Package ‘cobindR’

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Title Finding Co-occurring motifs of transcription factor binding sites

Description Finding and analyzing co-occurring motifs of transcription factor binding sites in groups of genes

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Imports methods, seqinr, yaml, rtfbs, gplots, mclust, gmp,
BiocGenerics (>= 0.13.8), IRanges, Biostrings, BSgenome,
biomaRt

Suggests RUnit

Enhances rGADEM, seqLogo, genoPlotR, parallel, VennDiagram,
RColorBrewer, vcd, MotiDb, snowfall

biocViews ChIPSeq, CellBiology, MultipleComparison, SequenceMatching

NeedsCompilation no

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cobindR-package

An R package for analyzing co-occurring transcription factor binding sites

Description

Many transcription factors (TFs) regulate gene expression by binding to specific DNA motifs near genes. Often the regulation of gene expression is not only controlled by one TF, but by many TFs together, that can either interact in a cooperative manner or interfere with each other. In recent years high throughput methods, like ChIP-Seq, have become available to produce large amounts of data, that contain potential regulatory regions. In silico analysis of transcription factor binding sites can help to interpret these enormous datasets in a convenient and fast way or narrow down the results to the most significant regions for further experimental studies.

cobindR provides a complete set of methods to analyse and detect pairs of TFs, including support of diverse input formats and different background models for statistical testing. Several visualization tools are implemented to ease the interpretation of the results.

Author(s)

Yue-Hien Lee, Robert Lehmann, Stefan Kroeger, Manuela Benary

See Also

The core class in this package: cobindr-class. The core function in this package: find.pairs.

bg_binding_sites

motif hits in the background sequences

Description

motif hits in the background sequences

Usage

## S4 method for signature 'cobindr'
bg_binding_sites(x)
## S4 replacement method for signature 'cobindr, data.frame'
bg_binding_sites(x) <- value

Arguments

x a cobindr object

value data.frame holding the binding site hits in the background sequences

Value

motif hits in background sequences (data.frame)
bg_pairs

Author(s)
Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
uid, name, sequences, bg_sequences, desc, configuration, binding_sites, pfm, bg_binding_sites, pairs, bg_pairs, pairs_of_interest

Examples

cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak bg_binding_sites'
cbr <- cobindr(cfg)
binding_sites(cbr)

bg_pairs
motif hit pairs in the background sequences

Description
motif hit pairs in the background sequences

Usage
## S4 method for signature 'cobindr'
bg_pairs(x)
## S4 replacement method for signature 'cobindr, data.frame'
bg_pairs(x) <- value

Arguments
x a cobindr object
value data.frame holding the binding site pairs in the background sequences

Value
background motif pairs (data.frame)

Author(s)
Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
uid, name, sequences, bg_sequences, desc, configuration, binding_sites, bg_binding_sites, pfm, pairs, bg_pairs, pairs_of_interest
Examples

cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak bg_pairs'
cbr <- cobindr(cfg)
bg_pairs(cbr)

Description

list of background sequence

Usage

## S4 method for signature 'cobindr'
bg_sequences(x)
## S4 replacement method for signature 'cobindr,list'
bg_sequences(x) <- value

Arguments

x a cobindr object

value list of background sequence of type SeqObj

Value

list of background sequences (SeqObj)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

uid.name.bg_sequences.bg_sequences.desc.configuration.binding_sites.bg_binding_sites.pfm.pairs.bg_pairs

Examples

cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak bg_pairs'
cbr <- cobindr(cfg)
length(bg_sequences(cbr))
bg_sequence_origin  background sequence origin note

Description
background sequence origin note

Usage
## S4 method for signature 'configuration'
bg_sequence_origin(x)
## S4 replacement method for signature 'configuration,character'
bg_sequence_origin(x) <- value

Arguments
  x  a cobindR configuration object
  value  a character

Value
background sequence origin (character)

Author(s)
Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
id,experiment_description,sequence_source,sequence_origin,sequence_type.bg_sequence_source.bg_sequence_type

Examples
cfg <- cobindRConfiguration()
bg_sequence_origin(cfg)

description  background sequence source note

Description
background sequence source note

Usage
## S4 method for signature 'configuration'
bg_sequence_source(x)
## S4 replacement method for signature 'configuration,character'
bg_sequence_source(x) <- value
**bg_sequence_type**

**Arguments**

- `x`: a cobindR configuration object
- `value`: a character

**Value**

background sequence source (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `bg_sequence_type`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`

**Examples**

```r
cfg <- cobindRConfiguration()
brown_sequence_source(cfg)
```

---

**Description**

background sequence type note

**Usage**

```r
## S4 method for signature 'configuration'
bg_sequence_type(x)
## S4 replacement method for signature 'configuration, character'
bg_sequence_type(x) <- value
```

**Arguments**

- `x`: a cobindR configuration object
- `value`: a character

**Value**

`bg_sequence_type` (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `bg_sequence_type`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`
Examples

```r
cfg <- cobindRConfiguration()
binding_sites_type(cfg)
```

### Description

motif hits on the foreground sequences

### Usage

```r
## S4 method for signature 'cobindr'
binding_sites(x)
## S4 replacement method for signature 'cobindr,data.frame'
binding_sites(x) <- value
```

### Arguments

- `x`: a cobindr object
- `value`: data.frame holding the binding site hits in the foreground sequences

### Value

motif hits in foreground sequences as data.frame

### Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

### See Also

- uid, name, sequences, bg_sequences, desc, configuration, binding_sites, bg_binding_sites, pfm, pairs, bg_pairs, pairs_of_interest

### Examples

```r
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seq.fasta',package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak binding_sites'
cbr <- cobindr(cfg)
binding_sites(cbr)
```
cobindr-class

Class "cobindr"

Description

Container for experiment run and its meta-data

Objects from the Class

Objects can be created by calls of the form `new("cobindr", conf, name, desc).

