

# Package ‘visualFields’

January 16, 2016

**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.

**Version** 0.4.3

**Date** 2016-01-15

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**URL** <http://people.eng.unimelb.edu.au/aturpin/opi/index.html>

**Depends** R (>= 2.14.0), stats, utils, gridBase, grid, flip (>= 2.1),  
matrixStats, Hmisc

**LazyData** yes

**License** GPL (>= 2.0)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2016-01-16 12:06:24

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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)

The visualFields Development Team

## 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

This work was supported by NIH grant number **R01EY007716**

## 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 <imarinfr@indiana.edu>

**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 <a href="#">vf</a> 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 <a href="#">quad2Dfit</a> , 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 inappropriate 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](#)

**Examples**

```
# DO NOT RUN
# to test this, load a file using e.g. loadvfcsv with control data and then run
# age1m <- ageLinearModel( vf )
```

---

 bebie

*Bebie curve*


---

### Description

Plots Bebie rank TD curve

### Usage

```
bebie( tdr, type = "conventional", diff = TRUE, percentiles = TRUE,
       correction = TRUE, txtfont = "mono", pointsize = 7, 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 mono
pointsize	size of the text with visual-sensitivity values. Default is 7
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 `nvt drank`, `perct drank`, and `perct drank adj` must exist in the `nv`-object, for the perimeter `tperimetry`, the pattern of locations `talgorithm`, and the presentation 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" )
```

---

colormapgraph

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


---

**Description**

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

**Usage**

```
colormapgraph( ncol = 3,
               mapval = visualFields::vfenv$nv$pmapsettings,
               notSeenAsBlack = TRUE,
               txtfont = "mono", pointsize = 7,
               outerSymbol = "circles", innerSymbol = "circles",
               outerSize = 1, innerSize = 1,
               outerInch = 0.2, innerInch = 0.1 )
```

**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. Default is nv\$pmapsettings
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

**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](#)**Examples**

```
# show a printout
#vflayout( vf91016right[15,] )
```

---

csplocmap	<i>xy-position mapping between CSP-custom-device convention (William H Swanson perimeter) and visualFields convention for patterns of location</i>
-----------	--

---

**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 Jansoniuous map

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

region region of the visual fields in comparison with ONH sector.

**Author(s)**

Ivan Marin-Franch

**References**

[1] N. M. Jansoniuous, 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	<i>xy-position mapping between FDP device convention and visualFields convention for patterns of location</i>
-----------	---

---

**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](#)

---

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](#)

**Examples**

```
# DO NOT RUN
#idx <- filterReliability( vf )
```

---

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, rankRef = c( "default" ) )
```

**Arguments**

td	vf-object with total-deviation values
correction	obtain general height as difference from mean normal "85th" percentile TD value? Default is FALSE
rankRef	the rank position to take as reference for general height. Default is "default". For "default" it looks at the type of visual field, p24d2 or p30d2, fullt or sitas, to get which is the position that corresponds, roughly with the 85th percentile

**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	<i>general height estimated from rank TD curve</i>
----------	--

---

**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 possibilities at the moment <code>isospaced</code> and <code>parallel</code> . In the option <code>isospaced</code> , 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 <code>parallel</code> , 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 <code>parallel</code> . For more details see [1] and [2]
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 <code>glm</code> fit. See <code>family</code> . Default is <code>logit</code>
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] Marin-Franch et al. TO COME SOON [2] Marin-Franch et al. TO COME SOON

**See Also**

[pdval](#), [ghpostd](#)

**Examples**

```
#####td <- tdval( vf91016right[15,] )
#####ghrank <- ghranktd( td )
```

---

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 <a href="#">wtd.quantile</a> 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 referring to mean must start with m and all referring 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](#)

**Examples**

```
# DO NOT RUN
# gperc <- gloperc()
```

---

hist_poplr	<i>histogram for PoPLR analysis</i>
------------	-------------------------------------

---

**Description**

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

**Usage**

