Package ‘corrDNA’

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Type Package

Title Finding Associations in Position-Wise Aligned DNA Sequence Dataset

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Imports mvtnorm

LazyData TRUE

Description Can be useful for finding associations among different positions in a position-wise aligned sequence dataset. The approach adopted for finding associations among positions is based on the latent multivariate normal distribution.

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NeedsCompilation no

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R topics documented:

assoc_comb ........................................... 2
assoc_Zi.Zj ............................................ 3
assoc_Zi.ZjR .......................................... 4
assoc_Zi.ZjY ........................................... 5
assoc_ZiR.ZjR ........................................ 6
assoc_ZiR.ZjY ........................................ 7
assoc_ZiY.ZjY ......................................... 8
don_dat .................................................. 9

Index 10
assoc_comb

Complete association matrix.

Description

All the six possible association matrices can be merged into a single matrix to visualize the overall association among positions as well as among the occurrences of nucleotides of different positions, in a position-wise aligned sequence dataset.

Usage

assoc_comb(x, rZiZj, rZiZjR, rZiZjY, rZiRZjR, rZiRZjY, rZiYZjY)

Arguments

x A dataframe of position-wise aligned sequence dataset having A, T, G and C only.

rZiZj An object generated by using the function assoc_Zi.Zj.
rZiZjR An object generated by using the function assoc_Zi.ZjR.
rZiZjY An object generated by using the function assoc_Zi.ZjY.
rZiRZjR An object generated by using the function assoc_ZiR.ZjR.
rZiRZjY An object generated by using the function assoc_ZiR.ZjY.
rZiYZjY An object generated by using the function assoc_ZiY.ZjY.

Details

All the six association matrices are required to be generated prior to merging them into a single matrix.

Value

A numeric matrix of order 3L by 3L for the dataset of L nucleotides long sequences.

Author(s)

Prabina Kumar Meher & A. R. Rao

Examples

data(don_dat)
kk <- don_dat[1:300,]
zizj <- assoc_Zi.Zj(x=kk)
zizjr <- assoc_Zi.ZjR(x=kk, rZiZj=zizj)
zizjy <- assoc_Zi.ZjY(x=kk, rZiZj=zizj)
zirzjr <- assoc_ZiR.ZjR(x=kk,rZiZj=zizj,rZiZjR=zizjr)
zirzjy <- assoc_ZiR.ZjY(x=kk,rZiZj=zizj,rZiZjR=zizjr,rZiZjY=zizjy)
**assoc_Zi.Zj**

**Description**

Finding association between variables of $i^{th}$ position and $j^{th}$ position. In any position wise aligned sequence dataset, occurrences of R=(A,G) and Y=(C, T) at each position can be explained by a standard normal variate $Z$ based on certain threshold value. So, an association between any two position in the dataset can be obtained which will be the association between the two standard normal variates at this two positions. However, the two normal variates representing the occurrences of R and Y are independent of each other at a given position.

**Usage**

```r
assoc Zi.Zj(x)
```

**Arguments**

- **x**: A dataframe of position wise aligned sequence dataset having A, T, G and C only.

**Details**

The user has to supply the sequence dataset in tab delimited format and not in FASTA format. Each sequence (row) should contain only standard nucleotides (A, T, G and C). Each sequence should be same length.

**Value**

A numeric matrix of order $L$ by $L$ for the dataset of $L$ nucleotides long sequences.

**Author(s)**

Prabina Kumar Meher & A. R. Rao

**Examples**

```r
data(don_dat)
kK <- don_dat[1:300,]
zizj <- assoc_Zi.Zj(x=kK)
zizj
define_Correlation <- assoc_comb(x=kK, rZiZj=rZiZj, rZiZjY=rZiZjY, rZiRZj=rZiRZj, rZiRZjY=rZiRZjY, rZiYZjY=rZiYZjY)
define_Correlation
```
Description
Finding association between variable $Z$ at $i^{th}$ position and $Z_R$ at $j^{th}$ position. Here, the standard normal variable $Z$ represents the occurrence of $R=(A,G)$ and $Y=(C,T)$ at each position in the position wise aligned dataset, whereas the standard normal variable $Z_R$ represents the occurrences of nucleotides $A$ and $G$ at any position based on some threshold value.

