Package 'pram'

November 12, 2026

Title Pooling RNA-seq datasets for assembling transcript models

Version 1.28.0

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.

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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), Seqinfo, 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

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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` *Build transcript models from aligned RNA-seq data*

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	A character string defining PRAM's model building method. Current available methods are: • plcf: pooling + cufflinks • plst: pooling + stringtie • cfmg: cufflinks + cuffmerge • stmg: stringtie + merging • cftc: cufflinks + taco • cf: cufflinks • st: stringtie Default: 'plcf'
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	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 http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz and MacOS http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz. Souce code can be obtained from http://cole-trapnell-lab.github.io/cufflinks/. Default: ''
stringtie	StringTie executable file. Required by mode 'plst', 'stmg', and 'st'. Executable can be downloaded for Linux http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz and MacOS http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz. Souce 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 and MacOS https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX_x86_64.tar.gz. Souce code can be obtained from https://tacorna.github.io. Default: ''
cufflinks_ref_fa	Genome reference fasta file for Cufflinks. If supplied, will be used for cufflinks's '–frag-bias-correct' and cuffmerge's '–ref-sequence' options. Default: ''

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` *Define intergenic genomic regions*

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: • hg19 • hg38 • mm9 • mm10 All the above genomes have sizes for all chromosomes including random and alt ones. Default: NULL

fchromsize	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, http://hgdownload.cse.ucsc.edu/ goldenpath/hg19/database/chromInfo.txt.gz Required to have at least two tab-delimited columns without any header: 1. chromosome name, e.g. chr1 2. chromosome length, e.g. 249250621 Both uncompressed and gzipped files are supported. Default: NULL
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 coordinatess. 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")
tgtdt = data.table::fread(ftgt, header=TRUE, sep="\t")


evalModel(mdldt, tgtdt)
```

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

finbam	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
iggrs	A GenomicRanges object defining intergenic regions
foutbam	Full name of an output BAM file to save all alignment fell into intergenic regions
max_uni_n_dup_aln	Maximum number of uniquely mapped fragments to report per each alignment. Default: 10
max_mul_n_dup_aln	Maximum number of multi-mapping fragments to report per each alignment. 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: • plcf: pooling + cufflinks • plst: pooling + stringtie • cfmg: cufflinks + cuffmerge • stmg: stringtie + merging • cftc: cufflinks + taco • cf: cufflinks • st: stringtie 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 http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz and MacOS http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.1.1.OSX_x86_64.tar.gz. Souce code can be obtained from http://cole-trapnell-lab.github.io/cufflinks/. Default: ""
stringtie	StringTie executable file. Required by mode 'plst', 'stmg', and 'st'. Executable can be downloaded for Linux http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.Linux_x86_64.tar.gz and MacOS http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.3.3b.OSX_x86_64.tar.gz. Souce

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 and MacOS https://github.com/tacorna/taco/releases/download/v0.7.0/taco-v0.7.0.OSX_x86_64.tar.gz. Souce 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 *Select transcript models*

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 — Minimium number of exons a transcript model required to have Default: 2

min_tr_len	Minimium length (bp) of exon(s) and intron(s) a transcript model required to have Default: 200
info_keys	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: c('transcript_id')

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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