

# Package ‘bgx’

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**Title** Bayesian Gene eXpression

**Version** 1.70.0

**Author** Ernest Turro, Graeme Ambler, Anne-Mette K Hein

**Maintainer** Ernest Turro <et341@cam.ac.uk>

**Description** Bayesian integrated analysis of Affymetrix GeneChips

**License** GPL-2

**Depends** R (>= 2.0.1), Biobase, affy (>= 1.5.0), gcrma (>= 2.4.1)

**Suggests** affydata, hgu95av2cdf

**biocViews** Microarray, DifferentialExpression

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**LinkingTo** Rcpp

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analysis.bgx

*Analyse BGX output.***Description**

Functions for plotting expression densities, differential expression densities, histogram of proportion of differentially expressed genes, etc.

**Usage**

```
plotExpressionDensity(bgxOutput, gene=NULL, normalize=c("none", "mean", "loess"), ...)
plotDEDensity(bgxOutput, gene=NULL, conditions=c(1,2), normalize=c("none", "mean", "loess"), normgenes=c(1:length(bgxOutput$genes)))
plotDEHistogram(bgxOutput, conditions=c(1,2), normalize=c("none", "mean", "loess"), normgenes=c(1:length(bgxOutput$genes)))
rankByDE(bgxOutput, conditions=c(1,2), normalize=c("none", "mean", "loess"), normgenes=c(1:length(bgxOutput$genes)))
plotDiffRank(bgxOutput, conditions=c(1,2), normalize=c("none", "mean", "loess"), normgenes=c(1:length(bgxOutput$genes)))
```

**Arguments**

bgxOutput	A list obtained from running <a href="#">readOutput.bgx</a> on a BGX output directory.
gene	Which gene to analyse. This can either be an index or a name.
conditions	Indices of conditions to compare.
normalize	"none": do not normalise posterior distributions of mu. "mean": normalise by scaling posterior distributions of mu for conditions > 1 to have the same mean as the posterior distribution of mu for condition 1. "loess": same as "mean" but use loess normalisation.
normgenes	Which genes to use for loess normalisation. By default, use all genes.
df	Residual degrees of freedom. Decrease to 6 if the histogram fit goes haywire.
absolute	Rank genes by absolute differential expression.
ymax	Specify upper limit of y axis.
...	Parameters to pass to density function (where applicable).

**Details**

`plotExpressionDensity` plots gene expression distributions under various conditions for the specified gene.

`plotDEDensity` plots the differential expression distribution between two conditions for a given gene.

`plotDEHistogram` plots a histogram of differential expression between two conditions and estimates the number of up and down regulated differentially expressed genes.

`rankByDE` ranks genes by differential expression and returns ordering and corresponding DE values in a matrix.

`plotDiffRank` plots 2.5-97.5% confidence intervals for ranked differential expression estimates.

**Value**

None, except plotDERank, which returns a matrix of genes ranked by differential expression.

**Author(s)**

Ernest Turro

**See Also**

[bgx](#), [standalone.bgx](#), [readOutput.bgx](#), [plotExpressionDensity](#), [plotDEDensity](#), [plotDEHistogram](#)

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bgx	<i>Fully Bayesian integrated approach to the analysis of Affymetrix GeneChip data</i>
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**Description**

'bgx' estimates Bayesian Gene eXpression (BGX) measures from an AffyBatch object.

'standalone.bgx' creates various files needed by the bgx standalone binary and places them in a directory. One of these files is 'infile.txt'. In order to run standalone BGX, compile it and run 'bgx <path\\_to\\_infile.txt>' from the command line.

**Usage**

```
bgx(aData, samplesets = NULL, genes = NULL, genesToWatch = NULL,
    burnin = 8192, iter = 16384, output = c("minimal", "trace", "all"),
    probeAff = TRUE, probecat_threshold = 100, adaptive = TRUE, rundir = ".")
```

```
standalone.bgx(aData, samplesets = NULL, genes = NULL, genesToWatch = NULL,
    burnin = 8192, iter = 16384, output = c("minimal", "trace", "all"),
    probeAff = TRUE, probecat_threshold = 100,
    adaptive = TRUE, batch_size = 50, optimalAR = 0.44, inputdir = "input")
```

**Arguments**

aData	An AffyBatch object.
samplesets	A numeric vector specifying which condition each array belongs to. E.g. if samplesets=c(2,2), then the first two replicates belong to one condition and the last two replicates belong to another condition. If NULL, each array is assumed to belong to a different condition. If the aData object contains information about the experiment design in its phenoData slot, this argument is not required.
genes	A numeric vector specifying which genes to analyse. If NULL, all genes are analysed.
genesToWatch	A numeric vector specifying which genes to monitor closely amongst those chosen to be analysed (see below for details).

