

# Package ‘XhybCasneuf’

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

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**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

**NeedsCompilation** no

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AffysTissue	<i>Affymetrix' CDF probe set pairs</i>
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## 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 >= 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 meant2hit and PSoftTarget 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 >= 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
```

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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
```

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XhybExamples-class      *Class "XhybExamples"*

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**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)
```

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