Package 'mgmtstp27'

May 21, 2024

Type Package

Title DNA methylation of MGMT promoter based on Infinium Platform
(27k, 450K and EPIC) from Illumina

Version 0.8

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Depends R (>= 4.2.1), minfi, lumi, ade4,methylumi,MASS

Suggests boot

Description This package contains R functions for the prediction of the DNA methylation status of MGMT promoter with data from Infinium platforms (HM-27K, HM450K, EPIC and EPICv2).

License GPL (>= 2)

Contents

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mgmtstp27-package   *Additional tools for the analysis of methylation data*

Description

Additional tools for the analysis of methylation data

Details

Package:	mgmtstp27
Type:	Package
Version:	0.1
Date:	2014-09-11
License:	GPL (>= 2)

Author(s)

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References

Bady, P., D. Sciuscio, A.-C. Diserens, J. Bloch, M. J. van den Bent, C. Marosi, P.-Y. Dietrich, M. Weller, L. Mariani, F. L. Heppner, D. R. McDonald, D. Lacombe, R. Stupp, M. Delorenzi, and M. E. Hegi. 2012. MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status. Acta Neuropathologica 124:547-560.

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gbm	*DNA methylation of MGMT promoter region from Infinium HM-450k and HM-27K platforms*

Description

DNA methylation of MGMT promoter region from Infinium HM-450k and HM-27K platforms (table S3 and S4 described in details Bady et al. 2012).

Usage

```
data("gbm")
```

Format

two data.frames corresponding to the tables S3 and S4 described in details Bady et al. (2012)

Details

The results published here are in part based upon data generated by The Cancer TCGA Genome Atlas pilot project established by the NCI and NHGRI. Information about TCGA and the investigators and institutions who constitute the TCGA research network can be found at (http://cancergenome.nih.gov). The dbGaP accession number to the specific version of the TCGA data set is phs000178.v8.p7.

Source

This two datasets correspond to the tables S3 and S4 from Bady et al. (2012).

References

Bady, P., D. Sciuscio, A.-C. Diserens, J. Bloch, M. J. van den Bent, C. Marosi, P.-Y. Dietrich, M. Weller, L. Mariani, F. L. Heppner, D. R. McDonald, D. Lacombe, R. Stupp, M. Delorenzi, and M. E. Hegi. 2012. MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status. Acta Neuropathologica 124:547-560.

The Cancer Genome Atlas Consortium Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature. 2008;455:1061-1068.

Noushmehr, H., D. Weisenberger, K. Diefes, H. Phillips, K. Pujara, B. Berman, F. Pan, C. Pelloski, E. Sulman, and K. Bhat. 2010. Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. Cancer Cell 17:510 - 522.

Examples

```
# table S3 (bady et al 2012)
data(NCHgbm450)
head(NCHgbm450)
# table S4 (bady et al 2012)
data(TCGAgbm27)
head(TCGAgbm27)
```

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mgmt   *set of tools related to prediction of the DNA methylation of MGMT promoter.*

Description

set of tools related to prediction of the DNA methylation of MGMT promoter.

Usage

```
MGMTpredict(x,level = 0.05,dispersion=FALSE,transpose=FALSE,ic.distrib="normal",cutoff=1,...)
MGMTsim(n=1000,proba=NULL,newdata=NULL,...)
MGMTqc.pop(object,sim=FALSE,n=1000,which.plot=1:6,mfrow=c(3,3),...)
MGMTqc.single(object,nsample=NULL,sim=FALSE,n=1000,which.plot=1:4,mfrow=c(2,3),...)
```

Arguments

x   a data.frame containing contining the M-values for the probes 'cg12981137' and 'cg12434587' (in row and columns).

object   an object of the class 'mgmt'.

level   a numeric value corresponding to level used to compute confidence intervals (level=0.05, by default).

dispersion   a logical value. If dispersion=TRUE, dispersion correction was used to compute Confidence intervals.

