

cdfenvs and oligonucleotide arrays

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Introduction

This document describes briefly how the package gets (or tries to get) the needed *cdfenvs*. Various issues like security and configuring the options for the package *affy* are outlined. To some extend, what is developped here could¹ be applied to the package *oligochips*.

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

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

Why and how

The *cdfenvs* are associative data structures to map efficiently a *probeset id* with indices for the corresponding probes. These indices are used to subset a matrix storing probe level intensities. Technically, a *cdfenv* is a **R environment**. The functions `get` and `multiget` (in *Biobase*) are a convenient way to access what is in an environment. Expert users only will consider modifying what is those environment.

In the case of *Affymetrix* data, the *cdfenvs* are built from the *.CDF* files. The package *makecdfenvs* is dedicated to the building of packages with *cdfenvs*. The simplest way to proceed is to have the package needed for the analysis installed. A number of *cdfenv* packages for *Affymetrix* chips are available for download on the *Bioconductor* data packages repository. This release (1.2.x) of the *affy* package has an option to allow automatic downloading and install of a *cdfenv* that would be found missing during an analysis. However, if you are using an *unconventional* chip, it is possible that *Bioconductor* has not created the appropriate package for your *.CDF* file. We recommend that you use the package *makecdfenvs* to create the appropriate source code for the *cdfenv* package you need. For Microsoft Windows binaries you need to do more, see <http://www.stats.ox.ac.uk/pub/R/rw-FAQ.html>. If you contribute the package to

¹Currently this would require a bit of effort, but it should become very easy very soon

Bioconductor a windows binary will be made for you (and everybody else). The last section outlines briefly how to change the associated *cdfenv*.

The complete structure of the options for the package is not completely described, but one can refer the source code for the function `.setAffyOptions()`. The entry *probesloc* in the options details the path used to look for the corresponding *cdfenv*. We introduce a simple function to display the content of the options for the obtention of the information about probe locations:

```
> print.probesloc.opt <- function(affy.opt, fields) {
+   all.fields <- c("what", "where", "autoload", "repository",
+     "installdir")
+   if (sum(!(fields %in% all.fields)) > 0)
+     stop(paste("'fields' can only contain elements of:",
+       paste(all.fields, collapse = " ")))
+   l <- lapply(affy.opt$probesloc, function(x) x[fields])
+   l <- lapply(l, function(x) {
+     unk <- is.na(names(x))
+     x[unk] <- rep(list(unk = NA), sum(unk))
+     x <- lapply(x, function(y) if (is.null(y))
+       "NULL"
+     else y)
+     return(x)
+   })
+   ul <- as.character(unlist(l))
+   m <- t(matrix(ul, nr = length(fields)))
+   colnames(m) <- fields
+   print(m)
+ }
```

The default search path for *cdfenvs* will be:

```
> affy.opt <- getOption("BioC")$affy
> print.probesloc.opt(affy.opt, c("what", "where", "autoload"))
```

	what	where	autoload
[1,]	"environment"	"<environment>"	"NA"
[2,]	"libPath"	"NULL"	"NA"
[3,]	"data"	"affy"	"NA"
[4,]	"bioC"	"E:/biocbld/bbs-2.1-bioc/tmpdir/Rinst549212774"	"NA"

The option *autoload* is only relevant where *what* is equal to *package*. Having it set to *TRUE* means that an attempt will be made to download the package if it is not found in `.libPaths()` or in the search path shown above.

The following function returns a set of options with any existing automatic download deactivated :

```

> deactivate.autoload <- function(affy.opt) {
+   l <- lapply(affy.opt$probesloc, function(x) {
+     i <- names(x) == "autoload"
+     x[i] <- list(FALSE)
+     return(x)
+   })
+   affy.opt$probesloc <- l
+   return(affy.opt)
+ }

```

It can be used to deactivate any automatic download:

```

> affy.opt <- getOption("BioC")$affy
> affy.opt.noauto <- deactivate.autoload(affy.opt)
> .setAffyOptions(affy.opt.noauto)

```

Security

The autoload mechanism can be perceived as a security breach. It is the case, but not more than any **R** package you might install (unless you inspect carefully the source of every single package you install).

By default the *cdfenv* packages are downloaded from the bioconductor repository. This can be changed through the options for the package. One might want to check what it is like on his/her local installation:

```

> print.probesloc.opt(affy.opt, c("what", "autoload", "repository"))

```

	what	autoload	repository
[1,]	"environment"	NA	NA
[2,]	"libPath"	NA	NA
[3,]	"data"	NA	NA
[4,]	"bioC"	NA	NA

If you do not have install permissions, you might consider installing the *cdfenvs* packages to a particular place. For that you need to change the *installdir* (passed to the function `install.packages`).

```

> my.installdir <- "mydir/is/here"
> has.installdir <- unlist(lapply(affy.opt$probesloc, function(x) if ("installdir" %in%
+   names(x)) grep("installdir", names(x)) else numeric(0))))
> l <- lapply(affy.opt$probesloc, function(x) {
+   if ("installdir" %in% names(x)) {
+     x$installdir <- my.installdir

```

```

+     }
+     return(x)
+ })
> affy.opt$probesloc <- 1
> .setAffyOptions(affy.opt)

```

Note that a given *cdfenv* package is searched as specified in the argument *where*. Depending on your settings, you might prefer updating the `.libPaths()` of your **R** session, or the field *where* for the *probelocs*).

Changing the associated *cdfenv*

If you do not care about mapping *probeset ids* with indices and only want to deal with probe intensities, or if you would like to make a custom *cdfenv* from scratch, you will have to modify the association between your **AffyBatch** object(s) and *cdfenvs*.

If you want to experiment with this feature of the package, we would recommend to create a dummy *cdfenv* and associate your **AffyBatch** to it:

```

> data(affybatch.example)
> dummymap.name <- "dummymap"
> assign(dummymap.name, new.env())
> affybatch.example@cdfName <- paste(dummymap.name, "cdf", sep = "")

```

As explained in the first part, the *affy* package will then find a matching environment in the current environment (`.GlobalEnv`) and will not try to find a package. Note: the environment should still be in the section *probelocs* of the package options.