Package

August 16, 2019

Title graph position weight matrix

Version 0.0.0.9000

Description This is to generate Graph Position Weight Matrix.

Depends R (>= 3.5.2)

License What license is it under?

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown

VignetteBuilder knitr

Imports ggplotify,
  ggplot2,
  gridExtra,
  grid,
  lattice,
  gridGraphics,
  base2grob,
  ggplot2,
  ggseqlogo

RoxygenNote 6.1.1.9000

R topics documented:

Barandseqlogo	*A function for generating barchart and seq-logo of co-factors of selected TF*

Usage

```
Barandseqlogo(NumberofTop, highestscore, cell, TF, Local = FALSE,
  path = "")
```

Arguments

NumberofTop   Number of top co-factors with higher co-binding

\itemhighestscoreCo-binding

\itemcellA character string, which is the name of cell under study.

\itemTFA character string which will be the Transcription Factor of interest.

\itemLocalA logical value, which will read a local .CSV file in case of TRUE. The file should contain two columns: scores, columnnames which are the co-binding percentages and IDs respectively.

\itempathThe path to .CSV file in case Local=TRUE.

This function generates a barchart of co-binding

BetaAdder	*A function to merge Beta Score matrices to generate a single matrix.*

Description

This function takes the class object and creates a merge of exclusive Beta Score Matrices by calculating the elementwise weighted average of them; up to the forking position. Weight of each matrix, is the overlapping percentage of intersectPeakmatrix.

Usage

```
BetaAdder(TheObject, sp)
```

Arguments

TheObject   is an object of S4 class that holds original matrices exported from the package TFregulomeR().

sp   is the forking position. User can define up to which position it is required to merge two matrices using this argument.

Value

This function receives a class object, and returns an updated class object.

Examples

```
This function is called within ClassAssignment() function.
```

ConvertToFTRANSFAC *Generating proper matrix similar to TRANSFAC format of all matrices.*

Description

This function generates a matrix of 5 column (Position,A,T, C, G) with redundant position numbers at Position column reflecting number of leafs and their PWMs.

Usage

```
ConvertToFTRANSFAC(TheObject)
```

Arguments

TheObject   This argument is an object of the class which holds the information ready to be plotted.

Value

This class receives a class Object which holds the plotting data, and updates it by adding the proper matrix of new format: FTRANSFAC.

FPWMPlotter *A function for generating the forked Position Weight Matrix*

Description

This function takes the generated class object and plots a forked position weight matrix.

Usage

```
FPWMPlotter(TheObject, Methylation = TRUE)
```

Arguments

Methylation   is a logical value. If it set on TRUE, Methylation level chart will also be plotted. If Flase, only sequence logos will be shown.

GraphDataObj   is an object of S4 class with modified and converted data ready to be plotted.

MatrixAdder	*A function to merge motif matrices to generate one matrix as parent node.*

Description

This function takes the object and creates a merge of all matrices by claculating the elementwise addition of them, up to a user specified position (Forking Position).

Usage

```
MatrixAdder(TheObject, sp)
```

Arguments

TheObject	is a object of S4 class that holds original matrices exported from the package TFregulomeR().
sp	is the forking position. User can define up to which position it is required to merge matrices using this argument.

Value

This function recieves a class object, and returns an updated class object by adding merged matrix to parentmatrix slot

Examples

```
This function is called whithin ClassAssignment() function.
```

ModifyBetaFormat	*A function for converting Beta Score matrices into proper data frames.*

Description

This function receives the S4 class object and converts Betalevel matrices into data frames for better plotting and browsing purposes.

Usage

```
ModifyBetaFormat(TheObject)
```

Arguments

TheObject	is an object of S4 class that holds original matrices exported from the package TFregulomeR().

Value

This function receives a class object, and returns an updated class object by modifying Beta Score Matrices.

Examples

```
This function is called within ClassAssignment() function.
```

ObjectGenerator | *A function togenerate a class object then assign proper data exported from TFregulomeR to its slots.*

Description

This function assigns proper data to their associated slots of a S4 classe. This information is either provided by user, or exported from TFregulomeR's dataware using user specified data.

Usage

```
ObjectGenerator(sp, peak_id_y_list, peak_id_x, height = 2, width = 3)
```

Arguments

sp	This argument, defines from which point on, the matrix needs to be forked, or in the other words, up to which point two exclusive matrices need to be aggregated.
peak_id_y_list	This argument is a list of TF ID's which will be intersected with Peak_id_x.
peak_id_x	This argument holds an id of TFBS compatible with TFregulomeR(). This is the target peak ID wich will be employed by IntersecPeakMatrix of TFregulomeR to extract desired data.
height	An argument which allows user to customize the height of final graph relative to screen.
width	An argument which allows user to customize the width of final graph relative to screen.

Value

This component, returns a class object which holds all the neccessary information for other functuins.

PlotMultiFTRANSFACFile

A function for storing .PDF of plots, by providing a .txt file of FPWMs concatination, in proper format.

Description

This function reads an stored .txt file of multiple FTRANSFAC matrices and generates the associated plot for each set then stores the figure as a PDF file. Name of each files indicates from each line the infomration is being imported to result to given plot.

Usage

```
PlotMultiFTRANSFACFile(File = "All.txt")
```

Arguments

File   the directory of .txt file of multiple FPWMs merged in proper format.

Value

Stores number of PDF files regarding the number of FPWMs provided within the file.

ReadFTRANSFACFile	*A function for generating a class object from a local file in proper format*

Description

This function reads an stored .txt file of FTRANSFAC format and constructs a class object from it. As default, the returned class Object does not contain Methylation Score matrices. If needed, files exported from TFregulomeR() with the same name and format should be provided before setting MEthylation==TRUE.

Usage

```
ReadFTRANSFACFile(File = "MM1_HSA_K562_CEBPB___4-FTRANSFAC.txt",
  Methylation = FALSE)
```

Arguments

File   the directory of .txt file

Methylation   a logical argument which indicates if Methylation Score files are provided and
                          needed to be included in Object or not.

Value

A class object for plotting. The Methylation Score matrices can be optionally ommitted or not.

StoreFTRANSFACFile	*Generation and storing a file of the standard TRANSFAC format*

Description

This function generates a .txt file of the format TRANSFAC with slight modifications in positions column.

Usage

```
StoreFTRANSFACFile(TheObject)
```

Arguments

TheObject   This argument is an object of the class which holds the information ready to be
                          plotted.IDs, Scores and Froked_PWM are mednatory.

Value

This function stores a .txt file at working directory, and returns name of the file for more convenience.

StoreMultiTRANSFACFile

Generating and storing a .txt file named "All.txt" which contains multiple FPWMs, contatinated together, respecting TRANSFAC format.

Description

This function generates a .txt file which holds number of the data structures needed for one set of plotting in FTRANSFAC format.

Usage

```
StoreMultiTRANSFACFile(List_sp, Listof_peak_id_y_list, List_peak_id_x)
```

Arguments

List_sp   List of forking position numbers for each one of FPWM.

Listof_peak_id_y_list
                 A list of lists. Each list within this list, is a set of IDs which are going to form one FPWM plot.

List_peak_id_x   A list of IDs. The ID in List_peak_id_x[i] will be employed to form multiple IntersecPeakMatrices with all the IDs exisiting in Listof_peak_id_y_list[i].

Value

This function stores a .txt file at working directory, and returns name of the file for more convenience.

Index