# Package 'TENxIO'

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**Description** Provides a structured S4 approach to importing data files from the 10X pipelines. It mainly supports Single Cell Multiome ATAC + Gene Expression data among other data types. The main Bioconductor data representations used are SingleCellExperiment and RaggedExperiment.

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`TENxFile` *TENxFile constructor function*

---

## Description

The `TENxFile` constructor function serves as the auto-recognizer function for 10X files. It can import several different file extensions, namely:

```
* H5 - on-disk HDF5
* MTX - matrix market
* .tar.gz - compressed tarball
```

## Usage

```
TENxFile(resource, extension, ...)
```

### Arguments

| | |
|---|---|
| resource | character(1) The path to the file |
| extension | character(1) The file extension for the given resource. It can usually be obtained from the file path. An override can be provided especially for ExperimentHub resources where the file extension is removed. |
| ... | Additional inputs to the low level class generator functions |

### Details

**Note** that the example below includes the use of a large ~ 4 GB ExperimentHub resource obtained from the 10X website.

### Value

A subclass of TENxFile according to the input file extension

### Examples

```
if (interactive()) {

    ## from ExperimentHub
    hub <- ExperimentHub::ExperimentHub()
    fname <- hub[["EH1039"]]
    TENxFile(fname, extension = "h5", group = "mm10", version = "2")
    TENxFile(fname, extension = "h5", group = "mm10", version = "2") |>
        metadata()

}
```

---

## TENxFile-class *TENxFile: General purpose class for 10X files*

---

### Description

The TENxFile class is the default representation for unrecognized subclasses. It inherits from the BiocFile class and adds a few additional slots. The constructor function can handle typical 10X file types. For more details, see the constructor function documentation.

### Usage

```
## S4 method for signature 'TENxFile'
metadata(x, ...)
```

### Arguments

| | |
|---|---|
| x | An object of class TENxFile, TENxFileList, TENxMTX, TENxH5, TENxPeaks, TENxTSV, or derivatives |
| ... | Additional arguments (not used) |

## Value

A list of metadata for the given object

## Functions

- `metadata(TENxFile)`: `metadata` method for `TENxFile` objects

## Slots

`extension` character(1) The file extension as extracted from the file path or overridden via the `ext` argument in the constructor function.

`colidx` integer(1) The column index corresponding to the columns in the file that will subsequently be imported

`rowidx` integer(1) The row index corresponding to rows in the file that will subsequently be imported

`remote` logical(1) Whether the file exists on the web, i.e., the `resource` is a URL

`compressed` logical(1) Whether the file is compressed with, e.g., `.gz`

---

`TENxFileList` *TENxFileList: Represent groups of files from 10X Genomic*

---

## Description

This constructor function is meant to handle `.tar.gz` tarball files from 10X Genomics.

## Usage

```
TENxFileList(..., version, compressed = FALSE)
```

## Arguments

| | |
|---|---|
| `...` | Typically, a file path to a tarball archive. Can be named arguments corresponding to file paths, or a named list of file paths. |
| `version` | character(1) The version in the tarball. See details. |
| `compressed` | logical(1) Whether or not the file provided is compressed, usually as `tar.gz` (default FALSE) |

## Details

These tarballs usually contain three files:

1. `matrix.mtx.gz` - the counts matrix
2. `features.tsv.gz` - row metadata usually represented as `rowData`
3. `barcodes.tsv.gz` - column names corresponding to cell barcode identifiers If all above files are in the tarball, the import method will provide a `SingleCellExperiment`. Otherwise, a simple list of imported data is given. Note that version "3" uses 'features.tsv.gz' and version "2" uses 'genes.tsv.gz'. If known, indicate the `version` argument in the `TENxFileList` constructor function.

