

# Package ‘proActiv’

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**Title** Estimate Promoter Activity from RNA-Seq data

**Version** 1.0.0

**Description** Most human genes have multiple promoters that control the expression of different isoforms. The use of these alternative promoters enables the regulation of isoform expression pre-transcriptionally. Alternative promoters have been found to be important in a wide number of cell types and diseases. proActiv is an R package that enables the analysis of promoters from RNA-seq data. proActiv uses aligned reads as input, and generates counts and normalized promoter activity estimates for each annotated promoter. In particular, proActiv accepts junction files from TopHat2 or STAR or BAM files as inputs. These estimates can then be used to identify which promoter is active, which promoter is inactive, and which promoters change their activity across conditions.

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**Imports** dplyr, GenomicRanges, GenomicFeatures, GenomicAlignments, GenomeInfoDb, IRanges, S4Vectors, methods, rlang, SummarizedExperiment, AnnotationDbi, DESeq2, data.table, tibble, Gviz, BiocParallel

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---

calculateJunctionReadCounts

*Calculate the total number of junction reads overlapping with the introns of each promoter for the input junction file*

---

### Description

Calculate the total number of junction reads overlapping with the introns of each promoter for the input junction file

### Usage

```
calculateJunctionReadCounts(
  promoterCoordinates,
  intronRanges,
  file = "",
  fileType = "",
  genome = ""
)
```

### Arguments

**promoterCoordinates** A GRanges object containing promoter coordinates and reduced exon coordinates by gene

**intronRanges** A GRanges object containing the annotated unique intron ranges. These ranges will be used for counting the reads

**file** character path for the input junction bed or bam file

fileType	character type of the junction bed file. Either 'tophat', 'star' or 'bam'
genome	character genome version

**Value**

The total number of junction reads overlapping with each promoter for the input annotated intron ranges

---

calculatePromoterReadCounts

*Calculate the promoter read counts using junction read counts approach for all the input junction files*

---

**Description**

Calculate the promoter read counts using junction read counts approach for all the input junction files

**Usage**

```
calculatePromoterReadCounts(
  promoterAnnotation,
  files = NULL,
  fileLabels = NULL,
  fileType = NULL,
  genome = NULL,
  numberOfCores = 1
)
```

**Arguments**

promoterAnnotation	A PromoterAnnotation object containing the reduced exon ranges, annotated intron ranges, promoter coordinates and the promoter id mapping
files	A character vector. The list of junction or BAM files for which the junction read counts will be calculated
fileLabels	A character vector. The labels of junction or BAM files for which the junction read counts will be calculated. These labels will be used as column names for the output data.frame object
fileType	A character. Type of the junction bed or bam file, either 'tophat', 'star' or 'bam'
genome	A character. Genome version used. Must be specified if input is a BAM file. Defaults to NULL
numberOfCores	A numeric value. The number of cores to be used for counting junction reads. Defaults to 1 (no parallelization). This parameter will be used as an argument to BiocParallel::bplapply

**Value**

A data.frame object. The number of junction reads per promoter (rows) for each sample (cols)

---

```
getAbsolutePromoterActivity
```

*Prepare the absolute promoter activity table including the promoter and gene ids*

---

### Description

Prepare the absolute promoter activity table including the promoter and gene ids

### Usage

```
getAbsolutePromoterActivity(
  junctionReadCounts,
  promoterAnnotation,
  log2 = TRUE,
  pseudocount = 1
)
```

### Arguments

junctionReadCounts	Matrix of junction read counts (rows: promoters, cols: samples)
promoterAnnotation	A PromoterAnnotation object containing the intron ranges, promoter coordinates and the promoter id mapping
log2	Logical indicating whether log2 read counts should be used (default: TRUE) or not
pseudocount	Number to be used for log2 as pseudocount if log2 is TRUE

### Value

data.frame of absolute promoter activity with promoter and gene ids

---

```
getGeneExpression
```

*Prepare the gene expression table including the gene ids*

---

### Description

Prepare the gene expression table including the gene ids

### Usage

```
getGeneExpression(absolutePromoterActivity)
```

### Arguments

absolutePromoterActivity	data.frame of absolute promoter activity with promoter and gene ids
--------------------------	---

**Value**

data.frame of gene expression with gene ids#'

---

*getRelativePromoterActivity*

*Prepare the relative promoter activity table including the promoter and gene ids*

---

**Description**

Prepare the relative promoter activity table including the promoter and gene ids

**Usage**

`getRelativePromoterActivity(absolutePromoterActivity, geneExpression)`

**Arguments**

`absolutePromoterActivity`

data.frame of absolute promoter activity with promoter and gene ids

`geneExpression` data.frame of gene expression with gene ids

**Value**

data.frame of relative promoter activity with promoter and gene ids

---

*normalizePromoterReadCounts*

*Normalize promoter read counts using DESeq2*

---

**Description**

Normalize promoter read counts using DESeq2

**Usage**

`normalizePromoterReadCounts(promoterReadCounts)`

**Arguments**

`promoterReadCounts`

A data.frame object. The number of junction reads per promoter (rows) for each sample (cols)

