

# Package ‘geneAttribution’

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**Type** Package

**Title** Identification of candidate genes associated with genetic variation

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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.

**License** Artistic-2.0

**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

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

<code>chr</code>	A character string representing a chromosome (e.g. "chr2")
<code>pos</code>	An integer representing a genomic position in the same genome build that gene models
<code>geneCoordinates</code>	A <code>GenomicRanges</code> object, as generated by <code>geneModels()</code>
<code>empiricalData</code>	A list of <code>GenomicRanges</code> objects, as generated by <code>loadBed()</code> . Optional
<code>lambda</code>	Float. Variable for exponential distribution. Default based on empirical eQTL data from multiple tissues. Optional
<code>maxDist</code>	Integer. Only genes within this distance of query locus are considered. Optional
<code>minPP</code>	Float. Genes with a posterior probability < <code>minPP</code> 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", "eqlHaplotypeBlocks.b38.bed", package="geneAttribution")
empirical <- loadBed(fileName)
geneAttribution("chr2", 127156000, geneLocs, empirical)
```

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 geneModels

*Load gene models*


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### 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"))
```

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 loadBed

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


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### 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))
```

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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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