or pattern-deviation values
`percentiles`	percentiles at which to calculate cutoff values
`type`	see `wtd.quantile` for a list of different options
`poolLocations`	assume that the shape of the empirical distributions at each location is the same and pool sensitivity, TD, or PD values per location. This is useful when the number of controls available is small. Sample size is increased at the expense of posible bias due to the fact that empirical distributions are not necessarily the same in each location

Details

gets the percentiles at each location. Since the number of visits per subject can be variable. To account for that, weighted quantile is used in which the weights for is the inverse of the number of visits for the subject

All the data passed to the function must belong to the same perimeter `tperimetry`, the same pattern of locations `talgorithm`, and the same presentation algorithm `tpattern`.

Value

percentiles for each location

Author(s)

Ivan Marin-Franch

References

[1] A. Heijl, G. Lindgren, and J. Olsson. *A package for the statistical analysis of visual fields*. Documenta Ophthalmologica Proceedings Series, 49, 1987

[2] A. Heijl, G. Lindgren, J. Olsson, and P. Asman. *Visual field interpretation with empiric probability maps*. Archives of Ophthalmology, 107, 1989

See Also

`gloperc`

`nvcspsgalpha` *IU normative reference values for Contrast Sensitiviy Perimetro. Alpha version!!!*

Description

Normative reference values or (normative values or nv for short) for Contrast Sensitivy Perimcery (CSP) from IU (William H Swanson and Victor E Malinovsky) databases.

Usage

```
data( nvcspsgalpha )
```

Format

This normative-value object is defined by some tables, variables, and sub-structures, some of which are mandatory and some which are not. This nv-object has the following objects:

`pmapsettings` **mandatory**. Information about which percentiles are used for location-wise analysis in this nv and their corresponding color coding for display. This is a table with four columns. First column specifies the percentiles (in percent) for `cutoffs` and the other three columns are the corresponding RGB values (defined from 0 to 1) specifying the color code to use for values below that percentile

`globalco` **mandatory**. Percentiles to be used for the analysis of globan indices such us mean deviation (MD), pattern standard deviation (PSD) or visual-field index (VFI)

`sgrnfl_zest` **mandatory**. The actual normative values for the presentaion algorithm ZEST at the array of test locations SGRNFL

`nvname` **mandatory**. Name assigned to this normative-value object

Author(s)

Ivan Marin-Franch, William H Swanson

See Also

`nvsapdefault`

`nvsapdefault` *SUNY-IU normative reference values for static automated perimetry*

Description

Normative reference values or (normative values or nv for short) for static automated perimetry (SAP) obtained from a combination of control subjects from SUNY and IU databases.

Usage

```
data( nvsapdefault )
```

Format

This normative-value object is defined by some tables, variables, and sub-structures, some of which are mandatory and some which are not. Importantly an age linear model must be included for test pattern (24-2) and presentation algorithm (e.g. SITA standard). Also important are the tables specifying the settings. Think of the normative-value object as a structure with several levels. The first level has three main substructures with settings:

`pmapsettings` **mandatory**. Information about which percentiles are used for location-wise analysis in this nv and their corresponding color coding for display. This is a table with four columns. First column specifies the percentiles (in percent) for `cutoffs` and the other three columns are the corresponding RGB values (defined from 0 to 1) specifying the color code to use for values below that percentile

`globalco` **mandatory**. Percentiles to be used for the analysis of globan indices such us mean deviation (MD), pattern standard deviation (PSD) or visual-field index (VFI)

`nvname` **mandatory**. Name assigned to this normative-value object From here age linear models, percentile values, etc are defined for combination of test patterns and presentation algorithms. It is important that the construction of the name for each of the normative-value for the particular test and presentation is in agreement with the values of `tperimetry` and `talgorithm` in `vf`. This is very important because it is the way `visualFields` can identify automatically which normative values are to be used with data for a particular visual field. For instance, for the test pattern 24-2 (`p24d2`) and the stimulus-presentation algorithm SITA standard (`sitas`), the substructure in the normative-values object must be called `p24d2_sitas`. This substructure itself is composed of other strutures and tables. These are

`demographics` **optional**. It has stats about the controls subjects used for the calculation of the normative values

`agelm` **mandatory**. A table with two columns, intercept and slope, specifying a linear model modeling the (linear) decrease at each location of the sensitivities in decibels (dB) per year. These were calculated with the `ageLinearModel`. See locations 26 and 35 have NAs. That is because these are the locations that correspond anatomically with the blind spot (see `vfsettings`) and are hence excluded from any analysis

`sds` **mandatory**. A table with three columns with the standard deviations for threshold sensitivities, total-deviation values (TD), and pattern-deviation values (PD)

TDpercloc **mandatory**. A table with as many columns as cutoff percentiles (rows) were defined in pmapsettings. Each column is the TD cutoff value for each percentile. It is used to get the probability map

PDpercloc **mandatory**. A table with as many columns as cutoff percentiles (rows) were defined in pmapsettings. Each column is the PD cutoff value for each percentile. It is used to get the probability map

percglo **mandatory**. A table with as many columns as cutoff percentiles (rows) were defined in globalco for global indices. Each row has a different statistical index. Most of them are not really used by convention. The statistical indices considered are mean and standard deviation of the threshold sensitivities (msens and ssens), mean and standard deviation of the TD values (mtdev and stdev), and mean and standard deviation of the PD values (mpdev and spdev). The two indices that are used by convention are mtdev and spdev, that is mean deviation (MD) and pattern standard deviation (PSD)

percvfi **mandatory**. A table with as many columns as cutoff percentiles (rows) were defined in globalco for global indices. This table has data only for the VFI (mvfi) and the standard deviation of the VFI at each locaton (svfi)

nvtdrank **optional**, but necessary to run bebie with the option diff = TRUE. A table with two columns, mean normal Bebie TD rank curve and the standard deviation at each ranked location.

perctdrank **optional**, but necessary to run bebie with the option percentiles = TRUE. A table with as many columns as cutoff percentiles (rows) were defined in pmapsettings. Each column is the TD cutoff value for each percentile

perctdrankadj7 **optional**, but necessary to run bebie with the option diff = TRUE and percentiles = TRUE. Same as perctdrank but the difference from mean normal Bebie TD rank curve analysis

Author(s)

Ivan Marin-Franch, William H Swanson

References

[1] ADD REFERENCE FOR 24-2

[2] H. J. Wyatt, M. W. Dul, and W. H. Swanson. *Variability of visual field measurements is correlated with the gradient of visual sensitivity*. Vision Research, 47, 2007.

[3] A. Shafi, W. H. Swanson, and M. W. Dul. *Structure and Function in Patients with Glaucomatous Defects Near Fixation*. Optometry and Vision Science, 88, 2011.

---

pdpmap *probability map for pattern deviation*

Description

gets probability map for pattern-deviation values

Usage

```
pdpmap( pd )
```

Arguments

pd	pattern-deviation values in dBs

Details

calculates the probability maps for pattern-deviation values

Value

returns the subjects's pattern-deviation probability map from the age-matched normative reference.

Author(s)

Ivan Marin-Franch

See Also

pdval, tdval, tdpmap

Examples

```
td  <- tdval( vf91016right )
pd  <- pdval( td )
pdp <- pdpmap( pd )
```

---

pdpmapghr *probability map for pattern deviation from global sensitivity estimate*

Description

gets probability map for pattern-deviation values obtained from estimates of general height rank

Usage

```
pdpmapghr( pd )
```

Arguments

pd	pattern-deviation values in dBs

Details

calculates the probability maps for pattern-deviation values obtained from estimates from general height rank

Value

returns the subjects's pattern-deviation probability map from the age-matched normative reference.

