Package 'SQN'

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Type Package

Title Subset Quantile Normalization

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Depends R (>= 2.6.0), mclust(>= 3.2), nor1mix(>= 1.0-7)

Description Normalization based a subset of negative control probes as described in 'Subset quantile normalization using negative control features'. Wu Z, Aryee MJ, J Comput Biol. 2010 Oct;17(10):1385-95 [PMID 20976876].

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Contents

SQN *subset quantile normalization*

Description

This function performs normalization based on a subset of negative controls whose distribution is expected to be unchanged in various samples. There is no restriction on the behavior of the rest of the measurements.

Usage

```
SQN(y, N.mix = 5, ctrl.id, model.weight = 0.9)
```

Arguments

y	A matrix of unnormalized data.
N.mix	Number of normal distributions in the mixture approximation.
ctrl.id	index of controls. Must be a vector smaller than nrow(y)
model.weight	weight given to the parametric normal mixture model

Value

A matrix of normalized data

Author(s)

Zhijin Wu

References

Wu Z and Aryee M. Subset Quantile Normalization using Negative Control Features (2010) Journal of Computational Biology, 17(10)

Examples

```
require(mclust)
require(nor1mix)
data(sqnData0)
Ynorm=SQN(sqnData0,ctrl.id=1:1000)  #after normalization
 par(mfrow=c(1,2))
  boxplot(sqnData0,main="before normalization")
  boxplot(sqnData0[1:1000,],add=TRUE,col=3,boxwex=.4)

 boxplot(Ynorm,main="after normalization")
  boxplot(Ynorm[1:1000,],add=TRUE,col=3,boxwex=.4)
 legend(.5,11,legend=c("probes for signal","negative control probes"),text.col=c(1,3),bg="white")
```

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sqnData0 *example data*

Description

Simulated data with two samples, each with 1000 negative controls and 5000 signal bearing probes

Usage

```
data(sqnData0)
```

Format

A matrix with two columns

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