Package 'VisiumIO'

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Title Import Visium data from the 10X Space Ranger pipeline

Version 1.6.3

Description The package allows users to readily import spatial data obtained from either the 10X website or from the Space Ranger pipeline. Supported formats include tar.gz, h5, and mtx files. Multiple files can be imported at once with *List type of functions. The package represents data mainly as SpatialExperiment objects.

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VisiumIO-package   *VisiumIO: Import Visium data from the 10X Space Ranger pipeline*

Description

The package allows users to readily import spatial data obtained from either the 10X website or
from the Space Ranger pipeline. Supported formats include tar.gz, h5, and mtx files. Multiple
files can be imported at once with *List type of functions. The package represents data mainly as
SpatialExperiment objects.

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See Also

Useful links:

- <https://github.com/waldronlab/VisiumIO>

- Report bugs at <https://github.com/waldronlab/VisiumIO/issues>

compareBarcodes	*Compare barcodes between raw and filtered data*

Description

This function compares the barcodes between raw and filtered data **depending** on the order of `processing`. Typically, the "raw" barcodes are compared to the "filtered" ones. The presence of raw barcodes in the filtered data are marked as `TRUE` in the resulting `data.frame`.

Usage

```
compareBarcodes(
  from_resource,
  to_resource,
  spacerangerOut,
  format = c("mtx", "h5"),
  processing = c("raw", "filtered"),
  ...
)
```

Arguments

`from_resource`	`character(1)` The path to the resource file whose barcodes are used as the basis of the comparison; typically, the "raw" feature barcodes are used.
`to_resource`	`character(1)` The path to the resource file whose barcodes are compared to the `from_resource`; typically, the "filtered" feature barcodes.
`spacerangerOut`	`character(1)` A single string specifying the path to the directory where the output of `spaceranger count` is located; typically (but not necessarily), this is the `outs` directory. The directory must contain the `(processing)_feature_bc_matrix` and `spatial` sub directories.
`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](#).
`processing`	`character(2)` A vector of length 2 that corresponds to the processing type. The processing types are typically "raw" and "filtered". These are the prefixes of the folder names `raw_feature_bc_matrix` and `filtered_feature_bc_matrix`. The order of the vector determines the comparison. By default, `processing = c("raw", "filtered")`, which means barcodes in the raw data are compared to the filtered data.
`...`	Additional arguments passed to `TENxH5` or `TENxFileList`.

Value

A `data.frame` with barcodes of the first element in the `processing` data type as the first column and a logical vector indicating whether the barcodes are found in the second element in `processing`. For example, if processing is `c("raw", "filtered")`, then the first column will be the barcodes in the `raw` data and the second column will be a logical vector indicating whether the barcodes are found in the `filtered` data.

Examples

```
if (interactive()) {
    compareBarcodes(
        from_resource = "V1_Adult_Mouse_Brain_raw_feature_bc_matrix.tar.gz",
        to_resource =
            "V1_Adult_Mouse_Brain_filtered_feature_bc_matrix.tar.gz",
    )

    compareBarcodes(
        from_resource =
            "V1_Adult_Mouse_Brain_raw_feature_bc_matrix.h5",
        to_resource =
            "V1_Adult_Mouse_Brain_filtered_feature_bc_matrix.h5"
    )

    compareBarcodes(spacerangerOut = "~/data/outs", format = "h5")

    compareBarcodes(
        spacerangerOut = "~/data/feature_bc_matrix", format = "mtx"
    )

    compareBarcodes(
        spacerangerOut = "~/data/folder_feature_bc_matrix", format = "mtx"
    )
}
```

---

st_invert_y	*Flip the Y-axis of cell or nucleus segmentations to align with H&E image*

Description

This function flips the Y-axis of cell or nucleus segmentations stored in an `sf` object to align with the H&E image. The Y-axis flipping is necessary because the origin (0,0) in image coordinates is at the top-left corner, while in Cartesian coordinates, the origin is at the bottom-left corner. The function takes into account the image height and scaling factor to accurately flip the Y-coordinates of the segmentations.

