

# Package ‘XhybCasneuf’

April 14, 2020

**Version** 1.24.0

**Date** 2007-06-21

**Title** EBI/PSB cross-hybridisation study package

**Author** Tineke Casneuf <tine@ebi.ac.uk>

**Maintainer** Tineke Casneuf <tine@ebi.ac.uk>

**Depends** R (>= 2.4.0), affy , ath1121501cdf , tinesath1cdf ,  
RColorBrewer , methods, grid

**Description** Cross-hybridisation study on the ATH1 Affymetrix GeneChip

**License** Artistic-2.0

**biocViews** ExperimentData, Tissue, MicroarrayData, TissueMicroarrayData

**git\_url** <https://git.bioconductor.org/packages/XhybCasneuf>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** 7e566ca

**git\_last\_commit\_date** 2019-10-29

**Date/Publication** 2020-04-14

## R topics documented:

AffysTissue . . . . .	1
CustomsTissue . . . . .	2
ex1 . . . . .	3
runSimulation . . . . .	4
XhybExamples-class . . . . .	5
<b>Index</b>	<b>6</b>

---

AffysTissue                      *Affymetrix’ CDF probe set pairs*

---

## Description

Affymetrix’ CDF probe set pairs

**Usage**

```
data(AffysTissue)
data(AffysTissueMC)
data(AffysTissue.noBl)
```

**Format**

These three data.frames contain data for Affymetrix' CDF's probe set pairs with  $Q75 \geq 55$ . The `pr` and `target` columns hold the names of probe set X and Y, respectively. Column `alSum` contains the  $Q75$  value of the alignment scores of X's reporters to the transcript of Y. The `meant2hit` and `PSofTarget` columns contain respectively the gene locus the probe set was designed to target and the probe set ID of the off-target Y, according to Affymetrix (extracted from ATH1-121501\\_annot.csv). The `peCC` column holds the pairs' Pearson correlation coefficient calculated on their expression intensities in the Tissue dataset (data originally from AtgenExpress Project).

`AffysTissue` is data.frame that contains all Affymetrix' CDF's probe set pairs with  $Q75 \geq 55$ . `AffysTissueMC` holds a subset of the pairs in `AffysTissue`, namely those whose metacorrelation coefficient is not NA are included. For `AffysTissue.noBl`, the pairs of `AffysTissue` that align to each other with BLAST in at least one direction with an E-value smaller than  $10^{-10}$  were omitted.

**Author(s)**

Tineke Casneuf <tine@ebi.ac.uk>

**References**

Casneuf, Van de Peer and Huber, AtgenExpress data used: Schmid, M., Davison, T. S., Henz, S. R., Pape, U. J., Demar, M., Vingron, M. Schoelkopf, B. Weigel, D., and Lohmann, J. (2005) A gene expression map of Arabidopsis development. *Nature Genetics*, 37, 501-506.

**See Also**

[CustomsTissue](#)

**Examples**

```
data(AffysTissue)
data(AffysTissueMC)
data(AffysTissue.noBl)

## see also the vignette
```

---

CustomsTissue

*Custom-made CDF's probe set pairs*

---

**Description**

Custom-made CDF's probe set pairs

**Usage**

```
data(CustomsTissue)
data(CustomsTissueMC)
data(CustomsTissue.noBl)
```

**Format**

These three data.frames contain data for the custom-made CDF's probe set pairs with  $Q75 \geq 55$ . The `pr` and `target` columns hold the names of probe set X and Y, respectively. Column `a1Sum` contains the  $Q75$  value of the alignment scores of X's reporters to the transcript of Y. The `peCC` column holds the pairs' Pearson correlation coefficient calculated on their expression intensities in the Tissue dataset (data originally from AtgenExpress Project).