Usage
assoc.Zi.ZjR(x, rzizj)

Arguments
x A dataframe of position wise aligned sequence dataset having A, T, G and C only.
rzizj An object generated by using the function assoc.Zi.Zj.

Details
The user has to supply the input dataset as well as the output generated from the function assoc.Zi.Zj.

Value
A numeric matrix of order $L$ by $L$ for the dataset of $L$ nucleotides long sequences.

Note
It may happen that the convergence will not reach after a certain number of iterations and will not produce any output. In such situation, the user is advised to exclude or include some positions, or otherwise include or exclude certain sequences. The user should exploit both options till convergence is reached.

Author(s)
Prabina Kumar Meher & A. R. Rao

Examples
data(don_dat)
kk <- don_dat[1:300,]
zizj <- assoc.Zi.Zj(x=kk)
zizjr <- assoc.Zi.ZjR(x=kk, rzizj=zizj)
zizjr
assoc_Zi.ZjY

Association between variable \( Z_i \) and \( Z_j \).

Description
Finding association between variable \( Z \) at \( i^{th} \) position and \( Z_y \) at \( j^{th} \) position. Here, the standard normal variable \( Z \) represents the occurrence of \( R=(A,G) \) and \( Y=(C, T) \) at each position in the position wise aligned dataset, whereas the the standard normal variable \( Z_R \) represents the occurrences of nucleotides A and G at any position based on some threshold values.

Usage
assoc_Zi.ZjY(x, rzizj)

Arguments
- \( x \) A dataframe of position wise aligned sequence dataset having A, T, G and C only.
- \( rzizj \) An object generated by using the function assoc_Zi.Zj.

Details
The user has to supply the input dataset as well as the output generated from the function assoc_Zi.Zj.

Value
A numeric matrix of order \( L \) by \( L \) for the dataset of \( L \) nucleotides long sequences.

Note
It may happen that the convergence will not reach after a certain number of iterations and will not produce any output. In such situation, the user is advised to exclude or include some positions, or otherwise include or exclude certain sequences. The user should exploit both options till convergence is reached.

Author(s)
Prabina Kumar Meher & A. R. Rao

Examples
```r
data(don_dat)
kk <- don_dat[1:300,]
zizj <- assoc_Zi.Zj(x=kk)
zizjy <- assoc_Zi.ZjY(x=kk, rzizj=zizj)
zizjy```
Description
Finding association between variable $Z_R$ at $i^{th}$ position and $Z_R$ at $j^{th}$ position. Here, the standard normal variable $Z_R$ represents the occurrences of nucleotides A and G at any position based on some threshold value.

Usage
assoc.ZiR.ZjR(x, rZiZj, rZiZjR)

Arguments
x
A dataframe of position wise aligned sequence dataset having A, T, G and C only.

rzizj
An object generated by using the function assoc.Zi.Zj.

rzizjr
An object generated by using the function assoc.Zi.ZJR.

Details
The user has to supply the input dataset as well as the outputs generated from the functions assoc.Zi.Zj and assoc.Zi.ZJR.

Value
A numeric matrix of order $L$ by $L$ for the dataset of $L$ nucleotides long sequences.

Note
It may happen that the convergence will not reach after a certain number of iterations and will not produce any output. In such situation, the user is advised to exclude or include some positions, or otherwise include or exclude certain sequences. The user should exploit both options till convergence is reached.

Author(s)
Prabina Kumar Meher & A. R. Rao

Examples

data(don_dat)
kk <- don_dat[1:300,]
ziZj <- assoc.Zi.Zj(x=kk)
ziZjR <- assoc.Zi.ZJR(x=kk, rZiZj=ziZj)
ziZjR <- assoc.ZiR.ZjR(x=kk, rZiZj=ziZj, rZiZjR=ziZjR)
Finding association between variable $Z_R$ at $i^{th}$ position and $Z_Y$ at $j^{th}$ position. Here, the standard normal variable $Z_Y$ represents the occurrences C and T at each position in the position wise aligned dataset, and the standard normal variable $Z_R$ represents the occurrences of nucleotides A and G at any position based on some threshold values.

**Usage**

