Package 'gcrma'

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Title Background Adjustment Using Sequence Information

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Description Background adjustment using sequence information

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Depends R (>= 2.6.0), affy (>= 1.23.2), graphics, methods, stats, utils

Imports Biobase, affy (>= 1.23.2), affyio (>= 1.13.3), XVector, Biostrings (>= 2.11.32), splines, BiocInstaller

Suggests affydata, tools, splines, hgu95av2cdf, hgu95av2probe

biocViews Microarray, OneChannel, Preprocessing

NeedsCompilation yes

R topics documented:

affinity.spline.coefs *Spline coefficients for estimation of affinity from probe sequence*

Description

Spline coefficients for estimation of affinity from probe sequence

Usage

```
data(affinity.spline.coefs)
```

See Also

compute.affinities

bg.adjust.affinities *Background adjustment with sequence information (internal function)*

Description

An internal function to be used by gcrma.

Usage

```
bg.adjust.fullmodel(pms,mms,ncs=NULL,apm,amm,anc=NULL,index.affinities,k=6
* fast + 0.25 * (1 - fast),rho=.7,fast=FALSE)
bg.adjust.affinities(pms,ncs,apm,anc,index.affinities,k=6
* fast + 0.25 * (1 - fast),fast=FALSE,nomm=FALSE)
```

Arguments

pms	PM intensities after optical background correction, before non-specific-binding correction.
mms	MM intensities after optical background correction, before non-specific-binding correction.
ncs	Negative control probe intensities after optical background correction, before non-specific-binding correction. If ncs=NULL, the MM probes are considered the negative control probes.
index.affinities	The index of pms with known sequences. (For some types of arrays the sequences of a small subset of probes are not provided by Affymetrix.)
apm	Probe affinities for PM probes with known sequences.
amm	Probe affinities for MM probes with known sequences.
anc	Probe affinities for Negative control probes with known sequences. This is ignored when ncs=NULL.
rho	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7

k	A tuning parameter. See details.
fast	Logical value. If TRUE a faster add-hoc algorithm is used.
nomm	Logical value indicating if MM intensities are available and will to be used to estimate background.

Details

Assumes PM=background1+signal,mm=background2, (log(background1),log(background2))' follow bivariate normal distribution, signal distribution follows power law. `bg.parameters.gcrma` and `sg.parameters.gcrma` provide adhoc estimates of the parameters.

the original gcrma uses an empirical Bayes estimate. this requires a complicated numerical integration. An add-hoc method tries to imitate the empirical Bayes estimate with a PM-B but values of PM-B<k going to k. This can be thought as a shrunken MVUE. For more details see Wu et al. (2003).

Value

a vector of same length as x.

Author(s)

Rafeal Irizarry, Zhijin(Jean) Wu

See Also

gcrma

`bg.adjust.gcrma` *GCRMA background adjust (internal function)*

Description

This function performs background adjustment (optical noise and non-specific binding on an `AffyBatch` project and returns an `AffyBatch` object in which the PM intensities are adjusted.

Usage

```
bg.adjust.gcrma(object,affinity.info=NULL,
      affinity.source=c("reference","local"),
      NCprobe=NULL,
      type=c("fullmodel","affinities","mm","constant"),
      k=6*fast+0.5*(1-fast),stretch=1.15*fast+1*(1-fast),correction=1,
      GSB.adjust=TRUE,
      rho=.7,optical.correct=TRUE,verbose=TRUE,fast=TRUE)
```

Arguments

object	an AffyBatch
affinity.info	NULL or an AffyBatch containing the affinities in the exprs slot. This object can be created using the function compute.affinities.
affinity.source	reference: use the package internal Non-specific binding data or local: use the experimental data in object. If local is chosen, either MM probes or a user-defined list of probes (see NCprobes) are used to estimate affinities.
NCprobe	Index of negative control probes. When set as NULL,the MM probes will be used. These probes are used to estimate parameters of non-specific binding on each array. These will be also used to estimate probe affinity profiles when affinity.info is not provided.
type	"fullmodel" for sequence and MM model. "affinities" for sequence information only. "mm" for using MM without sequence information.
k	A tuning factor.
stretch	.
correction	.
GSB.adjust	Logical value. If TRUE, probe effects in specific binding will be adjusted.
rho	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7
optical.correct	Logical value. If TRUE, optical background correction is performed.
verbose	Logical value. If TRUE messages about the progress of the function is printed.
fast	Logical value. If TRUE a faster ad hoc algorithm is used.

