

# Package ‘eds’

October 15, 2023

**Title** eds: Low-level reader for Alevin EDS format

**Version** 1.2.0

**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 dgCMatrx

### 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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