Package 'eds'

August 20, 2025

Title eds: Low-level reader for Alevin EDS format

Version 1.11.0

Description This packages provides a single function, readEDS.
This is a low-level utility for reading in Alevin EDS format into R.
This function is not designed for end-users but instead the package
is predominantly for simplifying package dependency graph for other
Bioconductor packages.

Depends Matrix

Imports Rcpp

Suggests knitr, tximportData, testthat (>= 3.0.0)

LinkingTo Rcpp

SystemRequirements C++11

License GPL-2

Encoding UTF-8

URL https://github.com/mikelove/eds

biocViews Sequencing, RNASeq, GeneExpression, SingleCell

VignetteBuilder knitr

LazyData true

RoxygenNote 7.1.2

Config/testthat/edition 3

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`readEDS` *A low-level utility function for quickly reading in Alevin EDS format*

Description

This provides a simple utility for reading in EDS format. Note that most users will prefer to use tximport or tximeta. This function and package exist in order to simplify the dependency graph for other packages.

Usage

```
readEDS(numOfGenes, numOfOriginalCells, countMatFilename, tierImport = FALSE)
```

Arguments

`numOfGenes`	number of genes
`numOfOriginalCells`	number of cells
`countMatFilename`	pointer to the EDS file, `quants_mat.gz`
`tierImport`	whether the `countMatFilename` refers to a quants tier file

Value

a genes x cells sparse matrix, of the class `dgCMatrix`

Examples

```
# point to files
dir0 <- system.file("extdata",package="tximportData")
samps <- list.files(file.path(dir0, "alevin"))
dir <- file.path(dir0,"alevin",samps[3],"alevin")
quant.mat.file <- file.path(dir, "quants_mat.gz")
barcode.file <- file.path(dir, "quants_mat_rows.txt")
gene.file <- file.path(dir, "quants_mat_cols.txt")

# readEDS() requires knowing the number of cells and genes
cell.names <- readLines(barcode.file)
gene.names <- readLines(gene.file)
num.cells <- length(cell.names)
num.genes <- length(gene.names)

# reading in the sparse matrix
mat <- readEDS(numOfGenes=num.genes,
               numOfOriginalCells=num.cells,
               countMatFilename=quant.mat.file)
```

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