Package ‘zFPKM’

January 21, 2025

Title A suite of functions to facilitate zFPKM transformations

Version 1.28.0

Description Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed chromosome data. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

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URL `https://github.com/ronammar/zFPKM/`

BugReports `https://github.com/ronammar/zFPKM/issues`

Imports checkmate, dplyr, ggplot2, tidyr, SummarizedExperiment

Suggests knitr, limma, edgeR, GEOquery, stringr, printr, rmarkdown

VignetteBuilder knitr

biocViews ImmunoOncology, RNASeq, FeatureExtraction, Software, GeneExpression

Depends R (>= 3.4.0)

LazyData true

RoxygenNote 6.0.1

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Contents

`zFPKM` *zFPKM Transformation*

Description

Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed promoter chromatin structure epigenetic data on six of the ENCODE cell lines. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

Usage

```
zFPKM(fpkmDF, assayName = "fpkm")
```

Arguments

`fpkmDF`	A SummarizedExperiment or data frame containing raw FPKM (or TPM) values. Each row corresponds to a gene/transcript and each column corresponds to a sample. NOTE: these are NOT log_2 transformed. Also, the rownames are gene/transcript names and NOT included as a separate column
`assayName`	When input is a SummarizedExperiment, names the specific assay. Typically one of "fpkm" or "tpm" [default = "fpkm"]

Value

zFPKM data frame

Author(s)

Ron Ammar, `<ron.ammar@bms.com>`

References

http://www.ncbi.nlm.nih.gov/pubmed/24215113

Examples

```
library(dplyr)
gse94802 <- "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE94nnn/GSE94802/suppl/GSE94802_Minkina_etal_normalized
temp <- tempfile()
download.file(gse94802, temp)
fpkm <- read.csv(gzfile(temp), row.names=1)
MyFPKMdf <- select(fpkm, -MGI_Symbol)

zfpkm <- zFPKM(MyFPKMdf)
```

`zFPKMPlot` *zFPKM Transformation*

Description

Perform the zFPKM transform on RNA-seq FPKM data. This algorithm is based on the publication by Hart et al., 2013 (Pubmed ID 24215113). Reference recommends using zFPKM > -3 to select expressed genes. Validated with encode open/closed promoter chromatin structure epigenetic data on six of the ENCODE cell lines. Works well for gene level data using FPKM or TPM. Does not appear to calibrate well for transcript level data.

Usage

```
zFPKMPlot(fpkmDF, assayName = "fpkm", FacetTitles = FALSE,
  PlotXfloor = -20)
```

Arguments

`fpkmDF`	A SummarizedExperiment or data frame containing raw FPKM (or TPM) values. Each row corresponds to a gene/transcript and each column corresponds to a sample. NOTE: these are NOT log_2 transformed. Also, the rownames are gene/transcript names and NOT included as a separate column
`assayName`	When input is a SummarizedExperiment, names the specific assay. Typically one of "fpkm" or "tpm" [default = "fpkm"]
`FacetTitles`	use to label each facet with the sample name [default = FALSE]
`PlotXfloor`	Lower limit for X axis (log2FPKM units) [default = -20] set to NULL to disable

Value

Displays plots of zFPKM distributions

Author(s)

Ron Ammar, `<ron.ammar@bms.com>`

References

`http://www.ncbi.nlm.nih.gov/pubmed/24215113`

Examples

```
library(dplyr)
gse94802 <- "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE94nnn/GSE94802/suppl/GSE94802_Minkina_etal_normalized
temp <- tempfile()
download.file(gse94802, temp)
fpkm <- read.csv(gzfile(temp), row.names=1)
MyFPKMdf <- select(fpkm, -MGI_Symbol)

zFPKMPlot(MyFPKMdf)
```

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