

Package ‘AID’

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Title Annotation-based transcript reconstruction and quantification

Version 0.0.1

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Description What the package does (one paragraph).

Depends R (>= 3.4.2)

License GPL

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

LinkingTo Rcpp, RcppArmadillo

Imports Rcpp, RcppArmadillo, Biostrings, GenomicAlignments, GenomicFeatures, GenomeInfoDb, IRanges, S4Vectors, GenomicRanges, gtools, igraph, np, rbamtools, Rsamtools, stringr, truncated, stats, utils, tidyr, dplyr

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aid	<i>use AID for transcript reconstruction and quantification</i>
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Description

use AID for transcript reconstruction and quantification

Usage

```
aid(gtf_path, bam_path, fasta_path, out_dir, readLen, strandmode = 0,  
    genes = NULL, pval = NULL, ncores = 5)
```

Arguments

gtf_path	A character specifying the full path of the GTF file.
bam_path	A character specifying full path of the BAM file. The BAM file should be sorted and indexed, with the BAI file in the same folder. The BAM file should be aligned using the GTF file as supplied by gtf_path.
fasta_path	A character specifying full path of the fasta file for genome sequences, used in GC-content bias correction.
out_dir	A character specifying the full path of the output directory.
readLen	An integer giving the length of the RNA-seq reads.
strandmode	An integer specifying the library type: 0 means unstranded, 1 means second-strand, and strandmode 2 means firststrand. Default is 0.
genes	An character vector specifying the ids of genes to be estimated. Must match the gene ids in the GTF file. Default is NULL, meaning that all genes in the GTF file will be estimated.
pval	An number specifying the threshold on p-values used in the likelihood ratio tests. Default is 0.01/(number of genes estimated).
ncores	A integer specifying the number of cores used for parallel computation. Default is 5.

Value

aid saves a GTF file with reconstructed transcripts and their FPKM values to x to the directory out_dir.

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