

# Package ‘mgmtstp27’

November 26, 2015

**Type** Package  
**Title** DNA methylation of MGMT promoter  
**Version** 0.6-3  
**Date** 2015-01-14  
**Author** Pierre Bady <pierre.bady@unil.ch>  
**Maintainer** Pierre Bady <pierre.bady@unil.ch>  
**Depends** R (>= 3.2.2), minfi, lumi, ade4, methylumi, MASS  
**Suggests** boot  
**Description** Prediction of the DNA methylation status of MGMT promoter with data from Infinium platforms (HM-27K and HM450K)  
**License** GPL (>= 2)

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mgmtstp27-package	<i>Additional tools for the analysis of methylation data</i>
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## 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)**

Author: Pierre Bady <pierre.bady@unil.ch>  
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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*

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**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	<i>set of tools related to prediction of the DNA methylation of MGMT promoter.</i>
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## 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 containing 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 specificity). 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 (Multi-variate 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

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 cantianing 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 using the cut-off provided 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(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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