Package 'mosaicsExample'

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Type Package

Title Example data for the mosaics package, which implements MOSAiCS,a statistical framework to analyze one-sample or two-sample
ChIP-seq data

Version 0.99.8

Depends R (>= 2.11.1)

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Description Data for the mosaics package, consisting of 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

R topics documented:

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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)
```

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exampleFit   *MOSAiCS Model Fit for STAT1 ChIP-seq Dataset*

Description

This is the MOSAiCS two-sample analysis model fit for `exampleBinData`.

Usage

```
data(exampleFit)
```

Format

`MosaicsFit` class object containing the model fit of MOSAiCS two-sample analysis.

Details

The model fit of MOSAiCS two-sample analysis for `exampleBinData`. See the vignette and Kuan et al. (2010) for more details.

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(exampleFit)
library(mosaics)
exampleFit

## End(Not run)
```

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