Package 'Fletcher2013a'

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Title Gene expression data from breast cancer cells under FGFR2 signalling perturbation

Version 1.44.0

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Description The package Fletcher2013a contains time-course gene expression data from MCF-7 cells treated under different experimental systems in order to perturb FGFR2 signalling. The data comes from Fletcher et al. (Nature Comms 4:2464, 2013) where further details about the background and the experimental design of the study can be found.

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Depends R (>= 2.15), limma

Imports Biobase ,VennDiagram, gplots,grid

License GPL (>= 2)

biocViews ExperimentData, ExpressionData, CancerData, BreastCancerData, MicroarrayData

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`Exp1` *Exp1 dataset: endogenous FGFRs experiments.*

Description

The data consists of 46 microarray samples from MCF-7 cells treated under different conditions, at 3 time points (0, 6 and 24 h). The data have been normalized (RMA algorithm) and are presented in the form of an `exprSet` object. The experiment was carried out on 4 Humanv4 arrays using 12 samples per array. The original arrays contain 48324 features, with an average of 22 beads per feature (Standard Deviation of 5). Additional description about sample groups can be retrieved from `phenoData` slot (see examples).

Usage

```
data(Exp1)
```

Format

The format is: An `ExpressionSet` object with covariates representing experimental conditions:

- `Sample`: Sample IDs.
- `Time`: Treatment time.
- `Replicates`: Biological replicates (numerical sequence).
- `UT`: Control group (vehicle).
- `E2`: E2 treatment group.
- `E2FGF10`: E2+FGF10 treatment group.
- `E2FGF10PD`: E2+FGF10+PD173074 treatment group.
- `Treatment`: Group names.
- `TreatmentGroups`: Group names with common starting point.
- `Target`: Group names for differential expression analysis (e.g. targets for limma). The corresponding constrasts can be retrived by `notes(Exp1)`.

Note

The differential expression analysis documented in the vignette is available at 'Exp1limma'.

Source

Michael NC Fletcher, Mauro AA Castro, Suet-Feung Chin, Oscar Rueda, Xin Wang, Carlos Caldas, Bruce AJ Ponder, Florian Markowetz, Kerstin B Meyer. Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 4:2464, 2013.

Examples

```
data(Exp1)
#gexp<-exprs(Exp1)
#geneids<-fData(Exp1)
#targets<-pData(Exp1)
#mycontrasts<-notes(Exp1)$contrasts

#limma pre-processed dataset
#data(Exp1limma)
```

Exp2 *Exp2 dataset: iF2 construct experiments.*

Description

The data consists of 71 microarray samples from MCF-7 cells treated under different conditions, at 3 time points (0, 6 and 24 h). The data have been normalized (RMA algorithm) and are presented in the form of an `exprSet` object. The experiment was carried out on 6 Humanv4 BeadChips using 12 samples per BeadChip. The original arrays contain 48324 features, with a mean of 22 beads per feature (Standard Deviation of 5). Additional description about sample groups can be retrieved from `phenoData` slot (see examples).

Usage

```
data(Exp2)
```

Format

The format is: An `ExpressionSet` object with covariates representing experimental conditions:

- `Sample`: Sample IDs.
- `Time`: Treatment time.
- `Replicates`: Biological replicates (numerical sequence).
- `UT`: Control group (vehicle).
- `E2`: E2 treatment group.
- `E2.AP20187`: E2+AP20187 treatment group.
- `E2.AP20187.PD`: E2+AP20187+PD173074 treatment group.
- `E2.FGF10`: E2+FGF10 treatment group.
- `Treatment`: Group names.
- `TreatmentGroups`: Group names with common starting point.
- `Target`: Group names for differential expression analysis (e.g. targets for limma). The corresponding constrasts can be retrived by `notes(Exp2)`.
- `TecRep`: Technical replicates.
- `isOriginal`: Simple vector mapping all samples (excluding technical replicates).

Note

The differential expression analysis documented in the vignette is available at 'Exp2limma'.

Source

Michael NC Fletcher, Mauro AA Castro, Suet-Feung Chin, Oscar Rueda, Xin Wang, Carlos Caldas, Bruce AJ Ponder, Florian Markowetz, Kerstin B Meyer. Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 4:2464, 2013.

Examples

```
data(Exp2)
#gexp<-exprs(Exp2)
#geneids<-fData(Exp2)
#targets<-pData(Exp2)
#mycontrasts<-notes(Exp2)$contrasts

#limma pre-processed dataset
#data(Exp2limma)
```

`Exp3` *Exp3 dataset: FGFR2b over-expression experiments.*

Description

The data consists of 125 microarray samples from MCF-7 cells treated under different conditions, at 5 time points (0, 3, 6, 12 and 24 h). The data have been normalized (RMA algorithm) and are presented in the form of an `exprSet` object. The experiment was carried out on 11 Humanv4 BeadChips using 12 samples per BeadChip. The original arrays contains 48324 features, with a mean of 22 beads per feature (Standard Deviation of 5). Additional description about sample groups can be retrieved from `phenoData` slot (see examples).

Usage

```
data(Exp3)
```

Format

The format is: An `ExpressionSet` object with covariates representing experimental conditions:

- `Sample`: Sample IDs.
- `Group`: Major experimental groups (MinusTet and PlusTet).
- `Time`: Treatment time.
- `Replicates`: Biological replicates (numerical sequence).
- `MinusTet.UT`: Control group (vehicle for MinusTet group).
- `MinusTet.E2`: E2 treatment group.

- `MinusTet.E2.FGF10`: E2+FGF10 treatment group.
- `PlusTet.UT`: Control group (vehicle for PlusTet group).
- `PlusTet.E2`: E2 treatment group.
- `PlusTet.E2.FGF10`: E2+FGF10 treatment group.
- `Treatment`: Group names (treatments).
- `Target`: Group names for differential expression analysis (e.g. targets for limma). The corresponding constrasts can be retrived by `notes(Exp3)`.

