Package ‘flowPlots’

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Type Package

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Title flowPlots: analysis plots and data class for gated flow cytometry data

Description Graphical displays with embedded statistical tests for gated ICS flow cytometry data, and a data class which stores "stacked" data and has methods for computing summary measures on stacked data, such as marginal and polyfunctional degree data.

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License Artistic-2.0

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Suggests vcd

NeedsCompilation no

R topics documented:

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The adultsNeonates example data set of "stacked" data.

Description

The adultsNeonates data is an example of stacked data from an ICS Flow Cytometry assay.

Usage

data(adultsNeonates)

Value

data frame with 1 column of marker combination percentages and several cols of 'demographic’ data describing the percentage in a given row.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

References

TR Kollmann, J Crabtree, A Rein-Weston, D Blimkie, F Thomai, X Wang, J Furlong, E Fortuno III, A Hajjar, N Hawkins, S Self, and C Wilson, The neonatal innate immune system is not less responsive than the adult but responds differently, 2009, J Immunology, 183, 7150-7160

See Also

StackedData

Examples

# Load adultsNeoates data
data(adultsNeonates)
computeMarginalData-methods

Method `computeMarginalData` from Class "StackedData"

Description

This function is a method of the StackedData class which computes the marginal data which can be stored in the marginalData slot of a StackedData object. This method relies on the marker data slot being assigned in the StackedData object.

Usage

```r
computeMarginalData(object, byVarNames, idVarName, percentVarName, groupVarName)
```

Arguments

- **object**: an object of the StackedData class
- **byVarNames**: character; the names of the variables specifying the subsets of interest in the data
- **idVarName**: character; the name of the id variable in the data
- **percentVarName**: character; the name of the variable holding the percentages to be summed when computing the pfd summary data
- **groupVarName**: character; the name of the variable specifying the group assignment in the data

Value

data frame of marginal data

Methods

```r
signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")
```

Compute the marginal data.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

`StackedData`, `marginalData`

Examples

```r
# Load stacked data
data(adultsNeonates)

# Create a stacked data object
stackedDataObject = new("StackedData", stackedData=adultsNeonates)

# Compute the marker data and set the marker data slot
markerNames = c("TNFa","IL6","IL12","IFNa")
markers = computeMarkers(markerNames,includeAllNegativeRow=TRUE)
markers(stackedDataObject) = markers
```
# Compute the marginal data and set the marginal data slot
byVarNames = c("stim", "concGroup", "cell")
marginalData = computeMarginalData(stackedDataObject, byVarNames, "id", "percentAll", "group")
marginalData(stackedDataObject) = marginalData

---

**computeMarkers-methods**

*Method computeMarkers from Class "StackedData"*

**Description**

This function is a method of the StackedData class which computes the markers which can be stored in the markers data slot of a StackedData object. The marker matrix should match the order of the rows in the stacked data file. The stacked data should be sorted so that the order of each 'stack' in the file is the same. This method can be used to compute a marker matrix. If that matrix does not match the order of the 'stack', then the user can generate the marker matrix separately and assign it to the marker the data slot in a StackedData object.

**Usage**

```r
computeMarkers(markerNames, includeAllNegativeRow)
```

**Arguments**

- `markerNames` character; vector of the names of the markers
- `includeAllNegativeRow` logical; TRUE, if the stacked data contains the all-negative row of markers; for example, TNFa-IFNg-IL2-, in this case with 3 markers.

**Value**

matrix of 0's and 1's; rows represent marker combinations, cols represent markers.

**Methods**

```r
signature(markerNames = "character", includeAllNegativeRow = "logical") Compute the markers. Include the all negative row if the data includes the all negative case, such as: TNFa-IFNg-IL2-, in this case with 3 markers.
```

**Author(s)**

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

**See Also**

`StackedData, markers`
Examples

# Compute the marker data
markerNames = c("TNFa","IL6","IL12","IFNa")
markers = computeMarkers(markerNames,includeAllNegativeRow=TRUE)

## If you're using a StackedData object to compute summary data

# Create a stacked data object
stackedDataObject = new("StackedData")

# Assign the markers to the marker data slot
markers(stackedDataObject) = markers

Description

This function is a method of the StackedData class which computes the polyfunctional degree (pfd) data (usually recorded as percentages of reactive cells) which can be stored in the pfdData slot of a StackedData object. PFD=1 refers to cells which are producing only one marker. PFD=2 refers to cells which are producing exactly two markers. Similarly, up to PFD=n, where n is the number of markers. This method relies on the marker data slot being assigned in the StackedData object.

