

# Package ‘mosaicsExample’

April 4, 2014

**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** 0.99.9

**Depends** R (>= 2.11.1)

**Date** 2011-03-08

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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](http://groups.google.com/group/mosaics_user_group)

**LazyLoad** yes

**biocViews** ExperimentData, ChIPseqData, Homo\_sapiens

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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)
```

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

**Examples**

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

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