Package ‘XhybCasneuf’

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AffysTissue

Affymetrix’ CDF probe set pairs

**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 `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)**

Tineke Casneuf <tine@ebi.ac.uk>

**References**


**See Also**

`CustomsTissue`

**Examples**

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

```r
## see also the vignette
```
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.ac.uk>

References


See Also

*AffysTissue*

Examples

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

## see also the vignette
## 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

## 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()
```

```r
## 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


Examples

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