

# Package ‘affydata’

December 31, 2024

**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** 2024-12-31

## Contents

Dilution . . . . .	2
Index	3

---

Dilution	<i>AffyBatch instance Dilution</i>
----------	------------------------------------

---

**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

# Index

## \* **datasets**

Dilution, [2](#)

Dilution, [2](#)