Note

The differential expression analysis documented in the vignette is available at 'Exp3limma'.

Source

Michael NC Fletcher, Mauro AA Castro, Suet-Feung Chin, Oscar Rueda, Xin Wang, Carlos Caldas, Bruce AJ Ponder, Florian Markowetz, Kerstin B Meyer. Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 4:2464, 2013.

Examples

```
data(Exp3)
#gexp<-exprs(Exp3)
#geneids<-fData(Exp3)
#targets<-pData(Exp3)
#mycontrasts<-notes(Exp3)$contrasts

#limma pre-processed dataset
#data(Exp3limma)
```

Fletcher2013a.pipelines

A pipeline to reproduce results for Fletcher et al. 2013.

Description

Pipeline functions to reproduce results in Fletcher et al. 2013.

Usage

```
Fletcher2013pipeline.limma(exprSet, par=list(method="global", adjust.method="BH", p.value=1e-2, lfc=
Fletcher2013pipeline.pca(exprSet)
Fletcher2013pipeline.deg(what="Exp1", idtype="probeid", response="all", mode="all")
Fletcher2013pipeline.supp()
```

Arguments

exprSet	Any ExpressionSet object available in the package Fletcher2013a: Exp1, Exp2 and Exp3.
par	a list with parameters for limma analysis (see decideTests) for details.
what	a single character value specifying an experimental system: "Exp1", "Exp2" or "Exp3".
idtype	a single character value specifying a signature report option: "probeid" or "entrez".
response	a single character value specifying how signatures should be consolidated across time points: "early", "late" or "all". (see Details for a detailed time-course dataset).
mode	a single character value specifying how signatures should be consolidated regarding the mode of action: "positive", "negative" or "all". (see Details for a detailed time-course dataset).

Details

These functions reproduce results of the differential expression analysis in Fletcher et al., 2013:

(1) Fletcher2013pipeline.limma: main function to run the limma analysis on the gene expression datasets.

(2) Fletcher2013pipeline.pca: complementary function to run a principal components analysis on the gene expression datasets.

(3) Fletcher2013pipeline.deg: function to extract retults computed in Fletcher2013pipeline.limma. Usefull to retrieve consolidated gene lists from the differential expression analyses. For detailed time-course information, please use the full pre-processed datasets Exp1limma, Exp2limma and Exp3limma.

(4) Fletcher2013pipeline.supp: this function generates additional figures for the vignette.

Value

All results will be saved in the current work directory.

Author(s)

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Source

Michael NC Fletcher, Mauro AA Castro, Suet-Feung Chin, Oscar Rueda, Xin Wang, Carlos Caldas, Bruce AJ Ponder, Florian Markowetz, Kerstin B Meyer. Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 4:2464, 2013.

Examples

```
## Not run:
data(Exp1)
#Fletcher2013pipeline.limma(Exp1)
#Fletcher2013pipeline.pca(Exp1)

## End(Not run)
```

---

siESR1 *Knockdown dataset: siESR1 in MCF-7 cells.*

Description

The data consists of 6 microarray samples after knocking down ESR1 in MCF-7 cells, retrived from GEO dataset (Series GSE18431). The data have been normalized (quantile normalization and log2 transformatoin) as described in the orifinal dataset, and are presented here in the form of an `exprSet` object.

Usage

```
data(siESR1)
```

Format

The format is: An `ExpressionSet` object with covariates representing experimental conditions:

- `Sample`: Sample IDs
- `Target`: Group names for differential expression analysis (e.g. targets for limma). The corresponding constrasts can be retrived by `notes(siESR1)`

Note

The differential expression analysis documented in the vignette is available at 'siESR1limma'.

Source

Park YY, Kim K, Kim SB, Hennessy BT et al. Reconstruction of nuclear receptor network reveals that NR2E3 is a novel upstream regulator of ESR1 in breast cancer. EMBO Mol Med 2012 Jan;4(1):52-67.

Examples

```
data(siESR1)
#notes(siESR1)

#limma pre-processed dataset
#data(siESR1limma)
```

siOTHERS *Knockdown dataset: siPTTG1, siSPDEF, siE2F2 and siELF3 in MCF-7 cells.*

Description

The data consists of 30 microarray samples after knocking down PTTG1, SPDEF, E2F2 or ELF3 in MCF-7 cells. The data have been normalized (RMA algorithm) and are presented in the form of an `exprSet` object. The experiment was carried out on 3 Humanv4 BeadChips using 30 arrays (1 samples per BeadChip). These arrays interrogate 48107 randomly-distributed bead-types, and in this experiment there was a mean of 22 beads per bead-type (Standard Deviation of 5). In total, there are 21642 genes being interrogated, with 7872 genes being interrogate by more than one bead-type and 13167 bead-types not being assigned to a gene symbol.

Usage

```
data(siOTHERS)
```

Format

The format is: An `ExpressionSet` object with covariates representing experimental conditions:

- `Sample`: Sample IDs.
- `Target`: Group names for differential expression analysis (e.g. targets for limma). The corresponding constrasts can be retrived by `notes(siOTHERS)`.

Note

The differential expression analysis documented in the vignette is available at 'siOTHERSlimma'.

Source

Michael NC Fletcher, Mauro AA Castro, Suet-Feung Chin, Oscar Rueda, Xin Wang, Carlos Caldas, Bruce AJ Ponder, Florian Markowetz, Kerstin B Meyer. Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 4:2464, 2013.

Examples

```
data(siOTHERS)
#notes(siOTHERS)

#limma pre-processed dataset
#data(siOTHERSlimma)
```

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