Package 'CAFE'

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Type Package

Title Chromosmal Aberrations Finder in Expression data

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Suggests RUnit, BiocGenerics, BiocStyle

Description Detection and visualizations of gross chromosomal aberrations using Affymetrix expression microarrays as input

License GPL-3

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Collate microProcess-improve.R selectSamples.R chromosomeStats.R rawPlot.R slidPlot.R discontPlot.R facetPlot.R

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CAFE-package *Chromosomal Aberrations Finder in Expression data*

Description

CAFE attempts to find chromosomal aberrations in microarray expression (mRNA) data. It contains several plotting functions to aid in visualizing these aberrations. It generally recapitulates the workflow described by Mayshar et al (see references), and implements several algorithms described by Friedrich et al (see references).

Details

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Author(s)

Sander Bollen

References

Friedrich, F., Kempe, a, Liebscher, V., & Winkler, G. (2008). Complexity Penalized M-Estimation. Journal of Computational and Graphical Statistics, 17(1), 201-224. doi:10.1198/106186008X285591

Mayshar, Y., Ben-David, U., Lavon, N., Biancotti, J.-C., Yakir, B., Clark, A. T., Plath, K., et al. (2010). Identification and classification of chromosomal aberrations in human induced pluripotent stem cells. Cell stem cell, 7(4), 521-31. doi:10.1016/j.stem.2010.07.017

Examples

```
## Not run:
setwd("/some/path/to/cel/files")
data <- ProcessCels()
# process cel files
samples <- c(1,2)
# select samples 1 and 2 to compare against the rest
chromosomeStats(data,chromNum="ALL",samples=samples)
```

```
# check for chromosomal gains
chromosomeStats(data,chromNum="ALL",samples=samples,alternative="less")
# check for chromosomal losses
bandStats(data,chromNum=1,samples=samples)
# check for band gains in chr1
bandStats(data,chromNum=1,samples=samples,alternative="less")
# check for band losses in chr1
rawPlot(data,chromNum=1,samples=samples,idiogram=TRUE)
# plot raw data with an ideogram
slidPlot(data,chromNum=1,samples=samples,idiogram=TRUE,combine=TRUE,k=100)
# moving average plot with ideogram
discontPlot(data,chromNum=1,samples=samples,idiogram=TRUE)
# discontinuous plot with ideogram


## End(Not run)
```

`armStats` *Find aberrations with chromosome arm resolution*

Description

Calculate significant chromosomal arms with various statistical tests

Usage

```
armStats(datalist, chromNum=1, arm="q",
samples=NULL, select="cli",test="fisher",
bonferroni = TRUE, enrichment = "greater")
```

Arguments

`datalist`	The CAFE datalist to be analyzed, i.e. the output of `ProcessCels`.
`chromNum`	The chromosome to be calculated. This can be `"ALL"` to calculate all chromosomes.
`arm`	Select which arm - `"q"` or `"p"` - to analyse
`samples`	A vector containing sample numbers to be analyzed
`select`	Signifies which type of sample selection prompt will be shown, if `samples=NULL`. Currently supported are `"cli"` for a command line interface and `"gui"` for a tcl/tk-based graphical user interface.
`test`	Signifies which statistical test to be used in the final calculation. Must be either `"fisher"` for an exact fisher test or `"chisqr"` for a chi square test.
`bonferroni`	If `bonferroni=TRUE`, will correct the p-values of the enrichment test with a bonferroni method.
`enrichment`	Test for over or underexpression. Can be set to `"greater"` or `"less"`.

Value

A named vector containing p-values.

Note

Technically speaking, the Fisher's exact test is better than the chi-square test; the Fisher's exact test gives an exact p-value, whereas the chi-square test only gives an approximation. However, the Fisher's exact test can get slow for large sample sizes, and the chi-square test becomes better with increasing sample size but does not slow down as much.

Author(s)

Sander Bollen

See Also

chromosomeStats bandStats

Examples

```
data("CAFE_data")
armStats(CAFE_data,chromNum="ALL",samples=c(1,3),arm="p")
```

---

bandStats *Find aberrations with cytoband resolution*

Description

Calculate significant chromosome bands with various statistical tests

Usage

```
bandStats(datalist, chromNum=1, samples=NULL, select="cli", test="fisher",
bonferroni = TRUE, enrichment = "greater")
```

Arguments

datalist	The CAFE datalist to be analyzed, i.e. the output of ProcessCels.
chromNum	The chromosome to be calculated. This can be "ALL" to calculate all chromosomes.
samples	A vector containing sample numbers to be analyzed
select	Signifies which type of sample selection prompt will be shown, if samples=NULL. Currently supported are "cli" for a command line interface and "gui" for a tcl/tk-based graphical user interface.
test	Signifies which statistical test to be used in the final calculation. Must be either "fisher" for an exact fisher test or "chisqr" for a chi square test.
bonferroni	If bonferroni=TRUE, will correct the p-values of the enrichment test with a bonferroni method.
enrichment	Test for over or underexpression. Can be set to "greater" or "less".

