

# Package ‘pram’

July 10, 2025

**Title** Pooling RNA-seq datasets for assembling transcript models

**Version** 1.24.0

**Description** Publicly available RNA-seq data is routinely used for retrospective analysis to elucidate new biology. Novel transcript discovery enabled by large collections of RNA-seq datasets has emerged as one of such analysis. To increase the power of transcript discovery from large collections of RNA-seq datasets, we developed a new R package named Pooling RNA-seq and Assembling Models (PRAM), which builds transcript models in intergenic regions from pooled RNA-seq datasets. This package includes functions for defining intergenic regions, extracting and pooling related RNA-seq alignments, predicting, selected, and evaluating transcript models.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**URL** <https://github.com/pliu55/pram>

**BugReports** <https://github.com/pliu55/pram/issues>

**Depends** R (>= 3.6)

**Imports** methods, BiocParallel, tools, utils, data.table (>= 1.11.8),  
GenomicAlignments (>= 1.16.0), rtracklayer (>= 1.40.6),  
BiocGenerics (>= 0.26.0), GenomeInfoDb (>= 1.16.0),  
GenomicRanges (>= 1.32.0), IRanges (>= 2.14.12), Rsamtools (>= 1.32.3), S4Vectors (>= 0.18.3)

**RoxygenNote** 6.1.0

**Suggests** testthat, BiocStyle, knitr, rmarkdown

**Collate** 'Param.R' 'Transcript.R' 'buildModel.R' 'defIgRanges.R'  
'evalModel.R' 'prepIgBam.R' 'runPRAM.R' 'selModel.R' 'util.R'

**VignetteBuilder** knitr

**biocViews** Software, Technology, Sequencing, RNASeq,  
BiologicalQuestion, GenePrediction, GenomeAnnotation,  
ResearchField, Transcriptomics

**SystemsRequirements** buildModel() and runPRAM() functions require external software Cufflinks, StringTie, and/or TACO. For details, please see the 'Required external software' section in vignette's 'Building transcript models: buildModel()'.

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|            |                                                          |
|------------|----------------------------------------------------------|
| buildModel | <i>Build transcript models from aligned RNA-seq data</i> |
|------------|----------------------------------------------------------|

---

Description

Build transcript models from aligned RNA-seq data

Usage

```
buildModel(in_bamv, out_gtf, method = "plcf", nthreads = 1,  
           tmpdir = NULL, keep_tmpdir = FALSE, cufflinks = "",  
           stringtie = "", taco = "", cufflinks_ref_fa = "")
```

**Arguments**

|                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| in_bamv          | A character vector of input BAM file(s). If mode 'cf' or 'st' is used, only one input RNA-seq BAM file is allowed. Currently, PRAM only supports strand-specific paired-end data with the first mate on the right-most of transcript coordinate, i.e., 'fr-firststrand' by Cufflinks's definition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| out_gtf          | An output GTF file of predicted transcript models                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| method           | <p>A character string defining PRAM's model building method. Current available methods are:</p> <ul style="list-style-type: none"> <li>• plcf: pooling + cufflinks</li> <li>• plst: pooling + stringtie</li> <li>• cfmg: cufflinks + cuffmerge</li> <li>• stmg: stringtie + merging</li> <li>• cftc: cufflinks + taco</li> <li>• cf: cufflinks</li> <li>• st: stringtie</li> </ul> <p>Default: 'plcf'</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| nthreads         | An integer defining the number of threads to-be-used. Default: 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| tmpdir           | A character string defining the full name of a folder for saving temporary files. If not tmpdir is give, PRAM will use R's tempdir().                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| keep_tmpdir      | Whether to keep temporary files afterwards. Default: False                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| cufflinks        | <p>Cufflinks executable. Required by mode 'plcf', 'cfmg', and 'cf'. For mode 'cfmg', executable files of Cuffmerge, Cuffcompare, and gtf_to_sam from the Cufflinks suite are assumed to be under the same folder as Cufflinks. All the executables are available to download for Linux <a href="http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz">http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz</a> and MacOS <a href="http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz">http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz</a>. Souce code can be obtained from <a href="http://cole-trapnell-lab.github.io/cufflinks/">http://cole-trapnell-lab.github.io/cufflinks/</a>. Default:</p> <p>”</p> |
| stringtie        | <p>StringTie executable file. Required by mode 'plst', 'stmg', and 'st'. Executable can be downloaded for Linux <a href="http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz">http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz</a> and MacOS <a href="http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz">http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz</a>. Souce code can be obtained from <a href="https://ccb.jhu.edu/software/stringtie/">https://ccb.jhu.edu/software/stringtie/</a>. Default:</p> <p>”</p>                                                                                                                                                                                                                                                                    |
| taco             | <p>TACO executable file. Required by mode 'cftc'. Executable can be downloaded for Linux <a href="https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.Linux_x86_64.tar.gz">https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.Linux_x86_64.tar.gz</a> and MacOS <a href="https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX_x86_64.tar.gz">https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX_x86_64.tar.gz</a>. Souce code can be obtained from <a href="https://tacorna.github.io">https://tacorna.github.io</a>. Default:</p> <p>”</p>                                                                                                                                                                                                                                                                           |
| cufflinks_ref_fa | <p>Genome reference fasta file for Cufflinks. If supplied, will be used for cufflinks's '-frag-bias-correct' and cuffmerge's '-ref-sequence' options. Default: ”</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

