Package 'MBAmethyl'

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Type Package

Title Model-based analysis of DNA methylation data

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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

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R topics documented:

`MBAmethyl-package` *Model-based analysis of DNA methylation data*

Description

This package provides functions for reconstructing DNA methylation values from raw measurements. It utilize 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
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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 paramter.

Usage

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

Arguments

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

Value

`ans.aic`	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.
`ans.bic`	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)
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fit <- MBAmethyl(Y, steps = 10)
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