

# Package ‘Fletcher2013b’

December 11, 2025

**Title** Master regulators of FGFR2 signalling and breast cancer risk

**Version** 1.46.0

**Author** Mauro Castro, Michael Fletcher, Florian Markowetz and Kerstin Meyer.

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

**Maintainer** Mauro Castro <mauro.a.castro@gmail.com>

**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\_22

**git\_last\_commit** 85a698b

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2025-12-11

## Contents

|                                   |          |
|-----------------------------------|----------|
| Fletcher2013b.pipelines . . . . . | 2        |
| miscellaneous . . . . .           | 3        |
| rtni.data . . . . .               | 4        |
| siRNA . . . . .                   | 5        |
| <b>Index</b>                      | <b>7</b> |

---

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 <a href="#">TNA-class</a> ).                                                                   |
| 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 <a href="#">tna.mra</a> ). |
| 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 <a href="#">p.adjust</a> for details).                                                |
| tnet           | a single character value specifying which transcriptional network should be 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 <a href="#">tni.dpi.filter</a> ).                         |
| 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**

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:
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 ( $\pm 35$  bp), including peak height and significance (in the form of  $-10 \cdot \log_{10}(\text{pvalue})$ ). Additional details about this and the other datasets are provided in the vignette.

## 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.

Grant CE, Bailey TL, Noble WS: FIMO: scanning for occurrences of a given motif. *Bioinformatics*, 27(7):1017-1018, 2011.

Venet, D., Dumont, J.E. & Detours, V. Most random gene expression signatures are significantly associated with breast cancer outcome. *PLoS Comput Biol*, 7:e1002240, 2011.

## Examples

```
data(miscellaneous)
```

---

rtni.data

*Transcriptional network datasets.*

---

## Description

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

## Usage

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

## Format

A set of TNI objects:

- `rtni1st`: A TF-centric network based on 2000 breast cancer gene expression profiles - Cohort I (Curtis, C. et al).
- `rtni2nd`: A TF-centric network based on 2000 breast cancer gene expression profiles - Cohort II (Curtis, C. et al).

- `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

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.

Curtis, C. et al. The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature*, 486:346-52, 2012.

Van Vlierberghe, P. et al. ETV6 mutations in early immature human T cell leukemias. *J Exp Med*, 208:2571-9, 2011.

### Examples

```
data(rtni1st)
```

---

|       |                                                                                           |
|-------|-------------------------------------------------------------------------------------------|
| siRNA | <i>Dataset from siRNA experiments used to reproduce results in Fletcher et al., 2012.</i> |
|-------|-------------------------------------------------------------------------------------------|

---

### 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

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(siRNA)
```

# Index

## \* datasets

- [miscellaneous](#), [3](#)
  - [rtnei.data](#), [4](#)
  - [siRNA](#), [5](#)
- [chromlen \(miscellaneous\)](#), [3](#)
- [consensus \(miscellaneous\)](#), [3](#)
- [ESR1bdsites \(miscellaneous\)](#), [3](#)
- [fimoESR1 \(miscellaneous\)](#), [3](#)
- [fimoFOXA1 \(miscellaneous\)](#), [3](#)
- [fimoGATA3 \(miscellaneous\)](#), [3](#)
- [Fletcher2013b](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013b.pipelines](#), [2](#)
- [Fletcher2013pipeline.consensusnet](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013pipeline.enrichmap](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013pipeline.mra1st](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013pipeline.mra2nd](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013pipeline.mraNormals](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [Fletcher2013pipeline.mraTALL](#)
  - [\(Fletcher2013b.pipelines\)](#), [2](#)
- [FOXA1bdsites \(miscellaneous\)](#), [3](#)
- [GATA3bdsites \(miscellaneous\)](#), [3](#)
- [metaPCNA \(miscellaneous\)](#), [3](#)
- [miscellaneous](#), [3](#)
- [p.adjust](#), [2](#)
- [randsites \(miscellaneous\)](#), [3](#)
- [risksites \(miscellaneous\)](#), [3](#)
- [rtnei.data](#), [4](#)
- [rtnei1st](#), [4](#)
- [rtnei1st \(rtnei.data\)](#), [4](#)
- [rtnei2nd](#), [4](#)
- [rtnei2nd \(rtnei.data\)](#), [4](#)
- [rtneiIDs \(rtnei.data\)](#), [4](#)
- [rtneiNormals](#), [4](#)
- [rtneiNormals \(rtnei.data\)](#), [4](#)
- [rtneiTALL](#), [4](#)
- [rtneiTALL \(rtnei.data\)](#), [4](#)
- [siESR1](#), [5](#)
- [siOTHERS](#), [5](#)
- [siRNA](#), [5](#)
- [SPDEFbdsites \(miscellaneous\)](#), [3](#)
- [tfs \(miscellaneous\)](#), [3](#)
- [tna.mra](#), [2](#)
- [tni.dpi.filter](#), [2](#)