Package ‘colocalized’

July 22, 2025

Type Package

Title Clusters of Colocalized Sequences

Version 0.2.0

Description
Also abbreviates to ``CCSeq''. Finds clusters of colocalized sequences in .bed annotation files
up to a specified cut-off distance. Two sequences are colocalized if they
are within the cut-off distance of each other, and clusters are sets of
sequences where each sequence is colocalized to at least one other sequence
in the cluster. For a set of .bed annotation tables provided in a list
along with a cut-off distance, the program will output a file containing
the locations of each cluster. Annotated .bed files are from
the 'pwmscan' application at <`https://ccg.epfl.ch/pwmtools/pwmscan.php`>.
Personal machines might crash or take excessively long depending
on the number of annotated sequences in each file and whether chromsearch()
or gensearch() is used.

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1.9000

Depends R (>= 3.0.0)

Imports foreach, doParallel, purrr, utils

NeedsCompilation no

Author Stefan Golas [cre, aut]

Maintainer Stefan Golas <`stefanmgolas@gmail.com`>

Repository CRAN

Date/Publication 2019-10-18 21:20:12 UTC

Contents

`chromsearch` *Search one chromsome*

Description

Search a single chromosome for clusters of TF binding sequences. Example produces a null result, test the same complex on "chr9" for a positive reading.

Usage

```
chromsearch(choose, n, chrom)
```

Arguments

`choose`	List of .bed tables
`n`	Cut-off distance between colocalized sequences
`chrom`	Chromosome to be searched given as e.g. "chr19"

Value

A table containing the addresses (as one dimensional intervals) of the members of every cluster, with some annotation data.

Examples

```
complex<-list(nfkb1,nfkb2,relb)
chromsearch(complex,150,"chrY")
```

`colocalized` *Colocalized cluster search.*

Description

Searches for clusters of colocalized transcription factor (TF) binding sequences. `colocalized(choose,chr,n)` searches for instances where the sequences from each table element in choose are colocalized to within a cut-off distance.

Usage

```
colocalized(choose, chr, n, cores)
```

Arguments

`choose`	List of .bed tables
`chr`	Chromosome
`n`	The cut-off distance
`cores`	Number of cores for parallel processing. Leaving this blank causes the program to use default (series) processing

Value

Table of clusters found in `chr`

Examples

```
complex<-list(nfkb1,nfkb2,relb)
colocalized(complex,"chrY",150)
```

`ColocalizedFullSearch` *Colocalized full search.*

Description

Wrapper for `colocalized` that searches every chromosome shared between the given .bed files.

Usage

```
ColocalizedFullSearch(choose, n, cores)
```

Arguments

`choose`	List of .bed tables
`n`	The cut-off distance
`cores`	Number of cores for parallel processing. Leaving this blank causes the program to use default (series) processing

Value

List of lists of each cluster found in each chromosome.

`colocalized_sequential` *Sequential cluster search*

Description

Search one chromosome for clusters using default non-parallel processing.

Usage

```
colocalized_sequential(choose, chr, n)
```

Arguments

`choose`	List of .bed tables
`chr`	Chromosome to be searched given as e.g. "chr19"
`n`	Cut-off distance between colocalized sequences

Value

Table containing the addresses (as one dimensional intervals) of the members of every cluster, with some annotation data.

Examples

```
complex<-list(nfkb1,nfkb2,relb)
colocalized_sequential(complex,"chrY",150)
```

`gensearch` *Whole genome search.*

Description

Search the whole genome for clusters of colocalized TF binding sequences.

Usage

```
gensearch(choose, n, cores)
```

Arguments

`choose`	List of .bed tables
`n`	The cut-off distance
`cores`	Number of cores for parallel processing. Leaving this blank causes the program to use default (series) processing

Value

Table containing the addresses (as one dimensional intervals) of the members of every cluster, with some annotation data.

`nfkb1` *NFKB1 bed file*

Description

nfkb1

Usage

`nfkb1`

`nfkb1`

Format

A dataframe with 230505 rows and 8 columns

Author(s)

Stefan Golas

Source

`https://ccg.epfl.ch/pwmtools/pwmscan.php`

`https://ccg.epfl.ch/pwmtools/pwmscan.php`

`nfkb2` *NFKB2 bed file*

Description

nfkb2

Usage

```
nfkb2
```

```
nfkb2
```

Format

A dataframe with 1901 rows and 8 columns

Author(s)

Stefan Golas

Source

https://ccg.epfl.ch/pwmtools/pwmscan.php

https://ccg.epfl.ch/pwmtools/pwmscan.php

`onedim_dist` *Create a colocalization matrix*

Description

Create a colocalization matrix

Usage

```
onedim_dist(bed1, bed2, n)
```

Arguments

`bed1`	A .bed table
`bed2`	A .bed table
`n`	The cut-off distance

Value

A colocalization matrix whose dimensions are the number of rows in `bed1` by the number of rows in `bed2`. Entry i,j is a 1 if the ith sequence in `bed1` is within the cut-off distance of the jth sequence in `bed2`, and 0 otherwise.

Examples

```
chr<-"chrY"
onedim_dist(nfkb1[which(nfkb1[,1]==chr),],nfkb2[which(nfkb2[,1]==chr),],150)
```

`relb` *RELB bed file*

Description

relb

Usage

```
relb

relb
```

Format

A dataframe with 1448 rows and 8 columns

Author(s)

Stefan Golas

Source

https://ccg.epfl.ch/pwmtools/pwmscan.php

https://ccg.epfl.ch/pwmtools/pwmscan.php

Index