

Package: target (via r-universe)

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Type Package

Title Predict Combined Function of Transcription Factors

Version 1.19.0

Description Implement the BETA algorithm for inferring direct target genes from DNA-binding and perturbation expression data Wang et al. (2013) <[doi:10.1038/nprot.2013.150](https://doi.org/10.1038/nprot.2013.150)>. Extend the algorithm to predict the combined function of two DNA-binding elements from comparable binding and expression data.

URL <https://github.com/MahShaaban/target>

BugReports <https://github.com/MahShaaban/target/issues>

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 3.6)

Imports BiocGenerics, GenomicRanges, IRanges, matrixStats, methods, stats, graphics, shiny

Suggests testthat (>= 2.1.0), knitr, rmarkdown, shinytest, shinyBS, covr

VignetteBuilder knitr

RoxygenNote 6.1.1

biocViews Software, StatisticalMethod, Transcription

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/target>

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associated_peaks	<i>Predict associated peaks</i>
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Description

This function selects overlapping peaks and regions, calculates the distance between them and score each peak.

Usage

```
associated_peaks(peaks, regions, regions_col, base = 1e+05)
```

Arguments

peaks	A GRanges object
regions	A GRanges object
regions_col	A character string
base	An integer to calculate distances relative to.

Value

A GRanges object. A similar object to peaks with three added metadata columns.

Examples

```
# load peaks and transcripts data
data("real_peaks")
data("real_transcripts")

# associated peaks
ap <- associated_peaks(real_peaks, real_transcripts, 'name2')
```

direct_targets	<i>Predict direct targets</i>
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Description

This function selects overlapping peaks and regions, calculates the distance between them, score each peak and region and calculate rank products of the regions.

Usage

```
direct_targets(peaks, regions, regions_col, stats_col, base = 1e+05)
```

Arguments

peaks	A GRanges object
regions	A GRanges object
regions_col	A character string
stats_col	A character string
base	An integer to calculate distances relative to.

Value

A GRanges object. A similar object to regions with several added metadata columns.

Examples

```
# load peaks and transcripts data
data("real_peaks")
data("real_transcripts")

# direct targets
dt <- direct_targets(real_peaks, real_transcripts, 'name2', 't')
```

find_distance	<i>Find the distance between peaks and regions</i>
---------------	--

Description

Calculate the distance between the elements of two GRanges objects.

Usage

```
find_distance(peaks, regions, how = "center")
```

Arguments

peaks	A GRanges object
regions	A GRanges object
how	A character string, default 'center'

Value

A vector of integers

Examples

```
library(IRanges)

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
find_distance(query, subject)
```

merge_ranges	<i>Merge peaks and regions GRanges</i>
--------------	--

Description

Merge two GRanges objects by overlaps

Usage

```
merge_ranges(peaks, regions)
```

Arguments

peaks	A GRanges object
regions	A GRanges object

Value

A DataFrame

Examples

```
library(IRanges)

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
mergeByOverlaps(query, subject)
```

plot_predictions *Plot the ECDF of ranks by groups*

Description

Plot the cumulative distribution function of chosen value (e.g. ranks) by a factor of the same length, group. Each group is given a color and a label.

Usage

```
plot_predictions(rank, group, colors, labels, ...)
```

Arguments

rank	A numeric vector
group	A factor of length equal that of rank
colors	A character vector of colors for each group
labels	A character vector of length equal the unique values in groups
...	Other arguments passed to points

Value

NULL.

Examples

```
# generate random values
rn1 <- rnorm(100)
rn2 <- rnorm(100, 2)
e <- c(rn1, rn2)

# generate grouping variable
g <- rep(c('up', 'down'), times = c(length(rn1), length(rn2)))

plot_predictions(e,
```

```
group = g,  
colors = c('red', 'green'),  
labels = c('up', 'down'))
```

rank_product	<i>Calculate the regions rank products</i>
--------------	--

Description

Calculate the rank products of the rank of the distances and the statistics.

Usage

```
rank_product(region_score, region_stat, region_id)
```

Arguments

region_score	A vector of numerics
region_stat	A vector of numerics
region_id	A vector of characters

Value

A vector of numerics

Examples

```
library(IRanges)  
  
query <- IRanges(c(1, 4, 9), c(5, 7, 10))  
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))  
distance <- find_distance(query, subject)  
peak_score <- score_peaks(distance, 100000)  
region_id <- c('region1', 'region1', 'region2')  
region_score <- score_regions(peak_score, region_id)  
region_stat <- c(30, 30, -40)  
rank_product(region_score, region_stat, region_id)
```

real_peaks	<i>AR peaks in LNCaP cell line</i>
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Description

Androgen receptor peaks from CHIP-Seq experiment in the LNCaP cell line.

