Package ‘Fletcher2013b’

April 2, 2024

Title Master regulators of FGFR2 signalling and breast cancer risk
Version 1.38.0
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Description This package reproduces the systems biology analysis for the data in pack-
age 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
git_url https://git.bioconductor.org/packages/Fletcher2013b
git_branch RELEASE_3_18
git_last_commit 40748fb
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-04-02

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Fletcher2013b.pipelines

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)
Mauro Castro <mauro.a.castro@gmail.com>
Source


Examples

```r
## Not run:
hits <- Fletcher2013pipeline.deg(what="Exp1")
mral1 <- Fletcher2013pipeline.mralst(hits=hits$E2FGF10)
## End(Not run)
```

miscellaneous

**Miscellaneous datasets.**

Description

Diferent 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).
rtni.data

- 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

data(miscellaneous)

data(rtni.data)  

Description

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

Usage

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

data(siRNA)
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