Value

A named vector containing p-values if testing a single chromosome. If chromNum="ALL", the output will be a two-column data frame, with cytoband names in the first column and p-values in the second column.

Note

Technically speaking, the Fisher's exact test is better than the chi-square test; the Fisher's exact test gives an exact p-value, whereas the chi-square test only gives an approximation. However, the Fisher's exact test can get slow for large sample sizes, and the chi-square test becomes better with increasing sample size but does not slow down as much.

Author(s)

Sander Bollen

See Also

chromosomeStats armStats

Examples

```
data(CAFE_data)
bandStats(CAFE_data,chromNum=17,samples=c(1,3),test="fisher")
```

CAFE_data *CAFE data set*

Description

Contains the dataset of GSE6561 and GSE10809 processed by ProcessCels

Usage

```
data("CAFE_data")
```

Format

A list containing two lists

`whole` A list containing a dataframe for each sample

`over` A list containing a dataframe for each sample, but with only those probes that are deemed overexpressed

The dataframes inside the lists contain the following columns:

`ID` Affymetrix probe IDs

`Sym` Gene symbols

`Value` Log2 transformed expression values

`LogRel` Log2 transformed relative expression values (to the median)

`Loc` Chromosomal locations

`Chr` Chromosome identifiers

Source

GSE6561: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6561

GSE10809: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE10809

Examples

```
data("CAFE_data")
```

`chromosomeStats` *Find aberrations with whole-chromosome resolution*

Description

Calculate significant chromosomes with various statistical tests

Usage

```
chromosomeStats(datalist, chromNum=1, samples=NULL, select="cli", test="fisher",
bonferroni = TRUE, enrichment = "greater")
```

Arguments

`datalist`	The CAFE datalist to be analyzed, i.e. the output of `ProcessCels`.
`chromNum`	The chromosome to be calculated. This can be `"ALL"` to calculate all chromosomes.
`samples`	A vector containing sample numbers to be analyzed
`select`	Signifies which type of sample selection prompt will be shown, if `samples=NULL`. Currently supported are `"cli"` for a command line interface and `"gui"` for a tcl/tk-based graphical user interface.
`test`	Signifies which statistical test to be used in the final calculation. Must be either `"fisher"` for an exact fisher test or `"chisqr"` for a chi square test.
`bonferroni`	If `bonferroni=TRUE`, will correct the p-values of the enrichment test with a bonferroni method.
`enrichment`	Test for over or underexpression. Can be set to `"greater"` or `"less"`.

Value

A named vector containing p-values.

Note

Technically speaking, the Fisher's exact test is better than the chi-square test; the Fisher's exact test gives an exact p-value, whereas the chi-square test only gives an approximation. However, the Fisher's exact test can get slow for large sample sizes, and the chi-square test becomes better with increasing sample size but does not slow down as much.

Author(s)

Sander Bollen

See Also

`bandStats` `armStats`

Examples

```
data("CAFE_data")
sam <- c(9,11)
chromosomeStats(CAFE_data,chromNum=17,samples=sam,test="fisher")
```

`cliSubset` *Subset data with a CLI*

Description

Provides command line interface for subsetting input datasets

Usage

```
cliSubset(datalist,alternative)
```

Arguments

`datalist`	the dataset to be subsetted
`alternative`	"greater" or "less"

Value

subset of input

Author(s)

Sander Bollen

See Also

`guiSubset`

Examples

```
## Not run:
datalist <- data("CAFE_data")
sub <- cliSubset(datalist,alternative="greater")

## End(Not run)
```

discontPlot *Plot with discontinuous smoother*

Description

Plots chromosome plots with a discontinuous smoother

Usage

```
discontPlot(datalist,samples=c(1,2),chromNum=1,gamma=300,idiogram=FALSE,
file="default")
```

Arguments

datalist	The CAFE datalist to be analyzed, i.e. the output of ProcessCels.
samples	A vector or sample numbers to be plotted
chromNum	the chromosome to be plotted
gamma	The gamma level can be roughly compared to the sliding window size in a normal continuous smoother. The gamma level determines how strict the algorithm functions; a higher level will correspond to fewer jumps. This can not be higher than the total number of probesets on the to-be-analyzed chromosome. Must be a positive integer.
idiogram	if TRUE, will overlay a chromosome idiogram over the chromosome plot
file	Specify a file name to store output png file

Value

Plot to file system; Returns a ggplot2 graph if chromNum!="ALL". When chromNum=="ALL", returns a list of ggplot2 graphs.

