

Package ‘maskBAD’

March 17, 2018

Version 1.22.0

Title Masking probes with binding affinity differences

Author Michael Dannemann <michael_dannemann@eva.mpg.de>

Maintainer Michael Dannemann <michael_dannemann@eva.mpg.de>

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:

exmask	1
newAffyBatch	2
newCdf	2
sequenceMask	3

Index	4
--------------	----------

exmask	<i>Output object of the function mask</i>
--------	---

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.

Source

??

References

??

newAffyBatch	<i>AffyBatch with reduced genes</i>
--------------	-------------------------------------

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

newCdf	<i>Object of type environment</i>
--------	-----------------------------------

Description

The environment object is part of the masked object newAffyBatch.

Usage

newCdf

Format

Object of type environment

Source

??

References

??

sequenceMask	<i>Object containing sequence information for probes.</i>
--------------	---

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

??

References

??

Index

*Topic **datasets**

exmask, [1](#)

newAffyBatch, [2](#)

newCdf, [2](#)

sequenceMask, [3](#)

exmask, [1](#)

newAffyBatch, [2](#)

newCdf, [2](#)

sequenceMask, [3](#)