Package 'scATAC.Explorer'

December 19, 2024

Title A Collection of Single-cell ATAC Sequencing Datasets and Corresponding Metadata

Version 1.13.0

Description
This package provides a tool to search and download a collection of publicly available single cell ATAC-seq datasets and their metadata. scATAC-Explorer aims to act as a single point of entry for users looking to study single cell ATAC-seq data.
Users can quickly search available datasets using the metadata table and download datasets of interest for immediate analysis within R.

License Artistic-2.0

Encoding UTF-8

LazyData FALSE

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

Imports methods, Matrix

Depends R (>= 4.1), SingleCellExperiment, BiocFileCache, data.table, utils, S4Vectors, zellkonverter

biocViews SingleCellData, SequencingData, ExpressionData, GEO, Tissue, Genome, PackageTypeData

BugReports https://github.com/shooshtarilab/scATACseq/issues

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`queryATAC` *A function to query scATAC-seq datasets available in this package*

Description

This function allows you to search and subset included scATAC-seq datasets. A named list of scATAC-seq_data objects matching the provided options will be returned. Some included datasets are represented using multiple matrices. Each matrix will be a seperate named object within the list. The returned list is named by matrix allow easy identification of data. If queryATAC is called without any options it will retrieve all available datasets in sparse matrix format. This should only be done on machines with a large amount of ram (>64gb) because some datasets are quite large. In most cases it is recommended to instead filter databases with some criteria.

Usage

```
queryATAC(
  accession = NULL,
  author = NULL,
  journal = NULL,
  year = NULL,
  pmid = NULL,
  sequence_tech = NULL,
  score_type = NULL,
  has_cluster_annotation = NULL,
  has_cell_type_annotation = NULL,
  organism = NULL,
  genome_build = NULL,
  broad_cell_category = NULL,
  tissue_cell_type = NULL,
  disease = NULL,
  metadata_only = FALSE,
  sparse = TRUE
)
```

Arguments

accession	Search by geo accession number. Good for returning individual datasets
author	Search by the author who published the dataset
journal	Search by the journal the dataset was published in.
year	Search by exact year or year ranges with '<', '>', or '-'. For example, you can return datasets newer than 2013 with '>2013'
pmid	Search by Pubmed ID associated with the study. Good for returning individual datasets
sequence_tech	Search by sequencing technology used to sample the cells.
score_type	Search by type of score (TPM, FPKM, raw count)
has_cluster_annotation	Return only those datasets that have clustering results available, or only those without (TRUE/FALSE)
has_cell_type_annotation	Return only those datasets that have cell-type annotations available, or only those without annotations (TRUE/FALSE)
organism	Search by source organism used in the study, for example human or mouse.
genome_build	Return datasets built only using specified genome build (ex. hg19)
broad_cell_category	Return datasets based on broad cell categories (ex. Hematopoetic cells). To view all cell categories available, explore the metadata table
tissue_cell_type	Return datasets based on tissue or cell types sampled (ex. PBMCs, Bone marrow, Oligodendrocytes)
disease	Return datasets based on sampled disease (ex. carcinoma, leukemia, diabetes)
metadata_only	Return rows of metadata instead of actual datasets. Useful for exploring what data is available without actually downloading data. Defaults to FALSE
sparse	Return expression as a sparse matrix. Reccomended to use sparse format, as dense formats tend to be excessively large.

Value

A list containing a table of metadata or one or more SingleCellExperiment objects

Examples

```
## Retrieve the metadata table to see what data is available
res <- queryATAC(metadata_only = TRUE)

## Retrieve a single dataset based on its accession number
res <- queryATAC(accession = "GSE129785")

## Retrieve the metadata of datasets between 2016 and 2020
res = queryATAC(year = "2016-2020", metadata_only = TRUE)
```

```
## Retrieve a filtered metadata table that only shows mouse
## datasets derived from blood cells with cell type annotations
res_mus <- queryATAC(has_cell_type_annotation = TRUE,
                organism = "Mus musculus",
                tissue_cell_type = "blood",
                metadata_only = TRUE)
```

---

saveATAC *A function to save a scATAC-seq dataset stored in a SingleCellExperiment*

Description

This function allows you to save the counts, peaks, cell ID's/barcodes, and any cell clustering data to disk in csv format. It takes two options: an object to save and a directory to save in. Multiple files will be created in the provided output directory, one for each type of data available in the scATAC_data object (counts, cell ID/Barcode, peak regions, cell type/cluster annotations).

Usage

```
saveATAC(object, outdir, format = "mtx")
```

Arguments

object	The SingleCellExperiment object to be written to disk, this should be an individual dataset returned by queryATAC.
outdir	The directory to save the data in, the directory should not exist yet.
format	The format to save the data in, the default is Matrix Market File Format. Alternative format is h5ad.

Value

Nothing

Examples

```
# Retrieve a previously identified dataset (see queryATAC) and save it to disk
res <- queryATAC(accession = 'GSE89362')[[1]]

saveATAC(res, output_directory_name)
```

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