Usage

computePFDData(object, byVarNames, idVarName, percentVarName, groupVarName)

Arguments

object an object of the StackedData class
byVarNames character; the names of the variables specifying the subsets of interest in the data
idVarName character; the name of the id variable in the data
percentVarName character; the name of the variable holding the percentages to be summed when computing the pfd summary data
groupVarName character; the name of the variable specifying the group assignment in the data

Value

data frame of pfd data

Methods

signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")

Computes the pfd data.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA
computePFDGroupStatsList

Compute Group Stats on PFD Data to Be Used In a Legend

Description

This function can be used with ternaryplot() to add PFD group stats to, say, the legend. The stats computed are group size (N), pfd group mean, and pfd group standard deviation.

Usage

computePFDGroupStatsList(groupPFDDataList, pfdValues=1:3, numDigitsMean=3, numDigitsSD=2)

Arguments

- groupPFDDataList: one list item per group, each list item contains a matrix of PFD percentages; the rows are subjects, and the columns are pfd categories.
- pfdValues: vector of the PFD values that the columns in each matrix in the groupPFDDataList represent; eg. 1:3 for (PFD1, PFD2, PFD3).
- numDigitsMean: return a mean rounded to this number of digits
- numDigitsSD: return a standard deviation rounded to this number of digits

Value

A list; each list item contains the stats for a group as a 3 element character vector containing the size of the group, the mean PFD, and the standard deviation of the PFD.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA
## Load PFD data to plot
```r
data(pfdDF)
pfdDataSubset = subset(pfdDF, stim=="LPS" & concGroup==3 & cell=="mDC")
```

## Prepare the PFD Data for a call to ternaryplot()
```r
ternaryData = makeTernaryData(pfdDataSubset, 1, 2, 3:4)
colnames(ternaryData) = c("PFD1", "PFD2", "PFD3-4")
```

## Make a ternary plot
```r
library(vcd)
ternaryplot(ternaryData, cex=.5, col=as.numeric(pfdDataSubset$group)*2, main="Stimulation = LPS, Concentration Group = 3, Cell = mDC")
```

## Compute Group Stats to use in the legend of the ternary plot
```r
adultPFDData = subset(pfdDataSubset, group=="adult", select=c(PFD1:PFD3))
neoPFDData = subset(pfdDataSubset, group=="neonate", select=c(PFD1:PFD3))
groupPFDDataList = list(adultPFDData, neoPFDData)
```

## Specifically, compute the PFD Group Stats List
```r
pfdGroupStatsList = computePFDGroupStatsList(groupPFDDataList, pfdValues=1:3, numDigitsMean=3, numDigitsSD=2)
groupNames = c("Adults","Neonates")
```

## Create group names for the legend based on the PFD Group Stats List
```r
legendNames = legendPFDStatsGroupNames(pfdGroupStatsList,groupNames)
grid_legend(0.8, 0.7, pch=c(20,20), col=c(2,4), legendNames, title = "Group (n), mean/sd: ", gp=gpar(cex=.8))
```
computeProfileData-methods

percentVarName character; the name of the variable holding the percentages to be summed when computing the pfd summary data

groupVarName character; the name of the variable specifying the group assignment in the data

Value

a list. Each element of the list is a data frame containing the component percents for a given degree of polyfunctionality (PFD), except for the max PFD since there is only one possible combination for the max PFD.

Methods

signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")

Compute the pfd parts data.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData, pfdPartsData

Examples

# Load stacked data
data(adultsNeonates)
# Create a stacked data object
stackedDataObject = new("StackedData", stackedData=adultsNeonates)

# Compute the marker data and set the marker data slot
markerNames = c("TNFa", "IL6", "IL12", "IFNa")
markers = computeMarkers(markerNames, includeAllNegativeRow=TRUE)
markers(stackedDataObject) = markers

# Compute the pfd parts data and set the pfd parts data slot
byVarNames = c("stim", "concGroup", "cell")
pfdPartsData = computePFDPartsData(stackedDataObject, byVarNames, "id", "percentAll", "group")
pfdPartsData(stackedDataObject) = pfdPartsData

computeProfileData-methods

Method computeProfileData from Class "StackedData"

Description

This function is a method of the StackedData class which computes the profile data which can be stored in the profileData slot of a StackedData object. This method relies on the marker data slot being assigned in the StackedData object. No computation is required. Instead, the marker combination percentages data is re-organized to be 'horizontal' rather than 'stacked' (vertical). This makes it ready for plotting via the GroupListBoxplot() function.
Usage

```r
computeProfileData(object, byVarNames, idVarName, percentVarName, groupVarName)
```

