Package 'nanonstringr'

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Type Package

Title Performs quality control and data normalization on the NanoString platform

Version 0.0.0.9008

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Description QC and batch adjustment operations for NanoString data.

Depends R (>= 3.2.0)

Imports dplyr, magrittr, assertthat

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LazyData TRUE

Suggests otta, testthat, knitr, rmarkdown, pander, stringr, tidyr, ggplot2

RoxygenNote 5.0.1

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

HKnorm *Normalization to Housekeeping Genes (Single-Patient sample)*

Description

Normalizes the gene expression of NanoString nCounter data to housekeeping genes. This is done by subtracting the average log housekeeping gene expression.

Usage

```
HKnorm(raw.data, corr = 1e-04)
```

Arguments

raw.data	matrix of raw counts obtained from nCounter (rows are genes). The first three columns must be labeled: c("Code.Class", "Name", "Accession") and contain that information.
corr	small correction on normalization

Value

A matrix of log normalized data in the same format but without reference genes.

Author(s)

Aline Talhouk

Examples

```
library(NanoStringNorm)
data(NanoString)
NanoString.mRNA[NanoString.mRNA$Name %in%
c(Eef1a1,Gapdh,Hprt1,Ppia,Sdha), Code.Class] <- Housekeeping

HKnorm(NanoString.mRNA)
```

NanoStringQC *QC for NanoString Data*

Description

Computes NanoString quality control parameters and flags

Usage

```
NanoStringQC(raw, exp, detect = 80, sn = 150, plots = TRUE, ttl = " ",
  explore = TRUE)
```

Arguments

raw	matrix of raw counts obtained from nCounter (rows are genes). The first three columns must be labeled: `c("Code.Class", "Name", "Accession")` and contain that information.
exp	matrix of annotations with rows in the same order as the columns of raw. Needs a column labeled File.Name with entries corresponding to sample names in raw count, also needs columns fov.counted and fov.count as well as binding.density. These fields can be extracted from the RCC files.
detect	percent threshold of genes over load that we would like to detect (not decimal).
sn	Signal to noise ratio of the housekeeping genes we are willing to tolerate
plots	logical; indicates whether plots to visualise the results are requested, defaults to TRUE
ttl	a string to show the title on the plots
explore	returns the plots only, defaults to TRUE

Value

matrix of annotations updated with normalization parameters

Author(s)

Aline Talhouk, Derek Chiu

Examples

```
# Load otta package for raw datasets and annotation matrix
library(otta)
data(rawOVCA2, rawPROT, rawOTTA, annot)

# Codeset 1, 2, 3 and annotations
cs1 <- rawOVCA2; cs2 <- rawPROT; cs3 <- rawOTTA; exp0 <- annot
exp0$geneRLF <- as.character(factor(exp0$geneRLF,
                    labels = c("HL1", "HL2", "HL3", "HuRef", "CS3", "mini", "CS1", "CS2")))

# Compute NanoString QC
exp.CS1 <- NanoStringQC(cs1, exp0[exp0$geneRLF == "CS1", ],
                        plots = FALSE, detect = 50, ttl = "CodeSet 1")
exp.CS2 <- NanoStringQC(cs2, exp0[exp0$geneRLF == "CS2", ],
                        plots = FALSE, sn = 100, ttl = "CodeSet 2")
exp.CS3 <- NanoStringQC(cs3, exp0[exp0$geneRLF == "CS3", ],
                        plots = TRUE, detect = 50, sn = 100, ttl = "CodeSet 3")
```

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nanostringr *nanostringr: Quality Control and normalization for nanostringr platform*

Description

The nanostringr package provides a novel set of tools used for quality control purposes in the NanoString platform. It includes batch adjustment using the ratio method thus far.

`ratioMethod` *Ratio method for batch adjustment*

Description

Batch adjustment by taking the ratio of a reference sample

Usage

```
ratioMethod(Y2, R1, R2)
```

Arguments

`Y2`	data run in the second batch, samples are rows and genes are columns
`R1`	reference data run in the first batch
`R2`	reference data run in the second batch

Value

The Y2 data adjusted to batch 1

Author(s)

Aline Talhouk

Examples

```
set.seed(12)
A <- matrix(rnorm(120), ncol = 10)
B <- matrix(rnorm(80), ncol = 10)
C <- matrix(rnorm(50), ncol = 10)
ratioMethod(A, B, C)
```

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