Package 'PWMEnrich.Hsapiens.background'

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Title H. sapiens background for PWMEnrich

Type Package

LazyLoad yes

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Description PWMEnrich pre-
compiled background objects for H. sapiens (human) and MotifDb H. sapiens motifs.

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PWMEnrich.Hsapiens.background package overview

Description

This package provides a set of pre-compiled genomic background files for the PWMEnrich package and H. sapiens (human). The backgrounds were pre-compiled using unique 2kb promoters in human.

- MotifDb.Hsap.PFM - a list of position frequency matrices (PFMs) from MotifDb
- MotifDb.Hsap - the corresponding PWMs generated by using the background frequencies of A,C,G,T in a set of 2kb human (hg19) promoters.
- PWMLogn.hg19.MotifDb.Hsap - pre-compiled threshold-free lognormal background for MotifDb human PWMs. The lognormal distribution is fitted to 500bp chunks of 2kb human (hg19) promoters.
- PWMCutoff4.hg19.MotifDb.Hsap, PWMCutoff5.hg19.MotifDb.Hsap - pre-compiled Z-score background with cutoff of 4 and 5 (base e) for MotifDb human PWMs. The number of hits is counted in 2kb human (hg19) promoters.
- PWMPvalueCutoff1e2.hg19.MotifDb.Hsap, PPWMPvalueCutoff1e3.hg19.MotifDb.Hsap, PPWMPvalueCutoff1e4.hg19.MotifDb.Hsap - pre-compiled Z-score background with P-value cutoff of 0.01, 0.001, and 0.0001 for MotifDb human PWMs. The number of hits with smaller P-value than cutoff is counted in 2kb human (hg19) promoters.

Usage

```
data(MotifDb.Hsap.PFM)
data(MotifDb.Hsap)
data(PWMLogn.hg19.MotifDb.Hsap)
data(PWMCutoff4.hg19.MotifDb.Hsap)
data(PWMCutoff5.hg19.MotifDb.Hsap)
data(PWMPvalueCutoff1e2.hg19.MotifDb.Hsap)
data(PWMPvalueCutoff1e3.hg19.MotifDb.Hsap)
data(PWMPvalueCutoff1e4.hg19.MotifDb.Hsap)
```

Details

All of these objects were created with the appropriate functions available in the PWMEnrich package (see Section 'See also'). We recommend using these functions to generate backgrounds for a custom set of background sequences and/or DNA motifs.

This package also contains the 2kb upstream sequences for human genes (hg19.upstream2000) which were removed from the BSgenome.Hsapiens.UCSC.hg19 package starting from Bioconductor version 3.0.

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See Also

makeBackground, makePWMLognBackground, makePWMCutoffBackground, makePWMEmpiricalBackground.

Examples

```
data(PWMLogn.hg19.MotifDb.Hsap)

res = motifEnrichment(DNAString("TGCATCAAGTGTGTAGTGCAAGTGAGTGATGAGTAGAAGTTGAGTGAGGTAGATGC"),
  PWMLogn.hg19.MotifDb.Hsap)

groupReport(res)[1:10]
```

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