Author(s)

Ivan Marin-Franch

See Also

pdval, tdval, tdpmap

Examples

```
td  <- tdval( vf91016right )
pd  <- pdvalghr( td )
pdp <- pdpmapghr( pd )
```

---

pdval *pattern deviation*

Description

gets pattern-deviation values

Usage

```
pdval( td )
```

Arguments

td	total-deviation values

Details

calculates pattern-deviation values using the (around) 85-th percentile. All in dBs.

Author(s)

Ivan Marin-Franch

See Also

pdpmap, tdval, tdpmap

Examples

```
td  <- tdval( vf91016right )
pd  <- pdval( td )
```

pdvalghr — *pattern deviation from general height rank (GHr)*

Description

gets the pattern-deviation from the estimator of general height rank (GHr)

Usage

```
pdvalghr( td )
```

Arguments

`td`	total-deviation values

Details

calculates pattern-deviation from the estimator of general height rank (GHr). All in dBs.

Author(s)

Ivan Marin-Franch

See Also

`pdval`, `pdpmap`, `pdpmapghr`, `tdval`, `tdpmap`

Examples

```
td  <- tdval( vf91016right )
pd  <- pdvalghr( td )
```

poplr — *permutation of Pointwise Linear Regression (PoPLR)*

Description

performs the PoPLR analysis from a series of visual-field threshold sensitivities, or TD or PD values over time

Usage

```
poplr( vf, nperm = 5000, sltest = NULL, truncVal = 1 )
```

Arguments

`vf`	`vf` object with threshold sensitivities, td, or pd values
`nperm`	number of permutations. Default is `5000`
`sltest`	values for the 1-tailed hypothesis test for all locations. The reference value is not restricted, but it should be either zero (was there any progression?) or negative (was the progression greater than test value?). Default is `NULL`
`truncVal`	p-value cut-off for truncation. Default is `1`

Author(s)

Ivan Marin-Franch

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

`poplr_cstat`, `poplr_pstat`, `vflayout_poplr`, `vfplot_plr`

Examples

```
res <- poplr( vf91016right )
```

`poplr_cstat` *permutation of pointwise linear regression (PoPLR): calculation of the combined statistic*

Description

For details see [1]

Usage

```
poplr_cstat( pval, truncVal = 1 )
```

Arguments

`pval`	p-values. Typically the ones obtained from `poplr_pstat`
`truncVal`	p-value cut-off for truncation. Default is `1`

Author(s)

Ivan Marin-Franch

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

poplr, poplr_pstat, vflayout_poplr, vfplot_plr

Examples

```
res <- poplr( vf91016right )
```

---

poplr_pstat — *Permutation of Pointwise Linear Regression (PoPLR): calculation of the p-value*

Description

For details see [1]

Usage

```
poplr_pstat( vf, porder, sltest = NULL )
```

Arguments

`vf`	visual-field data. It can be td or pd as well
`porder`	order of permunations of visual-fields sensitivities. Each row contains a permutation of tests from vf
`sltest`	values for the 1-tailed hypothesis test for each location. The reference values are not restricted, but they should be either zero (was there any progression?) or negative (was the progression greater than test value?). Default is `NULL`

Value

the function retunts two different structures depending on whehter the analysis is linear regression (`type = "slr"` or Spearman rank correlation `type = "rank"`). For `slr` analysis, the sturcture consists of four matrices with data: `pval` (p-value at each permutation and location of the significance of the 1-tailed hypothesis test specified by `sl_test` for each location), `se` (standard error), `sl` (slope), and `int` (intercept). For `rank` analysis, the sturcture consists of two matrices: `pval` (p-value at each permutation and location of the significance of the 1-tailed hypothesis test specified by `sl_test` for each location) and `rho` (the Spearman rank correlation)

Author(s)

Ivan Marin-Franch

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

poplr, poplr_cstat, vflayout_poplr, vfplot_plr

Examples

```
res <- poplr( vf91016right )
```

---

progols — *progression by linear ordinary least squares*

Description

makes a linear regression with projection in the future by projyears years

Usage

```
progols( tdate, index, projyears = 0,
         xlab = "years from first visit", ylab = "md",
         txtfont = "sans", pointsize = 10, cex = 1,
         markfl = FALSE, prggrp = 3 )
```

Arguments

`tdate`	visit date
`index`	index measured at the corresponding age
`xlab`	label for x-axis. Default is `age`
`ylab`	label for y-axis. Default is `md`
`projyears`	Years for projection. Default is `0`
`txtfont`	font of the text with visual-sensitivity values. Default is `sans`
`pointsize`	size of the text with visual-sensitivity values. Default is `10`
`cex`	a numerical value giving the amount by which plotting text and symbols should be magnified relative to the default. Default is `1`
`markfl`	Mark first and last data points? Default is `FALSE`
`prggrp`	How many datapoints to mark. Default is `3`

Author(s)

Ivan Marin-Franch

Examples

```
vfi <- vfindex( vf91016right )
progols( vfi$tdate, vfi$mvfi, ylab = "vfi" )
```

---

psi2oct — *Angle of incidence in the OCT scan corresponding to angle of incidence in optic nerve head*

Description

Obtains the angle of incidence in the circular oct scan from the average path that starts at an angle psi from the optic nerve head.

Usage

```
psi2oct( psi, diam = 12 )
```

Arguments

`psi`	Angle of incidence of the average bundle path on the optic nerve head
`diam`	Diameter of the scan. Default value is `12` in visual angle, which is the common diameter used in this types of OCT scans

Details

The operation `psi2oct( gloc2psi )` maps vf locations with RNFL angles so that the thickness that corresponds to each vf location can be estimated. This can be used in conjuction with `vf2gcloc` to correct for ganglion cell body displacement from vf location

Value

The angle of incidence in the circular oct scan

Author(s)

Ivan Marin-Franch

Examples

```
psi2oct( 90 + 45 )
```

quad2Dfit — *two-dimensional quadratic fitting for visual-field results*

Description

fits a 2D quadratic function using values in val as "observations" for the x and y coordinates in patternMap

Usage

```
quad2Dfit( val, patternMap, bspos )
```

Arguments

`val`	values at each location
`patternMap`	pattern of stimulus locations. It uses the x and y coordinates in conjunction with val to get the fitted values with the 2D model
`bspos`	position of the blind spot

Value

fitted values by a 2D quadratic function

Author(s)

Ivan Marin-Franch

See Also

`ageLinearModel`

retestconddist — *Conditional retest distribution*

Description

Computes the conditional retest distribution and the `( 1 - alpha / 2 )` conditional retest intervals

Usage

```
retestconddist( vf, nbase = 1, nfollow = 1, alpha = 0.1, typequantile = 7 )
```

Arguments

`vf`	Visual field data. It has to have as many visual fields as nbase + nfollow
`nbase`	Number of visual fields to be used as baseline
`nfollow`	Number of visual fields to be used as follow up.
`alpha`	Significance to derive the `( 1 - alpha / 2 )` conditional retest intervals. Default value is `0.1`
`typequantile`	An integer between 1 and 9 selecting one of the nine quantile algorithms detailed below to be used. Default value is 7

Value

conditional retest distribution and the `( 1 - alpha / 2 )` conditional retest intervals

Author(s)

Ivan Marin-Franch

References

[1] A. Heijl, A. Lindgren, and G. Lindgren. Test-retest variability in glaucomatous visual fields. American Academy of Ophthalmology, 180, 1989.