Value

None

Examples

```
fbams = c( system.file('extdata/bam/CMPRep1.sortedByCoord.clean.bam',
                      package='pram'),
            system.file('extdata/bam/CMPRep2.sortedByCoord.clean.bam',
                      package='pram') )

foutgtf = tempfile(fileext='.gtf')

## assuming the stringtie binary is in folder /usr/local/stringtie-1.3.3/
## you can run buildModel() by the following example
##
# buildModel(fbams, foutgtf, method='plst',
#            stringtie='/usr/local/stringtie-1.3.3/stringtie')
```

---

|             |                                          |
|-------------|------------------------------------------|
| defIgRanges | <i>Define intergenic genomic regions</i> |
|-------------|------------------------------------------|

---

Description

Define intergenic genomic regions

Usage

```
defIgRanges(in_gtf, chromgrs, genome = NULL, fchromsize = NULL,
            radius = 10000, feat = "exon", chroms = NULL)
```

Arguments

|          |                                                                                                                                                                                                                                                                                                    |
|----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| in_gtf   | An input GTF file for defining genomic coordinates of existing genes. Required to have 'gene_id' in the attribute column (column 9)                                                                                                                                                                |
| chromgrs | A GRanges object defining chromosome sizes.                                                                                                                                                                                                                                                        |
| genome   | Version of the genome. Will be used when 'chromgrs' is missing. Currently supported ones are: <ul style="list-style-type: none"><li>• hg19</li><li>• hg38</li><li>• mm9</li><li>• mm10</li></ul> All the above genomes have sizes for all chromosomes including random and alt ones. Default: NULL |

|            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| fchromsize | <p>Name of a file defining chromosome sizes. Will be used when 'chromgrs' and 'genome' are missing. It can be downloaded from UCSC, e.g. for hg19, <a href="http://hgdownload.cse.ucsc.edu/goldenpath/hg19/database/chromInfo.txt.gz">http://hgdownload.cse.ucsc.edu/goldenpath/hg19/database/chromInfo.txt.gz</a> Required to have at least two tab-delimited columns without any header:</p> <ol style="list-style-type: none"> <li>1. chromosome name, e.g. chr1</li> <li>2. chromosome length, e.g. 249250621</li> </ol> <p>Both uncompressed and gzipped files are supported. Default: NULL</p> |
| radius     | Region length (bp) of gene's upstream and downstream to be excluded from intergenic region. Default: 10,000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| feat       | Feature in the GTF file (column 3) to-be-used for defining genic region. Default: exon                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| chroms     | A vector of chromosomes names to define intergenic regions. e.g. c('chr10', 'chr11') Default: NULL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

**Value**

a GRanges object of intergenic regions

**Examples**

```
fgtf = system.file('extdata/gtf/defIgRanges_in.gtf', package='pram')

defIgRanges(fgtf, genome='hg38')
```