```
hist_poplr( scomb_obs, pcomb_obs, scomb, txtfont = "mono", pointsize = 7 )
```

**Arguments**

scomb_obs	observed S-statistic for the observed visual fields
pcomb_obs	p-value associated with the observed S-statistic for the observed visual fields
scomb	S-statistics calculated for the permutation of visual fields
txtfont	font of the text with visual-sensitivity values. Default is mono
pointsize	size of the text with visual-sensitivity values. Default is 7

**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\\_poplr](#)

**Examples**

```
#vflayout_poplr( vf91016right )
```

---

lidLensArtifact	<i>visual fields with lid or lens artifacts</i>
-----------------	---

---

**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](#)

**Examples**

```
# DO NOT EXECUTE
#idx <- lidLensArtifact( vf )
```



---

loadvfcsv	<i>load visual fields from a CSV file</i>
-----------	---

---

## 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](#)

## Examples

```
# DO NOT RUN
#filename <- # Add the file name with the control data
#vf      <- loadvfxml( filename = filename, patternMap = saplocmap$p24d2 )
```

---

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](#)

### Examples

```
# DO NOT RUN
#filename <- # Add the XML file name
#vf      <- loadvfxml( filename = filename, patternMap = saplocmap$p24d2 )
```

---

loadvxmlbatch	<i>loads visual fields from a set of XML files</i>
---------------	--

---

## Description

loads visual fields from a set of XML files

## Usage

```
loadvxmlbatch( 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](#)

## Examples

```
# DO NOT RUN
#filename <- # Add the file name with the XML files to load
#vf      <- loadvxmlbatch( filename = filename, patternMap = saplocmap$p24d2 )
```

---

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 <a href="#">wtd.quantile</a> 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 possible 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](#)

**Examples**

```
# DO NOT RUN
# lperc <- locper()
```

---

nvcspsgalpha	<i>IU normative reference values for Contrast Sensitivity Perimetry. Alpha version!!!</i>
--------------	---

---

**Description**

Normative reference values or (normative values or nv for short) for Contrast Sensitivity Perimetry (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 global indices such as mean deviation (MD), pattern standard deviation (PSD) or visual-field index (VFI)

`sgrnfl_zest` **mandatory**. The actual normative values for the presentation 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 global indices such as 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 structures 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)
- nvt drank **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	<i>probability map for pattern deviation</i>
--------	--

---

**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	<i>probability map for pattern deviation from global sensitivity estimate</i>
-----------	---

---

**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	<i>pattern deviation</i>
-------	--------------------------

---

**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	<i>pattern deviation from general height rank (GHR)</i>
----------	---

---

**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, type = "slr", truncVal = 1,
       sl_test = NULL, typecomb = "fisher", details = FALSE )
```

**Arguments**

<code>vf</code>	<code>vf</code> object with threshold sensitivities, td, or pd values
<code>nperm</code>	number of permutations. Default is 5000
<code>type</code>	Type of regression statistic: <code>slr</code> for simple linear regression and <code>rank</code> for Spearman correlation coefficient. Default is <code>slr</code>
<code>truncVal</code>	p-value cut-off for truncation. Default is 1
<code>sl_test</code>	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 0
<code>typecomb</code>	Combination type for p-values. Default is <code>fisher</code>
<code>details</code>	Whether to return all details of the permutation analysis or just final results. Default is <code>FALSE</code>

**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**

[hist\\_poplr](#), [poplr\\_cstat](#), [poplr\\_pstat](#), [vflayout\\_poplr](#), [vfplot\\_poplr](#)

**Examples**

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

---

poplr_cstat	<i>permutation of pointwise linear regression (PoPLR): calculation of the combined statistic</i>
-------------	--

---

**Description**

For details see [1]

**Usage**

