Package ‘XhybCasneuf’

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Title EBI/PSB cross-hybridisation study package

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RColorBrewer , methods, grid

Description Cross-hybridisation study on the ATH1 Affymetrix GeneChip

biocViews ExperimentData, Tissue, MicroarrayData, TissueMicroarrayData

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Contents

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 `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 >= 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)

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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 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)

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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