

Package ‘affyContam’

September 28, 2025

Title structured corruption of affymetrix cel file data

Version 1.66.0

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

Suggests hgu95av2cdf

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

License Artistic-2.0

LazyLoad yes

biocViews Infrastructure

git_url <https://git.bioconductor.org/packages/affyContam>

git_branch RELEASE_3_21

git_last_commit c70ca4b

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-09-28

Contents

setRectRegion	2
Index	4

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

* **models**

setRectRegion, [2](#)

getCircRegion (setRectRegion), [2](#)

getRectRegion (setRectRegion), [2](#)

setCircRegion (setRectRegion), [2](#)

setRectRegion, [2](#)