

Package ‘SpikeInSubset’

April 6, 2023

Title Part of Affymetrix's Spike-In Experiment Data

Version 1.38.0

Author Rafael Irizarry <rafa@jhu.edu> and Zhijin Wu

Description

Includes probe-level and expression data for the HGU133 and HGU95 spike-in experiments

Maintainer Rafael A. Irizarry <rafa@jhu.edu>

License LGPL

Depends R (>= 2.4.0), Biobase (>= 2.5.5), affy (>= 1.23.4)

biocViews ExperimentData, MicroarrayData

git_url <https://git.bioconductor.org/packages/SpikeInSubset>

git_branch RELEASE_3_16

git_last_commit 29f1e0e

git_last_commit_date 2022-11-01

Date/Publication 2023-04-06

R topics documented:

hgu133a.spikein.xhyb	1
SpikeIn	2

Index	3
--------------	----------

hgu133a.spikein.xhyb	<i>Cross hybridizers</i>
----------------------	--------------------------

Description

Probe Sets likely to crosshybridize to spiked-in probesets in the Affymetrix HGU133A spike in

This object is list. Each component of the list contains probeset names of possible crosshybridizers. The sequences of each spiked-in clone were collected and blasted against all HG-U133A target sequences. Target sequences are the ~600bp regions from which probes were selected. Thresholds of 100, 150 and 200bp were used and define the three components of the list.

Usage

```
data(hgu133a.spikein.xhyb)
```

Format

A list

Source

Simon Cawley <simon_cawley@affymetrix.com>

SpikeIn

Subset of Affymetrix SpikeIn Experiment Data

Description

Probe-level and pre-processed data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments.

Usage

```
data(spikein95)
data(rma95)
data(mas95)

data(spikein133)
data(rma133)
data(mas133)
```

Format

SpikeIn is [ProbeSet](#) containing the \$PM\$ and \$MM\$ intensities for a gene spiked in at different concentrations. Use pData to see the concentrations.

Source

spikein95 and spikein133 are instances of [ProbeSet](#) with the probe-level data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments respectively. rma95 and rma133 contain the data pre-processed with RMA. mas95 and mas133 contain the data preprocessed with mas5 (expression and present/absent calls). The calls are in objects called pacalls95 and pacalls133.

For more information see Irizarry, R.A., et al. NAR (2003) <http://www.biostat.jhsph.edu/~ririzarr/papers/index.html>

Index

* **datasets**

hgu133a.spikein.xhyb, [1](#)
SpikeIn, [2](#)

hgu133a.spikein.xhyb, [1](#)

mas133 (SpikeIn), [2](#)
mas95 (SpikeIn), [2](#)

pacalls133 (SpikeIn), [2](#)
pacalls95 (SpikeIn), [2](#)
ProbeSet, [2](#)

rma133 (SpikeIn), [2](#)
rma95 (SpikeIn), [2](#)

SpikeIn, [2](#)
spikein133 (SpikeIn), [2](#)
spikein95 (SpikeIn), [2](#)