Package 'CellMapperData'

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Type Package

Title Pre-processed data for use with the CellMapper package

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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

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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 cancatenated 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/exper 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' datsets 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 cancatenated to make a unified expression matrix of 463 arrays, and pre-processed using the CMprep function.

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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)
```

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