Usage

```
real_peaks
```

Format

```
A GRanges
```

Source

https://github.com/suwangbio/BETA/blob/master/BETA_test_data/3656_peaks.bed

See Also

[real_transcripts](#)

[sim_peaks](#)

Examples

```
# load data
data('real_peaks')

# locate the raw data
system.file('extdata', '3656_peaks.bed.gz', package = 'target')

# locate the source code for preparing the data
system.file('extdata', 'make-data.R', package = 'target')
```

real_transcripts	<i>Differential expression of DHT treated LNCaP cell line</i>
------------------	---

Description

The differential expression analysis output of LNCaP cell line treated with DHT for 16 hours compared to non-treated cells. The REFSEQ transcript identifiers were used to merge the data.frame with the transcript coordinates from the hg19 reference genome.

Usage

```
real_transcripts
```

Format

A GRanges

Source

https://github.com/suwangbio/BETA/blob/master/BETA_test_data/AR_diff_expr.xls

https://github.com/suwangbio/BETA/blob/master/BETA_1.0.7/BETA/references/hg19.refseq

See Also

[real_peaks](#)

[sim_transcripts](#)

Examples

```
# load data
data('real_transcripts')

# locate the raw data
system.file('extdata', 'AR_diff_expr.tsv.gz', package = 'target')
system.file('extdata', 'hg19.refseq', package = 'target')

# locate the source code for preparing the data
system.file('extdata', 'make-data.R', package = 'target')
```

score_peaks

Calculate peak scores

Description

Calculate the peak score based on the distance to a region of interest.

Usage

```
score_peaks(distance, base)
```

Arguments

distance A vector of integers

base An integer to calculate distances relative to.

Value

A vector of integers

Examples

```
library(IRanges)

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
distance <- find_distance(query, subject)
score_peaks(distance, 100000)
```

score_regions	<i>Calculate region scores</i>
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Description

Calculate the region score based on the distance to their assigned peaks.

Usage

```
score_regions(peak_score, region_id)
```

Arguments

peak_score	A vector of integers
region_id	A vector of character

Value

A vector of numerics

Examples

```
library(IRanges)

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
distance <- find_distance(query, subject)
peak_score <- score_peaks(distance, 100000)
region_id <- c('region1', 'region1', 'region2')
region_score <- score_regions(peak_score, region_id)
```

sim_peaks	<i>Simulated peaks</i>
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Description

is randomly generated peaks with random distances from the transcripts start sites (TSS) of chromosome 1 of the mm10 mouse genome.

Usage

```
sim_peaks
```

Format

A GRanges

See Also

[real_peaks](#)

[sim_transcripts](#)

Examples

```
# load data
data('sim_peaks')

# locate the source code for preparing the data
system.file('extdata', 'make-data.R', package = 'target')
```

sim_transcripts	<i>Simulated transcripts The transcripts chromosome 1 of the mm10 mouse genome with randomly singed statistics assigned to each.</i>
-----------------	--

Description

Simulated transcripts The transcripts chromosome 1 of the mm10 mouse genome with randomly singed statistics assigned to each.

Usage

```
sim_transcripts
```

Format

A GRanges

See Also[real_transcripts](#)[sim_transcripts](#)**Examples**

```
# load data
data('sim_transcripts')

# locate the source code for preparing the data
system.file('extdata', 'make-data.R', package = 'target')
```

target	target: <i>Predict Combined Function of Transcription Factors.</i>
--------	--

Description

Implement the BETA algorithm for inferring direct target genes from DNA-binding and perturbation expression data Wang et al. (2013) <doi: 10.1038/nprot.2013.150>. Extend the algorithm to predict the combined effect of two DNA-binding elements from comparable binding and expression data.

Details

Predicting associated peaks and direct targets

[associated_peaks](#) [direct_targets](#)

Plotting and testing predictions [plot_predictions](#) [test_predictions](#)

Internal target functions: [merge_ranges](#) [find_distance](#) [score_peaks](#) [score_regions](#) [rank_product](#)

target_app	<i>Run the shiny App</i>
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Description

Run the shiny App

Usage

```
target_app()
```

Value

Runs the shiny app

test_predictions	<i>Test the ECDF ranks of groups are from same distribution</i>
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Description

Test whether the cumulative distribution function of two groups are drawn from the same distribution.

Usage

```
test_predictions(rank, group, compare, ...)
```

Arguments

rank	A numeric vector
group	A factor of length equal that of rank
compare	A character vector of length two
...	Other arguments passed to ks.test

Value

An htest object

Examples

```
# generate random values
rn1 <- rnorm(100)
rn2 <- rnorm(100, 2)
e <- c(rn1, rn2)

# generate grouping variable
g <- rep(c('up', 'down'), times = c(length(rn1), length(rn2)))

# test
test_predictions(e,
                 group = g,
                 compare = c('up', 'down'))
```

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