Package ‘spatzie’

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Type Package

Title Identification of enriched motif pairs from chromatin interaction data

Version 1.8.0

Description Identifies motifs that are significantly co-enriched from enhancer-promoter interaction data. While enhancer-promoter annotation is commonly used to define groups of interaction anchors, spatzie also supports co-enrichment analysis between preprocessed interaction anchors. Supports BEDPE interaction data derived from genome-wide assays such as HiC, ChIA-PET, and HiChIP. Can also be used to look for differentially enriched motif pairs between two interaction experiments.

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URL https://spatzie.mit.edu

Depends R (>= 4.3)

Imports BiocGenerics, BSgenome, GenomeInfoDb, GenomicFeatures, GenomicInteractions, GenomicRanges, ggplot2, IRanges, MatrixGenerics, matrixStats, motifmatchr, S4Vectors, stats, SummarizedExperiment, TFBSTools, utils


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anchor_pair_enrich
Determine enriched motifs in anchors

Description

Determine whether motifs between paired bed regions have a statistically significant relationship. Options for significance are motif score correlation, motif count correlation, or hypergeometric motif co-occurrence.

Usage

anchor_pair_enrich(interaction_data, method = c("count", "score", "match"))

Arguments

- interaction_data: an interactionData object of paired genomic regions
- method: method for co-occurrence, valid options include:
  - count: correlation between counts (for each anchor, tally positions where motif score > 5 \times 10^{-5})
  - score: correlation between motif scores (for each anchor, use the maximum score over all positions)
  - match: association between motif matches (for each anchor, a match is defined if the is at least one position with a motif score > 5 \times 10^{-5})

Value

an interactionData object where obj$pair_motif_enrich contains the p-values for significance of seeing a higher co-occurrence than what we get by chance.

Score-based correlation

We assume motif scores follow a normal distribution and are independent between enhancers and promoters. We can therefore compute how correlated scores of any two transcription factor motifs are between enhancer and promoter regions using Pearson’s product-moment correlation coefficient:

\[
    r = \frac{\sum (x'_i - \bar{x}') (y'_i - \bar{y}')}{\sqrt{\sum (x'_i - \bar{x}')^2 \sum (y'_i - \bar{y}')^2}}
\]

where the input vectors \(x\) and \(y\) from above are transformed to vectors \(x'\) and \(y'\) by replacing the set of scores with the maximum score for each region:

\[
x'_i = \max x_i
\]

\(x'_i\) is then the maximum motif score of motif \(a\) in the promoter region of interaction \(i\), \(y'_i\) is the maximum motif score of motif \(b\) in the enhancer region of interaction \(i\), and \(\bar{x}'\) and \(\bar{y}'\) are the sample means.

Significance is then computed by transforming the correlation coefficient \(r\) to test statistic \(t\), which is Student \(t\)-distributed with \(n - 2\) degrees of freedom.

\[
t = \frac{r \sqrt{n - 2}}{\sqrt{1 - r^2}}
\]
All p-values are calculated as one-tailed p-values of the probability that scores are greater than or equal to \( r \).

**Count-based correlation**

Instead of calculating the correlation of motif scores directly, the count-based correlation metric first tallies the number of instances of a given motif within an enhancer or a promoter region, which are defined as all positions in those regions with motif score p-values of less than \( 5 \times 10^{-5} \). Formally, the input vectors \( x \) and \( y \) are transformed to vectors \( x'' \) and \( y'' \) by replacing the set of scores with the cardinality of the set:

\[ x''_i = |x_i| \]

And analogous for \( y'' \). Finally, the correlation coefficient \( r \) between \( x'' \) and \( y'' \) and its associated significance are calculated as described above.

**Match-based association**

Instance co-occurrence uses the presence or absence of a motif within an enhancer or promoter to determine a statistically significant association, thus \( x''' \) and \( y''' \) are defined by:

\[ x'''_i = 1_{x_i > 0} \]

Instance co-occurrence is computed using the hypergeometric test:

\[
p = \sum_{k=I_{ab}}^{P_a} \frac{\text{binom}(P_a, k) \text{binom}(n - P_a, E_b - k)}{\text{binom}(n, E_b)},
\]

where \( I_{ab} \) is the number of interactions that contain a match for motif \( a \) in the promoter and motif \( b \) in the enhancer, \( P_a \) is the number of promoters that contain motif \( a \) \( (P_a = \sum_i x'''_i) \), \( E_b \) is the number of enhancers that contain motif \( b \) \( (E_b = \sum_i y'''_i) \), and \( n \) is the total number of interactions, which is equal to the number of promoters and to the number of enhancers.

