

# Package ‘affyContam’

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**Title** structured corruption of affymetrix cel file data  
**Version** 1.64.0  
**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  
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**biocViews** Infrastructure  
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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

setRectRegion, [1](#)

getCircRegion (setRectRegion), [1](#)

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setCircRegion (setRectRegion), [1](#)

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