Slots

- uid: Object of class "character" -- unique id for internal representation
- name: Object of class "character" -- name of the experiment
- sequences: Object of class "list" -- list of sequence objects to be analyzed
- bg_sequences: Object of class "list" -- list of background sequences for statistical analyses
- desc: Object of class "character" -- verbal experiment description
- configuration: Object of class "configuration" -- the configuration object used to describe the experiment
- pfm: Object of class "list" -- list of pfms to be used
- pairs_of_interest: Object of class "factor" -- contains pairs for search

Methods

- `detrending` signature(object = "cobindr"): ...
- `find.pairs` signature(object = "cobindr"): ...
- `generate.background` signature(object = "cobindr"): ...
- `get.bindingsite.ranges` signature(object = "cobindr"): ...
- `get.pairs` signature(object = "cobindr"): ...
- `get.significant.pairs` signature(object = "cobindr"): ...
- `initialize` signature(.Object = "cobindr"): ...
- `input.pwm` signature(object = "cobindr"): ...
Author(s)
Manuela Benary <manuela.benary@cms.hu-berlin.de>

See Also
SeqObj configuration

Examples
showClass("cobindr")
Value
cobindR configuration object

Author(s)
Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
seqObj

Examples
cfg <- cobindRConfiguration()

comment
comment of cobindR SeqObj object

Description
comment of cobindR SeqObj object

Usage
## S4 method for signature 'SeqObj'
comment(x)
## S4 replacement method for signature 'SeqObj,character'
comment(x) <- value

Arguments
x a cobindR seqObj object
value comment to the sequence (character)

Value
comment (character)

Author(s)
Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
uid, name, species, comment, location, sequence

Examples
library(Biostrings)
so <- seqObj(DNAString("A"), id='', name='', species='', comment='', location='')
comment(so)
### Description

configuration of cobindr object

### Usage

```r
## S4 method for signature 'cobindr'
configuration(x)

## S4 replacement method for signature 'cobindr,configuration'
configuration(x) <- value
```

### Arguments

- `x`: a cobindr object
- `value`: returns the configuration object used in this cobindR object

### Value

cobindR configuration object

### Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

### See Also

- `uid`, `name`, `sequences`, `bg_sequences`, `desc`, `configuration`, `binding_sites`, `bg_binding_sites`, `pfm`, `pairs`, `bg_pairs`, `pairs_of_interest`

### Examples

```r
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak configuration'
cbr <- cobindr(cfg)
configuration(cbr)
```
configuration-class  

Class "configuration"

Description

Container for experiment description.

Objects from the Class

Objects can be created by calls of the form new("configuration", fname).

Slots

- id: Object of class "character" ~~ unique id for internal representation
- experiment_description: Object of class "character" ~~ verbal experiment description
- sequence_source: Object of class "character" ~~ file path or list of paths
- sequence_origin: Object of class "character" ~~ source of sequence data, e.g. ensembl
- sequence_type: Object of class "character" ~~ either ChipSeq or Fasta or BED are available
- bg_sequence_source: Object of class "character" ~~ file path or list of paths
- bg_sequence_origin: Object of class "character" ~~ how the background is obtained - either simulated or from fasta files or from gene ids
- bg_sequence_type: Object of class "character" ~~ determines the generation of the background sequences. Possible values: simulated, fasta and geneid
- species: Object of class "character" ~~ reference species
- downstream: Object of class "numeric" ~~ length of sequence downstream of reference point, e.g. transcription start site
- upstream: Object of class "numeric" ~~ length of sequence upstream of reference point, e.g. transcription start site
- max_distance: Object of class "numeric" ~~ maximal distance allowed between cooccurring transcription factor binding sites
- pairs: Object of class "character" ~~ list of pairs of interesting transcription factors
- pfm_path: Object of class "character" ~~ path to pfm matrix file
- threshold: Object of class "numeric" ~~ threshold for transcription factor binding site prediction
- fdrThreshold: Object of class "numeric" ~~ false discovery rate for filtering results (used in rtfbs)
- date: Object of class "character" ~~ data of experiment run
- path: Object of class "character" ~~ path of configuration file
- mart: Object of class "character" ~~ optional mirror for biomart
- pseudocount: Object of class "numeric" ~~ sets the pseudocount for the detrending analysis
- pValue: Object of class "numeric" ~~ optional p-Value for search with RGadem
Methods

```
initialize signature(.Object = "configuration"):
read.background.fasta signature(object = "configuration"):
read.pfm signature(object = "configuration"):
read.sequences signature(object = "configuration"):
write signature(x = "configuration", file = "character"):
```

Author(s)

Manuela Benary <manuela.benary@cms.hu-berlin.de>

See Also

SeqObj cobindr

Examples

```
showClass("configuration")
```

downstream range [bp] used in experiment

downstream

Description

downstream range [bp] used in experiment

Usage

```
## S4 method for signature 'configuration'
downstream(x)
## S4 replacement method for signature 'configuration,numeric'
downstream(x) <- value
```

Arguments

```
x
value
```

a cobindR configuration object

downstream distance [bp] of feature to be included (numeric)

Value

considered downstream range [bp]

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin, bg_species, bg_downstream, bg_upstream, max_distance, pairs, pfm_path, threshold, fdrThreshold, path, mart, pValue
**Examples**

```r
cfg <- cobindRConfiguration()
downstream(cfg)

experiment_description
```

**Description**

description of cobindR or configuration object

**Usage**

```r
## S4 method for signature 'configuration'
experiment_description(x)
## S4 replacement method for signature 'configuration,character'
experiment_description(x) <- value
## S4 method for signature 'cobindr'
experiment_description(x)
## S4 replacement method for signature 'cobindr,character'
experiment_description(x) <- value
```

**Arguments**

- `x` a cobindR or configuration object
- `value` description

**Value**

experiment description (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

`id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`

**Examples**

```r
cfg <- cobindRConfiguration()
experiment_description(cbr)
```

```r
cfg <- cobindRConfiguration()
experiment_description(cfg)

sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seq.fasta',package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak desc'
cbr <- cobindr(cfg)

experiment_description(cbr)
```
find.pairs

Description

find.pairs creates a data frame with all pairs in all sequences within the given distance.

Usage

find.pairs(x, background_scan = FALSE, n.cpu = NA)
get.bindingsite.ranges

**Arguments**

- **x**
  an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.

- **background_scan**
  logical flag, if `background_scan = TRUE` the pairs for the background sequences will be found.

- **n.cpu**
  number of CPUs to be used for parallelization. Default value is 'NA' in which case the number of available CPUs is checked and than used.

**Value**

- **runObj**
  an object of the class "cobindr" including the pairs of transcription factor binding sites

**Author(s)**

Yue-Hien Lee <>

**See Also**

- `plot.detrending`

---

Function converts predicted binding sites into a GRanges object (package: GenomicFeatures). This allows for easy interaction with other tools as well as output of different formats (bed, gff).