Author(s)

Sander Bollen

References

Friedrich, F., Kempe, a, Liebscher, V., & Winkler, G. (2008). Complexity Penalized M-Estimation. Journal of Computational and Graphical Statistics, 17(1), 201-224. doi:10.1198/106186008X285591

See Also

rawPlot slidPlot facetPlot

Examples

```
data("CAFE_data")
discontPlot(CAFE_data,samples=9,chromNum=17,gamma=300)
```

discontSmooth *A discontinuous smoother*

Description

Calculates discontinuous smoother

Usage

```
discontSmooth(y,gamma)
```

Arguments

y	input vector
gamma	The gamma level can be roughly compared to the sliding window size in a normal continuous smoother. The gamma level determines how strict the algorithm functions; a higher level will correspond to fewer jumps. This cannot be larger than length(y). Must be a positive integer.

Details

Uses the potts filter algorithm described by Friedrich et al.

Value

Vector with same length as input y

Author(s)

Sander Bollen

References

Friedrich, F., Kempe, a, Liebscher, V., & Winkler, G. (2008). Complexity Penalized M-Estimation. Journal of Computational and Graphical Statistics, 17(1), 201-224. doi:10.1198/106186008X285591

Examples

```
#generate piecewise vector with gaussian noise
y <- 1:450
y[1:150] <- 2
y[151:300] <- 3
y[301:450] <- 1
y <- y + rnorm(450)

#calculate smoother
y_smooth <- discontSmooth(y,20)
```

facetPlot *Plot all chromosomes horizontally next to each other*

Description

Plots all chromosomes in horizontal alignment next to each other, with optionally a moving average smoother applied to the data

Usage

```
facetPlot(datalist,samples=c(1,2),slid=FALSE,combine=FALSE,k=1,file="default")
```

Arguments

datalist	The CAFE datalist to be analyzed, i.e. the output of ProcessCels.
samples	A vector or sample numbers to be plotted
slid	If TRUE, use moving average smoother
combine	If TRUE, will plot the unaltered raw data in the background
k	The sliding window size. Must be a positive integer, smaller than the length of Affy IDs on the chromosome
file	Specify a file name to store output png file

Value

Plot to file system. Return a ggplot2 graph

Note

Makes heavy use of the ggplot2 package

Author(s)

Sander Bollen

References

H. Wickham. ggplot2: elegant graphics for data analysis. Springer New York, 2009.

See Also

slidPlot rawPlot discontPlot

Examples

```
data("CAFE_data")
facetPlot(CAFE_data,samples=9)
```

fisher.method *Combines pvalues by using Fisher's method*

Description

Combines pvalues by using Fisher's method

Usage

```
fisher.method(pvals)
```

Arguments

pvals	Vector of p values

Value

Combined p value

Author(s)

Sander Bollen

Examples

```
pvals <- runif(20) #generate 20 pvals
fisher.method(pvals)
```

guiSubset *Subset data with a GUI*

Description

Provides graphical user interface for subsetting input datasets

Usage

```
guiSubset(datalist,alternative)
```

Arguments

datalist	the dataset to be subsetted
alternative	"greater" or "less"

Value

Subset of input to variable guiSelectedSet in working directory

Author(s)

Sander Bollen

See Also

cliSubset

Examples

```
## Not run:
data("CAFE_data")
guiSubset(CAFE_data,alternative="greater")

## End(Not run)
```

ProcessCels *Processing CEL files*

Description

Normalizes and computes relative expressions for all CEL files in work directory

Usage

```
ProcessCels(threshold.over=1.5,threshold.under=(2/3),remove_method=1,
local_file=NULL)
```

