affyContam: structured corruption of CEL-level data

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August 4, 2008

1 Introduction

Microarray quality assessment is a major concern of microarray analysts. This package provides some simple approaches to *in silico* creation of quality problems in CEL-level data to help evaluate performance of quality metrics.
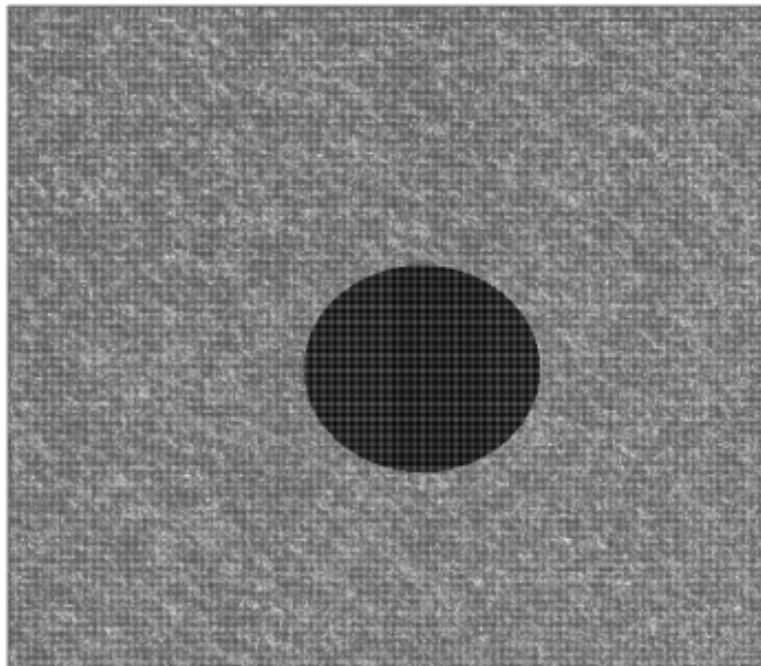
2 A small dataset

The *affydata* package includes a dataset called Dilution.

```
> library(affydata)
> data(Dilution)
> image(Dilution[, 1])
```

We can introduce a circular defect as follows:

```
> library(affyContam)
> dilc = setCircRegion(Dilution, chip = 1, cdfname = "hgu95av2cdf")

> image(dilc[, 1])
```

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Note that the extents of the region (which may be rectangular, see `setRectRegion`) can be varied using arguments to the set*Region functions. The distribution of intensity values used to reset the raw data can also be specified using the `valgen` parameter.