

Package: methylTFRAnnotationHg38 (via r-universe)

October 2, 2026

Title methylTFR Annotations for hg38

Description Precomputed transcription factor binding sites, motif GC frequency tables and a genome-wide GC distribution for use with the methylTFR package. Binding sites are genome-wide motif matches extended to the footprint window methylTFR reads across; the GC tables record how each motif's sites distribute over genome-wide GC quintiles, which is what allows a deviation score to be corrected for sequence composition. The data are hosted on AnnotationHub and retrieved on first use; this package provides the accessors and the documentation.

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Encoding UTF-8

Version 0.99.11

Depends R (>= 4.5.0)

Imports AnnotationHub, GenomicRanges, stats

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

VignetteBuilder knitr

biocViews AnnotationData, AnnotationHub, FunctionalAnnotation, SequenceAnnotation, Homo_sapiens

BugReports <https://github.com/EpigenomeInformatics/methylTFRAnnotationHg38/issues>

URL <https://github.com/EpigenomeInformatics/methylTFRAnnotationHg38>

Roxygen list(markdown = FALSE)

RoxygenNote 7.3.3

Config/testthat/edition 3

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

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

Date/Publication 2026-10-02 11:37:08 UTC

RemoteUrl <https://github.com/BiocStaging/methylTFRAnnotationHg38>

RemoteRef HEAD

RemoteSha bb0892c8b93c89362b23b1ab91e7fc4ec2429a4a

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methylTFRAnnotationHg38-package
methylTFRAnnotationHg38: methylTFR annotations for hg38

Description

Genome annotations that **methylTFR** needs to compute GC-bias-corrected transcription factor (TF) deviation scores from DNA methylation data on the Homo sapiens hg38 assembly.

Details

The package provides three kinds of resources, each with an accessor:

[getTFbindsites](#) Genome-wide TF binding sites, one GRanges per motif, extended to the footprint window (see [tf_bindsites](#)).

[getGCfreq](#) Motif GC frequency tables: how each motif's binding sites distribute over genome-wide GC quintiles (see [motif_gcfreq](#)).

[getGenomeGC](#) The genome-wide GC distribution in 30 nt windows (see [genomewide_GC](#)).

[availableMotifSets](#) lists the motif sets that can be requested. The three objects are passed to `methylTFR::run_methyltfr()`.

The data are too large to ship with the package. They are hosted on AnnotationHub, downloaded on first use and served from the local AnnotationHub cache afterwards. The metadata of every resource is listed in `system.file("extdata", "metadata.csv", package = "methylTFRAnnotationHg38")`, and the scripts that produced them are in `system.file("scripts", package = "methylTFRAnnotationHg38")`.

To read the `.rds` files from a local directory instead of AnnotationHub (for example on a machine without internet access), set `options(methylTFRAnnotationHg38.datadir = "/path/to/files")` or the environment variable `METHYL_TFRANNOTATION_HG38_DIR`.

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- Saarland University (NanoBioMed Young Investigator Grant) [funder]

See Also

vignette("methyLTFRAnnotationHg38")

availableMotifSets	<i>List the motif sets provided by this package</i>
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Description

Returns the names accepted by the motifSet argument of [getTFbindsites](#) and [getGCfreq](#).

Usage

```
availableMotifSets()
```

Value

A character vector of motif set names.

See Also

[methyLTFRAnnotationHg38](#) for an overview of the package.

Examples

```
availableMotifSets()
```

genomewide_GC	<i>Genome-wide GC distribution</i>
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Description

GC content of the hg38 genome in non-overlapping 30 nt windows. Returned by [getGenomeGC](#); the AnnotationHub record title is genomewide_GC_hg38.rds.

Format

A GRanges, one range per 30 nt window on the primary chromosomes, with metadata columns

GC_bias Numeric, GC fraction of the window (0 to 1); NaN for windows made of N.

GC_bin Integer, genome-wide GC quintile of the window, 1 (lowest) to 5 (highest).

and S4Vectors::metadata() entries gc_breaks (the six quintile boundaries), bin_scope ("genome": quantiles taken genome-wide) and step (window step, 30).

Details

methyLTFR overlaps each methylation call with these windows to assign it a GC bin; the motif tables in [motif_gcfreq](#) use the same boundaries.

Value

This page documents a data resource rather than a function; the object is returned by [getGenomeGC](#).

Source

Computed from the UCSC hg38 BSgenome package; see `system.file("scripts", "make-data.R", package = "methyLTFRAnnotationHg38")`.

See Also

[getGenomeGC](#), [methyLTFRAnnotationHg38](#)

Examples

```
# AnnotationHub records of this resource and their descriptions
md <- utils::read.csv(system.file("extdata", "metadata.csv",
  package = "methyLTFRAnnotationHg38")
))
md[grepl("genomewide_GC", md$title), c("title", "RDataClass")]

# Loading the resource downloads it from AnnotationHub on first use:
# gc <- getGenomeGC()
# table(gc$GC_bin); S4Vectors::metadata(gc)$gc_breaks
```

getGCfreq	<i>Load motif GC frequency tables</i>
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Description

Load the motif GC frequency tables for a motif set. Downloaded from AnnotationHub on first use and cached locally thereafter.

