Package ‘maskBAD’

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Version 1.18.0

Title Masking probes with binding affinity differences

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Depends R (>= 2.10), gcrma (>= 2.27.1), affy

Suggests hgu95av2probe

Description Package includes functions to analyze and mask microarray expression data.

License GPL version 2 or newer

biocViews Microarray

NeedsCompilation no

R topics documented:

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Description

This data is the output object of the function mask for the AffyBatch object newAffyBatch.

Usage

exmask

Format

List of 1 or 2 objects.
**newCdf**

**Source**

??

**References**

??

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**newAffyBatch**

*AffyBatch with reduced genes*

**Description**

This data is an AffyBatch object with a subset of 100 genes with human chimpanzee data (cdf hgu95av2) - 10 individuals each.

**Usage**

`newAffyBatch`

**Format**

AffyBatch object

**Source**

??

**References**

Khaitovich et al., Parallel Patterns of Evolution in the Genomes and Transcriptomes of Humans and Chimpanzees, Science 2005

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**newCdf**

*Object of type environment*

**Description**

The environment object is part of the masked object `newAffyBatch`.

**Usage**

`newCdf`

**Format**

Object of type environment

**Source**

??
sequenceMask

References
??

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<th>sequenceMask</th>
<th>Object containing sequence information for probes.</th>
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Description
This data is a table with information about sequence difference between human and chimpanzee for all available probes.

Usage
sequenceMask

Format
data.frame.

Source
??

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