

# 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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## Contents

|  |   |
|--|---|
| adultsNeonates . . . . .               | 2 |
| computeMarginalData-methods . . . . .  | 3 |
| computeMarkers-methods . . . . .       | 4 |
| computePFDData-methods . . . . .       | 5 |
| computePFDDGroupStatsList . . . . .    | 7 |
| computePFDDPartsData-methods . . . . . | 8 |

|                                      |           |
|--------------------------------------|-----------|
| computeProfileData-methods . . . . . | 9         |
| GroupListBoxplot . . . . .           | 11        |
| legendPFDStatsGroupNames . . . . .   | 14        |
| makeBarplotData . . . . .            | 15        |
| makeDataList . . . . .               | 16        |
| makeTernaryData . . . . .            | 17        |
| marginalData-methods . . . . .       | 19        |
| marginalDF . . . . .                 | 20        |
| markerMatrix . . . . .               | 21        |
| markers-methods . . . . .            | 21        |
| pfdData-methods . . . . .            | 22        |
| pfdDF . . . . .                      | 24        |
| pfdPartsData-methods . . . . .       | 24        |
| pfdPartsList . . . . .               | 26        |
| profileData-methods . . . . .        | 26        |
| profileDF . . . . .                  | 28        |
| readStackedData-methods . . . . .    | 28        |
| StackedData-class . . . . .          | 29        |
| stackedData-methods . . . . .        | 32        |
| <b>Index</b>                         | <b>34</b> |

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|                |   |
|----------------|---|
| adultsNeonates | <i>The adultsNeonates example data set of "stacked" data.</i> |
|----------------|---|

---

## 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 adultsNeonates 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**

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

**Arguments**

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

**Value**

data frame of marginal data

**Methods**

```
signature(object = "StackedData", byVarNames = "character", idVarName = "character", percentVarName = "ch")
Compute the marginal data.
```

**Author(s)**

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

**See Also**

[StackedData](#), [marginalData](#)

**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 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**

```
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-IL6-IL12-IFNa-

**Value**

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

**Methods**

`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
```

---

computePFDData-methods

*Method computePFDData from Class "StackedData"*

---

**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 = "ch")  
Computes the pfd data.

**Author(s)**

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

**See Also**

[StackedData](#), [pfdData](#)

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

---

`computePFDDGroupStatsList`*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

```
computePFDDGroupStatsList(groupPFDDDataList, pfdValues=1:3, numDigitsMean=3, numDigitsSD=2)
```

### Arguments

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

### See Also

[StackedData](#), [pfdData](#)

### Examples

```
## Load PFD data to 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 a ternary plot
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
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
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
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))

```

---

computePFDPartsData-methods

*Method computePFDPartsData from Class "StackedData"*

---

## Description

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

## Usage

```
computePFDPartsData(object, byVarNames, idVarName, percentVarName, groupVarName)
```

## Arguments

|                             |  |
|-----------------------------|--|
| <code>object</code>         | an object of the <code>StackedData</code> class  |
| <code>byVarNames</code>     | character; the names of the variables specifying the subsets of interest in the data                         |
| <code>idVarName</code>      | character; the name of the id variable in the data   |
| <code>percentVarName</code> | character; the name of the variable holding the percentages to be summed when computing the pfd summary data |
| <code>groupVarName</code>   | 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")  
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

```
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 = "ch")  
Compute the profile data.

**Author(s)**

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

**See Also**

[StackedData](#), [profileData](#)

**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 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
```

---

|                  |  |
|------------------|--|
| GroupListBoxplot | <i>A Boxplot Function With Embedded Statistical Tests for Comparing Groups</i> |
|------------------|--|

