

# HowTo BGX

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## 1 Introduction

This vignette describes how to use *bgx*, a C++ implementation of a Bayesian hierarchical integrated approach to the modelling and analysis of Affymetrix GeneChip arrays. The model and methodology is described in Hein et al, 2005.

There are two ways to run *bgx*: (1) through R and (2) as a standalone binary. Both ways make use of probe level GeneChip data, which you must obtain as GeneChip CEL files.

## 2 Reading in the CEL files

When you load *bgx*, several required packages from the Bioconductor<sup>1</sup> project are automatically loaded.

```
> library(bgx)
```

The *affy* package allows you to read CEL files into an `AffyBatch` object. This can be achieved by changing your working directory to wherever the CEL files are stored and executing:

```
> aData <- ReadAffy()
```

This will read in the CEL files in alphabetical order and save the data in the `aData` object. Alternatively, you can specify the specific files you would like to read in by adding their paths to the argument list, for example:

```
> aData <- ReadAffy("CEL/choe/chipC-rep1.CEL", "CEL/choe/chipS-rep2.CEL")
```

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<sup>1</sup><http://bioconductor.org>

### 3 Running BGX through R

A basic execution of the program can be performed by simply passing an **AffyBatch** object as a single parameter to the **bgx** function and saving the result in an **ExpressionSet** object. The result will hold array-specific gene expression values and their corresponding standard errors in `assayData(eset)$exprs` and `assayData(eset)$se.exprs` respectively.

```
> eset <- bgx(aData)
```

A more elaborate scenario would involve splitting the arrays into a number of conditions using the *samplesets* argument<sup>2</sup>; specifying which genes to analyse with the *genes* argument; specifying whether to take into account probe affinity with *probeAff*; setting the number of burn-in and post burn-in runs with the *burnin* and *iter* arguments respectively; setting the set of parameters to save with the *output* argument<sup>3</sup>; and specifying where to save the runs with *rundir*. Execute `help(bgx)` in R for a full explanation of all the parameters.

As an example, let us analyse the **Dilution** data set and save the results in the current working directory ("."):

```
> library(affydata)
> library(hgu95av2cdf)
> data(Dilution)
> eset <- bgx(Dilution, samplesets=c(2,2), probeAff=FALSE, burnin=2048, iter=8192,ge
```

The **eset** object will contain gene expression information for each gene under each condition (not necessarily each array). You may obtain the gene expression measure using the **exprs** function. For instance:

```
> exprs(eset)[10:40,] # Shorthand for assayData(eset)$exprs[10:40,]
```

	condition 1	condition 2
947_at	6.54444	6.25029
948_s_at	4.84583	4.45123
949_s_at	4.84665	4.55750
950_at	4.48827	4.27474
951_at	2.70152	2.49357
952_at	1.58622	1.94747
953_g_at	5.28392	4.89309

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<sup>2</sup>Note that if your **AffyBatch** object contains information on the experimental design in the **phenoData** slot, you do not need to use the *samplesets* argument.

<sup>3</sup>*output* can be set to either "minimal", "trace" or "all". See the documentation for an explanation of what these levels mean

954_s_at	6.36809	6.09223
955_at	6.60929	6.33914
956_at	7.00133	6.70313
957_at	4.62867	4.25959
958_s_at	5.53495	5.18097
959_at	1.90068	1.65003
960_g_at	5.22854	4.93502
961_at	1.71897	1.60414
962_at	2.46971	2.01055
963_at	4.55256	4.25666
964_at	4.27345	3.96223
965_at	2.17875	1.15486
966_at	4.44520	3.96493
967_g_at	4.85540	4.59308
968_i_at	3.33662	3.63703
969_s_at	4.80061	4.41228
970_r_at	6.29191	6.17022
971_s_at	2.03316	2.89112
973_at	4.35829	4.09485
974_at	2.27413	2.23694
975_at	4.26401	3.96236
976_s_at	3.52073	3.17471
977_s_at	4.83872	4.59583
978_at	3.19150	2.26953

Run `help(ExpressionSet)` in R for more information.

Note that *samplesets* should be set to an array specifying the number of replicates in each condition. If set to (3,2), `bgx` will treat the first three arrays read into R as replicates under condition 1 and the next two as replicates under condition 2. You should make sure that all condition 1 files are read in first and all condition 2 files are read in second by `ReadAffy()`. You may check the order of the samples in your `AffyBatch` object by using the `sampleNames` function:

```
> sampleNames(Dilution)
[1] "20A" "20B" "10A" "10B"
```

## 4 Running BGX as a standalone binary

Occasionally it may be useful to run `bgx` as a standalone binary from the command line<sup>4</sup>. In this case, you should use the `standalone.bgx` function instead of the `bgx` function.

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<sup>4</sup>You can compile it by tweaking 'src/Makefile.standalone' to your specifications and running 'make -f Makefile.standalone' from the 'src' directory.

