

# Package ‘flowType’

March 26, 2013

**Type** Package

**Title** Phenotyping Flow Cytometry Assays

**Version** 1.4.0

**Date** 2011-04-27

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**Description** Phenotyping Flow Cytometry Assays using multidimensional expansion of single dimensional partitions.

**Imports** Biobase, graphics, grDevices, methods, flowCore, flowMeans, sfsmisc, rrcov, flowClust, flowMerge, stats

**Depends** R (>= 2.10)

**Suggests** xtable

**biocViews** FlowCytometry

**License** Artistic-2.0

**LazyLoad** yes

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 flowType-package

*flowType: Phenotyping Flow Cytometry Assays*


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## Description

flowType uses a simple threshold, Kmeans, flowMeans, or flowClust to partition every channel to a positive and a negative cell population. These partitions are then combined to generate a set of multi-dimensional phenotypes.

## Details

Package:	flowType
Type:	Package
Version:	0.0.1
Date:	2011-04-27
License:	Artistic-2.0
LazyLoad:	yes
Depends:	methods

For a given FCS file, the flowType function extracts a the phenotypes and reports their cell frequencies (number of cells) and mean fluorescence intensity (MFI)s.

## Author(s)

Nima Aghaeepour

## References

Nima Aghaeepour, Pratip K. Chattopadhyay, Anuradha Ganesan, Kieran O'Neill, Habil Zare, Adrin Jalali, Holger H. Hoos, Mario Roederer, and Ryan R. Brinkman. Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays. submitted to Bioinformatics, 2011.

## Examples

```
#Load the library
library(flowType)
data(DLBCLExample)
MarkerNames <- c('Time', 'FSC-A', 'FSC-H', 'SSC-A', 'IgG', 'CD38', 'CD19', 'CD3', 'CD27', 'CD20', 'NA', 'NA')

#These markers will be analyzed
PropMarkers <- 3:5
MFIMarkers <- PropMarkers
MarkerNames <- c('FS', 'SS', 'CD3', 'CD5', 'CD19')

#Run flowType
Res <- flowType(DLBCLExample, PropMarkers, MFIMarkers, 'flowMeans', MarkerNames);

MFIs=Res@MFIs;
Proportions=Res@CellFreqs;
Proportions <- Proportions / max(Proportions)
```

```

#Select the 30 largest phenotypes
index=order(Proportions,decreasing=TRUE)[1:30]
bp=barplot(Proportions[index], axes=FALSE, names.arg=FALSE)
text(bp+0.2, par("usr")[3]+0.02, srt = 90, adj = 0, labels = names(Proportions[index]), xpd = TRUE, cex=0.8)
axis(2);
axis(1, at=bp, labels=FALSE);
title(xlab='Phenotype Names', ylab='Cell Proportion')

#These phenotype can be analyzed using a predictive model (e.g., classification or regression)

```

---

DLBCLExample

*DLBCLExample*


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### Description

A flow cytometry sample from a patient with DLBC lymphoma. The full dataset is available through the FlowCAP project (<http://flowcap.flowsite.org>).

### Usage

```
data(DLBCLExample)
```

### Format

A flowFrame describing expression values of 3 markers and 3796 cells. Each column represents a marker and each row represents a cell.

### Examples

```
data(DLBCLExample)
```

---

flowType

*flowType: Phenotyping Flow Cytometry Assays*


---

### Description

flowType uses a simple threshold, Kmeans, flowMeans or flowClust to partition every channel to a positive and a negative cell population. These partitions are then combined to generate a set of multi-dimensional phenotypes.

### Usage

```
flowType(Frame, PropMarkers = NA, MFIMarkers = NA, Methods = "kmeans", MarkerNames="NULL")
```

**Arguments**

Frame	A flowFrame (after transformation) that is going to be phenotyped.
PropMarkers	A vector of the indexes or names of the markers for which cell proportions must be measured.
MFIMarkers	A vector of the indexes or names of the markers for which MFIs must be measured.
Methods	A vector of strings of length 1 or PropMarkers. Values can be "Kmeans", "flowMeans", "flowClust", or a numerical value. If only one method is provided the same method will be used for all of the channels.
MarkerNames	A vector of names for the channels. If NULL, the names provided in Frame will be used.

**Value**

CellFreqs:	Object of class "numeric" containing the cell frequencies measured for each phenotype. Phenotype names are assigned as labels.
MFIs:	Object of class "matrix" containing the measured MFIs for each phenotype. Phenotype names are assigned as column labels and marker names as row labels.
PropMarkers	A vector of the indexes or names of the markers for which cell proportions must be measured.
MFIMarkers	A vector of the indexes or names of the markers for which MFIs must be measured.
MarkerNames	A vector of names for the channels. If NULL, the names provided in Frame will be used.
Partitions	A matrix where each column shows the partitioning of the respective channel. 1 and 2 correspond to negative and positive, respectively.

