

# Package ‘mosaicsExample’

July 18, 2023

**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** 1.39.0

**Depends** R (>= 2.11.1)

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**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](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** 4cb411b

**git\_last\_commit\_date** 2023-04-25

**Date/Publication** 2023-07-18

## R topics documented:

exampleBinData . . . . . 2

**Index** . . . . . 3

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`exampleBinData`*STAT1 ChIP-seq Dataset*

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**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/](http://works.bepress.com/sunduz_keles/19/)).

**Examples**

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

# Index

\* **datasets**

exampleBinData, [2](#)

exampleBinData, [2](#)