**Usage**

`get.bindingsite.ranges(x, ...)`

**Arguments**

- **x**
  An object of the class "cobindr", which will hold the predicted binding site locations.

- **...**
  optional additional parameters

**Value**

A GRanges object holding the positions of all predicted transcription factor binding sites relative to the input sequence.

**Author(s)**

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>
See Also

get.pairs write.bindingsites write.bindingsites.table

Examples

# export(get.bindingsite.ranges(runObj), "tfbs_hits.gff3")

description

Function returns the results of findPairs() as a data frame. The data.frame consists of 6 columns, namely

- a unique id for each pair,
- the unique id of the sequence, where the pair was found,
- the names of the corresponding PFM's,
- the unique id for each PFM, and
- the distance window in which the pair occurs.

Usage

## S4 method for signature 'cobindr'
get.pairs(x, background = FALSE)

Arguments

x an object of the class "cobindr", which holds all necessary information about the
sequences and the predicted binding sites.

background logical flag. If background is 'TRUE' the pairs found in the background se-
quencies are used.

Author(s)

Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also

get.significant.pairs, write.bindingsites, write.sequences, write
get.significant.pairs function to returns the results of detrending as a data.frame

Description

get.significant.pairs returns a data.frame of observed distances between the specified pair of PWMs in the foreground set of the sequences as well as the background set of sequences. The distance distribution for the pair in the background is used for detrending.

Usage

```r
## S4 method for signature 'cobindr'
get.significant.pairs(x, pwm1, pwm2, bin_length=20, z_value=3, overlap=0, abs.distance=FALSE)
```

Arguments

- `x` an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- `pwm1` name of the first PWM
- `pwm2` name of the second PWM
- `bin_length` defines size of bins for distance analysis, default value is 20 nucleotides
- `z_value` level of significance
- `overlap` number of nucleotides which are allowed for an overlap
- `abs.distance` logical flag

Author(s)

Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also

`plot.detrending`, `get.pairs`, `find.pairs`

---

id of cobindR configuration object

Description

id of cobindR configuration object.

Usage

```r
## S4 method for signature 'configuration'
id(x)
## S4 replacement method for signature 'configuration,character'
id(x) <- value
```
Arguments

x          a cobindR configuration object
value      the identifier of the configuration object

Value

id (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin, species, downstream, upstream, max_distance, pairs, pfm_path, threshold, fdrThreshold, path, mart, pValue

Examples

cfg <- cobindRConfiguration()
id(cfg)

---

location  location of cobindR SeqObj object

Description

location of cobindR seqObj object (e.g. chr1)

Usage

## S4 method for signature 'SeqObj'
location(x)
## S4 replacement method for signature 'SeqObj,character'
location(x) <- value

Arguments

x          a cobindR seqObj object
value      the location description of the sequence

Value

returns location (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

uid, name, species, location, comment, sequence
Examples

```r
library(Biostrings)
so <- seqObj(DNAString("A"), id='', name='', species='', comment='', location='')
location(so)
```

---

**Description**

biomart of cobindR configuration object. Set to "ensembl" as default

**Usage**

```r
## S4 method for signature 'configuration'
mart(x)
## S4 replacement method for signature 'configuration,character'
mart(x) <- value
```

**Arguments**

- `x` a cobindR configuration object
- `value` name of biomart to retrieve sequence data

**Value**

`mart` (character)

**Author(s)**

Rob Lehmann <rlehmann@biologie.hu-berlin.de>

**See Also**

`id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_type`

**Examples**

```r
cfg <- cobindRConfiguration()
mart(cfg)
```
max_distance

max_distance of cobindR configuration object

Description

max_distance of cobindR configuration object.

Usage

## S4 method for signature 'configuration'
max_distance(x)
## S4 replacement method for signature 'configuration,numeric'
max_distance(x) <- value

Arguments

x
a cobindR configuration object

value
the maximal distance of two hits to be considered a pair

Value

max_distance (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin, species, downstream, upstream, max_distance, pairs, pfm_path, threshold, fdrThreshold, path, mart, pValue

Examples

cfg <- cobindRConfiguration()
max_distance(cfg)

name

name of cobindR SeqObj object

Description

name of cobindR seqObj object.
**pairs**

**Usage**

```r
## S4 method for signature 'SeqObj'
name(x)
## S4 method for signature 'cobindR'
name(x)
## S4 replacement method for signature 'SeqObj,character'
name(x) <- value
## S4 replacement method for signature 'cobindR,character'
name(x) <- value
```

**Arguments**

- `x`: a cobindR seqObj object
- `value`: the name describing the sequence object

**Value**

`name` (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

`uid`, `name`, `species`, `location`, `comment`, `sequence`

**Examples**

```r
library(Biostrings)
so <- seqObj(DNAString('A'), id='', name='', species='', comment='', location='')
name(so)
```

```
pairs  motif hit pairs in the foreground sequences
```

**Description**

motif hit pairs in the foreground sequences

**Usage**

```r
## S4 method for signature 'configuration'
pairs(x)
## S4 replacement method for signature 'configuration,character'
pairs(x) <- value
## S4 method for signature 'cobindR'
pairs(x)
## S4 replacement method for signature 'cobindR,data.frame'
pairs(x) <- value
```
pairs_of_interest

Arguments

x a cobindR configuration object
value for a configuration object, pairs is a character specifying the motif pairs which should be considered. for a cobindR object, pairs is a data.frame holding the detected motif pairs.

Value

pairs (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin, species, downstream, upstream, max_distance, pairs, pfm_path, threshold, path, mart, pValue

Examples

```r
cfg <- cobindRConfiguration()
pairs(cfg)
```

Description

pairs_of_interest of cobindr object.

Usage

```r
## S4 method for signature 'cobindr'
pairs_of_interest(x)
## S4 replacement method for signature 'cobindr,factor'
pairs_of_interest(x) <- value
```

Arguments

x a cobindr object
value factors specifying the motif pairs that are to be evaluated

Value

pairs_of_interest (factor)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>
**path**

See Also

uid, name, sequences, bg_sequences, desc, configuration, binding_sites, bg_binding_sites, pfm, pairs, bg_pairs

Examples

cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package = 'cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak pairs_of_interest'
cbr <- cobindr(cfg)
pairs_of_interest(cbr)

---

**path**

path of cobindR configuration object

Description

path of cobindR configuration object.

