

# Package ‘TMEexplorer’

October 12, 2021

**Title** A Collection of Tumour Microenvironment Single-cell RNA Sequencing Datasets and Corresponding Metadata

**Version** 1.2.1

**Description** This package provides a tool to search and download a collection of tumour microenvironment single-cell RNA sequencing datasets and their metadata. TMEexplorer aims to act as a single point of entry for users looking to study the tumour microenvironment at the single cell level. Users can quickly search available datasets using the metadata table and then download the ones they are interested in for analysis.

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** FALSE

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown

**Imports** methods, Matrix

**Depends** R (>= 4.1), SingleCellExperiment, BiocFileCache

**biocViews** CancerData, SingleCellData, RNASeqData, SequencingData, ExpressionData, GEO, PackageTypeData

**BugReports** <https://github.com/shooshtarilab/TMEexplorer/issues>

**git\_url** <https://git.bioconductor.org/packages/TMEexplorer>

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 80da7f6

**git\_last\_commit\_date** 2021-05-20

**Date/Publication** 2021-10-12

**Author** Erik Christensen [aut, cre],  
Alaine Naidas [aut],  
Parisa Shooshtari [aut]

**Maintainer** Erik Christensen <echris3@uwo.ca>

## R topics documented:

queryTME . . . . .	2
saveTME . . . . .	3

## Index

	5
--	---

---

### queryTME

*A function to query TME datasets available in this package*

---

#### Description

This function allows you to search and subset included TME datasets. A list of tme\_data objects matching the provided options will be returned, if queryTME is called without any options it will retrieve all available datasets. 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

```
queryTME(
  geo_accession = NULL,
  score_type = NULL,
  has_signatures = NULL,
  has_truth = NULL,
  tumour_type = NULL,
  author = NULL,
  journal = NULL,
  year = NULL,
  pmid = NULL,
  sequence_tech = NULL,
  organism = NULL,
  metadata_only = FALSE,
  sparse = FALSE
)
```

#### Arguments

geo_accession	Search by geo accession number. Good for returning individual datasets
score_type	Search by type of score (TPM, FPKM, raw count)
has_signatures	Return only those datasets that have cell-type gene signatures available, or only those without (TRUE/FALSE)
has_truth	Return only those datasets that have cell-type annotations available, or only those without annotations
tumour_type	Search by type of tumour represented by the dataset
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.
organism	Search by source organism used in the study, for example human or mouse.
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. Uses less memory but is less convenient to view, recommended only if encounter memory issues with dense data. Defaults to FALSE.

### 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 <- queryTME(metadata_only = TRUE)

## Retrieve a filtered metadata table that only shows datasets with
## cell type annotations and cell type gene signatures
res <- queryTME(has_truth = TRUE, has_signatures = TRUE, metadata_only = TRUE)

## Retrieve a single dataset identified from the table
res <- queryTME(geo_accession = "GSE72056")
```

## saveTME

*A function to save a TME dataset*

### Description

This function allows you to save the expression, labels, and cell types 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 tme\_data object (expression, gene signatures, cell type annotations).

### Usage

```
saveTME(object, outdir)
```

### Arguments

object	The tme_data object to be written to disk, this should be an individual dataset returned by queryTME.
outdir	The directory to save the tme_data in, the directory should not exist yet.

### Value

Nothing

**Examples**

```
# Retrieve a previously identified dataset (see queryTME) and save it to disk
res <- queryTME(geo_accession = 'GSE72056')[[1]]

saveTME(res, output_directory_name)
```

# Index

## \* **tumour**

queryTME, [2](#)

saveTME, [3](#)

queryTME, [2](#)

saveTME, [3](#)