```
poplr_cstat( pval, typecomb = "fisher", truncVal = 1, minmax = TRUE,
             spatialwtd = NULL, distance = NULL, eccwtd = NULL )
```

**Arguments**

pval	p-values. Typically the ones obtained from <a href="#">poplr_pstat</a>
typecomb	Combination type for p-values. Default is fisher, by now the only one implemented
truncVal	p-value cut-off for truncation. Default is 1
minmax	whether to use minimum p-value if empty combination statistic after truncation. Default is TRUE
spatialwtd	Weights for spatial autocorrelation. Typically the p-values, the slope, or the Spearman rank correlation obtained with <a href="#">poplr_pstat</a> . If NULL, then the weights are all 1
distance	Pairwise distances between locations. Default is NULL
eccwtd	Eccentricity-related weights. Ask Neil. Default is NULL

**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](#), [hist\\_poplr](#), [poplr\\_pstat](#), [vflayout\\_poplr](#), [vfplot\\_poplr](#)

**Examples**

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

---

poplr_pstat	<i>Permutation of Pointwise Linear Regression (PoPLR): calculation of the p-value</i>
-------------	---

---

**Description**

For details see [1]

**Usage**

```
poplr_pstat( vf, porder, type = "slr", sl_test = NULL )
```

**Arguments**

vf	visual-field data. It can be td or pd as well
porder	order of permutations of visual-fields sensitivities. Each row contains a permutation of tests from vf
type	Type of regression statistic: slr for simple linear regression and rank for Spearman correlation coefficient. Default is slr
sl_test	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 returns two different structures depending on whether the analysis is linear regression (type = "slr" or Spearman rank correlation type = "rank"). For slr analysis, the structure 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 structure 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](#), [hist\\_poplr](#), [poplr\\_cstat](#), [vflayout\\_poplr](#), [vfplot\\_poplr](#)

**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 = 5,
         xlab = "years from first visit", ylab = "md",
         txtfont = "mono", pointsize = 12, cex = 1 )
```

**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 5
txtfont	font of the text with visual-sensitivity values. Default is mono
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. Default is 1

**Author(s)**

Ivan Marin-Franch

**Examples**

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

---

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 = visualFields::saplocmap$p24d2,
           bspos = visualFields::vfsettings$p24d2$bs )
```

**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](#)

**Examples**

```
# DO NOT RUN
# to test this, load a file using e.g. loadvfcsv with control data and then run
# age1m <- ageLinearModel( vf )
```

---

ringmapgraph	<i>ring legend for p-values</i>
--------------	---------------------------------

---

**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**

[vfcormap](#)



**Examples**

```
ringmapgraph()
```

---

saplocmap	<i>xy-position mapping between HFA device convention and visualFields convention for patterns of location</i>
-----------	---

---

**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 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

<code>vf</code>	<code>vf</code> -object with sensitivity thresholds
<code>smooth</code>	whether to use a function to smooth the results or not. Default is TRUE
<code>smoothFunction</code>	If <code>smooth</code> is true, the function to use for smoothing. Default is <code>quad2Dfit</code> , 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 deviation.

### Author(s)

Ivan Marin-Franch

### See Also

[ageLinearModel](#), [locperc](#), [quad2Dfit](#)

### Examples

```
#sdnv( vf )
```

---

sdnvghr	<i>standard deviations of normative values of PD from general-height-rank</i>
---------	---

---

### 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 <a href="#">quad2Dfit</a> , 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 deviation.

### Author(s)

Ivan Marin-Franch

### See Also

[ageLinearModel](#), [locperc](#), [quad2Dfit](#)

### Examples

```
#sdnvghr( vf )
```

---

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", "0D" )
```

---

tdpmap	<i>probability map for total deviation</i>
--------	--

---

**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	<i>total-deviation rank curve</i>
--------	-----------------------------------

---

**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	<i>percentiles for adjusted TD rank curve</i>
---------------	---