**Author(s)**

Jennifer Hammelman
Konstantin Krismer

**Examples**

```r
## Not run:
genome_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!is.in%in%rownames(utils::installed.packages()))) {
  BiocManager::install(genome_id, update = FALSE, ask = FALSE)
}

genome <- BSgenome::getBSgenome(genome_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz", package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
```
anchor_pair_example_count

```
yy1_pd_interaction <- filter_motifs(yy1_pd_interaction, 0.4)
yy1_pd_count_corr <- anchor_pair_enrich(yy1_pd_interaction, method = "count")

## End(Not run)

res <- anchor_pair_enrich(spatzie::scan_interactions_example_filtered,
    method = "score")
```

---

**anchor_pair_example_count**  
*spatzie count correlation data set*

**Description**  
This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs, filtered for motifs present in at least 10 interactions with count correlation. It serves as unit test data.

**Usage**  
`data(anchor_pair_example_count)`

**Format**  
An interactionData object

---

**anchor_pair_example_match**  
*spatzie match association data set*

**Description**  
This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs, filtered for motifs present in at least 10 interactions with using the hypergeometric test. It serves as unit test data.

**Usage**  
`data(anchor_pair_example_match)`

**Format**  
A interactionData object
Description

This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs, filtered for motifs present in at least 10 interactions with score correlation. It serves as unit test data.

Usage

data(anchor_pair_example_score)

Format

An interactionData object

compare_motif_pairs  Compare pairs of motifs between two interaction datasets

Description

Compute the log-likelihood ratio that a motif pair is differential between two interaction datasets. Note that motif pair significance should have been computed using the same method for both datasets.

Usage

compare_motif_pairs(
  interaction_data1,
  interaction_data2,
  differential_p = 0.05
)

Arguments

interaction_data1
  an interactionData object of paired genomic regions that has been scanned for significant motif:motif interactions

interaction_data2
  an interactionData object of paired genomic regions that has been scanned for significant motif:motif interactions

differential_p
  threshold for significance of differential p-value
**Value**

a matrix of the log likelihood ratio of motif pairs that are significantly differential between two interactionData sets

**Author(s)**

Jennifer Hammelman

**Examples**

```r
pheatmap::pheatmap(compare_motif_pairs(spatzie::int_data_k562,
      spatzie::int_data_mslcl, 5e-06),
      fontsize = 6)
```

**Description**

This is a matrix containing example result from compare_motif_pairs. It serves as unit test data.

**Usage**

data(compare_pairs_example)

**Format**

A matrix

**filter_motifs**

Filter motifs based on occurrence within interaction data

**Description**

Select a subset of motifs that are in at least a threshold fraction of regions. Motif subsets are selected separately for anchor one and anchor two regions.

**Usage**

```r
filter_motifs(interaction_data, threshold)
```

**Arguments**

- interaction_data: an interactionData object of paired genomic regions
- threshold: fraction of interactions that should contain a motif for a motif to be considered
filter_pairs_example

Value

an interactionData object where obj$anchor1_motif_indices and obj$anchor2_motif_indices have been filtered to motifs that are present in a threshold fraction of interactions

Author(s)

Jennifer Hammelman

Examples

```r
## Not run:
genome_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!(genome_id %in% rownames(utils::installed.packages()))) {
  BiocManager::install(genome_id, update = FALSE, ask = FALSE)
}
genome <- BSgenome::getBSgenome(genome_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz", package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
yy1_pd_interaction <- filter_motifs(yy1_pd_interaction, 0.4)
## End(Not run)

res <- filter_motifs(spatzie::scan_interactions_example, threshold = 0.1)
```

Description

This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs, filtered for motifs present in at least 10 interactions with score correlation, and filtered for pairs with p < 0.5. It serves as unit test data.

Usage

data(filter_pairs_example)

Format

An interactionData object
**filter_pair_motifs**  
*Filter significant motif interactions*

**Description**

Multiple hypothesis correction applied to filter for significant motif interactions.

