

Package: PscanRBackgrounds (via r-universe)

October 7, 2026

Type Package

Title Precomputed Promoter Backgrounds for PscanR

Version 0.99.3

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 (>= 4.5.0)

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>

RoxygenNote 8.0.0

Config/testthat/edition 3

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository <https://biocstaging.r-universe.dev>

Date/Publication 2026-10-06 09:27:42 UTC

RemoteUrl <https://github.com/BiocStaging/PscanRBackgrounds>

RemoteRef HEAD
RemoteSha 7c2a404c2f16c5eb203d8589bf0d91e6e5b1eacc

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PscanRBackgrounds-resources
<i>PscanR promoter backgrounds, version 2</i>

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](https://doi.org/10.5281/zenodo.23183695), [doi:10.5281/zenodo.23183713](https://doi.org/10.5281/zenodo.23183713), [doi:10.5281/zenodo.23183720](https://doi.org/10.5281/zenodo.23183720)), and archived together in [doi:10.5281/zenodo.21821764](https://doi.org/10.5281/zenodo.21821764). See the installed scripts/make-data.R.

References

Zambelli F, Pesole G, Pavese 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](https://doi.org/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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* **datasets**

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