---

### 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, groupColorVector=c(2,4,5,6,7,9,3,10,11,8,1), boxlty=1, boxlwd=1,
  medlty=1, medlwd=3, medpch=NA, medcex=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", xylabCEX=1, xylabFont=1, xAxisLabels=NA, xAxisCEX=1, xAxisFont=1,
  xAxisRotation=1, xMtext="", xMtextCEX=1, xMtextFont=1, xAtMtext=0, yAxisCEX=1, yAxisFont=1,
  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

|                               |  |
|-------------------------------|--|
| <code>dataList</code>         | 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. |
| <code>ymaxBoxplot</code>      | ymax for the boxplot will be set by R's <code>boxplot()</code> fcn, unless set here, default=NA  |
| <code>addToYmax2</code>       | this value is added to ymax if printing p-vals and N's, default=.2   |
| <code>addToYmax1</code>       | this value is added to ymax if only printing p-vals or N's, default=.1   |
| <code>boxWidth</code>         | width of the box, default=.10  |
| <code>boxColor</code>         | color of the box, default=8  |
| <code>boxOutliers</code>      | print or suppress outlier points on the plot, default=TRUE   |
| <code>groupColorVector</code> | 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)   |
| <code>boxlty</code>           | Box outline type, default=1  |
| <code>boxlwd</code>           | Box outline width, default=1   |
| <code>medlty</code>           | median line type, default=1  |
| <code>medlwd</code>           | median line width, default=3   |
| <code>medpch</code>           | median point character, default=NA   |
| <code>medcex</code>           | 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          | legend X location, default=NA   |
| legendY          | legend Y location, default=NA   |
| legendCEX        | point size for legend text, default=1   |
| legendPCH        | symbol or character to print next to legend names, default=1  |
| legendColors     | colors of the points or lines next to the legend names, default=1:length(legendGroupNames)                |
| legendLTY        | line type to print next to legend names, default=NA   |
| legendLWD        | width of line to print next to legend names, default=NA   |
| legendTitle      | legend title, default=NA  |
| legendPoints     | print points next to legend names, default=TRUE   |
| legendLines      | print lines next to legend names, default=FALSE   |
| printPoints      | overlay the points on the boxplot, default=TRUE   |
| pointChar        | symbol or character to plot, default=1  |
| pointCEX         | size of point plotted, default=1  |
| pointColor       | color of point plotted – can be single value, vector, matrix, or list, default=1:length(legendGroupNames) |
| pointJitter      | amount to scatter points around group x position, default=.25   |
| mainTitle        | text for main title, default="Boxplots"   |
| mainTitleCEX     | size of main title, default=1   |
| mainTitleFont    | regular or bold font, default=1   |
| mainTitleLine    | margin line on which to print main title - minimum is 0, default=1  |
| testTitleCEX     | size of stat test title, default=1  |
| testTitleFont    | regular or bold font, default=1   |
| testTitleLine    | margin line on which to print title - minimum is 0, default=0   |
| xlabel           | label for X axis, default="X Axis"  |
| ylabel           | label for Y axis, default="Y Axis"  |
| xylabCEX         | size of x and y axes labels, default=1  |
| xylabFont        | regular or bold font for X and Y axes labels, default=1   |
| xAxisLabels      | labels for ticks on x axis, default=NA  |
| xAxisCEX         | size of labels on x ticks, default=1  |
| xAxisFont        | regular or bold font for x tick labels, default=1   |
| xAxisRotation    | horizontal or vertical x tick labels, default=1   |
| xMtext           | text to place in x-axis margin, default=""  |
| xMtextCEX        | size of text to place in x-axis margin, default=1   |
| xMtextFont       | regular or bold font for text in x-axis margin, default=1   |
| xAtMtext         | x position for text in x-axis margin, size of y tick labels, default=0                                    |

|                          |  |
|--------------------------|--|
| yAxisCEX                 | size of y tick labels, default=1                         |
| yAxisFont                | regular or bold font for y axis tick labels, default=1   |
| yAxisRotation            | horizontal or vertical y tick labels, default=1          |
| plotBoxLWD               | line width of box drawn around entire plot, default=1    |
| testsRoundDigits         | number of digits to report in p-value, default=2         |
| pCEX                     | size of p-value text, default=1                          |
| 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 group boxplot of marginal data
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)
```

---

legendPFDDStatsGroupNames

*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

```
legendPFDDStatsGroupNames(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 will have dimensions (16,2).

