Package 'triform'

October 30, 2019

Type Package

Title Triform finds enriched regions (peaks) in transcription factor
ChIP-sequencing data

Version 1.29.0

Date 2016-02-11

Encoding UTF-8

Depends R (>= 2.11.0), IRanges, yaml

Imports BiocGenerics, IRanges (>= 2.5.27), yaml

Suggests RUnit

Description The Triform algorithm uses model-free statistics to
identify peak-like distributions of TF ChIP sequencing reads,
taking advantage of an improved peak definition in combination
with known profile characteristics.

License GPL-2

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biocViews Sequencing, ChIPSeq

git_url https://git.bioconductor.org/packages/triform

git_branch master

git_last_commit 706e658

git_last_commit_date 2019-10-29

Date/Publication 2019-10-29

R topics documented:

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triform-package   *Triform finds peaks in ChIP-sequencing data.*

Description

The Triform method uses model-free statistics to identify peak-like distributions of sequencing reads, taking advantage of an improved peak definition in combination with known profile characteristics.

Details

Package:	triform
Type:	Package
Version:	1.0
Date:	2012-06-01
License:	GPL-3

It is recommended to make a configuration file in YAML format first. Then run functions "preprocess" and "triform" to find peaks in BED-formatted ChIP-sequencing data.

Author(s)

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Examples

```
## Not run:
preprocess("./config.yml")
triform("./config.yml")

## End(Not run)
```

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preprocess   *Preprocess BED-files with reads to calculate chromosome coverage*

Description

Given a directory with BED-files describing ChIP-seq reads, makes coverage files (1 pr chromosome) describing tag counts along the chromosomes. Reads in all available BED-files in the given directory is first converted to IRanges objects and saved as RData files. The preprocessing ends by creating one file for each chromosome, with the calculated coverage on the different strands for different BED-files.

Usage

```
preprocess(configPath = "./config.yml", params=list())
```

Arguments

`configPath`	Path to a configuration file in YAML format (see config.yml), or NULL.
`params`	A list of parameters (see details).

Details

The preprocess function computes the chromosome tag-coverage along each chromosome. Parameters supplied in params can include the following:

- READ.PATH Path to BED files with reads.
- COVER.PATH Path for coverage files (preprocessing output).
- READ.WIDTH Read width (w)

Value

Used for its side-effect.

Author(s)

Karl Kornacker <<kornacker@midohio.twcbc.com>> and Tony Handstad <<tony.handstad@gmail.com>>

Examples

```
## Not run:
# Run preprocessing using a configuration file in YAML format:
preprocces(configPath = "./config.yml")

# Run preprocessing without using a configuration file:
preprocces(configPath = NULL, params=list(READ.PATH="./tmp",
          COVER.PATH="./chrcovers", READ.WIDTH=100))

## End(Not run)
```

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triform	*Run Triform peak detection algorithm.*

Description

Runs Triform according to configuration file or given parameters.
Triform uses chromosome coverage files prepared by the preprocessing function.

Usage

```
triform(configPath = "./config.yml", params=list())
```

Arguments

`configPath`	Path to a configuration file in YAML format, or NULL.
`params`	A list of parameters values (see details)

Details

If configPath is NULL, all the other arguments must be supplied in params.
Values in params will overwrite values as set in the configuration file. The following list explains
the parameters for the triform algorithm:

- COVER.PATH Path for coverage files (from preprocessing).
- OUTPUT.PATH Path for output file.
- TARGETS Filenames for TF experiments. (Named according to replicate, i.e. myTF_rep1.bed
  for replicate 1.
- CONTROLS Filnames for control experiments (Named according to replicate).
- MAX.P Minimum p-value, used to calculate min.z
- MIN.WIDTH Minimum peak width (min.n)
- MIN.QUANT Quantile of enrichment ratios, used to calculate min.er
- MIN.SHIFT Minimum inter-strand lag between peak coverage distributions.
- FLANK.DELTA Fixed spacing between central and flanking locations.
- CHRS A list of chromosomes to be processed.

Value

Output is saved to the outputpath.

Author(s)

Karl Kornacker <<kornacker@midohio.twcbc.com>> and Tony Handstad <<tony.handstad@gmail.com>>

See Also

preprocess

Examples

```
## Not run:
# Run Triform with configuration file:
triform(configPath = "./config.yml")

# Run Triform with arguments instead of configuration file:
triform(configPath=NULL, params=list(COVER.PATH = "./chrcovers",
       OUTPUT.PATH = "./Triform_output.csv",
       CONTROLS = c("backgr_huds_Gm12878_rep1", "backgr_huds_Gm12878_rep2"),
       TARGETS = c("srf_huds_Gm12878_rep1", "srf_huds_Gm12878_rep2"),
       MAX.P = 0.1, MIN.WIDTH = 10, MIN.QUANT = 0.375, MIN.SHIFT = 10,
       FLANK.DELTA = 150, CHRS = c("chrY")))

## End(Not run)
```

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