

# puma

April 19, 2010

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bcomb

*Combining replicates for each condition*

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## Description

This function calculates the combined signal for each condition from replicates using Bayesian models. The inputs are gene expression levels and the probe-level standard deviation associated with expression measurement for each gene on each chip. The outputs include gene expression levels and standard deviation for each condition. This function was originally part of the **pplr** package. Although this function can be called directly, it is recommended to use the [pumaComb](#) function instead, which can work directly on [ExpressionSet](#) objects, and can automatically determine which arrays are replicates.

## Usage

```
bcomb(e, se, replicates, method=c("map", "em"),  
      gsnorm=FALSE, nsample=1000, eps=1.0e-6)
```

## Arguments

<code>e</code>	a data frame containing the expression level for each gene on each chip.
<code>se</code>	a data frame containing the standard deviation of gene expression levels.
<code>replicates</code>	a vector indicating which chip belongs to which condition.
<code>method</code>	character specifying the method algorithm used.
<code>gsnorm</code>	logical specifying whether do global scaling normalisation or not.
<code>nsample</code>	integer. The number of sampling in parameter estimation.
<code>eps</code>	a numeric, optimisation parameter.

## Details

Each element in replicate represents the condition of the chip which is in the same column order as in the expression and standard deviation matrix files.

Method "map" uses MAP of a hierarchical Bayesian model with Gamma prior on the between-replicate variance (Gelman et.al. p.285) and shares the same variance across conditions. This method is fast and suitable for the case where there are many conditions.

Method "em" uses variational inference of the same hierarchical Bayesian model as in method "map" but with conjugate prior on between-replicate variance and shares the variance across conditions.

The parameter nsample should be large enough to ensure stable parameter estimates. Should be at least 1000.

### Value

The result is a data frame with components named 'M1', 'M2', and so on, which represent the mean expression values for condition 1, condition 2, and so on. It also has components named 'Std1', 'Std2', and so on, which represent the standard deviation of the gene expression values for condition 1, condition 2, and so on.

### Author(s)

Xuejun Liu, Marta Milo, Neil D. Lawrence, Magnus Rattray

### References

Gelman,A., Carlin,J.B., Stern,H.S., Rubin,D.B., Bayesian data analysis. London: Chapman & Hall; 1995.

Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) Probe-level variances improve accuracy in detecting differential gene expression, technical report available upon request.

### See Also

Related methods [pumaComb](#), [mmgmos](#) and [pp1r](#)

### Examples

```
data(exampleE)
data(exampleStd)
r<-bcomb(exampleE,exampleStd,replicates=c(1,1,1,2,2,2),method="map")
```

---

calcAUC

*Calculate Area Under Curve (AUC) for a standard ROC plot.*

---

### Description

Calculates the AUC values for one or more ROC plots.

### Usage

```
calcAUC(scores, truthValues, includedProbesets = 1:length(truthValues))
```

**Arguments**

- `scores` A vector of scores. This could be, e.g. one of the columns of the statistics of a [DEResult](#) object.
- `truthValues` A boolean vector indicating which scores are True Positives.
- `includedProbesets` A vector of indices indicating which scores (and `truthValues`) are to be used in the calculation. The default is to use all, but a subset can be used if, for example, you only want a subset of the probesets which are not True Positives to be treated as False Positives.

**Value**

A single number which is the AUC value.

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [plotROC](#) and [numFP](#).

**Examples**

```
class1a <- rnorm(1000,0.2,0.1)
class2a <- rnorm(1000,0.6,0.2)
class1b <- rnorm(1000,0.3,0.1)
class2b <- rnorm(1000,0.5,0.2)
scores_a <- c(class1a, class2a)
scores_b <- c(class1b, class2b)
classElts <- c(rep(FALSE,1000), rep(TRUE,1000))
print(calcAUC(scores_a, classElts))
print(calcAUC(scores_b, classElts))
```

---

calculateFC

*Calculate differential expression between conditions using FC*

---

**Description**

Automatically creates design and contrast matrices if not specified. This function is useful for comparing fold change results with those of other differential expression (DE) methods such as [pumaDE](#).

**Usage**

```
calculateFC(
  eset
  , design.matrix = createDesignMatrix(eset)
  , contrast.matrix = createContrastMatrix(eset)
)
```

## Arguments

`eset` An object of class [ExpressionSet](#)  
`design.matrix` A design matrix  
`contrast.matrix` A contrast matrix

## Details

The `eset` argument must be supplied, and must be a valid [ExpressionSet](#) object. Design and contrast matrices can be supplied, but if not, default matrices will be used. These should usually be sufficient for most analyses.

## Value

An object of class [DEResult](#).

## Author(s)

Richard D. Pearson

## See Also

Related methods [pumaDE](#), [calculateLimma](#), [calculateTtest](#), [createDesignMatrix](#) and [createContrastMatrix](#) and class [DEResult](#)

## Examples

```
if (require(affydata)) {  
  data(Dilution)  
  eset_rma <- rma(Dilution)  
  # Next line used so eset_rma only has information about the liver factor  
  # The scanner factor will thus be ignored, and the two arrays of each level  
  # of the liver factor will be treated as replicates  
  pData(eset_rma) <- pData(eset_rma)[,1, drop=FALSE]  
  FCRes <- calculateFC(eset_rma)  
  topGeneIDs(FCRes, numberOfGenes=6)  
  plotErrorBars(eset_rma, topGenes(FCRes))  
}
```

---

`calculateLimma`

*Calculate differential expression between conditions using limma*

---

## Description

Runs a default analysis using the **limma** package. Automatically creates design and contrast matrices if not specified. This function is useful for comparing **limma** results with those of other differential expression (DE) methods such as [pumaDE](#).

## Usage

```
calculateLimma(  
  eset  
  , design.matrix = createDesignMatrix(eset)  
  , contrast.matrix = createContrastMatrix(eset)  
  )
```

## Arguments

eset	An object of class <a href="#">ExpressionSet</a>
design.matrix	A design matrix
contrast.matrix	A contrast matrix

## Details

The `eset` argument must be supplied, and must be a valid [ExpressionSet](#) object. Design and contrast matrices can be supplied, but if not, default matrices will be used. These should usually be sufficient for most analyses.

## Value

An object of class [DEResult](#).

## Author(s)

Richard D. Pearson

## See Also

Related methods [pumaDE](#), [calculateTtest](#), [calculateFC](#), [createDesignMatrix](#) and [createContrastMatrix](#) and class [DEResult](#)

## Examples

```
if (require(affydata)) {  
  data(Dilution)  
  eset_rma <- rma(Dilution)  
  # Next line used so eset_rma only has information about the liver factor  
  # The scanner factor will thus be ignored, and the two arrays of each level  
  # of the liver factor will be treated as replicates  
  pData(eset_rma) <- pData(eset_rma)[,1, drop=FALSE]  
  limmaRes <- calculateLimma(eset_rma)  
  topGeneIDs(limmaRes, numberOfGenes=6)  
  plotErrorBars(eset_rma, topGenes(limmaRes))  
}
```

---

calculateTtest	<i>Calculate differential expression between conditions using T-test</i>
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---

### Description

Automatically creates design and contrast matrices if not specified. This function is useful for comparing T-test results with those of other differential expression (DE) methods such as [pumaDE](#).

### Usage

```
calculateTtest(  
  eset  
  , design.matrix = createDesignMatrix(eset)  
  , contrast.matrix = createContrastMatrix(eset)  
  )
```

### Arguments

eset	An object of class <a href="#">ExpressionSet</a>
design.matrix	A design matrix
contrast.matrix	A contrast matrix

### Details

The `eset` argument must be supplied, and must be a valid [ExpressionSet](#) object. Design and contrast matrices can be supplied, but if not, default matrices will be used. These should usually be sufficient for most analyses.

### Value

An object of class [DEResult](#).

### Author(s)

Richard D. Pearson

### See Also

Related methods [pumaDE](#), [calculateLimma](#), [calculateFC](#), [createDesignMatrix](#) and [createContrastMatrix](#) and class [DEResult](#)

### Examples

```
eset_test <- new("ExpressionSet", exprs=matrix(rnorm(400,8,2),100,4))  
pData(eset_test) <- data.frame("class"=c("A", "A", "B", "B"))  
TtestRes <- calculateTtest(eset_test)  
plotErrorBars(eset_test, topGenes(TtestRes))
```

---

clusterApplyLBDots *clusterApplyLB with dots to indicate progress*

---

### Description

This is basically the `clusterApplyLB` function from the **snow** package, but with dots displayed to indicate progress.

### Usage

```
clusterApplyLBDots(cl, x, fun, ...)
```

### Arguments

<code>cl</code>	cluster object
<code>x</code>	array
<code>fun</code>	function or character string naming a function
<code>...</code>	additional arguments to pass to standard function

### Author(s)

Richard D. Pearson (modified from original **snow** function)

---

clusterNormE *Zero-centered normalisation*

---

### Description

This function normalise the data vector to have zero mean.

### Usage

```
clusterNormE(x)
```

### Arguments

<code>x</code>	a vector which contains gene expression level on log2 scale.
----------------	--

### Details

Vector `x` is related to a gene and each element is related to a chip.

### Value

The return vector is in the same format as the input `x`.

### Author(s)

Xuejun Liu, Magnus Rattray

**See Also**

See Also as [pumaClust](#)

**Examples**

```
data(Clust.exampleE)
Clust.exampleE.centered<-t(apply(Clust.exampleE, 1, clusterNormE))
```

---

clusterNormVar	<i>Adjusting expression variance for zero-centered normalisation</i>
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**Description**

This function adjusts the variance of the gene expression according to the zero-centered normalisation.

**Usage**

```
clusterNormVar(x)
```

**Arguments**

x a vector which contains the variance of gene expression level on log2 scale.

**Details**

Vector x is related to a gene and each element is related to a chip.

**Value**

The return vector is in the same format as the input x.

**Author(s)**

Xuejun Liu, Magnus Rattray

**See Also**

See Also as [pumaClust](#)

**Examples**

```
data(Clust.exampleE)
data(Clust.exampleStd)
Clust.exampleVar<-Clust.exampleStd^2
Clust.exampleStd.centered<-t(apply(cbind(Clust.exampleE,Clust.exampleVar), 1, clusterNorm
```



---

Clust.exampleE      *The example data of the mean gene expression levels*

---

**Description**

This data is an artificial example of the mean gene expression levels.

**Usage**

```
data(Clust.exampleE)
```

**Format**

A 700x20 matrix including 700 genes and 20 chips. Every 100 genes belong to one cluster from the first gene. There are 7 clusters.

**Source**

Liu, X. Lin, K., Andersen, B. Rattray, M. (2007) Including probe-level uncertainty in model-based gene expression clustering, BMC Bioinformatics, 8(98).

**See Also**

[Clust.exampleStd](#)

---

Clust.exampleStd      *The example data of the standard deviation for gene expression levels*

---

**Description**

This data is an artificial example of the standard deviation for gene expression levels.

**Usage**

```
data(Clust.exampleStd)
```

**Format**

A 700x20 matrix including 700 genes and 20 chips. Every 100 genes belong to one cluster from the first gene. There are 7 true clusters.

**Source**

Liu, X. Lin, K., Andersen, B. Rattray, M. (2007) Including probe-level uncertainty in model-based gene expression clustering, BMC Bioinformatics, 8(98).

**See Also**

[Clust.exampleE](#)

---

compareLimmapumaDE *Compare pumaDE with a default Limma model*

---

## Description

This function compares the identification of differentially expressed (DE) genes using the `pumaDE` function and the `limma` package.

