

# Package ‘maskBAD’

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**Version** 1.38.0

**Title** Masking probes with binding affinity differences

**Author** Michael Dannemann <mi chael\_dannemann@eva.mpg.de>

**Maintainer** Michael Dannemann <mi chael\_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>

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

**Source**

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**References**

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

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**References**

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

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newCdf	<i>Object of type environment</i>
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**Description**

The environment object is part of the masked object newAffyBatch.

**Usage**

```
newCdf
```

**Format**

Object of type environment

**Source**

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**References**

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

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