affy: Import Methods (HowTo)

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1 Introduction

This document describes briefly how to write import methods for the `affy` package. As one might know, the Affymetrix data are originally stored in files of type `.CEL` and `.CDF`. The package extracts and store the information contained in `R` data structures using file parsers. This document outlines how to get the data from other sources than the current[1] file formats.

As usual, loading the package in your `R` session is required.

```
R> library(affy) ##load the affy package
```

note: this document only describes the process for .CEL files

Knowing the slots of `Cel` and `AffyBatch` objects will probably help you to achieve your goals. You may want to refer to the respective help pages. Try `help(Cel)`, `help(AffyBatch)`.

2 How-to

2.1 Cel objects

The functions `getNrowForCEL` and `getNcolForCEL` are assumed to return the number of rows and the number of columns in the `.CEL` file respectively

You will also need to have access to the X and Y position for the probes in the `.CEL}`file. The functions `getPosXForCel` and `getPosYForCEL` are assumed to return the X and Y positions respectively. The corresponding probe intensities are assumed to be returned by the function `getIntensitiesForCEL`.

If you stored **all** the X and Y values that were in the `.CEL`, the functions verb+getNrowForCEL+ and `getNcolForCEL` can written:

---

[1]today's date is early 2003

```
> getNrowForCEL <- function() max(getPosXForCEL())
> getNcolForCEL <- function() max(getPosYForCEL())
```

You will also need the name for the corresponding `.CDF` (although you will probably no need the `.CDF` file itself, the cdf packages available for download will probably be enough).

```
import.celfile <- function(celfile, ...) {

  cel.nrow <- getNrowForCEL(celfile)
  cel.ncol <- getNcolForCEL(celfile)
  x <- matrix(NA, nr=cel.nrow, nc=cel.ncol)

  cel.intensities <- getIntensitiesForCEL(celfile)

  cel.posx <- getPosXForCEL(celfile) # +1 if indexing starts at 0 (like in .CEL)
  cel.posy <- getPosYForCEL(celfile) # idem

  x[cbind(cel.posx, cel.posy)] <- cel.intensities

  mycdfName <- whatcdf("aCELfile.CEL")

  myCel <- new("Cel", exprs=x, cdfName=mycdfName)

  return(myCel)
}
```

The function `import.celfile` can now replace the function `read.celfile` in the `affy` package

2.2   AffyBatch objects

(scratch) the use of . . . should make you able to override the function read.celfile by a hack like:

```
read.celfile <- import.celfile
```

The function `read.affybatch` should now function using your `import.celfile`