**Value**

A data.frame object. The normalized number of junction reads per promoter (rows) for each sample (cols) using DESeq2 counts function. Requires 'DESeq2' package to be installed

---

plotPromoters

*Visualizes promoter activity and transcript model for a gene of interest*


---

## Description

Visualizes promoter activity and transcript model for a gene of interest

## Usage

```
plotPromoters(
  result,
  gene,
  txdb,
  ranges,
  cex.title = 0.9,
  cex.axis = 0.9,
  cex.main = 1,
  blk.width = 500,
  blk.fill = "grey",
  blk.border = "darkgrey",
  label.col = "black",
  label.size = 0.7,
  arrow.width = NULL,
  arrow.fill = "transparent",
  arrow.border = "grey"
)
```

## Arguments

result	A SummarizedExperiment object with assays giving promoter counts and activity with gene expression stored as column data and promoter gene id mapping stored as row data
gene	A character vector of length 1. Single gene of interest to be plotted
txdb	A TxDb object. The txdb must correspond to the genome version used in running proActiv. Here, it is recommended to use the same txdb in generating promoter annotations
ranges	A list of GRanges. Each entry in the list should correspond to a transcript that will be visualized, with Genomic Ranges giving the exons corresponding to that transcript
cex.title	A numeric value. Size of axis labels. Defaults to 0.9
cex.axis	A numeric value. Size of axis and axis ticks. Defaults to 0.9
cex.main	A numeric value. Size of plot name. Defaults to 1
blk.width	A numeric value. The width of promoters blocks in the data track. Defaults to 500 (bases)
blk.fill	A character vector of length 1. The fill colour of the promoter blocks in the data track. Defaults to 'grey'
blk.border	A character vector of length 1. The border colour of the promoter blocks in the data track. Defaults to 'darkgrey'

label.col	A character vector of length 1. The font colour of the promoter ID label in the annotation track. Defaults to 'black'
label.size	A numeric value. The size of the promoter ID label in the annotation track. Defaults to 0.7
arrow.width	A numeric value. The width of promoter arrows in the annotation track. This value is internally calculated based on the gene of interest
arrow.fill	A character vector of length 1. The fill colour of the promoter arrows in the annotation track. Defaults to 'transparent'
arrow.border	A character vector of length 1. The border colour of the promoter arrows in the annotation track. Defaults to 'grey'

### Value

Outputs a plot of the promoters of the gene of interest across conditions, along with a model of transcripts belonging to the gene

### Examples

```
## First, run proActiv to generate a summarizedExperiment result
files <- list.files(system.file('extdata/vignette/junctions',
                              package = 'proActiv'),
                  full.names = TRUE)
promoterAnnotation <- promoterAnnotation.gencode.v34.subset
result <- proActiv(files = files,
                  promoterAnnotation = promoterAnnotation,
                  condition = rep(c('A549', 'HepG2'), each=3),
                  ncores = 1)
## Read in pre-computed ranges
txdb <- AnnotationDbi::loadDb(system.file('extdata/vignette/annotations',
                                         'gencode.v34.annotation.rap1gap.sqlite',
                                         package = 'proActiv'))
## Declare a gene of interest
gene <- 'ENSG00000076864.19'
## Call plot
plotPromoters(result = result, gene = gene, txdb = txdb)
```

---

preparePromoterAnnotation

*Prepares promoter annotation from a gtf or txdb*

---

### Description

Prepares promoter annotation from a gtf or txdb

### Usage

```
preparePromoterAnnotation(txdb, file, species)
```

**Arguments**

txdb	A txdb object. The txdb of the annotation version for which promoters will be identified. Either 'txdb' or 'file' argument must be specified, but not both.
file	A character object. The file path to a gtf/gff or txdb of the annotation version for which promoters will be identified. Either 'txdb' or 'file' argument must be specified, but not both.
species	A character object. The genus and species of the organism to be used in keepStandardChromosomes(). Supported species can be seen with names(genomeStyles()).

**Value**

A PromoterAnnotation object. The annotated intron ranges, promoter coordinates and the promoter id mapping are attributes of the promoter annotation data.

**Examples**

```
txdbPath <- system.file('extdata/vignette/annotations/',
                       'gencode.v34.annotation.subset.sqlite',
                       package = 'proActiv')
txdb <- AnnotationDbi::loadDb(txdbPath)
promoterAnnotation <- preparePromoterAnnotation(txdb = txdb,
                                                species = 'Homo_sapiens')
```

---

 proActiv

*Estimates promoter counts and activity in a single command*


---

**Description**

Estimates promoter counts and activity in a single command

**Usage**

```
proActiv(
  files,
  promoterAnnotation,
  fileLabels = NULL,
  condition = NULL,
  genome = NULL,
  ncores = 1
)
```