Usage

```r
## S4 method for signature 'configuration'
path(x)

## S4 replacement method for signature 'configuration,character'
path(x) <- value
```

Arguments

- `x`: a cobindR configuration object
- `value`: the path of the loaded configuration file

Value

path (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequences

Examples

cfg <- cobindRConfiguration()
path(cfg)
pfm

pfm list used in experiment

Description

pfm list used in experiment

Usage

```r
## S4 method for signature 'cobindr'
pfm(x)
## S4 replacement method for signature 'cobindr,list'
pfm(x) <- value
```

Arguments

- `x`: a cobindr object
- `value`: a list of motif matrices

Value

pfm (list of motif matrices)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

uid, name, sequences, bg_sequences, desc, configuration, binding_sites, bg_binding_sites, pfm, pairs, bg_pairs, pfm

Examples

```r
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta', package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak pfm'
cbr <- cobindr(cfg)
pfm(cbr)
```
Description

path to pfms to be used

Usage

```r
## S4 method for signature 'configuration'
 pfm_path(x)
## S4 replacement method for signature 'configuration,character'
 pfm_path(x) <- value
```

Arguments

- `x`: a cobindR configuration object
- `value`: the path to the folder containing the motif matrices to be used

Value

`pfm_path` (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

- `id`
- `experiment_description`
- `sequence_source`
- `sequence_origin`
- `sequence_type`
- `bg_sequence_source`
- `bg_sequence_origin`
- `bg_sequence_type`
- `species`
- `downstream`
- `upstream`
- `max_distance`
- `pairs`
- `pfm_path`
- `threshold`
- `fdrThreshold`
- `path`
- `mart`
- `pValue`

Examples

```r
cfg <- cobindRConfiguration()
pfm_path(cfg)
```

plot.detrending

function to plot distances between a pair of PWMs

Description

plot.detrending plots a histograms of observed distances between the specified pair of PWMs in the foreground set of the sequences as well as the background set of sequences. The distance distribution for the pair in the background is used for detrending.

Usage

```r
## S4 method for signature 'cobindr'
 plot.detrending(x, pwm1, pwm2, bin_length=20, z_value=3, overlap=0,
                 abs.distance=FALSE)
```
Arguments

x an object of the class "cobindr", which will hold all necessary information about
the sequences and the hits.
pwm1 name of the first PWM
pwm2 name of the second PWM
bin_length defines size of bins for distance analysis, default value is 20 nucleotides
z_value level of significance
overlap number of nucleotides which are allowed for an overlap
abs.distance logical flag

Author(s)

Yue-Hien Lee

See Also

plot.pairdistribution, plot.pairdistance

plot.gc function to visualize GC content or CpG content of input sequences

Description

plot.gc calculates the GC (or CpG) content based on a window size for each sequence and plots the
content for all sequences as a heatmap over position and sequence.

Usage

## S4 method for signature 'cobindr'
plot.gc(x, seq.ids, cpg = F, wind.size = 50,
sig.test = F, hm.margin = c(4, 10), frac = 10, n.cpu = NA)

Arguments

x an object of the class "cobindr", which will hold all necessary information about
the sequences.
seq.ids list of sequence identifiers, for which the GC (or CpG) content will be plotted.
cpg logical flag, if cpg=TRUE the CpG content rather than the GC content will be
calculated and plotted.
wind.size integer describing the window size for GC content calculation
sig.test logical flag, if sig.test=TRUE wilcoxon.test is performed per individual window
against all windows in other sequence at the same position. The significance test
might be slow for large number of sequences
hm.margin optional argument providing the margin widths for the heatmap (if sig.test=FALSE)
frac determines the overlap between consecutive windows as fraction wind.size/frac
n.cpu number of CPUs to be used for parallelization. Default value is 'NA' in which
case the number of available CPUs is checked and than used.
plot.pairdistance

Author(s)
Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also
testCpG

Examples

library(Biostrings)

n <- 50 # number of input sequences
l <- 100 # length of sequences
bases <- c("A","C","G","T") # alphabet
# generate random input sequences with two groups with differing GC content
seqs <- sapply(1:(3*n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(0.3,0.22,0.2,0.28)), collapse=""))
seqs <- append(seqs, sapply(1:(n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(0.25,0.25,0.25,0.25)), collapse="")))
# save sample sequences in fasta file
tmp.file <- tempfile(pattern = "cobindr_sample_seq", tmpdir = tempdir(), fileext = ".fasta")
writeXStringSet(DNAStringSet(seqs), tmp.file)

cfg <- new("configuration")
slot(cfg, "sequence_type") <- "fasta"
slot(cfg, "sequence_source") <- tmp.file
# avoid complaint of validation mechanism
slot(cfg, "pfm_path") <- system.file("extdata/pfms", package="cobindR")
slot(cfg, "pairs") <- ""

runObj <- new("cobindr", cfg, "test")

plot.gc(runObj, cpg = TRUE)

unlink(tmp.file)

---

plot.pairdistance function to plot the distance of the pairs in the sequences

Description

For a specified pair of PWMs the function creates histogram plot of distances between pairs of TFs as specified by pwm1 and pwm2

Usage

## S4 method for signature 'cobindr'
plot.pairdistance(x, pwm1, pwm2, breaks=50, main=NA, xlab=NA, ylab=NA, background=FALSE)
Arguments

- `x`: an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- `pwm1`: name of the first PWM
- `pwm2`: name of the second PWM
- `breaks`: number of breaks to separate the distance distribution into
- `main`: figure title
- `xlab`: label for the x-axis of the figure
- `ylab`: label for the y-axis of the figure
- `background`: flag allowing to plot foreground or background distance distribution

Author(s)

Manuela Benary <manuela.benary@cms.hu-berlin.de>

See Also

- `plot.pairdistribution`
plot.positionprofile function to plot a profile over the total number of predicted transcription factor binding sites for each PWM.

Description

plot.positionprofile provides position-wise profile plot over total number of predicted TFBS for each PWM over all input sequences. Windowing is used to provide a smoother appearance, the window size can be adjusted with the window parameter.

Usage

## S4 method for signature 'cobindr'
plot.positionprofile(x, wind.len = 50)

Arguments

x
an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.

wind.len
integer, defining the length of the window for counting the hits.

