Package 'QuantNorm'

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Title Quantile Normalization Methods for Batch Effect Correction

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Description
The QuantNorm function can help classify RNA-seq measurements from different batches.

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Depends stats, base, R (>= 3.3.1)

RoxygenNote 6.0.1

R topics documented:

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humanmouse   *Brain RNA-Seq data for both human and mouse.*

Description

Brain RNA-Seq data for both human and mouse.

Usage

humanmouse

Format

A data frame with 15041 rows and 62 columns

Source

http://web.stanford.edu/group/barres_lab/brainseq2/brainseq2.html

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QuantNorm *Conducting batch effect correction by quantile normalization*

Description

Conducting batch effect correction by quantile normalization

Usage

```
QuantNorm(dat, batch, method = "refB", iter = 1, logdat = TRUE,
  standardize = FALSE)
```

Arguments

dat | The original p*n batch effect data with n subjects and p RNA-seq measurements.

batch | The vector of length n indicating which batch the subjects belong to.

method | Method for the quantile normalization. There are three options: "refB", "ref1" and "block".

iter | Times of iteration for "refB" and "ref1" methods when no standardization is applied.

logdat | Whether conducting log transformation to data or not.

standardize | Whether conducting standardization [(dat - mean)/var] to data or not.

Value

The corrected 1-correlation matrix between subjects.

Examples

```
library(rgl) #for 3D PCA display

data("humanmouse")

#Numbering the cells by cell types
celltype <- c(rep(1,8),rep(7,6),rep(1,12),rep(2,1),rep(3,5),rep(4,3),rep(5,2),rep(6,4),
              rep(1,2),rep(1,4),rep(2,2),rep(3,6),rep(4,2),rep(5,2),rep(6,3))

#Assigning the batch number that the 62 subjects belonging to.
batches <- c(rep(1,41),rep(2,21))

#Plot the 3D PCA for the uncorrected batch effect data
plot3d(princomp(1-cor(humanmouse,method='spearman'))$scores[,1:3], col=celltype)

#QuantNorm correction
ccc <- QuantNorm(humanmouse,batches,iter=10)
plot3d(princomp(ccc)$scores[,1:3], col=celltype, size=10)
```

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