---

**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 <a href="#">wtd.quantile</a> 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 <a href="#">tdrankglm</a> , 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**

```
# DO NOT EXECUTE
#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**

<code>tdr</code>	table with TD rank curve
<code>familytxt</code>	family of distributions to use with <code>glm</code> fit. See <a href="#">family</a> . Default is gaussian
<code>link</code>	link function to use with <code>glm</code> fit. See <a href="#">family</a> . Default is logit
<code>rankCentral</code>	central ranked positions to use in the fit. By default it is NULL, so that all rank locations are used for the fit
<code>scaleFactor</code>	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

**References**

References?

**See Also**

[tdrank](#), [tdrankperc](#)

**Examples**

```
#tdrankglm()
```



---

tdranknv	<i>normative values for TD rank curve</i>
----------	---

---

**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 <a href="#">tdrankglm</a> , 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

**References**

References?

**See Also**

[tdrank](#), [tdrankglm](#)

**Examples**

```
#tdranknv()
```

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 <a href="#">wtd.quantile</a> 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 <a href="#">tdrankglm</a> , 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

### References

References?

### See Also

[tdrank](#), [tdrankglm](#)

### Examples

```
#tdrankperc()
```

---

tdval	<i>total deviation</i>
-------	------------------------

---

**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 )
```

---

vf91016csp1vf	<i>a vf-object with CSP sample data with</i>
---------------	--

---

**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](#)

---

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 = visualFields::vfenv$nv$pmapsettings )
```

**Arguments**

`map`                    array with the percentile for TD or PD probability map  
`mapval`                mapping values to use. Default is `nv$pmapsettings`

**Author(s)**

Chaitanya Khadilkar, Ivan Marin-Franch

**See Also**

[vfplot](#), [vfgrayscale](#)

**Examples**

```
# DO NOT EXECUTE
#vfcolormap( map )
```

---

vfdemographics	<i>demographics and statistics of sample in visual-fields object vf</i>
----------------	---

---

**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	<i>environment with the current normative values used visualFields</i>
-------	--

---

**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	<i>gray scales for sensitivities</i>
-------------	--------------------------------------

---

**Description**

maps sensitivity values to grayscales

**Usage**

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

**Arguments**

<code>sens</code>	an array with sensitivity values
<code>age</code>	age of the subject
<code>algorithm</code>	algorithm used in the visual test
<code>pattern</code>	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**

[vfieldcolormap](#)

**Examples**

```
# DO NOT EXECUTE
#vfieldgrayscale( sens )
```

---

vfielddefault

*Settings of visual field index*

---

**Description**

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

**Usage**

```
data( vfielddefault )
```

**Format**

vfieldsettings 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	<i>visual field index</i>
---------	---------------------------

---

**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, vfishet = visualFields::vfdefault )
```

**Arguments**

vf	stimulus sensitivities in dBs
td2pdcutoff	cutoff 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
vfishet	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	<i>probability values for visual field index</i>
-------------	--

---

### Description

calculates the probability values for visual field index

### Usage

```
vfindexpmap( vfi )
```

### Arguments

vfi                    visual fields index

### Details

calculates the probability 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](#), [loperc](#)

### Examples

```
# DO NOT EXECUTE  
#vfiperc( vals )
```

---

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,
          ffamily = "serif", sizetxt = 12,
          sizetxtSmall = 8, ffamilyvf = "serif",
          pointsize = 5,
          outerSymbol = "circle", outerInch = 0.13,
          innerSymbol = "circle", innerInch = outerInch / 1.9,
          lengthLines = 0, thicknessLines = 0 )
```

**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.
ffamily	Family font for the text in the form. Default is "Helvetica"
sizetxt	Text size for main text in the form. Default is 12
sizetxtSmall	Text size for details in the form. Default is 8
ffamilyvf	Family font for the number in the vfpots (TD, PD, etc). Default is "Times"
pointsize	Point size for numbers in the vfplots (TD, PD, etc). Default is 5
outerSymbol	Type of outer symbol. Default is "circle"
outerInch	Inches of outer symbol. Default is 0.13
innerSymbol	Type of inner symbol. Default is "circle"
innerInch	Inches of inner symbol. Default is outerInch / 1.9
lengthLines	Length of lines. Default is 0
thicknessLines	Line thickness. Default is 0

**Author(s)**

Ivan Marin-Franch

**See Also**

[vflayout\\_poplr](#), [vflayout\\_legoplot](#)

**Examples**

