

Package: MBAmethyl (via r-universe)

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Type Package

Title Model-based analysis of DNA methylation data

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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)

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biocViews DNAMethylation, MethylationArray

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/MBAmethyl>

RemoteRef HEAD

RemoteSha 20922209709deb5da57f010f35658d6740c49b8f

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

Author(s)

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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

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 $i = 1, \dots, p$;
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)
Y <- theta0 * phi0 + error
fit <- MBAmethyl(Y, steps = 10)
```

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