Arguments

- `object` an object of the StackedData class
- `byVarNames` character; the names of the variables specifying the subsets of interest in the data
- `idVarName` character; the name of the id variable in the data
- `percentVarName` character; the name of the variable holding the percentages to be summed when computing the pfd summary data
- `groupVarName` character; the name of the variable specifying the group assignment in the data

Value

data frame of profile data

Methods

- `signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")`
  Compute the profile data.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

- `StackedData`
- `profileData`

Examples

```r
# Load stacked data
data(adultsNeonates)
# Create a stacked data object
stackedDataObject = new("StackedData", stackedData=adultsNeonates)

# Compute the marker data and set the marker data slot
markerNames = c("TNFa","IL6","IL12","IFNa")
markers = computeMarkers(markerNames,includeAllNegativeRow=TRUE)
markers(stackedDataObject) = markers

# Compute the profile percent data and set the profile percent data slot
byVarNames = c("stim", "concGroup", "cell")
profilePercent = computeProfileData(stackedDataObject, byVarNames, "id", "percentAll", "group")
profileData(stackedDataObject) = profilePercent
```
A Boxplot Function With Embedded Statistical Tests for Comparing Groups

Description

A function which creates boxplots side-by-side, with points overlaid, to compare groups. Group sizes and p-values from tests comparing groups can be printed on the plot.

Usage

GroupListBoxplot(dataList, ymaxBoxplot=NA, addToYmax2=.2, addToYmax1=.1, boxWidth=.10, boxColor=8, boxOutliers=TRUE, boxGroupColors=c(2,4,5,6,7,9,3,10,11,8,1), boxLty=1, boxLwd=3, boxPch=NA, boxCex=NA, legendInclude=TRUE, legendGroupNames=paste("Group ", 1:length(dataList), sep=""), legendX=NA, legendY=NA, legendCex=1, legendPCH=1, legendColors=1:length(legendGroupNames), legendLTY=NA, legendLWD=NA, legendTitle=NA, legendPoints=TRUE, legendLines=FALSE, printPoints=TRUE, pointChar=1, pointCex=1, pointColor=1:length(legendGroupNames), pointJitter=.25, mainTitle="Boxplots", mainTitleCex=1, mainTitleFont=1, mainTitleLine=1, testTitleCex=1, testTitleFont=1, testTitleLine=0, xLabel="X Axis", yLabel="Y Axis", xLabelCex=1, xLabelFont=1, xAxisRotation=1, xAtMtext=0, yAxisRotation=1, plotBoxLwd=1, testsRoundDigits=2, pCex=1, pFont=1, yP=NA, pValueLabel="p", betweenGroupTestsCompute=TRUE, pairedGroups=FALSE, printNs=TRUE, nCex=1, nFont=1, yN=NA)

Arguments

dataList A list of data frames. Each data frame contains the data for a group. Each column in the data frame represents a time point or category point on the plot.

ymaxBoxplot ymax for the boxplot will be set by R's boxplot() fcn, unless set here, default=NA

addToYmax2 this value is added to ymax if printing p-vals and N's, default=.2

addToYmax1 this value is added to ymax if only printing p-vals or N's, default=.1

boxWidth width of the box, default=.10

boxColor color of the box, default=8

boxOutliers print or suppress outlier points on the plot, default=TRUE

groupColorVector Vector of unique colors for a set of up to 11 groups, default=c(2,4,5,6,7,9,3,10,11,8,1)

boxLty Box outline type, default=1

boxLwd Box outline width, default=1

medLty median line type, default=1

medLwd median line width, default=3

medPch median point character, default=NA

medCex median point size expansion, default=NA

legendInclude Print legend on plot, default=TRUE

legendGroupNames names to use in the legend items, default=paste("Group ", 1:length(dataList), sep="")
legendX  
legendY  
legendCEX  
legendPCH  
legendColors  
legendLTY  
legendLWD  
legendTitle  
legendPoints  
legendLines  
printPoints  
pointChar  
pointCEX  
pointColor  
pointJitter  
mainTitle  
mainTitleCEX  
mainTitleFont  
mainTitleLine  
testTitleCEX  
testTitleFont  
testTitleLine  
xlabel  
ylabel  
xylabsCEX  
xylabsFont  
xAxisLabels  
xAxisCEX  
xAxisFont  
xAxisRotation  
xtext  
xMtextCEX  
xMtextFont  
xAtMtext  
yAxisCEX  
yAxisFont  
yAxisRotation  
plotBoxLWD  
testsRoundDigits  
pCEX
pFont  regular or bold font for p-value text, default=1
yP     y position for p-value text, default=NA
pvalueLabel label to use to precede numerical p-value, default="p"
betweenGroupTestsCompute include group comparison p-values in plots, default=TRUE
pairedGroups  are the groups paired?, default=FALSE
printNs include sample sizes on plots, default=TRUE
nCEX size of the sample size text to print, default=1
nFont regular or bold text for n’s, default=1
yN y position for the sample size text, default=NA

