

# Package: maskBAD (via r-universe)

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**Version** 1.57.0

**Title** Masking probes with binding affinity differences

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**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

**Config/pak/sysreqs** zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

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**RemoteRef** HEAD

**RemoteSha** 729bc1d801a194a7204fc733972afa57e828a377

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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**

??

**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**

??

**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**

??

**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**

??

**References**

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