---

evalModel

---

*Evaluate transcript model*


---

**Description**

Evaluate trascript model's precision and recall on exon nucleotides, splice junctions, and splice patterns by comparing them to transcript targets

**Usage**

```
evalModel(model_exons, target_exons)

## S4 method for signature 'GRanges,GRanges'
evalModel(model_exons, target_exons)

## S4 method for signature 'character,character'
evalModel(model_exons, target_exons)

## S4 method for signature 'data.table,data.table'
```

```
evalModel(model_exons, target_exons)

## S4 method for signature 'character,data.table'
evalModel(model_exons, target_exons)
```

### Arguments

**model\_exons**      genomic coordinates for transcript model exons  
**target\_exons**    genomic coordinates for transcript target exons

### Value

a data table of precision, recall, number of true positive, false negative, false positive for all three evaluated features

### Methods (by class)

- **model\_exons = GRanges, target\_exons = GRanges:** Both **model\_exons** and **target\_exons** are GRanges objects to define genomic coordinates of exons. Required to have a meta-data column named 'trid' to define each exon's transcript ID.
- **model\_exons = character, target\_exons = character:** Both **model\_exons** and **target\_exons** are GTF files with full names. Each GTF file is required to have a 'transcript\_id' tag in column 9.
- **model\_exons = data.table, target\_exons = data.table:** Both **model\_exons** and **target\_exons** are data.table objects to define exon genomic coordinates. Required to have the following columns:
  - chrom: exon's chromosome, e.g. 'chr8'
  - start: exon's start position
  - end: exon's end position
  - strand: exon's strand, '+' or '-'
  - trid: exon's transcript ID
- **model\_exons = character, target\_exons = data.table:** The **model\_exons** is a GTF file with full name and **target\_exons** is a data.table object. Requirements for GTF and data.table are the same as above

### Examples

```
fmdl = system.file('extdata/benchmark/plcf.tsv', package='pram')
ftgt = system.file('extdata/benchmark/tgt.tsv', package='pram')

mdldt = data.table::fread(fmdl, header=TRUE, sep="\t")
tgtgt = data.table::fread(ftgt, header=TRUE, sep="\t")

evalModel(mdldt, tgtgt)
```

---

`prepIgBam`*Extract alignments in intergenic regions from BAM files*

---

**Description**

Extract alignments in intergenic regions from BAM files

**Usage**

```
prepIgBam(finbam, iggrs, foutbam, max_uni_n_dup_aln = 10,  
          max_mul_n_dup_aln = 10)
```

**Arguments**

|                                |                                                                                                                                                                                                                        |
|--------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>finbam</code>            | Full name of an input RNA-seq BAM file. Currently, PRAM only supports strand-specific paired-end data with the first mate on the right-most of transcript coordinate, i.e., 'fr-firststrand' by Cufflinks's definition |
| <code>iggrs</code>             | A GenomicRanges object defining intergenic regions                                                                                                                                                                     |
| <code>foutbam</code>           | Full name of an output BAM file to save all alignment fell into intergenic regions                                                                                                                                     |
| <code>max_uni_n_dup_aln</code> | Maximum number of uniquely mapped fragments to report per each alignment.<br>Default: 10                                                                                                                               |
| <code>max_mul_n_dup_aln</code> | Maximum number of multi-mapping fragments to report per each alignment.<br>Default: 10                                                                                                                                 |

**Value**

None

**Examples**

```
finbam = system.file('extdata/bam/CMPRep2.sortedByCoord.raw.bam',  
                     package='pram')  
  
iggrs = GenomicRanges::GRanges('chr10:77236000-77247000:+')  
  
foutbam = tempfile(fileext='.bam')  
  
prepIgBam(finbam, iggrs, foutbam)
```