transpose	a logical value (transpose=TRUE, when the probes are organized by rows).
ic.distrib	a character value indicating the probability distribution used to compute confidence intervals ("student" or "normal", by default ic.distrib="normal").
cutt-off	a numeric value identifying the cut-off used to calculate the DNA methylation state of MGMT promoter (1= better classification, 2= balance among sensitivity and specificty). By default, cutoff is equal to 1.
n	number of simulated samples
newdata	an object of the class 'mgmt' containing containing the M-values for the probes 'cg12981137' and 'cg12434587' (in columns).
sim	a logical value.If sim=TRUE, the reference is obtained by simulation (Multivariate distribution. If sim=FALSE (by default), the reference is the training data.
nsample	a numerical value identifying the sample of interest (only used in the function MGMTqc.single, bydefault nsample=1).
which.plot	a vector telling which plots to produce.
mfrow	parameter for the array of figures to be drawn .
...	further arguments passed to or from other methods

Details

For EPIC v2 infinium platform, the function uses the two probes "cg12434587_BC11" and "cg12981137_TC11" (which will be renamed as "cg12434587" and "cg12981137"). The selection of these two probes is based on the concordance of the annotation information and the sequences of the probes (see variable "AlleleA_ProbeSeq" from manifest file). add information about simulation and QC graphical ouput.

Value

The function 'MGMTsim' return a data.frame containing two simulated M-values corresponding to the probes 'cg12981137' and 'cg12434587'. The function 'MGMTpredict' return data.frame contianing the following information:

sample	sample(row) names
cg12434587	M-value for the probe 'cg12434587'
cg12981137	M-value for the probe 'cg12981137'
pred	probability that MGMT promoter is methylated
lower	lower limit of the confidence intervals for the probability
upper	upper limit of the confidence intervals for the probability
state	DNA methylation state of MGMT promoter (U,M)using the cut-off provided in Bady et al. (2012)
extended	DNA methylation state of MGMT promoter (U,u,m,M) using the cut-off provided and confidence interval in Bady et al. (2012)

Author(s)

P.BADY

References

Bady, P., D. Sciuscio, A.-C. Diserens, J. Bloch, M. J. van den Bent, C. Marosi, P.-Y. Dietrich, M. Weller, L. Mariani, F. L. Heppner, D. R. McDonald, D. Lacombe, R. Stupp, M. Delorenzi, and M. E. Hegi. 2012. MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status. Acta Neuropathologica 124:547-560.

Examples

```
data(MGMTSTP27)
training1 <- MGMTSTP27$data
pred1 <- MGMTpredict(training1)
sim1 <- MGMTsim(n=100,newdata=pred1)
qqplot(pred1[,"cg12434587"],sim1[,"cg12434587"])
MGMTqc.pop(pred1)
```

MGMTSTP27   *Model to predict MGMTSTP27*

Usage

```
data("MGMTSTP27")
```

Format

an object 'glm' with additional numerical vector called 'perf' containing performance information.

perf a numeric vector containing information

Details

The function MGMTpredict provides prediction of DNA methylation status of MGMT promoter as described in Bady et al (2012). The model is an object glm with an additional numerical vector called 'perf' containing performance information.

Source

The model is presented in details in Bady et al. (2012).

References

Bady, P., D. Sciuscio, A.-C. Diserens, J. Bloch, M. J. van den Bent, C. Marosi, P.-Y. Dietrich, M. Weller, L. Mariani, F. L. Heppner, D. R. McDonald, D. Lacombe, R. Stupp, M. Delorenzi, and M. E. Hegi. 2012. MGMT methylation analysis of glioblastoma on the Infinium methylation BeadChip identifies two distinct CpG regions associated with gene silencing and outcome, yielding a prediction model for comparisons across datasets, tumor grades, and CIMP-status. Acta Neuropathologica 124:547-560.

Examples

```
data(MGMTSTP27)
MGMTSTP27
# maximization of good classification
MGMTSTP27$perf1
# balance amon specificity and sensitivity
MGMTSTP27$perf2
```

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