burnin	Number of burn-in iterations.
iter	Number of post burn-in iterations.
output	One of "minimal", "trace" or "all". See below for details.
probeAff	Stratify the mean (lambda) of the cross-hybridisation parameter (H) by categories according to probe-level sequence information.
probecat_threshold	Minimum amount of probes per probe affinity category.
adaptive	Adapt the variance of the proposals for Metropolis Hastings objects (that is: S, H, Lambda, Eta, Sigma and Mu).
batch_size	Size of batches for calculating acceptance ratios and updating jumps.
optimalAR	Optimal acceptance ratio.
rundir	The directory in which to save the output runs.
inputdir	The name of the directory in which to place the input files for the standalone binary.

### Details

- `genesToWatch` Specify the subset of genes for which thinned samples from the full posterior distributions of  $\log(S+1)$  (x) and  $\log(H+1)$  (y) are collected.
- `output` Output the following to disk:
  - "minimal" The gene expression measure (`muave`), thinned samples from the full posterior distributions of `mu` (`mu.[1..c]`), where 'c' is the number of conditions, the integrated autocorrelation time (IACT) and the Markov chain Monte Carlo Standard Error (MCSE) for each gene under each condition. Note that the IACT and MCSE are calculated from the thinned samples of `mu`.
  - "trace" The same as "minimal" plus thinned samples from the full posterior distributions of `sigma2` (`sigma2.[1..c]`), `lambda` (`lambda.[1..s]`), `eta2` (`eta2`), `phi` (`phi`) and `tau2` (`tau2`), where 's' is the number of samples. If there are probes with unknown sequences, output a thinned trace of their categorisation.
  - "all" The same as "trace" plus acceptance ratios for S (`sacc`), H (`hacc`), `mu` (`muacc`), `sigma` (`sigmaacc`), `eta` (`etaacc`) and `lambda` (`lambdasacc`).

### Value

`'bgx'` returns an `ExpressionSet` object containing gene expression information for each gene under each condition (not each replicate).

`'standalone.bgx'` returns the path to the BGX input files.

### Note

The `bgx()` method and the `bgx` standalone binary create a directory in the working directory called `'run.x'` (x:1,2,3,...), wherein files are placed for further detailed analysis.

### Author(s)

Ernest Turro

## References

Turro, E., Bochkina, N., Hein, A., Richardson, S. (2007) BGX: a Bioconductor package for the Bayesian integrated analysis of Affymetrix GeneChips. *BMC Bioinformatics* 2007, 8:439.

Hein, A., Richardson, S. (2006) A powerful method for detecting differentially expressed genes from GeneChip arrays that does not require replicates. *BMC Bioinformatics* 2006, 7:353.

Hein, A., Richardson, S., Causton, H., Ambler, G., Green., P. (2005) BGX: a fully Bayesian integrated approach to the analysis of Affymetrix GeneChip data. *Biostatistics*, 6, 3, pp. 349-373.

Hekstra, D., Taussig, A. R., Magnasco, M., and Naef, F. (2003) Absolute mRNA concentrations from sequence-specific calibration of oligonucleotide array. *Nucleic Acids Research*, 31. 1962-1968.

G.O. Roberts, J.S. Rosenthal (September, 2006) Examples of Adaptive MCMC.

## Examples

```
# This example requires the 'affydata' and 'hgu95av2cdf' packages
if(require(affydata) && require(hgu95av2cdf)) {
  data(Dilution)
  eset <- bgx(Dilution, samplesets=c(2,2), probeAff=FALSE, burnin=4096, iter=8192,
    genes=c(12500:12599), output="all", rundir=file.path(tempdir()))
}
```

---

mcmc.bgx

*Internal wrapper function for calling the bgx C++ function.*

---

## Description

This internal function calls the bgx method in a loaded bgx shared object (bgx.so/bgx.dll)

## Usage

```
mcmc.bgx(pm, mm, samplesets, probesets, numberCategories, categories, unknownProbeSeqs, numberOfUnknow
  numberGenesToWatch, whichGenesToWatch, whichProbesToWatch, iter, burnin,
  adaptive, batch_size=50, optimalAR=0.44, output, samplenames = "unknown",
  subsample = ifelse(iter > 1024, iter/1024, 1), seed = 192492, rundir)
```

## Arguments

pm	Perfect Match probes
mm	MisMatch probes
samplesets	A numeric vector specifying which condition each array belongs to. E.g. if samplesets=c(2,2), then the first two replicates belong to one condition and the last two replicates belong to another condition. If NULL, each array is assumed to belong to a different condition.
probesets	A numeric vector specifying how probes are grouped into probesets.