Arguments

threshold.over	Determines the threshold, as a multiple of median value, where probes are considered overexpressed. Default is 1.5
threshold.under	Determines the threshold, as a fraction of median value, where probes are considered underexpressed. Default is 2/3
remove_method	Determines which method is used to remove multiple probesets that are annotated to map to the same gene. The default option, 1, will keep 1 probeset with the following priority: 1): nnn_at; 2): nnn_a_at; 3): nnn_s_at; 4): nnn_x_at; 5): lowest nnn if multiple probes still exist If remove_method=2, probesets will *only* be removed if several probesets of the same gene map to the exact same location. In the case that many probesets map to the same location, one probeset will be retained according to the priority of option 1 above. If remove_method=0, no multiple probesets will be removed
local_file	Use a local - previously downloaded - UCSC file (e.g. http://hgdownload.soe.ucsc.edu/goldenPath/hg affyU133Plus2.txt.gz) instead of directly retrieving the file instead.

Details

this function uses the RMA algorithm to normalize *.CEL files in work directory. It then computes relative expressions for every probe on every sample. Locations for probesets are downloaded from UCSC, as the standard BioConductor annotations do not map probeset location (they only map the location to the corresponding gene). Multiple probesets belonging to the same gene are removed as described above. The function then determines which probes are overexpressed and underexpressed relative to the median probeset values across all samples. Finally,the relative expressions are log2-transformed.

Value

list

$whole	named list, where each element is a data.frame corresponding to a *.CEL file - containing columns: 1): "ID" (Affy ID number); 2): "Sym" (gene Symbol); 3): "Value" (Expression values); 4): "LogRel" (Relative expressions); 5): "Loc" (Chromosomal locations); 6): "Chr" (Chromosome number); 7): "Band" (Cytoband); 8): "Arm" (Chromosomal arm)
$over	same as $whole, but contains only those probes which are deemed overexpressed
$under	same as $whole, but contains only those probes which are deemd underexpressed

Author(s)

Sander Bollen

Examples

```
## Not run:
data <- ProcessCels()

## End(Not run)
```

---

rawPlot *Plot without any smoother*

Description

Makes chromosome plot using raw data values

Usage

```
rawPlot(datalist,samples=c(1,2),chromNum=1,idiogram=FALSE,file="default")
```

Arguments

datalist	The CAFE datalist to be analyzed, i.e. the output of ProcessCels.
samples	A vector or sample numbers to be plotted
chromNum	The chromosome to be analyzed
idiogram	If TRUE, will plot a chromosome idiogram over the plot
file	Specify a file name to store output png file

Value

Plot to file system; Returns a ggplot2 graph if chromNum!="ALL". When chromNum=="ALL", returns a list of ggplot2 graphs.

Author(s)

Sander Bollen

See Also

slidPlot facetPlot discontPlot

Examples

```
data("CAFE_data")
rawPlot(CAFE_data,samples=8,chromNum=17)
```

---

slidPlot *Plot with sliding average smoother*

Description

Plots chromosome plots with a moving average smoother

Usage

```
slidPlot(datalist,samples=c(1,2),chromNum=1,combine=FALSE,k=1,idiogram=FALSE,file="default")
```

Arguments

datalist	The CAFE datalist to be analyzed, i.e. the output of ProcessCels.
samples	A vector of sample numbers to be plotted
chromNum	The chromosome to be analyzed
combine	If TRUE, will plot the unaltered raw data in the background
k	The sliding window size. Must be a positive integer, smaller than the total number of probesets on the chromosome
idiogram	If TRUE, will plot a chromosome idiogram over the plot
file	Specify a file name to store output png fileS

Value

Plot to file system; Returns a ggplot2 graph if chromNum!="ALL". When chromNum=="ALL", returns a list of ggplot2 graphs.

Note

Makes heavy use of the ggplot2 package.

Author(s)

Sander Bollen

References

H. Wickham. ggplot2: elegant graphics for data analysis. Springer New York, 2009.

See Also

rawPlot facetPlot discontPlot

Examples

```
data("CAFE_data")
slidPlot(CAFE_data,samples=9,chromNum=17,k=50,combine=TRUE)
```

`slidSmooth` *A moving average smoother*

Description

Calculates moving average smoother

Usage

```
slidSmooth(x,k)
```

Arguments

x	input vector
k	The moving average window size. Must be an integer value greater than 0, and no larger than `length(y)`.

Value

Vector with same length as input y

Author(s)

Sander Bollen

Examples

```
#generate piecewise vector with gaussian noise
y <- 1:450
y[1:150] <- 2
y[151:300] <- 3
y[301:450] <- 1
y <- y + rnorm(450)

#calculate smoother
y_smooth <- slidSmooth(y,20)
```

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