

# Package ‘maskBAD’

October 16, 2018

**Version** 1.24.0

**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, hgu95av2cdf

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

**License** GPL (>= 2)

**biocViews** Microarray

**git\_url** <https://git.bioconductor.org/packages/maskBAD>

**git\_branch** RELEASE\_3\_7

**git\_last\_commit** dc49d4c

**git\_last\_commit\_date** 2018-04-30

**Date/Publication** 2018-10-15

## R topics documented:

exmask . . . . .	1
newAffyBatch . . . . .	2
newCdf . . . . .	2
sequenceMask . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

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

*Object containing sequence information for probes.*

---

**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](#)