```r
assoc_zir.zjy(x, rzizj, rzizjr, rzizjy)
```

**Arguments**

- **x**: A dataframe of position wise aligned sequence dataset having A, T, G and C only.
- **rzizj**: An object generated by using the function `assoc_zi.zj`.
- **rzizjr**: An object generated by using the function `assoc_zi.zjr`.
- **rzizjy**: An object generated by using the function `assoc_zi.zjy`.

**Details**

The user has to supply the input dataset as well as the outputs generated from the functions `assoc_zi.zj`, `assoc_zi.zjr` and `assoc_zi.zjy`.

**Value**

A numeric matrix of order $L$ by $L$ for the dataset of $L$ nucleotides long sequences.

**Note**

It may happen that the convergence will not reach after a certain number of iterations and will not produce any output. In such situation, the user is advised to exclude or include some positions, or otherwise include or exclude certain sequences. The user should exploit both options till convergence is reached.

**Author(s)**

Prabina Kumar Meher & A. R. Rao
Examples

data(don_dat)
kk <- don_dat[1:300,]
zizj <- assoc_Zi.Zj(x=kk)
zizjr <- assoc_Zi.ZjR(x=kk, rZiZj=zizj)
zizjy <- assoc_Zi.ZjY(x=kk, rZiZj=zizj)
zirzjy <- assoc_ZiR.Zjy(x=kk, rZiZj=zizj, rZiZjR=zizjr, rZiZjY=zizjy)
zirzjy

== assoc_ZiY.ZjY ==

Association between variable $Z_{iY}$ and $Z_{jY}$.

Description

Finding association between variable $Z_Y$ at $i^{th}$ position and $Z_Y$ at $j^{th}$ position. Here, the standard normal variable $Z_Y$ represents the occurrences of nucleotides C and T at any position based on some threshold values.

Usage

assoc_ZiY.ZjY(x, rZiZj, rZiZjY)

Arguments

- **x**: A dataframe of position wise aligned sequence dataset having A, T, G and C only.
- **rZiZj**: An object generated by using the function `assoc_Zi.Zj`.
- **rZiZjY**: An object generated by using the function `assoc_Zi.ZjY`.

Details

The user has to supply the input dataset as well as the outputs generated from the functions `assoc_Zi.Zj` and `assoc_Zi.ZjY`.

Value

A numeric matrix of order $L$ by $L$ for the dataset of $L$ nucleotides long sequences.

Note

It may happen that the convergence will not reach after a certain number of iterations and will not produce any output. In such situation, the user is advised to exclude or include some positions, or otherwise include or exclude certain sequences. The user should exploit both options till convergence is reached.
**Author(s)**
Prabina Kumar Meher & A. R. Rao

**Examples**

```r
data(don_dat)
kk <- don_dat[1:300,]
zizj <- assoc_zi.Zj(x=kk)
zizjy <- assoc_zi.zjy(x=kk, rZiZj=zizj)
ziyzjy <- assoc_ziY.ZjY(x=kk, rZiZj=zizj, rZiZjY=zizjy)
ziyzjy
```

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**don_dat**

A sample dataset of human donor splice sites.

**Description**
This dataset comprises 1000 donor splice site sequences, where each sequence is of length 20 with 10 at the exon end and 10 at the intron start excluding the conserved di-nucleotide GT at the beginning of intron. This dataset was randomly taken from true donor splice sites of HS3D dataset.

**Usage**

```r
data(don_dat)
```

**References**

**Examples**

```r
data(don_dat)
```
Index

assoc_comb, 2
assoc_Zi.Zj, 2, 3, 4-8
assoc_Zi.ZjR, 2, 4, 6, 7
assoc_Zi.ZjY, 2, 5, 7, 8
assoc_ZiR.ZjR, 2, 6
assoc_ZiR.ZjY, 2, 7
assoc_ZiY.ZjY, 2, 8

don_dat, 9