## Value

Either a `SingleCellExperiment` or a list of imported data

## Examples

```
fl <- system.file(
    "extdata", "pbmc_granulocyte_sorted_3k_ff_bc_ex_matrix.tar.gz",
    package = "TENxIO", mustWork = TRUE
)

## Method 1 (tarball)
TENxFileList(fl)

## metadata before import
metadata(TENxFileList(fl))

## import() method
import(TENxFileList(fl))

## metadata after import
import(TENxFileList(fl)) |>
    metadata()

## untar to simulate folder output
dir.create(tdir <- tempfile())
untar(fl, exdir = tdir)

## Method 2 (folder)
TENxFileList(tdir)
import(TENxFileList(tdir))

## Method 3 (list of TENxFile objects)
files <- list.files(tdir, recursive = TRUE, full.names = TRUE)
names(files) <- basename(files)
filelist <- lapply(files, TENxFile)

TENxFileList(filelist, compressed = FALSE)

## Method 4 (SimpleList)
TENxFileList(as(filelist, "SimpleList"), compressed = FALSE)

## Method 5 (named arguments)
TENxFileList(
    barcodes.tsv.gz = TENxFile(files[1]),
    features.tsv.gz = TENxFile(files[2]),
    matrix.mtx.gz = TENxFile(files[3])
)

unlink(tdir, recursive = TRUE)
```

TENxFileList-class *TENxFileList: A list-like representation for TENxFiles*

## Description

This class was designed to mainly handle tarballs from 10X Genomics. The typical file extension for these tarballs is `.tar.gz`.

## Usage

```
## S4 method for signature 'TENxFileList'
path(object, ...)

## S4 method for signature 'TENxFileList'
decompress(manager, con, ...)

## S4 method for signature 'TENxFileList,ANY,ANY'
import(con, format, text, ...)

## S4 method for signature 'TENxFileList'
metadata(x, ...)
```

## Arguments

| | |
|---|---|
| `object` | An object containing paths. Even though it will typically contain a single path, `object` can actually contain an arbitrary number of paths. |
| `...` | Additional arguments (not used) |
| `manager` | A `ConnectionManager` internal instance; currently not used. |
| `con` | The connection from which data is loaded or to which data is saved. If this is a `character` vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |
| `format` | The format of the output. If missing and `con` is a file name, the format is derived from the file extension. This argument is unnecessary when `con` is a derivative of BiocFile. |
| `text` | If `con` is missing, this can be a character vector directly providing the string data to import. |
| `x` | An object of class `TENxFile`, `TENxFileList`, `TENxMTX`, `TENxH5`, `TENxPeaks`, `TENxTSV`, or derivatives |

### Details

These tarballs usually contain three files:

1. `matrix.mtx.gz` - the counts matrix
2. `features.tsv.gz` - row metadata usually represented as `rowData`
3. `barcodes.tsv.gz` - column names corresponding to cell barcode identifiers Note that version '2' includes `genes.tsv.gz` instead of `features.tsv.gz` in version '3'.

An additional `ref` argument can be provided when the file contains multiple `feature_type` in the file or "Type" in the `rowData`. By default, the first type reported in `table()` is set as the `mainExpName` in the `SingleCellExperiment` object.

### Value

A `TENxFileList` class object

### Functions

- `path(TENxFileList)`: Obtain file paths for all files in the object as a vector
- `decompress(TENxFileList)`: An intermediate method for decompressing (via untar) the contents of a `.tar.gz` file list
- `import(con = TENxFileList, format = ANY, text = ANY)`: Recursively import files within a `TENxFileList`
- `metadata(TENxFileList)`: `metadata` method for `TENxFileList` objects

### Slots

`listData` list() The data in list format

`extension` character() A vector of file extensions for each file

`compressed` logical(1) Whether the file is compressed as `.tar.gz`

`version` character(1) The version number of the tarball usually either '2' or '3'

---

## `TENxFragments` *TENxFragments: Import fragments files from 10X*

---

### Description

TENxFragments: Import fragments files from 10X

### Usage

```
TENxFragments(resource, yieldSize = 200, which = GRanges(), ...)
```

### Arguments

| | |
|---|---|
| resource | character(1) The file path to the fragments resource, usually a compressed tabix file with extension .tsv.gz. |
| yieldSize | numeric() The number of records to read by default, 200 records will be imported. A warning will be emitted if not modified. |
| which | GRanges() A GRanges indicating the regions of interest. This get sent to RSamtools as the param input. |
| ... | Further arguments to the class generator function (currently not used) |

