Package 'MAAPER'

August 14, 2021

Title Analysis of Alternative Polyadenylation Using 3' End-Linked Reads

Version 1.1.1

Description A computational method developed for model-based analysis of alternative polyadenylation (APA) using 3' end-linked reads. It accurately assigns 3' RNA-seq reads to polyA sites through statistical modeling, and generates multiple statistics for APA analysis. Please also see Li WV, Zheng D, Wang R, Tian B (2021) <doi:10.1186/s13059-021-02429-5>.

License GPL-3

Encoding UTF-8

RoxygenNote 7.1.1

Imports parallel, GenomicRanges, GenomicAlignments, GenomicFeatures, GenomeInfoDb, stats, utils, Rsamtools, IRanges, MASS

URL https://github.com/Vivianstats/MAAPER, https://genomebiology.biomedcentral.com/articles/10.1186/s13059-021-02429-5

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

maaper *Model-based analysis of alternative polyadenylation using 3' end-linked reads*

Description

Model-based analysis of alternative polyadenylation using 3' end-linked reads

Usage

```
maaper(
  gtf,
  pas_annotation,
  output_dir,
  bam_c1,
  bam_c2,
  read_len,
  ncores = 1,
  num_pas_thre = 25,
  frac_pas_thre = 0.05,
  dist_thre = 600,
  num_thre = 50,
  run = "all",
  subset = NULL,
  region = "all",
  gtf_rds = NULL,
  verbose = FALSE,
  paired = FALSE,
  bed = FALSE
)
```

Arguments

gtf	A character specifying the full path of the GTF file (reference genome);
pas_annotation	A list containing the pas annotation. MAAPER provides processed annotation information from PolyA_DB v3 on its Github page.
output_dir	A character specifying the full path of the output directory, which is used to store all intermdediate and final outputs.
bam_c1	A character vector specifying the full paths to the bam files for condition 1 (control). The length of the vector equals the number of samples.
bam_c2	A character vector specifying the full paths to the bam files for condition 2 (experiment). The length of the vector equals the number of samples.
read_len	An integer specifying the read length.
ncores	An integer specifying the number of cores used in parallel computation.
num_pas_thre	An integer specifying the threhold on PAS's read number. Defaults to 25.

frac_pas_thre	A numeric specifying the threshold on PAS's fraction. Defaults to 0.05.
dist_thre	An integer specifying the threshold on fragment length. Defaults to 600.
num_thre	An integer specifying the threhold on gene's read number. Defaults to 50.
run	"all" (default) or "skip-train". For test and debug only.
subset	A character vector specifying genes' Ensembl IDs if only a subset of genes need to be analyzed. Check the pas_annotation files for ID formats.
region	"all" (default). For test and debug only.
gtf_rds	NULL (default). For test and debug only.
verbose	FALSE (default). For test and debug only.
paired	A boolean indicating whether to perform paired test instead of unpaired test (defaults to FALSE).
bed	Aboolean indicating whether bedGraph files should be output for visualization in genome browser.

Value

maaper saves two text files, gene.txt and pas.txt, to out_dir. pas.txt contains the gene names, predicted PASs, and their corresponding fractions in the two conditions. gene.txt contains the genes' PAS number, p values, RED, RLDu, and RLDi scores.

Author(s)

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Examples

```
## Not run:
# data used in this example can be found on the package's Github page
pas_annotation = readRDS("./mouse.PAS.mm9.rds")
gtf = "./gencode.mm9.chr19.gtf"
bam_c1 = "./NT_chr19_example.bam"
bam_c2 = "./AS_4h_chr19_example.bam"
maaper(gtf, pas_annotation, output_dir = "./",
       bam_c1, bam_c2, read_len = 76, ncores = 1)

## End(Not run)
```

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