## Usage

```
compareLimmapumaDE(
  eset_mmgmos
  , eset_comb = NULL
  , eset_other = eset_mmgmos
  , limmaRes = calculateLimma(eset_other)
  , pumaDERes = pumaDE(eset_comb)
  , contrastMatrix = createContrastMatrix(eset_mmgmos)
  , numberToCompareForContrasts = 3
  , numberToCompareForVenn = 100
  , plotContrasts = TRUE
  , contrastsFilename = NULL
  , plotOther = FALSE
  , otherFilename = "other"
  , plotBcombContrasts = FALSE
  , bcombContrastsFilename = "bcomb_contrasts"
  , plotVenn = FALSE
  , vennFilename = "venn.pdf"
  , showTopMatches = FALSE
  , returnResults = FALSE
)
```

## Arguments

- |                          |   |
|--------------------------|---|
| <code>eset_mmgmos</code> | An object of class <code>ExpressionSet</code> , that includes both expression levels as well as standard errors of the expression levels. This will often have been created using <code>mmgmos</code> , but might also have been created by <code>mgmos</code> , or any other method capable of providing standard errors.  |
| <code>eset_comb</code>   | An object of class <code>ExpressionSet</code> , includes both expression levels as well as standard errors of the expression levels for each unique condition in an experiment (i.e. created from combining the information from each replicate). This will usually have been created using <code>pumaComb</code> .   |
| <code>eset_other</code>  | An object of class <code>ExpressionSet</code> , that includes expression levels, and may optionally also include standard errors of the expression levels. This is used for comparison with <code>eset_mmgmos</code> , and might have been created by any summarisation method, e.g. <code>rma</code> .   |
| <code>limmaRes</code>    | A list with two elements, usually created using the function <code>calculateLimma</code> . The first element is a matrix of p-values. Each column represent one contrast. Within each column the p-values are ordered. The second element is a matrix of row numbers, which can be used to map p-values back to probe sets. If not supplied this will be automatically created from <code>eset_other</code> . |

<code>pumaDERes</code>	A list with two elements, usually created using the function <code>pumaDE</code> . The first element is a matrix of PPLR values. Each column represent one contrast. Within each column the PPLR values are ordered. The second element is a matrix of row numbers, which can be used to map PPLR values back to probe sets. If not supplied this will be automatically created from <code>eset_comb</code> .
<code>contrastMatrix</code>	A contrast matrix. If not supplied this will be created from <code>eset_mmgmos</code>
<code>numberToCompareForContrasts</code>	An integer specifying the number of most differentially expressed probe sets (genes) that will be used in comparison charts.
<code>numberToCompareForVenn</code>	An integer specifying the number of most differentially expressed probe sets (genes) that will be used for comparison in the Venn diagram.
<code>plotContrasts</code>	A boolean specifying whether or not to plot the most differentially expressed probe sets (genes) for each contrast for the <code>eset_mmgmos ExpressionSet</code> .
<code>contrastsFilename</code>	A character string specifying a file name stem for the PDF files which will be created to hold the contrast plots for the <code>eset_mmgmos ExpressionSet</code> . The actually filenames will have the name of the contrast appended to this stem.
<code>plotOther</code>	A boolean specifying whether or not to plot the most differentially expressed probe sets (genes) for each contrast for the <code>eset_other ExpressionSet</code> .
<code>otherFilename</code>	A character string specifying a file name stem for the PDF files which will be created to hold the contrast plots for the <code>eset_other ExpressionSet</code> . The actually filenames will have the name of the contrast appended to this stem.
<code>plotBcombContrasts</code>	A boolean specifying whether or not to plot the most differentially expressed probe sets (genes) for each contrast for the <code>eset_comb ExpressionSet</code> .
<code>bcombContrastsFilename</code>	A character string specifying a file name stem for the PDF files which will be created to hold the contrast plots for the <code>eset_comb ExpressionSet</code> . The actually filenames will have the name of the contrast appended to this stem.
<code>plotVenn</code>	A boolean specifying whether or not to plot a Venn diagram showing the overlap in the most differentially expressed probe sets (genes) as identified from the two different methods being compared.
<code>vennFilename</code>	A character string specifying the filename for the PDF file which will hold the Venn diagram showing the overlap in the most differentially expressed probe sets (genes) as identified from the two different methods being compared.
<code>showTopMatches</code>	A boolean specifying whether or not to show the probe sets which are deemed most likely to be differentially expressed.
<code>returnResults</code>	A boolean specifying whether or not to return a list containing results generated.

**Value**

The main outputs from this function are a number of PDF files.

The function only returns results if `returnResults=TRUE`

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [pumaDE](#) and [calculateLimma](#)

---

```
createContrastMatrix
```

*Automatically create a contrast matrix from an [ExpressionSet](#) and optional design matrix*

---

**Description**

To appear

**Usage**

```
createContrastMatrix(eset, design=NULL)
```

**Arguments**

<code>eset</code>	An object of class <a href="#">ExpressionSet</a> .
<code>design</code>	A design matrix

**Details**

The **puma** package has been designed to be as easy to use as possible, while not compromising on power and flexibility. One of the most difficult tasks for many users, particularly those new to microarray analysis, or statistical analysis in general, is setting up design and contrast matrices. The **puma** package will automatically create such matrices, and we believe the way this is done will suffice for most users' needs.

It is important to recognise that the automatic creation of design and contrast matrices will only happen if appropriate information about the levels of each factor is available for each array in the experimental design. This data should be held in an [AnnotatedDataFrame](#) class. The easiest way of doing this is to ensure that the [AnnotatedDataFrame](#) object holding the raw CEL file data has an appropriate `phenoData` slot. This information will then be passed through to any [ExpressionSet](#) object created, for example through the use of [mmgmos](#). The `phenoData` slot of an [ExpressionSet](#) object can also be manipulated directly if necessary.

Design and contrast matrices are dependent on the experimental design. The simplest experimental designs have just one factor, and hence the `phenoData` slot will have a matrix with just one column. In this case, each unique value in that column will be treated as a distinct level of the factor, and hence [pumaComb](#) will group arrays according to these levels. If there are just two levels of the factor, e.g. A and B, the contrast matrix will also be very simple, with the only contrast of interest being A vs B. For factors with more than two levels, a contrast matrix will be created which reflects all possible combinations of levels. For example, if we have three levels A, B and C, the contrasts of interest will be A vs B, A vs C and B vs C. In addition, if the `others` argument is set to TRUE, the following additional contrasts will be created: A vs other (i.e. A vs B & C), B vs other and C vs other. Note that these additional contrasts are experimental, and not currently recommended for use in calculating differential expression.

If we now consider the case of two or more factors, things become more complicated. There are now two cases to be considered: factorial experiments, and non-factorial experiments. A factorial experiment is one where all the combinations of the levels of each factor are tested by at least one array (though ideally we would have a number of biological replicates for each combination of factor levels). The `estrogen` case study from the package vignette is an example of a factorial experiment.

A non-factorial experiment is one where at least one combination of levels is not tested. If we treat the example used in the `puma-package` help page as a two-factor experiment (with factors “level” and “batch”), we can see that this is not a factorial experiment as we have no array to test the conditions “level=ten” and “batch=B”. We will treat the factorial and non-factorial cases separately in the following sections.

#### Factorial experiments

For factorial experiments, the design matrix will use all columns from the `phenoData` slot. This will mean that `pumaComb` will group arrays according to a combination of the levels of all the factors.

#### Non-factorial designs

For non-factorial designed experiments, we will simply ignore columns (right to left) from the `phenoData` slot until we have a factorial design or a single factor. We can see this in the example used in the `puma-package` help page. Here we have ignored the “batch” factor, and modelled the experiment as a single-factor experiment (with that single factor being “level”).

### Value

The result is a matrix. See the code below for an example.

### Author(s)

Richard D. Pearson

### See Also

Related methods `createDesignMatrix` and `pumaDE`

### Examples

```
# This is a simple example based on a real data set. Note that this is an "unbalanced" de

# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
#   data(Dilution)
#   eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
createContrastMatrix(eset_mmgmos)

# The following shows a set of 15 synthetic data sets with increasing complexity. We first

# single 2-level factor
eset1 <- new("ExpressionSet", exprs=matrix(0,100,4))
pData(eset1) <- data.frame("class"=c(1,1,2,2))

# single 2-level factor - unbalanced design
eset2 <- new("ExpressionSet", exprs=matrix(0,100,4))
```



```

eset13 <- new("ExpressionSet", exprs=matrix(0,100,16))
pData(eset13) <- data.frame(
  "fac1"=c("a","a","a","a","a","a","a","a","b","b","b","b","b","b","b","b")
  ,"fac2"=c(0,0,0,0,1,1,1,1,0,0,0,0,1,1,1,1)
  ,"fac3"=c(2,2,3,3,2,2,3,3,2,2,3,3,2,2,3,3)
  ,"fac4"=c("X","Y","X","Y","X","Y","X","Y","X","Y","X","Y","X","Y","X","Y") )

# "Un-analysable" data set - all arrays are from the same class
eset14 <- new("ExpressionSet", exprs=matrix(0,100,4))
pData(eset14) <- data.frame("class"=c(1,1,1,1))

# "Non-factorial" data set - there are no arrays for fac1="b" and fac2=2. In this case on
eset15 <- new("ExpressionSet", exprs=matrix(0,100,6))
pData(eset15) <- data.frame("fac1"=c("a","a","a","a","b","b"), "fac2"=c(1,1,2,2,1,1))

createContrastMatrix(eset1)
createContrastMatrix(eset2)
createContrastMatrix(eset3)
createContrastMatrix(eset4)
createContrastMatrix(eset5)
createContrastMatrix(eset6)
createContrastMatrix(eset7)
createContrastMatrix(eset8)
createContrastMatrix(eset9)
# For the last 4 data sets, the contrast matrices get pretty big, so we'll just show the
colnames(createContrastMatrix(eset10))
colnames(createContrastMatrix(eset11))
# Note that the number of contrasts can rapidly get very large for multi-factorial experi
colnames(createContrastMatrix(eset12))
# For this final data set, note that the puma package does not currently create interacti
colnames(createContrastMatrix(eset13))

# "Un-analysable" data set - all arrays are from the same class - gives an error. Note t
# createContrastMatrix(eset14)
# "Non-factorial" data set - there are no arrays for fac1="b" and fac2=2. In this case on
createContrastMatrix(eset15)

```

---

createDesignMatrix *Automatically create a design matrix from an ExpressionSet*

---

## Description

Automatically create a design matrix from an ExpressionSet.

## Usage

```
createDesignMatrix(eset)
```

## Arguments

eset                    An object of class [ExpressionSet](#).

## Details

The **puma** package has been designed to be as easy to use as possible, while not compromising on power and flexibility. One of the most difficult tasks for many users, particularly those new to microarray analysis, or statistical analysis in general, is setting up design and contrast matrices. The **puma** package will automatically create such matrices, and we believe the way this is done will suffice for most users' needs.

It is important to recognise that the automatic creation of design and contrast matrices will only happen if appropriate information about the levels of each factor is available for each array in the experimental design. This data should be held in an `AnnotatedDataFrame` class. The easiest way of doing this is to ensure that the `AnnotatedDataFrame` object holding the raw CEL file data has an appropriate `phenoData` slot. This information will then be passed through to any `ExpressionSet` object created, for example through the use of `mmgmos`. The `phenoData` slot of an `ExpressionSet` object can also be manipulated directly if necessary.

Design and contrast matrices are dependent on the experimental design. The simplest experimental designs have just one factor, and hence the `phenoData` slot will have a matrix with just one column. In this case, each unique value in that column will be treated as a distinct level of the factor, and hence `pumaComb` will group arrays according to these levels. If there are just two levels of the factor, e.g. A and B, the contrast matrix will also be very simple, with the only contrast of interest being A vs B. For factors with more than two levels, a contrast matrix will be created which reflects all possible combinations of levels. For example, if we have three levels A, B and C, the contrasts of interest will be A vs B, A vs C and B vs C.

If we now consider the case of two or more factors, things become more complicated. There are now two cases to be considered: factorial experiments, and non-factorial experiments. A factorial experiment is one where all the combinations of the levels of each factor are tested by at least one array (though ideally we would have a number of biological replicates for each combination of factor levels). The `estrogen` case study from the package vignette is an example of a factorial experiment.

A non-factorial experiment is one where at least one combination of levels is not tested. If we treat the example used in the `puma-package` help page as a two-factor experiment (with factors "level" and "batch"), we can see that this is not a factorial experiment as we have no array to test the conditions "level=ten" and "batch=B". We will treat the factorial and non-factorial cases separately in the following sections.

### Factorial experiments

For factorial experiments, the design matrix will use all columns from the `phenoData` slot. This will mean that `pumaComb` will group arrays according to a combination of the levels of all the factors.

### Non-factorial designs

For non-factorial designed experiments, we will simply ignore columns (right to left) from the `phenoData` slot until we have a factorial design or a single factor. We can see this in the example used in the `puma-package` help page. Here we have ignored the "batch" factor, and modelled the experiment as a single-factor experiment (with that single factor being "level").

## Value

The result is a matrix. See the code below for an example.