Usage

```
getGCfreq(motifSet = "altius")
```

Arguments

motifSet	Motif set to load. One of availableMotifSets(): altius, cisbpv2, jaspar2020, jaspar2020_distal. Case-insensitive.
----------	---

Details

Each table describes the GC composition around one motif's binding sites. Column j corresponds to the j -th 30 nt window along the (extended) binding site; row i gives the fraction of binding sites whose window at that position falls into genome-wide GC quintile i (row 1 lowest, row 5 highest GC). Columns therefore sum to one. **methyITFR** combines these fractions with the observed methylation per GC bin to obtain the methylation a motif would be expected to show from sequence composition alone. See [motif_gcfreq](#) for the data format.

Value

A named list of numeric matrices with five rows (GC quintiles), one matrix per motif.

See Also

[motif_gcfreq](#), [getTFbindsites](#), [getGenomeGC](#)

Examples

```
# Point the package at a temporary directory holding a small mock
# table so the example runs without downloading from AnnotationHub.
mock_dir <- file.path(tempdir(), "gcfreq_example")
dir.create(mock_dir, showWarnings = FALSE)
freq <- matrix(c(0.1, 0.2, 0.4, 0.2, 0.1), nrow = 5, ncol = 3)
saveRDS(list(MA0001.1 = freq), file.path(mock_dir,
"altius_motif_gcfreq.rds"))
old_opt <- options(methylTFRAnnotationHg38.datadir = mock_dir)

gcfreqs <- getGCfreq("altius")
gcfreqs$MA0001.1
colSums(gcfreqs$MA0001.1)
```

```
options(old_opt)
unlink(mock_dir, recursive = TRUE)
```

getGenomeGC

Load the genome-wide GC distribution

Description

Load the genome-wide GC distribution for hg38. Downloaded from AnnotationHub on first use and cached locally thereafter.

Usage

```
getGenomeGC(assembly = "hg38")
```

Arguments

assembly	Genome assembly. Only "hg38" (the default) is available in this package; case-insensitive.
----------	--

Details

The genome is tiled into non-overlapping 30 nt windows. Each window carries its GC fraction and its genome-wide GC quintile. **methyITFR** uses the table to assign every methylation call to a GC bin. See [genomewide_GC](#) for the data format.

The package serves a single assembly, so the argument can be left out. It is kept so that code written as `getGenomeGC("hg38")` works; any other assembly is an error.

Value

A GRanges with metadata columns GC_bias (GC fraction of the window) and GC_bin (quintile, 1 to 5).

See Also

[genomewide_GC](#), [getGCfreq](#)

Examples

```
# Point the package at a temporary directory holding a small mock
# object so the example runs without downloading from AnnotationHub.
mock_dir <- file.path(tempdir(), "genomegc_example")
dir.create(mock_dir, showWarnings = FALSE)
gr <- GenomicRanges::GRanges(c("chr1:1-30", "chr1:31-60", "chr1:61-90"))
gr$GC_bias <- c(0.30, 0.43, 0.63)
gr$GC_bin <- c(1L, 3L, 5L)
saveRDS(gr, file.path(mock_dir, "genomewide_GC_hg38.rds"))
old_opt <- options(methyITFRAnnotationHg38.datadir = mock_dir)
```

```

getGenomeGC()

options(old_opt)
unlink(mock_dir, recursive = TRUE)

```

getTFbindsites	<i>Load transcription factor binding sites</i>
----------------	--

Description

Load genome-wide transcription factor binding sites for a motif set. Downloaded from AnnotationHub on first use and cached locally thereafter.

Usage

```
getTFbindsites(motifSet = "altius")
```

Arguments

motifSet	Motif set to load. One of availableMotifSets(): altius, cisbpv2, jaspar2020, jaspar2020_distal. Case-insensitive.
----------	---

Details

Each element of the returned list holds the binding sites of one motif. Every range is the motif match extended by 200 bp on either side, the footprint window across which **methyITFR** reads methylation. See [tf_bindsites](#) for the data format.

Sets ending in _distal only have their own GC frequency table; they share the binding sites of the base set. Passing a _distal name here returns the base set's binding sites.

Value

A GRangesList with one GRanges per motif, named by motif ID.

See Also

[tf_bindsites](#), [getGCfreq](#)

Examples

```

# Point the package at a temporary directory holding a small mock
# object so the example runs without downloading from AnnotationHub.
mock_dir <- file.path(tempdir(), "tfbs_example")
dir.create(mock_dir, showWarnings = FALSE)
mock_grl <- GenomicRanges::GRangesList(
  MA0001.1 = GenomicRanges::GRanges(
    c("chr1:1001-1411", "chr2:5001-5411"),
    strand = c("+", "-")
  )
)

```

```

)
saveRDS(mock_grl, file.path(mock_dir, "altius_tf_bindsites.rds"))
old_opt <- options(methylTFRAnnotationHg38.datadir = mock_dir)

getTFbindsites("altius")

options(old_opt)
unlink(mock_dir, recursive = TRUE)

```

motif_gcfreq

Motif GC frequency tables

Description

Per-motif tables describing the GC composition around each motif's binding sites on hg38. Returned by [getGCfreq](#); the AnnotationHub record titles are <motifSet>_motif_gcfreq.rds.

