

Package ‘XhybCasneuf’

December 2, 2025

Version 1.48.0
Date 2007-06-21
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
git_url <https://git.bioconductor.org/packages/XhybCasneuf>
git_branch RELEASE_3_22
git_last_commit cd755c7
git_last_commit_date 2025-10-29
Repository Bioconductor 3.22
Date/Publication 2025-12-02

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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 ≥ 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 ≥ 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 ≥ 55 . CustomsTissueMC holds a subset of the pairs in CustomsTissue, namely those whose metacorre-lation 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	<i>Cross-hybridisation example</i>
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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	<i>Cross-hybridisation simulation</i>
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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
```

XhybExamples-class	<i>Class "XhybExamples"</i>
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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

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

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