### Value

A RaggedExperiment object class

### Examples

```
fr <- system.file(
    "extdata", "pbmc_3k_atac_ex_fragments.tsv.gz",
    package = "TENxIO", mustWork = TRUE
)

tfr <- TENxFragments(fr)

fra <- import(tfr)
```

---

## TENxFragments-class *TENxFragments: A class to represent fragments data as* GRanges

---

### Description

This class is designed to work mainly with fragments.tsv.gz files from 10x pipelines.

### Usage

```
## S4 method for signature 'TENxFragments,ANY,ANY'
import(con, format, text, ...)
```

### Arguments

| | |
|---|---|
| con | The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |

| | |
|---|---|
| format | The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of BiocFile. |
| text | If con is missing, this can be a character vector directly providing the string data to import. |
| ... | Parameters to pass to the format-specific method. |

## Details

Fragments data from 10x can be quite large. In order to speed up the initial exploration of the data, we use a default of **200** records for loading. Users can change this default value by specifying a new one via the `yieldSize` argument in the constructor function.

## Value

A `TENxFragments` class object

## Methods (by generic)

- `import(con = TENxFragments, format = ANY, text = ANY)`: Import method for representing fragments.tsv.gz data from 10x via `Rsamtools` and `RaggedExperiment`

## Slots

`which` GRanges() A GRanges indicating the regions of interest. This get sent to `RSamtools` as the `param` input.

`yieldSize` numeric() The number of records to read by default, 200 records will be imported. A warning will be emitted if not modified.

---

`TENxH5` *TENxH5: Represent H5 files from 10X*

---

## Description

This constructor function was developed using the PBMC 3K dataset from 10X Genomics (version 3). Other versions are supported and input arguments `version` and `group` can be overridden.

## Usage

```
TENxH5(resource, version, group, ranges, rowidx, colidx, ...)
```

## Arguments

| | |
|---|---|
| resource | character(1) The path to the file |
| version | character(1) There are currently two recognized versions associated with 10X data, either version "2" or "3". See details for more information. |
| group | character(1) The HDF5 group embedded within the file structure, this is usually either the "matrix" or "outs" group but other groups are supported as well (e.g., "mm10"). |
| ranges | character(1) The HDF5 internal folder location embedded within the file that points to the ranged data information, e.g., "/features/interval". Set to NA_character_ if range information is not present. |
| rowidx, colidx | numeric() A vector of indices corresponding to either rows or columns that will dictate the data imported from the file. The indices will be passed on to the [ method of the TENxMatrix representation. |
| ... | Additional inputs to the low level class generator functions |

## Details

The various TENxH5 methods including rowData and rowRanges, provide a snapshot of the data using a length 12 head and tail subset for efficiency. In contrast, methods such as dimnames and dim give a full view of the dimensions of the data. The show method provides relevant information regarding the dimensions of the data including metadata such as rowData and "Type" column, if available. The term "projection" refers to the data class that will be provided once the data file is imported.

An additional ref argument can be provided when the file contains multiple feature_type in the file or "Type" in the rowData. By default, the first type reported in table() is set as the mainExpName in the SingleCellExperiment object.

For data that do not contain genomic coordinate information, the TENxH5 will fail to read "/features/interval" and will set the ranges argument to NA_character_.

The data version "3" mainly includes a "matrix" group and "interval" information within the file. Version "2" data does not include ranged-based information and has a different directory structure compared to version "3". See the internal data.frame: TENxIO:::h5.version.map for a map of fields and their corresponding file locations within the H5 file. This map is used to create the rowData structure from the file.

