Modifying existing CDF environments to make alternative CDF environments

Laurent Gautier

April 15, 2011

Introduction

First we need to load the package:

```
> library(altcdfenvs)
```

The *Plasmodium* / *Anopheles* is taken as an example:

```
> library(plasmodiumanophelescdf)
```

One will adapt easily the code below for other chips.

How to build a CdfEnvAffy object from the cdfenv package

The first step is to wrap the naked enviroment in the package *plasmodiumanophelescdf* in an object:

```
> planocdf <- wrapCdfEnvAffy(plasmodiumanophelescdf, 712, 712,
+     "plasmodiumanophelescdf")
> print(planocdf)
```

```
Instance of class CdfEnvAffy:
 name     : plasmodiumanophelescdf
 chip-type: plasmodiumanophelescdf
 size     : 712 x 712
 22769 probe set(s) defined.
```

The numbers 712 and 712 correspond to the dimension of the array. If you do not know these numbers for your chip, the easiest (for the moment) is to read CEL data in an `AffyBatch` and call the function `print` on this object. Hopefully, the cdf packages offered on the bioconductor website will be modified, which will make this step (and the complication to know the dimension of the chip) unncessary.

How to subset an environment using probe set ids

(see the vignette 'n-genomes chips')

How to work with given index / XY coordinates

Getting index

The method `indexProbes` is implemeted for objects of class `AltCdfEnvs`

One can directly work on the CDF data, without having to load CEL data.

Removing probe sets

The function `removeIndex` let one remove probe sets given their index.

Multiple use of index

When crafting an AltCdfEnv, it can happen that probe indexes are used by several probe sets.

The `unique.CdfEnvAffy` is designed to help one to deal with the issue.

How to use this environment

(see the vignette 'n-genomes chips')