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[1] 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")
```

[1] `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[2]; 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[3]; 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       6.56098     6.26997
948_s_at     4.85790     4.49876
949_s_at     4.83961     4.56556
950_at       4.52997     4.29875
951_at       3.17393     2.44307
952_at       2.73888     2.56612
953_g_at     5.36699     4.92927
```

[2]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.

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

```
954_s_at     6.37191     6.10189
955_at       6.62872     6.35100
956_at       7.01201     6.71214
957_at       4.72135     4.34800
958_s_at     5.54409     5.21718
959_at       1.57482     1.86354
960_g_at     5.20786     4.92868
961_at       2.03527     1.66524
962_at       2.14763     2.55365
963_at       4.60264     4.28778
964_at       4.28678     4.13439
965_at       1.03681     1.26713
966_at       4.47805     4.10522
967_g_at     4.84897     4.66133
968_i_at     3.67266     2.90894
969_s_at     4.87544     4.51131
970_r_at     6.31486     6.17551
971_s_at     3.43529     2.95454
973_at       4.45409     4.13214
974_at       2.01042     2.06738
975_at       4.32565     4.13869
976_s_at     3.86750     3.44907
977_s_at     4.94816     4.62901
978_at       2.65994     2.81188
```

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[4]. In this case, you should use the `standalone.bgx` function instead of the `bgx` function.

[4]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[5], 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

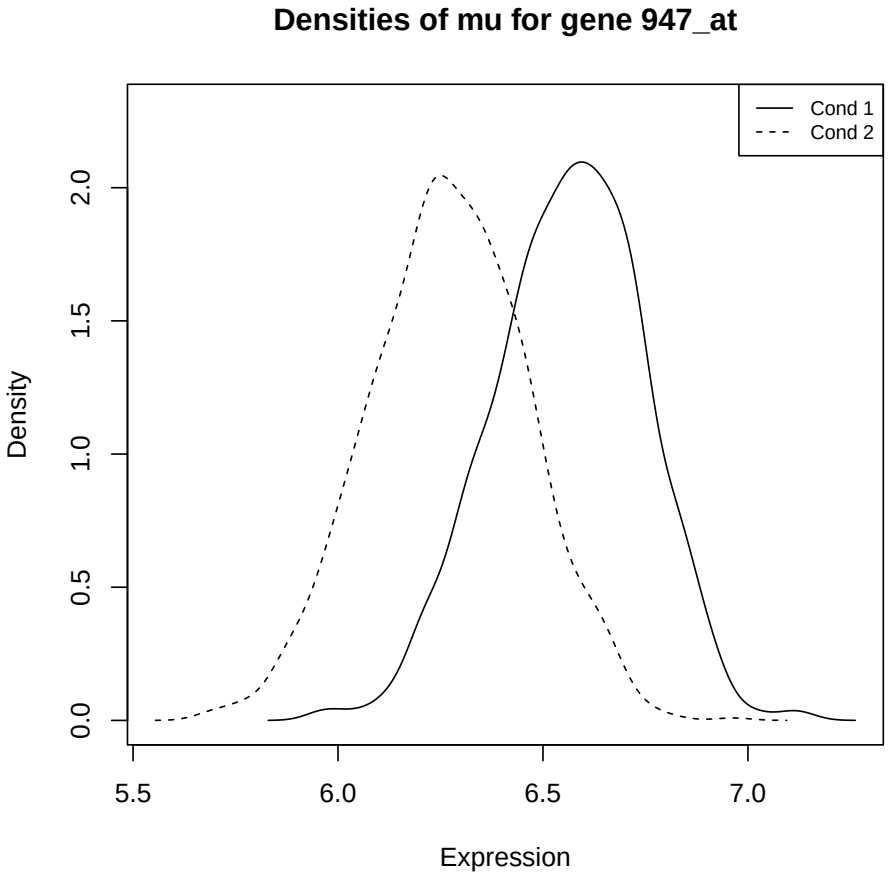
If you wish to analyse the output in detail, you should first read the output into a list as follows:

```
> 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)
```

[5]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
AFFX-HSAC07/X00351_5_at	83	35.264039
956_at	19	34.426614
AFFX-HUMGAPDH/M33197_5_at	90	32.603083
941_at	4	30.761823
955_at	18	30.120320
AFFX-HUMGAPDH/M33197_M_at	92	26.166322
947_at	10	24.066835
AFFX-HSAC07/X00351_M_at	85	23.781085
954_s_at	17	20.713868
953_g_at	16	19.738269
AFFX-HUMGAPDH/M33197_3_at	88	18.643602
946_at	9	17.263210

AFFX-hum_alu_at	87	16.196821
958_s_at	21	15.306843
AFFX-BioDn-3_at	70	14.365100
969_s_at	32	13.084924
AFFX-HUMISGF3A/M97935_3_at	94	12.876558
AFFX-HUMISGF3A/M97935_MB_at	97	12.210429
982_at	44	11.920631
957_at	20	11.042587
AFFX-HSAC07/X00351_3_at	81	10.833132
948_s_at	11	10.325586
993_at	54	8.787360
977_s_at	39	8.776448
AFFX-HUMISGF3A/M97935_MA_at	96	8.739451

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