## Value

Usually, a SingleCellExperiment instance

## See Also

import section in TENxH5

## Examples

```
h5f <- system.file(
    "extdata", "pbmc_granulocyte_ff_bc_ex.h5",
```

```
    package = "TENxIO", mustWork = TRUE
)

TENxH5(h5f)

import(TENxH5(h5f))

h5f <- system.file(
    "extdata", "10k_pbmc_ATACv2_f_bc_ex.h5",
    package = "TENxIO", mustWork = TRUE
)

## Optional ref input, most frequent Type used by default
th5 <- TENxH5(h5f, ranges = "/features/id", ref = "Peaks")
th5
TENxH5(h5f, ranges = "/features/id")
import(th5)
```

---

TENxH5-class *TENxH5: The HDF5 file representation class for 10X Data*

---

## Description

This class is designed to work with 10x Single Cell datasets. It was developed using the PBMC 3k 10X dataset from the CellRanger v2 pipeline.

## Usage

```
## S4 method for signature 'TENxH5'
rowData(x, use.names = TRUE, ...)

## S4 method for signature 'TENxH5'
dim(x)

## S4 method for signature 'TENxH5'
dimnames(x)

## S4 method for signature 'TENxH5'
genome(x)

## S4 method for signature 'TENxH5'
rowRanges(x, ...)

## S4 method for signature 'TENxH5,ANY,ANY'
import(con, format, text, ...)

## S4 method for signature 'TENxH5'
show(object)
```

## Arguments

| | |
|---|---|
| x | A TENxH5 object |
| use.names | For rowData: Like mcols(x), by default rowData(x) propagates the rownames of x to the returned DataFrame object (note that for a SummarizedExperiment object or derivative, the rownames are also the names i.e. rownames(x) is always the same as names(x)). Setting use.names=FALSE suppresses this propagation i.e. it returns a DataFrame object with no rownames. Use this when rowData(x) fails, which can happen when the rownames contain NAs (because the rownames of a SummarizedExperiment object or derivative can contain NAs, but the rownames of a DataFrame object cannot).<br>For combineRows and combineCols: See Combining section below. |
| ... | For assay, arguments in ... are forwarded to assays.<br>For rbind, cbind, ... contains SummarizedExperiment objects (or derivatives) to be combined.<br>For other accessors, ignored. |
| con | The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |
| format | The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of BiocFile. |
| text | If con is missing, this can be a character vector directly providing the string data to import. |
| object | A TENxH5 class object |

## Details

The data version "3" mainly includes a "matrix" group and "interval" information within the file. Version "2" data does not include ranged-based information and has a different directory structure compared to version "3". See the internal data.frame: TENxIO:::h5.version.map for a map of fields and their corresponding file locations within the H5 file. This map is used to create the rowData structure from the file.

## Value

A TENxH5 class object

## Methods (by generic)

- rowData(TENxH5): Generate the rowData ad hoc from a TENxH5 file
- dim(TENxH5): Get the dimensions of the data as stored in the file
- dimnames(TENxH5): Get the dimension names from the file

- `genome(TENxH5)`: Read genome string from file
- `rowRanges(TENxH5)`: Read interval data and represent as GRanges
- `import(con = TENxH5, format = ANY, text = ANY)`: Import TENxH5 data as a SingleCellExperiment; see section below
- `show(TENxH5)`: Display a snapshot of the contents within a TENxH5 file before import

## Slots

`version` character(1) There are currently two recognized versions associated with 10X data, either version "2" or "3". See details for more information.

`group` character(1) The HDF5 group embedded within the file structure, this is usually either the "matrix" or "outs" group but other groups are supported as well.

`ranges` character(1) The HDF5 internal folder location embedded within the file that points to the ranged data information, e.g., "/features/interval".

## import

The `import` method uses `DelayedArray::TENxMatrix` to represent matrix data. Generally, version 3 datasets contain associated genomic coordinates. The associated feature data, as displayed by the `rowData` method, is queried for the "Type" column which will indicate that a `splitAltExps` operation is appropriate. If a `ref` input is provided to the constructor function `TENxH5`, it will be used as the main experiment; otherwise, the most frequent category in the "Type" column will be used. For example, the Multiome ATAC + Gene Expression feature data contains both 'Gene Expression' and 'Peaks' labels in the "Type" column.