numberCategories	Number of probe affinity categories.
categories	A numeric vector specifying which category each probe belongs to.
unknownProbeSeqs	A numeric vector specifying which probes lack sequence information.
numberOfUnknownProbeSeqs	Number of probes lacking sequence information.
numberGenesToWatch	How many genes to monitor closely.
whichGenesToWatch	A numeric vector specifying which genes to monitor closely.
whichProbesToWatch	The starting position for each probe in each gene to monitor closely.
iter	Number of post burn-in iterations.
burnin	Number of burn-in iterations.
adaptive	Use adaptive MCMC for better mixing.
batch_size	Batch size for adaptive MCMC.
optimalAR	Optimal acceptance ratio.
output	One of "minimal", "trace", "diagnostic" or "mcse".
samplenames	Vector of names for each array.
subsample	Subsampling interval.
seed	Seed for PRNG.
rundir	The directory in which to place the output run directories.

### Details

See [bgx](#) for more details.

### Value

The name of the output directory.

### Note

You shouldn't call this function directly, but if you do, make sure the appropriate shared object is loaded.

### Author(s)

Ernest Turro

### See Also

[bgx](#), [standalone.bgx](#)

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readOutput.bgx      *Read in the output from a BGX run.*

---

**Description**

readOutput.bgx reads in output from BGX which can then be fed into BGX analysis functions.

**Usage**

```
readOutput.bgx(...)
```

**Arguments**

...      Paths of BGX output directories. If you specify more than one path, then the runs will be combined such that each condition from each run is treated as a different different from all the others.

**Details**

See [bgx](#) for more details.

**Value**

A list containing data from the BGX output.

**Author(s)**

Ernest Turro

**See Also**

[bgx](#), [standalone.bgx](#), [plotExpressionDensity](#), [plotDEDensity](#), [plotDEHistogram](#)

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saveAffinityPlot.bgx      *Save a plot of affinity categorisation.*

---

**Description**

This internal function saves a plot showing how probes were categorised into affinity categories.

**Usage**

```
saveAffinityPlot.bgx(originalAffinities, categories, dir, probecat_threshold)
```

**Arguments**

originalAffinities	The affinities of the probes.
categories	The categories of the probes.
dir	Name of a directory in which to save the plot.
probecat_threshold	The minimum number of probes per category that was used to categorise the probes.

**Author(s)**

Ernest Turro

**References**

See [bgx](#)

**See Also**

[bgx](#)

---

setupVars.bgx

*Initialise variables needed to run BGX simulation.*

---

**Description**

This internal function initialises several variables, which it returns in a list.

**Usage**

```
setupVars.bgx(data, samplesets, genes, genesToWatch, probeAff, probecat_threshold, rounding_dec_place)
```

**Arguments**

data	An AffyBatch object.
samplesets	A numeric vector specifying which condition each array belongs to. E.g. if <code>samplesets=c(2,2)</code> , then the first two replicates belong to one condition and the last two replicates belong to another condition. If NULL, each array is assumed to belong to a different condition.
genes	A numeric vector specifying which genes to analyse. If NULL, all genes are analysed.
genesToWatch	A numeric vector specifying which genes to monitor closely amongst those chosen to be analysed (see below for details).
probeAff	Stratify the mean ( $\lambda$ ) for the cross-hybridisation parameter (H) by categories according to probe-level sequence information.



probecat\_threshold  
Minimum amount of probes per probe affinity category.

rounding\_dec\_places  
The initial probe categorisation is done by rounding affinities to the nearest rounding\_dec\_places decimal places. 1 is a good value.

**Value**

A list:

pm Perfect Match probes.

mm MisMatch probes.

samplesets A numeric vector specifying which condition each array belongs to. E.g. if samplesets=c(2,2), then the first two replicates belong to one condition and the last two replicates belong to another condition. If NULL, each array is assumed to belong to a different condition.

probesets A numeric vector specifying how probes are grouped into probesets.

numberOfCategories  
Number of probe affinity categories.

categories A numeric vector specifying which category each probe belongs to.

unknownProbeSeqs  
A numeric vector specifying which probes lack sequence information.

numberOfUnknownProbeSeqs  
Number of probes lacking sequence information.

genesToWatch A numeric vector specifying which genes to monitor closely.

firstProbeInEachGeneToWatch  
The starting position for each probe in each gene to monitor closely.

numArrays  
Number of arrays.

**Note**

This function shouldn't be called directly.

**Author(s)**

Ernest Turro

**References**

See [bgx](#)

**See Also**

[bgx](#)

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