

Package ‘CellMapperData’

March 29, 2021

Type Package

Title Pre-processed data for use with the CellMapper package

Version 1.16.0

Date 2016-10-05

Author Brad Nelms

Maintainer Brad Nelms <bnelms.research@gmail.com>

Description Experiment data package. Contains microarray data from several large expression compendia that have been pre-processed for use with the CellMapper package. This pre-processed data is recommended for routine searches using the CellMapper package.

License Artistic-2.0

Depends ExperimentHub, CellMapper

Suggests BiocStyle

biocViews ExperimentData, MicroarrayData, ExpressionData

git_url <https://git.bioconductor.org/packages/CellMapperData>

git_branch RELEASE_3_12

git_last_commit d6d5b69

git_last_commit_date 2020-10-27

Date/Publication 2021-03-29

R topics documented:

CellMapperData-package 1

Index 4

CellMapperData-package

Pre-processed data for use with the CellMapper package

Description

Contains microarray data from several large expression compendia that have been pre-processed for use with the CellMapper package. All datasets are CellMapperList objects that were pre-processed using the CMprep function; these can be provided directly to the CMsearch function. These pre-processed datasets are recommended for routine searches using the CellMapper package.

Details

Contains the following six pre-processed datasets:

EH170: pre-processed microarray samples from microdissected human brain regions. Normalized microarray data were downloaded from the Allen Brain Atlas in February 2014 at the link: <http://human.brain-map.org/static/download> (the 6 files listed under the heading "Complete normalized microarray datasets"). The six normalized datasets were then loaded into R and concatenated to make a unified expression matrix of 3702 arrays, and pre-processed using the CMprep function.

EH171: pre-processed microarray samples from the Affymetrix HG_U133PlusV2 platform. The data were obtained from the GSE64985 Bioconductor package and pre-processed using the CMprep function. The original dataset contained 9395 arrays from diverse biological samples.

EH172: pre-processed microarray samples from the Affymetrix HG_U133A platform. The data were obtained from the E.MTAB.62 Bioconductor package and pre-processed using the CMprep function. The original dataset contained 5372 arrays from diverse biological samples.

EH173: pre-processed microarray samples from the Affymetrix MG_U74Av2 platform. Normalized microarray data were downloaded from Array Express accession E-MTAB-27 (<https://www.ebi.ac.uk/arrayexpress/e-MTAB-27/>) and processed with the R package `bias.0.0.3` to reduce the influence of technical bias (Eklund, et al. 2008). Then Mouse Entrez IDs were then mapped to their corresponding human orthologs as described in Nelms, et al. 2016, and the expression matrix was pre-processed with the CMprep function. The original dataset contained 1332 arrays from diverse biological samples.

EH174: pre-processed microarray samples from the human intestine. An intestine-specific subset of the 'Engreitz' and 'Lukk' datasets was obtained as described in Section 5.2 of the CellMapper package vignette. The unprocessed data contained 582 microarrays from the 'Engreitz' dataset and 130 microarrays from the 'Lukk' dataset.

EH175: pre-processed microarray samples from the human kidney. Normalized microarray data were downloaded from the Gene Expression Omnibus from the following accessions: GSE32691, GSE35488, GSE37455, GSE37460, and GSE47185. The five normalized datasets were then loaded into R and concatenated to make a unified expression matrix of 463 arrays, and pre-processed using the CMprep function.

Author(s)

Brad Nelms

Maintainer: Brad Nelms <bnelms.research@gmail.com>

References

B.D. Nelms, L. Waldron, L.A. Barrera, A.W. Weflen, J.A. Goettel, G. Guo, R.K. Montgomery, M.R. Neutra, D.T. Breault, S.B. Snapper, S.H. Orkin, M.L. Bulyk, C. Huttenhower and W.I. Lencer. CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. *Genome Biology* 2016, 17(1).

Hawrylycz MJ, Lein ES, Guillozet-Bongaarts AL, Shen EH, Ng L, Miller J a, van de Lagemaat LN, Smith K A, Ebbert A, Riley ZL, Abajian C, Beckmann CF, Bernard A, Bertagnolli D, Boe AF, Cartagena PM, Chakravarty MM, Chapin M, Chong J, Dalley R A, Daly BD, Dang C, Datta S, Dee N, Dolbear T a, Faber V, Feng D, Fowler DR, Goldy J, Gregor BW, et al. An anatomically comprehensive atlas of the adult human brain transcriptome. *Nature* 2012, 489:391-9.

Engreitz JM, Daigle BJ, Marshall JJ, Altman RB. Independent component analysis: mining microarray data for fundamental human gene expression modules. *J Biomed Inform* 2010, 43:932-44.

Lukk M, Kapushesky M, Nikkil" a J, Parkinson H, Goncalves A, Huber W, Ukkonen E, Brazma A. A global map of human gene expression. *Nat Biotechnol* 2010, 28:322-4.

Zheng-Bradley X, Rung J, Parkinson H, Brazma A. Large scale comparison of global gene expression patterns in human and mouse. *Genome Biol* 2010, 11:R124.

Eklund AC, Szallasi Z. Correction of technical bias in clinical microarray data improves concordance with known biological information. *Genome Biol* 2008, 9:R26.

See Also

[CMsearch](#), [CMprep](#)

Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
x <- query(hub, "CellMapperData")
x
## Not run:
## download Brain Atlas resource (EH170)
BrainAtlas <- x[[1]]

## End(Not run)
```

Index

* **datasets, CellMapper**

CellMapperData-package, [1](#)

CellMapperData

(CellMapperData-package), [1](#)

CellMapperData-package, [1](#)

CMprep, [3](#)

CMsearch, [3](#)