## Author(s)

Richard D. Pearson



**See Also**

Related methods [createContrastMatrix](#), [pumaComb](#) and [pumaDE](#)

**Examples**

```
# This is a simple example based on a real data set. Note that this is an "unbalanced" de

# Next 4 lines commented out to save time in package checks, and saved version used
#   # if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
createDesignMatrix(eset_mmgmos)

# The following shows a set of 15 synthetic data sets with increasing complexity. We first

# single 2-level factor
eset1 <- new("ExpressionSet", exprs=matrix(0,100,4))
pData(eset1) <- data.frame("class"=c(1,1,2,2))

# single 2-level factor - unbalanced design
eset2 <- new("ExpressionSet", exprs=matrix(0,100,4))
pData(eset2) <- data.frame("class"=c(1,2,2,2))

# single 3-level factor
eset3 <- new("ExpressionSet", exprs=matrix(0,100,6))
pData(eset3) <- data.frame("class"=c(1,1,2,2,3,3))

# single 4-level factor
eset4 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset4) <- data.frame("class"=c(1,1,2,2,3,3,4,4))

# 2x2 factorial
eset5 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset5) <- data.frame("fac1"=c("a","a","a","a","b","b","b","b"), "fac2"=c(1,1,2,2,1,1,2,2))

# 2x2 factorial - unbalanced design
eset6 <- new("ExpressionSet", exprs=matrix(0,100,10))
pData(eset6) <- data.frame("fac1"=c("a","a","a","b","b","b","b","b","b","b"), "fac2"=c(1,1,2,2,3,3,1,1,2,2))

# 3x2 factorial
eset7 <- new("ExpressionSet", exprs=matrix(0,100,12))
pData(eset7) <- data.frame("fac1"=c("a","a","a","a","b","b","b","b","c","c","c","c"), "fac2"=c(1,1,2,2,3,3,1,1,2,2,3,3))

# 2x3 factorial
eset8 <- new("ExpressionSet", exprs=matrix(0,100,12))
pData(eset8) <- data.frame(
  "fac1"=c("a","a","a","a","a","a","b","b","b","b","b","b"),
  "fac2"=c(1,1,2,2,3,3,1,1,2,2,3,3) )

# 2x2x2 factorial
eset9 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset9) <- data.frame(
  "fac1"=c("a","a","a","a","b","b","b","b")
  "fac2"=c(1,1,2,2,1,1,2,2))
```

```

, "fac3"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# 3x2x2 factorial
eset10 <- new("ExpressionSet", exprs=matrix(0,100,12))
pData(eset10) <- data.frame(
  "fac1"=c("a", "a", "a", "a", "b", "b", "b", "b", "c", "c", "c", "c")
  , "fac2"=c(1,1,2,2,1,1,2,2,1,1,2,2)
  , "fac3"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# 3x2x2 factorial
eset11 <- new("ExpressionSet", exprs=matrix(0,100,12))
pData(eset11) <- data.frame(
  "fac1"=c("a", "a", "a", "a", "a", "a", "b", "b", "b", "b", "b", "b")
  , "fac2"=c(1,1,2,2,3,3,1,1,2,2,3,3)
  , "fac3"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# 3x2x2 factorial
eset12 <- new("ExpressionSet", exprs=matrix(0,100,18))
pData(eset12) <- data.frame(
  "fac1"=c("a", "a", "a", "a", "a", "a", "b", "b", "b", "b", "b", "b", "c", "c", "c", "c", "c", "c")
  , "fac2"=c(1,1,2,2,3,3,1,1,2,2,3,3,1,1,2,2,3,3)
  , "fac3"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# 2x2x2x2 factorial
eset13 <- new("ExpressionSet", exprs=matrix(0,100,16))
pData(eset13) <- data.frame(
  "fac1"=c("a", "a", "a", "a", "a", "a", "a", "a", "b", "b", "b", "b", "b", "b", "b", "b")
  , "fac2"=c(0,0,0,0,1,1,1,1,0,0,0,0,1,1,1,1)
  , "fac3"=c(2,2,3,3,2,2,3,3,2,2,3,3,2,2,3,3)
  , "fac4"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# "Un-analysable" data set - all arrays are from the same class
eset14 <- new("ExpressionSet", exprs=matrix(0,100,4))
pData(eset14) <- data.frame("class"=c(1,1,1,1))

# "Non-factorial" data set - there are no arrays for fac1="b" and fac2=2. In this case on
eset15 <- new("ExpressionSet", exprs=matrix(0,100,6))
pData(eset15) <- data.frame("fac1"=c("a", "a", "a", "a", "b", "b"), "fac2"=c(1,1,2,2,1,1))

# "pseduo 2 factor" data set - second factor is informative
eset16 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset16) <- data.frame("fac1"=c("a", "a", "b", "b"), "fac2"=c(1,1,1,1))

# "pseduo 2 factor" data set - first factor is informative
eset17 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset17) <- data.frame("fac1"=c("a", "a", "a", "a"), "fac2"=c(1,1,2,2))

# "pseudo 3 factor" data set - first factor is uninformative so actually a 2x2 factorial
eset18 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset18) <- data.frame(
  "fac1"=c("a", "a", "a", "a", "a", "a", "a", "a")
  , "fac2"=c(1,1,2,2,1,1,2,2)
  , "fac3"=c("X", "Y", "X", "Y", "X", "Y", "X", "Y") )

# "pseudo 3 factor" data set - first and third factors are uninformative so actually a si
eset19 <- new("ExpressionSet", exprs=matrix(0,100,8))
pData(eset19) <- data.frame(

```

```

"fac1"=c("a","a","a","a","a","a","a","a")
,"fac2"=c(1,1,2,2,1,1,2,2)
,"fac3"=c("X","X","X","X","X","X","X","X") )

createDesignMatrix(eset1)
createDesignMatrix(eset2)
createDesignMatrix(eset3)
createDesignMatrix(eset4)
createDesignMatrix(eset5)
createDesignMatrix(eset6)
createDesignMatrix(eset7)
createDesignMatrix(eset8)
createDesignMatrix(eset9)
createDesignMatrix(eset10)
createDesignMatrix(eset11)
createDesignMatrix(eset12)
createDesignMatrix(eset13)

# "Un-analysable" data set - all arrays are from the same class - gives an error. Note th
# createDesignMatrix(eset14)
# "Non-factorial" data set - there are no arrays for fac1="b" and fac2=2. In this case on
createDesignMatrix(eset15)

```

---

create\_eset\_r

*Create an ExpressionSet from a PPLR matrix*


---

## Description

This is really an internal function called from `pumaComb`. It is used to create an [ExpressionSet](#) object from the output of the `bcomb` function (which was originally part of the `pplr` package. Don't worry about it!

## Usage

```

create_eset_r(
  eset
  , r
  , design.matrix=createDesignMatrix(eset)
)

```

## Arguments

<code>eset</code>	An object of class <a href="#">ExpressionSet</a> . The phenotype information from this is used as the phenotype information of the returned object
<code>r</code>	A data frame with components named 'M1', 'M2', and so on, which represent the mean expression values for condition 1, condition 2, and so on. It also has components named 'Std1', 'Std2', and so on, which represent the standard deviation of the gene expression values for condition 1, condition 2, and so on. This type of data frame is output by function <a href="#">bcomb</a>
<code>design.matrix</code>	A design matrix.

**Value**

An object of class [ExpressionSet](#).

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [pumaComb](#) and [bcomb](#)

---

 DEResult

---

*Class DEResult*


---

**Description**

Class to contain and describe results of a differential expression (DE) analysis. The main components are `statistic` which hold the results of any statistic (e.g. p-values, PPLR values, etc.), and `FC` which hold the fold changes.

**Creating Objects**

DEResult objects will generally be created using one of the functions [pumaDE](#), [calculateLimma](#), [calculateFC](#) or [calculateTtest](#).

Objects can also be created from scratch:

```
new("DEResult")
new("DEResult", statistic=matrix() , FC=matrix() , statisticDescription="unknown"
, DEMethod="unknown" )
```

**Slots**

**statistic:** Object of class "matrix" holding the statistics returned by the DE method.

**FC:** Object of class "matrix" holding the fold changes returned by the DE method.

**statisticDescription:** A text description of the contents of the `statistic` slot.

**DEMethod:** A string indicating which DE method was used to create the object.

**Methods**

Class-specific methods.

`statistic(DEResult)`, `statistic(DEResult, matrix) <-` Access and set the `statistic` slot.

`FC(DEResult)`, `FC(DEResult, matrix) <-` Access and set the `FC` slot.

`statisticDescription(DEResult)`, `statisticDescription(DEResult, character) <-` Access and set the `statisticDescription` slot.

`DEMethod(DEResult)`, `DEMethod(DEResult, character) <-` Access and set the `DEMethod` slot.

`pLikeValues(object, contrast=1, direction="either")` Access the statistics of an object of class `DEResult`, converted to "p-like values". If the object holds information on more than one contrast, only the values of the statistic for contrast number `contrast` are given. Direction can be "either" (meaning we want order genes by probability of being either up- or down-regulated), "up" (meaning we want to order genes by probability of being up-regulated), or "down" (meaning we want to order genes by probability of being down-regulated). "p-like values" are defined as values between 0 and 1, where 0 identifies the highest probability of being differentially expressed, and 1 identifies the lowest probability of being differentially expressed. We use this so that we can easily compare results from methods that provide true p-values (e.g. `calculateLimma`) and methods that do not provide p-values (e.g. `pumaDE`). For objects created using `pumaDE`, this returns 1-PPLR if the direction is "up", PPLR if direction is "down", and  $1 - \text{abs}(2 * (\text{PPLR} - 0.5))$  if direction is "either". For objects created using `calculateLimma` or `calculateTtest`, this returns the p-value if direction is "either",  $((p - 1 * \text{sign}(\text{FC})) / 2) + 0.5$ , if the direction is "up", and  $((1 - p * \text{sign}(\text{FC})) / 2) + 0.5$  if the direction is "down". For all other methods, this returns the rank of the appropriate statistic, scaled to lie between 0 and 1. `contrast` will be returned.

`topGenes(object, numberOfGenes=1, contrast=1, direction="either")` Returns the index numbers (row numbers) of the genes determined to be most likely to be differentially expressed. `numberOfGenes` specifies the number of genes to be returned by the function. If the object holds information on more than one contrast, only the values of the statistic for contrast number `contrast` are given. Direction can be "either" (meaning we want order genes by probability of being either up- or down-regulated), "up" (meaning we want to order genes by probability of being up-regulated), or "down" (meaning we want to order genes by probability of being down-regulated). Note that genes are ordered by "p-like values" (see `pLikeValues`). `object` is an object of class `DEResult`.

`topGeneIDs(object, numberOfGenes=1, contrast=1, direction="either")` Returns the Affy IDs (row names) of the genes determined to be most likely to be differentially expressed. `numberOfGenes` specifies the number of genes to be returned by the function. If the object holds information on more than one contrast, only the values of the statistic for contrast number `contrast` are given. Direction can be "either" (meaning we want order genes by probability of being either up- or down-regulated), "up" (meaning we want to order genes by probability of being up-regulated), or "down" (meaning we want to order genes by probability of being down-regulated). Note that genes are ordered by "p-like values" (see `pLikeValues`). `object` is an object of class `DEResult`.

`numberOfProbesets(object)` Returns the number of probesets (number of rows) in an object of class `DEResult`. This method is synonymous with `numberOfGenes`.

`numberOfGenes(object)` Returns the number of probesets (number of rows) in an object of class `DEResult`. This method is synonymous with `numberOfProbesets`.

`numberOfContrasts(object)` Returns the number of contrasts (number of columns) in an object of class `DEResult`.

`write.results(object) signature(x = "DEResult")`: writes the statistics and related fold changes (FCs) to files. It takes the same arguments as `write.table`. The argument "file" does not need to set any extension. The different file marks and extension "csv" will be added automatically. The default file name is "tmp". In the final results, statistics are in the file "tmp\_statistics.csv", and FCs are in "tmp\_FCs.csv" respectively.

Standard generic methods:

`show(object)` Informatively display object contents.

### Author(s)

Richard D. Pearson

**See Also**

Related methods [pumaDE](#), [calculateLimma](#), [calculateFC](#) or [calculateTtest](#).

**Examples**

```
## Create an example DEResult object
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
#   data(Dilution)
#   eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)

# Next line used so eset_mmgmos only has information about the liver factor
# The scanner factor will thus be ignored, and the two arrays of each level
# of the liver factor will be treated as replicates
pData(eset_mmgmos) <- pData(eset_mmgmos)[,1,drop=FALSE]

# To save time we'll just use 100 probe sets for the example
eset_mmgmos_100 <- eset_mmgmos[1:100,]
eset_comb <- pumaComb(eset_mmgmos_100)

esetDE <- pumaDE(eset_comb)

## Use some of the methods
statisticDescription(esetDE)
DEMethod(esetDE)
numberOfProbesets(esetDE)
numberOfContrasts(esetDE)
topGenes(esetDE)
topGenes(esetDE, 3)
pLikeValues(esetDE)[topGenes(esetDE, 3)]
topGeneIDs(esetDE, 3)
topGeneIDs(esetDE, 3, direction="down")

## save the expression results into files
write.reslts(esetDE, file="example")
```

---

erfc

*The complementary error function*


---

**Description**

This function calculates the complementary error function of an input  $x$ .

**Usage**

```
erfc(x)
```

**Arguments**

$x$  a numeric, the input.

**Details**

erfc is implemented using the function `qnorm`.

**Value**

The return is a numeric.

**Author(s)**

Xuejun Liu

**See Also**

[qnorm](#)

**Examples**

```
erfc(0.5)
```

---

eset\_mmgmos

*An example ExpressionSet created from the Dilution data with mmgmos*

---

**Description**

This data is created by applying `mmgmos` to the `Dilution AffyBatch` object from the `affydata` package.

**Usage**

```
data(eset_mmgmos)
```

**Format**

An object of class [ExpressionSet](#).

