Package ‘emtdata’

March 28, 2024

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

Version  1.10.0

Description  This package provides pre-processed RNA-seq data where the epithelial to mesenchymal transition was induced on cell lines. These data come from three publications Cursons et al. (2015), Cursons et al. (2018) and Foroutan et al. (2017). In each of these publications, EMT was induces across multiple cell lines following treatment by TGFb among other stimulants. This data will be useful in determining the regulatory programs modified in order to achieve an EMT. Data were processed by the Davis laboratory 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/emtdata

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

NeedsCompilation  no

VignetteBuilder  knitr

Config/testthat/edition  3

License  GPL-3

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

git_branch  RELEASE_3_18

git_last_commit  630cb37

git_last_commit_date  2023-10-24
**asDGEList**

**Description**

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

**Usage**

```r
asDGEList(se, assay_name = "counts")
```

**Arguments**

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

**Value**

a DGEList object

**Examples**

```r
library(ExperimentHub)

eh = ExperimentHub()
query(eh, 'emtdata')
cursons2018_se = eh['EH5440']
cursons2018_dge = asDGEList(cursons2018_se)
```
**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()
etm_datasets <- query(eh, "emtdata")
```
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 (TGFβ). 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.

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 (TGFβ). 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

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

asDGEList, 2

cursos2015_se, 3
cursos2018_se, 4

foroutan2017_se, 4

SummarizedExperiment::colData(), 3–5