# mosaicsExample

March 19, 2011

---

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)
```

---

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

### Examples

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

## End(Not run)
```

# Index