**Source**

see [Dilution](#)

---

`exampleE`*The example data of the mean gene expression levels*

---

**Description**

This data is an artificial example of the mean gene expression levels from golden spike-in data set in Choe et al. (2005).

**Usage**

```
data(exampleE)
```

**Format**

A 200x6 matrix including 200 genes and 6 chips. The first 3 chips are replicates for C condition and the last 3 chips are replicates for S condition.

**Source**

Choe,S.E., Boutros,M., Michelson,A.M., Church,G.M., Halfon,M.S.: Preferred analysis methods for Affymetrix GeneChips revealed by a wholly defined control dataset. *Genome Biology*, 6 (2005) R16.

**See Also**

[exampleStd](#)

---

`exampleStd`*The example data of the standard deviation for gene expression levels*

---

**Description**

This data is an artificial example of the standard deviation for gene expression levels from golden spike-in data set in Choe et al. (2005).

**Usage**

```
data(exampleStd)
```

**Format**

A 200x6 matrix including 200 genes and 6 chips. The first 3 chips are replicates for C condition and the last 3 chips are replicates for S condition.

**Source**

Choe,S.E., Boutros,M., Michelson,A.M., Church,G.M., Halfon,M.S.: Preferred analysis methods for Affymetrix GeneChips revealed by a wholly defined control dataset. *Genome Biology*, 6 (2005) R16.



**See Also**

[exampleE](#)

---

exprReslt-class      *Class exprReslt*

---

**Description**

This is a class representation for Affymetrix GeneChip probe level data. The main component are the intensities, estimated expression levels and the confidence of expression levels from multiple arrays of the same CDF type. In extends [ExpressionSet](#).

**Objects from the Class**

Objects can be created by calls of the form `new("exprReslt", ...)`.

**Slots**

**prcfive:** Object of class "matrix" representing the 5 percentile of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**prctwfive:** Object of class "matrix" representing the 25 percentile of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**prcfifty:** Object of class "matrix" representing the 50 percentile of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**prcsevfive:** Object of class "matrix" representing the 75 percentile of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**prcninfive:** Object of class "matrix" representing the 95 percentile of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**exprs:** Object of class "matrix" representing the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**se.exprs:** Object of class "matrix" representing the standard deviation of the observed expression levels. This is a matrix with columns representing patients or cases and rows representing genes.

**phenoData:** Object of class "phenoData" inherited from [ExpressionSet](#).

**description:** Object of class "MIAME". For compatibility with previous version of this class description can also be a "character". The class `characterOrMIAME` has been defined just for this.

**annotation:** A character string identifying the annotation that may be used for the [ExpressionSet](#) instance.

**notes:** Object of class "character" Vector of explanatory text

**Extends**

Class "ExpressionSet", directly.

## Methods

- se.exprs** signature(object = "exprReslt"): obtains the standard error of the estimated expression levels.
- se.exprs<-** signature(object = "exprReslt"): replaces the standard error of the estimated expression levels.
- prcfifty** signature(object = "exprReslt"): obtains the 50 percentile of the estimated expression levels.
- prcfifty<-** signature(object = "exprReslt"): replaces the 50 percentile of the estimated expression levels.
- prcfive** signature(object = "exprReslt"): obtains the 5 percentile of the estimated expression levels.
- prcfive<-** signature(object = "exprReslt"): replaces the 5 percentile of the estimated expression levels.
- prcninfive** signature(object = "exprReslt"): obtains the 95 percentile of the estimated expression levels.
- prcninfive<-** signature(object = "exprReslt"): replaces the 95 percentile of the estimated expression levels.
- prcsevfive** signature(object = "exprReslt"): obtains the 75 percentile of the estimated expression levels.
- prcsevfive<-** signature(object = "exprReslt"): replaces the 75 percentile of the estimated expression levels.
- prctwfive** signature(object = "exprReslt"): obtains the 25 percentile of the estimated expression levels.
- prctwfive<-** signature(object = "exprReslt"): replaces the 25 percentile of the estimated expression levels.
- show** signature(object = "exprReslt"): renders information about the exprReslt in a concise way on stdout.
- write.results** signature(x = "exprReslt"): writes the expression levels and related confidences to files. It takes the same arguments as `write.table`. The argument "file" does not need to set any extension. The different file marks and extension "csv" will be added automatically. The default file name is "tmp". In the final results, expression levels are in the file "tmp\exprs.csv", standard deviations in "tmp\se.csv", 5 percentiles in "tmp\prctile5.csv", likewise, 25, 50, 75 and 95 percentiles in "tmp\prctile25.csv", "tmp\prctile50.csv", "tmp\prctile75.csv" and "tmp\prctile95.csv" respectively.

## Author(s)

Xuejun Liu, Magnus Rattray, Marta Milo, Neil D. Lawrence, Richard D. Pearson

## See Also

Related method `mmgmos` and related class `ExpressionSet`.

## Examples

```
## load example data from package affydata
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
```

```
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)

## save the expression results into files
write.reslts(eset_mmgmos, file="example")
```

---

hgu95aphis

*Estimated parameters of the distribution of  $\phi$* 


---

### Description

The pre-estimated parameters of log normal distribution of  $\phi$ , which is the fraction of specific signal binding to mismatch probe.

### Usage

```
data(hgu95aphis)
```

### Format

The format is: num [1:3] 0.171 -1.341 0.653

### Details

The current values of hgu95aphis are estimated from Affymetrix spike-in data sets. It was loaded in the method "mmgmos".

hgu95aphis[1:3] is respectively the mode, mean and variance of the log normal distribution of  $\phi$ , and hgu95aphis[1] is also the initial value of  $\phi$  in the model optimisation.

---

justmgMOS

*Compute mgmos Directly from CEL Files*


---

### Description

This function converts CEL files into an `exprResult` using mgmos.

### Usage

```
justmgMOS(..., 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="",
           background=TRUE, gsnorm=c("median", "none", "mean", "meanlog"), savepar

just.mgmos(..., filenames=character(0),
```

```
phenoData=new("AnnotatedDataFrame"),
description=NULL,
notes="",
compress=getOption("BioC")$affy$compress.cel,
background=TRUE, gsnorm=c("median", "none", "mean", "meanlog"), savepa
```

### 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?
celfile.path	a character denoting the path <a href="#">ReadAffy</a> should look for cel files.
sampleNames	a character vector of sample names to be used in the <a href="#">AffyBatch</a> .
phenoData	an <a href="#">AnnotatedDataFrame</a> object.
description	a <a href="#">MIAME</a> object.
notes	notes.
background	Logical value. If TRUE, then perform background correction before applying mgmos.
gsnorm	character. specifying the algorithm of global scaling normalisation.
savepar	Logical value. If TRUE, then the estimated parameters of the model are saved in file <code>par\_mgmos.txt</code> and <code>phi\_mgmos.txt</code> .
eps	Optimisation termination criteria.

### Details

This method should require much less RAM than the conventional method of first creating an [AffyBatch](#) and then running [mgmos](#).

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 algorithms of global scaling normalisation can be one of "median", "none", "mean", "meanlog". "mean" and "meanlog" are mean-centered normalisation on raw scale and log scale respectively, and "median" is median-centered normalisation. "none" will result in no global scaling normalisation being applied.

### Value

An `exprResult`.

### See Also

Related class [exprResult-class](#) and related method [mgmos](#)

## Description

This function converts CEL files into an `exprResult` using `mmgmos`.

## Usage

```
justmmgMOS(..., 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="",
            background=TRUE, gsnorm=c("median", "none", "mean", "meanlog"), savepar=FALSE)

just.mmgmos(..., filenames=character(0),
            phenoData=new("AnnotatedDataFrame"),
            description=NULL,
            notes="",
            compress=getOption("BioC")$affy$compress.cel,
            background=TRUE, gsnorm=c("median", "none", "mean", "meanlog"), savepar=FALSE)
```

## Arguments

<code>...</code>	file names separated by comma.
<code>filenames</code>	file names in a character vector.
<code>widget</code>	a logical specifying if widgets should be used.
<code>compress</code>	are the CEL files compressed?
<code>celfile.path</code>	a character denoting the path <code>ReadAffy</code> should look for cel files.
<code>sampleNames</code>	a character vector of sample names to be used in the <code>AffyBatch</code> .
<code>phenoData</code>	an <code>AnnotatedDataFrame</code> object
<code>description</code>	a <code>MIAME</code> object
<code>notes</code>	notes
<code>background</code>	Logical value. If <code>TRUE</code> , then perform background correction before applying <code>mmgmos</code> .
<code>gsnorm</code>	character. specifying the algorithm of global scaling normalisation.
<code>savepar</code>	Logical value. If <code>TRUE</code> , the the estimated parameters of the model are saved in file <code>par\_mmgmos.txt</code> and <code>phi\_mmgmos.txt</code> .
<code>eps</code>	Optimisation termination criteria.

## Details

This method should require much less RAM than the conventional method of first creating an [AffyBatch](#) and then running [mmgmos](#).

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 algorithms of global scaling normalisation can be one of "median", "none", "mean", "meanlog". "mean" and "meanlog" are mean-centered normalisation on raw scale and log scale respectively, and "median" is median-centered normalisation. "none" will result in no global scaling normalisation being applied.

## Value

An `exprResult`.

## See Also

Related class [exprResult-class](#) and related method [mmgmos](#)

---

legend2

*A legend which allows longer lines*

---

## Description

This function can be used to add legends to plots. This is almost identical to the `legend` function, accept it has an extra parameter, `seg.len` which allows the user to change the lengths of lines shown in legends.

## Usage

```
legend2(x, y = NULL, legend, fill = NULL, col = par("col"),
        lty, lwd, pch, angle = 45, density = NULL, bty = "o", bg = par("bg"),
        box.lwd = par("lwd"), box.lty = par("lty"), pt.bg = NA, cex = 1,
        pt.cex = cex, pt.lwd = lwd, xjust = 0, yjust = 1, x.intersp = 1,
        y.intersp = 1, adj = c(0, 0.5), text.width = NULL, text.col = par("col"),
        merge = do.lines && has.pch, trace = FALSE, plot = TRUE,
        ncol = 1, horiz = FALSE, title = NULL, inset = 0, seg.len = 2)
```

## Arguments

<code>x, y</code>	the x and y co-ordinates to be used to position the legend. They can be specified by keyword or in any way which is accepted by <a href="#">xy.coords</a> : See Details.
<code>legend</code>	a character or <a href="#">expression</a> vector. of length $\geq 1$ to appear in the legend. Other objects will be coerced by <a href="#">as.graphicsAnnot</a> .
<code>fill</code>	if specified, this argument will cause boxes filled with the specified colors (or shaded in the specified colors) to appear beside the legend text.
<code>col</code>	the color of points or lines appearing in the legend.
<code>lty, lwd</code>	the line types and widths for lines appearing in the legend. One of these two <i>must</i> be specified for line drawing.

<code>pch</code>	the plotting symbols appearing in the legend, either as vector of 1-character strings, or one (multi character) string. <i>Must</i> be specified for symbol drawing.
<code>angle</code>	angle of shading lines.
<code>density</code>	the density of shading lines, if numeric and positive. If <code>NULL</code> or negative or <code>NA</code> color filling is assumed.
<code>bty</code>	the type of box to be drawn around the legend. The allowed values are <code>"o"</code> (the default) and <code>"n"</code> .
<code>bg</code>	the background color for the legend box. (Note that this is only used if <code>bty != "n"</code> .)
<code>box.lty</code> , <code>box.lwd</code>	the line type and width for the legend box.
<code>pt.bg</code>	the background color for the <code>points</code> , corresponding to its argument <code>bg</code> .
<code>cex</code>	character expansion factor <b>relative</b> to current <code>par("cex")</code> .
<code>pt.cex</code>	expansion factor(s) for the points.
<code>pt.lwd</code>	line width for the points, defaults to the one for lines, or if that is not set, to <code>par("lwd")</code> .
<code>xjust</code>	how the legend is to be justified relative to the legend x location. A value of 0 means left justified, 0.5 means centered and 1 means right justified.
<code>yjust</code>	the same as <code>xjust</code> for the legend y location.
<code>x.intersp</code>	character interspacing factor for horizontal (x) spacing.
<code>y.intersp</code>	the same for vertical (y) line distances.
<code>adj</code>	numeric of length 1 or 2; the string adjustment for legend text. Useful for y-adjustment when <code>labels</code> are <code>plotmath</code> expressions.
<code>text.width</code>	the width of the legend text in x ( <code>"user"</code> ) coordinates. (Should be positive even for a reversed x axis.) Defaults to the proper value computed by <code>strwidth(legend)</code> .
<code>text.col</code>	the color used for the legend text.
<code>merge</code>	logical; if <code>TRUE</code> , "merge" points and lines but not filled boxes. Defaults to <code>TRUE</code> if there are points and lines.
<code>trace</code>	logical; if <code>TRUE</code> , shows how <code>legend</code> does all its magical computations.
<code>plot</code>	logical. If <code>FALSE</code> , nothing is plotted but the sizes are returned.
<code>ncol</code>	the number of columns in which to set the legend items (default is 1, a vertical legend).
<code>horiz</code>	logical; if <code>TRUE</code> , set the legend horizontally rather than vertically (specifying <code>horiz</code> overrides the <code>ncol</code> specification).
<code>title</code>	a character string or length-one expression giving a title to be placed at the top of the legend. Other objects will be coerced by <code>as.graphicsAnnot</code> .
<code>inset</code>	inset distance(s) from the margins as a fraction of the plot region when legend is placed by keyword.
<code>seg.len</code>	numeric specifying length of lines in legend.

