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chromsearch	<i>Search one chromosome</i>
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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

<code>choose</code>	List of .bed tables
<code>chr</code>	Chromosome
<code>n</code>	The cut-off distance
<code>cores</code>	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

<code>choose</code>	List of .bed tables
<code>n</code>	The cut-off distance
<code>cores</code>	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.

nfbk1	<i>NFKB1 bed file</i>
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Description

nfbk1

Usage

nfbk1

nfbk1

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>

nfk2	<i>NFKB2 bed file</i>
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Description

nfk2

Usage

nfk2

nfk2

Format

A dataframe with 1901 rows and 8 columns

Author(s)

Stefan Golas

Source

<https://ccg.epfl.ch/pwmtools/pwmtools.php>

<https://ccg.epfl.ch/pwmtools/pwmtools.php>

onedim_dist	<i>Create a colocalization matrix</i>
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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 i th sequence in bed1 is within the cut-off distance of the j th sequence in bed2, and 0 otherwise.

Examples

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

relb	<i>RELB bed file</i>
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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>

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