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

plot.positions

plot.positions function to plot hits for each PWM on the individual sequence

Description

plot.positions plots hits for each PWM on the individual sequence. Which sequences to plot can be specified by providing a list of sequence identifiers seq.ids. Which PWMs to plot can be specified as list of PWMs. The total height of the plot can be adjusted via argument height.

Usage

## S4 method for signature 'cobindr'
plot.positions(x, seq.ids, pwms, main, order.seq = FALSE, wind.size = 400, frac = 10)
plot.positions.simple

Arguments

x an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
seq.ids list of sequence identifiers, for which the positions of TFBS will be plotted.
pwms list of PWMs, for which the positions will be visualized. If no list is given, all PWMs in runObj are used.
main title for the plot, if no title is given than 'predicted TFBS positions per sequence' will be used
order.seq logical flag, if TRUE similar patterns of TFBS are shown together. This is computationally expensive for large numbers of sequences.
wind.size integer describing the windows which will be used to enhance clustering of TFBS patterns. Necessary if order.seq=TRUE
frac integer

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de

Description

plot.positions plots hits for each PWM on the individual sequence. Which sequences to plot can be specified by providing a list of sequence identifiers seq.ids. Which PWMs to plot can be specified as list of PWMs. The total height of the plot can be adjusted via argument height.

Usage

## S4 method for signature 'cobindr'
plot.positions.simple(x, seq.ids, pwms, main)

Arguments

x an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
seq.ids list of sequence identifiers, for which the positions of TFBS will be plotted.
pwms list of PWMs, for which the positions will be visualized. If no list is given, all PWMs in runObj are used.
main title for the plot, if no title is given than 'predicted TFBS positions per sequence' will be used

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de

See Also

plot.positionprofile
plot.tfbs.heatmap  

**Function to do plot a heatmap of overlaps between all specified PWMs**

### Description

plot.tfbs.heatmap plots a heatmap of overlaps between all specified PWMs. For each overlap, the significance is determined based on the hypergeometric test. If a file path is specified in pdf.name, the diagram will be written into the specified file.

### Usage

```r
## S4 method for signature 'cobindr'
plot.tfbs.heatmap(x, pwms, include.empty.seqs = FALSE)
```

### Arguments

- **x**
  - an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.

- **pwms**
  - list of PWMs, for which the overlap will be visualized. If no list is given, all PWMs in runObj are used.

- **include.empty.seqs**
  - logical flag, if include.empty.seqs == TRUE, sequences without hits of the specified PWMs are also included in the diagram.

### Details

In this plot for each pair of PWMs the overlap of sequences with hits of the given PWMs is calculated. The number of sequences in each overlap are color-coded in the heatmap. For each overlap the significance is calculated using the hypergeometric test. If the significance is below 0.05 (or below 0.01), the corresponding field is marked with one (or two) *

### Warning

- unknown identifier if the list of PWMs contains unknown PWM identifiers a warning is given and the method stops
- no hits if no hits are found in the object, the method gives a warning and stops

### Author(s)

Manuela Benary <manuela.benary@cms.hu-berlin.de>

### See Also

plot.tfbs.venndiagram
plot.tfbs.venndiagram function visualize the overlaps of PWM hits over the sequences.

Description

The distribution of PWM hits over the sequences is visualized as Venn diagram. If a list of PWM names is provided, only these PWMs are included in the Venn diagram. If `include.empty.seqs == TRUE`, sequences without hits of the specified PWMs are also included in the diagram. If a file path is specified in `pdf.name`, the diagram will be written into the specified file.

Usage

```r
## S4 method for signature 'cobindr'
plot.tfbs.venndiagram(x, pwms, include.empty.seqs = FALSE)
```

Arguments

- `x`: an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- `pwms`: list of PWMs, which shall be visualized in the Venn-Diagram. If no list is given, all PWMs in the runObj are used. The package "VennDiagram" only allows Venn plots with up to 4 elements.
- `include.empty.seqs`: logical flag, if `include.empty.seqs == TRUE`, sequences without hits of the specified PWMs are also included in the diagram.

Warning

- unknown identifier: if the list of PWMs contains unknown PWM identifiers a warning is given and the method stops
- too many PWMs: if more than 4 PWMs are listed a warning is given and the method stops
- no hits: if no hits are found in the object, the method gives a warning and stops

Author(s)

Manuela Benary <manuela.benary@cms.hu-berlin.de>

References

using the package "VennDiagram" (http://www.biomedcentral.com/1471-2105/12/35/)

See Also

- `plot.tfbs.heatmap`
plot.tfbslogo

function to plot sequence logos based on hits of tools

Description

plot.tfbslogo produces a sequence logo based on all hits per position weight matrix. If a file path is specified in pdf.name, sequences logos will be written into the specified file.

Usage

## S4 method for signature 'cobindr'
plot.tfbslogo(x, pwms)

Arguments

x Object

pwms vector of names of position weight matrices used for searching the sequences. For each pwm a new sequence logo based on the hits is produced.

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

predicted2pwm

function to convert predicted TFBS hits into a PWM

Description

function converts for each input PWM the predicted TFBS hits into a PWM. Function is intended to be used together with the sequence logo creation function 'plot.tfbslogo'.

Usage

## S4 method for signature 'cobindr'
predicted2pwm(x, as.pfm=FALSE)

Arguments

x object of class "cobindr" describing the sequences and the predicted TFBS.

as.pfm logical flag, to indicate whether the function should return a PFM (TRUE) or a PWM (FALSE)

Value

predPwm positional frequency matrix based on consensus matrix

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>
Description

pseudocount of cobindR configuration object. Set to 10 as default

Usage

```r
## S4 method for signature 'configuration'
pseudocount(x)
## S4 replacement method for signature 'configuration,character'
pseudocount(x) <- value
```

Arguments

- `x`: a cobindR configuration object
- `value`: pseudocount for detrending analysis, i.e. the default number in each distance bin.

