Package ‘SVM2CRMdata’

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Type Package

Title An example dataset for use with the SVM2CRM package

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Author Guidantonio Malagoli Tagliazucchi

Maintainer Guidantonio Malagoli Tagliazucchi
`<guidantonio.malagolitagliazucchi@unimore.it>`

Description An example dataset for use with the SVM2CRM package.

License LGPL (>= 2)

Depends R(>= 3.2.0)

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`CD4-H2AK5ac.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

```
"CD4-H2AK5ac.sort.txt"
```

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`CD4-H2AK9ac.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

```
"CD4-H2AK9ac.sort.txt"
```

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`CD4-H3K23ac.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

`"CD4-H3K23ac.sort.txt"`

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`CD4-H3K27ac.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

`"CD4-H3K27ac.sort.txt"`

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`CD4_matrixInputSVMbin100window1000`

Histone modification map from CD4

Description

The first step of the analysis with SVM2CRM is the preprocessing of the data. Basically, SVM2CRM allow to import bed files in the working directory using cisREfindbed. This function import bed files, and then perfomed codify the signals of each histone marks considering the windows size defined by the user. Specially this function require diverse parameters. A vector with the list of bed files that the user want use. The bin.size and the windows size that respectivelly repsent the size of bin used to normalized the data (e.g. 100bp) and windows size that the use want use to describe the signal of each histone marks (e.g. 1000bp). Finally, the user can set a function to smooth the signal of the histone marks inside da particular windows (e.g. median). During this step cisREfindbed generate a data.frame that contains on the column the histone marks, and on the rows the corresponding signals genome-wide.

Usage

```
data(CD4_matrixInputSVMbin100window1000)
```

Format

A data.frame where in the rows there are the genomic regions while in the columns the signals of histone modifications

Source

see Wang Z et al., 2008

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`GSM393946.distal.p300fromTSS` *A bed file of p300 genomic regions*

Description

A bed file of p300 genomic regions.

Usage

```
"GSM393946.distal.p300fromTSS.txt"
```

Format

The output of getSignal

Source

see Wang Z et al., 2008

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`H3K27me3.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

```
"H3K27me3.sort.txt"
```

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`H3K4me1.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

```
"H3K4me1.sort.txt"
```

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`H3K4me2.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

```
"H3K4me2.sort.txt"
```

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`H3K4me3.sort` *Histone modification ChIP-seq data in CD4*

Description

Histone modification ChIP-seq data in CD4.

Usage

`"H3K4me3.sort.txt"`

Format

A bed file

Source

created with a custom script

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`p300.distal.fromTSS` *P300 binding sites from CD4*

Description

This file contain the genomic regions with the p300 binding sites that have a distance of 1000kb from TSSs.

Usage

`"p300.distal.fromTSS.txt"`

Format

A bed file format with chromosome, start, end

Source

see Wang Z et al., 2008

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`random.region.hg18.nop300` *A bed file with the coordinates of random regions in Hg18*

Description

A bed file with the coordinates of random regions in Hg18, created using a custom script and bedtools (Quinlan AR., et al 2010).

Usage

```
"random.region.hg18.nop300.txt"
```

Format

A bed file format with chromosome, start, end

Source

created with a custom script

References

Quinlan AR, Hall IM. BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics. 2010 Mar 15;26(6):841-2.

`SVM2CRMdata` *An example dataset for the SVM2CRM package*

Description

This dataset contain raw ChIPseq data of H2AK9ac, H3K23ac, H3K27ac, H3K27me3, H3K4me1, H3K4me3 in CD4+ T-cells. Data were downloaded from: Wang Z et al., 2008

Author(s)

Guidantonio Malagoli Tagliazucchi <guidantonio.malagolitagliazucchi@unimore.it>

Examples

```
dataDir <- system.file("data", package="SVM2CRMdata")
setwd(dataDir)
dir()
```

`train_negative` *Random genomic regions of ChIP-seq without enhancers*

Description

This file contain the output of getSignal using a little number of histone marks and database of random regions without enhancers.

Usage

```
data("train_negative")
```

Format

The output of getSignal

Source

see Wang Z et al., 2008

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

`train_positive` *ChIP-seq signal in correspondence of enhancers*

Description

This file contain the output of getSignal using a little number of histone marks and database of enhancers.

Usage

```
data("train_positive")
```

Format

The output of getSignal

Source

see Wang Z et al., 2008

References

Wang Z, Zang C, Rosenfeld JA, Schones DE, Barski A, Cuddapah S, Cui K, Roh TY,Peng W, Zhang MQ, Zhao K. Combinatorial patterns of histone acetylations and methylations in the human genome. Nat Genet. 2008 Jul;40(7):897-903.

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