MiChip

April 19, 2010

`boxplotDataNoFile` *Create Boxplot of data*

Description

Creates a boxplot of expression data contained in a matrix.

Usage

```
boxplotDataNoFile(dmat, exptname, dlevel)
```

Arguments

`dmat`	matrix containing expression data to be boxplotted
`exptname`	Name of the experiment, used to build plot title
`dlevel`	Stage of the experiment e.g. raw, summarized, normalized

Examples

```
#Create a boxplot containing normalized expression data for myexpt
## Not run: boxplotDataNoFile(dmat, "MyExpt", "mednormed")
```

`boxplotData` *Create Boxplot of data*

Description

Creates a boxplot of expression data contained in a matrix and writes this to a file.

Usage

```
boxplotData(dmat, exptname, dlevel)
```

Arguments

`dmat`	matrix containing expression data to be boxplotted
`exptname`	Name of the experiment, used to build filename
`dlevel`	Stage of the experiment e.g. raw, summarized, normalized

Examples

```
#Create a file of a boxplot containing normalized expression data for myexpt
## Not run:
boxplotData(dmat, "MyExpt", "mednormed")

## End(Not run)
```

`correctForFlags` *Corrects for spots flagged as not present*

Description

Spots flagged with a -ve quality flag value by the scanner may be regarded as not present. This method sets their intensity to NA.

Usage

```
correctForFlags(eset, intensityCutoff=0)
```

Arguments

`eset` `ExpressionSet` containing intensity values and flags to be filtered

`intensityCutoff` value of lowest acceptable intensity value in the experiment

Examples

```
#Correct ExpressionSet for flags of spots marked as unreadable
## Not run:
myCorrectedEset <-correctForFlags(eset, intensityCutoff=0)

## End(Not run)
```

`MiChip` *Introduction to the MiChip Package*

Description

Alibrary for processing MiChip hybridizations

Author(s)

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myForgivingMedian *Produce Median from Probe Intensity values*

Description

Creates a median to summarize the intensities for individual probes, giving that not all probes will have a valid intensity reading

Usage

```
myForgivingMedian(mat, minSumlength=0)
```

Arguments

`mat`	matrix of data to calculate the median from
`minSumlength`	The lowest acceptable length of the matrix to calculate a median

Examples

```
#Calculate the median of a matrix omiting NAs
## Not run:
myForgivingMedian(mat, minSumlength=0)

## End(Not run)
```

naOmitMedian *Calculates the median of an array excluding NAs*

Description

Calculates the median of an array excluding NAs

Usage

```
naOmitMedian(mat, madAdjust=FALSE)
```

Arguments

`mat`	A single dimensional matrix
`madAdjust`	if `TRUE` then summarized data will be filtered according to the MAD median absolute deviation and set to `NA` if the median is less than MAD

Examples

```
#Calculate the median of matrix mat omiting NAs
## Not run:
myMedian <-naOmitMedian(mat, madAdjust=TRUE)

## End(Not run)
```

normalizePerChipMedian

Normalize to median intensity

Description

Normalizes intensity values to the median of each chip

Usage

```
normalizePerChipMedian(eset)
```

Arguments

eset	ExpressionSet containing chip intensity values to be normalized

Examples

```
#Normalize expression data in an Eset to the median
## Not run:
normedDataEset <- normalizePerChipMedian(eset)

## End(Not run)
```

outputAnnotatedDataMatrix

Outputs a tab delimited file from an ExpressionSet

Description

Takes an ExpressionSet and outputs a tab delimited file containing feature annotation to the left and hyb specific expression/flag data to the right

Usage

```
outputAnnotatedDataMatrix(eset, exptname, stage, dataElement)
```

Arguments

eset	ExpressionSet containing the matrix and annotation to output
exptname	a string containing the name of the experiment. Used to build file name
stage	a string containing the stage of the data in the matrix e.g. normalized
dataElement	a string containing the name of the data element in the ExpressionSet to be output

Examples

```
#Write out an annotated tab delimited file for the normalized data
## Not run:
outputAnnotatedDataMatrix(normedEset, "MyMicroArrayExpt","Median_Normalized", "exprs")
## End(Not run)
```

`panelCor` *Add Pearson Correlation value to plots*

Description

Adds a pearson correlation value to the scatter plots

Usage

```
panelCor(x,y, digits=2, prefix="r=")
```

Arguments

`x`	matrix of x values
`y`	matrix of y values to correlate with x
`digits`	number of digits to display
`prefix`	The string prefix that should be display on the scatterplot panel

Examples

```
#Calculate the median of a matrix omiting NAs
## Not run:
panelCor(x,y, digits=2, prefix="r=")

## End(Not run)
```

`parseRawData` *Parse raw data files to create an ExpressionSet*

Description

Loads all the gpr scanner output files in a particular directory and returns an `ExpressionSet` of the hybridizations in a MiChip experiment

Usage

```
parseRawData(datadir=".", pat="gpr")
```

Arguments

datadir	a directory containing one or my files of scanner output from MiChip hybridizations
pat	a string containing the three letter extension of the scanner output files

Examples

```
## Not run:
## Load all *.gpr files in current directory
parseRawData(datadir=".", pat="gpr")


## Load all *.gpr files in a specified directory , windows
parseRawData(datadir="c:\mydata\grpdata\expt1\", pat="gpr")


## Load all *.gpr files in a specified directory, linux
parseRawData(datadir="/home/myuser/gprdata/extp1/", pat="gpr")

## End(Not run)
```

plotIntensitiesScatter

Plot pairwise intensity scatter

Description

Creates a pairwise set of scatter plots from a data matrix and writes it out to file

