

Package ‘mosaicsExample’

October 1, 2024

Type Package

Title Example data for the mosaics package, which implements MOSAiCS and MOSAiCS-HMM, a statistical framework to analyze one-sample or two-sample ChIP-seq data for transcription factor binding and histone modification

Version 1.43.0

Depends R (>= 2.11.1)

Date 2015-04-30

Author Dongjun Chung, Pei Fen Kuan, Rene Welch, Sunduz Keles

Maintainer Dongjun Chung <dongjun.chung@gmail.com>

Description Data for the mosaics package, consisting of (1) chromosome 22 ChIP and control sample data from a ChIP-seq experiment of STAT1 binding and H3K4me3 modification in MCF7 cell line from ENCODE database (HG19) and (2) chromosome 21 ChIP and control sample data from a ChIP-seq experiment of STAT1 binding, with mappability, GC content, and sequence ambiguity scores of human genome HG18.

License GPL (>= 2)

URL http://groups.google.com/group/mosaics_user_group

LazyLoad yes

biocViews ExperimentData, ChIPseqData, Homo_sapiens

git_url <https://git.bioconductor.org/packages/mosaicsExample>

git_branch devel

git_last_commit 8627375

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-10-01

Contents

| | |
|--------------------------|----------|
| exampleBinData | 2 |
| Index | 3 |

`exampleBinData`*STAT1 ChIP-seq Dataset*

Description

This is the STAT1 ChIP-seq dataset used in Kuan et al. (2010).

Usage

```
data(exampleBinData)
```

Format

`BinData` class object containing bin-level ChIP data, control sample data, mappability score, GC content score, and sequence ambiguity score.

Details

ChIP data and control sample data are chromosome 21 data from a ChIP-seq experiment of STAT1 binding in interferon-gamma-stimulated HeLa S3 cells (Rozowsky et al., 2009). Mappability score, GC content score, and sequence ambiguity score are calculated from human genome HG18. See the vignette of R package `mosaics` and Kuan et al. (2010) for more details.

Source

Rozowsky, J, G Euskirchen, R Auerbach, D Zhang, T Gibson, R Bjornson, N Carriero, M Snyder, and M Gerstein (2009), "PeakSeq enables systematic scoring of ChIP-Seq experiments relative to controls", *Nature Biotechnology*, 27, pp. 66–75.

References

Kuan, PF, D Chung, JA Thomson, R Stewart, and S Keles (2010), "A Statistical Framework for the Analysis of ChIP-Seq Data", submitted (http://works.bepress.com/sunduz_keles/19/).

Examples

```
## Not run:
data(exampleBinData)
library(mosaics)
exampleBinData

## End(Not run)
```

Index

* **datasets**

exampleBinData, [2](#)

exampleBinData, [2](#)