

# Package ‘CpGFilter’

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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

**Encoding** UTF-8

**NeedsCompilation** no

**Repository** CRAN

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CpGFilterICC

*CpG filtering method based on intra-class correlation coefficients.***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**

|                              |  |
|------------------------------|--|
| <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>REML</code>            | If TRUE, Restricted Maximum Likelihood (REML) method will be used; Otherwise, Maximum Likelihood (ML) method will be used. Default is FALSE.   |
| <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**

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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