`CustomsTissue` is data.frame that contains all custom-made CDF's probe set pairs with  $Q75 \geq 55$ . `CustomsTissueMC` holds a subset of the pairs in `CustomsTissue`, namely those whose metacorrelation coefficient is not NA are included. For `CustomsTissue.noBl`, the pairs of `CustomsTissue` that align to each other with BLAST in at least one direction with an E-value smaller than  $10^{-10}$  were omitted.

**Author(s)**

Tineke Casneuf <tine@ebi.c.uk>

**References**

Casneuf, Van de Peer and Huber, AtgenExpress data used: Schmid, M., Davison, T. S., Henz, S. R., Pape, U. J., Demar, M., Vingron, M. Schoelkopf, B. Weigel, D., and Lohmann, J. (2005) A gene expression map of Arabidopsis development. *Nature Genetics*, 37, 501-506.

**See Also**

[AffysTissue](#)

**Examples**

```
data(CustomsTissue)
data(CustomsTissueMC)
data(CustomsTissue.noBl)

## see also the vignette
```

---

ex1

*Cross-hybridisation example*

---

**Description**

Cross-hybridisation example

**Usage**

```
data(ex1)
data(ex2)
data(ex3)
```

**Format**

These objects contain the data of three examples of cross-hybridisation.

**Author(s)**

Tineke Casneuf <tine@ebi.ac.uk>

**References**

Casneuf, Van de Peer and Huber. Submitted.

**Examples**

```
data(ex1)
data(ex2)
data(ex3)

plotExample(ex1)
plotExample(ex2)
plotExample(ex3)
```

```
## see also the vignette
```

---

runSimulation

*Cross-hybridisation simulation*

---

**Description**

Cross-hybridisation simulation

**Usage**

```
runSimulation()
```

**Format**

runSimulation is a function that will run the simulation we ran for our study. By modifying the parameters, users can play with it themselves.

**Author(s)**

Tineke Casneuf <tine@ebi.ac.uk>

**References**

Casneuf, Van de Peer and Huber (Submitted).

**Examples**

```
runSimulation()
```

```
## see also the vignette
```

---

XhybExamples-class      *Class "XhybExamples"*

---

**Description**

Class containing information of cross-hybridisation examples

**Objects from the Class**

Objects can be created by calls of the form `new("XhybExamples", ...)`.

**Slots**

X: Object of class "character" contains the ID of probe set X

Y: Object of class "character" contains the ID of probe set Y

IVX: Object of class "numeric" contains the expression intensities of X in the Tissue dataset

IVY: Object of class "numeric" contains the expression intensities of Y in the Tissue dataset

IVXi: Object of class "matrix" contains the expression intensities of X's reporters in the Tissue dataset

ai: Object of class "numeric" contains the alignment scores of X's reporters to Y's transcript sequence

**Methods**

**plotExample** signature(ex = "XhybExamples"): ...

**Author(s)**

Tineke Casneuf <tine@ebi.ac.uk>

**References**

Casneuf, Van de Peer and Huber (submitted); AtgenExpress data used: Schmid, M., Davison, T. S., Henz, S. R., Pape, U. J., Demar, M., Vingron, M. Schoelkopf, B. Weigel, D., and Lohmann, J. (2005) A gene expression map of Arabidopsis development. *Nature Genetics*, 37, 501-506.

**Examples**

```
data(ex1)
data(ex2)
data(ex3)
plotExample(ex1)
plotExample(ex2)
plotExample(ex3)
```

# Index

## \*Topic **classes**

XhybExamples-class, 5

## \*Topic **datasets**

AffysTissue, 1

CustomsTissue, 2

ex1, 3

## \*Topic **manip**

runSimulation, 4

AffysTissue, 1, 3

AffysTissueMC (AffysTissue), 1

CustomsTissue, 2, 2

CustomsTissueMC (CustomsTissue), 2

ex1, 3

ex2 (ex1), 3

ex3 (ex1), 3

plotExample (XhybExamples-class), 5

plotExample, XhybExamples-method  
(XhybExamples-class), 5

runSimulation, 4

XhybExamples-class, 5