

# Package ‘jmosaics’

October 9, 2013

**Type** Package

**Title** Joint analysis of multiple ChIP-Seq data sets

**Version** 1.0.0

**Date** 2013-01-29

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**Depends** R (>= 2.15.2), mosaics

**Description** jmosaics detects enriched regions of ChIP-seq data sets jointly.

**License** GPL (>= 2)

**LazyLoad** yes

**biocViews** ChIPseq, Sequencing, Transcription, Genetics, Bioinformatics

## R topics documented:

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| jmosaics-package | <i>Joint analysis of multiple ChIP-seq data sets</i> |
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## Description

Joint analysis of multiple ChIP-seq data sets

## Details

```

Package:  jmosaics
Type:    Package
Version:  1.0
Date:    2012-06-24
License:  GPL(>=2)
LazyLoad: yes

```

readBinsMultiple match coordinates for multiple datasets, jmosaicsPattern call E\_LAYER and B\_LAYER peaks

### Author(s)

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### References

jMOSAICS: Joint Analysis of Multiple ChIP-seq Datasets

### Examples

```

## step by step not run
## Not run:
bin1 <- readBins(type = c("chip", "M", "GC", "N", "input"),
  fileName = c("h3k27me3_chip_chr10.txt",
    "/M_chr10.txt", "/GC_chr10.txt", "/N_chr10.txt",
    "h3k27me3_input_chr10.txt"))
bin2 <- readBins(type = c("chip", "M", "GC", "N", "input"),
  fileName = c("h3k4me1_chip_chr10.txt",
    "/M_chr10.txt", "/GC_chr10.txt", "/N_chr10.txt",
    "h3k4me1_input_chr10.txt"))
origin_bin <- list(bin1, bin2)

## End(Not run)

data("jmosaics_example_data")
bin <- readBinsMultiple(origin_bin)
fit1 <- mosaicsFit(bin[[1]], analysisType = "IO")
fit2 <- mosaicsFit(bin[[2]], analysisType = "IO")
fit <- list(fit1, fit2)
result <- jmosaicsPattern(fit, region_length=1, FDR=0.01, thres=c(10,10), type=c('B', 'E', 'Pattern'), patternInfo=

```

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jmosaicsPattern      *Call peaks and obtain combinatorial enrichment patterns*

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## Description

Call peaks and obtain combinatorial enrichment patterns

## Usage

```
jmosaicsPattern(fit_all, region_length, FDR, thres=NULL, type=c('B', 'E', 'Pattern'), patternInfo='FALSE')
```

## Arguments

|               |   |
|---------------|---|
| fit_all       | A list of fitted MOSAiCS models obtained using function mosaicsFit.   |
| region_length | Region length, the number of bins covered by each region.   |
| FDR           | False discovery rate.   |
| thres         | A peak within initial peak is removed if its ChIP tag counts are less than thres. thres could be NULL or a numeric vector, corresponding to each dataset. If NULL, no threshold for average ChIP tag counts for all data sets would be used. Default is NULL. |
| type          | a vector of characters to decide which objects would be returned. Possible values are 'E': return E_LAYER result; 'B': return B_LAYER result and 'Pattern': return Pattern (enrichment pattern).  |
| patternInfo   | Parameter for returning information on regions. Possible values are TRUE (return information on regions) or FALSE (do not return information on regions). Default is FALSE.   |

## Details

The function returns objects based on 'type'. 'B\_LAYER' object is a list of regions which are enriched in at least one dataset. Peak information can be accessed by 'chrID', 'PeakStart', 'PeakStop', 'Postprob'(P(B=0|data information)), 'aveChipCount E\_\*', 'aveInputCount E\_\*'. \* indicates the index of the datasets, for example: aveChipCount E\_1 is the average tagCount for the first dataset. Each list of 'E\_LAYER' object reports enriched regions for each dataset which can be accessed by 'chrID', 'PeakStart', 'PeakStop', 'Postprob'(P(E=0|data sets)), 'aveChipCount', 'maxChipCount', 'aveInputCount', 'aveInputCountScaled', 'aveLog2Ratio'. If region length is 1, it can be accessed by 'chrID', 'PeakStart', 'PeakStop', 'Postprob', 'ChipCount', 'InputCount', 'Input-CountScaled', 'Log2Ratio'. In the object of Pattern, it reports the enrichment patterns to the regions which cover the whole genome. When the region covering more than one bin, to get the average ChIP and input tagCount would be time consuming, the argument of 'patternInfo' let users decide whether to report the average ChIP and input tagCount.

**Value**

A list with following components:

|         |   |
|---------|---|
| E_LAYER | lists of enriched E regions, each list includes enriched regions for each data set. |
| B_LAYER | list of enriched B regions.   |
| Pattern | list of regions annotated with patterns.  |

**Author(s)**

Xin Zeng

**Examples**

```
data("jmosaics_example_data")
bin <- readBinsMultiple(origin_bin)
fit1 <- mosaicsFit(bin[[1]], analysisType = "IO")
fit2 <- mosaicsFit(bin[[2]], analysisType = "IO")
fit <- list(fit1,fit2)
result <- jmosaicsPattern(fit, region_length=1, FDR=0.01, thres=c(10,10), type=c('B','E','Pattern'), patternInfo=)
```

---

jmosaics\_example\_data *ChIP-seq data of Histone H3K4me1 and H3K27me3.*

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**Description**

This is an example chr10 ChIP-seq data of Histone H3K4me1 and H3K27me3.

**Usage**

```
data("jmosaics_example_data")
```

**Format**

jmosaics\_example\_data names of included datasets.

**Examples**

```
data(jmosaics_example_data)
jmosaics_example_data
```

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|            |   |
|------------|---|
| origin_bin | <i>ChIP-seq data of Histone H3K4me1 and H3K27me3.</i> |
|------------|---|

---

**Description**

This is an example chr10 ChIP-seq data of Histone H3K4me1 and H3K27me3.

**Usage**

```
data("jmosaics_example_data")
```

**Format**

origin\_bin a list of bin-level data sets.

**Examples**

```
data(jmosaics_example_data)
str(origin_bin)
```

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|------------------|---|
| readBinsMultiple | <i>Match coordinates for multiple data sets</i> |
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**Description**

Match coordinates for multiple data sets

**Usage**

```
readBinsMultiple(dataset)
```

**Arguments**

dataset      A list of bin-level data sets.

**Details**

Bin-level data can be generated by readBins from mosaics package for each data set. This function is used to match the coordinates of multiple data sets to get the shared regions.

**Value**

List of Bin-level data sets.

**Author(s)**

Xin Zeng

**Examples**

```
data("jmosaics_example_data")  
bin<- readBinsMultiple(origin_bin)
```

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