Examples

```
vfcondretest <- retestconddist( vf91016left[c(1:4),], nbase = 2, nfollow = 2 )
```

`ringmapgraph` *ring legend for p-values*

Description

It geneartes ring legend for p-values

Usage

```
ringmapgraph( ncol = 3, mapval = NULL, txtfont = "mono", pointsize = 7,
              outerSymbol = "circles", innerSymbol = "circles",
              outerSize = 1, innerSize = 1,
              outerInch = 0.2, innerInch = 0.1,
              outerBorderThickness = 2, innerBorderThickness = 2 )
```

Arguments

`ncol`	number of columns in where to show the color symbols. Default is `3`
`mapval`	map and cutoff values to be used for the generation of the color map. Default is `NULL`
`txtfont`	font of the text with visual-sensitivity values. Default is `mono`
`pointsize`	size of the text with visual-sensitivity values. Default is `7`
`outerSymbol`	The outer symbol at all locations. Can be any of circles, squares, rectangles, stars. Default is `circle`
`innerSymbol`	The inner symbol at all locations. Can be any of circles, squares, rectangles, stars. Default is `circle`
`outerSize`	Size of the outer symbol. Default is `1`
`innerSize`	Size of the inner symbol. Default is `1`
`outerInch`	Maximum size of the outer symbol in inches. Default is `0.2`
`innerInch`	Maximum size of the inner symbol in inches. Default is `0.1`
`outerBorderThickness`	Thickness of outer border for outer symbol denoting statistical significance. Default is `2`
`innerBorderThickness`	Thickness of the inner border that represents statistical significance. Default is `2`

Author(s)

Ivan Marin-Franch

See Also

`vfcolormap`

`saplocmap` *xy-position mapping between HFA device convention and visualFields convention for patterns of location*

Description

A table with relevant information about test location data for each pattern of locations, 24-2, 10-2, and 30-2, and the conventional Goldman size III stimulus. The G1 pattern is also included for the Goldman size III, size V and size VI stimuli. The convention for visualFields is to use always a right-eye format. That is, a left eye would be "flipped" left-right and location number are counted row-wise from top-left to bottom-right. Information about the size of the stimulus and the corresponding angle of incidence and slope with Jansonious map [1] are included.

Usage

```
data( saplocmap )
```

Format

The structure saplocmap has 1 table for the test pattern `p24d2`. The table has six columns:

`xod` stimulus x position

`yod` stimulus y position

`loc` sequential location number in the original device

`size` size of the stimulus presentation

`jmangle` angle of incidence in blind spot from Jansonious map

`jmslope` orientation of an average bundle at that position of the visual field as calculated from the Jansonious map

`region` region of the visual fields in comparison with ONH sector. Garway-Heath map

Author(s)

Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. *A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research*, 49, 2009.

See Also

`fdplocmap`

---

sdnv *standard deviations of normative values*

Description

get the standard deviations at each location for normative values: sensitivities, total-deviation, and pattern-deviation values

Usage

```
sdnv( vf, smooth = TRUE, smoothFunction = quad2Dfit )
```

Arguments

`vf`	`vf`-object with sensitivity thresholds
`smooth`	whether to use a function to smooth the results or not. Default is `TRUE`
`smoothFunction`	If `smooth` is true, the function to use for smoothing. Default is `quad2Dfit`, a 2D quadratic fit to resulting data. This function is not really a smoothing procedure, but a parametric fit

Details

calculates total-deviation and pattern-deviation values and, from them, their standard deviation at each location

Value

returns a 3-column data frame with SDs per location. Each row is a location. Column 1 is for sensitivities, column 2 for total deviation, and column 3 for pattern deiation.

Author(s)

Ivan Marin-Franch

See Also

ageLinearModel, locperc, quad2Dfit

`sdnvghr` *standard deviations of normative values of PD from general-height-rank*

Description

get the standard deviations of PD values from general-height-rank estimates at each location for normative values

Usage

```
sdnvghr( vf, smooth = TRUE, smoothFunction = quad2Dfit )
```

Arguments

`vf`	`vf`-object with sensitivity thresholds
`smooth`	whether to use a function to smooth the results or not. Default is `TRUE`
`smoothFunction`	If `smooth` is true, the function to use for smoothing. Default is `quad2Dfit`, a 2D quadratic fit to resulting data. This function is not really a smoothing procedure, but a parametric fit

Details

calculates total-deviation and pattern-deviation values and, from them, their standard deviation at each location

Value

returns a 3-column data frame with SDs per location. Each row is a location. Column 1 is for sensitivities, column 2 for total deviation, and column 3 for pattern deiation.

Author(s)

Ivan Marin-Franch

See Also

ageLinearModel, locperc, quad2Dfit

---

setnv *set normative values and location map*

Description

set normative values and stimuli location map to be used with visualFields

Usage

```
setnv( nvtxt = "nvsapdefault" )
```

Arguments

nvtxt	char. Name of the normative reference values to be used. It must be an existing structure

Details

sets normative values and stimuli location map to be used with visualFields

Author(s)

Ivan Marin-Franch

See Also

getnv

Examples

```
setnv()
```

stimLoc *stimulus location and size*

Description

plots the stimulus location and size

Usage

```
stimLoc( perimetry, pattern, eye, txtfont = "mono", pointsize = 7,
         xminmax = 29, yminmax = 29 )
```

Arguments

perimetry	type of perimetry
pattern	pattern used in the perimetry
eye	eye being tested
txtfont	font of the text with visual-sensitivity values. Default is mono
pointsize	size of the text with visual-sensitivity values. Default is 7
xminmax	minimum and maximum limits on the x axis. Default is 29
yminmax	minimum and maximum limits on the y axis. Default is 29

Author(s)

Ivan Marin-Franch

See Also

saplocmap

Examples

```
stimLoc( "sap", "p24d2", "OD" )
```

tdpmap *probability map for total deviation*

Description

gets probability map for total-deviation values

Usage

```
tdpmap( td )
```

Arguments

td	total-deviation values in dBs

Details

calculates the probability maps for total-deviation values

Author(s)

Ivan Marin-Franch

See Also

tdval, pdval, pdpmap

Examples

```
td  <- tdval( vf91016right )
tdp <- tdpmap( td )
```

tdrank *total-deviation rank curve*

Description

get total-deviation rank curve

Usage

```
tdrank( td )
```

Arguments

td	total deviation values

Details

calculates total-deviation rank curve.

Author(s)

Ivan Marin-Franch

See Also

`tdrankperc`

Examples

```
td <- tdval( vf91016right )
tdr <- tdrank( td  )
```

---

tdrankadjperc *percentiles for adjusted TD rank curve*

Description

gets percentiles for adjusted TD rank curve

Usage

```
tdrankadjperc( td, percentiles = c( 0.5, 1, 2, 5, 95 ), type = "conventional",
               typequantiles = c( "quantile", "(i-1)/(n-1)", "i/(n+1)", "i/n" ),
               smooth = TRUE, smoothFunction = tdrankglm )
```

Arguments

`td`	`vf`-object with total-deviation values
`type`	whether to use a `conventional` way to plot the rank TD curve or `ghrank` type where the `vf` object passed is the reconstructed within-normal TD rank curve. Default is `conventional`
`percentiles`	percentiles at which to calculate cutoff values
`typequantiles`	see `wtd.quantile` for a list of different options
`smooth`	whether to use a function to smooth the results or not. Default is TRUE
`smoothFunction`	if `smooth` is `TRUE` is true, the function to use for smoothing. Default is `tdrankglm`, a GLM fit which was proven to do a good fit for average over subject of TD rank curves. This function is not really a smoothing procedure, but a parametric fit

Value

percentiles for adjusted TD rank curves

Author(s)

Ivan Marin-Franch

See Also

tdrank, tdrankperc

Examples

```
tdrankadjperc( td )
```

tdrankglm — *GLM fit for TD rank curve*

Description

gets a generalized linear model fit for TD rank curve

Usage

```
tdrankglm( tdr, familytxt = c( "gaussian" ), link = make.link( "logit" ),
                  rankCentral = NULL, scaleFactor = 52.4 )
```

