

# R documentation

of ‘testProbes.Rd’

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testProbes

*Test Illumina CpG Probes for potential problems*

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## Description

Test Illumina CpG probes for potential problems, useful for removing hits that may be unlikely to be reproduced

## Usage

```
testProbes(  
  betas,  
  manifest = c("450k", "EPIC"),  
  beadcounts = NULL,  
  detection = NULL,  
  nb = 0.2,  
  np = 0.2,  
  nvar = 0.5,  
  ot,  
  nbCount = 3,  
  nbThresh = 0.05,  
  pvCount = 0.05,  
  pvThresh = 0.01,  
  nvarThresh = 0.05  
)
```

## Arguments

betas	A matrix contain beta values, or a RGChannelSet(Extended), or a methylumiSet
manifest	Specify which manifest to use
beadcounts	Default: NULL, provide with a matrix containing beadcounts. Bead counts values will be used in calculation of nb for each probe.

detection	Default: NULL, provide with a matrix containing detection P values. Detection p-values will be used in calculation of np for each probe.
nb	A value between 0 and 1, the percentage of dataset a probe has failed in bead count. Probes failed in more than 20% of datasets in terms of bead count will be filtered out. However, all probes can be tested by nb=0.
np	A value between 0 and 1, the percentage of dataset a probe has failed in detection p-value. Probes failed in more than 20% of datasets in terms of detection p-values will be filtered out. However, all probes can be tested by np=0.
nvar	A value between 0 and 1, sample variance is used to filter out low variance having probes. Nvar parameter is adjusted to 0.5 which means the probe showing a low variation for more than 50% of the time will be failed in test. The last two messages clarify how many type I and type II probes were determined within the 5% in terms of variation.
ot	a character vector representing the types of probes as I or II.
nbCount	refers to physical bead counts to test the probes determined as lower than 3.
pvCount	the detection p-value to test probes. Default is 0.05 (5%).
pvThresh	the detection p-value threshold, corresponding to > 0.01 value. Probes are failed when they show > 0.05 detection p-value in > 1% of samples.
nvarThresh	the density of variation a probe can be in.
nbTresh	a proportion of the sample. The TestProbes function filters probes when the nbCount is less than 3 (<3) and nbThresh > 5% of the samples.

### Value

For minfi package & beta-values: A data.frame of nrow(betas) x 3 columns specifying which probes have failed which tests.

For methylumi package: MethylumiSet object. Analysis is stored under betas@featureData@data\$Variation.

### Author(s)

Tyler Gorrie-Stone <tgorri@essex.ac.uk>

### Examples

```
data("melon") #Sample dataset from watermelon package
betas <- betas(melon) #extracting beta values from melon object
test_betas <- testProbes(betas, ot = ot)

library(minfiData)
data("RGsetEx")
test_RG <- testProbes(RGsetEx)

data("melon")
test_melon <- testProbes(melon)
```

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