Author(s)
N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also
boxplot

Examples

# Create Sample dataList
group1DataFrame = as.data.frame(cbind(1:3,4:6))
group2DataFrame = as.data.frame(cbind(4:6,7:9))
datalist = list(group1DataFrame, group2DataFrame)

# Make the plot
GroupListBoxplot(datalist, xlabel="Cytokine", ylabel="Percent of CD4 Cells",
 xAxisLabels=c("IFNg","TNFa"), mainTitle="Compare Innate Immune Response",
 legendGroupNames=c("Group 1","Group 2"))

## -- Adults vs. Neonates Data -----------------------------------
## Marginal Data boxplot
# Get the data
data(marginalDF)
marginalDataSubset = subset(marginalDF, stim=="LPS" & concGroup==3 & cell=="mDC")
datalist = makeDataList(marginalDataSubset, "group", 1:5)

# Make the boxplot of marginal data
GroupListBoxplot(datalist, xlabel="Cytokine", ylabel="Percent of All Cells",
 xAxisLabels=c("TNF","IL6","IL12","IFNa","AnyMarker"),
 mainTitle="Stimulation = LPS and Concentration Group = 3 and Cell = mDC",
 legendGroupNames=c("Adults","Neonates"), pointColor=c(2,4), testTitleCEX=.8, nCEX=.8,
 pCEX=.8, legendColor=c(2,4), legendCEX=.7)
Create Group Names With Embedded Stats to Use in a Plot Legend

Description

This function returns a vector of groupNames of the form: "Adults (25) 1.5/.6", which represents
the group name, number of subjects in the group, the pfd mean / pfd standard deviation, where pfd
= polyfunctional degree.

Usage

legendPFDStatsGroupNames(pfdGroupStatsList, groupNames)

Arguments

pfdGroupStatsList
a list of vectors containing the pfd group stats of group size, pfd group mean,
and pfd group standard deviation

groupNames
a vector of group names, such as c("Adult", "Neonate")

Value

character vector; the length is equal to the number of groups. Each element of the vector contains
the formatted stats for a group. For a subset of the adultsNeonates data, the 2-element vector result
looks like this: "Adults (24), 1.47/0.10" "Neonates (30), 1.41/0.13"

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData

Examples

## Load the PFD data and prepare it for a call to ternaryplot()

data(pfdDF)
pfdDataSubset = subset(pfdDF, stim="LPS" & concGroup==3 & cell=="mDC")
ternaryData = makeTernaryData(pfdDataSubset, 1, 2, 3:4)
colnames(ternaryData) = c("PFD1", "PFD2", "PFD3-4")

## Make a ternary plot

library(vcd)
ternaryplot(ternaryData, cex=.5, col=as.numeric(pfdDataSubset$group)*2, main="Stimulation = LPS,
Concentration Group = 3, Cell = mDC")

## Compute PFD Stats to print in plot legend

adultPFDData = subset(pfdDataSubset, group="adult", select=c(PFD1:PFD3))
neoPFDData = subset(pfdDataSubset, group="neonate", select=c(PFD1:PFD3))
groupPFDDataList = list(adultPFDData, neoPFDData)
pfdGroupStatsList = computePFDGroupStatsList(groupPFDDataList, pfdValues=1:3, numDigitsMean=3,
    numDigitsSD=2)
groupNames = c("Adults","Neonates")

## Create group names including the PFD Stats for the legend
legendNames = legendPFDStatsGroupNames(pfdGroupStatsList, groupNames)

## Add the legend to the ternary plot
grid_legend(0.8, 0.7, pch=c(20,20), col=c(2,4), legendNames, title = "Group (n), mean/sd:",
gp=gpar(cex=.8))

makeBarplotData

Prepare Profile Data for a Call to Barplot()

Description

This function takes a dataframe of profile data and prepares a matrix of data for input to barplot()

Usage

makeBarplotData(profileData, profileColumns, groupVariableName)

Arguments

profileData dataframe of profile data, such as cell categories of cells
profileColumns the columns of profileData to include in the barplot
groupVariableName the column in the dataframe containing the group info

Value

a matrix whose rows represent different profile categories and whose columns represent different
groups. Each cell in the matrix contains the mean value for the group for a given profile category. For
profile data with 16 cytokine combinations for each of 2 groups, the matrix returned with have
dimensions (16,2).