Arguments

`tdr`	table with TD rank curve
`familytxt`	family of distributions to use with `glm` fit. See `family`. Default is `gaussian`
`link`	link function to use with `glm` fit. See `family`. Defaulut is `logit`
`rankCentral`	central ranked positions to use in the fit. By default it is `NULL`, so that all rank locations are used for the fit
`scaleFactor`	scale to use for ranks to make them be between 0 and 1. Default is `52.4`

Details

details

Value

fitted values of the generalized linear model fit for TD rank curve

Author(s)

Ivan Marin-Franch

See Also

tdrank, tdrankperc

`tdranknv` *normative values for TD rank curve*

Description

gets percentiles for TD rank curve

Usage

```
tdranknv( td, smooth = TRUE, smoothFunction = tdrankglm )
```

Arguments

`td`	table with total-deviation values
`smooth`	whether to use a function to smooth the results or not. Default is TRUE
`smoothFunction`	if `smooth` is `TRUE`, the function to use for smoothing. Default is `tdrankglm`, a GLM fit which was proven to do a good fit for average over subject of TD rank curves. This function is not really a smoothing procedure, but a parametric fit

Details

details

Value

percentiles for TD rank curves

Author(s)

Ivan Marin-Franch

See Also

`tdrank`, `tdrankglm`

tdrankperc *percentiles for TD rank curve*

Description

gets percentiles for TD rank curve

Usage

```
tdrankperc( td, percentiles = c( 0.5, 1, 2, 5, 95 ),
                   type = c( "quantile", "(i-1)/(n-1)", "i/(n+1)", "i/n" ),
                   smooth = TRUE, smoothFunction = tdrankglm )
```

Arguments

`td`	table with total-deviation values
`percentiles`	percentiles at which to calculate cutoff values
`type`	see `wtd.quantile` for a list of different options
`smooth`	whether to use a function to smooth the results or not. Default is TRUE
`smoothFunction`	if `smooth` is `TRUE` is true, the function to use for smoothing. Default is `tdrankglm`, a GLM fit which was proven to do a good fit for average over subject of TD rank curves. This function is not really a smoothing procedure, but a parametric fit

Details

details

Value

percentiles for TD rank curves

Author(s)

Ivan Marin-Franch

See Also

`tdrank`, `tdrankglm`

tdval — *total deviation*

Description

gets total-deviation values

Usage

```
tdval( vf )
```

Arguments

vf	stimulus sensitivities in dBs

Details

calculates the normative reference sensitivities for healthy subjects of the same age as the subject and obtains differences between the visual field sensitivities and mean normal sensitivities. All in dBs.

Author(s)

Ivan Marin-Franch

See Also

tdpmap, pdval, pdpmap

Examples

```
td <- tdval( vf91016right )
```

vf2gcloc — *Calculates the location of the GC soma corresponding to vf locations*

Description

Calculates the corresponding location of the GC soma for a list of vf locations. See [1,2]

Usage

```
vf2gcloc( xy )
```

Arguments

xy	data frame with the xy VF locations in degrees of visual angle

Value

returns GC soma position in degrees of visual angle

Author(s)

Ivan Marin-Franch

References

[1] D. C. Hood, A. S. Raza, D. M. C. G. V., J. G. Odel, V. C. Greenstein, J. M. Liebmann, and R. Ritch. Initial arcuate defects within the central 10 degrees in glaucoma. Investigative Ophthalmology and Visual Science, 52(2):940-946, 2011.

[2] A. S. Raza, J. Cho, D. M. C. G. V., H. Wang, X. Zhang, R. H. Kardon, J. M. Liebmann, R. Ritch, and D. C. Hood. Retinal ganglion cell layer thickness and local visual field sensitivity in glaucoma. Archives of Ophthalmology, 129(12):1529-1536, 2011.

Examples

```
vf2gcloc( data.frame( x = 1, y = 1 ) )
```

---

vf91016csp1vf *a vf-object with CSP sample data with*

Description

a vf-object with sample data for the examples in visualFields's help. This is real data for the right eye, but the ages have been changed to protect anonymity of the subject

Usage

```
data( vf91016csp1vf )
```

Format

the format is as in vf but for CSP format (see csplocmap)

Author(s)

Ivan Marin-Franch, William H Swanson, Victor E Malinovsky

See Also

vf

`vf91016left` *a vf-object with SAP sample data*

Description

a vf-object with sample data for the examples in `visualFields`'s help. This is real data for the right eye, but the ages have been changed to protect anonymity of the subject

Usage

```
data( vf91016left )
```

Format

the format is as explained in `vf` with columns L1 .. L54 containing sensitivity thresholds

Author(s)

Ivan Marin-Franch, William H Swanson, Victor E Malinovsky

See Also

`vf`

`vf91016right` *a vf-object with SAP sample data*

Description

a vf-object with sample data for the examples in `visualFields`'s help. This is real data for the right eye, but the ages have been changed to protect anonymity of the subject

Usage

```
data( vf91016right )
```

Format

the format is as explained in `vf` with columns L1 .. L54 containing sensitivity thresholds

Author(s)

Ivan Marin-Franch, William H Swanson, Victor E Malinovsky

See Also

`vf`

vfArtes2014 *Short-term retest static automated perimetry data*

Description

Thirty patients recruited from the glaucoma clinics at the Queen Elizabeth Health Sciences Centre in Halifax, Nova Scotia. Each patient underwent 12 visual fields in 12 consecutive weekly sessions.

Usage

```
data( vfArtes2014 )
```

Format

It is a `vf`-object

Author(s)

Paul H Artes, David P Crabb

References

[1] P. H. Artes, N. O'Leary, M. T. Nicolela, B. C. Chauhan, and D. P. Crabb. Visual field progression in glaucoma: What is the specificity of the guided progression analysis? American Academy of Ophthalmology, 121(10):2023-2027, 2014.

vfaverage *average of vf-objects*

Description

computes the location averages of vf-object

Usage

```
vfaverage( vf )
```

Arguments

`vf`	a vf-object with more than 1 entry

Value

returns the location average of vf.

Author(s)

Ivan Marin-Franch

Examples

```
vfaverage( vf91016left )
```

`vfcolormap` *Color code for TD or PD probability maps*

Description

returns the RGB values specifying the color code for the TD or PD probability maps

Usage

```
vfcolormap( map, mapval = NULL )
```

Arguments

`map`	array with the percentile for TD or PD probability map
`mapval`	map and cutoff values to be used for the generation of the color map. If `NULL`, then go to current `nv$pmapsettings`. Default is `NULL`

Author(s)

Chaitanya Khadilkar, Ivan Marin-Franch

See Also

`vfplot`, `vfgrayscale`

`vfdemographics` *demographics and statistics of sample in visual-fields object vf*

Description

gets demographics and weighted statistics of sample in visual-fields object vf

Usage

```
vfdemographics( vf )
```

Arguments

vf A vf-object with sensitivity thresholds, total-deviation or pattern-deviation values

Value

returns a table with demographics and weighted statistics

Author(s)

Ivan Marin-Franch

Examples

```
vfdemog <- vfdemographics( vf91016right )
```

---

vfenv *environment with the current normative values used* visualFields

---

Description

environment containing the current version of normative values to be used with visualFields. The default used is nvsapdefault

Usage

```
data(vfenv)
```

Format

It has as many element as the version of normative values used plus one with the name of the version used. To set a structure as the new dataset use setnv. The structure has to be similar to nvsapdefault.