Value

pseudocount (numeric)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

`id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pseudocount`, `pValue`

Examples

```r
cfg <- cobindRConfiguration()
pseudocount(cfg)
```
pValue

pValue threshold used for motif hit finding

Description

pValue threshold used for motif hit finding

Usage

```r
## S4 method for signature 'configuration'
pValue(x)
## S4 replacement method for signature 'configuration,numeric'
pValue(x) <- value
```

Arguments

- `x`: a cobindR configuration object
- `value`: the p-value threshold used for hit searching

Value

pValue threshold (numeric)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

`id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`

Examples

```r
cfg <- cobindRConfiguration()
pValue(cfg)
```

rtfbs

function performs TFBS prediction using the package rtfbs

Description

function performs TFBS prediction using the package rtfbs

Usage

```r
## S4 method for signature 'cobindr'
rtfbs(x, append = F, background_scan = FALSE, n.cpu = NA)
```
Arguments

- **x**: an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- **append**: logical flag, if append=TRUE the binding sites will be appended to already existing results
- **background_scan**: logical flag, if background_scan=TRUE the background sequences will be searched for transcription factor binding sites
- **n.cpu**: number of CPUs to be used for parallelization. Default value is 'NA' in which case the number of available CPUs is checked and than used.

Value

- **x**: an object of the class "cobindr" including the predicted transcription factor binding sites

Author(s)

Yue-Hien Lee <>

References

uses the package "rtfbs" (http://cran.r-project.org/web/packages/rtfbs/index.html)

See Also

search.pwm, search.gadem

Examples

```
# use simulated sequences
library(Biostrings)

n <- 400 # number of input sequences
l <- 500 # length of sequences
n.hits <- 250 # number of 'true' binding sites
bases <- c("A","C","G","T") # alphabet
# generate random input sequences with two groups with differing GC content
seqs <- sapply(1:(3*n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.3,.22,.2,.28)), collapse=""))
seqs <- append(seqs, sapply(1:(n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.25,.25,.25,.25)), collapse="")))
path <- system.file("extdata/pfms/myod.tfpfm",package="cobindR")
motif <- read.transfac.pfm(path)[[1]] # get PFM of binding site
# add binding sites with distance specificity
for(position in c(110, 150)) {
  hits <- apply(apply(motif, 2, function(x) sample(x=bases, size=n.hits, prob=x, replace=TRUE)), 1, paste, collapse="")
  pos.hits <- round(rnorm(n.hits, mean=position, sd=8))
  names(pos.hits) <- sample(1:n, n.hits)
  for(i in 1:n.hits) substr(seqs[as.integer(names(pos.hits)[i])],
    start=pos.hits[i], stop=pos.hits[i]+ncol(motif)) <- hits[i]
```

## S4 method for signature 'cobindr'
search.gadem(x, deNovo = FALSE, append = F, background_scan = FALSE)

### Arguments

- **x**: an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- **deNovo**: logical flag, if deNOVO=TRUE a denovo search is startet. Otherwise the given PFM s are used as seed.
- **append**: logical flag, if append=TRUE the binding sites will be appended to already existing results
- **background_scan**: logical flag, if background_scan=TRUE the function will search for binding sites in the set of background sequences

### Value

- **x**: an object of the class "cobindr" including the predicted transcription factor binding sites
Author(s)
Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

References
uses package "rGADEM" (http://www.bioconductor.org/packages/release/bioc/html/rGADEM.html)

See Also
rtfbs, search.pwm

Examples
############################################################
# use simulated sequences
library(Biostrings)

n <- 600 # number of input sequences
l <- 150 # length of sequences
n.hits <- 600 # number of 'true' binding sites
bases <- c("A","C","G","T") # alphabet

# generate random input sequences with two groups with differing GC content
seqs <- sapply(1:(3*n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.3,.22,.2,.28)), collapse=""))
seqs <- append(seqs, sapply(1:(n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.25,.25,.25,.25)), collapse="")))
path <- system.file("extdata/pfms/myod.tfpfm",package="cobindR")
motif <- read.transfac.pfm(path)[[,1]] # get PFM of binding site

# add binding sites with distance specificity
for(position in c(70, 90)) {
  hits <- apply(apply(motif, 2, function(x) sample(x=bases, size=n.hits, prob=x, replace=TRUE)), 1, paste, collapse='')
pos.hits <- round(rnorm(n.hits, mean=position, sd=8))
names(pos.hits) <- sample(1:n, n.hits)
  for(i in 1:n.hits) substr(seqs[as.integer(names(pos.hits)[i])], start=pos.hits[i], stop=pos.hits[i]+ncol(motif)) <- hits[i]
}

# save sample sequences in fasta file
tmp.file <- tempfile(pattern = "cobindr_sample_seq", tmpdir = tempdir(), fileext = ".fasta")
writeXStringSet(DNAStringSet(seqs), tmp.file)
# run cobindr
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- tmp.file
sequence_origin(cfg) <- 'artificial sequences'
pfm_path(cfg) <- system.file("extdata/pfms",package="cobindR")
pairs(cfg) <- 'V$MYOD_01 V$MYOD_01'
runObj <- cobindr(cfg, name= "cobindr test using sampled sequences")

# perform tfbs prediction using rGADEM - commented out due to long time required
# runObj.bs <- search.gadem(runObj)
# show results
# plot.positions(runObj.bs)

# clean up
unlink(tmp.file)
**Description**

function to predict transcription factor binding sites using the method matchPWM from package Biostrings

**Usage**

```r
## S4 method for signature 'cobindr'
search.pwm(x, min.score = "80%", append = FALSE, background_scan = FALSE, n.cpu = NA)
```

**Arguments**

- `x`: an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.
- `min.score`: minimal score to define threshold for hits (default = .8)
- `append`: logical flag, if append=TRUE the binding sites will be appended to already existing results
- `background_scan`: logical flag, if background_scan=TRUE the background sequences will be searched for transcription factor binding sites
- `n.cpu`: number of CPUs to be used for parallelization. Default value is 'NA' in which case the number of available CPUs is checked and than used.