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

GroupListBoxplot
makeDataList

Prepare Data in a Data Frame for a Call to GroupListBoxplot()

Description

This function makes a list of data, where each item of the list is a data frame and contains data for a group. The list can be used as input for a call to GroupListBoxplot().

Usage

makeDataList(theData, groupVariableName, columnsToKeep)

Arguments

theData data.frame containing data for 1 or more groups

groupVariableName character; name of the column in theData identifying group

columnsToKeep numeric vector specifying the column numbers in theData to include in the list of data.

Value

a list; each item of the list is a data frame and contains data for a group. The rows of each data frame are for subject. The cols of each data frame represent categories to be plotted on the x-axis.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

GroupListBoxplot
Examples

```r
# Load the data
data(marginalDF)
marginalDataSubset = subset(marginalDF, stim="LPS" & concGroup==3 & cell="mDC")

# Make a data list
dataList = makeDataList(marginalDataSubset, "group", 1:5)

# Make a plot using the data list
GroupListBoxplot(dataList, xlabel="Cytokine", ylabel="Percent of All Cells", xAxisLabels=c("TNFa","IL6","IL12","IFNa","AnyMarker"), mainTitle="Stimulation = LPS and Concentration Group = 3 and Cell = mDC", legendGroupNames=c("Adults","Neonates"), pointColor=c(2,4), testTitleCEX=.8, nCEX=.8, pCEX=.8, legendColor=c(2,4), legendCEX=.7)
```

### makeTernaryData

#### Description

This function takes a dataframe of polyfunctional degree (pfd) data and prepares a matrix with 3 columns (e.g., PFD1, PFD2, PFD3, or PFD1-2, PFD3-4, PFD5-6) to use as input to ternaryplot() in the vcd pkg. If multiple columns are specified for one of the three columns, the percentages for the multiple columns will be summed.

#### Usage

```r
makeTernaryData(pfdData, columns1, columns2, columns3, columnNames=c("PFD=1","PFD=2","PFD=3"))
```

#### Arguments

- **pfdData**: data frame containing data for 1 or more groups
- **columns1**: numeric; column(s) of pfd data to place in the first column of the matrix
- **columns2**: numeric; column(s) of pfd data to place in the second column of the matrix
- **columns3**: numeric; column(s) of pfd data to place in the third column of the matrix
- **columnNames**: (optional) character vector of names for the three columns of the matrix

#### Value

matrix of 3 columns; rows = subjects, cols = data for each point on the triangle

#### Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

#### See Also

- StackedData
**Examples**

```r
## Load the PFD Data to plot in a ternary plot
data(pfdDF)
pfdDataSubset = subset(pfdDF, stim=="LPS" & concGroup==3 & cell=="mDC")

## Prepare the PFD Data for a call to ternaryplot()
ternaryData = makeTernaryData(pfdDataSubset, 1, 2, 3:4)
colnames(ternaryData) = c("PFD1", "PFD2", "PFD3-4")

## Make the ternary plot
library(vcd)
ternaryplot(ternaryData, cex=.5, col=as.numeric(pfdDataSubset$group)*2, main="Stimulation = LPS, Concentration Group = 3, Cell = mDC")

## Prepare a legend with group stats
adultPFDData = subset(pfdDataSubset, group=="adult", select=c(PFD1:PFD3))
neoPFDData = subset(pfdDataSubset, group=="neonate", select=c(PFD1:PFD3))
groupPFDDataList = list(adultPFDData, neoPFDData)
pfdGroupStatsList = computePFDGroupStatsList(groupPFDDataList, pfdValues=1:3, numDigitsMean=3, numDigitsSD=2)
groupNames = c("Adults","Neonates")
legendNames = legendPFDStatsGroupNames(pfdGroupStatsList,groupNames)
grid_legend(0.8, 0.7, pch=c(20,20), col=c(2,4), legendNames, title = "Group (n), mean/sd:", gp=gpar(cex=.8))
```

---

**Description**

This function is a method of the StackedData class which can retrieve the marginalData from a StackedData object or which can assign the marginalData data slot of a StackedData object.

**Usage**

```r
# Get the marginal data from a StackedData object
marginalData(object)

# Set the marginal data slot of a StackedData object
## S4 replacement method for signature 'StackedData'
marginalData(object) <- value
```

**Arguments**

- `object` an object of the StackedData class
- `value` a replacement value
**Value**

data frame of marginal data.

**Methods**

signature(object="StackedData") Get the value of the marginalData slot in the stackedDataObject.

signature(object = "StackedData", value = "data.frame") Set the value of the marginalData slot in the stackedDataObject.

