Package ‘bodenmiller’

October 12, 2022

Type Package

Title Profiling of Peripheral Blood Mononuclear Cells using CyTOF

Version 0.1.1

Depends R (>= 3.1.0)

Suggests ggplot2, cytofan, dplyr, reshape2, RColorBrewer, knitr, rmarkdown

Description
This data package contains a subset of the Bodenmiller et al, Nat Biotech 2012 dataset for testing single cell, high dimensional analysis and visualization methods.

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Encoding UTF-8

LazyData TRUE

LazyDataCompression xz

URL `https://github.com/yannabraham/bodenmiller`

BugReports `https://github.com/yannabraham/bodenmiller/issues`

VignetteBuilder knitr

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

`refAnnots` *Reference Annotation*

Description

A `data.frame` containing the source file and cell type for every cell in `refPhenoMat` and `refFuncMat`. See Bodenmiller et al 2012 for details.

Usage

```
refAnnots
```

Format

a data.frame with 15792 rows and 2 variables:

- Sourcethe name of the source (fcs) file
- Cellsthe cell type for the corresponding row in `refPhenoMat` or `refFuncMat`

Source

`https://reports.cytobank.org/105/v2/`

`refFuncMat` *Reference Matrix (Functional)*

Description

a `matrix` containing the signal intensity for functional markers measured using CyTOF on different cell types. See Bodenmiller et al 2012 for details.

Usage

```
refFuncMat
```

Format

a matrix with 15792 rows and 14 variables:

- pStat1
- pSlp76
- pBtk
- pPlcg2
- pErk
- pLat
- pS6
- pNFkB
- pp38
- pStat5
- pAkt
- pSHP2
- pZap70
- pStat3

Source

`https://reports.cytobank.org/105/v2/`

`refPhenoMat` *Reference Matrix (Phenotypic)*

Description

a `matrix` containing the signal intensity for phenotypic markers measured using CyTOF on different cell types. See Bodenmiller et al 2012 for details.

Usage

```
refPhenoMat
```

Format

a matrix with 15792 rows and 9 variables:

- CD20
- IgM
- CD4
- CD33

- HLA-DR
- CD14
- CD7
- CD3
- CD123

Source

https://reports.cytobank.org/105/v2/

`untreatedAnnots` *Untreated Samples with 4 Different Treatments (Annotation)*

Description

A `data.frame` containing the source file, cell type and stimulation for every cell in `refPhenoMat` and `refFuncMat`. Stimulations include BCR/FcR-XL, PMA/Ionomycin and vanadate.See Bodenmiller et al 2012 for details.

Usage

```
untreatedAnnots
```

Format

a data.frame with 15792 rows and 2 variables:

- Sourcethe name of the source (fcs) file
- Treatmentthe treatment for the corresponding row in `refPhenoMat` or `refFuncMat`
- Cellsthe cell type for the corresponding row in `refPhenoMat` or `refFuncMat`

Source

https://reports.cytobank.org/105/v2/

`untreatedFuncMat` *Untreated Samples with 4 Different Treatments (Functional)*

Description

a `matrix` containing the signal intensity for functional markers measured using CyTOF on different cell types, after stimulation with BCR/FcR-XL, PMA/Ionomycin and vanadate. See Bodenmiller et al 2012 for details.

Usage

```
untreatedFuncMat
```

Format

a matrix with 15792 rows and 14 variables:

- pStat1
- pSlp76
- pBtk
- pPlcg2
- pErk
- pLat
- pS6
- pNFkB
- pp38
- pStat5
- pAkt
- pSHP2
- pZap70
- pStat3

Source

`https://reports.cytobank.org/105/v2/`

`untreatedPhenoMat` *Untreated Samples with 4 Different Treatments (Phenotypic)*

Description

a `matrix` containing the signal intensity for phenotypic markers measured using CyTOF on different cell types, after stimulation with BCR/FcR-XL, PMA/Ionomycin and vanadate. See Bodenmiller et al 2012 for details.

Usage

```
untreatedPhenoMat
```

Format

a matrix with 15792 rows and 9 variables:

- CD20
- IgM
- CD4
- CD33
- HLA-DR
- CD14
- CD7
- CD3
- CD123

Source

`https://reports.cytobank.org/105/v2/`

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