

description of gcrma

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1 Introduction

The *gcrma* package is part of the Bioconductor¹ project.

2 Getting Started: From probe level data to expression values

You will need to install the *affy* package, and the a package containing 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.

¹<http://www.bioconductor.org/>

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)
```