It takes the same arguments as `bgx`, with the addition of *dirname*, which should specify where you would like to save the input files required by the standalone binary.

```
aData <- ReadAffy() # Read in 6 arrays across two conditions
                  # in alphabetical order
standalone.bgx(aData, samplesets=c(3,3), genes=c(1:650,1000:1200),
  burnin=16384, iter=65536, output="minimal",
  dirname="input-choe3replicates")
```

Once you have saved the input files, you should locate the binary, make sure it is executable<sup>5</sup>, and pass the path to the newly created `infile.txt` file as a single argument. For example:

```
./bgx ../input-choe3replicates/infile.txt
```

## 5 Detailed analysis of the output

If you wish to analyse the output in detail, you should first read the output into a list as follows:

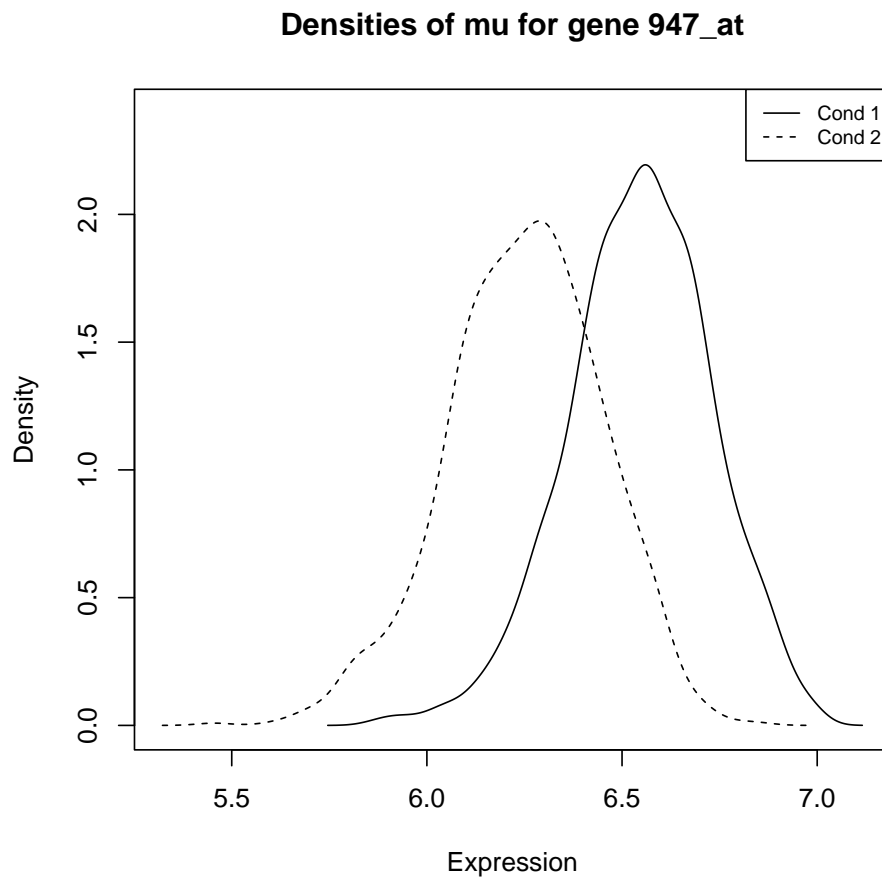
```
> bgxOutput <- readOutput.bgx("run.1")
```

You may then pass the `bgxOutput` object to any of several analysis functions. For instance, to view the gene expression distributions under the various conditions for gene 10, you could do:

```
> plotExpressionDensity(bgxOutput, gene=10)
```

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<sup>5</sup>Under Unix-like environments, you can type `chmod +x bgx` at the command prompt to do this.



In order to get a list of ranked differential expression values, you could do:

```
> rankedGeneList <- rankByDE(bgxOutput)
> print(rankedGeneList[1:25,]) # print top 25 DEG
```

	Position	DiffExpression
941_at	4	36.347898
956_at	19	31.947193
955_at	18	30.719990
AFFX-HUMGAPDH/M33197_5_at	89	29.730292
AFFX-HSAC07/X00351_5_at	83	28.877642
AFFX-HUMGAPDH/M33197_M_at	91	25.443945
947_at	10	25.033984
AFFX-HSAC07/X00351_M_at	85	24.970413
954_s_at	17	22.723817
946_at	9	22.693250
958_s_at	21	21.205970
AFFX-HUMGAPDH/M33197_3_at	87	18.793519

AFFX-HUMISGF3A/M97935_MB_at	96	17.405426
953_g_at	16	16.603250
AFFX-BioDn-3_at	70	15.625753
982_at	44	14.335130
AFFX-HUMISGF3A/M97935_3_at	93	13.916216
AFFX-HUMISGF3A/M97935_MA_at	95	12.615134
948_s_at	11	12.404184
AFFX-HSAC07/X00351_3_at	81	12.382537
969_s_at	32	12.107360
993_at	54	12.089784
957_at	20	11.909911
960_g_at	23	9.688060
949_s_at	12	9.650797

Run `help(analysis.bgx)` for more detailed usage instructions on the analysis functions.