

# Package ‘MAAPER’

July 21, 2025

**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](https://doi.org/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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**Repository** CRAN

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## 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 intermediate 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 threshold 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 threshold 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           | A boolean 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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