Package 'PAIR'

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Title SNP array normalization

Version 1.0

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Description Paired Allelic log-Intensity-Ratio based normalization algo-rithm for SNP-CGH arrays

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biocViews Microarray, Normalization

LazyData yes

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R topics documented:

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hist.y   *Calculate piece-wise mean intensity values*

Description

Calculate the piece-wise mean intensity values of a sequence of mean intensity values.

Usage

hist.y (y, ave.num, hist.b, plotTF=FALSE),

Arguments

y a vector of data from array-CGH, ROMA, or other copy number experiments

ave.num number of observations to be average.

hist.b number of breaks for generating the histogram

plotTF whether or not to generating plots

Details

For "y", "ave.num", "hist.b"

Data that are NA, Inf, NaN will not be allowed

Value

...

HMMvit   *HMM based change point detection by viterbi algorithm*

Description

Find the most possible path of a HMM via viterbi algorithm

Usage

HMMvit (sd.2n, Obs, factor.y, plotTF),

Arguments

sd.2n the initial value of standard deviation of the observation in two-copy state

Obs the sequence of observations

factor.y multiplication factor value for mean/sd ratio

plotTF whether or not to generating plots

Details

For "sd.2n", "Obs", "factor.y"
Data that are NA, Inf, NaN will not be allowed

Value
...

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mod.y   *modality test*

Description

Modality test for a sequence of observations.

Usage

mod.y (x, n.group, ite),

Arguments

x a vector of data from array-CGH, ROMA, or other copy number experiments

n.group number of mode to be used

ite number of maximum iteration

Details

For "x", "n.group", "ite"
Data that are NA, Inf, NaN will not be allowed

Value
...

PAIR   *Perform PAIR normalization*

Description

Main function for perform PAIR normalization

Usage

PAIR (T.file, C.file, gt.file, ann.file, optionTF, plotTF),

Arguments

T.file name of the tumor data file

C.file name of the paired control data file

gt.file name of the genotype file for the paired control sample

ann.file name of the annotation file

optionTF whether or not performing the optional individual normalization

plotTF whether or not to generate plots

Details

For "T.file", "C.file"
Both files should be saved in .txt format, and should look like the following:

```
       id        chrom pos    A.probe  B.probe
SNP_A-1886933    1 785989   556.5000 552.8333
SNP_A-1902458    1 1130727 1021.6667 386.6667
SNP_A-2131660    1 1156131  355.3333 627.5000
SNP_A-4221087    1 1268847  802.8333 318.5000
SNP_A-1884606    1 1506035  415.3333 382.1667
```

Note that data both before log-transformed and after log-transformation data are acceptable.
Rows should be sorted by "chrom" and "pos".

For "gt.file"
The genotype files for the paired normal samples should be saved in .txt format, and should look like the following:

```
       id        gt
SNP_A-1780520 BB
```

```
SNP_A-1780618 BB
SNP_A-1780632 AB
SNP_A-1780654 AA
SNP_A-4192495 AB
```

For "ann.file"

The annotation file should be saved in .txt format, and should look like the following:

```
     id          chrom   pos
SNP_A-1780619    1  50661138
SNP_A-1780618    4 104675512
SNP_A-1780617   18  26599922
SNP_A-1780778    5  65190626
SNP_A-1780616   12  93021674
```

Value

...

Examples

normalized.logR = PAIR(T.file, C.file, gt.file, ann.file, plotTF=TRUE)