Package ‘tissueTreg’

March 28, 2024

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

Version  1.22.0

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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

Imports

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

git_branch  RELEASE_3_18

git_last_commit  6b37bb0

git_last_commit_date  2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-28

R topics documented:

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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


Examples

```r
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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