Textual description of gcrma

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1 Introduction

The *gcrma* package is part of the Bioconductor[1] project. The following terms are used throughout this document:

probe oligonucleotides of 25 base pair length used to probe RNA targets.

perfect match probes intended to match perfectly the target sequence.

PM intensity value read from the perfect matches.

mismatch the probes having one base mismatch with the target sequence intended to account for non-specific binding.

MM intensity value read from the mis-matches.

probe pair a unit composed of a perfect match and its mismatch.

affyID an identification for a probe set (which can be a gene or a fraction of a gene) represented on the array.

probe pair set *PM*s and *MM*s related to a common *affyID*.

CEL **files** contain measured intensities and locations for an array that has been hybridized.

CDF **file** contain the information relating probe pair sets to locations on the array.

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[1] http://www.bioconductor.org/

2 Getting Started: From probe level data to expression values

You will need the following libraries: affy, MASS and a library containint probe sequence data (such as hgu95av2probe). The first thing you need to do is **load the package**.

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

2.1 Quick start

If all you want is to go from probe level data (*Cel* files) to expression measures here are some quick ways.

   The quickest way of reading in data and getting expression measures is the following:

1. Create a directory, move all the relevant *CEL* files to that directory

2. Start R in that directory.

3. If using the Rgui for Microsoft Windows make sure your working directory contains the *Cel* files (use "File -> Change Dir" menu item).

4. Load the library.

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

5. Read in the data and create an expression, using RMA for example.

   ```
   R> Data <-  ReadAffy() ##read data in working directory
   R> eset <- gcrma(Data)
   ```