

Package: PWMEnrich.Hsapiens.background (via r-universe)

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Maintainer Diego Diez <diego10ruiz@gmail.com>

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Title H. sapiens background for PWMEnrich

Type Package

LazyLoad yes

Author Robert Stojnic

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

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PWMEnrich.Hsapiens.background-package

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.
- PPWMPvalueCutoff1e2.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(PPWMPvalueCutoff1e2.hg19.MotifDb.Hsap)
data(PPWMPvalueCutoff1e3.hg19.MotifDb.Hsap)
data(PPWMPvalueCutoff1e4.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.

Author(s)

Robert Stojnic
Cambridge Systems Biology Centre
University of Cambridge, UK
Maintainer: Robert Stojnic <robert.stojnic@gmail.com>

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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