

# Package ‘affyContam’

April 4, 2014

**Title** structured corruption of affymetrix cel file data

**Version** 1.20.0

**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](#)