

Package ‘geneAttribution’

June 18, 2025

Type Package

Title Identification of candidate genes associated with genetic variation

Version 1.35.0

Date 2016-10-16

Author Arthur Wuster

Maintainer Arthur Wuster <wustera@gene.com>

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.

License Artistic-2.0

biocViews SNP, GenePrediction, GenomeWideAssociation, VariantAnnotation, GenomicVariation

Imports utils, GenomicRanges, org.Hs.eg.db, BiocGenerics, GenomeInfoDb, 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 devel

git_last_commit d1614f7

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-06-18

Contents

geneAttribution	2
geneModels	3
loadBed	3
normP	4

Index**5**

geneAttribution	<i>geneAttribution: Identification of candidate genes associated with noncoding genetic variation</i>
-----------------	---

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 <code>geneModels()</code>
empiricalData	A list of GenomicRanges objects, as generated by <code>loadBed()</code> . 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("CYR1", "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	<i>Normalize likelihoods and return probabilities</i>
-------	---

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)
```

Index

geneAttribution, [2](#)
geneAttribution-package
 (geneAttribution), [2](#)
geneModels, [3](#)

loadBed, [3](#)

normP, [4](#)