## See Also

TENxH5

---

`TENxIO` *TENxIO: A Bioconductor package for importing 10X Genomics files*

---

## Description

The package provides file classes based on `BiocIO` for common file extensions found in the 10X Genomics website.

## Supported file types

Here is a table of supported file and file extensions and their imported classes:

| Extension | Class | Imported as |
|---|---|---|
| .h5 | TENxH5 | SingleCellExperiment w/ TENxMatrix |
| .mtx / .mtx.gz | TENxMTX | SummarizedExperiment w/ dgCMatrix |
| .tar.gz | TENxFileList | SingleCellExperiment w/ dgCMatrix |
| peak_annotation.tsv | TENxPeaks | GRanges |

| | | |
|---|---|---|
| fragments.tsv.gz | TENxFragments | RaggedExperiment |
| .tsv / .tsv.gz | TENxTSV | tibble |

## Author(s)

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## See Also

Useful links:

- https://github.com/waldronlab/TENxIO
- Report bugs at https://github.com/waldronlab/TENxIO/issues

---

TENxMTX *TENxMTX: Represent Matrix Market Format Files from 10X*

---

## Description

This constructor function accepts `.mtx` and `.mtx.gz` compressed formats for eventual importing. It is mainly used with tarball files from 10X Genomics, where more annotation data is included. Importing solely the `.mtx` format will provide users with a `SummarizedExperiment` with an assay of class `dgCMatrix` from the `Matrix` package. Currently, other formats are not supported but if you'd like to request support for a format, please open an issue on GitHub.

## Usage

```
TENxMTX(resource, compressed = FALSE, ...)
```

## Arguments

| | |
|---|---|
| `resource` | character(1) The path to the file |
| `compressed` | logical(1) Whether the resource file is compressed (default FALSE) |
| `...` | Additional inputs to the low level class generator functions |

## Value

A `SummarizedExperiment` instance with a `dgCMatrix` in the assay

## Examples

```
mtxf <- system.file(
    "extdata", "pbmc_3k_ff_bc_ex.mtx",
    package = "TENxIO", mustWork = TRUE
)

con <- TENxMTX(mtxf)

import(con)
```

---

TENxMTX-class *TENxMTX: The Matrix Market representation class for 10X Data*

---

## Description

This class is designed to work with 10x MTX datasets, particularly from the multiome pipelines.

## Usage

```
## S4 method for signature 'TENxMTX,ANY,ANY'
import(con, format, text, ...)
```

## Arguments

| | |
|---|---|
| con | The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |
| format | The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of BiocFile. |
| text | If con is missing, this can be a character vector directly providing the string data to import. |
| ... | Parameters to pass to the format-specific method. |

## Details

The TENxMTX class is a straightforward implementation that allows the user to import a Matrix Market file format using Matrix::readMM. Currently, it returns a SummarizedExperiment with an internal dgCMatrix assay. To request other formats, please open an issue on GitHub.

## Value

A TENxMTX class object

### Methods (by generic)

- `import(con = TENxMTX, format = ANY, text = ANY)`: Import method mainly for mtx.gz files from 10x

### Slots

`compressed` logical(1) Whether or not the file is in compressed format, usually gzipped (`.gz`).

---

`TENxPeaks` *Import 10x peak annotation files from 10x*

---

### Description

This constructor function is designed to work with the files denoted with "peak_annotation" in the file name. These are usually produced as tab separated value files, i.e., `.tsv`.

### Usage

```
TENxPeaks(resource, extension, ...)
```

### Arguments

| | |
|---|---|
| `resource` | character(1) The path to the file |
| `extension` | character(1) The file extension for the given resource. It can usually be obtained from the file path. An override can be provided especially for `ExperimentHub` resources where the file extension is removed. |
| `...` | Additional inputs to the low level class generator functions |

### Details

The output class allows handling of peak data. It can be used in conjunction with the `annotation` method on a `SingleCellExperiment` to add peak information to the experiment. The ranged data is represented as a `GRanges` class object.