... same variables as in the corresponding normative values version used. See default value of nv$nvname

nv$nvname char. Name of the variable with the normative values to use. Default is "nvsapdefault"

Author(s)

Ivan Marin-Franch

See Also

getnv,setnv

`vfgrayscale` *gray scales for sensitivities*

Description

maps sensitivity values to grayscales

Usage

```
vfgrayscale( sens, age, pattern, algorithm )
```

Arguments

`sens`	an array with sensitivity values
`age`	age of the subject
`algorithm`	algorithm used in the visual test
`pattern`	pattern used in the visual test

Details

This function maps sensitivity values to grayscales. The grayscale depends on age of the person, test pattern and algorithm

Value

returns the RGB values for the gray scale

Author(s)

Ivan Marin-Franch

See Also

`vfcolormap`

vfidefault *Settings of visual field index*

Description

Specifies the weighting to be applied at each location for averaging.

Usage

```
data( vfidefault )
```

Format

vfisettings contains structures for different patterns of location testing. For instance, p24d2 or p30d2. Each structure contains 2 items:

`regweights` the actual weights to be applied to each region

`locregions` mapping between locations in the visual-field testing pattern and regions with the same weight

Author(s)

Ivan Marin-Franch

References

[1] B. Bengtsson and A. Heijl. *A visual field index for calculation of glaucoma rate of progression*. American Journal of Ophthalmology, 145, 2008

vfindex *visual field index*

Description

calculates the visual field index. It can be parametrized by re-defining which locations go to which weighting regions and the actual weights per region.

Usage

```
vfindex( vf, td2pdcutoff = -20, perc = 5, vfiset = visualFields::vfidefault )
```

Arguments

- `vf` stimulus sensitivities in dBs
- `td2pdcutoff` cutof value for mean deviation. See `perc` below for an explanation of how both criteria work in conjunction. Default is -20
- `perc` percentile at which to check whether the 85th TD percentile is within normal limits or not. If it is not and mean deviation is lower than `td2pdcutoff`, then TD probability maps are to be used instead of PD probability maps. Default is 5th percentile
- `vfiset` settings to be applied for the calculation of VFI

Details

calculates the visual field index. It can be parametrized by re-defining which locations go to which weighting regions and the actual weights per region.

Author(s)

Ivan Marin-Franch

References

[1] B. Bengtsson and A. Heijl. *A visual field index for calculation of glaucoma rate of progression*. American Journal of Ophthalmology, 145, 2008

See Also

`vfstats`, `vfstatspmap`, `vfindexpmap`

Examples

```
vfi <- vfindex( vf91016right )
```

`vfindexpmap` *probability values for visual field index*

Description

calculates the probability values for visual field index

Usage

```
vfindexpmap( vfi )
```

Arguments

- `vfi` visual fields index

Details

calculates the proability values for visual field index (see vfindex)

Author(s)

Ivan Marin-Franch

References

[1] B. Bengtsson and A. Heijl. *A visual field index for calculation of glaucoma rate of progression*. American Journal of Ophthalmology, 145, 2008

See Also

vfstats, vfstatspmap, vfindex

Examples

```
vfi  <- vfindex( vf91016right )
vfip <- vfindexpmap( vfi )
```

---

vfiperc *percentiles for visual field index*

Description

gets the percentiles for visual field index

Usage

```
vfiperc( vals, percentiles = c( 0.5, 1, 2, 5, 95 ),
         type = c( "quantile", "(i-1)/(n-1)", "i/(n+1)", "i/n" ) )
```

Arguments

vals	vf-object with vfi values
percentiles	percentiles at which to calculate cutoff values
type	see wtd.quantile for a list of different options

Value

percentiles for visual field index

Author(s)

Ivan Marin-Franch

References

[1] B. Bengtsson and A. Heijl. *A visual field index for calculation of glaucoma rate of progression*. American Journal of Ophthalmology, 145, 2008

See Also

vfindex, vfstats, gloperc, locperc

---

vflayout *printout with results for the visual field*

Description

creates a printout with results for the visual field. This includes sensitivity threshold values with a gray scale plot, and TD and PD values with color coding for the probability map

Usage

```
vflayout( vf, pwidth = 8.27, pheight = 11.69, margin = 0.25, filename = NULL,
                  showaxis = FALSE, colaxis = "black" )
```

Arguments

vf	vf-object with sensitivity thresholds
pwidth	width of the page (in inches). Default is 8.27
pheight	height of the page (in inches). Default is 11.69
margin	margins of the page (in inches). Default is 0.25
filename	file name to save the printout as pdf. If it is saved to pdf, it won't be displayed in the screen. Default is NULL.
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Author(s)

Ivan Marin-Franch

See Also

vflayoutghr, vfplot, vfplotloc

Examples

```
vflayout( vf91016right[15,] )
```

vflayoutghr *printout with results for the visual field*

Description

creates a printout with results for the visual field. This includes sensitivity threshold values with a gray scale plot, and TD and PD values (from general-height-rank estimates) with color coding for the probability map

Usage

```
vflayoutghr( vf, pwidth = 8.27, pheight = 11.69, margin = 0.25, filename = NULL,
                    showaxis = FALSE, colaxis = "black" )
```

Arguments

vf	vf-object with sensitivity thresholds
pwidth	width of the page (in inches). Default is 8.27
pheight	height of the page (in inches). Default is 11.69
margin	margins of the page (in inches). Default is 0.25
filename	file name to save the printout as pdf. If it is saved to pdf, it won't be displayed in the screen. Default is NULL.
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Author(s)

Ivan Marin-Franch

See Also

vflayout, vfplot, vfplotloc

Examples

```
vflayoutghr( vf91016right[15,] )
```

vflayout_poplr — *layout displaying the PoPLR analysis*

Description

the function performs the PoPLR analysis (see poplr) with default values and presents the results in form of a A4 printout

Usage

```
vflayout_poplr( vf, grp = 3, nperm = 5000, sparklines = TRUE,
                plotType = "td", summaryIndex1 = "md", summaryIndex2 = "gh",
                  ttail = "left", sltest = NULL, truncVal = 1,
                  pwidth = 8.27, pheight = 11.69,
                  margin = 0.25, filename = NULL,
                  colorMapType = "pval", colorScale = NULL,
                  showaxis = FALSE, colaxis = "black" )
```

Arguments

`vf`	`vf` object with threshold sensitivities, td, or pd values
`grp`	how many visual fields to group. Default is `3`
`nperm`	number of permutations. Default is `5000`
`sparklines`	Whether or not to show sparklines. Default is `TRUE`
`plotType`	Type of plot to show. It can be visual sensitivities (`vf`), total-deviation values (`td`), or pattern-deviation values (`pd`). Default is `td`
`summaryIndex1`	Which summary index to use for the first global progression analysis. Default is `md`
`summaryIndex2`	Which summary index to use for the second global progression analysis. Default is `gh`
`ttail`	type of alternative in the significant test: `left`, `right`, `both`. Default is `left`
`sltest`	values for the 1-tailed hypothesis test for all locations. The reference value is not restricted, but it should be either zero (was there any progression?) or negative (was the progression greater than test value?). Default is `NULL`
`truncVal`	p-value cut-off for truncation. Default is `1`
`pwidth`	width of the page (in inches). Default is `8.27`
`pheight`	height of the page (in inches). Default is `11.69`
`margin`	margins of the page (in inches). Default is `0.25`
`filename`	file name to save the printout as pdf. If it is saved to pdf, it won't be displayed in the screen. Default is `NULL`.
`colorMapType`	what does color map categorizes. It can be `pvals`, `slopes`, or years `blind`. Default is `pvals`

colorScale	Color mapping to use. Default is NULL. A different default is given depending on colorMapType
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Author(s)

Ivan Marin-Franch, Chaitanya Khadilkar

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

vflayout, poplr, poplr_cstat, poplr_pstat, vfplot_plr

Examples

```
vflayout_poplr( vf91016right )
```

---

vflayout_progress   *progression analysis layout*

Description

A layout showing graphs and stats for progression analysis.

