Package ‘Fletcher2013b’

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Title Master regulators of FGFR2 signalling and breast cancer risk
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Description This package reproduces the systems biology analysis for the data in package Fletcher2013a using RTN.
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A pipeline to reproduce results for Fletcher et al. 2013.

Description

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

Usage

Fletcher2013pipeline.mra1st(hits, minRegulonSize=20, idtype="probeid", pAdjustMethod="holm", tnet="dpi", eps=0, pValueCutoff=1e-4, verbose=TRUE, ...)
Fletcher2013pipeline.mra2nd(hits, minRegulonSize=20, idtype="probeid", pAdjustMethod="holm", tnet="dpi", eps=0, pValueCutoff=1e-4, verbose=TRUE, ...)
Fletcher2013pipeline.mraNormals(hits, minRegulonSize=20, idtype="probeid", pAdjustMethod="holm", tnet="dpi", eps=0, pValueCutoff=1e-4, verbose=TRUE, ...)
Fletcher2013pipeline.mraTALL(hits, minRegulonSize=20, idtype="probeid", pAdjustMethod="holm", tnet="dpi", eps=0, pValueCutoff=0.01, verbose=TRUE, ...)
Fletcher2013pipeline.consensusnet()
Fletcher2013pipeline.enrichmap()

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)
```

miscellaneous

Miscellaneous datasets.

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*log10(pvalue)). Additional details about this and the other datasets are provided in the vignette.

### Source


### Examples

```r
data(miscellaneous)
```

---

### Description

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

### Usage

```r
data(rtni1st)
data(rtni2nd)
data(rtniNormals)
data(rtniTALL)
```
siRNA

Format
A set of TNI objects:

• rtniNormals: A TF-centric network based on normal breast gene expression profiles (Curtis, C. et al).
• rtniTALL: A TF-centric network based non-breast cancer gene expression profiles, derived from T-cell acute lymphoblastic leukaemia (Van Vlierberghe, P. et al.).
• rtniIDs: A data.frame with gene ids.

Source

Examples

data(rtni1st)

| 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`.

**Source**


**Examples**

```r
data(siRNA)
```
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