### Value

A `GRanges` class object of peak locations

### Examples

```
fi <- system.file(
    "extdata", "pbmc_granulocyte_sorted_3k_ex_atac_peak_annotation.tsv",
    package = "TENxIO", mustWork = TRUE
)
peak_file <- TENxPeaks(fi)
peak_anno <- import(peak_file)
peak_anno
```

```
example(TENxH5)

## Add peaks to an existing SCE
## First, import the SCE from an example H5 file
h5f <- system.file(
    "extdata", "pbmc_granulocyte_ff_bc_ex.h5",
    package = "TENxIO", mustWork = TRUE
)
con <- TENxH5(h5f)
sce <- import(con)
## auto-import peaks when using annotation<-
annotation(sce, name = "peak_annotation") <- peak_file
annotation(sce)
```

---

`TENxPeaks-class` *TENxPeaks: The class to represent 10x Peaks files*

---

## Description

This class is designed to work with the files denoted with "peak_annotation" in the file name. These are usually produced as tab separated value files, i.e., `.tsv`.

## Usage

```
## S4 method for signature 'TENxPeaks,ANY,ANY'
import(con, format, text, ...)

## S4 replacement method for signature 'SingleCellExperiment,ANY'
annotation(object, ...) <- value

## S4 method for signature 'SingleCellExperiment'
annotation(object, ...)
```

## Arguments

| | |
|---|---|
| `con` | The connection from which data is loaded or to which data is saved. If this is a `character` vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |
| `format` | The format of the output. If missing and `con` is a file name, the format is derived from the file extension. This argument is unnecessary when `con` is a derivative of BiocFile. |
| `text` | If `con` is missing, this can be a character vector directly providing the string data to import. |

| | |
|---|---|
| ... | Parameters to pass to the format-specific method. |
| object | The object to export. |
| value | The annotation information to set on object. |

## Details

This class is a straightforward class for handling peak data. It can be used in conjunction with the annotation method on a SingleCellExperiment to add peak information to the experiment. The ranged data is represented as a GRanges class object.

## Value

A TENxPeaks class object

## Functions

- import(con = TENxPeaks, format = ANY, text = ANY): Import a peaks_annotation file from 10x as a GRanges representation
- annotation(object = SingleCellExperiment) <- value: Replacement method to add annotation data to a SingleCellExperiment
- annotation(SingleCellExperiment): Extraction method to obtain annotation data from a SingleCellExperiment representation

---

# TENxTSV-class *TENxTSV: A class to represent 10x tab separated values files*

---

## Description

This class is general purpose for reading in tabular data from the 10x Genomics website with the .tsv file extension. The class also supports compressed files, i.e., those with the .tsv.gz extension.

## Usage

```
## S4 method for signature 'TENxTSV,ANY,ANY'
import(con, format, text, ...)

TENxTSV(resource, compressed = FALSE, ...)

## S4 method for signature 'TENxTSV'
metadata(x, ...)
```

## Arguments

| | |
|---|---|
| con | The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection. |
| format | The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of BiocFile. |
| text | If con is missing, this can be a character vector directly providing the string data to import. |
| ... | Parameters to pass to the format-specific method. |
| resource | character(1) The path to the file |
| compressed | logical(1) Whether the resource file is compressed (default FALSE) |
| x | A TENxTSV object |

## Details

Typical .tsv files obtained from the 10X website are compressed and contain information relevant to 'barcodes' and 'features'. Currently, the code only supports files such as features.tsv.* and barcodes.tsv.*.

## Value

A TENxTSV class object; a tibble for the import method

## Functions

- import(con = TENxTSV, format = ANY, text = ANY): General import method for tsv files from 10x; using readr::read_tsv and returning a tibble representation
- metadata(TENxTSV): metadata method for TENxTSV objects

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