Package: CpGFilter (via r-universe)

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Type Package

Title CpG Filtering Method Based on Intra-Class Correlation Coefficients

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Description Filter CpGs based on Intra-class Correlation Coefficients (ICCs) when replicates are available. ICCs are calculated by fitting linear mixed effects models to all samples including the un-replicated samples. Including the large number of un-replicated samples improves ICC estimates dramatically. The method accommodates any replicate design.

License GPL-3

Depends R (>= 3.1.0)

Imports stats, matrixStats

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NeedsCompilation no

Repository CRAN

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Description

Filter CpGs based on Intra-class Correlation Coefficients (ICCs). ICCs are calculated by fitting linear mixed effects models to all samples including the un-replicated samples. Including the large number of un-replicated samples improves ICC estimates dramatically. The method accommodates any replicate design.

Usage

```
CpGFilterICC(dat, rep.design, REML = FALSE, logit.transform = TRUE, verbose = TRUE)
```

Arguments

dat	a matrix of CpG beta-values, row - CpG, column - sample
rep.design	a vector indicating the replicate design, it could be factor, character or numeric vectors. Example - c(1, 2, 3, 4, 4, 4, 5, 5) OR c('S1', 'S2', 'S2', 'S2', 'S1')
REML	If TRUE, Restricted Maximum Likelihood (REML) method will be used; Otherwise, Maximum Likelihood (ML) method will be used. Default is FALSE.
logit.transform	
	If TRUE, beta-value will be converted into M-value; Default is TRUE.
verbose	If TRUE, print run information

Value

ICCs for all probes

Author(s)

Jun Chen

References

Chen J, Just A, et al. CpGFilter:Model-based CpG probe filtering with replicates for epigenome-wide association studies (2016). Bioinformatics, 32(3): 469–471

Examples

```
require(CpGFilter)
# 10 samples replicated twice, 5 samples replicated four times.
rep.design <- c(1:100, 101:110, 101:110, 111:115, 111:115, 111:115, 111:115)
rho <- CpGFilterICC(matrix(rnorm(140*1000), 1000, 140), rep.design, logit=FALSE)
```

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