

Microarray Data Analysis using Bioconductor<http://www.bioconductor.org>**Using getBioC to obtain Bioconductor packages**

- From your R session, type:
 - > `source("http://www.bioconductor.org/getBioC.R")`
 this will download the getBioC functionality into your R session.
- To install Bioconductor packages, use the function "getBioC" as follows. To download and install the default packages, type:
 - > `getBioC()`
 For a different subset of packages, use the following values for the libName argument (or "all" for all packages)
 1. "all" - gets all packages (warning: This is a very large set)
 2. "affy" - gets packages [affy](#), [affycomp](#), [affydata](#), [affyPLM](#), [annaffy](#), [gcrma](#), [makecdfenv](#), [matchprobes](#), plus "exprs".
 3. "cdna" - gets packages [marray](#), [vsn](#), plus "exprs".
 4. "default" - gets all packages from "affy", "cdna" and "exprs"
 5. "exprs" - gets packages [Biobase](#), [annotate](#), [edd](#), [genefilter](#), [geneploter](#), [globaltest](#), [ROC](#), [MAGEML](#), [multtest](#), [limma](#), [pamr](#), [siggenes](#) and [vsn](#).

Using affy package

- Save all the .CEL files for the analysis and the corresponding .CDF file for the particular array in one directory. If you are connected to internet then R will get .CDF file
- Run R from that directory
- In R GUI write
 - `library(affy)`
 - `Data <- ReadAffy() # Reads in Data`
- Creating Expression Intensity Values
 1. RMA Expression Intensities (<http://stat-www.berkeley.edu/users/bolstad/RMAExpress/RMAExpress.html>)
 - `eset <- rma(Data)`
 OR
 - `eset <- expresso(Data, normalize.method="quantile.robust", bgcorrect.method="rma", pmcorrect.method="pmonly", summary.method="medianpolish")`
 - `write.exprs(eset, file="myDataRMA.txt")`
 2. DChip Expression Intensities (<http://www.dchip.org/>)
 - `eset <- expresso(Data, normalize.method="invariantset", bgcorrect=FALSE, pmcorrect.method="pmonly", summary.method="liwong")`
 - `write.exprs(eset, file="myDataDChip.txt")`
 3. MAS 5.0 Expression Intensities (<http://www.affymetrix.com/analysis>)
 - `eset <- mas5(Data)`
 OR
 - `eset <- expresso(Data, normalize=FALSE, bgcorrect.method="mas", pmcorrect.method="mas", summary.method="mas")`
 - `write.exprs(eset, file="myDataMAS5.txt")`
 - `Calls <- mas5calls(Data)`