Package ‘Fletcher2013b’

February 1, 2017

Title Master regulators of FGFR2 signalling and breast cancer risk.

Version 1.10.0

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Description This package reproduces the systems biology analysis for the data in package Fletcher2013a using RTN.

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Depends R (>= 2.15), Fletcher2013a, RTN (>= 1.1.2), RedeR (>= 1.8.1), igraph

Imports RColorBrewer

License GPL (>= 2)

biocViews ExperimentData, ChIPSeqData, CancerData, BreastCancerData, SNPData

URL http://dx.doi.org/10.1038/ncomms3464

InstallableEverywhere yes

NeedsCompilation no

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Fletcher2013b.gsea.regulons

Supplementary GSEA analyses to reproduce results for Fletcher et al. 2013.

Description

Supplementary functions to reproduce results for Fletcher et al. 2013.

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Usage

Fletcher2013gsea.regulons(what = "Exp1", timepoint = 6, verbose = TRUE)

Arguments

what
a single character value specifying one of the experimental systems implemented in the study (Options: 'Exp1', 'Exp2', and 'Exp3').

timepoint
a single integer value specifying a timepoint of the experimental system (Options: 6 or 24).

verbose
a single logical value specifying to display detailed messages (when verbose=TRUE) or not (when verbose=FALSE).

Value

All results will be saved in the current work directory.

Author(s)

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Source


Examples

## Not run:
Fletcher2013gsea.regulons(what="Exp1")
## End(Not run)
Arguments

- **hits**: a character vector of gene identifiers for those considered as hits (see TNA-class).
- **minRegulonSize**: a single integer or numeric value specifying the minimum number of elements in a regulon that must map to elements of the gene universe (see tna.mra).
- **idtype**: a single character value specifying the input gene id (Options: 'probeid' or 'entrez').
- **pAdjustMethod**: a single character value specifying the p-value adjustment method to be used (see p.adjust for details).
- **tnet**: a single character value specifying which transcriptional network should to used to compute the MRA analysis. Options: "dpi" and "ref".
- **eps**: a single numeric value specifying the threshold under which Aracne algorithm should apply the dpi filter (see tni.dpi.filter).
- **pValueCutoff**: a single numeric value specifying the cutoff for p-values considered significant.
- **verbose**: a single logical value specifying to display detailed messages (when verbose=TRUE) or not (when verbose=FALSE).
- **...**: other arguments passed to the RTN package.

Value

All results will be saved in the current work directory.

Author(s)

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Source


Examples

```r
## Not run:
hits <- Fletcher2013pipeline.deg(what="Exp1")
mra1 <- Fletcher2013pipeline.mra1st(hits=hits$E2FGF10)

## End(Not run)```
Description

Different data sets used to produce a variety of analyses and figures in Fletcher et al., 2013.

Usage

data(miscellaneous)

Format

A set of miscellaneous data objects:

- **risksites**: a data.frame with top 1385 risk SNPs derived from UK2 GWAS study for breast cancer (mapped to genome assembly NCBI36/hg18).
- **randsites**: a data.frame with random SNPs derived from Affy SNP-6 array (sites mapped to hg19).
- **chromlen**: a vector listing human chromosome length (genome assembly NCBI36/hg18).
- **ESR1bdsites**: a data.frame listing ChIP-seq ESR1 binding sites in MCF-7 cells (mapped to genome assembly NCBI36/hg18).
- **FOXA1bdsites**: a data.frame listing ChIP-seq FOXA1 binding sites in MCF-7 cells (mapped to genome assembly NCBI36/hg18).
- **GATA3bdsites**: a data.frame listing ChIP-seq GATA3 binding sites in MCF-7 cells (mapped to genome assembly NCBI36/hg18).
- **SPDEFbdsites**: a data.frame listing ChIP-seq SPDEF binding sites in MCF-7 cells (mapped to genome assembly NCBI36/hg18).
- **fimoESR1**: a list with ESR1 motifs mapped across the human genome. TRANSFAC PWM was used as input for the FIMO DNA motif identification tool, Grant et al., 2011 (mapped to hg19).
- **fimoFOXA1**: a list with FOXA1 motifs mapped across the human genome. TRANSFAC PWM was used as input for the FIMO DNA motif identification tool, Grant et al., 2011 (mapped to hg19).
- **fimoGATA3**: a list with GATA3 motifs mapped across the human genome. TRANSFAC PWM was used as input for the FIMO DNA motif identification tool, Grant et al., 2011 (mapped to hg19).
- **metaPCNA**: a vector listing genes from the metaPCNA proliferation-based gene signature (Venet, D. et al., 2011).
- **consensus**: a list with consensus breast cancer master regulators described in Fletcher et al., 2013.
- **tfs**: a vector listing the transcription factors used to compute the transcriptional networks `rtni1st`, `rtni2nd`, `rtniNormals` and `rtniTALL`.

Details

ChIP-seq datasets are representative of 3 independent experiments, with peaks overlapping in at least 2 out of 3 replicates (taking one as reference). All peaks are provided related to the summit positions (+- 35 bp), including peak height and significance (in the form of $-10 \times \log_{10}(pvalue)$). Additional details about this and the other datasets are provided in the vignette.
Source


Examples

data(miscellaneous)

rtini.data

Transcriptional network datasets.

Description

The datasets consist of a transcriptional networks computed by the package RTN.

Usage

data(rtini1st)
data(rtini2nd)
data(rtiniNormals)
data(rtiniTALL)

Format

A set of TNI objects:

- rtiniTALL: A TF-centric network based non-breast cancer gene expression profiles, derived from T-cell acute lymphoblastic leukaemia (Van Vlierberghe, P. et al.).
- rtiniIDs: A data.frame with gene ids.

Source


siRNA

Dataset from siRNA experiments used to reproduce results in Fletcher et al., 2012.

Description
The data consists of differentially expressed genes in MCF-7 cells after knockdown experiments.

Usage
data(siRNA)

Format
A list object:
- siRNA$ESR1: differentially expressed genes in MCF-7 cells after knocking down ESR1 gene.
- siRNA$SPDEF: differentially expressed genes in MCF-7 cells after knocking down SPDEF gene.
- siRNA$PTTG1: differentially expressed genes in MCF-7 cells after knocking down PTTG1 gene.

Note
The differential expression analysis is documented in the package 'Fletcher2013a', and row gene expression data is available at siOTHERS and siESR1.

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