

Package ‘bodenmiller’

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Type Package

Title Profiling of Peripheral Blood Mononuclear Cells using CyTOF

Version 0.1.1

Depends R (>= 3.1.0)

Suggests ggplot2, cytofان, 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

Author Yann Abraham [aut, cre],
Bernd Bodenmiller [aut]

Maintainer Yann Abraham <yann.abraham@gmail.com>

Repository CRAN

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refAnnots	<i>Reference Annotation</i>
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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:

- Source the name of the source (fcs) file
- Cell the cell type for the corresponding row in [refPhenoMat](#) or [refFuncMat](#)

Source

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

refFuncMat	<i>Reference Matrix (Functional)</i>
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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:

- Source the name of the source (fcs) file
- Treatment the treatment for the corresponding row in [refPhenoMat](#) or [refFuncMat](#)
- Cell the 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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