Package 'PscanRBackgrounds'

November 12, 2026

Type Package

Title Precomputed Promoter Backgrounds for PscanR

Version 0.99.7

Description Provides ExperimentHub metadata and documentation for the promoter-background score distributions used by PscanR transcription factor binding motif enrichment analyses. Each of the 105 backgrounds is a separate ExperimentHub resource, covering the JASPAR 2020, 2022 and 2024 CORE collections, seven genome assemblies of five organisms, and five promoter windows. The files are hosted on Zenodo, one record per JASPAR release, and archived together in a version-specific Zenodo record.

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Encoding UTF-8

Depends R (>= 4.6.0)

Imports ExperimentHub

Suggests BiocStyle, ExperimentHubData, knitr, rmarkdown, testthat (>= 3.0.0)

biocViews ExperimentHub, Genome, Homo_sapiens_Data, Mus_musculus_Data, Drosophila_melanogaster_Data, Saccharomyces_cerevisiae_Data, Arabidopsis_thaliana_Data

VignetteBuilder knitr

URL https://github.com/Federico77z/PscanRBackgrounds, https://doi.org/10.5281/zenodo.21821764

BugReports https://github.com/Federico77z/PscanRBackgrounds/issues

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`PscanRBackgrounds-package`
Precomputed promoter backgrounds for PscanR

Description

PscanRBackgrounds provides ExperimentHub metadata and documentation for the precomputed promoter-background score distributions used by the PscanR motif enrichment package. Each background is a separate ExperimentHub resource; see PscanRBackgrounds-resources for their content and naming, and the package vignette for retrieval.

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See Also

Useful links:

- https://github.com/Federico77z/PscanRBackgrounds
- doi:10.5281/zenodo.21821764
- Report bugs at https://github.com/Federico77z/PscanRBackgrounds/issues

Examples

```
path <- system.file("extdata", "metadata.csv", package = "PscanRBackgrounds")
metadata <- utils::read.csv(path)
nrow(metadata)
table(metadata$Species)
```

`PscanRBackgrounds-resources`

PscanR promoter backgrounds, version 2

Description

One ExperimentHub resource per combination of JASPAR CORE release (2020, 2022, 2024), genome assembly (hg38, hs1, mm10, mm39, dm6, sacCer3, TAIR9) and promoter window (200u_50d, 450u_50d, 500u_0d, 950u_50d, 1000u_0d), for 105 resources in total.

Format

Each resource is a tab-separated text file. The first line is the header `[SHORT TFBS MATRIX]`; each following line holds a JASPAR matrix identifier, the number of promoters, the mean score and the score standard deviation. The resources use the `FilePath` dispatch class, so retrieval returns the path to the locally cached file.

Details

For each motif of the JASPAR collection matching the organism's taxonomic group, PscanR scans every unique promoter sequence of the assembly over the given window, keeps the best normalized PWM score per promoter, and records the number of promoters with the mean and standard deviation of those scores. PscanR compares foreground promoters against these statistics.

Resource titles have the form `PscanR_bg_v2_J<release>_<assembly>_<up>u_<down>d_<source>`, for example `PscanR_bg_v2_J2020_hg38_200u_50d_UCSC`. The installed `extdata/catalog_v2.tsv` lists, for every resource, the annotation source and retrieval date, promoter, motif and annotation hashes, the PscanR scanner version and commit, and the SHA-256 checksum of the file. PscanR users normally retrieve a background with PscanR's own retrieval function, which verifies that checksum.

License

The backgrounds are distributed under CC BY 4.0. See the installed `DATA_SOURCES.md` for upstream attribution.

Source

Generated with the pipeline at https://github.com/Federico77z/PscanRBackgrounds-pipeline. The files are hosted on Zenodo, one record per JASPAR release (doi:10.5281/zenodo.23183695, doi:10.5281/zenodo.23183713, doi:10.5281/zenodo.23183720), and archived together in doi:10.5281/zenodo.21821764. See the installed `scripts/make-data.R`.

References

Zambelli F, Pesole G, Pavesi G. (2009). Pscan: finding over-represented transcription factor binding site motifs in sequences from co-regulated or co-expressed genes. Nucleic Acids Research. doi:10.1093/nar/gkp464.

Examples

```
metadata <- utils::read.csv(system.file(
    "extdata", "metadata.csv", package = "PscanRBackgrounds"
))
head(metadata[c("Title", "Genome", "Species")])
catalog <- utils::read.delim(system.file(
    "extdata", "catalog_v2.tsv", package = "PscanRBackgrounds"
))
table(catalog$assembly, catalog$jaspar_release)
```

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