Package ‘XhybCasneuf’

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### Description

Affymetrix' CDF probe set pairs

### Usage

```r
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 `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)

Tineke Casneuf <tine@ebi.ac.uk>

### References


### See Also

- [CustomsTissue](#)

### Examples

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

```r
## see also the vignette
```
CustomsTissue

---

CustomsTissue  
Custom-made CDF's probe set pairs

Description

Custom-made CDF's probe set pairs

Usage

```r
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)

Tineke Casneuf <tine@ebi.c.uk>

References


See Also

AffysTissue

Examples

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

## see also the vignette
```
**runSimulation**

---

**ex1**

*Cross-hybridisation example*

---

**Description**

Cross-hybridisation example

**Usage**

```r
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**

```r
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

class 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"

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

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data(ex2)
data(ex3)
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plotExample(ex2)
plotExample(ex3)
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