```
# show a printout
#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 )
```

**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.

**Author(s)**

Ivan Marin-Franch

**See Also**

[vflayout\\_poplr](#), [vflayout\\_legoplot](#)

**Examples**

```
# show a printout
#vflayoutghr( vf91016right[15,] )
```

---

vflayout\_legoplot      *legoplot visualization for change in sensitivities over time of visual fields*

---

### Description

displays a legoplot visualization for change in sensitivities over time of visual fields

### Usage

```
vflayout_legoplot( vf, grp = 3, pwidth = 8.27, pheight = 11.69,
                  margin = 0.25, filename = NULL,
                  ffamily = "serif", sizetxt = 12,
                  sizetxtSmall = 8,
                  ffamilyvf = "serif", pointsize = 6,
                  txtcolorlego = "red", pointsizelego = 16,
                  outerSymbol = "circle", outerInch = 0.12,
                  innerSymbol = "circle", innerInch = outerInch / 1.9,
                  inch2axisunits = 12.528,
                  lengthLines = 0, thicknessLines = 0,
                  outerSymbollego = "square", outerInchlego = 0.36,
                  innerSymbollego = "circle", innerInchlego = 0.16 )
```

### Arguments

vf	vf-object with sensitivity thresholds
grp	how many visual fields to group. Default is 3
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.
ffamily	Family font for the text in the form. Default is "Helvetica"
sizetxt	Text size for main text in the form. Default is 12
sizetxtSmall	Text size for details in the form. Default is 8
ffamilyvf	Font family for text in lego plots. Default is "Times"
pointsize	Point size for text in lego plots. Default is 6
txtcolorlego	Text color for lego plots. Default is "red"
pointsizelego	Point size for text of lego plots. Default is 16
outerSymbol	Type of outer symbol. Default is "circle"
outerInch	Inches of outer symbol. Default is 0.12
innerSymbol	Type of inner symbol. Default is "circle"

innerInch	Inches of inner symbol. Default is outerInch / 1.9
inch2axisunits	Conversion factor inches to axis units. Default is 12.528
lengthLines	Length of lines. Default is 0
thicknessLines	Line thickness. Default is 0
outerSymbollego	Type of outer lego symbol. Default is "square"
outerInchlego	Inches of outer lego symbol. Default is 0.36
innerSymbollego	Type of inner lego symbol. Default is "circle"
innerInchlego	Inches of inner lego symbol. Default is 0.16

**Author(s)**

Ivan Marin-Franch

**See Also**

[vflayout](#), [vflayout\\_poplr](#)

**Examples**

```
#vflayout_legoplot( vf91016right )
```

---

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,
                plotType = "vf", truncVal = 1,
                type = "slr", typecomb = "fisher",
                pwidth = 8.27, pheight = 11.69,
                margin = 0.25, filename = NULL,
                colorMapType = "pval", colorScale = NULL,
                ringMapType = NULL, ringScale = NULL,
                impairedVision = 10, rangeNormal = NULL,
                ffamily = "serif", sizetxt = 12,
                sizetxtSmall = 8,
                ffamilyvf = "serif", pointsize = 7,
                outerSymbol = "circle", outerInch = 0.12,
                innerSymbol = "circle", innerInch = outerInch / 1.9,
```

```

    inch2axisunits = 12.528,
    lengthLines = 0, thicknessLines = 0,
    outerInchpoplr = 0.185,
    innerInchpoplr = outerInchpoplr / 1.9,
    lengthLinespoplr = 0, borderThickness = 1.5 )