**Value**

- `x`: an object of the class "cobindr" including the predicted transcription factor binding sites

**Author(s)**

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

**References**

uses matchPWM from package "Biostrings" (http://www.bioconductor.org/packages/release/bioc/html/Biostrings.html)

**See Also**

`rtfbs`, `search.gadem`
# Examples

```r
# use simulated sequences
library(Biostrings)

n <- 400 # number of input sequences
l <- 500 # length of sequences
n.hits <- 250 # number of 'true' binding sites
bases <- c("A","C","G","T") # alphabet
# generate random input sequences with two groups with differing GC content
seqs <- sapply(1:(3*n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.3,.22,.2,.28)), collapse=""))
seqs <- append(seqs, sapply(1:(n/4), function(x) paste(sample(bases, l, replace=TRUE, prob=c(.25,.25,.25,.25)), collapse=""))
path <- system.file("extdata/pfms/myod.tfpf",package='cobindR')
motif <- read.transfac.pfm(path)[[1]] # get PFM of binding site
# add binding sites with distance specificity
for(position in c(110, 150)) {
  hits <- apply(apply(motif, 2, function(x) sample(x=bases, size=n.hits, prob=x, replace=TRUE)), 1, paste, collapse="")
  pos.hits <- round(rnorm(n.hits, mean=position, sd=8))
  names(pos.hits) <- sample(1:n, n.hits)
  for(i in 1:n.hits) substr(seqs[as.integer(names(pos.hits)[i])], start=pos.hits[i], stop=pos.hits[i]+ncol(motif)) <- hits[i]
}
# save sample sequences in fasta file
tmp.file <- tempfile(pattern = "cobindr_sample_seq", tmpdir = tempdir(), fileext = ".fasta")
writeXStringSet(DNAStringSet(seqs), tmp.file)
# run cobindr
runObj <- cobindr(cfg, name="cobindr test using sampled sequences")
# perform tfbs prediction using matchPWM
runObj.bs <- search.pwm(runObj, min.score = 90)
# show results
plot.positionprofile(runObj.bs)
# clean up
unlink(tmp.file)
```

---

### seqObj

**cobindR SeqObj object constructor**

**Description**

cobindR SeqObj object constructor

**Usage**

```r
## S4 method for signature
## 'DNAString,character,character,character,character,character,character'
seqObj(seq,id,name,species,comment,location)
```
SeqObj-class

Arguments

seq  DNAString object holding the sequence
id   id (character)
name id (character)
species id (character)
comment id (character)
location id (character)

Value

cobindR SeqObj object

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

cobindRConfiguration

Examples

library(Biostrings)
so <- seqObj(DNAString('A'), id='', name='', species='', comment='', location='')
sequence(so)

SeqObj-class  Class "SeqObj"

Description

Container for DNA sequence and its meta-data.

Objects from the Class

Objects can be created by calls of the form new("SeqObj", seq, id, species, name, comment, location).

Slots

uid: Object of class "character" ~~ unique id for internal representation
name: Object of class "character" ~~ biological reference name, if available
species: Object of class "character" ~~ reference species
location: Object of class "character" ~~ location on the reference genome
comment: Object of class "character" ~~ comments and notes
sequence: Object of class "DNAString" ~~ the sequence
Methods

  initialize signature(.Object = "SeqObj"): ...
  rtfbs.intern signature(object = "SeqObj"): ...
  write.fasta signature(sequences = "SeqObj"): ...

Author(s)

  Manuela Benary <manuela.benary@cms.hu-berlin.de>

See Also

  cobindr configuration

Examples

  showClass("SeqObj")

  sequence (DNAString)

Description

  returns sequence of cobindR SeqObj object.

Usage

  ## S4 method for signature 'SeqObj'
  sequence(x)
  ## S4 replacement method for signature 'SeqObj,DNAString'
  sequence(x) <- value

Arguments

  x  a cobindR seqObj object

  value  DNAString of the actual DNA sequence in this SeqObj

Value

  sequence (DNAString)

Author(s)

  Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

  uid,name,species,location,comment,sequence

Examples

  library(Biostrings)
  so <- seqObj(DNAString("A"), id='', name='', species='', comment='',location='')
  sequence(so)
sequences

---

sequences

**sequences of cobindr object**

---

**Description**

sequences of cobindr object.

**Usage**

```r
## S4 method for signature 'cobindr'
sequences(x)

## S4 replacement method for signature 'cobindr,list'
sequences(x) <- value
```

**Arguments**

- `x` a cobindr object
- `value` the list of input sequences of type SeqObj

**Value**

sequences (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

`uid`, `name`, `sequences`, `bg_sequences`, `desc`, `configuration`, `binding_sites`, `bg_binding_sites`, `pfm`, `pairs`, `bg_pairs`, `pairs_of_interest`

**Examples**

```r
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/sox_oct_example_vignette_seqs.fasta',package='cobindR')
sequence_origin(cfg) <- 'Mouse Embryonic Stem Cell Example ChIP-Seq Oct4 Peak Sequences'
cbr <- cobindr(cfg)
length(sequences(cbr))
```
**sequence_origin**

returns sequence_origin of cobindR configuration object.

**Usage**

```r
## S4 method for signature 'configuration'
sequence_origin(x)
## S4 replacement method for signature 'configuration,character'
sequence_origin(x) <- value
```

**Arguments**

- `x` a cobindR configuration object
- `value` the origin of the sequence

**Value**

sequence_origin (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `sequ...
**sequence_type**

**Arguments**

- `x` a cobindR configuration object  
- `value` the source of which the sequence is retrieved

**Value**

- `sequence_source` (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`

**Examples**

```r
cfg <- cobindRConfiguration()  
sequence_source(cfg)
```

---

**Description**

sequence type of cobindR configuration object

**Usage**

```r
## S4 method for signature 'configuration'
sequence_type(x)
```

```r
## S4 replacement method for signature 'configuration,character'
sequence_type(x) <- value
```

**Arguments**

- `x` a cobindR configuration object  
- `value` the type of the sequence used in this experiment (e.g. promotor)

**Value**

- `sequence_type` (character)

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`
Examples

cfg <- cobindRConfiguration()
sequence_type(cfg)

Arguments

object a cobindR configuration object
value name of species in this experiment or SeqObj

Value

sequence / experiment species (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin

downstream, upstream, max_distance, pairs, pfm_path, threshold, fdrThreshold, path, mart, pValue

Examples

cfg <- cobindRConfiguration()
species(cfg)
testCpG

function to cluster sequences based on their CpG and GC content

Description

diagnostical function - GC content and CpG content are clustered using 2D gaussian models (Mclust). FALSE is returned if > max.clust (default=1) subgroups are found using the bayesian information criterion (BIC). If do.plot=TRUE, the results are visualized.

Usage

## S4 method for signature 'cobindr'
testCpG(x, max.clust = 4, do.plot = F, n.cpu = NA)

Arguments

x an object of the class "cobindr", which will hold all necessary information about the sequences and the hits.

max.clust integer describing the maximal number of clusters which are used for separating the data.

do.plot logical flag, if do.plot=TRUE a scatterplot for the GC and CpG content for each sequence is produced and the clusters are color coded.

n.cpu number of CPUs to be used for parallelization. Default value is 'NA' in which case the number of available CPUs is checked and than used.

