# Package 'SQN'

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Type Package	
Title Subset Quantile Normalization	
Version 1.0.6	
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<b>Depends</b> R (>= 2.6.0), mclust(>= 3.2), nor1mix(>= 1.0-7)	
<b>Description</b> 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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Repository CRAN	
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R topics documented:	
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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.

2 sqnData0

#### 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")
```

sqnData0

example data

## **Description**

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

### Usage

```
data(sqnData0)
```

sqnData0 3

## **Format**

A matrix with two columns

# **Index**

```
* datasets
sqnData0, 2
mix.qn(SQN), 1
SQN, 1
sqnData0, 2
```