## Details

Arguments `x`, `y`, `legend` are interpreted in a non-standard way to allow the coordinates to be specified *via* one or two arguments. If `legend` is missing and `y` is not numeric, it is assumed that the second argument is intended to be `legend` and that the first argument specifies the coordinates.

The coordinates can be specified in any way which is accepted by `xy.coords`. If this gives the coordinates of one point, it is used as the top-left coordinate of the rectangle containing the legend. If it gives the coordinates of two points, these specify opposite corners of the rectangle (either pair of corners, in any order).

The location may also be specified by setting `x` to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". This places the legend on the inside of the plot frame at the given location. Partial argument matching is used. The optional `inset` argument specifies how far the legend is inset from the plot margins. If a single value is given, it is used for both margins; if two values are given, the first is used for `x`- distance, the second for `y`-distance.

“Attribute” arguments such as `col`, `pch`, `lty`, etc, are recycled if necessary. `merge` is not.

Points are drawn *after* lines in order that they can cover the line with their background color `pt.bg`, if applicable.

See the examples for how to right-justify labels.

## Value

A list with list components

<code>rect</code>	a list with components <code>w</code> , <code>h</code> positive numbers giving <b>width</b> and <b>height</b> of the legend's box. <code>left</code> , <code>top</code> <code>x</code> and <code>y</code> coordinates of upper left corner of the box.
<code>text</code>	a list with components <code>x</code> , <code>y</code> numeric vectors of length <code>length(legend)</code> , giving the <code>x</code> and <code>y</code> coordinates of the legend's text(s).

returned invisibly.

## Author(s)

Richard Pearson (modified from original **graphics** package function.)

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

## See Also

[legend](#)



**Examples**

```
x <- seq(-pi, pi, len = 65)
plot(x, sin(x), type = "l", ylim = c(-1.2, 1.8), col = 3, lty = 2)
points(x, cos(x), pch = 3, col = 4)
lines(x, tan(x), type = "b", lty = 1, pch = 4, col = 6)
title("legend(..., lty = c(2, -1, 1), pch = c(-1,3,4), merge = TRUE)",
      cex.main = 1.1)
legend2(-1, 1.9, c("sin", "cos", "tan"), col = c(3,4,6),
        text.col = "green4", lty = c(2, -1, 1), pch = c(-1, 3, 4),
        merge = TRUE, bg = 'gray90', seg.len=6)
```

---

license.puma

---

*Print puma license*


---

**Description**

This function prints the license under which puma is made available.

**Usage**

```
license.puma()
```

**Value**

Null.

**Author(s)**

Richard Pearson (based on the license.cosmo function from the cosmo package)

**Examples**

```
license.puma()
```

---

matrixDistance

---

*Calculate distance between two matrices*


---

**Description**

This calculates the mean Euclidean distance between the rows of two matrices. It is used in the function [pumaPCA](#)

**Usage**

```
matrixDistance(
  matrixA
, matrixB
)
```

**Arguments**

<code>matrixA</code>	the first matrix
<code>matrixB</code>	the second matrix

**Value**

A numeric giving the mean distance

**Author(s)**

Richard D. Pearson

**See Also**

Related class [pumaPCA](#)

**Examples**

```
show(matrixDistance(matrix(1,2,2),matrix(2,2,2)))
```

---

mgmos

*modified gamma Model for Oligonucleotide Signal*

---

**Description**

This function converts an object of class [AffyBatch](#) into an object of class [exprResult](#) using the modified gamma Model for Oligonucleotide Signal (multi-mgMOS). This function obtains confidence of measures, standard deviation and 5, 25, 50, 75 and 95 percentiles, as well as the estimated expression levels.

**Usage**

```
mgmos (
  object
  ,background=FALSE
  ,replaceZeroIntensities=TRUE
  ,gsnorm=c("median", "none", "mean", "meanlog")
  ,savepar=FALSE
  ,eps=1.0e-6
)
```

**Arguments**

<code>object</code>	an object of <a href="#">AffyBatch</a>
<code>background</code>	Logical value. If TRUE, perform background correction before applying <code>mmgmos</code> .
<code>replaceZeroIntensities</code>	Logical value. If TRUE, replace 0 intensities with 1 before applying <code>mmgmos</code> .
<code>gsnorm</code>	character. specifying the algorithm of global scaling normalisation.
<code>savepar</code>	Logical value. If TRUE the estimated parameters of the model are saved in file <code>par\_mmgmos.txt</code> and <code>phi\_mmgmos.txt</code> .
<code>eps</code>	Optimisation termination criteria.

## Details

The obtained expression measures are in log base 2 scale.

The algorithms of global scaling normalisation can be one of "median", "none", "mean", "meanlog". "mean" and "meanlog" are mean-centered normalisation on raw scale and log scale respectively, and "median" is median-centered normalisation. "none" will result in no global scaling normalisation being applied.

There are 4\*n columns in file par\\_mgmos.txt, n is the number of chips. Every 4 columns are parameters for a chip. Among every 4 columns, the first one is for 'alpha' values, the 2nd one is for 'a' values, The 3rd column is for 'c' and the final column is values for 'd'.

## Value

An object of class `exprResult`.

## Author(s)

Xuejun Liu, Magnus Rattray, Marta Milo, Neil D. Lawrence

## References

Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips, *Bioinformatics*, 21:3637-3644.

Milo,M., Niranjana,M., Holley,M.C., Rattray,M. and Lawrence,N.D. (2004) A probabilistic approach for summarising oligonucleotide gene expression data, technical report available upon request.

Milo,M., Fazeli,A., Niranjana,M. and Lawrence,N.D. (2003) A probabilistic model for the extraction of expression levels from oligonucleotide arrays, *Biochemical Society Transactions*, 31: 1510-1512.

Peter Spellucci. DONLP2 code and accompanying documentation. Electronically available via <http://plato.la.asu.edu/donlp2.html>

## See Also

Related class [exprResult-class](#) and related method [mmgmos](#)

## Examples

```
## Code commented out to speed up checks
## load example data from package affydata
# if (require(affydata)) data(Dilution)

## use method mgMOS to calculate the expression levels and related confidence
## of the measures for the example data
# eset<-mgmos(Dilution)
```

mmgmos

*Multi-chip modified gamma Model for Oligonucleotide Signal***Description**

This function converts an object of class `AffyBatch` into an object of class `exprReslt` using the Multi-chip modified gamma Model for Oligonucleotide Signal (multi-mgMOS). This function obtains confidence of measures, standard deviation and 5, 25, 50, 75 and 95 percentiles, as well as the estimated expression levels.

**Usage**

```
mmgmos (
  object
  ,background=FALSE
  ,replaceZeroIntensities=TRUE
  ,gsnorm=c("median", "none", "mean", "meanlog")
  ,savepar=FALSE
  ,eps=1.0e-6
  ,orig.phis = FALSE
  ,addConstant = 0
)
```

**Arguments**

<code>object</code>	an object of <code>AffyBatch</code>
<code>background</code>	Logical value. If TRUE, perform background correction before applying <code>mmgmos</code> .
<code>replaceZeroIntensities</code>	Logical value. If TRUE, replace 0 intensities with 1 before applying <code>mmgmos</code> .
<code>gsnorm</code>	character. specifying the algorithm of global scaling normalisation.
<code>savepar</code>	Logical value. If TRUE the estimated parameters of the model are saved in file <code>par\_mmgmos.txt</code> and <code>phi\_mmgmos.txt</code> .
<code>eps</code>	Optimisation termination criteria.
<code>orig.phis</code>	Logical value. If TRUE, use phi values created from <code>hgu95a</code> array.
<code>addConstant</code>	numeric. This is an experimental feature and should not generally be changed from the default value.

**Details**

The obtained expression measures are in log base 2 scale.

The algorithms of global scaling normalisation can be one of "median", "none", "mean", "meanlog". "mean" and "meanlog" are mean-centered normalisation on raw scale and log scale respectively, and "median" is median-centered normalisation. "none" will result in no global scaling normalisation being applied.

There are  $2*n+2$  columns in file `par\_mmgmos.txt`,  $n$  is the number of chips. The first  $n$  columns are 'alpha' values for  $n$  chips, the next  $n$  columns are 'a' values for  $n$  chips, column  $2*n+1$  is 'c' values and the final column is values for 'd'. The file `phi\_mmgmos.txt` keeps the final optimal value of 'phi'.

**Value**

An object of class `exprReslt`.

**Author(s)**

Xuejun Liu, Magnus Rattray, Marta Milo, Neil D. Lawrence

**References**

Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips, *Bioinformatics* 21: 3637-3644.

Milo,M., Niranjana,M., Holley,M.C., Rattray,M. and Lawrence,N.D. (2004) A probabilistic approach for summarising oligonucleotide gene expression data, technical report available upon request.

Milo,M., Fazeli,A., Niranjana,M. and Lawrence,N.D. (2003) A probabilistic model for the extraction of expression levels from oligonucleotide arrays, *Biochemical Society Transactions*, 31: 1510-1512.

Peter Spellucci. DONLP2 code and accompanying documentation. Electronically available via <http://plato.la.asu.edu/donlp2.html>

**See Also**

Related class [exprReslt-class](#) and related method [mgmos](#)

**Examples**

```
## Code can be commented out to speed up checks, but left in for now for debugging (June)
## load example data from package affydata
if (require(affydata)) data(Dilution)

## use method mmgMOS to calculate the expression levels and related confidence
## of the measures for the example data
eset<-mmgmos(Dilution)
```

---

normalisation.gs     *Global scaling normalisation*

---

**Description**

This function is only included for backwards compatibility with the **pplr** package. This function is now superseded by [pumaNormalize](#).

This function does the global scaling normalisation.

**Usage**

```
normalisation.gs(x)
```

**Arguments**

`x`                    a matrix or data frame which contains gene expression level on log2 scale.

**Details**

Each row of `x` is related to a gene and each column is related to a chip.

**Value**

The return matrix is in the same format as the input `x`.

**Author(s)**

Xuejun Liu, Marta Milo, Neil D. Lawrence, Magnus Rattray

**See Also**

See Also as [bcomb](#)

**Examples**

```
data(exampleE)
exampleE.normalised<-normalisation.gs(exampleE)
data(Clust.exampleE)
Clust.exampleE.normalised<-normalisation.gs(Clust.exampleE)
```

---

numFP

*Number of False Positives for a given proportion of True Positives.*

---

**Description**

Often when evaluating a differential expression method, we are interested in how well a classifier performs for very small numbers of false positives. This method gives one way of calculating this, by determining the number of false positives for a set proportion of true positives.

**Usage**

```
numFP(scores, truthValues, TPRate = 0.5)
```

**Arguments**

<code>scores</code>	A vector of scores. This could be, e.g. one of the columns of the statistics of a <a href="#">DEResult</a> object.
<code>truthValues</code>	A boolean vector indicating which scores are True Positives.
<code>TPRate</code>	A number between 0 and 1 identify the proportion of true positives for which we wish to determine the number of false positives.

**Value**

An integer giving the number of false positives.

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [plotROC](#) and [calcAUC](#).

**Examples**

```
class1a <- rnorm(1000,0.2,0.1)
class2a <- rnorm(1000,0.6,0.2)
class1b <- rnorm(1000,0.3,0.1)
class2b <- rnorm(1000,0.5,0.2)
scores_a <- c(class1a, class2a)
scores_b <- c(class1b, class2b)
classElts <- c(rep(FALSE,1000), rep(TRUE,1000))
print(numFP(scores_a, classElts))
print(numFP(scores_b, classElts))
```

---

numOfFactorsToUse *Determine number of factors to use from an ExpressionSet*

---

**Description**

This is really an internal function used to determine how many factors to use in design and contrast matrices

**Usage**

```
numOfFactorsToUse (eset)
```

**Arguments**

eset                   An object of class [ExpressionSet](#).

**Value**

An integer denoting the number of factors to be used.

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [createDesignMatrix](#) and [createContrastMatrix](#)

**Examples**

```
# Next 4 lines commented out to save time in package
# checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
numOfFactorsToUse(eset_mmgmos)
```

---

numTP	<i>Number of True Positives for a given proportion of False Positives.</i>
-------	--

---

### Description

Often when evaluating a differential expression method, we are interested in how well a classifier performs for very small numbers of true positives. This method gives one way of calculating this, by determining the number of true positives for a set proportion of false positives.

