

Package ‘MBAmethyl’

April 16, 2025

Type Package

Title Model-based analysis of DNA methylation data

Version 1.42.0

Date 2014-10-03

Author Tao Wang, Mengjie Chen

Maintainer Tao Wang <tao.wang.tw376@yale.edu>

Description This package provides a function for reconstructing DNA methylation values from raw measurements. It iteratively implements the group fused lars to smooth related-by-location methylation values and the constrained least squares to remove probe affinity effect across multiple sequences.

Depends R (>= 2.15)

License Artistic-2.0

biocViews DNAMethylation, MethylationArray

git_url <https://git.bioconductor.org/packages/MBAmethyl>

git_branch RELEASE_3_21

git_last_commit 32f32b8

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-04-15

Contents

MBAmethyl-package	2
MBAmethyl	3
Index	5

MBAmethyl-package

Model-based analysis of DNA methylation data

Description

This package provides functions for reconstructing DNA methylation values from raw measurements. It utilizes both the information from biological replicates and neighboring probes by explicitly modeling the probe-specific effect and encouraging the neighboring similarity by a group fused lasso penalty.

Details

Package: MBAmethyl
 Type: Package
 Version: 0.99.0
 Date: 2014-08-24
 License: Artistic-2.0

Author(s)

Tao Wang, Mengjie Chen

Maintainer: Tao Wang <tao.wang.tw376@yale.edu>

References

~~ Literature or other references for background information ~~

Examples

```

p <- 80
n <- 40
K <- 2
k <- K - 1
cp <- numeric()
L <- c(0, floor(p / K) * (1 : k), p)
cp <- floor(p / K) * (1 : k) + 1

## phi0: probe effects; theta0: true methylation values; part: partition of probe indices
phi0 <- runif(p, 0.5, 2.0)
theta0 <- matrix(0, p, n)
part <- list()

for (s in 1 : K) {
  part[[s]] <- (L[s] + 1) : L[s + 1]
}
```

```

    phi0[part[[s]]] <- phi0[part[[s]]] / sqrt(mean(phi0[part[[s]]]^2))
  }

  theta0[part[[1]], ] <- rep(1, length(part[[1]]))
  theta0[part[[2]], ] <- rep(1, length(part[[2]]))

  error <- matrix(runif(p * n, 0, 0.1), p, n)
  Y <- theta0 * phi0 + error
  fit <- MBAmethyl(Y, steps = 10)

```

MBAmethyl

*Model-based analysis of DNA methylation data***Description**

This function reconstructs DNA methylation values from raw measurements. It iteratively implements the group fused lars to smooth related-by-location methylation values and the constrained least squares to remove probe affinity effect across multiple sequences. It also contains a criterion-based method (AIC or BIC) for selecting the tuning parameter.

Usage

```
MBAmethyl(Y, wts = .defaultWeights(nrow(Y)), steps = min(dim(Y)) - 1)
```

Arguments

<code>Y</code>	An observed matrix ($p \times n$) of methylation values (beta values); p is the number of probes and n is the number of samples;
<code>wts</code>	A pre-specified vector of weights. By default, we use the probe index-dependent weight scheme, $\text{wts}_i = \sqrt{p / i / (p - i)}$ for $i = 1, \dots, p$;
<code>steps</code>	Limit the number of steps taken. One can use this option to perform early stopping.

Value

<code>ans.aic</code>	A list corresponds to the AIC, containing estimated beta values, estimated probed effects, estimated change-point locations, residual sum of squares, and degree of freedom.
<code>ans.bic</code>	A list corresponds to the BIC, containing estimated beta values, estimated probed effects, estimated change-point locations, residual sum of squares, and degree of freedom.

Author(s)

Tao Wang, Mengjie Chen

References

paper under review

Examples

```
p <- 80
n <- 40
K <- 2
k <- K - 1
cp <- numeric()
L <- c(0, floor(p / K) * (1 : k), p)
cp <- floor(p / K) * (1 : k) + 1

## phi0: probe effects; theta0: true methylation values; part: partition of probe indices
phi0 <- runif(p, 0.5, 2.0)
theta0 <- matrix(0, p, n)
part <- list()

for (s in 1 : K) {
  part[[s]] <- (L[s] + 1) : L[s + 1]
  phi0[part[[s]]] <- phi0[part[[s]]] / sqrt(mean(phi0[part[[s]]]^2))
}

theta0[part[[1]], ] <- rep(1, length(part[[1]]))
theta0[part[[2]], ] <- rep(1, length(part[[2]]))

error <- matrix(runif(p * n, 0, 0.1), p, n)
Y <- theta0 * phi0 + error
fit <- MBAmethyl(Y, steps = 10)
```

Index

- * **methylation**

- MBAmethyl, [3](#)

- * **package**

- MBAmethyl-package, [2](#)

MBAmethyl, [3](#)

MBAmethyl-package, [2](#)