

# Package ‘affyContam’

February 21, 2025

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

**Version** 1.65.0

**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

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**License** Artistic-2.0

**LazyLoad** yes

**biocViews** Infrastructure

**git\_url** <https://git.bioconductor.org/packages/affyContam>

**git\_branch** devel

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

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### 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)
```

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## \* **models**

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