Format

A named list with one numeric matrix per motif (names are motif IDs, matching the names of the corresponding [tf_bindsites](#) list). Each matrix has

5 rows Genome-wide GC quintiles, from lowest (row 1) to highest (row 5) GC. Quintile boundaries are the ones stored with [genomewide_GC](#), so both objects share one scale.

one column per window position A 30 nt window slides one base at a time along the binding site (motif plus 200 bp on either side, padded by a further 65 bp so edge windows are complete). Column *j* is the *j*-th window.

Entries are the fraction of the motif's binding sites whose window at that position falls into each quintile; every column sums to one. Windows containing N are ignored.

Details

The tables are what make the methylTFR deviation score bias-corrected. A motif whose sites sit in GC-rich sequence overlaps hypomethylated CpG islands more often; combining these fractions with the observed methylation per GC bin gives the methylation expected from sequence composition alone, which is then subtracted.

Available motif sets:

jaspar2020 JASPAR2020 CORE matrices for *Homo sapiens* (629 PWMs), scanned genome-wide.
cisbpv2 CIS-BP v2 human PWMs (human_pwm_v2 from **chromVARmotifs**), scanned genome-wide.

altius Vierstra motif archetypes v1.0 (286 archetype clusters), taken from the published hg38 archetype scan and de-duplicated by motif score.

jaspar2020_distal A GC frequency table only: as **jaspar2020**, but restricted to binding sites overlapping distal regulatory regions (Ensembl Regulatory Build v104). Use it together with the unrestricted **jaspar2020** binding sites.

Value

This page documents a data resource rather than a function; the object is returned by [getGCfreq](#).

Source

Built with methylTFRAnnotationBuilder (<https://github.com/EpigenomeInformatics/methylTFRAnnotationBuilder>) from BSgenome sequences; see `system.file("scripts", "make-data.R", package = "methylTFRAnnotationHg38")` and `system.file("extdata", "metadata.csv", package = "methylTFRAnnotationHg38")` for the exact sources and versions.

See Also

[getGCfreq](#), [methylTFRAnnotationHg38](#)

Examples

```
# AnnotationHub records of this resource and their descriptions
md <- utils::read.csv(system.file("extdata", "metadata.csv",
  package = "methylTFRAnnotationHg38"
))
md[grepl("_motif_gcfreq", md$Title), c("Title", "RDataClass")]

# Loading the resource downloads it from AnnotationHub on first use:
# gcfreqs <- getGCfreq("jaspar2020")
# length(gcfreqs); dim(gcfreqs[[1]]); colSums(gcfreqs[[1]])
```

tf_bindsites

Transcription factor binding sites

Description

Genome-wide predicted transcription factor binding sites on hg38. Returned by [getTFbindsites](#); the AnnotationHub record titles are <motifSet>_tf_bindsites.rds.

Format

A GRangesList with one GRanges per motif, named by motif ID. Each range is a motif match on the primary chromosomes (chr1-22, X, Y; chrM excluded) extended by 200 bp on either side of the match, so all ranges of a motif have the same width (motif width + 400 bp). The strand of the match is kept; there are no metadata columns. Coordinates are 1-based.

Details

Available motif sets:

jaspar2020 JASPAR2020 CORE matrices for *Homo sapiens* (629 PWMs), scanned genome-wide.
 cisbpv2 CIS-BP v2 human PWMs (human_pwm_v2 from **chromVARmotifs**), scanned genome-wide.

altius Vierstra motif archetypes v1.0 (286 archetype clusters), taken from the published hg38 archetype scan and de-duplicated by motif score.

jaspar2020_distal A GC frequency table only: as jaspar2020, but restricted to binding sites overlapping distal regulatory regions (Ensembl Regulatory Build v104). Use it together with the unrestricted jaspar2020 binding sites.

Value

This page documents a data resource rather than a function; the object is returned by [getTFbindsites](#).

Source

See [motif_gcfreq](#).

See Also

[getTFbindsites](#), [methy1TFRAnnotationHg38](#)

Examples

```
# AnnotationHub records of this resource and their descriptions
md <- utils::read.csv(system.file("extdata", "metadata.csv",
  package = "methy1TFRAnnotationHg38"
))
md[grepl("_tf_bindsites", md$title), c("title", "RDataClass")]

# Loading the resource downloads it from AnnotationHub on first use:
# tfbs <- getTFbindsites("jaspar2020")
# length(tfbs); head(lengths(tfbs)); tfbs[[1]]
```

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