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 re-
ter to Dai, J, Wang, X, Chen, H and others (2021) "Incorporating increased variability in discov-
Depends R (>= 3.5.0)
Imports matrixStats, stats, foreach, parallel, doParallel
License GPL (>= 2)
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Suggests knitr, markdown
VignetteBuilder knitr
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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 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 334 rows and 3 variables:

- **group**: Whether the sample is normal or tumor, normal:0, tumor:1
- **gender**: Female or Male
- **age**: age (31–90)

**Examples**

`data(covariate)`
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

\[ \text{dmvc}(\beta = \text{beta, covariate = covariate, npermut=100, permut.seed=100, corenumber=1}) \]

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

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