**Author(s)**

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

**See Also**

StackedData, marginalData

**Examples**

```r
# Load the marginal data and set the marginal data slot
data(marginalDF)
# Create a stacked data object
stackedDataObject = new("StackedData")
# Set the marginal data slot
marginalData(stackedDataObject) = marginalDF

# Get the marginal data from the stacked data object
marginalData = marginalData(stackedDataObject)
```

---

**Description**

The marginal data computed from the adultsNeonates data.

**Usage**

data(marginalDF)

**Value**

data frame; There are (n+1) columns in the data frame for the marginal percentages; one col for each marker and 1 col for "anyMarker", which is the sum of the individual marker cols. The data frame also has cols of 'demographic' data describing each row of percentages.

**Author(s)**

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA
**See Also**

StackedData

**Examples**

```r
# Load marginal data
data(marginalDF)
```

---

**Description**

The markers data created to match the order of the marker combinations in each subset of interest in the adultsNeonates data.

**Usage**

```r
data(markerMatrix)
```

**Value**

matrix of 0's and 1's; rows = marker combinations, cols = marker names.

**Author(s)**

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

**See Also**

StackedData

**Examples**

```r
# Load marker data
data(markerMatrix)
```

---

**Description**

This function is a method of the StackedData class which retrieves the markers from a StackedData object or which assigns the markers data slot of a StackedData object.
Usage

# Get the marker matrix from a StackedData object.
markers(object)

# Set the marker matrix slot of a StackedData object.
## S4 replacement method for signature 'StackedData'
markers(object) <- value

Arguments

object an object of the StackedData class
value a replacement value

Value

matrix of markers data.

Methods

signature(object = "StackedData") Get the marker matrix from the object.
signature(object = "StackedData", value = "matrix") Set the value of the markers data slot in the object.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData, markers

Examples

# Load the marker data and set the marker data slot
data(markerMatrix)

# Create a stacked data object
stackedDataObject = new("StackedData")

# Set the marker data slot
markers(stackedDataObject) = markerMatrix

# Get the marker data from the stacked data object
markers = markers(stackedDataObject)
Description
This function is a method of the StackedData class which retrieves the pfdData from a StackedData object or which assigns the pfdData data slot of a StackedData object.

Usage

```r
# Get the pfdData from a StackedData object.
pfdData(object)

# Set the pfdData slot of a StackedData object.
## S4 replacement method for signature 'StackedData'
pfdData(object) <- value
```

Arguments

- `object`: an object of the StackedData class
- `value`: a replacement value

Value
data frame of pfd data.

Methods

- `signature(object = "StackedData")` Get the pfdData from the object.
- `signature(object = "StackedData", value = "data.frame")` Set the value of the pfdData slot in the object.

Author(s)
N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also
- `StackedData, pfdData`

Examples

```r
# Load the pfd data and set the pfd data slot
data(pfdDF)

# Create a stacked data object
stackedDataObject = new("StackedData")

# Set the pfd data slot
pfdData(stackedDataObject) = pfdDF
```
# Get the pfd data from the stacked data object
pfdData = pfdData(stackDataObject)

pfdDF

An example of pfdData

Description
The polyfunctional degree (pfd) data computed from the adultsNeonates data.

Usage
data(pfdDF)

Value
data frame; The data frame contains n columns of PFD percentages of reactive cells, where n is the number of markers in the data set, as well as 'demographic' data for each row of percentages. PFD=1 refers to the percentages of reactive cells which are producing only one marker, irregardless of which marker. PFD=2 refers to cells which are producing exactly two markers. Similarly, up to PFD=n markers.

Author(s)
N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also
StackedData

Examples
# Load pfd data
data(pfdDF)

Method pfdPartsData from Class "StackedData"

Description
This function is a method of the StackedData class which retrieves the pfdPartsData from a StackedData object or which assigns the pfdPartsData data slot of a StackedData object.

Usage

# Get the pfdPartsData from a Stacked Data object.
pfdPartsData(object)

# Set the pfdPartsData of a Stacked Data object.
# S4 replacement method for signature 'StackedData'
pfdPartsData(object) <- value
**Arguments**

- **object** an object of the StackedData class
- **value** a replacement value

**Value**

a list. Each element of the list is a data frame containing the component percents for a given degree of polyfunctionality (PFD), except for the max PFD since there is only one possible combination for the max PFD.

**Methods**

- **signature(object = "StackedData")** Get the pfdPartsData from the object.
- **signature(object = "StackedData", value = "list")** Set the value of the pfdPartsData slot in the object.

**Author(s)**

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

**See Also**

StackedData, pfdPartsData

**Examples**

```r
# Load the pfdParts data and set the pfdParts data slot
data(pfdPartsList)

# Create a stacked data object
stackedDataObject = new("StackedData")

# Set the pfdParts data slot
pfdPartsData(stackedDataObject) = pfdPartsList

# Get the pfd parts data
pfdPartsData = pfdPartsData(stackedDataObject)
```

---

**Description**

The pfd parts data computed from the adultsNeonates data.

