

Package ‘CpGFilter’

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Type Package

Title CpG Filtering Method Based on Intra-class Correlation Coefficients

Version 1.0

Date 2014-10-31

Author Jun Chen

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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-2

NeedsCompilation no

Repository CRAN

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CpGFilter-package *CpG filtering method based on linear mixed effects model.*

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.

Details

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Version: 1.0
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License: GPL-2

Author(s)

Jun Chen <chen.jun2@mayo.edu>

References

CpGFilter:Model-based CpG probe filtering with replicates for epigenome-wide association studies (2014). Submitted.

Examples

```
require(CpGFilter)
rep.design <- c(1:900, 901:910, 901:910, 911:915, 911:915, 911:915, 911:915)
rho <- CpGFilterICC(matrix(rnorm(940*10000), 10000, 940), rep.design, logit=FALSE)
```

B2M

Convert CpG Beta value to M value

Description

Convert CpG Beta value to M value

Usage

B2M(x)

Arguments

x Matrix of CpG Beta values

Value

Matrix of CpG M values

References

CpGFilter:Model-based CpG probe filtering with replicates for epigenome-wide association studies (2014). Submitted.

CpGFilterICC	<i>CpG filtering method based on intra-class correlation coefficients.</i>
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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, logit.transform = TRUE, verbose = TRUE)
```

Arguments

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

Value

ICCs for all probes

Author(s)

Jun Chen

References

CpGFilter:Model-based CpG probe filtering with replicates for epigenome-wide association studies (2014). Submitted.

Examples

```
require(CpGFilter)
rep.design <- c(1:900, 901:910, 901:910, 911:915, 911:915, 911:915, 911:915)
rho <- CpGFilterICC(matrix(rnorm(940*10000)), 10000, 940), rep.design, logit=FALSE)
```

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