

# Package ‘affydata’

April 3, 2025

**Version** 1.55.0

**Date** 2011-10

**Title** Affymetrix Data for Demonstration Purpose

**Author** Laurent Gautier <laurent@cbs.dtu.dk>

**Maintainer** Robert D Shear <rshear@ds.dfci.harvard.edu>

**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>

**git\_branch** devel

**git\_last\_commit** 427aebc

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-03

## Contents

Dilution . . . . .	2
Index	3

---

Dilution

*AffyBatch instance Dilution*

---

**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

# Index

\* **datasets**

Dilution, [2](#)

Dilution, [2](#)