**Usage**

data(pfdPartsList)
profileData-methods

Value

a list: pdfPartsData is a list of data frames. The first data frame holds the compositional percentages for PFD=1; that is, of the cells producing only one marker, the percentage of cells which express marker1, the percentage of cells which produce marker2, etc. For example, if there are 4 markers, the data frame for PFD=1 will have a percentage column for each marker, and the sum of those 4 cols will equal 100. The second data frame has n-choose-2 columns of percentages, where n is the number of markers and 2 is the polyfunctional degree; i.e. the 2 in PFD=2. And, so on. The length of the list is (maxPFD-1), since there is only 1 way to achieve maxPFD; that is, all markers are positive when PFD=maxPFD. Each data frame also contains 'demographic' data describing each row of percentages.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData

Examples

# Load pfd parts data
data(pfdPartsList)

profileData-methods  Method profileData from Class "StackedData"

Description

This function is a method of the StackedData class which retrieves the profileData from a StackedData object or which assigns the profileData data slot of a StackedData object.

Usage

# Get the profileData from a StackedData object.
profileData(object)

# Set the profileData slot of a StackedData object.
## S4 replacement method for signature 'StackedData'
profileData(object) <- value

Arguments

object an object of the StackedData class
value a replacement value

Value
data frame of profile data.
Methods

signature(object = "StackedData") Get the profileData from the object.
signature(object = "StackedData", value = "data.frame") Set the value of the profileData slot in the object.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData, profileData

Examples

# Load the profile data, create a stackedData object and set the profile data slot
data(profileDF)
# Create a stacked data object
stackedDataObject = new("StackedData")
# Set the profile data slot
profileData(stackedDataObject) = profileDF

# Get the profile data from the stacked data object
profileData = profileData(stackedDataObject)

ProfileDF

Description

An example of profileData

The profile data computed from the adultsNeonates data.

Usage

data(profileDF)

Value

A data frame containing cols for the percentages for each of the marker combinations (the profile percentages), as well as 'demographic' data describing each row of percentages. For example, if there are 4 markers in the data set, there will be 2^4 columns for the profile percentages if all possible combinations are included. If the all-negative combination is excluded, there will be (2^4-1) cols of profile percentages.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData
Examples

# Load profile data
data(profileDF)

stackedDataFrame = readStackedData(fileName=system.file("extdata","adultsNeonates.csv", package="flowPlots"))
StackedData-class

### Description

Stacked data refers to gated data originating from an ICS Flow Cytometry experiment where the marker combinations for a subset of interest, say a given cell type, stimulus, and concentration, are "stacked". A common type of marker is a cytokine. A subset of stacked data could look like this:

```
  id  group stim concGroup cell percentAll count totalCount percentReactive cytCombo
a2004 adult LPS  3 mDC  0.00  0   700   0.000000 TNFa+IL6+IL12+IFNa+
a2004 adult LPS  3 mDC  0.43  3   700   0.940625 TNFa+IL6+IL12+IFNa-
a2004 adult LPS  3 mDC  0.00  0   700   0.000000 TNFa+IL6+IL12-IFNa+
a2004 adult LPS  3 mDC 21.86 153  700  47.818750 TNFa+IL6+IL12-IFNa-
a2004 adult LPS  3 mDC  0.00  0   700   0.000000 TNFa+IL6-IL12+IFNa+
a2004 adult LPS  3 mDC  0.29  2   700   0.634375 TNFa+IL6-IL12+IFNa-
a2004 adult LPS  3 mDC  0.00  0   700   0.000000 TNFa+IL6-IL12-IFNa+
a2004 adult LPS  3 mDC 19.71 138  700  43.115625 TNFa+IL6-IL12-IFNa-
```

### Details

The marker combinations in the stacked data should be ordered within each subset of interest (for example: subjectID, celltype, concentration, and stimulation) to match the marker matrix. If the data are not in this order, it should be sorted into this order before using the computeProfileData, computeMarginalData, computePFFData, computePFFPartsData methods. The computeMarkers method can be used to compute the marker matrix used by these methods. If the matrix computed does not match the order of your data, then you can supply your own marker matrix, assign it to the marker data slot of a StackedData object, and then use the `compute` methods to compute the other types of data.

