Package ‘CAFE’
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Author Sander Bollen
Maintainer Sander Bollen <sander.h.bollen@gmail.com>
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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

Package: CAFE
Type: Package
Version: 0.6.9.5
Date: 2013-05-16
License: GPLv3

Author(s)

Sander Bollen

References


Examples

```r
## 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
```
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
bandStats

See Also

chromosomeStats bandStats

Examples

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

Description

Find aberrations with cytoband resolution

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.
CAFE_data

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

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

**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

**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


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


Examples

```r
#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)
```

Description

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

Usage

```r
facetPlot(datalist,samples=c(1,2),slid=FALSE,combine=FALSE,k=1,file="default")
```
**fisher.method**

**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**


**See Also**

- slidPlot
- rawPlot
- discontPlot

**Examples**

```r
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**

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

**Arguments**

- **pvals**  
Vector of p values
**Value**

Combined p value

**Author(s)**

Sander Bollen

**Examples**

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

---

**Description**

Provides graphical user interface for subsetting input datasets

**Usage**

```r
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**

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

## End(Not run)
```
ProcessCels

### Description

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

### Usage

```r
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/hg19/database/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

- **$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" (Chromosomal arm); 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 deemed underexpressed

Author(s)

Sander Bollen

Examples

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

```
rawPlot                 Plot without any smoother
```

Description

Makes chromosome plot using raw data values

Usage

```r
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

```r
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

See Also
rawPlot facetPlot discontPlot

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