Usage

```
vflayout_progress( vf, plotType, grp = 2, nperm = 5000,
                   colorMapType = "pval", colorScale = NULL,
                   filename = NULL,
                   pwidth = 8.27, pheight = 11.69, margin = 0.25,
                   showaxis = FALSE, colaxis = "black" )
```

Arguments

vf	vf object with threshold sensitivities, td, or pd values
plotType	Type of plot to show. It can be visual sensitivities (vf), total-deviation values (td), or pattern-deviation values (pd)
grp	how many visual fields to group. Default is 3
nperm	number of permutations. Default is 5000

colorMapType	what does color map categorizes. It can be pvals, slopes, or years blind. Default is pvals
colorScale	Color mapping to use. Default is NULL. A different default is given depending on colorMapType
filename	file name to save the printout as pdf. If it is saved to pdf, it won't be displayed in the screen. Default is NULL.
pwidth	width of the page (in inches). Default is 8.27
pheight	height of the page (in inches). Default is 11.69
margin	margins of the page (in inches). Default is 0.25
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Author(s)

Ivan Marin-Franch

See Also

vflayout, vflayout_poplr

Examples

```
vflayout_progress( vf91016left, plotType = "td" )
```

---

vfobject *visualField objects*

Description

This is the main object of the visualFields package. It is essentially a dataframe, but with a fixed number of columns (with pre-determined names) for information about the subject and test data and a variable number of columns for the perimetry results. These can be the sensitivities, or total-deviation values, or pattern-deviation values obtained from static automated perimetry (SAP), frequency-doubling perimetry (FDP), or any other perimetry device. (The number of columns for tested locations is variable as is different for different testing patterns, 24-2, 30-2, 10-2, etc.) Mean deviation, pattern standard deviation, vfi, etc are stored too in a visualField-type object

Details

The fixed columns of the visualField object with information about subject and test are:

- **id** subject identification number
- **tperimetry** test perimetry. The type of perimetry analysis performed. Possible values include "sap" and "fdp". The value of this column, tperimetry, is used in conjunction with the value in talgorithm, and tpattern to find the corresponding normative values (see help on nv) to use for data analysis (e.g. calculation of total-deviation and pattern-deviation values and probability maps). At the moment, only normative values for SAP, 24-2, SITA standard, is distributed with visualFields. Nevertheless, visualFields contains a number of functions that can be used for the generation of normative values (see getnv, ageLinearModel, sdnv, tdval, pdval, locperc, vfstats, vfindex, gloperc, vfiperc, setnv).
- **talgorithm** test algorithm. The algorithm used for the perimetric test. Posible values are sitas and zest. At the moment, only normative values for SAP, 24-2, SITA standard, is distributed with visualFields
- **tpattern** test pattern. The pattern of locations used for the perimetric test. Posible values are p24d2 or p10d2. At the moment, only normative values for SAP, 24-2, SITA standard, is distributed with visualFields
- **tdate** test date
- **ttime** test time
- **stype** type of subject. Values can be ctr for controls, pwg for patients with glaucoma, sus for suspect subjects. This is just for information to display in the printouts
- **sage** subject age. Important for the calculation of total-deviation values and probabiliby maps.
- **seye** eye tested
- **sbsx** estimated x-position of the blind spot in degrees of angle of vision
- **sbsy** estimated y-position of the blind spot in degrees of angle of vision
- **sfp** false positives
- **sfn** false negatives
- **sfl** fixation losses
- **sduration** total duration of the test
- **spause** total time of pause

The reminder of the columns can be different things. For threshold sensitivity values, and total-deviation and pattern-deviation values, and their corresponding probability maps, they are:

- **L1 .. L54 .. L68 .. L76** location number. There are up to 54 locations for the 24-2, up to 68 for the 10-2, and 76 for the 30-2. Information about the position of the locations, the size of the stimulus, and the x and y coordinates in degrees of visual angles are specified in saplocmap (for SAP) fdplocmap (for FDP)

For statistical values of the visual-fields results (mean deviation, pattern standard deviation, and others) and their corresponding probability mapped value, they are:

msens	mean sensitivity value; or the probability mapped value
ssens	standard deviation of the sensitivity values; or the probability mapped value
mtdev	mean deviation (mean value of the total-deviation values; or the probability mapped value)
stdev	standard deviation of the total-deviation values; or the probability mapped value
mpdev	mean value of the pattern-deviation values; or the probability mapped value)
stdev	standard pattern deviation (standard deviation pattern-deviation values; or the probability mapped value

For visual field index (VFI) value and the corresponding probability mapped value, they are:

mvfi	visual field indes (VFI); or the probability mapped value
svfi	standard deviation of the VFI at each location; or the probability mapped value

Author(s)

Ivan Marin-Franch

See Also

vfsettings

Examples

```
# DO NOT EXECUTE
# one can load sensitivities using loadvfcsv or loadvfxml the data so
# vf <- loadvfcsv( filename = "foo.csv", , patternMap = saplocmap$p24d2 )
# calculate total deviation values using \code{\link{visualFields}} normative values for
# SAP SITAS 24-2 (and Goldman size III stimulus)
# td <- tdval( vf )
# calculate pattern deviation values using total deviation values SAP SITAS 24-2
# pd <- tdval( td )
# OR
# pd <- tdval( tdval( vf ) )
# calculate total deviation proabiliby maps
# tdp <- tdpmap( td )
# calculate pattern deviation proabiliby maps
# pdp <- pdpmap( pd )
```

---

vfplot *visual field plot*

Description

plots location-specific sensitivity thresholds, or TD or PD values at each location of the visual field with the corresponding color code for the probability map

Usage

```
vfplot( vf, plotType = "vf",
               xmin = NULL, xmax = NULL, ymin = NULL, ymax = NULL,
               notSeenAsBlack = TRUE, newWindow = FALSE,
               txtfont = "sans", pointsize = 10, width = 6,
               showaxis = FALSE, colaxis = "black" )
```

Arguments

- `vf` — `vf`-object with sensitivity thresholds, or TD or PD values
- `plotType` — Type of plot to show. It can be visual sensitivities (`vf`), total-deviation values (`td`), or pattern-deviation values (pd). Default is `vf`
- `xmin, xmax, ymin, ymax` — minimum and maximum limits on the x and y axes, in degrees of visual angle. If `NULL`, then the limits are the maximum and minimum location values + 2.5 percent of the range. Default is `NULL`.
- `notSeenAsBlack` — whether to plot non-seen as black. Default is `TRUE`
- `newWindow` — whether to generate a new window for the plot. This becomes important when working with RStudio. Default value is `TRUE`
- `txtfont` — font face of the text with visual-sensitivity values. Default is `sans`
- `pointsize` — size of the text with visual-sensitivity values. Default is `10`
- `width` — width of the window. height is calculated using the width, xmin, xmax, ymin, and ymax. Default is `6`
- `showaxis` — Whether to show axis or not. Default is `FALSE`
- `colaxis` — Color of the axis to show, if `showaxis` is `TRUE`. Default is `black`

Details

This function The vfplot function operates on a single row of visual fileds (vf). Depending on the plot type it will generate a plot representing the sensitivity at each location. The color scheme elucidates the degree of sensitivity at that location. Locations with zero sensitivity are shown in black. Blind spots have been excluded fronm the plot

Author(s)

Chaitanya Khadilkar, Ivan Marin-Franch

See Also

`vfplotloc`

Examples

```
vfplot( vf91016right[15,], plotType = "td" )
```

`vfplotloc` *visual field data plot*

Description

plots location-specific data at each location of the visual field. It is the function called by `vfplot`

