Package 'CGHregions'

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Type Package

Title Dimension Reduction for Array CGH Data with Minimal Information Loss.

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Author Sjoerd Vosse & Mark van de Wiel

Maintainer Sjoerd Vosse <info@vossewebdevelopment.nl>

Depends R (>= 2.0.0), methods, Biobase, CGHbase

Description Dimension Reduction for Array CGH Data with Minimal Information Loss

License GPL (http://www.gnu.org/copyleft/gpl.html)

Collate CGHRegions.R private.R

biocViews Microarray, CopyNumberVariation, Visualization

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`CGHregions-package` *Dimension Reduction for Array CGH Data with Minimal Information Loss.*

Description

CGHregions takes as input array CGH data (log2-ratios) that have been segmented (i.e., split into chromosomal segments of similar log2-ratios) and called (i.e., a copy number assigned to each segment) on a per-sample basis and adjusts the segmentation so that break-points that are in similar locations across multiple samples are set to be in identical locations. Segmented and called data can be obtained by using the CGHcall package. The resulting dimensionality reduction facilitates downstream analysis in a variety of ways (e.g., reduces severity of multiple hypothesis testing, facilitates clustering and visualization, reduces computer memory requirements).

Details

Package:	CGHregions
Type:	Package
Version:	0.99.0
Date:	2008-04-29
License:	GPL

Author(s)

Mark van de Wiel and Sjoerd Vosse Maintainer: Mark van de Wiel <mark.vdwiel@vumc.nl>

References

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics, 2*, 55-63.

`CGHregions` *Dimension Reduction for Array CGH Data with Minimal Information Loss*

Description

Dimension Reduction for Array CGH Data with Minimal Information Loss

Usage

```
CGHregions(input, averror=0.01)
```

Arguments

input	An object of class cghCall, a character string or a dataframe. See details for information on the latter two.
averror	Maximal information loss allowed.

Details

Please read the article and the supplementary information for detailed information on the algorithm.

If the input is not an object of class cghCall it should be either a dataframe or a tabseparated textfile (textfiles must contain a header). The first three columns should contain the name, chromosome and position in bp for each array target respectively. The chromosome and position column must contain numbers only. Following these is a column with log2 ratios for each of your samples. If the input type is a textfile, missing values should be represented as 'NA' or an empty field.

The algorithm reduces the call matrix to a smaller matrix that contains regions rather than individual clones. The regions consist of consequtive clones the signatures of which are very much alike. The dimension reduction is potentially for testing and clustering puposes. The amount of information lost by this dimension reduction is controlled by averror. The larger averror, the less regions will result.

Value

This function returns an object of class cghRegions

Author(s)

Mark van de Wiel and Sjoerd Vosse Maintainer: Mark van de Wiel <mark.vdwiel@vumc.nl>

References

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics, 2*, 55-63.

Examples

```
data(WiltingCalled)
result <- CGHregions(WiltingCalled)
```

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