Package ‘tissueTreg’

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Title TWGBS and RNA-seq data from tissue T regulatory cells from mice

Version 1.29.0

Author Charles Imbusch [aut, cre],
Michael Delacher [aut],
Markus Feuerer [aut],
Benedikt Brors [aut]

Maintainer Charles Imbusch <`c.imbusch@dkfz.de`>

Description The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues as obtained in the study (Delacher and Imbusch 2017, PMID: 28783152).
Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

Depends R (>= 3.5)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Suggests BiocStyle, knitr, rmarkdown, testthat, ExperimentHub, bsseq, SummarizedExperiment, ggplot2, reshape2

VignetteBuilder knitr

biocViews ExperimentData, Tissue, Mus_musculus_Data, SequencingData, RNASeqData

URL `https://github.com/cimbusch/tissueTreg`

RoxygenNote 6.0.1

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

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`tissueTreg` *Epigenomes and transcriptomes of tissue resident regulatory T cells*

Description

The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues. Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

Source

Delacher, M, Imbusch, CD, Weichenhan, D, Breiling, A, Hotz-Wagenblatt, A, Träger, U, Hofer, AC, Kägebein, D, Wang, Q, Frauhammer, F, Mallm, JP, Bauer, K, Herrmann, C, Lang, PA, Brors, B, Plass, C, Feuerer, M (2017). Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. Nat. Immunol., 18, 10:1160-1172.

Examples

```
eh <- ExperimentHub::ExperimentHub()

# RNA-seq RPKM data:
se_rpkms <- eh[["EH1074"]]

# Whole genome bisulfite sequencing data as bsseq objects:
tregs_per_sample <- eh[["EH1072"]]
tregs_per_tissue <- eh[["EH1073"]]
```

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