Usage

```
vfplotloc( vals, patternMap, loccol, vftiles, vfhull,
                  xmin, xmax, ymin, ymax,
                  txtfont = "sans", pointsize = 10,
                  showaxis = FALSE, colaxis = "black" )
```

Arguments

`vals`	sensitivity threshold, TD or PD values, or other location-specific values
`patternMap`	locations where to plot symbols, the TD and PD values
`loccol`	color to apply to each location. Typically calculated from the normative values
`vftiles`	Tiles for the tessellation calculated with Voronoi polygons
`vfhull`	Hull defined for the visual field test.
`xmin, xmax, ymin, ymax`	minimum and maximum limits on the x and y axes, in degrees of visual angle.
`txtfont`	font of the text with visual-sensitivity values. Default is `sans`
`pointsize`	size of the text with visual-sensitivity values. Default is `10`
`showaxis`	Whether to show axis or not. Default is `FALSE`
`colaxis`	Color of the axis to show, if `showaxis` is `TRUE`. Default is `black`

Details

The vfplot function operates on a single row of visual fileds (vf). Depending on the plot type it will generate a plot representing the sensitivity at each location. The color scheme elucidates the degree of sensitivity at that location. Locations with zero sensitivity are shown in black. Blind spots have been excluded fronm the plot

Author(s)

Chaitanya Khadilkar, Ivan Marin-Franch

See Also

`vfplot`

vfplot_legoplot *legoplot for PoPLR analysis*

Description

legoplot for PoPLR analysis

Usage

```
vfplot_legoplot( vals, patternMap, vftiles, vfhull,
                         loccolout, loccolin, radius = 2,
                         xmin = NULL, xmax = NULL, ymin = NULL, ymax = NULL,
                         txtfont = "sans", pointsize = 10,
                         showaxis = FALSE, colaxis = "black" )
```

Arguments

vals	values to show in the lego-plot, typically differences between baseline and final visual field tests
patternMap	locations where to plot symbols, the TD and PD values
vftiles	Tiles for the tessellation calculated with Voronoi polygons
vfhull	Hull defined for the visual field test.
loccolout	color of the polygon surrinding the circle in the lego piece
loccolin	color of the circle in the inside of the lego piece
radius	Radius of the circle inside the lego piece. Default is 2.
xmin, xmax, ymin, ymax	minimum and maximum limits on the x and y axes, in degrees of visual angle. If NULL, then the limits are the maximum and minimum location values + 2.5 percent of the range. Default is NULL.
txtfont	font face of the text with visual-sensitivity values. Default is sans
pointsize	size of the text with visual-sensitivity values. Default is 10
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Details

Shows the legoplots

Author(s)

Ivan Marin-Franch, Paul H Artes

Examples

```
vflayout_poplr( vf91016right )
```

---

vfplot_plr *plot with the PLR analysis*

Description

plots the slope values and the corresponding probabiliby category for each location

Usage

```
vfplot_plr( sl, pval, vfinfo, newWindow = FALSE,
                   xmin = NULL, xmax = NULL, ymin = NULL, ymax = NULL,
                   colorMapType = "pval", colorScale = NULL,
                   txtfont = "sans", pointsize = 10, width = 6,
                   showaxis = FALSE, colaxis = "black" )
```

Arguments

sl	slopes
pval	pvalues calculated for the slope
vfinfo	information about the visual field
newWindow	boolean value- TRUE will generate a new window for the plot. Default value is TRUE
xmin, xmax, ymin, ymax	minimum and maximum limits on the x and y axes, in degrees of visual angle. If NULL, then the limits are the maximum and minimum location values + 2.5 percent of the range. Default is NULL.
colorMapType	what does color map categorizes. It can be pvals, slopes, or years blind. Default is pvals
colorScale	Color mapping to use. Default is NULL. A different default is given depending on colorMapType
txtfont	font of the text with visual-sensitivity values. Default is sans
pointsize	size of the text with visual-sensitivity values. Default is 10
width	width of the window. height is calucated using the width, xminmax and yminmax
showaxis	Whether to show axis or not. Default is FALSE
colaxis	Color of the axis to show, if showaxis is TRUE. Default is black

Details

The vfplot function operates on a single row of visual fileds (vf). Depending on the plot type it will generate a plot representing the sensitivity at each location. The color scheme elucidates the degree of sensitivity at that location. Locations with zero sensitivity are shown in black. Blind spots have been excluded fronm the plot

Author(s)

Ivan Marin-Franch, Paul H Artes, Chaitanya Khadilkar

References

[1] N. O'Leary, B. C. Chauhan, and P. H. Artes. *Visual field progression in glaucoma: estimating the overall significance of deterioration with permutation analyses of pointwise linear regression (PoPLR)*. Investigative Ophthalmology and Visual Science, 53, 2012

See Also

`poplr`, `poplr_cstat`, `poplr_pstat`, `vflayout_poplr`

Examples

```
res <- poplr( vf91016right )
vfplot_plr( res$sl, res$pval, res$vfdata )
```

`vfplot_sparklines` *Sparklines*

Description

Sparklines to print on top of vfplots

Usage

```
vfplot_sparklines( vf, ylim = c( -5, 35 ), collin = NULL, ... )
```

Arguments

`vf`	`vf`-object with sensitivity thresholds, or TD or PD values
`ylim`	y-limit for the plots for the sparkline.
`collin`	color for each sparkline to be plotted. Default is `NULL`, then all plotted in dark gray
`...`	Arguments to be passed to methods, such as graphical parameters.

Details

Plots sparklines on top of other vfplots. It is used for the PLR plot in the PoPLR layout.

Author(s)

Paul H Artes

Examples

```
vflayout_poplr( vf91016right )
```

`vfsegmentcoord` *calculate line segments to plot in `vfplot` representing the overall orientation of the retinal nerve fibre layer bundles according to Jansonious map [1]*

Description

This function geneartes coordinates for the line segments to be plotted

Usage

```
vfsegmentcoord( lineMap, length = 2.5 )
```

Arguments

`lineMap`	patternMap having x,y and slope values
`length`	length of the line segment in inches. Default is `3.75`

Details

This function geneartes coordinates for the line segments to be plotted. Based on the location (x,y) and slope, this function claculates the coordinate set (x1,y1),(x2,y2) which is used to plot the line segments

Author(s)

Chaitanya Khadilkar, Ivan Marin-Franch

References

[1] N. M. Jansonius, J. Nevalainen, B. Selig, L. M. Zangwill, P. A. Sample, W. M. Budde, J. B. Jonas, W. A. Lagreze, P. J. Airaksinen, R. Vonthein, L. A. Levin, J. Paetzold, and U. Schiefer. *A mathematical description of nerve fiber bundle trajectories and their variability in the human retina. Vision Research*, 49, 2009.

`vfselectvisit` *select visits per subject from a vf-object*

Description

select a determined amount of visits a vf-object. This is done if the interest is to select the last n visits, or the first n visits, or visits within a range, etc

Usage

```
vfselectvisit( vf, sel = "last", numTests = 1,
               beginDate = NA, endDate = NA )
```

Arguments

`vf`	a vf-object
`sel`	Type of selection, do we want visits from `last`, from first `first`, within a `date` range, or specific visit numbers. Default is `last`
`numTests`	number of tests to select from `last`, `first`, or a `date` range. If `sel` is an array of indices or set to a `date` range, `numTests` is overruled. Default is `1`
`beginDate`	when `sel = "date"` is date from (inclusive). If it is `NA`, then the data is set to `1900-01-01`. Default is `NA`
`endDate`	when `sel = "date"` is date to (inclusive). If it is `NA`, then the data is set to today. Default is `NA`

Value

returns the subselected visits per subject. For those subject for which at least `numTests` visits could not be selected are completely removed

Author(s)

Ivan Marin-Franch

Examples

```
vfselectvisit( vf91016left )
```

`vfsettings` *Settings of visualField object*

Description

Specifies the structure of a vf object (see `vf`) and information pertaining test patterns and their statistical analysis.

