Package ‘XhybCasneuf’

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License Artistic-2.0
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R topics documented:

AffysTissue Affymetrix’ CDF probe set pairs

Description

Affymetrix’ CDF probe set pairs

Usage

data(AffysTissue)
data(AffysTissueMC)
data(AffysTissue.noBl)
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**


**See Also**

CustomsTissue

**Examples**

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

## see also the vignette
```

## Custom-made CDF’s probe set pairs

**Description**

Custom-made CDF’s probe set pairs

**Usage**

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


See Also

AffysTissue

Examples

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

### see also the vignette

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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
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

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