**Arguments**

files	A character vector. The list of input files for which the junction read counts will be calculated
promoterAnnotation	A PromoterAnnotation object containing the intron ranges, promoter coordinates and the promoter id mapping



fileLabels	A character vector. The labels of input files for which the junction read counts will be calculated. These labels will be used as column names for each output data.frame object. If not provided, filenames will be used as labels. Defaults to NULL
condition	A character vector. The condition to which each sample belong to. Must correspond to the order of the files. If supplied, results are summarized by condition. Defaults to NULL
genome	A character. Genome version. Must be specified if input file type is a BAM file. Defaults to NULL
ncores	A numeric value. The number of cores to be used for counting junction reads. Defaults to 1 (no parallelization). This parameter will be used as an argument to BiocParallel::bplapply

**Value**

A SummarizedExperiment object with assays giving promoter counts and activity with gene expression stored as metadata. rowData contains promoter metadata and absolute promoter activity summarized across conditions (if condition is provided)

**Examples**

```
files <- list.files(system.file('extdata/vignette/junctions',
                             package = 'proActiv'),
                  full.names = TRUE, pattern = 'replicate5')
promoterAnnotation <- promoterAnnotation.gencode.v34.subset
result <- proActiv(files = files,
                  promoterAnnotation = promoterAnnotation,
                  condition = rep(c('A549', 'HepG2'), each=1),
                  fileLabels = NULL,
                  ncores = 1)
```

---

PromoterAnnotation-class

*S4 class for promoter annotation data for a specific annotation version*

---

**Description**

S4 class for promoter annotation data for a specific annotation version

**Usage**

```
PromoterAnnotation(
  intronRanges = GRanges(),
  promoterIdMapping = data.frame(),
  promoterCoordinates = GRanges()
)
```

```
intronRanges(x)
```

```

## S4 method for signature 'PromoterAnnotation'
intronRanges(x)

promoterIdMapping(x)

## S4 method for signature 'PromoterAnnotation'
promoterIdMapping(x)

promoterCoordinates(x)

## S4 method for signature 'PromoterAnnotation'
promoterCoordinates(x)

intronRanges(x) <- value

## S4 replacement method for signature 'PromoterAnnotation'
intronRanges(x) <- value

promoterIdMapping(x) <- value

## S4 replacement method for signature 'PromoterAnnotation'
promoterIdMapping(x) <- value

promoterCoordinates(x) <- value

## S4 replacement method for signature 'PromoterAnnotation'
promoterCoordinates(x) <- value

```

### Arguments

intronRanges	A GRanges object containing annotated intron ranges
promoterIdMapping	A data.frame containing mapping between transcript, TSS, promoter and gene ids
promoterCoordinates	A GRanges object containing promoter coordinates
x	A PromoterAnnotation object
value	intronRanges, promoterIdMapping or promoterCoordinates to be assigned

### Value

A promoter annotation object with three slots: intronRanges, promoterIdMapping and promoterCoordinates

### Functions

- intronRanges: Getter for intronRanges
- intronRanges, PromoterAnnotation-method: Getter for intronRanges
- promoterIdMapping: Getter for promoterIdMapping
- promoterIdMapping, PromoterAnnotation-method: Getter for promoterIdMapping
- promoterCoordinates: Getter for promoterCoordinates

- promoterCoordinates, PromoterAnnotation-method: Getter for promoterCoordinates
- intronRanges<-: Setter for intronRanges
- intronRanges<- , PromoterAnnotation-method: Setter for intronRanges
- promoterIdMapping<-: Setter for promoterIdMapping
- promoterIdMapping<- , PromoterAnnotation-method: Setter for promoterIdMapping
- promoterCoordinates<-: Setter for promoterCoordinates
- promoterCoordinates<- , PromoterAnnotation-method: Setter for promoterCoordinates

### Slots

**intronRanges** A GRanges object. The intron ranges annotated with the promoter information.

**promoterIdMapping** A data.frame object. The id mapping between transcript ids, names, TSS ids, promoter ids and gene ids.

**promoterCoordinates** A GRanges object. Promoter coordinates (TSS) with gene id and internal promoter state

### Examples

```
promoterAnnotation <- PromoterAnnotation()
intronRanges(promoterAnnotation) <- intronRanges(
  promoterAnnotation.gencode.v34.subset)
promoterIdMapping(promoterAnnotation) <- promoterIdMapping(
  promoterAnnotation.gencode.v34.subset)
promoterCoordinates(promoterAnnotation) <- promoterCoordinates(
  promoterAnnotation.gencode.v34.subset)
```

---

```
promoterAnnotation.gencode.v34.subset
```

*Promoter annotation for Gencode.v34 (subset)*

---

### Description

Promoter annotation for Gencode.v34 (chr1:10,000,000 - 30,000,000)

### Usage

```
promoterAnnotation.gencode.v34.subset
```

### Format

A PromoterAnnotation (S4 Class) object containing all promoter annotation objects for Gencode.v34 chr1:10,000,000-30,000,000. The object has 3 slots:

**intronRanges** A GRanges object of 4,523 ranges corresponding to introns, annotated with the associated transcript.

**promoterIdMapping** The id mapping between transcript names, promoter ids and gene ids for Gencode v34.

**promoterCoordinates** A GRanges object of 1,380 ranges showing the tss coordinate for each promoter of Gencode v34 chr1:10,000,000-30,000,000, annotated with the associated gene id, coordinate of the 3' end of the first reduced exon, and intron id.

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