

Package ‘MiChip’

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Title MiChip Parsing and Summarizing Functions

Author Jonathon Blake <blake@embl.de>

Maintainer Jonathon Blake <blake@embl.de>

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Description This package takes the MiChip miRNA microarray .grp scanner output files and parses these out, providing summary and plotting functions to analyse MiChip hybridizations. A set of hybridizations is packaged into an ExpressionSet allowing it to be used by other BioConductor packages.

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| | |
|-------------|-------------------------------|
| boxplotData | <i>Create Boxplot of data</i> |
|-------------|-------------------------------|

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)
```

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")
```

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

A library for processing MiChip hybridizations

Author(s)

Jonathon Blake

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 omitting NAs
## Not run:
myForgivingMedian(mat, minSumlength=0)

## End(Not run)
```

| | |
|--------------|--|
| naOmitMedian | <i>Calculates the median of an array excluding NAs</i> |
|--------------|--|

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 | <i>Normalize to median intensity</i> |
|------------------------|--------------------------------------|

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/expt1/", 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 matrix 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=".", minSumlength, madAdjust = FALS
```

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, minSumLength=0, madAdjust=TRUE)
```

```
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=".", minSumlength, madAdjust = FA
```

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=".", minSumlength=0, madA

## End(Not run)
```

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