Details

The returned value is an AffyBatch object, in which the PM probe intensities have been background adjusted. The rest is left the same as the starting AffyBatch object.

The tunning factor k will have different meainngs if one uses the fast (ad hoc) algorithm or the empirical bayes approach. See Wu et al. (2003)

Value

An AffyBatch.

Author(s)

Rafeal Irizarry

Examples

```
if(require(affydata) & require(hgu95av2probe) & require(hgu95av2cdf)){
        data(Dilution)
        ai <- compute.affinities(cdfName(Dilution))
        Dil.adj<-bg.adjust.gcrma(Dilution,affinity.info=ai,type="affinities")
    }
```

bg.parameters.ns *Estimation of non-specific Binding Background Parameters*

Description

An internal function to be used by gcrma

Usage

```
bg.parameters.ns(x,affinities,affinities2=NULL,affinities3=NULL,span=.2)
```

Arguments

x	PM or MM intensities after optical background correction, before non-specific-binding correction.
affinities	Probe affinities for probes with known sequences.Used to estimate the function between non-specific binding and affinities.
affinities2	Probe affinities for the probes whoes expected non-specific binding intensity is to be predicted.
affinities3	Probe affinities for another extra group of probes whoes expected non-specific binding intensity is to be predicted.
span	The span parameter passed to loess function

Value

a vector of same length as x.

Author(s)

Rafeal Irizarry, Zhijin (Jean) Wu

See Also

gcrma

compute.affinities *Probe Affinity computation*

Description

An internal function to calculate probe affinities from their sequences.

Usage

```
compute.affinities(cdfname,verbose=TRUE)
compute.affinities2(cdfname,verbose=TRUE)
check.probes(probepackage,cdfname)
```

Arguments

cdfname	Object of class character representing the name of CDF file associated with the arrays in the AffyBatch.
probepackage	character representing the name of the package with the probe sequence information.
verbose	Logical value. If TRUE messages about the progress of the function is printed.

Details

The affinity of a probe is described as the sum of position-dependent base affinities. Each base at each position contributes to the total affinity of a probe in an additive fashion. For a given type of base, the positional effect is modeled as a spline function with 5 degrees of freedom.

Use compute.affinities2 if there are no MM probes.

check.probes makes sure things are matching as they should.

Value

compute.affinities returns an AffyBatch with the affinities for PM probes in the pm locations and the affinities for MM probes in the mm locations. NA will be added for probes with no sequence information.

Author(s)

Rafeal Irizarry

References

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.

See Also

gcrma,affinity.spline.coefs

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gcrma *Robust Multi-Array expression measure using sequence information*

Description

This function converts an AffyBatch into an ExpressionSet using the robust multi-array average (RMA) expression measure with help of probe sequence.

Usage

```
gcrma(object,affinity.info=NULL,
      affinity.source=c("reference","local"),NCprobe=NULL,
      type=c("fullmodel","affinities","mm","constant"),
      k=6*fast+0.5*(1-fast),stretch=1.15*fast+1*(1-fast),correction=1,
      GSB.adjust=TRUE,
      rho=.7,optical.correct=TRUE,verbose=TRUE,fast=TRUE,
      subset=NULL,normalize=TRUE,...)
```

Arguments

object	an AffyBatch
affinity.info	NULL or an AffyBatch containing the affinities in the exprs slot. This object can be created using the function compute.affinities.
affinity.source	reference: use the package internal Non-specific binding data or local: use the experimental data in object. If local is chosen, either MM probes or a user-defined list of probes (see NCprobes) are used to estimate affinities.
NCprobe	Index of negative control probes. When set as NULL,the MM probes will be used. These probes are used to estimate parameters of non-specific binding on each array. These will be also used to estimate probe affinity profiles when affinity.info is not provided.
type	"fullmodel" for sequence and MM model. "affinities" for sequence information only. "mm" for using MM without sequence information.
k	A tuning factor.
stretch	.
correction	.
GSB.adjust	Logical value. If TRUE, probe effects in specific binding will be adjusted.
rho	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7
optical.correct	Logical value. If TRUE, optical background correction is performed.
verbose	Logical value. If TRUE messages about the progress of the function is printed.
fast	Logical value. If TRUE a faster ad hoc algorithm is used.
subset	a character vector with the the names of the probesets to be used in expression calculation.
normalize	logical value. If 'TRUE' normalize data using quantile normalization.
...	further arguments to be passed (not currently implemented - stub for future use).

