

Package: hgammaR (via r-universe)

October 12, 2026

Type Package

Title Incorporation of chromatin interaction and epigenetic profiles
to predict risk genes

Version 0.99.3

Description Combines chromatin interaction (e.g. PLAC-seq/Hi-C) data
with regulatory region annotations (e.g. promoters, enhancers,
H3K27ac) to link non-coding GWAS SNPs to their putative target
genes, producing MAGMA-compatible gene annotation files for
downstream gene-level association testing.

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URL <https://github.com/aydanasg/hgammaR>

BugReports <https://github.com/aydanasg/hgammaR/issues>

Encoding UTF-8

RoxygenNote 7.3.1

biocViews Software, Epigenetics, ChIPSeq, GeneRegulation, SNP,
GenomeAnnotation, FunctionalGenomics, GeneTarget, HiC

Imports TxDb.Hsapiens.UCSC.hg19.knownGene (>= 3.2.2), org.Hs.eg.db (>=
3.18.0), GenomicRanges (>= 1.54.1), IRanges (>= 2.36.0),
S4Vectors (>= 0.40.2), ChIPseeker (>= 1.38.0), stats

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

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs
libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libbz2-dev libicu-
dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

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

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AnnotationFileHmagma	<i>Gene level analysis carried out by magma</i> (https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004219)
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Description

Generates an annotation file for magma input

Usage

```
AnnotationFileHmagma(  
  hic,  
  regulatoryRegions = NULL,  
  promoterRegions = NULL,  
  enhancerRegions = NULL,  
  snps,  
  annotated_genes,  
  snpgeneexon,  
  AnnotationFile  
)
```

Arguments

hic	Dataframe of chromatin interaction data with 6 columns in the format: "chrom1", "start1", "end1", "chrom2", "start2", "end2". Chromosome columns should have "chr" before the number
regulatoryRegions	Dataframe of regulatory regions (H3K27ac) in the .bed format (chr, start, end). Chromosome columns should have "chr" before the number
promoterRegions	Dataframe of promoters in the .bed format (chr, start, end). Chromosome columns should have "chr" before the number
enhancerRegions	Dataframe of enhancers in the .bed format (chr, start, end). Chromosome columns should have "chr" before the number
snps	Dataframe of reference snps. This could be the ".bim" file from g1000 reference genome in the format: "chr", "position", "rsid"

annotated_genes	Dataframe of reference genes. This should contain columns with names "chr", "start", "end", "ensg". Chromosome columns should have "chr" before the number
snpgeneexon	Dataframe of genes and snps within it. This should contain columns with names "rsid", "ensg"
AnnotationFile	Path prefix for the output file; ".transcript.annot" is appended

Value

Function generates gene level analysis files (.genes.raw, .genes.out, .log.suppl, .log)

Examples

```
data("test_dataset.microglia.hg19")
out <- tempfile()
AnnotationFileHmagma(
  hic = hic, promoterRegions = promoterRegions, enhancerRegions = enhancerRegions,
  snps = snps, annotated_genes = annotated_genes, snpgeneexon = snpgeneexon,
  AnnotationFile = out
)
```

GeneLevelAnalysis_hmagma	<i>Gene level analysis carried out by magma</i> (https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004219)
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Description

Generates an annotation file for magma input

Usage

```
GeneLevelAnalysis_hmagma(magma, g1000, gwas, AnnotationFile, output)
```

Arguments

magma	Path to magma binary file, should be in a './magma' format
g1000	Path to 1,000 Genomes reference data files (.bin, .bed, .fam, .synonyms). Include the name of the of the files in the path (e.g. /path_to_g1000/g1000_eur). Obtain from https://cncr.nl/research/magma/ under Auxiliary files.
gwas	Path to the GWAS summary statistics to be used where rsid column name is "SNP", p-value column name is "P", and sample size column name is "N"
AnnotationFile	Annotation file generated using AnnotationFileHmagma() or SampledDownAnnotation()
output	Name of the output file

Value

Function generates gene level analysis files (.genes.raw, .genes.out, .log.suppl, .log)

Examples

```
# Requires a local MAGMA installation and 1000 Genomes reference files;
# skipped automatically when magma is not found on the PATH.
magma_path <- Sys.which("magma")
if (nzchar(magma_path)) {
  GeneLevelAnalysis_hmagma(
    magma = magma_path,
    g1000 = "/path/to/g1000_eur",
    gwas = "/path/to/gwas_summary_stats.txt",
    AnnotationFile = "/path/to/annotation.transcript.annot",
    output = tempfile()
  )
} else {
  message("magma not found on PATH; skipping example.")
}
```

