

# Package ‘SQN’

July 2, 2014

**Type** Package

**Title** subset quantile normalization

**Version** 1.0.5

**Date** 2012-08-06

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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].

**License** LGPL (>= 2.0)

**Repository** CRAN

**Date/Publication** 2012-08-13 17:24:15

**NeedsCompilation** no

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SQN *subset quantile normalization*

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### 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

<code>y</code>	A matrix of unnormalized data.
<code>N.mix</code>	Number of normal distributions in the mixture approximation.
<code>ctrl.id</code>	index of controls. Must be a vector smaller than <code>nrow(y)</code>
<code>model.weight</code>	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*

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**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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