Usage

```
data( vfsettings )
```

Format

This structure contains a variable specifying the number of columns with patient and subject data, `locini` and several sub-structures with relevant information pertaining different pattern of locations and their analysis. Information exists for the test patterns `p24d2`, `p30d2`, `p10d2`, and `sgrnfl`. Each sub-structure contains three items:

`bs` locations that correspond to the ananomical region where the blind spot is. For 24-2, those are locations 26 and 35. There are non for the 10-2

`locnum` total number of locations of the testing pattern in which stimuli are presented. For 24-2 there are 54 locations, for 30-2 there are 76, for 10-2 there are 68

`locrPD` specifies the rank TD value to be used for the derivation of TD. For 24-2, that ranked location would be 7, corresponding approximately (but not very) to the 85th percentile. For 30-2 the ranked locatoion taken is 10, but this needs fixing???. The way PD is calculated really for 30-2 is by taking the 24-2 locations and finding the seventh largest

Author(s)

Ivan Marin-Franch

See Also

`vf`

`vfShafi2011` *SUNY-IU control data for static automated perimetry 10-2 SITA Standard*

Description

SUNY-IU control data for static automated perimetry 10-2 SITA Standard

Usage

```
data( vfShafi2011 )
```

Format

It is a vf-object

Author(s)

Ivan Marin-Franch, William H Swanson, Harry J Wyatt, Mitchell W Dul

References

[1] H. J. Wyatt, M. W. Dul, and W. H. Swanson. *Variability of visual field measurements is correlated with the gradient of visual sensitivity*. Vision Research, 47, 2007.

[2] A. Shafi, W. H. Swanson, and M. W. Dul. *Structure and Function in Patients with Glaucomatous Defects Near Fixation*. Optometry and Vision Science, 88, 2011.

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vfsort *sort vf-objects*

Description

sorts a vf-object by id, eye tested, and date and time of test

Usage

```
vfsort( vf, decreasing = FALSE )
```

Arguments

`vf`	a vf-object
`decreasing`	logical. Should the sort order be increasing or decreasing?. Default is `FALSE`

Value

return a sorted vf

Author(s)

Ivan Marin-Franch

Examples

```
vfsort( vf91016left, decreasing = TRUE )
```

`vfstats` *visual field stats*

Description

calculates the visual field stats

Usage

```
vfstats( vf )
```

Arguments

vf	vf-object with sensitivity thresholds

Details

calculates the visual field stats: mean sensitivity (msens), std of sensitivities (ssens), mean total deviation (mtdev), std of total deviation (stdev), mean pattern deviation (mpdev), std of pattern deviation (spdev). All are weighted means and stds

Author(s)

Ivan Marin-Franch

References

[1] A. Heijl, G. Lindgren, and J. Olsson. *A package for the statistical analysis of visual fields*. Documenta Ophthalmologica Proceedings Series, 49, 1987

See Also

vfstatspmap, vfindex, vfindexpmap

Examples

```
vfs <- vfstats( vf91016right )
```

vfstatspmap *probability values for visual field global indices*

Description

calculates the probability values for visual field global indices

Usage

```
vfstatspmap( vfindices )
```

Arguments

vfindices	visual fields global indices

Details

calculates the proability values for visual field global indices (see vfstats)

Author(s)

Ivan Marin-Franch

References

[1] A. Heijl, G. Lindgren, and J. Olsson. *A package for the statistical analysis of visual fields*. Documenta Ophthalmologica Proceedings Series, 49, 1987

See Also

vfstats, vfindex, vfindexpmap

Examples

```
vfs  <- vfstats( vf91016right )
vfsp <- vfstatspmap( vfs )
```

vftessellation — *Voronoi tessellation of vf spatial testing locations*

Description

calculates the Voronoi tessellation of vf spatial testing locations

Usage

```
vftessellation( locmap, dist = 3 )
```

Arguments

`locmap`	a vf-object
`dist`	This function calculates the outer convex hull of the Voronoi diagram. This parameter specifies how much in degrees we want to extend the outer convex hull. Default is 3 degrees

Value

returns the Voronoi diagrams and the outer convex hull of the visual field area tested.

Author(s)

Ivan Marin-Franch

Examples

```
vftess <- vftessellation( saplocmap$p24d2 )
```

xmlblock — *extracts a block from the XML file*

Description

extracts a block from the XML file

Usage

```
xmlblock( tag, xmllines, capitalize = TRUE )
```

Arguments

`tag`	tag to look at
`xmllines`	lines from loaded XML files
`capitalize`	Whether we need to capitalize or not. Default is `TRUE`

Value

returns an array of characters with all that is inside a block corresponding to a particular tag

Author(s)

Ivan Marin-Franch

See Also

loadvfxml, loadvfcsv, xmlitem

---

xmldevval *extracts total-deviation values, pattern-deviation values, total-deviation probability values, and pattern-deviation probability values*

Description

extracts total-deviation values, pattern-deviation values, total-deviation probability values, and pattern-deviation probability values

Usage

```
xmldevval( xmllines, patternMap, typeData = c( "td" ),
           group = c( 4, 3, 2, 1, 0 ),
           cutoffs = c( 0.5, 1, 2, 5, 95 ) )
```

Arguments

xmllines	lines from loaded XML files
patternMap	pattern of stimulus locations. Default is saplocmap$p24d2
typeData	Type of data to load; visual field (vf), total deviations (td), pattern deviations (pd), global indices (gi), visual-field index (vfi), total-deviation p-values (tdp), pattern-deviation p-values (pdp), global indices probability maps (gip), visual-field-index probability map (vfip). Default is vf
group	for probability maps: the probability group coding
cutoffs	for probability maps: the corresponding pvalue for each group code

Value

total-deviation values, pattern-deviation values, total-deviation probability values, and pattern-deviation probability values

Author(s)

Ivan Marin-Franch

See Also

loadvfxml, xmlvfval

`xmlitem` *extracts from a loaded XML file the info of a tag*

Description

extracts from a loaded XML file the info of a tag

Usage

```
xmlitem( tag, xmllines, capitalize = TRUE )
```

Arguments

`tag`	tag to look at
`xmllines`	lines from loaded XML files
`capitalize`	Whether we need to capitalize or not. Default is `TRUE`

Details

extracts from a loaded XML file the info of a tag

Author(s)

Ivan Marin-Franch

See Also

loadvfxml, loadvfcsv,xmlblock

`xmlvfval` *extracts visual-field sensitivity values*

Description

extracts visual-field sensitivity values

Usage

```
xmlvfval( xmllines, patternMap, extractionType = c( "average" ) )
```

Arguments

`xmllines`	lines from loaded XML files
`patternMap`	pattern of stimulus locations. Default is `saplocmap$p24d2`
`extractionType`	what type of extraction we want: all re-tested sensitivities `"all"` or just the mean `"average"` over re-tested values? Default is `"average"`

Author(s)

Ivan Marin-Franch

See Also

`loadvfxml`, `xmldevval`

`xmlvfxy` *dxtraction of (x,y)-coordinates of tested locations*

Description

extracts the (x,y)-coordinates of tested locations

Usage

```
xmlvfxy( xmllines )
```

Arguments

`xmllines`	lines from loaded XML files

Details

extracts the (x,y)-coordinates of tested locations. To be used only for custom locations, not when we know that the testing pattern is 24-2, or 30-2, etc

Value

(x,y)-coordinates of tested locations

Author(s)

Ivan Marin-Franch

See Also

`loadvfxml`, `xmlvfval`

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