

# Package ‘BAC’

October 8, 2015

**Type** Package

**Title** Bayesian Analysis of Chip-chip experiment

**Version** 1.28.0

**Date** 2007-11-20

**Author** Raphael Gottardo

**Maintainer** Raphael Gottardo <raph@stat.ubc.ca>

**Depends** R (>= 2.10)

**Description** This package uses a Bayesian hierarchical model to detect enriched regions from ChIP-chip experiments

**License** Artistic-2.0

**biocViews** Microarray, Transcription

**NeedsCompilation** yes

## R topics documented:

BAC . . . . .	1
CallRegions . . . . .	3
ER . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

BAC *Bayesian Analysis of ChIP-chip tiling arrays*

---

## Description

Bayesian Analysis of ChIP-chip tiling arrays

## Usage

BAC(C, I, B=15000, verbose=FALSE, w=5)

**Arguments**

C	The matrix of control measurements. Rows correspond to probes and columns to samples.
I	The matrix of IP measurements. Rows correspond to probes and columns to samples.
B	Number of iterations used the MCMC. Default to 15000.
verbose	Logical parameter. If TRUE, some progression
w	The window size. Default to 5. See details below for more about this parameter.

**Details**

The window size should be calculated in function of the resolution and the shearing resolution. For example, for Affymetrix human tiling arrays, the shearing resolution is 500-1000bps, the tiling resolution is 35bps and the probe length is 25bps. Then one would expect a bound region to contain  $500-1000/(35+25) \sim 8-16$  probes. Thus we decided to set *w* to 5. Note that the exact value of *w* is not crucial.

**Value**

The marginal posterior probabilities and the joint posterior probabilities computed from the Bayesian hierarchical model. We recommend using the joint posterior probabilities to call enriched regions.

**Author(s)**

Raphael Gottardo, <raph@stat.ubc.ca>

**See Also**

CallRegions

**Examples**

```
# Load the data
data(ER)
# Only select the first 5000 probes for speed-up
ER<-ER[1:5000,]
# Calculate the joint posterior probabilities
#Only use 100 iterations for speed up (You should use more! See default value)
BAConER<-BAC(ER[,5:7], ER[,2:4], B=100,verbose=FALSE,w=5)
# For Regions using 0.5 cut-off for the joint posterior probabilities
ERregions<-CallRegions(ER[,1],BAConER$jointPP,cutoff=0.5,maxGap=500)
# Create the BED file
nRegions<-max(ERregions)
BED<-matrix(0,nRegions,4)
for(i in 1:nRegions)
{
  BED[i,2:3]<-range(ER[ERregions==i,1])
  #The score should be between 0 and 1000
  BED[i,4]<-max(BAConER$jointPP[ERregions==i])*1000
}
```

```
}  
BED<-data.frame(BED)  
# The ER data is a subset of chr 21  
BED[,1]<-"chr21"  
names(BED)<-c("chrom", "chromStart", "chromEnd", "Score")  
# print it  
print(BED)
```

---

CallRegions	<i>Call and merge regions using joint posterior probabilities calculated by BAC.</i>
-------------	--

---

### Description

Call and merge regions using joint posterior probabilities calculated by BAC.

### Usage

```
CallRegions(position, jointPP, cutoff=0.5, maxGap=500)
```

### Arguments

position	A vector containing the probe genomic positions
jointPP	A vector containing the joint posterior probabilities as returned by BAC.
cutoff	The cutoff used to call regions.
maxGap	The maximum gap allowed between regions. Regions that are less than maxGap bps away will be merged.

### Value

A vector containing the region index for each probe. Probes with the same positive index belong to the same region, whereas probe with index zero are background probes (not part of a bound region). These indices can be used to form a BED file, see example below.

### Author(s)

Raphael Gottardo, <raph@stat.ubc.ca>

### See Also

BAC

**Examples**

```

# Load the data
data(ER)
# Only select the first 5000 probes for speed-up
ER<-ER[1:5000,]
# Calculate the joint posterior probabilities
#Only use 100 iterations for speed up (You should use more! See default value)
BAConER<-BAC(ER[,5:7], ER[,2:4], B=100,verbose=FALSE,w=5)
# For Regions using 0.5 cut-off for the joint posterior probabilities
ERregions<-CallRegions(ER[,1],BAConER$jointPP,cutoff=0.5,maxGap=500)
# Create the BED file
nRegions<-max(ERregions)
BED<-matrix(0,nRegions,4)
for(i in 1:nRegions)
{
  BED[i,2:3]<-range(ER[ERregions==i,1])
  #The score should be between 0 and 1000
  BED[i,4]<-max(BAConER$jointPP[ERregions==i])*1000
}
BED<-data.frame(BED)
# The ER data is a subset of chr 21
BED[,1]<- "chr21"
names(BED)<-c("chrom", "chromStart", "chromEnd", "Score")
# print it
print(BED)

```

ER

---

*Chromosome-Wide Mapping of Estrogen Receptor Binding Reveals  
Long-Range Regulation Requiring the Forkhead Protein FoxA1*

---

**Description**

This is a subset of the data containing 30000 probes on chromosome 21.

**Usage**

```
data(ER)
```

**Source**

<http://www.cell.com/content/article/abstract?uid=PIIS0092867405004538>

**References**

Cell, Vol 122, 33-43, 15 July 2005

# Index

\*Topic **datasets**

ER, [4](#)

\*Topic **models**

BAC, [1](#)

CallRegions, [3](#)

BAC, [1](#)

CallRegions, [3](#)

ER, [4](#)