Value

result logical flag, FALSE is returned if more than one subgroups are found using the bayesian information criterion (BIC)

gc matrix with rows corresponding to sequences and columns corresponding to GC and CpG content

Author(s)

Robert Lehmann <r.lehmann@biologie.hu-berlin.de>

References

the method uses clustering functions from the package "mclust" (http://www.stat.washington.edu/mclust/)

See Also

plot.gc
threshold

Examples

cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/example.fasta', package='cobindR')
# avoid complaint of validation mechanism
pfm_path(cfg) <- system.file('extdata/pfms',package='cobindR')
pairs(cfg) <- ''
runObj <- cobindr(cfg)
testCpG(runObj, max.clust = 2, do.plot = TRUE)

Description

threshold used in motif hit finding

Usage

### S4 method for signature 'configuration'
threshold(x)
### S4 replacement method for signature 'configuration,numeric'
threshold(x) <- value

Arguments

- **x**: a cobindR configuration object
- **value**: the hit threshold

Value

threshold (numeric)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

id, experiment_description, sequence_source, sequence_origin, sequence_type, bg_sequence_source, bg_sequence_origin, species, downstream, upstream, max_distance, pairs, pfm_path, threshold, fdrThreshold, path, mart, pValue

Examples

cfg <- cobindRConfiguration()
threshold(cfg)
uid  
uid of cobindR SeqObj object

Description

uid of cobindR seqObj object.

Usage

```r
## S4 method for signature 'SeqObj'
uid(x)
## S4 method for signature 'cobindr'
uid(x)
## S4 replacement method for signature 'SeqObj,character'
uid(x) <- value
## S4 replacement method for signature 'cobindr,character'
uid(x) <- value
```

Arguments

- `x` a cobindR seqObj object
- `value` the unique id of the sequence or cobindr object

Value

uid (character)

Author(s)

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

See Also

uid, name, species, location, comment, sequence

Examples

```r
library(Biostrings)
so <- seqObj(DNAString('A'), id='', name='', species='', comment='', location='')
uid(so)
```
upstream  

**Description**

upstream range [bp] used in experiment

**Usage**

```r
## S4 method for signature 'configuration'
upstream(x)
## S4 replacement method for signature 'configuration,numeric'
upstream(x) <- value
```

**Arguments**

- `x`: a cobindR configuration object
- `value`: upstream distance [bp] of feature to be included (numeric)

**Value**

- considered upstream range [bp]

**Author(s)**

Rob Lehmann <r.lehmann@biologie.hu-berlin.de>

**See Also**

- `id`, `experiment_description`, `sequence_source`, `sequence_origin`, `sequence_type`, `bg_sequence_source`, `bg_sequence_origin`, `species`, `downstream`, `upstream`, `max_distance`, `pairs`, `pfm_path`, `threshold`, `fdrThreshold`, `path`, `mart`, `pValue`

**Examples**

```r
cfg <- cobindRConfiguration()
upstream(cfg)
```

---

**write.bindingsites**  

**writes predicted binding sites as a BED file.**

**Description**

writes predicted binding sites as a BED file.

**Usage**

```r
## S4 method for signature 'cobindr'
write.bindingsites(x, file = NULL, background = FALSE)
```
Arguments

- **x**: an object of the class "cobindr", which holds all necessary information about the sequences and the predicted binding sites.
- **file**: path to file. If filename is 'NULL' a filename is generated based on the name of the object of class "cobindr".
- **background**: logical flag. If background is 'TRUE' the binding sites found in the background sequences are used.

Note

At the moment write.bindingsites() only works for sequences based on gene ids. Otherwise please use write.bindingsites.table().

Author(s)

Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also

write.bindingsites.table, write.pairs, write.sequences, write

---

**write.bindingsites.table**

*function to write predicted TFBS into a tab-separated file.*

Description

function to write predicted TFBS into a tab-separated file.

Usage

```r
## S4 method for signature 'cobindr'
write.bindingsites.table(x, file = NULL)
```

Arguments

- **x**: an object of the class "cobindr", which will hold all necessary information about the sequences and the predicted binding sites.
- **file**: path to file. If filename is 'NULL' a filename is generated based on the name of the object of class "cobindr".

Author(s)

Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also

write.pairs, write.bindingsites, write.sequences, write
write.pairs function to write output of findPairs into file

Description
Function writes the results of findPairs() as a tab-separated file. The file consists of 6 columns, namely
- a unique id for each pair,
- the unique id of the sequence, where the pair was found,
- the names of the corresponding PFM s,
- the unique id for each PFM, and
- the distance window in which the pair occurs.

Usage
## S4 method for signature 'cobindr'
write.pairs(x, file = NULL, background = FALSE)

Arguments
- x: an object of the class "cobindr", which holds all necessary information about the sequences and the predicted binding sites.
- file: path to file. If filename is 'NULL' a filename is generated based on the name of the object of class "cobindr".
- background: logical flag. If background is 'TRUE' the pairs found in the background sequences are used.

Author(s)
Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also
write.bindingsites.table, write.bindingsites, write.sequences, write

write.sequences writes the sequences of a cobindr-object into a fasta file.

Description
writes the sequences of a cobindr-object into a fasta file.

Usage
## S4 method for signature 'cobindr'
write.sequences(x, slotname = "sequences", file = NULL)
Arguments

- **x**: an object of the class "cobindr", which will hold all necessary information about the sequences.
- **slotname**: string, describing whether to use foreground sequences (default) or background sequences
- **file**: path to file. If filename is 'NULL' a filename is generated based on the name of the object of class "cobindr".

Author(s)

Stefan Kroeger <kroeger@informatik.hu-berlin.de>

See Also

`write.bindingsites.table`, `write.bindingsites`, `write.pairs`, `write`

Examples

```r
cfg <- cobindRConfiguration()
sequence_type(cfg) <- 'fasta'
sequence_source(cfg) <- system.file('extdata/example.fasta', package='cobindR')
# avoid complaint of validation mechanism
pfm_path(cfg) <- system.file('extdata/pfms',package='cobindR')
pairs(cfg) <- ''
runObj <- cobindr(cfg)
write.sequences(runObj, file = file.path(tempfile("example.txt", tempdir())))
```
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