runPRAM

*Predict intergenic transcript models from RNA-seq***Description**

Predict intergenic transcript models from RNA-seq

**Usage**

```
runPRAM(in_gtf, in_bamv, out_gtf, method, cufflinks = "",
        stringtie = "", taco = "")
```

**Arguments**

|           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| in_gtf    | An input GTF file for defining genomic coordinates of existing genes. Required to have 'gene_id' in the attribute column (column 9)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| in_bamv   | A character vector of input BAM file(s). If mode 'cf' or 'st' is used, only one input RNA-seq BAM file is allowed. Currently, PRAM only supports strand-specific paired-end data with the first mate on the right-most of transcript coordinate, i.e., 'fr-firststrand' by Cufflinks's definition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| out_gtf   | An output GTF file of predicted transcript models                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| method    | A character string defining PRAM's model building method. Current available methods are: <ul style="list-style-type: none"> <li>• plcf: pooling + cufflinks</li> <li>• plst: pooling + stringtie</li> <li>• cfmg: cufflinks + cuffmerge</li> <li>• stmg: stringtie + merging</li> <li>• cfte: cufflinks + taco</li> <li>• cf: cufflinks</li> <li>• st: stringtie</li> </ul> Default: 'plcf'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| cufflinks | Cufflinks executable. Required by mode 'plcf', 'cfmg', and 'cf'. For mode 'cfmg', executable files of Cuffmerge, Cuffcompare, and gtf_to_sam from the Cufflinks suite are assumed to be under the same folder as Cufflinks. All the executables are available to download for Linux <a href="http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz">http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz</a> and MacOS <a href="http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz">http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz</a> . Source code can be obtained from <a href="http://cole-trapnell-lab.github.io/cufflinks/">http://cole-trapnell-lab.github.io/cufflinks/</a> . Default: "" |
| stringtie | StringTie executable file. Required by mode 'plst', 'stmg', and 'st'. Executable can be downloaded for Linux <a href="http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz">http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz</a> and MacOS <a href="http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz">http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz</a> . Source                                                                                                                                                                                                                                                                                                                                                                                                          |

code can be obtained from <https://ccb.jhu.edu/software/stringtie/>. Default: ”

taco TACO executable file. Required by mode 'cftc'. Executable can be downloaded for Linux [https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.Linux\\_x86\\_64.tar.gz](https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.Linux_x86_64.tar.gz) and MacOS [https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX\\_x86\\_64.tar.gz](https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX_x86_64.tar.gz). Source code can be obtained from <https://tacorna.github.io>. Default: ”

## Value

None

## Examples

```
in_gtf = system.file('extdata/demo/in.gtf', package='pram')

in_bamv = c(system.file('extdata/demo/SZP.bam', package='pram'),
            system.file('extdata/demo/TLC.bam', package='pram'))

pred_out_gtf = tempfile(fileext='.gtf')

## assuming the stringtie binary is in folder /usr/local/stringtie-1.3.3/
## you can run runPRAM() by the following example
##
# runPRAM(in_gtf, in_bamv, pred_out_gtf, method='plst',
#         stringtie='/usr/local/stringtie-1.3.3/stringtie')
```

---

|          |                                 |
|----------|---------------------------------|
| selModel | <i>Select transcript models</i> |
|----------|---------------------------------|

---

## Description

Select transcript models

## Usage

```
selModel(fin_gtf, fout_gtf, min_n_exon = 2, min_tr_len = 200,
         info_keys = c("transcript_id"))
```

## Arguments

|            |                                                                                                                                     |
|------------|-------------------------------------------------------------------------------------------------------------------------------------|
| fin_gtf    | Character of an input GTF file that contains transcript models. Required to have 'transcript_id' in the attribute column (column 9) |
| fout_gtf   | Character of an output GTF file that contains selected transcript models                                                            |
| min_n_exon | Minimum number of exons a transcript model required to have Default: 2                                                              |

|                         |                                                                                                                                                                                                |
|-------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>min_tr_len</code> | Minimum length (bp) of exon(s) and intron(s) a transcript model required to have Default: 200                                                                                                  |
| <code>info_keys</code>  | A vector of characters defining the attributes in input GTF file's column 9 to be saved in the output GTF file. 'transcript_id' will always be saved. Default: <code>c('transcript_id')</code> |

**Value**

None

**Examples**

```
fin_gtf = system.file('extdata/gtf/selModel_in.gtf', package='pram')  
  
fout_gtf = tempfile(fileext='.gtf')  
  
selModel(fin_gtf, fout_gtf)
```

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