# Package ‘colocalized’

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**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.

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1.9000

**Depends** R (>= 3.0.0)

**Imports** foreach, doParallel, purrr, utils

**NeedsCompilation** no

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**Repository** CRAN

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`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.

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## `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

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