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)

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References

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

Examples

require(mclust)
require(norqmix)
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")

Description

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

Usage

data(sqndata0)
sqnData0

**Format**

A matrix with two columns
Index

* Topic **datasets**
  sqndata0, 2

mix.qn (SQN), 1

SQN, 1

sqndata0, 2