**Author(s)**

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

**See Also**

[GroupListBoxplot](#)

**Examples**

```
data(profileDF)
profileDataSubset = subset(profileDF, stim=="LPS" & concGroup==3 & cell=="mDC")
profileColumns = 1:16
barplotData = makeBarplotData(profileDataSubset, profileColumns, groupVariableName="group")
barplotDataWithLegend = cbind(barplotData, NA, NA)
barColors = gray(0:15/15)[16:1]
barplot(barplotDataWithLegend, col=barColors, main="Stimulation = LPS
        Concentration Group = 3
        Cell = mDC")
legendNames = rownames(barplotData)
legend(2.75, 100, legend=legendNames[16:1], col=barColors[16:1], cex=.8, pch=20)
```

---

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**

```
# 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

*Prepare PFD Data for a Call to ternaryplot()*

---

**Description**

This function takes a dataframe of polyfunctional degree (pfd) data and prepares a matrix with 3 columns (egs. 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**

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

**Arguments**

|             |  |
|-------------|--|
| pfdfData    | 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**

```
## 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))
```

---

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

---

### 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

```
# 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

```
# 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)
```

---

marginalDF

*An example of marginalData*

---

## 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

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

---

|              |  |
|--------------|--|
| markerMatrix | <i>An example of the markers data.</i> |
|--------------|--|

---

**Description**

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

**Usage**

```
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**

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

---

|                 |  |
|-----------------|--|
| markers-methods | <i>Method markers from Class "StackedData"</i> |
|-----------------|--|

---

**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)
```

---

pfdData-methods

*Method pfdData from Class "StackedData"*

---

**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**

```
# 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**

```
# 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(stackedDataObject)
```

---

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)
```

---

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

---

### Description

This function is a method of the StackedData class which retrieves the pfdPartsData from a Stacked-Data 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**

```
# 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)
```

---

`pdfPartsList`*An example of pdfPartsData*

---

**Description**

The pdf parts data computed from the adultsNeonates data.

**Usage**

```
data(pdfPartsList)
```

**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 pdf parts data
data(pdfPartsList)
```

---

`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`*An example of profileData*

---

**Description**

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)
```

---

`readStackedData-methods`*Method readStackedData from Class "StackedData"*

---

**Description**

This function is a method of the StackedData class which reads a csv file of stacked data into a data frame, which can be stored in the stackedData data slot of a StackedData object. This function is a wrapper for the R base function, `read.csv()`, for users not so familiar with R.

**Usage**

```
readStackedData(fileName)
```

**Arguments**

fileName            character; the full name of the file containing stacked data in csv format.

**Value**

data frame of stacked data.

**Methods**

signature(fileName = "character") Wrapper function for read.csv() to read a file of stacked data.

**Author(s)**

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

**See Also**

[StackedData](#), [read.csv](#)

**Examples**

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

---

StackedData-class            *Class "StackedData"*

---

**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`, `computePFDDData`, `computePFDPartsData` 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:

```
stackedDataObject = new("StackedData", stackedData=NA, profileData=NA, marginalData=NA,
  pfdData=NA, pfdPartsData=NA, markers=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")
computePFDDData 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")
pfData signature(object = "StackedData", value = "data.frame")
pfDataParts 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](#), [pfData](#), [pfDataParts](#), [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)
markers(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 pfData data and set the pfData data slot
byVarNames = c("stim", "concGroup", "cell")
pfData = computePFData(stackedDataObject, byVarNames, "id", "percentAll", "group")
pfData(stackedDataObject) = pfData

# Compute the pfData parts data and set the pfData 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