### Usage

```
numTP(scores, truthValues, FPRate = 0.5)
```

### Arguments

scores	A vector of scores. This could be, e.g. one of the columns of the statistics of a <a href="#">DEResult</a> object.
truthValues	A boolean vector indicating which scores are True Positives.
FPRate	A number between 0 and 1 identify the proportion of false positives for which we wish to determine the number of true positives.

### Value

An integer giving the number of true positives.

### Author(s)

Richard D. Pearson

### See Also

Related methods [numFP](#), [plotROC](#) and [calcAUC](#).

### Examples

```
class1a <- rnorm(1000,0.2,0.1)
class2a <- rnorm(1000,0.6,0.2)
class1b <- rnorm(1000,0.3,0.1)
class2b <- rnorm(1000,0.5,0.2)
scores_a <- c(class1a, class2a)
scores_b <- c(class1b, class2b)
classElts <- c(rep(FALSE,1000), rep(TRUE,1000))
print(numTP(scores_a, classElts))
print(numTP(scores_b, classElts))
```



---

orig\_pplr

*Probability of positive log-ratio*


---

### Description

This is the original version of the `pplr` function as found in the **pplr** package. This should give exactly the same results as the `pplr` function. This function is only included for testing purposes and is not intended to be used. It will not be available in future versions of **puma**.

This function calculates the probability of positive log-ratio (PPLR) between any two specified conditions in the input data, mean and standard deviation of gene expression level for each condition.

### Usage

```
orig_pplr(e, control, experiment)
```

### Arguments

<code>e</code>	a data frame containing the mean and standard deviation of gene expression levels for each condition.
<code>control</code>	an integer denoting the control condition.
<code>experiment</code>	an integer denoting the experiment condition.

### Details

The input of 'e' should be a data frame comprising of  $2*n$  components, where  $n$  is the number of conditions. The first  $1,2,\dots,n$  components include the mean of gene expression values for conditions  $1,2,\dots,n$ , and the  $n+1, n+2,\dots,2*n$  components contain the standard deviation of expression levels for condition  $1,2,\dots,n$ .

### Value

The return is a data frame. The description of the components are below.

<code>index</code>	The original row number of genes.
<code>cM</code>	The mean expression levels under control condition.
<code>sM</code>	The mean expression levels under experiment condition.
<code>cStd</code>	The standard deviation of gene expression levels under control condition.
<code>sStd</code>	The standard deviation of gene expression levels under experiment condition.
<code>LRM</code>	The mean log-ratio between control and experiment genes.
<code>LRStd</code>	The standard deviation of log-ratio between control and experiment genes.
<code>stat</code>	A statistic value which is $-\text{mean}/(\sqrt{2}*\text{standard deviation})$ .
<code>PPLR</code>	Probability of positive log-ratio.

### Author(s)

Xuejun Liu, Marta Milo, Neil D. Lawrence, Magnus Rattray

## References

Liu, X., Milo, M., Lawrence, N.D. and Rattray, M. (2005) Probe-level variances improve accuracy in detecting differential gene expression, technical report available upon request.

## See Also

Related method [bcomb](#)

## Examples

```
data(exampleE)
data(exampleStd)
r<-bcomb(exampleE, exampleStd, replicates=c(1,1,1,2,2,2), method="map")
p<-orig_pplr(r, 1, 2)
```

---

plotErrorBars      *Plot mean expression levels and error bars for one or more probesets*

---

## Description

This produces plots of probesets of interest.

## Usage

```
plotErrorBars(
  eset
  , probesets = if(dim(exprs(eset))[1] <= 12) 1:dim(exprs(eset))[1] else 1
  , arrays = 1:dim(pData(eset))[1] # default is to use all
  , xlab = paste(colnames(pData(eset))[1:numOfFactorsToUse(eset)], collapse=":")
  , ylab = "Expression Estimate"
  , xLabels = apply(
      as.matrix(pData(eset)[arrays, 1:numOfFactorsToUse(eset)])
      , 1
      , function(mat) {paste(mat, collapse=":")}
    )
  , ylim = NA
  , numOfSEs = qnorm(0.975)
  , globalYlim = FALSE # Not yet implemented!
  , plot_cols = NA
  , plot_rows = NA
  , featureNames = NA
  , showGeneNames = TRUE
  , showErrorBars = if(
    length(assayDataElement(eset, "se.exprs"))==0 ||
    length(assayDataElement(eset, "se.exprs")) == sum(is.na(assayDataElement(eset, "se.exprs")))
  ) FALSE else TRUE
  , plotColours = FALSE
  , log.it = if(max(exprs(eset)) > 32) TRUE else FALSE
  , eset_comb = NULL
  , jitterWidth = NA
  , qtpcrData = NULL
```

```
, ...
)
```

### Arguments

<code>eset</code>	An object of class <code>ExpressionSet</code> . This is the main object being plotted.
<code>probesets</code>	A vector of integers indicating the probesets to be plotted. These integers refer to the row numbers of the <code>eset</code> .
<code>arrays</code>	A vector of integers indicating the arrays to be shown on plots.
<code>xlab</code>	Character string of title to appear on x-axis
<code>ylab</code>	Character string of title to appear on y-axis
<code>xLabels</code>	Vector of strings for labels of individual points on x-axis.
<code>ylim</code>	2-element numeric vector showing minimum and maximum values for y-axis.
<code>numOfSEs</code>	Numeric indicating the scaling for the error bars. The default value give error bars that include 95% of expected values.
<code>globalYlim</code>	Not yet implemented!
<code>plot_cols</code>	Integer specifying number of columns for multi-figure plot.
<code>plot_rows</code>	Integer specifying number of rows for multi-figure plot.
<code>featureNames</code>	A vector of strings for <code>featureNames</code> (Affy IDs). This is an alternative (to the <code>probesets</code> argument) way of specifying probe sets.
<code>showGeneNames</code>	Boolean indicating whether to use Affy IDs as titles for each plot.
<code>showErrorBars</code>	Boolean indicating whether error bars should be shown on plots.
<code>plotColours</code>	A vector of colours to plot.
<code>log.it</code>	Boolean indicating whether expression values should be logged.
<code>eset_comb</code>	An object of class <code>ExpressionSet</code> . This is a secondary object to be plotted on the same charts as <code>eset</code> . This should be an object created using <code>pumaComb</code> which holds the values created by combining information from the replicates of each condition.
<code>jitterWidth</code>	Numeric indicating the x-axis distance between replicates of the same condition.
<code>qtPCRData</code>	A 2-column matrix of qRT-PCR values (or other data to be plotted on the same charts).
<code>...</code>	Additional arguments to be passed to <code>plot</code> .

### Value

This function has no return value. The output is the plot created.

### Author(s)

Richard D. Pearson

**Examples**

```
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
plotErrorBars(eset_mmgmos)
plotErrorBars(eset_mmgmos, 1:6)
```

---

plotHistTwoClasses *Stacked histogram plot of two different classes*

---

**Description**

Stacked histogram plot of two different classes

**Usage**

```
plotHistTwoClasses (
  scores
  , class1Elements
  , class2Elements
  , space=0
  , col=c("white", "grey40")
  , xlab="PPLR"
  , ylab="Number of genes"
  , ylim=NULL
  , las=0 # axis labels all perpendicular to axes
  , legend=c("non-spike-in genes", "spike-in genes")
  , inset=0.05
  , minScore=0
  , maxScore=1
  , numofBars=20
  , main=NULL
)
```

**Arguments**

scores	A numeric vector of scores (e.g. from the output of <a href="#">pumaDE</a> )
class1Elements	Boolean vector, TRUE if element is in first class
class2Elements	Boolean vector, TRUE if element is in second class
space	Numeric. x-axis distance between bars
col	Colours for the two different classes
xlab	Title for the x-axis
ylab	Title for the y-axis
ylim	2-element numeric vector showing minimum and maximum values for y-axis.

las	See <a href="#">par</a> . Default of 0 means axis labels all perpendicular to axes.
legend	2-element string vector giving text to appear in legend for the two classes.
inset	See <a href="#">legend</a>
minScore	Numeric. Minimum score to plot.
maxScore	Numeric. Maximum score to plot.
numOfBars	Integer. Number of bars to plot.
main	String. Main title for the plot.

**Value**

This function has no return value. The output is the plot created.

**Author(s)**

Richard D. Pearson

**Examples**

```
class1 <- rnorm(1000,0.2,0.1)
class2 <- rnorm(1000,0.6,0.2)
class1[which(class1<0)] <- 0
class1[which(class1>1)] <- 1
class2[which(class2<0)] <- 0
class2[which(class2>1)] <- 1
scores <- c(class1, class2)
class1elts <- c(rep(TRUE,1000), rep(FALSE,1000))
class2elts <- c(rep(FALSE,1000), rep(TRUE,1000))
plotHistTwoClasses(scores, class1elts, class2elts, ylim=c(0,300))
```

---

plot-methods

*Plot method for pumaPCARes objects*

---

**Description**

This is the method to plot objects of class pumaPCARes. It will produce a scatter plot of two of the principal components

**Usage**

```
## S4 method for signature 'pumaPCARes,missing':
plot(..., firstComponent = 1, secondComponent = 2, useFileNames = FALSE, phenoty
```

**Arguments**

... Optional graphical parameters to adjust different components of the plot

firstComponent Integer identifying which principal component to plot on the x-axis

secondComponent Integer identifying which principal component to plot on the x-axis

useFileNames Boolean. If TRUE then use filenames as plot points. Otherwise just use points.

```

phenotype      Phenotype information
legend1pos     String indicating where to put legend for first factor
legend2pos     String indicating where to put legend for second factor

```

### Examples

```

# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
pumapca_mmgmos <- pumaPCA(eset_mmgmos)
plot(pumapca_mmgmos)

```

---

plotROC

*Receiver Operator Characteristic (ROC) plot*

---

### Description

Plots a Receiver Operator Characteristic (ROC) curve.

### Usage

```

plotROC(
  scoresList
  ,truthValues
  ,includedProbesets=1:length(truthValues)
  ,legendTitles=1:length(scoresList)
  ,main = "PUMA ROC plot"
  ,lty = 1:length(scoresList)
  ,col = rep(1,length(scoresList))
  ,lwd = rep(1,length(scoresList))
  ,yaxisStat = "tpr"
  ,xaxisStat = "fpr"
  ,downsampling = 100
  ,showLegend = TRUE
  ,showAUC = TRUE
  ,...
)

```

### Arguments

```

scoresList      A list, each element of which is a numeric vector of scores.
truthValues     A boolean vector indicating which scores are True Positives.
includedProbesets
                A vector of indices indicating which scores (and truthValues) are to be used in
                the calculation. The default is to use all, but a subset can be used if, for example,
                you only want a subset of the probesets which are not True Positives to be treated
                as False Positives.
legendTitles    Vector of names to appear in legend.

```

main	Main plot title
lty	Line types.
col	Colours.
lwd	Line widths.
yaxisStat	Character string identifying what is to be plotted on the y-axis. The default is "tpr" for True Positive Rate. See <a href="#">performance</a> function from <b>ROCR</b> package.
xaxisStat	Character string identifying what is to be plotted on the x-axis. The default is "fpr" for False Positive Rate. See <a href="#">performance</a> function from <b>ROCR</b> package.
downsampling	See details for <a href="#">plot.performance</a> from the <b>ROCR</b> package.
showLegend	Boolean. Should legend be displayed?
showAUC	Boolean. Should AUC values be included in legend?
...	Other parameters to be passed to plot.

### Value

This function has no return value. The output is the plot created.

### Author(s)

Richard D. Pearson

### See Also

Related method [calcAUC](#)

### Examples

```
class1a <- rnorm(1000,0.2,0.1)
class2a <- rnorm(1000,0.6,0.2)
class1b <- rnorm(1000,0.3,0.1)
class2b <- rnorm(1000,0.5,0.2)
scores_a <- c(class1a, class2a)
scores_b <- c(class1b, class2b)
scores <- list(scores_a, scores_b)
classElts <- c(rep(FALSE,1000), rep(TRUE,1000))
plotROC(scores, classElts)
```

---

plotWhiskers

*Standard errors whiskers plot*

---

### Description

A plot showing error bars for genes of interest.

**Usage**

```
plotWhiskers (
  eset
  , comparisons=c(1,2)
  , sortMethod = c("logRatio", "PPLR")
  , numGenes=50
  , xlim
  , main = "PUMA Whiskers plot"
  , highlightedGenes=NULL
)
```

**Arguments**

eset	An object of class <a href="#">ExpressionSet</a> .
comparisons	A 2-element integer vector specifying the columns of data to be compared.
sortMethod	The method used to sort the genes. "logRatio" is fold change. PPLR is Probability of Positive Log Ratio (as determined by the <a href="#">pumaDE</a> method).
numGenes	Integer. Number of probesets to plot.
xlim	The x limits of the plot. See <a href="#">plot.default</a> .
main	A main title for the plot. See <a href="#">plot.default</a> .
highlightedGenes	Row numbers of probesets to highlight with an asterisk.

