Package 'DMtest'

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Type Package

Title Differential Methylation Tests (DMtest)

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Description Several tests for differential methylation in methylation array data, including one-sided differential mean and variance test. Methods used in the package refer to Dai, J, Wang, X, Chen, H and others (2021) ``Incorporating increased variability in discovering cancer methylation markers'', Biostatistics, submitted.

Depends R (>= 3.5.0)

Imports matrixStats,stats,foreach,parallel,doParallel

License GPL (>= 2)

NeedsCompilation no

LazyData true

RoxygenNote 7.1.1

Suggests knitr, markdown

VignetteBuilder knitr

Repository CRAN

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Contents

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beta   *Example DNA methylation data for dmvc function*

Description

DNA methylation data from TCGA-COAD

Usage

```
data(beta)
```

Format

An object of class `"matrix"` with with 500 rows and 334 columns. Each row is a CpG, each column is a sample

Examples

```
data(beta)
```

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covariate   *Example covariate data for dmvc function*

Description

Covariate data for 334 TCGA-COAD samples

Usage

```
data(covariate)
```

Format

An object of class `"matrix"` with with 334 rows and 3 vaiables.

group Whether the sample is normal or tumor, normal:0, tumor:1

gender Female or Male

age age (31–90)

Examples

```
data(covariate)
```

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dmvc	*Perform DMC, DVC, DMVC, and DMVC+ tests for genome-wide CpGs in methylation arrays.*

Description

This function implements an algorithm for computing various tests of mean and variance differences, including the DMVC+ test that specifically addresses the hypermethylation and hypervariability for cancer-specific CpGs

Usage

```
dmvc(beta = beta, covariate = covariate, npermut=100,permut.seed=100,
corenumber=1)
```

Arguments

beta	Methylation beta value matrix, row for CpGs, column for samples. The matrix has sample name as the column names, and CpG names as the row names.
covariate	covariate matrix, a data frame including all covariates in the regression model, whose row represents for samples, column represents different covariates. The matrix has sample names as the row names. The matrix must include a "group" column, which is a binary indicator (0 for normal and 1 for tumor) to define two groups of samples to be compared.
npermut	The number of permutations for computing the correlation that is needed for the joint tests
permut.seed	The random seed used by permutation for joint tests
corenumber	The number of cores to be used for joint tests; if corenumber>1, a parallel computing version will be used to speed up the computation

Value

A data frame with the following columns.

Mean_normal	Mean of beta values for normal samples.
Mean_tumor	Mean of beta values for tumor samples.
Mean_all	Mean of beta values for all samples.
SD_normal	Standard deviation of beta values for normal samples.
SD_tumor	Standard deviation of beta values for tumor samples.
SD_all	Standard deviation of beta values for all samples.
DMCP	p-value from DMC test.
DVCP	p-value from DVC test.
Joint1P	Joint test for DMVC+ (test for hypermethylation and increased variance in cancer samples).

Joint2P	Joint test for DMVC (test for differential methylation in both direction and increased variance in cancer samples).
LRT1	Likelihood ratio test statistics for joint test1.
LRT2	Likelihood ratio test statistics for joint test2.
pho	Correlation value computed by permutations.

References

Dai, J, Wang, X, Chen, H and others. (2021). Incorporating increased variability in discovering cancer methylation markers, Biostatistics, submitted.

Examples

```
data(beta)
data(covariate)
out=dmvc(beta=beta,covariate=covariate)
```

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