Package ‘MBAmethyl’

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Type Package
Title Model-based analysis of DNA methylation data
Version 1.8.0
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Author Tao Wang, Mengjie Chen
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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
NeedsCompilation no

R topics documented:

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

Author(s)

Tao Wang, Mengjie Chen

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References

~~ Literature or other references for background information ~~

Examples

```r
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)
```

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**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**

- **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 $i = 1, \ldots, p$;
- **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**

```r
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[[s]]] <- rnorm(n, 0, 2)
}
```
theta0[[1]], ] <- rep(1, length(part[[1]]))
theta0[[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)
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