```

## 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
plotType	Type of plot to show. It can be visual sensitivities (vf), total-deviation values (td), or pattern-deviation values (pd)
truncVal	p-value cut-off for truncation. Default is 1
type	Type of regression statistic: slr for simple linear regression and rank for Spearman correlation coefficient. Default is slr
typecomb	Combination type for p-values. Default is fisher
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
ringMapType	what concentric rings categorizes. It can be pvals or slopes, or years blind. Default is NULL, for which no rings are shown.
ringScale	Ring mapping to use. Default is NULL. A different default is given depending on ringMapType
rangeNormal	range to indicate which slopes are normal. All significance from data points within the range will be removed. Default is NULL.
impairedVision	sensitivity below which it is considered impairment. Default is 10
ffamily	Family font for the text in the form. Default is "Helvetica"
sizetxt	Text size for main text in the form. Default is 12
sizetxtSmall	Text size for details in the form. Default is 8
ffamilyvf	Font family for text in lego plots. Default is "Times"
pointsize	Point size for text in lego plots. Default is 7
outerSymbol	Type of outer symbol. Default is "circle"
outerInch	Inches of outer symbol. Default is 0.12
innerSymbol	Type of inner symbol. Default is "circle"



innerInch	Inches of inner symbol. Default is outerInch / 1.9
inch2axisunits	Conversion factor inches to axis units. Default is 12.528
lengthLines	Line length. Default is 0
thicknessLines	Line thickness. Default is 0
outerInchpoplr	Size of outer symbols for PoPLR graph. Default is 0.185
innerInchpoplr	Size of inner symbols for PoPLR graph. Default is outerInchpoplr / 1.9
lengthLinespoplr	length of lines. Default is 0
borderThickness	Border thickness. Default is 1.5

**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](#), [vflayout\\_legoplot](#), [poplr](#), [hist\\_poplr](#), [poplr\\_cstat](#), [poplr\\_pstat](#), [vfplot\\_poplr](#)

**Examples**

```
#vflayout_poplr( vf91016right )
```

---

vobject

*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:

<b>id</b>	subject identification number
<b>tperimetry</b>	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 <a href="#">visualFields</a> . Nevertheless, <a href="#">visualFields</a> 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).
<b>talgorithm</b>	test algorithm. The algorithm used for the perimetric test. Possible values are sitas and zest. At the moment, only normative values for SAP, 24-2, SITA standard, is distributed with <a href="#">visualFields</a>
<b>tpattern</b>	test pattern. The pattern of locations used for the perimetric test. Possible values are p24d2 or p10d2. At the moment, only normative values for SAP, 24-2, SITA standard, is distributed with <a href="#">visualFields</a>
<b>tdate</b>	test date
<b>ttime</b>	test time
<b>stype</b>	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
<b>sage</b>	subject age. Important for the calculation of total-deviation values and probability maps.
<b>seye</b>	eye tested
<b>sbsx</b>	estimated x-position of the blind spot in degrees of angle of vision
<b>sbsy</b>	estimated y-position of the blind spot in degrees of angle of vision
<b>sfp</b>	false positives
<b>sfn</b>	false negatives
<b>sfl</b>	fixation losses
<b>sduration</b>	total duration of the test
<b>spause</b>	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:

<b>L1 .. L54 .. L68 .. L76</b>	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:

<b>msens</b>	mean sensitivity value; or the probability mapped value
<b>ssens</b>	standard deviation of the sensitivity values; or the probability mapped value
<b>mtdev</b>	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 index (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 probability maps
# tdp <- tdpmap( td )
# calculate pattern deviation probability 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, notSeenAsBlack = TRUE, newWindow = FALSE,
        txtfont = "serif", pointsize = 7, width = 6,
        xminmax = 29, yminmax = 29,
        outerSymbol = "circles", innerSymbol = "circles",
        outerSize = 1, innerSize = 1,
        outerInch = 0.14, innerInch = 0.08,
        lengthLines = 4.25, thicknessLines = 2 )
```

**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)
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 Helvetica
pointsize	size of the text with visual-sensitivity values. Default is 7
width	width of the window. height is calculated using the width, xminmax, and yminmax. Default is 6
xminmax	minimum and maximum limits on the x axis, in degrees of visual angle. Default is 29
yminmax	minimum and maximum limits on the y axis, in degrees of visual angle. Default is 29
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	Relative size of the outer symbol. Default is 1
innerSize	Relative size of the inner symbol. Default is 1
outerInch	Maximum size of the outer symbol in inches. Default is 0.14
innerInch	Maximum size of the inner symbol in inches. Default is 0.08
lengthLines	length of the lines denoting the orientation of the RNFL bundle. Default is 4.25
thicknessLines	thickness of the lines denoting the orientation of the RNFL bundle. Default is 2

**Details**

This function The vfplot function operates on a single row of visual fields (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 from the plot

**Author(s)**

Chaitanya Khadilkar, Ivan Marin-Franch

**See Also**

[vcolormap](#)

**Examples**

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

---

vplotloc	<i>visual field data plot</i>
----------	-------------------------------

---

**Description**

plots location-specific data at each location of the visual field. It is the function called by [vplot](#)

**Usage**

```
vplotloc( vals, eye, patternMap, outerColor, innerColor = NULL, bs = NULL,
          axesCol = "black", txtfont = "mono", pointsize = 7,
          txtcolor = NULL, xminmax = 29, yminmax = 29, outerSymbol = "circles",
          innerSymbol = "circles", outerSize = 1, innerSize = 1,
          outerInch = 0.2, innerInch = 0.1, lengthLines = 0,
          thicknessLines = 0, outerBorderColor = NULL, innerBorderColor = NULL,
          outerBorderThickness = 2, innerBorderThickness = 2 )
```

**Arguments**

vals	sensitivity threshold, TD or PD values, or other location-specific values
eye	eye being tested
patternMap	locations where to plot symbols, the TD and PD values
outerColor	colors to use for the outer symbols in the graph
innerColor	colors to use for the inner symbols in the graph. Default is NULL, meaning white
bs	location of the blind spot. Default is NULL meaning do not show blind spot
axesCol	color of the axes. Default is black
txtfont	font of the text with visual-sensitivity values. Default is mono
pointsize	size of the text with visual-sensitivity values. Default is 7
txtcolor	color of text. Default is black
xminmax	minimum and maximum limits on the x axis
yminmax	minimum and maximum limits on the y axis
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	Relative size of the outer symbol. Default is 1
innerSize	Relative 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
lengthLines	length of the lines denoting the orientation of the RNF bundle
thicknessLines	thickness of the lines denoting the orientation of the RNF bundle
outerBorderColor	Border for outer symbol denoting statistical significance. Default is NULL
innerBorderColor	Color of the inner border that represents statistical significance. Default is NULL.
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

### Details

The vfplot function operates on a single row of visual fields (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 from the plot

### Author(s)

Chaitanya Khadilkar, Ivan Marin-Franch

### See Also

[vfplot](#)

### Examples

```
# DO NOT EXECUTE
#vfplotloc( vals )
```

---

vfplot\_poplr *plot with the PoPLR analysis*

---

### Description

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

### Usage