```

# 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

|                     |   |
|---------------------|---|
| <code>object</code> | an object of the <code>StackedData</code> class |
| <code>value</code>  | 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 `stackedData` 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
```

# Index

adultsNeonates, [2](#), [31](#)

boxplot, [13](#)

computeMarginalData  
(computeMarginalData-methods),  
[3](#)

computeMarginalData, StackedData, character, character, character, character-method  
(computeMarginalData-methods),  
[3](#)

computeMarginalData-methods, [3](#)

computeMarkers  
(computeMarkers-methods), [4](#)

computeMarkers, character, logical-method  
(computeMarkers-methods), [4](#)

computeMarkers-methods, [4](#)

computePFDData  
(computePFDData-methods), [5](#)

computePFDData, StackedData, character, character, character, character-method  
(computePFDData-methods), [5](#)

computePFDData-methods, [5](#)

computePFDDGroupStatsList, [7](#)

computePFDDPartsData  
(computePFDDPartsData-methods),  
[8](#)

computePFDDPartsData, StackedData, character, character, character, character-method  
(computePFDDPartsData-methods),  
[8](#)

computePFDDPartsData-methods, [8](#)

computeProfileData  
(computeProfileData-methods), [9](#)

computeProfileData, StackedData, character, character, character, character-method  
(computeProfileData-methods), [9](#)

computeProfileData-methods, [9](#)

GroupListBoxplot, [11](#), [16](#), [17](#)

legendPFDDStatsGroupNames, [14](#)

makeBarplotData, [15](#)

makeDataList, [16](#)

makeTernaryData, [17](#)

marginalData, [3](#), [19](#), [31](#)

marginalData (marginalData-methods), [19](#)

marginalData, StackedData-method  
(marginalData-methods), [19](#)

marginalData-methods, [19](#)

marginalData<- (marginalData-methods),  
[19](#)

marginalData<-, StackedData-method  
(marginalData-methods), [19](#)

marginalData<--methods  
(marginalData-methods), [19](#)

marginalDF, [20](#)

markerMatrix, [21](#)

markers, [5](#), [22](#), [31](#)

markers (markers-methods), [21](#)

markers, StackedData-method  
(markers-methods), [21](#)

markers-methods, [21](#)

markers<- (markers-methods), [21](#)

markers<-, StackedData-method  
(markers-methods), [21](#)

markers<--methods (markers-methods), [21](#)

pfddata, character, character, character, character-method  
pfddata (pfddata-methods), [22](#)

pfddata, StackedData-method  
(pfddata-methods), [22](#)

pfddata-methods, [22](#)

pfddata<- (pfddata-methods), [22](#)

pfddata<-, StackedData-method  
(pfddata-methods), [22](#)

pfddata<--methods (pfddata-methods), [22](#)

pfddf, [24](#)

pfddpartsdata, [9](#), [25](#), [31](#)

pfddpartsdata (pfddpartsdata-methods), [24](#)

pfddpartsdata, StackedData-method  
(pfddpartsdata-methods), [24](#)

pfddpartsdata-methods, [24](#)

`pfPartsData<-` (`pfPartsData-methods`),  
24

`pfPartsData<-`, `StackedData-method`  
(`pfPartsData-methods`), 24

`pfPartsData<--methods`  
(`pfPartsData-methods`), 24

`pfPartsList`, 26

`profileData`, 10, 27, 31

`profileData` (`profileData-methods`), 26

`profileData`, `StackedData-method`  
(`profileData-methods`), 26

`profileData-methods`, 26

`profileData<-` (`profileData-methods`), 26

`profileData<-`, `StackedData-method`  
(`profileData-methods`), 26

`profileData<--methods`  
(`profileData-methods`), 26

`profileDF`, 28

`read.csv`, 29

`readStackedData`  
(`readStackedData-methods`), 28

`readStackedData`, `character-method`  
(`readStackedData-methods`), 28

`readStackedData-methods`, 28

`StackedData`, 3, 5–7, 9, 10, 14, 18–29, 33

`StackedData` (`StackedData-class`), 29

`stackedData` (`stackedData-methods`), 32

`stackedData`, `StackedData-method`  
(`stackedData-methods`), 32

`StackedData-class`, 29

`stackedData-methods`, 32

`stackedData<-` (`stackedData-methods`), 32

`stackedData<-`, `StackedData-method`  
(`stackedData-methods`), 32

`stackedData<--methods`  
(`stackedData-methods`), 32