

Package 'PWMEnrich.Dmelanogaster.background'

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Title D. melanogaster background for PWMEnrich

Type Package

LazyLoad yes

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Description PWMEnrich pre-compiled background objects for Drosophila melanogaster and JASPAR insects motifs.

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datasets-bg-JASPAR *Pre-compiled backgrounds for JASPAR database for D. melanogaster.*

Description

A set of pre-compiled backgrounds for enrichment analysis of motifs from the JASPAR insects motif database. The backgrounds were pre-compiled using unique promoters of *Drosophila melanogaster*.

- `PWMLogn.dm3.jaspar.insects` - 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.jaspar.insects`, `PWMCutoff5.dm3.jaspar.insects` - 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.jaspar.insects`, `PPWMPvalueCutoff1e3.dm3.jaspar.insects`, `PPWMPvalueCutoff1e4.dm3.jaspar.insects` - 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).
- `PWMGEV.dm3.jaspar.insects` - pre-compiled generalized extreme value (GEV) distribution with location, scale and shape parameters fitted using linear regression on fragments of size 200-2000bp on all unique 2kb *Drosophila Melanogaster* (dm3) promoters.

Usage

```
data(PWMLogn.dm3.jaspar.insects)
data(PWMCutoff4.dm3.jaspar.insects)
data(PWMCutoff5.dm3.jaspar.insects)
data(PWMGEV.dm3.jaspar.insects)
data(PWMPvalueCutoff1e2.dm3.jaspar.insects)
data(PWMPvalueCutoff1e3.dm3.jaspar.insects)
data(PWMPvalueCutoff1e4.dm3.jaspar.insects)
```

Details

For convenience this package contains already pre-compiled set of backgrounds for *D. melanogaster*. These contain both the parameters of background distributions and JASPAR position frequency matrices converted to PWMs using the same background (with a pseudo-count of 1 *shared* between the four nucleotides proportional to nucleotide background frequencies).

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

See Also

[makeBackground](#), [makePWMLognBackground](#), [makePWMCutoffBackground](#), [makePWMEmpiricalBackground](#)

Examples

```
data(PWMLogn.dm3.jaspar.insects)

motifEnrichment(DNAString("TGCATCAAGTGTGTAGTGCGATGAATGC"), PWMLogn.dm3.jaspar.insects)
```

`datasets-JASPAR`*JASPAR database of Position Frequency Matrices and PWMs*

Description

The JASPAR (<http://jaspar.genereg.net/>) database retrieved on April 2012. Contains the Position Frequency Matrices (PFMs) for a number of transcription factors.

Usage

```
data(jaspar.insects.PFM)
data(jaspar.insects)
```

Details

The `jaspar.insects.PFM` object contain a list of motifs in matrix format where rows are the four nucleotides (A,C,G,T). JASPAR identifiers have been stripped for clarity.

The PWMs (`jaspar.insects`) were generated by using the background frequencies of A,C,G,T in a set of 10031 2kb promoters in *D. Melanogaster*.

See Also

`datasets-bg-JASPAR`.

Examples

```
data(jaspar.insects.PFM)
data(jaspar.insects)
```

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