```
vfplot_poplr( sl, pval, vfinfo, newWindow = FALSE, txtfont = "mono",
              pointsize = 7, width = 6,
              xminmax = 29, yminmax = 29,
              outerSymbol = "circles", innerSymbol = "circles",
              outerSize = 1, innerSize = 1,
              outerInch = 0.24, innerInch = 0.12,
              lengthLines = 0, thicknessLines = 0,
              colorMapType = "pval", colorScale = NULL,
              ringMapType = NULL, ringScale = NULL,
              impairedVision = 10, borderThickness = 2,
              idxNotSeen = NULL, rangeNormal = NULL,
              conormal = NULL )
```

### 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
txtfont	font of the text with visual-sensitivity values. Default is mono
pointsize	size of the text with visual-sensitivity values. Default is 7
width	width of the window. height is calculated using the width, xminmax and yminmax
xminmax	minimum and maximum limits on the x axis
yminmax	minimum and maximum limits on the y axis
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	Relative size of the outer symbol. Default is 1
innerSize	Relative 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

lengthLines	length of the lines denoting the orientation of the RNF bundle
thicknessLines	thickness of the lines denoting the orientation of the RNF bundle
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
ringMapType	what concentric rings categorizes. It can be pvals or slopes, or years blind. Default is NULL, for which no rings are shown.
ringScale	Ring mapping to use. Default is NULL. A different default is given depending on ringMapType
impairedVision	sensitivity below which it is considered impairment. Default is 10
borderThickness	Thickness of the borders if ringMapType is not NULL. Default is 5
idxNotSeen	index of locations that are not seen. These locations will be displayed with a solid black circle. Default is NULL.
rangeNormal	range to indicate which slopes are normal. All significance from data points within the range will be removed. Default is NULL.
conormal	if a rangeNormal is defined, then this specifies the within-normal category. Default is NULL. If colorMapType = "pval", then it is 95, if colorMapType = "slope", then it is 0.5

### Details

The vfplot function operates on a single row of visual fields (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 from the plot

### 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

[poplr](#), [hist\\_poplr](#), [poplr\\_cstat](#), [poplr\\_pstat](#), [vflayout\\_poplr](#)

### Examples

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



---

vfsegmentcoord	<i>calculate line segments to plot in <code>vfplot</code> representing the overall orientation of the retinal nerve fibre layer bundles according to Jansoniuous map [1]</i>
----------------	--

---

## 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. Jansoniuous, 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.

## Examples

```
# DO NOT EXECUTE
#vfsegmentcoord( lineMap,length )
```

---

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 sgrnf1. Each sub-structure contains three items:

bs locations that correspond to the anatomical region where the blind spot is. For 24-2, those are locations 26 and 35. There are none 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 location 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.

---

vfsort	<i>sort vf-objects</i>
--------	------------------------

---

**Description**

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

**Usage**

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

**Arguments**

<code>vf</code>	a <code>vf</code> -object
<code>decreasing</code>	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	<i>visual field stats</i>
---------	---------------------------

---

### 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	<i>probability values for visual field global indices</i>
-------------	---

---

**Description**

calculates the probability values for visual field global indices

**Usage**

```
vfstatspmap( vfindices )
```

**Arguments**

vfindices      visual fields global indices

**Details**

calculates the probability 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 )
```

---

xmlblock	<i>extracts a block from the XML file</i>
----------	---

---

**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**

[loadvxml](#), [loadvfcsv](#), [xmlitem](#)

**Examples**

```
# DO NOT RUN
#xmlblock( tag, xmllines )
```

---

xmldevval	<i>extracts total-deviation values, pattern-deviation values, total-deviation probability values, and pattern-deviation probability values</i>
-----------	--

---

**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**

[loadvxml](#), [xmlvval](#)

**Examples**

```
# DO NOT RUN
#xmldevval( xmllines, patternMap = saplocmap$p24d2 )
```

---

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
xmlines	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**

[loadvxml](#), [loadvfcsv](#), [xmlblock](#)

**Examples**

```
# DO NOT RUN
#xmlitem( tag, xmlines )
```

---

xmlvfval	<i>extracts visual-field sensitivity values</i>
----------	---

---

**Description**

extracts visual-field sensitivity values

**Usage**

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

**Arguments**

xmlines	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**

[loadvxml](#), [xmldevval](#)

**Examples**

```
# DO NOT RUN
#xmlvfval( xmllines, patternMap = saplocmap$p24d2 )
```

---

xmlvfxy	<i>dxttraction of (x,y)-coordinates of tested locations</i>
---------	---

---

**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](#)

**Examples**

```
# DO NOT RUN
#xmldevval( xmllines )
```

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