Package 'asmn'

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Title All sample mean normalization.

Description Performs all sample mean normalization using raw data output from BeadStudio and MethyLumiM data.

Version 1.2.0

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Depends R (>= 3.0.2)

Imports methylumi, stats, Biobase

Suggests TCGAMethylation450k, IlluminaHumanMethylation450k.db

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biocViews DNAMethylation, TwoChannel, Preprocessing, QualityControl

LazyData true

R topics documented:

`normalize_asmn` *Perform all sample mean normalization.*

Description

This function normalizes either raw data output from BeadStudio or data of type `MethyLumiSet`.

Usage

```
normalize_asmn(normfactors, rawdata, featuredata, methylumidata = NULL,
  type = "raw")
```

Arguments

normfactors	The output from norm_factors
rawdata	A data.frame, or matrix containing the methylation values the user wishes to normalize. Must contain column names that specify the detection signal type (A or B) and have the number of rows equal the number of CpG sites to be analyzed.
featuredata	A data.frame containing information for each row of rawdata specifying the ID of the CpG sites, the Infinium design type (I or II), and the color channel (red or green). This determines which normalization factors are used.
methylumidata	A MethyLumiSet data object containing the methylated/unmethylated sites as well as color channel identifiers accessed using fData. See the vignette for this package for an example using this type of data.
type	One of either "raw" (default) or "methylumi" indicating the type of data supplied by the user.

Examples

```
ids <- seq(from = 10, to = 59)
n <- length(ids)
reds.s <- data.frame(matrix(rep(round(abs(rnorm(n, 4, 1))), 30), nrow=30))
names(reds.s) <- paste("X", ids, ".Signal_Red", sep = "")
greens.s <- data.frame(matrix(rep(round(abs(rnorm(n, 5, 2))), 30), nrow = 30))
names(greens.s) <- paste("X", ids, ".Signal_Grn", sep = "")
dat <- data.frame(reds.s, greens.s)
dat <- dat[,order(names(dat))]
indices <- sample(1:30, 30, replace = FALSE)
TargetID.s <- rep(NA, 30)
TargetID.s[indices[1:9]] <- "NORM_A"
TargetID.s[indices[10:18]] <- "NORM_T"
TargetID.s[indices[19:25]] <- "NORM_C"
TargetID.s[indices[25:30]] <- "NORM_G"
controldata.s <- data.frame(TargetID = TargetID.s, dat)
normfactors <- norm_factors(controldata=controldata.s, subjects=NULL)
ncpg <- 100
IlmnIDs.s <- paste("cg00", seq(1:ncpg), sep = "")
Infinium_Design_type.s <- sample(c("I", "II"), size=ncpg, replace = TRUE)
Color_Channel.s <- vector()
Color_Channel.s[Infinium_Design_type.s == "I"] <- sample(c("Red", "Grn"), size = length(Color_Channel.s[Infinium_
featuredata.s <- data.frame(IlmnIDs = IlmnIDs.s, Infinium_Design_Type = Infinium_Design_type.s, Color_Channel = Co
signalA.s <- data.frame(matrix(rep(round(abs(rnorm(n, 4000, 2000))), ncpg), nrow=ncpg))
names(signalA.s) <- paste("X", ids, ".Signal_A", sep = "")
signalB.s <- data.frame(matrix(rep(round(abs(rnorm(n, 5000, 2000))), ncpg), nrow = ncpg))
names(signalB.s) <- paste("X", ids, ".Signal_B", sep = "")
dat <- data.frame(signalA.s, signalB.s)
mydata.s <- dat[,order(names(dat))]

newbetas <- normalize_asmn(normfactors=normfactors, rawdata=mydata.s, featuredata=featuredata.s, methylumidata =
```

norm_factors *Create normalization factors.*

Description

Using either raw data from BeadStudio or MethyLumiSet data, this function creates normalization factors using either all subjects' means or a subset.

Usage

```
norm_factors(controldata, subjects = NULL, methylumidata = NULL,
  type = "raw")
```

Arguments

controldata	A data.frame containing the red and green color channels for all control samples in raw format output from BeadStudio. May also contain detection p-values for each subject. Must contain a column called TargetID, which contains the CpG site identifiers. Either this or methylumidata must be supplied.
subjects	Optional. User can specify the index or names of a given subject or range of subjects to use in the creation of the normalization factors as oppposed to using all the samples.
methylumidata	A MethyLumiSet object containing control data (which can be accessed using the normctls function). See the vignette for this package for an example using this type of data.
type	One of either "raw" (default) or "methylumi" indicating the type of data supplied by the user.

Value

A list of length two containing the normalization factors for each subject in each color channel.

Examples

```
ids <- seq(from = 10, to = 59)
n <- length(ids)
reds.s <- data.frame(matrix(rep(round(abs(rnorm(n, 4, 1))), 30), nrow=30))
names(reds.s) <- paste("X", ids, ".Signal_Red", sep = "")
greens.s <- data.frame(matrix(rep(round(abs(rnorm(n, 5, 2))), 30), nrow = 30))
names(greens.s) <- paste("X", ids, ".Signal_Grn", sep = "")
dat <- data.frame(reds.s, greens.s)
dat <- dat[,order(names(dat))]
indices <- sample(1:30, 30, replace = FALSE)
TargetID.s <- rep(NA, 30)
TargetID.s[indices[1:9]] <- "NORM_A"
TargetID.s[indices[10:18]] <- "NORM_T"
TargetID.s[indices[19:25]] <- "NORM_C"
```

```
TargetID.s[indices[25:30]] <- "NORM_G"
controldata.s <- data.frame(TargetID = TargetID.s, dat)

normfactors <- norm_factors(controldata=controldata.s, subjects=NULL, type = "raw")
normfactors <- norm_factors(controldata=controldata.s, subjects=1, type = "raw")
```

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