**Usage**

```r
filter_pair_motifs(interaction_data, method = "fdr", threshold = 0.05)
```

**Arguments**

- `interaction_data`  
an interactionData object of paired genomic regions
- `method`  
statistical method for multiple hypothesis correction, defaults to Benjamini-Hochberg ("fdr") (see `p.adjust` for options)
- `threshold`  
p-value threshold for significance cut-off

**Value**

an interactionData object where `obj$pair_motif_enrich` contains multiple hypothesis corrected p-values for significance of seeing a higher co-occurrence than what we get by chance and `obj$pair_motif_enrich_sig` contains only motifs that have at least one significant interaction.

**Author(s)**

Jennifer Hammelman

**Examples**

```r
## Not run:
genome_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!(genome_id %in% rownames(utils::installed.packages()))) {  
  BiocManager::install(genome_id, update = FALSE, ask = FALSE)
}  
genome <- BSgenome::getBSgenome(genome_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz",  
  package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
yy1_pd_interaction <- filter_motifs(yy1_pd_interaction, 0.4)
yy1_pd_score_corr <- anchor_pair_enrich(yy1_pd_interaction, method = "score")
yy1_pd_score_corr_adj <- filter_pair_motifs(yy1_pd_score_corr)

## End(Not run)
```
find_ep_coenrichment

Description

Identifies co-enriched pairs of motifs in enhancer-promoter interactions selected from a data frame of general genomic interactions.

If `identify_ep`: Promoters and enhancers are identified using genomic annotations, where anchors close to promoter annotations (within 2500 base pairs) are considered promoters and all other anchors are considered gene-distal enhancers. Only interactions in `int_raw_data` between promoters and enhancers are used for motif co-enrichment analysis.

If `!identify_ep`: Instead of automatically identifying promoters and enhancers based on genomic annotations, all interactions in `int_raw_data` must be preprocessed in a way that anchor 1 contains promoters and anchor 2 contains enhancers. Motif co-enrichment analysis is performed under this assumption.

Calls functions `scan_motifs`, `filter_motifs`, and `anchor_pair_enrich` internally.

Usage

```r
find_ep_coenrichment(
  int_raw_data,
  motifs_file,
  motifs_file_matrix_format = c("pfm", "ppm", "pwm"),
  genome_id = c("hg38", "hg19", "mm9", "mm10"),
  identify_ep = TRUE,
  cooccurrence_method = c("count", "score", "match"),
  filter_threshold = 0.4
)
```

Arguments

- `int_raw_data` a `GenomicInteractions` object or a data frame with at least six columns:
  - column 1: character; genomic location of interaction anchor 1 - chromosome (e.g., "chr3")
  - column 2: integer; genomic location of interaction anchor 1 - start coordinate
  - column 3: integer; genomic location of interaction anchor 1 - end coordinate
  - column 4: character; genomic location of interaction anchor 2 - chromosome (e.g., "chr3")
  - column 5: integer; genomic location of interaction anchor 2 - start coordinate
  - column 6: integer; genomic location of interaction anchor 2 - end coordinate

- `motifs_file` JASPAR format matrix file containing multiple motifs to scan for, gz-zipped files allowed
find_ep_coenrichment

motifs_file_matrix_format
type of position-specific scoring matrices in motifs_file, valid options include:

- pfm: position frequency matrix, elements are absolute frequencies, i.e., counts (default)
- ppm: position probability matrix, elements are probabilities, i.e., Laplace smoothing corrected relative frequencies
- pwm: position weight matrix, elements are log likelihoods

genome_id
ID of genome assembly interactions in int_raw_data were aligned to, valid options include: hg19, hg38, mm9, and mm10, defaults to hg38

identify_ep
logical, set FALSE if enhancers and promoters should not be identified based on genomic annotations, but instead assumes anchor 1 contains promoters and anchor 2 contains enhancers, for all interactions in int_raw_data, defaults to TRUE, i.e., do identify enhancers and promoters of interactions in int_raw_data based on genomic interactions and filter all interactions which are not between promoters and enhancers

coopurrence_method
method for co-occurrence, valid options include:

- count: correlation between counts (for each anchor, tally positions where motif score > 5 \times 10^{-5})
- score: correlation between motif scores (for each anchor, use the maximum score over all positions)
- match: association between motif matches (for each anchor, a match is defined if the is at least one position with a motif score

See anchor_pair_enrich for details.

