

# Package ‘affydata’

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**Title** Affymetrix Data for Demonstration Purpose

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**Depends** R (>= 2.4.0), affy (>= 1.23.4)

**Imports** methods

**Suggests** hgu95av2cdf, hgu133acdf

**Description** Example datasets of a slightly large size. They represent ‘real world examples’, unlike the artificial examples included in the package affy.

**License** GPL (>= 2)

**biocViews** ExperimentData, OneChannel, Microarray

## R topics documented:

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Dilution	<i>AffyBatch</i> instance <i>Dilution</i>
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### Description

This [AffyBatch-class](#) object represents part of a dilution experiment dataset.

### Usage

```
data(Dilution)
```

### Format

An [AffyBatch-class](#) object containing 4 arrays.

**Source**

Two sources of cRNA A (human liver tissue) and B (Central Nervous System cell line) have been hybridized to human array (HGU95A) in a range of proportions and dilutions. This data set is taken from arrays hybridized to source A at 10.0 and 20  $\mu\text{g}$ . We have two replicate arrays for each generated cRNA. Three scanners have been used in this study. Each array replicate was processed in a different scanner.

For more information see Gautier et al., *affy - Analysis of Affymetrix GeneChip data at the probe level* <http://bioinformatics.oxfordjournals.org/content/20/3/307.full.pdf> *Bioinformatics*, 2004

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\*Topic **datasets**

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