Details

Note that this expression measure is given to you in log base 2 scale. This differs from most of the other expression measure methods.

The tuning factor k will have different meanings if one uses the fast (add-hoc) algorithm or the empirical Bayes approach. See Wu et al. (2003)

Value

An ExpressionSet.

Author(s)

Rafeal Irizarry

Examples

```
if(require(affydata) & require(hgu95av2probe) & require(hgu95av2cdf)){
     data(Dilution)
     ai <- compute.affinities(cdfName(Dilution))
     Dil.expr<-gcrma(Dilution,affinity.info=ai,type="affinities")
}
```

`gcrma.engine` *GCRMA background adjust engine(internal function)*

Description

This function adjust for non-specific binding when all arrays in the dataset share the same probe affinity information. It takes matrices of PM probe intensities, MM probe intensities, other negative control probe intensities(optional) and the associated probe affinities, and return one matrix of non-specific binding corrected PM probe intensities.

Usage

```
gcrma.engine(pms,mms,ncs=NULL,
                          pm.affinities=NULL,mm.affinities=NULL,anc=NULL,
                          type=c("fullmodel","affinities","mm","constant"),
                          k=6*fast+0.5*(1-fast),
                     stretch=1.15*fast+1*(1-fast),correction=1,GSB.adjust=TRUE,rho=0.7,
                          verbose=TRUE,fast=FALSE)
```

Arguments

`pms`	The matrix of PM intensities
`mms`	The matrix of MM intensities
`ncs`	The matrix of negative control probe intensities. When left as`NULL`, the MMs are considered the negative control probes.
`pm.affinities`	The vector of PM probe affinities. Note: This can be shorter than the number of rows in `pms` when some probes do not have sequence information provided.
`mm.affinities`	The vector of MM probe affinities.
`anc`	The vector of Negative Control probe affinities. This is ignored if MMs are used as negative controls (`ncs=NULL`)
`type`	"fullmodel" for sequence and MM model. "affinities" for sequence information only. "mm" for using MM without sequence information.
`k`	A tuning factor.
`stretch`	.
`correction`	.
`GSB.adjust`	Logical value. If `TRUE`, probe effects in specific binding will be adjusted.
`rho`	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7
`verbose`	Logical value. If `TRUE` messages about the progress of the function is printed.
`fast`	Logicalvalue. If `TRUE` a faster add-hoc algorithm is used.

Details

Note that this expression measure is given to you in log base 2 scale. This differs from most of the other expression measure methods.

The tunning factor k will have different meainngs if one uses the fast (add-hoc) algorithm or the empirical bayes approach. See Wu et al. (2003)

Value

A matrix of PM intensties.

Author(s)

Rafeal Irizarry & Zhijin Wu

See Also

gcrma.engine2

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gcrma.engine2 *GCRMA background adjust engine(internal function)*

Description

This function adjust for non-specific binding when each array has its own probe affinity information. It takes an AffyBatch object of probe intensities and an AffyBatch of probe affinity, returns one matrix of non-specific binding corrected PM probe intensities.

Usage

```
gcrma.engine2(object,pmIndex=NULL,mmIndex=NULL,
              NCprobe=NULL,affinity.info,
              type=c("fullmodel","affinities","mm","constant"),
              k=6*fast+0.5*(1-fast),
             stretch=1.15*fast+1*(1-fast),correction=1,GSB.adjust=TRUE,rho=0.7,
              verbose=TRUE,fast=TRUE)
```

Arguments

object	an AffyBatch. Note: this is an internal function. Optical noise should have been corrected for.
pmIndex	Index of PM probes.This will be computed within the function if left NULL
mmIndex	Index of MM probes.This will be computed within the function if left NULL
NCprobe	Index of negative control probes. When set as NULL,the MM probes will be used. These probes are used to estimate parameters of non-specific binding on each array. These will be also used to estimate probe affinity profiles when affinity.info is not provided.
affinity.info	NULL or an AffyBatch containing the affinities in the exprs slot. This object can be created using the function compute.affinities.
type	"fullmodel" for sequence and MM model. "affinities" for sequence information only. "mm" for using MM without sequence information.

k	A tuning factor.
stretch	.
correction	.
GSB.adjust	Logical value. If TRUE, probe effects in specific binding will be adjusted.
rho	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7
verbose	Logical value. If TRUE messages about the progress of the function is printed.
fast	Logicalvalue. If TRUE a faster add-hoc algorithm is used.

