Package 'AIDE'

November 8, 2019

Title Annotation-assisted transcript reconstruction and quantification

Version 1.0.0

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Description Annotation-assisted transcript reconstruction and quantification.

Depends R (>= 3.4)

License GPL

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

LinkingTo Rcpp, RcppArmadillo

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

R topics documented:

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aide   *use AIDE for transcript reconstruction and quantification*

Description

use AIDE for transcript reconstruction and quantification

Usage

```
aide(gtf_path, bam_path, fasta_path, out_dir, readLen, strandmode = 0,
  genes = NULL, pval = NULL, ncores = 5, mode = "regular",
  ne = 25, gene_model_path = NULL, flag = 0)
```

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`	An integer specifying the number of cores used for parallel computation. Default is 5.
`mode`	An character specifying running mode (used in tests). Default is "regular".
`ne`	An integer indicating complex genes.
`gene_model_path`	
	An character specifying path to gene models.
`flag`	Used in tests.

Value

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

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