**Value**

This function has no return value. The output is the plot created.

**Author(s)**

Richard D. Pearson

**See Also**

Related method [pumaDE](#)

---

pplr

*Probability of positive log-ratio*

---

**Description**

**WARNING** - this function is generally not expected to be used, but is intended as an internal function. It is included for backwards compatibility with the **pplr** package, but may be deprecated and then hidden in future. Users should generally use [pumaDE](#) instead.

This function calculates the probability of positive log-ratio (PPLR) between any two specified conditions in the input data, mean and standard deviation of gene expression level for each condition.

**Usage**

```
pplr(e, control, experiment, sorted=TRUE)
```



**Arguments**

<code>e</code>	a data frame containing the mean and standard deviation of gene expression levels for each condition.
<code>control</code>	an integer denoting the control condition.
<code>experiment</code>	an integer denoting the experiment condition.
<code>sorted</code>	Boolean. Should PPLR values be sorted by value? If FALSE, PPLR values are returned in same order as supplied.

**Details**

The input of 'e' should be a data frame comprising of  $2*n$  components, where  $n$  is the number of conditions. The first  $1,2,\dots,n$  components include the mean of gene expression values for conditions  $1,2,\dots,n$ , and the  $n+1, n+2,\dots,2*n$  components contain the standard deviation of expression levels for condition  $1,2,\dots,n$ .

**Value**

The return is a data frame. The description of the components are below.

<code>index</code>	The original row number of genes.
<code>cM</code>	The mean expression levels under control condition.
<code>sM</code>	The mean expression levels under experiment condition.
<code>cStd</code>	The standard deviation of gene expression levels under control condition.
<code>sStd</code>	The standard deviation of gene expression levels under experiment condition.
<code>LRM</code>	The mean log-ratio between control and experiment genes.
<code>LRStd</code>	The standard deviation of log-ratio between control and experiment genes.
<code>stat</code>	A statistic value which is $-\text{mean}/(\sqrt{2}*\text{standard deviation})$ .
<code>PPLR</code>	Probability of positive log-ratio.

**Author(s)**

Xuejun Liu, Marta Milo, Neil D. Lawrence, Magnus Rattray

**References**

Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) Probe-level variances improve accuracy in detecting differential gene expression, technical report available upon request.

**See Also**

Related methods [pumaDE](#) and [bcomb](#)

**Examples**

```
data(exampleE)
data(exampleStd)
r<-bcomb(exampleE,exampleStd,replicates=c(1,1,1,2,2,2),method="map")
p<-pplr(r,1,2)
```

---

pplrUnsorted	<i>Return an unsorted matrix of PPLR values</i>
--------------	---

---

**Description**

Returns the output from [pplr](#) as an unsorted matrix (i.e. sorted according to the original sorting in the original matrix)

**Usage**

```
pplrUnsorted(p)
```

**Arguments**

`p` A matrix as output by [pplr](#).

**Value**

A matrix of PPLR values

**Author(s)**

Richard D. Pearson

**See Also**

Related method [pplr](#)

---

pumaClust	<i>Propagate probe-level uncertainty in model-based clustering on gene expression data</i>
-----------	--

---

**Description**

This function clusters gene expression using a Gaussian mixture model including probe-level measurement error. The inputs are gene expression levels and the probe-level standard deviation associated with expression measurement for each gene on each chip. The outputs is the clustering results.

**Usage**

```
pumaClust(e=NULL, se=NULL, efile=NULL, sefile=NULL,  
subset=NULL, gsnorm=FALSE, clusters,  
iter.max=100, nstart=10, eps=1.0e-6, del0=0.01)
```

**Arguments**

<code>e</code>	either a valid <a href="#">ExpressionSet</a> object, or a data frame containing the expression level for each gene on each chip.
<code>se</code>	data frame containing the standard deviation of gene expression levels.
<code>efile</code>	character, the name of the file which contains gene expression measurements.
<code>sefile</code>	character, the name of the file which contains the standard deviation of gene expression measurements.
<code>subset</code>	vector specifying the row number of genes which are clustered on.
<code>gsnorm</code>	logical specifying whether do global scaling normalisation or not.
<code>clusters</code>	integer, the number of clusters.
<code>iter.max</code>	integer, the maximum number of iterations allowed in the parameter initialisation.
<code>nstart</code>	integer, the number of random sets chosen in the parameter initialisation.
<code>eps</code>	numeric, optimisation parameter.
<code>del0</code>	numeric, optimisation parameter.

**Details**

The input data is specified either as an [ExpressionSet](#) object (in which case `se`, `efile` and `sefile` will be ignored), or by `e` and `se`, or by `efile` and `sefile`.

**Value**

The result is a list with components

`cluster`: vector, containing the membership of clusters for each gene; `centers`: matrix, the center of each cluster; `centersigs`: matrix, the center variance of each cluster; `likelipergene`: matrix, the likelihood of belonging to each cluster for each gene; `bic`: numeric, the Bayesian Information Criterion score.

**Author(s)**

Xuejun Liu, Magnus Rattray

**References**

Liu, X., Lin, K.K., Andersen, B., and Rattray, M. (2006) Propagating probe-level uncertainty in model-based gene expression clustering, technical report available upon request.

Liu, X., Milo, M., Lawrence, N.D. and Rattray, M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips, *Bioinformatics*, 21(18):3637-3644.

**See Also**

Related method [mmgmos](#)

**Examples**

```
data(Clust.exampleE)
data(Clust.exampleStd)
pumaClust.example<-pumaClust(Clust.exampleE, Clust.exampleStd, clusters=7)
```

pumaComb

*Combining replicates for each condition***Description**

This function calculates the combined (from replicates) signal for each condition using Bayesian models. The inputs are gene expression levels and the probe-level standard deviations associated with expression measurements for each gene on each chip. The outputs include gene expression levels and standard deviation for each condition.

**Usage**

```
pumaComb (
  eset
  , design.matrix=NULL
  , method="em"
  , numOfChunks=1000
  , save_r=FALSE
  , cl=NULL
  , parallelCompute=FALSE
)
```

**Arguments**

<code>eset</code>	An object of class <a href="#">ExpressionSet</a> .
<code>design.matrix</code>	A design matrix.
<code>method</code>	Method "map" uses MAP of a hierarchical Bayesian model with Gamma prior on the between-replicate variance (Gelman et.al. p.285) and shares the same variance across conditions. This method is fast and suitable for the case where there are many conditions.  Method "em" uses variational inference of the same hierarchical Bayesian model as in method "map" but with conjugate prior on between-replicate variance and shares the variance across conditions. This is generally much slower than "map", but is recommended where there are few conditions (as is usually the case).
<code>numOfChunks</code>	An integer defining how many chunks the data is divided into before processing. There is generally no need to change the default value.
<code>save_r</code>	Will save an internal variable <code>r</code> to a file. Used for debugging purposes.
<code>cl</code>	A "cluster" object. See <a href="#">makeCluster</a> function from <b>snow</b> package for more details (if available).
<code>parallelCompute</code>	Boolean identifying whether processing in parallel should occur.

**Details**

It is generally recommended that data is normalised prior to using this function. Note that the default behaviour of `mmgmos` is to normalise data so this shouldn't generally be an issue. See the function [pumaNormalize](#) for more details on normalisation.

**Value**

The result is an [ExpressionSet](#) object.

**Author(s)**

Xuejun Liu, Marta Milo, Neil D. Lawrence, Magnus Rattray

**References**

Gelman,A., Carlin,J.B., Stern,H.S., Rubin,D.B., Bayesian data analysis. London: Chapman & Hall; 1995.

Liu,X., Milo,M., Lawrence,N.D. and Rattray,M. (2005) Probe-level variances improve accuracy in detecting differential gene expression, technical report available upon request.

**See Also**

Related methods [pumaNormalize](#), [bcomb](#), [mmgmos](#) and [pumaDE](#)

**Examples**

```
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)

# Next line shows that eset_mmgmos has 4 arrays, each of which is a different
# condition (the experimental design is a 2x2 factorial, with both liver and
# scanner factors)
pData(eset_mmgmos)

# Next line shows expression levels of first 3 probe sets
exprs(eset_mmgmos)[1:3,]

# Next line used so eset_mmgmos only has information about the liver factor
# The scanner factor will thus be ignored, and the two arrays of each level
# of the liver factor will be treated as replicates
pData(eset_mmgmos) <- pData(eset_mmgmos)[,1,drop=FALSE]

# To save time we'll just use 100 probe sets for the example
eset_mmgmos_100 <- eset_mmgmos[1:100,]
eset_comb <- pumaComb(eset_mmgmos_100)

# We can see that the resulting ExpressionSet object has just two conditions
# and 1 expression level for each condition
pData(eset_comb)
exprs(eset_comb)[1:3,]
```

---

pumaDE

*Calculate differential expression between conditions*

---

## Description

The function generates lists of genes ranked by probability of differential expression (DE). This uses the PPLR method.

## Usage

```
pumaDE(  
  eset  
  , design.matrix = createDesignMatrix(eset)  
  , contrast.matrix = createContrastMatrix(eset)  
  )
```

## Arguments

<code>eset</code>	An object of class <a href="#">ExpressionSet</a> .
<code>design.matrix</code>	A design matrix
<code>contrast.matrix</code>	A contrast matrix

## Details

A separate list of genes will be created for each contrast of interest.

Note that this class returns a [DEResult-class](#) object. This object contains information on both the PPLR statistic values (which should generally be used to rank genes for differential expression), as well as fold change values (which are generally not recommended for ranking genes, but which might be useful, for example, to use as a filter). To understand more about the object returned see [DEResult-class](#), noting that when created a [DEResult](#) object with the `pumaDE` function, the `statistic` method should be used to return PPLR values. Also note that the `pLikeValues` method can be used on the returned object to create values which can more readily be compared with p-values returned by other methods such as variants of t-tests (limma, etc.).

While it is possible to run this function on data from individual arrays, it is generally recommended that this function is run on the output of the function [pumaComb](#) (which combines information from replicates).

## Value

An object of class [DEResult-class](#).

## Author(s)

Richard D. Pearson

## See Also

Related methods [calculateLimma](#), [calculateFC](#), [calculateTtest](#), [pumaComb](#), [mmgmos](#), [pplr](#), [createDesignMatrix](#) and [createContrastMatrix](#)

**Examples**

```

# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)

# Next line shows that eset_mmgmos has 4 arrays, each of which is a different
# condition (the experimental design is a 2x2 factorial, with both liver and
# scanner factors)
pData(eset_mmgmos)

# Next line shows expression levels of first 3 probe sets
exprs(eset_mmgmos)[1:3,]

# Next line used so eset_mmgmos only has information about the liver factor
# The scanner factor will thus be ignored, and the two arrays of each level
# of the liver factor will be treated as replicates
pData(eset_mmgmos) <- pData(eset_mmgmos)[,1,drop=FALSE]

# To save time we'll just use 100 probe sets for the example
eset_mmgmos_100 <- eset_mmgmos[1:100,]
eset_comb <- pumaComb(eset_mmgmos_100)

pumaDEResults <- pumaDE(eset_comb)

topGeneIDs(pumaDEResults,6) # Gives probeset identifiers
topGenes(pumaDEResults,6) # Gives row numbers
statistic(pumaDEResults)[topGenes(pumaDEResults,6),] # PPLR scores of top six genes
FC(pumaDEResults)[topGenes(pumaDEResults,6),] # Fold-change of top six genes

```

---

pumaDEUnsorted      *Return an unsorted matrix of PPLR values*

---

**Description**

Returns the output from [pumaDE](#) as an unsorted matrix (i.e. sorted according to the original sorting in the ExpressionSet)

**Usage**

```
pumaDEUnsorted(pp)
```

**Arguments**

pp                    A list as output by [pumaDE](#).

**Value**

A matrix of PPLR values

**Author(s)**

Richard D. Pearson

**See Also**Related method [pumaDE](#)

---

`pumaFull`*Perform a full PUMA analysis*

---

**Description**

Full analysis including pumaPCA and mmgmos/pumaDE vs rma/limma comparison

**Usage**

```
pumaFull (
  affybatch = NULL
  , data_dir = getwd()
  , load_affybatch = FALSE
  , calculate_eset = TRUE
  , calculate_pumaPCAs = TRUE
  , calculate_bcomb = TRUE
  , mmgmosComparisons = FALSE
)
```

**Arguments**

`affybatch` An object of class [AffyBatch](#).

`data_dir` A character string specifying where data files are stored.

`load_affybatch` Boolean. Load a pre-existing AffyBatch object? Note that this has to be named "affybatch.rda" and be in the `data_dir` directory.