SampledDownAnnotation *Gene level analysis carried out by magma*
 (<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004219>)

Description

Generates an annotation file for magma input

Usage

```
SampledDownAnnotation(
  hic,
  regulatoryRegions,
  snps,
  annotated_genes,
  snpgeneexon,
  loopNumber,
  sampleDownNumber,
  AnnotationFile
)
```

Arguments

hic	Dataframe of chromatin interaction data with 6 columns in the format: "chrom1", "start1", "end1", "chrom2", "start2", "end2". Chromosome columns should have "chr" before the number
regulatoryRegions	Dataframe of regulatory regions (H3K27ac) in the .bed format (chr, start, end). Chromosome columns should have "chr" before the number

snps	Dataframe of reference snps. This could be the ".bim" file from g1000 reference genome in the format: "chr", "position", "rsid"
annotated_genes	Dataframe of reference genes. This should contain columns with names "chr", "start", "end", "ensg". Chromosome columns should have "chr" before the number
snpgeneexon	Dataframe of genes and snps within it. This should contain columns with names "rsid", "ensg"
loopNumber	Number to sample down the loop number to. This is useful when comparing more than one sample to ensure that the difference is not down to the difference in loop number
sampleDownNumber	Number of times sample down the loop number randomly
AnnotationFile	Path where to save the sampled down annotation files

Value

Function generates sampled down gene level analysis files (.genes.raw, .genes.out, .log.suppl, .log)

Examples

```
data("test_dataset.microglia.hg19")
out <- tempfile()
SampledDownAnnotation(
  hic = hic, regulatoryRegions = regulatoryRegions, snps = snps,
  annotated_genes = annotated_genes, snpgeneexon = snpgeneexon,
  loopNumber = 5000, sampleDownNumber = 1, AnnotationFile = out
)
```

test_dataset.microglia.hg19

Example microglia PLAC-seq dataset

Description

A small, randomly subsampled set of objects used to demonstrate the hmagmaR workflow in the package vignette and examples. Load with `data("test_dataset.microglia.hg19")`. Because the rows are drawn independently at random from each source table (rather than hand-picked around loci known to overlap), results produced from this dataset are illustrative only and not biologically meaningful.

Usage

```
hic
```

```
promoterRegions
```

enhancerRegions

regulatoryRegions

snps

annotated_genes

snpgeneexon

gwas

Format

Eight objects are provided:

hic A data frame/tibble of 20,000 microglia PLAC-seq chromatin interactions (Nott et al., 2019), with columns chr1, start1, end1, chr2, start2, end2, plus interaction-calling metadata (count, expected, fdr, ClusterLabel, ClusterSize, ClusterType, ClusterNegLog10P, ClusterSummit).

promoterRegions A data frame of 12,709 microglia promoter regions (Nott et al., 2019) in BED-like format: chr, start, end.

enhancerRegions A data frame of 44,090 microglia enhancer regions (Nott et al., 2019) in BED-like format: chr, start, end.

regulatoryRegions A data frame identical to promoterRegions, provided for functions such as SampledDownAnnotation() that take a single combined regulatory-region table instead of separate promoter and enhancer tables.

snps A data table of 20,000 reference SNPs subsampled from 1000 Genomes (European ancestry), with columns chr, Position, SNP.

annotated_genes A data table of 20,000 reference gene coordinates, with columns chr, start, end, ensq.

snpgeneexon A data table of 20,000 SNPs falling within exons/promoters of a gene, with columns rsid, ensq.

gwas A data table of 20,000 example GWAS summary statistics rows, with columns SNP, CHR, BP, A1, A2, FRQ, BETA, SE, P, N.

An object of class tbl_df (inherits from tbl, data.frame) with 20000 rows and 14 columns.

An object of class data.frame with 12709 rows and 3 columns.

An object of class data.frame with 44090 rows and 3 columns.

An object of class data.frame with 12709 rows and 3 columns.

An object of class data.table (inherits from data.frame) with 20000 rows and 3 columns.

An object of class data.table (inherits from data.frame) with 20000 rows and 4 columns.

An object of class data.table (inherits from data.frame) with 20000 rows and 2 columns.

An object of class data.table (inherits from data.frame) with 20000 rows and 10 columns.

Source

Subsampled from microglia PLAC-seq interactions and regulatory regions (Nott et al., 2019, <https://doi.org/10.1126/science.aay0793>), 1000 Genomes reference SNPs, and example GWAS summary statistics.

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