**Author(s)**

Nima Aghaeepour

**References**

Nima Aghaeepour, Pratip K. Chattopadhyay, Anuradha Ganesan, Kieran O'Neill, Habil Zare, Adrin Jalali, Holger H. Hoos, Mario Roederer, and Ryan R. Brinkman. Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays. submitted to Bioinformatics, 2011.

**Examples**

```
#Load the library
library(flowType)
data(DLBCLExample)
MarkerNames <- c('Time', 'FSC-A', 'FSC-H', 'SSC-A', 'IgG', 'CD38', 'CD19', 'CD3', 'CD27', 'CD20', 'NA', 'NA')

#These markers will be analyzed
PropMarkers <- 3:5
MFIMarkers <- PropMarkers
MarkerNames <- c('FS', 'SS', 'CD3', 'CD5', 'CD19')

#Run flowType
```

```

Res <- flowType(DLBCLExample, PropMarkers, MFIMarkers, 'flowMeans', MarkerNames);

MFIs=Res@MFIs;
Proportions=Res@CellFreqs;
Proportions <- Proportions / max(Proportions)

#Select the 30 largest phenotypes
index=order(Proportions,decreasing=TRUE)[1:30]
bp=barplot(Proportions[index], axes=FALSE, names.arg=FALSE)
text(bp+0.2, par("usr")[3]+0.02, srt = 90, adj = 0, labels = names(Proportions[index]), xpd = TRUE, cex=0.8)
axis(2);
axis(1, at=bp, labels=FALSE);
title(xlab='Phenotype Names', ylab='Cell Proportion')

#These phenotype can be analyzed using a predictive model (e.g., classification or regression)

```

---

getLabels

*getLabels: Returns the labels of the cells in a given phenotype.*


---

## Description

Returns the labels of the cells in a given phenotype in a Phenotypes object.

## Usage

```
getLabels(Phenotypes, PhenotypeNumber)
```

## Arguments

Phenotypes	An object of class Phenotypes as produced by the flowType function.
PhenotypeNumber	A numeric or character value representing the phenotypes number of name, respectively.

## Value

Membership Labels:

A vector of length of the number of events. 1 and 2 represent the cells that are not-included and included in the phenotype respectively.

## Author(s)

Nima Aghaeepour

## References

Nima Aghaeepour, Pratip K. Chattopadhyay, Anuradha Ganesan, Kieran O'Neill, Habil Zare, Adrin Jalali, Holger H. Hoos, Mario Roederer, and Ryan R. Brinkman. Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays. submitted to Bioinformatics, 2011.

## Examples

```
#See the vigentte
```

HIVData

*HIVData*

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**Description**

A flow cytometry dataset from a HIV+ patients PBMC by the Scott lab of the Simon Fraser University and the Spina lab of the University of California San Diego.

**Usage**

```
data(HIVData)
```

**Format**

A flowSet describing expression values of 11 markers and 500 cells (sampled uniformly) for 19 HIV+ and 12 normal subjects.

**Examples**

```
data(HIVData)
## maybe str(x) ; plot(x) ...
```

---

HIVMetaData

*HIVMetaData*

---

**Description**

The meta-data of a flow cytometry dataset from a HIV+ patients PBMC by the Scott lab of the Simon Fraser University and the Spina lab of the University of California San Diego.

**Usage**

```
data(HIVMetaData)
```

**Format**

A matrix describing the FCS filename, patient label (HIV+ or normal) and tube number of every assay.

**Examples**

```
data(HIVMetaData)
## maybe str(x) ; plot(x) ...
```

---

plot *Methods for Function plot*

---

**Description**

Methods for function plot

**Usage**

```
## S4 method for signature 'Phenotypes,flowFrame'  
plot(x, y, ...)  
## S4 method for signature 'Phenotypes,numeric'  
plot(x, y, Frame,...)  
## S4 method for signature 'Phenotypes,character'  
plot(x, y, Frame,...)
```

**Arguments**

x	An object of class Phenotypes as generated by the flowType package.
y	A flowFrame or a numeric/character value representing the phenotype that needs to be plotted depending on the signature of the function
Frame	A flowFrame (might be optional depending on the signature of the function)
...	Extra parameters that will be passed to the generic plot function

**Author(s)**

Nima Aghaeepour <<naghaeep@bccrc.ca>>

**See Also**

[flowType](#)

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summary-methods *~~ Methods for Function summary ~~*

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**Description**

*~~ Methods for function summary ~~*

**Methods**

signature(object = "Phenotypes") Prints basic characteristics of a Phenotypes object.

**See Also**

[flowType](#)

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