Package 'geneAttribution'

November 12, 2026

Type Package

Title Identification of candidate genes associated with genetic variation

Version 1.38.0

Date 2025-07-24

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Description Identification of the most likely gene or genes through which variation at a given genomic locus in the human genome acts. The most basic functionality assumes that the closer gene is to the input locus, the more likely the gene is to be causative. Additionally, any empirical data that links genomic regions to genes (e.g. eQTL or genome conformation data) can be used if it is supplied in the UCSC .BED file format.

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biocViews SNP, GenePrediction, GenomeWideAssociation, VariantAnnotation, GenomicVariation

Imports utils, GenomicRanges, org.Hs.eg.db, BiocGenerics, Seqinfo, GenomicFeatures, IRanges, rtracklayer

Suggests TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Hsapiens.UCSC.hg19.knownGene, knitr, rmarkdown, testthat

RoxygenNote 5.0.1

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/geneAttribution

git_branch RELEASE_3_23

git_last_commit 73393b2

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`geneAttribution` *geneAttribution: Identification of candidate genes associated with noncoding genetic variation*

Description

Identification of the most likely gene or genes through which variation at a given genomic locus in the human genome acts. The most basic functionality assumes that the closer gene is to the input locus, the more likely the gene is to be causative. Additionally, any empirical data that links genomic regions to genes (e.g. eQTL or genome conformation data) can be used if it is supplied in UCSC .bed file format. A typical workflow requires loading gene models and empirical data, then running geneAttribution() on the locus of interest

Given genomic coordinate, return normalized probability for each gene

Usage

```
geneAttribution(chr, pos, geneCoordinates, empiricalData, lambda = 7.61e-06,
  maxDist = 1e+06, minPP = 0.01)
```

Arguments

`chr`	A character string representing a chromosome (e.g. "chr2")
`pos`	An integer representing a genomic position in the same genome build that gene models
`geneCoordinates`	A GenomicRanges object, as generated by geneModels()
`empiricalData`	A list of GenomicRanges objects, as generated by loadBed(). Optional
`lambda`	Float. Variable for exponential distribution. Default based on empirical eQTL data from multiple tissues. Optional
`maxDist`	Integer. Only genes within this distance of query locus are considered. Optional
`minPP`	Float. Genes with a posterior probability < minPP are lumped as "Other". Can be set to 0 when all genes should be reported. Optional

Value

A sorted, numeric vector of normalized gene probabilities

Examples

```
geneLocs <- geneModels()
fileName <- system.file("extdata", "eqtlHaplotypeBlocks.b38.bed", package="geneAttribution")
empirical <- loadBed(fileName)
geneAttribution("chr2", 127156000, geneLocs, empirical)
```

`geneModels` *Load gene models*

Description

Get gene models as a GenomicRanges object, with gene names in the symbol column For hg19, you may want to use TxDb.Hsapiens.UCSC.hg19.knownGene and for GRCh38, TxDb.Hsapiens.UCSC.hg38.knownGene (set as default)

Usage

```
geneModels(txdb = TxDb.Hsapiens.UCSC.hg38.knownGene::TxDb.Hsapiens.UCSC.hg38.knownGene,
 maxGeneLength = 1e+06, genesToInclude, genesToExclude)
```

Arguments

`txdb`	GenomicFeatures TxDb object containing genomic coordinates of genes
`maxGeneLength`	An integer. Gene models that are longer than this are excluded. Optional
`genesToInclude`	A character vector of gene symbols of genes to include (e.g. only protein coding genes). Optional
`genesToExclude`	A character vector of gene symbols of genes to exclude. Optional

Value

A GenomicRanges object containing human gene models

Examples

```
geneModels()
geneModels(genesToInclude = c("CYYR1", "ADAMTS1", "ADAMTS5", "N6AMT1", "LTN1"))
```

loadBed *Load UCSC *.BED files containing empirical data*

Description

Required *.BED file format (tab-separated): chr start end name (optional column: score). Sample files supplied with package are limited to chromosome 2.

Usage

```
loadBed(files, weights)
```

Arguments

files	A character vector containing *.BED file names
weights	An integer vector containing weighting for each bed file. Optional

Value

A list of GenomicRanges objects containing the data from the *.BED files, with weightings in the score column

Examples

```
fileName1 <- system.file("extdata", "hiCRegions.b38.bed", package="geneAttribution")
fileName2 <- system.file("extdata", "eqtlHaplotypeBlocks.b38.bed", package="geneAttribution")
loadBed(c(fileName1, fileName2), c(2, 5))
```

normP *Normalize likelihoods and return probabilities*

Description

Normalize likelihoods and return probabilities

Usage

```
normP(pVector, minPP = 0)
```

Arguments

pVector	A numeric vector of pre-normalization likelihoods
minPP	A float. Genes with a posterior probability < minPP are lumped as "Other". Optional

Value

A sorted, numeric vector of normalized probabilities

Examples

```
normP(c(5, 1, 1, 1, 1, 1, 0.1))
normP(c(5, 1, 1, 1, 1, 1, 0.1), minPP=0.1)
```

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