

Package ‘affyContam’

October 8, 2013

Title structured corruption of affymetrix cel file data

Version 1.18.0

Author V. Carey

Description structured corruption of cel file data to demonstrate QA effectiveness

Depends R (>= 2.7.0), tools, methods, utils, Biobase, affy, affydata

Maintainer V. Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

biocViews Infrastructure, Bioinformatics

R topics documented:

setRectRegion 1

Index 3

| | |
|---------------|------------------------------------------------------------------------------------------|
| setRectRegion | <i>set a rectangular or circular region in an affybatch to a specified set of values</i> |
|---------------|------------------------------------------------------------------------------------------|

Description

set a rectangular or circular region in an affybatch to a specified set of values

Usage

```
setRectRegion(x, chip=1, xinds=251:350, yinds=251:350, vals=10, valgen=NULL)
setCircRegion(x, chip=1, center=c(350,350), rad=100, vals=10, valgen=NULL)
getRectRegion(x, chip=1, xinds=251:350, yinds=251:350)
getCircRegion(x, chip=1, center=c(350,350), rad=100)
```

Arguments

| | |
|--------|-----------------------------------------------------------------------------------------------------------------|
| x | AffyBatch instance |
| chip | sample index |
| xinds | x coordinates to be contaminated |
| yinds | y coordinates to be contaminated |
| vals | values to be assigned to rectangle elements |
| center | geometric center of circle to be altered |
| rad | radius of circle to be altered, in xy units of the chip addressing system used by xy2indices in the cdf package |
| valgen | function of parameter n that generates n values to be inserted in the altered region |

Value

set* functions return AffyBatch instance with intensities modified as requested

get* functions return numeric vectors of intensities as requested.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
library(affydata)
data(Dilution)
opar = par(no.readonly=TRUE)
par(mfrow=c(2,2))
hist(Dilution, main="original")
image(Dilution[,1], main="original")
#
# we will contaminate in two ways: thin line at fixed low intensity, and
# circular blob at moderate random intensity
#
ab = setRectRegion(Dilution, 1, xinds=25:30, yinds=1:620,
  vals=10)
ab = setCircRegion(ab, 1, valgen=function(n){
  rnorm(n, 350,50)})
hist(ab, main="chip 1 contaminated by normal")
image(ab[,1], main="chip 1 contaminated")
ex = getCircRegion(Dilution, 1)
length(ex)
ab = setCircRegion(Dilution, 1, vals=pmin(2*ex,65535))
image(ab[,1], main="chip 1 contaminated by doubling")
par(opar)
```

Index

*Topic **models**

setRectRegion, [1](#)

getCircRegion (setRectRegion), [1](#)

getRectRegion (setRectRegion), [1](#)

setCircRegion (setRectRegion), [1](#)

setRectRegion, [1](#)