

# Package

June 9, 2020

**Title** Forked Position Weight Matrix.

**Version** 0.0.0.9000

**Description** This package generates a Forked Position Weight Matrix which is helpful to have a better insight about characteristics of Transcription Factor Dimers.

**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,  
stringr,  
cowplot,  
reader

**RoxygenNote** 7.1.0

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Barandseqlogo	<i>A function for generating barchart and seq-logo of co-factors of selected TF</i>
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## Description

This function generates a barchart of co-binding Percentage for each co-factor of selected TF, along with seq-logo for each of co-factors.

## Usage

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

## Arguments

NumberofTop	Number of top co-factors with higher co-binding Percentage to be illustrated
highestscore	Co-binding Percentage which will be the minimum percentage of the shown co-factors.
cell	A character string, which is the name of cell under study.
TF	A character string which will be the Transcription Factor of interest.
Local	A 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.
path	The path to .CSV file in case Local=TRUE.
Methylation	Is a logic argument which indicates if user wants Methylation Score to be plotted on top of sequence logos or not.

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BetaAdder	<i>A function to merge Beta Score matrices to generate a single matrix.</i>
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### 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.

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ConvertToFTRANSFAC	<i>Generating proper matrix similar to TRANSFAC format of all matrices.</i>
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### 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.
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### Value

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

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Ensembles	<i>A function for generating the object for TF in different cell lines</i>
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### Description

This function browses all the cell lines of a given TF and augments the provided motif with added cell lines to represent the impact of cell line on motif structure

### Usage

```
Ensembles(sp, tfname, tfID, CelllinesNumb)
```

### Arguments

sp	Forking point for final plot
tfname	The name of target tf in strings
tfID	the targeted motif using MethMotif IDs as the target cell line under study.
CelllinesNumb	Maximum number of cell lines to be considered

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ensemblesfunc	<i>A function for exporting the motif matrix and augmenting it with additional cell lines</i>
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### Description

This function

### Usage

```
ensemblesfunc(tfname = "JUN", tfID = "MM1_HSA_K562_JUN")
```

### Arguments

tfname	The name of target tf in strings
the	targeted motif using MethMotif IDs as the target cell line under study.

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FPWMPLOTTER

*A function for generating the forked Position Weight Matrix*


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### 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 FALSE, 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.*


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### Description

This function takes the object and creates a merge of all matrices by calculating 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 receives a class object, and returns an updated class object by adding merged matrix to parentmatrix slot

### Examples

This function is called within ClassAssignment() function.

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ModifyBetaFormat	<i>A function for converting Beta Score matrices into proper data frames.</i>
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### 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().
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### 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.

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ObjectGenerator	<i>A function to generate a class object then assign proper data exported from TFregulomeR to its slots.</i>
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### 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 which 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 necessary information for other functions.

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PlotMultiFTRANSFACFile

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

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**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 information 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.

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ReadFTRANSFACFile

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

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**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 omitted or not.

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StoreFTRANSFACFile	<i>Generation and storing a file of the standard TRANSFAC format</i>
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**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 Forked_PWM are mandatory.
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**Value**

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

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StoreMultiTRANSFACFile	<i>Generating and storing a .txt file named "All.txt" which contains multiple FPWMs, concatenated together, respecting TRANSFAC format.</i>
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**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 existing 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.



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storeTRANSFAC	<i>A function for storing TRANSFAC files of the forked matrices.</i>
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### Description

This function generates files of regular TRANSFAC format in order to further analysis and evaluation. Each file name holds the name of Transfactor of interest, and the co-factor that is under analysis in the current matrix.

### Usage

```
storeTRANSFAC(TheObject)
```

### Arguments

TheObject	the input is the object of FPWM class that holds the raw matrices directly exported from TFregulomeR().
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ToTFBStools	<i>A function for generating object of TFBStools holding PFM of each forked matrix.</i>
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### Description

This function generates a TFBStools object of each matrix present in FPWM class object, and returns a list containing all the objects.

### Usage

```
ToTFBStools(TheObject)
```

### Arguments

TheObject	is the object of the FPWM class. It needs to contain the matrices, IDs and parent matrix.
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