Details

Note that this expression measure is given to you in log base 2 scale. This differs from most of the other expression measure methods.

The tunning factor k will have different meainngs if one uses the fast (add-hoc) algorithm or the empirical bayes approach. See Wu et al. (2003)

Value

A matrix of PM intensties.

Author(s)

Rafeal Irizarry & Zhijin Wu

See Also

gcrma.engine

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justGCRMA *Compute GCRMA Directly from CEL Files*

Description

This function converts CEL files into an ExpressionSet using the robust multi-array average (RMA) expression measure with help of probe sequences.

Usage

```
just.gcrma(..., filenames=character(0),
           phenoData=new("AnnotatedDataFrame"),
           description=NULL,
           notes="", compress=getOption("BioC")$affy$compress.cel,
           normalize=TRUE, bgversion=2, affinity.info=NULL,
           type=c("fullmodel","affinities","mm","constant"),
           k=6*fast+0.5*(1-fast), stretch=1.15*fast+1*(1-fast),
           correction=1, rho=0.7, optical.correct=TRUE,
           verbose=TRUE, fast=TRUE, minimum=1, optimize.by =
           c("speed","memory"),
           cdfname = NULL, read.verbose = FALSE)
```

```
justGCRMA(..., filenames=character(0),
          widget=getOption("BioC")$affy$use.widgets,
          compress=getOption("BioC")$affy$compress.cel,
          celfile.path=getwd(),
          sampleNames=NULL,
          phenoData=NULL,
          description=NULL,
          notes="",
          normalize=TRUE,
          bgversion=2, affinity.info=NULL,
          type=c("fullmodel","affinities","mm","constant"),
          k=6*fast+0.5*(1-fast), stretch=1.15*fast+1*(1-fast),
          correction=1, rho=0.7, optical.correct=TRUE,
          verbose=TRUE, fast=TRUE, minimum=1,
          optimize.by = c("speed","memory"),
          cdfname = NULL, read.verbose = FALSE)
```

Arguments

...	file names separated by comma.
filenames	file names in a character vector.
widget	a logical specifying if widgets should be used.
compress	are the CEL files compressed?
phenoData	a AnnotatedDataFrame object.
description	a MIAME object.
notes	notes.
affinity.info	NULL or a list of three components: apm,amm and index, for PM probe affinities, MM probe affinities, the index of probes with known sequence, respectively.
type	"fullmodel" for sequence and MM model. "affinities" for sequence information only. "mm" for using MM without sequence information.
k	A tuning factor.
rho	correlation coefficient of log background intensity in a pair of pm/mm probes. Default=.7.
stretch	.
correction	.
normalize	Logical value. If TRUE, then normalize data using quantile normalization.
optical.correct	Logical value. If TRUE, then optical background correction is performed.
verbose	Logical value. If TRUE, then messages about the progress of the function is printed.
fast	Logical value. If TRUE, then a faster add-hoc algorithm is used.
optimize.by	"speed" will use a faster algorithm but more RAM, and "memory" will be slower, but require less RAM.
bgversion	integer value indicating which RMA background to use 1: use background similar to pure R rma background given in affy version 1.0 - 1.0.2 2: use background similar to pure R rma background given in affy version 1.1 and above.
minimum	.

celfile.path	a character denoting the path 'ReadAffy' should look for cel files.
sampleNames	a character vector of sample names to be used in the 'AffyBatch'.
cdfname	Used to specify the name of an alternative cdf package. If set to NULL, the usual cdf package based on Affymetrix' mappings will be used. Note that the name should not include the 'cdf' on the end, and that the corresponding probe package is also required to be installed. If either package is missing an error will result.
read.verbose	Logical value. If TRUE, then messages will be printed as each celfile is read in.

Details

This method should require much less RAM than the conventional method of first creating an AffyBatch and then running gcrma.

This is a simpler version than gcrma, so some of the arguments available in gcrma are not available here. For example, it is not possible to use the MM probes to estimate background. Instead, the internal NSB estimates are used (which is also the default for gcrma).

Note that this expression measure is given to you in log base 2 scale. This differs from most of the other expression measure methods.

The tuning factor k will have different meanings if one uses the fast (add-hoc) algorithm or the empirical Bayes approach. See Wu et al. (2003)

fast.bkg and mem.bkg are two internal functions.

Value

An ExpressionSet object.

Author(s)

James W. MacDonald

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