Package ‘EMTscoreData’

April 23, 2026

Title Single-cell RNA-seq datasets of EMT responses from Cook et al. (2020)

Version 0.99.10

Description Provides 12 single-cell RNA-seq datasets profiling epithelial–mesenchymal transition (EMT) in human cancer cell lines (MCF7, OVCA420, DU145, and A549) under TGF-beta stimulation, kinase inhibition, and time-course conditions, as reported by Cook DP and Vanderhyden BC (2020). The datasets are distributed via ExperimentHub as SingleCellExperiment objects.

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Imports SummarizedExperiment, Seurat, SingleCellExperiment, AnnotationHub, ExperimentHub, ggplot2

Suggests BiocFileCache, SeuratObject, knitr, rmarkdown, googledrive, BiocStyle, testthat (>= 3.0.0)

VignetteBuilder knitr

biocViews ExperimentHub, SingleCellData, ExpressionData, CancerData, RNASeqData

URL `https://github.com/wenmm/EMTscoreData`

BugReports `https://github.com/wenmm/EMTscoreData/issues`

Encoding UTF-8

LazyData false

RoxygenNote 7.3.3

NeedsCompilation no

Config/testthat/edition 3

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The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines A549 treated with EGF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load A549 EGF dataset
A549_EGF <- eh[["EH10292"]]
```

`A549_TGFB1` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines A549 treated with TGFB1

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load A549 TGFB1 dataset
A549_TGFB1 <- eh[["EH10293"]]
```

`A549_TNF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines A549 treated with TNF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load A549 TNF dataset
A549_TNF <- eh[["EH10291"]]
```

`DU145_EGF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines DU145 treated with EGF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load DU145 EGF dataset
DU145_EGF <- eh[["EH10289"]]
```

`DU145_TGFB1` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines DU145 treated with TGFB1

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load DU145 TGFB1 dataset
DU145_TGFB1 <- eh[["EH10290"]]
```

`DU145_TNF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines DU145 treated with TNF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load DU145 TNF dataset
DU145_TNF <- eh[["EH10288"]]
```

`MCF7_EGF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines MCF7 treated with EGF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load MCF7 EGF dataset
MCF7_EGF <- eh[["EH10283"]]
```

`MCF7_TGFB1` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines MCF7 treated with TGFB1

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load MCF7 TGFB1 dataset
MCF7_TGFB1 <- eh[["EH10284"]]
```

`MCF7_TNF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines MCF7 treated with TNF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load MCF7 TNF dataset
MCF7_TNF <- eh[["EH10282"]]
```

`OVCA420_EGF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines OVCA420 treated with EGF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load OVCA420 EGF dataset
OVCA420_EGF <- eh[["EH10286"]]
```

`OVCA420_TGFB1` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines OVCA420 treated with TGFB1

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load OVCA420 TGFB1 dataset
OVCA420_TGFB1 <- eh[["EH10287"]]
```

`OVCA420_TNF` *EMTscoreData: Single-cell RNA-seq datasets for EMTscore*

Description

The EMTscoreData package provides 12 single-cell RNA-seq datasets from Cook DP, Vanderhyden BC (2020). Context specificity of the EMT transcriptional response. Nature Communications 11(1):2142.

Format

SingleCellExperiment object containing scRNA-seq profiles for cell line and treatment.

Details

These datasets profile epithelial-mesenchymal transition (EMT) in human cancer cell lines OVCA420 treated with TNF

Each dataset was processed into a SingleCellExperiment object and saved as an .rda file.

The datasets can be accessed via `ExperimentHub` using the provided accessors. Each object contains gene expression matrices and associated cell metadata, such as treatment.

Value

SingleCellExperiment dataset

References

Cook DP, Vanderhyden BC. Context specificity of the EMT transcriptional response. *Nature Communications* 2020 May 1;11(1):2142.

Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, "EMTscoreData")

#Example: load OVCA420 TNF dataset
OVCA420_TNF <- eh[["EH10285"]]
```

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