R documentation
of ‘bacom.Rd’ etc.
October 28, 2010

**bacom**

*Bayesian analysis of copy number mixtures for DNA copy number data*

**Description**

'bacom' calls Java class Noticcor to perform normal tissue contamination correction using Bayesian analysis of copy number mixtures (BACOM).

**Usage**

```r
bacom(chrID, copyNumber, alleleA, alleleB, isGenotypeAB, segMean)
```

**Arguments**

- **chrID**: a character vector of chromosome ID, the same length as copyNumber.
- **copyNumber**: a numeric vector of DNA copy numbers (the normal segments have mean 2).
- **alleleA**: a numeric vector of allele A, the same length as copyNumber.
- **alleleB**: a numeric vector of allele B, the same length as copyNumber.
- **isGenotypeAB**: a boolean vector indicating whether the corresponding loci are genotype AB, the same length as copyNumber.
- **segMean**: a numeric vector of segment means, the same length as copyNumber.

**Value**

'bacom' returns the estimated fraction of normal cells in the sample.

**Note**

'bacom' requires R package ‘rJava’ and Java Virtual Machine installed and configured properly. `rJava` can be installed as any other R package from CRAN using `install.packages('rJava')`. `rJava` requires JDK 1.4 or higher to be installed. For `rJava` installation details, please refer to: [http://www.rforge.net/rJava/index.html](http://www.rforge.net/rJava/index.html).
References


Examples

```r
alpha <- bacom(chrID, copyNumber, alleleA, alleleB, isGenotypeAB, segMean)
```

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**plot.cna.bacom**

Plot DNA copy number profiles for BACOM

Description

`plot.cna.bacom` plots DNA copy number profiles.

Usage

```r
plot.cna.bacom(copyNumber, chrID, segMean, alpha,  
position = 1:length(copyNumber),  
ylim = c(-1, 6), chrToPlot=paste(1:22),  
isPlotSegMeanBeforeCorrection = TRUE,  
isShowLegend = TRUE, isShowAlpha = TRUE)
```

Arguments

- `copyNumber`: a vector of copy number profile.
- `chrID`: a character vector of chromosome IDs.
- `segMean`: segment means.
- `alpha`: percentage of normal cell contamination.
- `position`: a vector of x-axis indices (consecutive numbers or physical locations).
- `ylim`: y-axis limit.
- `chrToPlot`: a character vector of chromosome IDs to be plotted.
- `isPlotSegMeanBeforeCorrection`: TRUE if to plot segment mean before correction.
- `isShowLegend`: TRUE if to show legend on the figure.
- `isShowAlpha`: TRUE if to show the value of alpha on the figure.

Examples

```r
plot.cna.bacom(copyNumber, chrID, segMean, alpha)
```
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