Package 'PWMEnrich.Dmelanogaster.background'

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Maintainer Diego Diez <diego10ruiz@gmail.com>

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Title D. melanogaster background for PWMEnrich

Type Package

LazyLoad yes

Author Robert Stojnic

Description PWMEnrich pre-compiled background objects for Drosophila melanogaster and MotifDb D. melanogaster motifs.

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PWMEnrich.Dmelanogaster.background package overview

Description

This package provides a set of pre-compiled genomic background files for the PWMEnrich package and D. melanogaster. The backgrounds were pre-compiled using unique promoters of Drosophila melanogaster.

- MotifDb.Dmel.PFM - a list of 740 position frequency matrices (PFMs) from MotifDb
- MotifDb.Dmel - the corresponding PWMs generated by using the background frequencies of A,C,G,T in a set of 10031 2kb promoters in D. Melanogaster.
- PWMLogn.dm3.MotifDb.Dmel - pre-compiled threshold-free lognormal background for JASPAR insects PWMs. The lognormal distribution is fitted to 1kb fragments of 10031 2kb Drosophila Melanogaster (dm3) promoters. For each gene one promoter is taken (from the first transcript).
- PWMCutoff4.dm3.MotifDb.Dmel, PWMCutoff5.dm3.MotifDb.Dmel - pre-compiled Z-score background with cutoff of 4 and 5 (base e) for JASPAR insects PWMs. The number of hits above the score cutoff is counted in 10031 2kb Drosophila Melanogaster (dm3) promoters. For each gene one promoter is taken (from the first transcript).
- PWMPvalueCutoff1e2.dm3.MotifDb.Dmel, PPWMPvalueCutoff1e3.dm3.MotifDb.Dmel, PPWMPvalueCutoff1e4 - pre-compiled Z-score background with P-value cutoff of 0.01, 0.001, and 0.0001 for JASPAR insects PWMs. The number of hits with smaller P-value than cutoff is counted in 10031 2kb Drosophila Melanogaster (dm3) promoters. For each gene one promoter is taken (from the first transcript).

Usage

```
data(MotifDb.Dmel.PFM)
data(MotifDb.Dmel)
data(PWMLogn.dm3.MotifDb.Dmel)
data(PWMCutoff4.dm3.MotifDb.Dmel)
data(PWMCutoff5.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e2.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e3.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e4.dm3.MotifDb.Dmel)
```

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 Drosophila genes (dm3.upstream2000) which were removed from the BSgenome.Dmelanogaster.UCSC.dm3 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.dm3.MotifDb.Dmel)

res = motifEnrichment(DNAString("TGCATCAAGTGTGTAGTGCGATGAATGC"), PWMLogn.dm3.MotifDb.Dmel)

head(motifRankingForGroup(res))
```

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