Package 'BAC'

October 15, 2018

Type Package

Title Bayesian Analysis of Chip-chip experiment

Version 1.40.0

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

git_url https://git.bioconductor.org/packages/BAC

git_branch RELEASE_3_7

git_last_commit 48e4c99

git_last_commit_date 2018-04-30

Date/Publication 2018-10-15

R topics documented:

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)~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` *Call and merge regions using joint posterior probabilities calculated by BAC.*

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