filter_threshold
fraction of interactions that should contain a motif for a motif to be considered, see filter_motifs, defaults to 0.4

Value

a list with the following items:

- int_data: GenomicInteractions object; promoter-enhancer interactions
- int_data_motifs: interactionData object; return value of scan_motifs
- filtered_int_data_motifs: interactionData object; return value of filter_motifs
- annotation_pie_chart: ggplot2 plot; return value of plotInteractionAnnotations
- motif_cooccurrence: interactionData object; return value of anchor_pair_enrich

Author(s)

Jennifer Hammelman
Konstantin Krismer

Examples

```r
## Not run:
interactions_file <- system.file("extdata/yy1_interactions.bedpe.gz",
package = "spatzie")
```
get_specific_interactions

Get interactions that contain a specific motif pair

Description
Select interactions that contain anchor1_motif within anchor 1 and anchor2_motif within anchor 2.

Usage
get_specific_interactions(
  interaction_data,
  anchor1_motif = NULL,
  anchor2_motif = NULL
)

Arguments
  interaction_data
    an interactionData object of paired genomic regions
  anchor1_motif
    Motif name from interactionData$anchor1_motifs
  anchor2_motif
    Motif name from interactionData$anchor2_motifs

Value
a GenomicInteractions object containing a subset subset of interactions that contain an instance of anchor1_motif in anchor 1 and anchor2_motif in anchor 2

Author(s)
Jennifer Hammelman
Examples

```r
## Not run:
genome_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!(genome_id %in% rownames(utils::installed.packages()))) {
  BiocManager::install(genome_id, update = FALSE, ask = FALSE)
}
genome <- BSgenome::getBSgenome(genome_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz",
                           package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
yy1_pd_interaction <- filter_motifs(yy1_pd_interaction, 0.4)
yy1_yy1_interactions <- get_specific_interactions(
  yy1_pd_interaction,
  anchor1_motif = "YY1",
  anchor2_motif = "YY1")

## End(Not run)

res <- get_specific_interactions(spatzie::int_data_yy1,
                                 anchor1_motif = "YY1",
                                 anchor2_motif = "YY1")
```

Description

This object contains genomic interactions obtained by mouse YY1 ChIA-PET and serves as example and unit test data. The same data set is used in the vignette.

Usage

```r
data(interactions_yy1)
```

Format

A `GenomicInteractions` object
interactions_yy1_enhancer

Mouse YY1 Enhancer - Promoter Interactions Data Set - YY1 enhancers

Description

This is a GenomicInteractions object containing processed results from YY1 ChIA-PET of interactions that contain a YY1 motif in the enhancer (anchor 2) region. It serves as unit test data.

Usage

data(interactions_yy1_enhancer)

Format

A GenomicInteractions object

interactions_yy1_ep

Mouse YY1 Enhancer - Promoter Interactions Data Set - YY1 enhancers/promoters

Description

This is a GenomicInteractions object containing processed results from YY1 ChIA-PET of interactions that contain a YY1 motif in the promoter (anchor 1) region and a YY1 motif in the enhancer (anchor 2) region. It serves as unit test data.

Usage

data(interactions_yy1_ep)

Format

A GenomicInteractions object
interactions_yy1_promoter

Mouse YY1 Enhancer - Promoter Interactions Data Set - YY1 promoters

Description

This is a GenomicInteractions object containing processed results from YY1 ChIA-PET of interactions that contain a YY1 motif in the promoter (anchor 1) region. It serves as unit test data.

Usage

data(interactions_yy1_promoter)

Format

A GenomicInteractions object

int_data_k562

K562 Enhancer - Promoter Interactions Data Set

Description

This object contains genomic interactions obtained by human RAD21 ChIA-PET from K562 cells and serves as unit test data.

Usage

data(int_data_k562)

Format

An interactionData object
**int_data_mslcl**  
*MSLCL Enhancer - Promoter Interactions Data Set*

**Description**

This object contains genomic interactions obtained by human RAD21 ChIA-PET from MSLCL cells and serves as unit test data.

**Usage**

`data(int_data_mslcl)`

**Format**

An `interactionData` object

---

**int_data_yy1**  
*Mouse YY1 Enhancer - Promoter Interactions Data Set*

**Description**

This object contains genomic interactions obtained by mouse YY1 ChIA-PET and serves as example and unit test data.