`calculate_eset` Boolean. Calculate ExpressionSet from `affybatch` object? If FALSE, files named "eset\_mmgmos.rda" and "eset\_rma.rda" must be available in the `data_dir` directory.

`calculate_pumaPCAs` Boolean. Calculate pumaPCA from `eset_mmgmos` object? If FALSE, a file named "pumaPCA\_results.rda" must be available in the `data_dir` directory.

`calculate_bcomb` Boolean. Calculate pumaComb from `eset_mmgmos` object? If FALSE, files named "eset\_comb.rda" and "eset\_normd\_comb.rda" must be available in the `data_dir` directory.

`mmgmosComparisons` Boolean. If TRUE, will compare mmgmos with default settings, with mmgmos used with background correction.



**Value**

No return values. Various objects are saved as .rda files during the execution of this function, and various PDF files are created.

**Author(s)**

Richard D. Pearson

**See Also**

Related methods [pumaDE](#), [createDesignMatrix](#) and [createContrastMatrix](#)

**Examples**

```
## Code commented out to ensure checks run quickly
# if (require(affydata)) data(Dilution)
# pumaFull(Dilution)
```

---

pumaNormalize      *Normalize an ExpressionSet*

---

**Description**

This is used to apply a scaling normalization to set of arrays. This normalization can be at the array scale (thus giving all arrays the same mean or median), or at the probeset scale (thus giving all probesets the same mean or median).

It is generally recommended that the default option (median array scaling) is used after running [mmgmos](#) and before running [pumaComb](#) and/or [pumaDE](#). There are however, situations where this might not be the recommended, for example in time series experiments where it is expected that there will be general up-regulation or down-regulation in overall gene expression levels between time points.

**Usage**

```
pumaNormalize(
  eset
  ,arrayScale = c("median", "none", "mean", "meanlog")
  ,probesetScale = c("none", "mean", "median")
  ,probesetNormalisation = NULL
  ,replicates = list(1:dim(exprs(eset))[2])
)
```

**Arguments**

<code>eset</code>	An object of class <a href="#">ExpressionSet</a> .
<code>arrayScale</code>	A method of scale normalisation at the array level.
<code>probesetScale</code>	A method of scale normalisation at the probe set level.
<code>probesetNormalisation</code>	If not NULL normalises the expression levels to have zero mean and adjusts the variance of the gene expression according to the zero-centered normalisation.
<code>replicates</code>	List of integer vectors indicating which arrays are replicates.

**Value**

An object of class `ExpressionSet` holding the normalised data.

**Author(s)**

Richard D. Pearson

**See Also**

Methods `mmgmos`, `pumaComb` and `pumaDE`

**Examples**

```
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
apply(exprs(eset_mmgmos), 2, median)
eset_mmgmos_normd <- pumaNormalize(eset_mmgmos)
apply(exprs(eset_mmgmos_normd), 2, median)
```

---

puma-package

*puma - Propagating Uncertainty in Microarray Analysis*

---

**Description**

Most analyses of Affymetrix GeneChip data are based on point estimates of expression levels and ignore the uncertainty of such estimates. By propagating uncertainty to downstream analyses we can improve results from microarray analyses. For the first time, the `puma` package makes a suite of uncertainty propagation methods available to a general audience. `puma` also offers improvements in terms of scope and speed of execution over previously available uncertainty propagation methods. Included are summarisation, differential expression detection, clustering and PCA methods, together with useful plotting functions.

**Details**

Package: puma  
Type: Package  
Version: 1.2.1  
Date: 2007-06-26  
License: LGPL excluding donlp2

For details of using the package please refer to the Vignette

**Author(s)**

Richard Pearson, Xuejun Liu, Guido Sanguinetti, Marta Milo, Neil D. Lawrence, Magnus Rattray  
Maintainer: Richard Pearson <richard.pearson@postgrad.manchester.ac.uk>

## References

- Milo, M., Niranjana, M., Holley, M. C., Rattray, M. and Lawrence, N. D. (2004) A probabilistic approach for summarising oligonucleotide gene expression data, technical report available upon request.
- Liu, X., Milo, M., Lawrence, N. D. and Rattray, M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips, *Bioinformatics*, 21(18):3637-3644.
- Sanguinetti, G., Milo, M., Rattray, M. and Lawrence, N. D. (2005) Accounting for probe-level noise in principal component analysis of microarray data, *Bioinformatics*, 21(19):3748-3754.
- Rattray, M., Liu, X., Sanguinetti, G., Milo, M. and Lawrence, N. D. (2006) Propagating uncertainty in Microarray data analysis, *Briefings in Bioinformatics*, 7(1):37-47.
- Liu, X., Milo, M., Lawrence, N. D. and Rattray, M. (2006) Probe-level measurement error improves accuracy in detecting differential gene expression, *Bioinformatics*, 22(17):2107-2113.
- Liu, X., Lin, K., Andersen, B., Rattray, M. (2007) Including probe-level uncertainty in model-based gene expression clustering, *BMC Bioinformatics*, 8(98).
- Pearson, R. D., Liu, X., Sanguinetti, G., Milo, M., Lawrence, N. D., Rattray, M. (2008) In preparation.

## Examples

```
# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)
pumapca_mmgmos <- pumaPCA(eset_mmgmos)
plot(pumapca_mmgmos)
eset_mmgmos_100 <- eset_mmgmos[1:100,]
eset_comb <- pumaComb(eset_mmgmos_100)
esetDE <- pumaDE(eset_comb)
```

---

```
pumaPCAExpectations-class
      Class pumaPCAExpectations
```

---

## Description

This is a class representation for storing a set of expectations from a pumaPCA model. It is an internal representation and shouldn't normally be instantiated.

## Objects from the Class

Objects can be created by calls of the form `new("pumaPCAExpectations", ...)`.

## Slots

- x:** Object of class "matrix" representing x
- xxT:** Object of class "array" representing xxT
- logDetCov:** Object of class "numeric" representing logDetCov

**Methods**

This class has no methods defined

**Author(s)**

Richard D. Pearson

**See Also**

Related method [pumaPCA](#) and related class [pumaPCARes](#).

---

pumaPCAModel-class *Class pumaPCAModel*

---

**Description**

This is a class representation for storing a pumaPCA model. It is an internal representation and shouldn't normally be instantiated.

**Objects from the Class**

Objects can be created by calls of the form `new ("pumaPCAModel", ...)`.

**Slots**

**sigma:** Object of class "numeric" representing sigma

**m:** Object of class "matrix" representing m

**Cinv:** Object of class "matrix" representing Cinv

**W:** Object of class "matrix" representing W

**mu:** Object of class "matrix" representing mu

**Methods**

This class has no methods defined

**Author(s)**

Richard D. Pearson

**See Also**

Related method [pumaPCA](#) and related class [pumaPCARes](#).

pumaPCA

*PUMA Principal Components Analysis***Description**

This function carries out principal components analysis (PCA), taking into account not only the expression levels of genes, but also the variability in these expression levels.

The various other pumaPCA... functions are called during the execution of pumaPCA

**Usage**

```
pumaPCA(
  eset
  , latentDim          = if(dim(exprs(eset))[2] <= 3)
    dim(exprs(eset))[[2]]-1
  else
  3
  , sampleSize        = if(dim(exprs(eset))[1] <= 1000)
    dim(exprs(eset))[[1]]
  else
  1000 ## Set to integer or FALSE for all
  , initPCA           = TRUE ## Initialise parameters with PCA
  , randomOrder       = FALSE ## Update parameters in random order
  , optimMethod       = "BFGS" ## ?optim for details of methods
  , stoppingCriterion = "deltaW" ## can also be "deltaL"
  , tol               = 1e-3 ## Stop when delta update < this
  , stepChecks        = FALSE ## Check likelihood after each update?
  , iterationNumbers  = TRUE ## Show iteration numbers?
  , showUpdates       = FALSE ## Show values after each update?
  , showTimings       = FALSE ## Show timings after each update?
  , showPlot          = FALSE ## Show projection plot after each update?
  , maxIters          = 500 ## Number of EM iterations.
  , transposeData     = FALSE ## Transpose eset matrices?
  , returnExpectations = FALSE
  , returnData        = FALSE
  , returnFeedback    = FALSE
  , pumaNormalize     = TRUE
)
```

**Arguments**

eset	An object of class <a href="#">ExpressionSet</a> .
latentDim	An integer specifying the number of latent dimensions (kind of like the number of principal components).
sampleSize	An integer specifying the number of probesets to sample (default is 1000), or FALSE, meaning use all the data.
initPCA	A boolean indicating whether to initialise using standard PCA (the default, and generally quicker and recommended).
randomOrder	A boolean indicating whether the parameters should be updated in a random order (this is generally not recommended, and the default is FALSE).

`optimMethod` See `?optim` for details of methods.  
`stoppingCriterion` If set to "deltaW" will stop when W changes by less than `tol`. If "deltaL" will stop when L (lambda) changes by less than `tol`.  
`tol` Tolerance value for `stoppingCriterion`.  
`stepChecks` Boolean. Check likelihood after each update?  
`iterationNumbers` Boolean. Show iteration numbers?  
`showUpdates` Boolean. Show values after each update?  
`showTimings` Boolean. Show timings after each update?  
`showPlot` Boolean. Show projection plot after each update?  
`maxIters` Integer. Maximum number of EM iterations.  
`transposeData` Boolean. Transpose eset matrices?  
`returnExpectations` Boolean. Return expectation values?  
`returnData` Boolean. Return expectation data?  
`returnFeedback` Boolean. Return feedback on progress of optimisation?  
`pumaNormalize` Boolean. Normalise data prior to running algorithm (recommended)?

**Value**

An object of class `pumaPCARes`

**Author(s)**

Richard D. Pearson

**See Also**

Related methods `pumaDE`, `createDesignMatrix` and `createContrastMatrix`

**Examples**

```

# Next 4 lines commented out to save time in package checks, and saved version used
# if (require(affydata)) {
# data(Dilution)
# eset_mmgmos <- mmgmos(Dilution)
# }
data(eset_mmgmos)

pumapca_mmgmos <- pumaPCA(eset_mmgmos)
plot(pumapca_mmgmos)

```

---

pumaPCARes-class    *Class pumaPCARes*

---

### Description

This is a class representation for storing the outputs of the `pumaPCA` function. Objects of this class should usually only be created through the `pumaPCA` function.

### Objects from the Class

Objects can be created by calls of the form `new("pumaPCARes", ...)`.

### Slots

**model:** Object of class "pumaPCAModel" representing the model parameters  
**expectations:** Object of class "pumaPCAExpectations" representing the model expectations  
**varY:** Object of class "matrix" representing the variance in the expression levels  
**Y:** Object of class "matrix" representing the expression levels  
**phenoData:** Object of class "AnnotatedDataFrame" representing the phenotype information  
**timeToCompute:** Object of class "numeric" representing the time it took `pumaPCA` to run  
**numberOfIterations:** Object of class "numeric" representing the number of iterations it took `pumaPCA` to converge  
**likelihoodHistory:** Object of class "list" representing the history of likelihood values while `pumaPCA` was running  
**timingHistory:** Object of class "list" representing the history of how long each iteration took while `pumaPCA` was running  
**modelHistory:** Object of class "list" representing the history of how the model was changing while `pumaPCA` was running  
**exitReason:** Object of class "character" representing the reason `pumaPCA` halted. Can take the values "Update of Likelihood less than tolerance x", "Update of W less than tolerance x", "Iterations exceeded", "User interrupt", "unknown exit reason"

### Methods

**plot** signature(x="pumaPCARes-class"): plots two principal components on a scatter plot.

**write.reslts** signature(x = "pumaPCARes-class"): writes the principal components for each array to a file. It takes the same arguments as `write.table`. The argument "file" does not need to set any extension. The file name and extension "csv" will be added automatically. The default file name is "tmp".

### Author(s)

Richard D. Pearson

### See Also

Related method `pumaPCA` and related class `pumaPCARes`.

---

```
removeUninformativeFactors
```

*Remove uninformative factors from the phenotype data of an [ExpressionSet](#)*

---

### Description

This is really an internal function used to remove uninformative factors from the phenotype data. Uninformative factors here are defined as those which have the same value for all arrays in the [ExpressionSet](#).

### Usage

```
removeUninformativeFactors(eset)
```

### Arguments

`eset` An object of class [ExpressionSet](#).

### Value

An [ExpressionSet](#) object with the same data as the input, except for a new `phenoData` slot.

### Author(s)

Richard D. Pearson

### See Also

Related methods [createDesignMatrix](#) and [createContrastMatrix](#)

### Examples

```
eset_test <- new("ExpressionSet", exprs=matrix(rnorm(400,8,2),100,4))
pData(eset_test) <- data.frame("informativeFactor"=c("A", "A", "B", "B"), "uninformativeF
eset_test2 <- removeUninformativeFactors(eset_test)
pData(eset_test)
pData(eset_test2)
```



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