Package ‘SQN’

October 12, 2022

Type Package
Title Subset Quantile Normalization
Version 1.0.6
Date 2022-06-10
Author Zhijin(Jean) Wu, Martin Aryee
Maintainer Martin Aryee <martin.aryee@gmail.com>
Depends R (>= 2.6.0), mclust(>= 3.2), nor1mix(>= 1.0-7)
License LGPL (>= 2.0)
NeedsCompilation no
Repository CRAN
Date/Publication 2022-06-10 16:00:02 UTC

R topics documented:

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SQN</td>
<td>subset quantile normalization</td>
</tr>
</tbody>
</table>

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")

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

* datasets
  sqnData0, 2

mix.qn (SQN), 1

SQN, 1
sqnData0, 2