**Usage**

`data(int_data_yy1)`

**Format**

An `interactionData` object
plot_motif_occurrence

Plot motif occurrence

Description

Plots a histogram of motif values (either counts, instances, or scores) for anchor 1 and anchor 2 regions.

Usage

```r
plot_motif_occurrence(
  interaction_data,
  method = c("counts", "instances", "scores")
)
```

Arguments

- **interaction_data**: an interactionData object of paired genomic regions
- **method**: way to interpret motif matching for each anchor region as "counts" number of motifs per region, "instances" motif present or absent each region, or "scores" maximum motif PWM match score for each region

Value

plot containing histogram for each anchor

Author(s)

Jennifer Hammelman

Examples

```r
## Not run:
genome_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!isTRUE(rownames(utils::available.packages()))) {
  BiocManager::install(genome_id, update = FALSE, ask = FALSE)
}
genome <- BSgenome::getBSgenome(genome_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz",
                          package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
yy1_pd_interaction <- filter_motifs(yy1_pd_interaction, 0.4)
plot_motif_occurrence(yy1_pd_interaction, "counts")
## End(Not run)
```
scan_interactions_example

Interactions scanned for motifs - interactionData object

Description
This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs and serves as unit test data.

Usage
data(scan_interactions_example)

Format
An interactionData object

scan_interactions_example_filtered

Interactions with motifs filtered for significance - interactionData object

Description
This object contains genomic interactions obtained by mouse YY1 ChIA-PET scanned for mouse transcription factor motifs and filtered for motifs present in at least 10

Usage
data(scan_interactions_example_filtered)

Format
An interactionData object
**scan_motifs**  

*Scans interaction file for motif instances*

---

**Description**

Uses motifmatchR to scan interaction regions for given motifs.

**Usage**

```r
scan_motifs(int_data, motifs, genome)
```

**Arguments**

- `int_data`: a `GenomicInteractions` object of paired genomic regions
- `motifs`: a TFBS tools matrix of DNA binding motifs
- `genome`: `BSgenome` object or `DNAStringSet` object, must match chromosomes from interaction data file

**Value**

An interaction data object where `obj$anchor1_motifs` and `obj$anchor2_motifs` contain information about the scores and matches to motifs from anchor one and anchor two of interaction data genomic regions

**Author(s)**

Jennifer Hammelman

**Examples**

```r
## Not run:
genie_id <- "BSgenome.Mmusculus.UCSC.mm9"
if (!(genie_id %in% rownames(utils::installed.packages()))) {
  BiocManager::install(genie_id, update = FALSE, ask = FALSE)
}
genie <- BSgenome::getBSgenome(genie_id)

motifs_file <- system.file("extdata/motifs_subset.txt.gz", 
                          package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")

yy1_pd_interaction <- scan_motifs(spatzie::interactions_yy1, motifs, genome)
## End(Not run)

motifs_file <- system.file("extdata/motifs_subset.txt.gz", 
                          package = "spatzie")
motifs <- TFBSTools::readJASPARMatrix(motifs_file, matrixClass = "PFM")
```
left <- GenomicRanges::GRanges(
  seqnames = c("chr1", "chr1", "chr1"),
  ranges = IRanges::IRanges(start = c(1, 15, 20),
                           end = c(10, 35, 31)))
right <- GenomicRanges::GRanges(
  seqnames = c("chr1", "chr2", "chr2"),
  ranges = IRanges::IRanges(start = c(17, 47, 41),
                           end = c(28, 54, 53)))
test_interactions <- GenomicInteractions::GenomicInteractions(left, right)

# toy DNAStringSet to replace BSgenome object
seqs <- c("chr1" = "CCACTAGCCACCGCTACTGTTAGCGTGATTGAAACTAAATCGTATGAAAATCC",
         "chr2" = "CTACAAACTAGGAATTTAGGCAAACCTGTGTTAAAATCTTAGCTCATTCATTAAT")
toy_genome <- Biostrings::DNAStringSet(seqs, use.names = TRUE)
res <- scan_motifs(test_interactions, motifs, toy_genome)

---

Description

Looks for motifs which are significantly co-enriched from enhancer-promoter interaction data, derived from assays such as as HiC, ChIA-PET, etc. It can also look for differentially enriched motif pairs between to interaction experiments.

Author(s)

Jennifer Hammelman
Konstantin Krismer
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