# Package 'affydata'

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**Version** 1.53.0

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**Title** Affymetrix Data for Demonstration Purpose

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**URL** https://bioconductor.org/packages/affydata

**BugReports** https://github.com/rafalab/affydata/issues

**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, Tissue, MicroarrayData, TissueMicroarrayData

**git_url** https://git.bioconductor.org/packages/affydata

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## Contents

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| Dilution | *AffyBatch instance Dilution* |
|---|---|

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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 $\mu$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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