Package ‘tissueTreg’

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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
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R topics documented:

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<th>Epigenomes and transcriptomes of tissue resident regulatory T cells</th>
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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

    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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