Usage

```
plotIntensitiesScatter(dmat, controls=NULL, exptname, maintitle)
```

Arguments

dmat	matrix containing data from an experiment to be plotted
controls	matrix of row numbers containing control data to be plotted in a different colour
exptname	Name of the experiment, used for build the filename
maintitle	String used to build the maintitle of the graph

Examples

```
#Plot the pairwise intensities from myexpt
## Not run:
plotIntensitiesScatter(dmat, NULL, "MyExpt", "Median_Normalized")

## End(Not run)
```

`removeUnwantedRows` *Removes unwanted rows from data matrix*

Description

Due to the requirements of spotting the chips, some of the spots are empty. Others contain controls or features from another species that may not be wanted in the analysis. This method removes them

Usage

```
removeUnwantedRows(rawData, filters)
```

Arguments

`rawData`	`ExpressionSet` containing matrix of data to be filtered
`filters`	list of strings to be to be filtered from annotation gene name column

Examples

```
#Removes empty and control spots from data matrix
## Not run:
filters=c("empty", "control")
filteredData <- removeUnwantedRows(rawData, filters)
## End(Not run)
```

`returnAnnotatedDataMatrix` *returns and annotated data matrix from an ExpressionSet*

Description

Takes an `ExpressionSet` and returns a data martix of feature annotation to the left and hyb specific expression/flag data to the right

Usage

```
returnAnnotatedDataMatrix(eset, dataElement)
```

Arguments

`eset`	`ExpressionSet` containing the matrix and annotation to output
`dataElement`	a string containing the name of the data element in the ExpressionSet to be output

Examples

```
#Write out an annotated tab delimited file for the normalized data
## Not run:
returnAnnotatedDataMatrix(normedEset,"exprs")
## End(Not run)
```

`setIntensityCutoff` *Sets a cutoff for the lowest intensity value*

Description

Any value less than the cutoff value will be set to NA. This allows near background intensity values to be excluded

Usage

```
setIntensityCutoff(dmat, intensityCutoff)
```

Arguments

`dmat`	matrix of intensity values to which the cutoff value is applied
`intensityCutoff`	value of lowest acceptable intensity value in the experiment

Examples

```
#Set all the values under 50 in a matrix to NA
## Not run:
dmatOver50 <- setIntensityCutoff(dmat, 50)

## End(Not run)
```

`standardRemoveRows` *Removes a standard list of features for MiChip processing*

Description

Removes all empty spots, control spots, U6 RNA, non human spots from an `ExpressionSet` in the standard fashion. A wrapper for removeUnwantedRows

Usage

```
standardRemoveRows(rawData)
```

Arguments

`rawData`	`ExpressionSet` containing the matrix to be filtered

Examples

```
#Filter standard rows from an ExpressionSet
## Not run:
myfilterdEset <-standardRemoveRows(rawData)

## End(Not run)
```

summarizeIntensitiesAsMedian

Summarizes the probe intensity as median of replicates spotted

Description

As the probes are spotted onto the in quaduplet or duplicate the values have to be combined in some way. This function takes the median of the intensities for the spots. Effectively the mean for duplicates. If less than half of the spots are present an NA is added

Usage

```
summarizeIntensitiesAsMedian(eset,minSumlength=0, madAdjust=FALSE)
```

Arguments

`eset`	ExpressionSet containing probe intensity data to be summarized
`minSumlength`	The lowest acceptable length of the matrix to calculate a median
`madAdjust`	if `TRUE` then summarized data will be filtered according to the MAD median absolute deviation and set to `NA` if the median is less than MAD

Examples

```
#Calculate the median of a matrix omiting NAs
## Not run:
summarizeIntensitiesAsMedian(eset,minSumlength=0,madAdjust=TRUE)

## End(Not run)
```

workedExampleMedianNormalize

Worked Example of MiChip Processing

Description

Loads a set of hybridizations into a matrix and them proceeds to filter, summarize and median normalize them

Usage

```
workedExampleMedianNormalize(exptname, intensityCutoff=0, datadir=".", minSumlen
```

Arguments

exptname string indicating the name of the experiment

intensityCutoff
The intensity value for accepting the spots intensity value in the experiment

datadir The directory where hybridization files are found.

minSumlength Minimum exceptable number of values to summarize intensity value.

madAdjust if TRUE then summarized data will be filtered according to the MAD median absolute deviation and set to NA if the median is less than MAD

Examples

```
#Normalize data in the current directory to the median per chip
datadir <- system.file("extdata", package="MiChip")
myNormedEset <-workedExampleMedianNormalize("MyExpt", intensityCutoff=0, datadir, minSuml
```

---

workedExampleNotNormalizedData
Worked Example of MiChip Processing

Description

Loads a set of hybridizations into a matrix and them proceeds to filter and summarize these data

Usage

```
workedExampleNotNormalizedData(exptname, intensityCutoff=0, datadir=".", minSuml
```

Arguments

exptname string indicating the name of the experiment

intensityCutoff
The intensity value for accepting the spots intensity value in the experment

datadir The directory contain data from the experiment

minSumlength Minimum exceptable number of values to summarize intensity value.

madAdjust if TRUE then summarized data will be filtered according to the MAD median absolute deviation and set to NA if the median is less than MAD

Examples

```
#Summarizes the data in the current directory
## Not run:
mySummarizedEset <-workedExampleNotNormalizedData("MyExpt", intensityCutoff=0, datadir=".

## End(Not run)
```

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