Package 'mgmtstp27'

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Type Package

Title DNA methylation of MGMT promoter

Version 0.1

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Depends R (>= 3.1.1), minfi, lumi, ade4,methylumi,MASS

Suggests boot

Description prediction of the DNA methylation of MGMT promoter with data from infinium platform in glioma population

License GPL (>= 2)

R topics documented:

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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)

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

Usage

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

Format

two data.frames corresponding to the table 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)
```

---

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,...)
MGMTsim(n=1000,proba=NULL,newdata=NULL,...)
MGMTqc(object,sim=FALSE,n=1000,proba=NULL,...)
```

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).
n	number of simulated samples
proba	prevalance of methylated MGMT promoter.
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.
...	further arguments passed to or from other methods

Details

information about simulation and QC grphical 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 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
MGMTSTP27$perf
```

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