### Objects from the Class

Objects can be created by calls of the form:

```r
  stackedDataObject = new("StackedData", stackedData=NA, profileData=NA, marginalData=NA, ...
```

### Slots

- `stackedData`: "data.frame" of stacked data
- `profileData`: "data.frame" of profile data
- `marginalData`: "data.frame" of marginal data
- `pfdData`: "data.frame" of pfd data
- `pfdPartsData`: "list" of "data.frame"'s of pfd parts data
- `markers`: "matrix" of marker data
Methods

computeMarginalData signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")
computeMarkers signature(markerNames = "character", includeAllNegativeRow = "logical")
computePFDData signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")
computePFDPartsData signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")
computeProfileData signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "character", groupVarName = "character")

# getters
marginalData signature(object = "StackedData")
markers signature(object = "StackedData")
pfdData signature(object = "StackedData")
pfdPartsData signature(object = "StackedData")
profileData signature(object = "StackedData")
stackedData signature(object = "StackedData")

# setters
marginalData signature(object = "StackedData", value = "data.frame")
markers signature(object = "StackedData", value = "matrix")
pfdData signature(object = "StackedData", value = "data.frame")
pfdPartsData signature(object = "StackedData", value = "list")
profileData signature(object = "StackedData", value = "data.frame")
stackedData signature(object = "StackedData", value = "data.frame")

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

markers, profileData, marginalData, pfdData, pfdPartsData, adultsNeonates

Examples

# View the Data Slots in StackedData
showClass("StackedData")

# Load stacked data
data(adultsNeonates)
# Create a stacked data object
stackedDataObject = new("StackedData", stackedData=adultsNeonates)

# Compute the marker data and set the marker data slot
# The marker matrix computed here matches the order of the marker combinations
# in the adultsNeonates stacked data within each subset of interest
markerNames = c("TNFa","IL6","IL12","IFNa")
markers = computeMarkers(markerNames,includeAllNegativeRow=TRUE)
makers(stackedDataObject) = markers

# Compute the profile data and set the profile data slot
byVarNames = c("stim", "concGroup", "cell")
profileData = computeProfileData(stackedDataObject, byVarNames, "id", "percentAll", "group")
profileData(stackedDataObject) = profileData
# Compute the marginal data and set the marginal data slot
byVarNames = c("stim", "concGroup", "cell")
marginalData = computeMarginalData(stackedDataObject, byVarNames, "id", "percentAll", "group")
marginalData(stackedDataObject) = marginalData

# Compute the pfd data and set the pfd data slot
byVarNames = c("stim", "concGroup", "cell")
pfdData = computePFDData(stackedDataObject, byVarNames, "id", "percentAll", "group")
pfdData(stackedDataObject) = pfdData

# Compute the pfd parts data and set the pfd parts data slot
byVarNames = c("stim", "concGroup", "cell")
pfdPartsData = computePFDPartsData(stackedDataObject, byVarNames, "id", "percentAll", "group")
pfdPartsData(stackedDataObject) = pfdPartsData

# Get the data from the stacked data object
markers = markers(stackedDataObject)
profileData = profileData(stackedDataObject)
marginalData = marginalData(stackedDataObject)
pfdData = pfdData(stackedDataObject)
pfdPartsData = pfdPartsData(stackedDataObject)

---

**stackedData-methods**  
*Method stackedData from Class "StackedData"*

**Description**

This function is a method of the StackedData class which retrieves the stackedData from a StackedData object or which assigns the stackedData data slot of a StackedData object.

**Usage**

```r
# Get the stacked data from the StackedData object
stackedData(object)

# Set the stacked data slot of a StackedData object
## S4 replacement method for signature 'StackedData'
stackedData(object) <- value
```

**Arguments**

- **object**
  - an object of the StackedData class
- **value**
  - a replacement value

**Value**

data frame of stacked data.
Methods

signature(object = "StackedData") Get the stackedData from the object.
signature(object = "StackedData", value = "data.frame") Set the value of the stacked-Data slot in the object.

Author(s)

N. Hawkins, Fred Hutchinson Cancer Research Center, Seattle, WA

See Also

StackedData

Examples

## Set the stacked data slot WHILE creating a new stacked data object

# Load stacked data
data(adultsNeonates)
# Create a stacked data object
stackedDataObject = new("StackedData", stackedData=adultsNeonates)

## Set the stacked data slot AFTER creating a new stacked data object

# Load stacked data
data(adultsNeonates)
# Create a stacked data object
stackedDataObject = new("StackedData")
# Set the stacked data slot
stackedData(stackedDataObject) = adultsNeonates

## Set the stacked data slot after creating a new stacked data object

stackedDataFrame = readStackedData(fileName=system.file("extdata","adultsNeonates.csv", package="flowPlots")
stackedDataObject = new("StackedData")
stackedData(stackedDataObject) = stackedDataFrame
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