

# XhybCasneuf

October 5, 2010

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`AffysTissue`

*Affymetrix' CDF probe set pairs*

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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  $Q75 \geq 55$ . 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
```

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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 `alSum` 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
```

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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)
```

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*

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**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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