Package ‘emtdatat’

August 15, 2024

Title  An ExperimentHub Package for data sets with an Epithelial to
Mesenchymal Transition (EMT)

Version  1.12.0

Description  This package provides pre-processed RNA-seq data where the epithelial to mesenchy-
mal transition was induced on cell lines. These data come from three publications Cur-
sons et al. (2015), Cursons et al. (2018) and Foroutan et al. (2017). In each of these publica-
tions, EMT was induces across multiple cell lines following treat-
ment by TGFb among other stimulants. This data will be useful in determining the regula-
tory programs modified in order to achieve an EMT. Data were processed by the Davis labora-
tory in the Bioinformatics division at WEHI.

biocViews  ExperimentHub, Homo_sapiens_Data, RNASeqData, ExpressionData

Encoding  UTF-8

LazyData  true

Roxygen  list(markdown = TRUE)

RoxygenNote  7.1.1

Depends  R (>= 4.1)

Imports  edgeR, ExperimentHub, SummarizedExperiment

Suggests  testthat (>= 3.0.0), stringr, plyr, prettydoc, BiocStyle,
          Homo.sapiens, RColorBrewer, rmarkdown, BiocFileCache, knitr

URL  https://github.com/DavisLaboratory/emtdatat

BugReports  https://github.com/DavisLaboratory/emtdatat/issues

NeedsCompilation  no

VignetteBuilder  knitr

Config/testthat/edition  3

License  GPL-3

git_url  https://git.bioconductor.org/packages/emtdatat

git_branch  RELEASE_3_19

git_last_commit  bd5ca34

git_last_commit_date  2024-04-30
asDGEList

Convert a SummarizedExperiment object to a DGEList object

Description

This function converts a SummarizedExperiment object to a DGEList object to enhance differential expression analysis using the edgeR package.

Usage

asDGEList(se, assay_name = "counts")

Arguments

se a SummarizedExperiment object.
assay_name a character, specifying the assay to retrieve.

Value

a DGEList object

Examples

library(ExperimentHub)

eh = ExperimentHub()
query(eh, 'emtdata')

cursors2018_se = eh[['EH5440']]
cursors2018_dge = asDGEList(cursors2018_se)
EGF or hypoxia treatment of Breast Cancer Cell lines from Cursons et al. (2015)

Description

Dataset used in Cursons et al. 2015. Where parallel ‘deep sequencing’ of RNA (RNA-Seq) were conducted to examine the changes in expression profiles between breast cancer cell lines PMC42-ET, PMC42-LA and MDA-MB-468 cells.

Format

A SummarizedExperiment object, containing gene expression data of different sub-lines of human breast cancer cell lines. The `SummarizedExperiment::colData()` function can be used to access the sample annotations.

Details

For PMC42 cell lines, cells were treated for 3 or 7 days in the presence or absence of 10 ng/ml EGF. For MDA-MB-468 cells, cells were treated for 7 days in the presence or absence of either 10 ng/ml EGF or kept under Hypoxia.

There are 3 biological replicates per condition which were summed. Samples were sequenced on the Illumina HiSeq 2000, 100bp paired end.

Data from this publication were downloaded from EMBL-EBI ENA and processed into a SummarizedExperiment object. Sample annotations were modified from the original publication and SRA portal.

References


Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
emt_datasets <- query(eh, "emtdata")
```
Description

Cursons et al. used the Human Mammary Epithelial Cells (HMLE) cell line dataset. A mesenchymal HMLE (mesHMLE) phenotype was induced following treatment with transforming growth factors (TGFb). The mesHMLE subline was then treated with mir200c to reinduce an epithelial phenotype. All mRNA RNA-seq was collected using the Illumina HiSeq 2500 with a paired end read length of 100bp.

Format

A SummarizedExperiment object, containing gene expression data of the Human Mammary Epithelial Cells (HMLE) cell line. The `SummarizedExperiment::colData()` function can be used to access the sample annotations.

Details

Data from this publication were downloaded from the European Nucleotide Archive (ENA) and processed into a SummarizedExperiment object. Sample annotations were modified from the original publication.

References


Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
etm_datasets <- query(eh, "emtdata")
```

Description

Foroutan et al. collected data from multiple different studies where various cell lines (from various tissues of origin) were stimulated with transforming growth factor beta (TGFb) to induce an epithelial to mesenchymal transition (EMT). Since the data were from different studies (and platforms), the surrogate variable analysis (SVA) and ComBat approaches were applied to correct for batch effects.
Format

A SummarizedExperiment object, containing gene expression data of human cell lines treated with TGFβ. The `SummarizedExperiment::colData()` function can be used to access the sample annotations.

Details

Data from this publication were downloaded from figshare and processed into a SummarizedExperiment object. Sample annotations were retrieved from the original publication.

References


Examples

```r
library(ExperimentHub)
eh <- ExperimentHub()
etm_datasets <- query(eh, "emtdata")
```
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