Usage

```
st_invert_y(sf, type = c("POINT", "POLYGON"), img_height, scalef)
```

Arguments

sf	sf an sf class object read from a .geojson file.
type	character(1) "POINT" for cell centroid, or "POLYGON" for cell segmentation mask. Default is "POINT".
img_height	numeric(1) The total length along the Y axis of the image. Obtained by reading in hires or lowres .png under /spatial folder with magick::image_read().
scalef	numeric(1) The scaling factor from a /spatial/scalefactors_json.json file

Value

an sf object with Y-axis of the points or polygons flipped

Author(s)

Estella YiXing Dong

Examples

```
geojson_file <- system.file(
    file.path("extdata", "segmented_outputs", "cell_segmentations.geojson"),
    mustWork = TRUE, package = "VisiumIO"
)
geo_data <- sf::st_read(geojson_file, quiet = TRUE)
st_invert_y(
    sf = geo_data, type = "POLYGON", img_height = 3886, scalef = 0.079
)
```

TENxGeoJSON-class   *Import 10X Genomics GeoJSON files*

Description

TENxGeoJSON is a class to represent and import GeoJSON files from 10X Genomics. It is a composed class of TENxIO::TENxFile.

Usage

```
TENxGeoJSON(resource)

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

Arguments

resource	character(1) The path to the file
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.
...	Additional inputs to the low level class generator functions

Details

Typically, the user will not create an object of this class directly but rather use the `TENxVisium()` constructor function to create an object of this class in the background.

Value

TENxGeoJSON(): An object of class TENxGeoJSON

import-method: An `sf` and `data.frame` with the GeoJSON data

See Also

https://www.10xgenomics.com/support/software/xenium-ranger/3.0/analysis/segmentation-inputs

Examples

```
segout_folder <- system.file(
    file.path("extdata", "segmented_outputs"),
    package = "VisiumIO"
)
geojsonres <- file.path(segout_folder, "cell_segmentations.geojson")

TENxGeoJSON(geojsonres)

TENxGeoJSON(geojsonres) |>
  import()
```

TENxSpatialCSV-class   *Represent and import spatial CSV data from 10X Genomics*

Description

TENxSpatialCSV is a class to represent and import spatial CSV files with specific column names. It is a composed class of TENxIO::TENxFile and contains additional slots for the column names and whether the CSV is a list-type of file.

Usage

```
TENxSpatialCSV(resource, colnames = .TISSUE_POS_COLS)

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

Arguments

resource	character(1) The path to the file
colnames	character() A vector specifying the column names of the CSV, defaults to c("barcode", "in_tissue", "array_row", "array_col", "pxl_row_in_fullres", "pxl_col_in_fullres"). Mainly used for the "positions" CSV type of file which does not include column names in the file.

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.

...   Additional inputs to the low level class generator functions

Details

Typically, the user will not create an object of this class directly but rather use the [TENxVisium()](#)
constructor function to create an object of this class in the background. The column names are set to
the default values of c(″barcode″, ″in_tissue″, ″array_row″, ″array_col″, ″pxl_row_in_fullres″,
″pxl_col_in_fullres″). The column names can be changed by specifying the colnames argu-
ment in the constructor function.

Set the option "VisiumIO.csvreader" to either "data.table" or "readr" to use the data.table::fread
or readr::read_csv functions, respectively. These options are useful when the CSV file is rela-
tively large and the user wants to use faster read-in options. Note that the outputs will still be con-
verted to DataFrame when incorporated to the SpatialExperiment or SingleCellExperiment
object.

Value

TENxSpatialCSV: An object of class [TENxSpatialCSV](#)

import-method: A DataFrame object containing the data from the CSV file

Slots

isList logical(1) A scalar specifying whether the CSV is a list-type of file

colnames character() A vector specifying the column names of the CSV

variant character(1) A scalar specifying the variant of the CSV file "positions", "cell_boundaries",
    or "other". The variant is determined by the name of the CSV file within the constructor func-
    tion. Values include "positions", "cell_boundaries", and "other".

compressed logical(1) A scalar specifying whether the CSV is compressed (mainly with a .gz
    file extension).

Examples

```
sample_dir <- system.file(
    file.path("extdata", "10xVisium", "section1"),
    package = "VisiumIO"
)
spatial_dir <- Filter(
  function(x) endsWith(x, "spatial"), list.dirs(sample_dir)
)
csvresource <- file.path(spatial_dir, "tissue_positions_list.csv")
TENxSpatialCSV(csvresource)
```

```
head(import(TENxSpatialCSV(csvresource)), 4)

import(TENxSpatialCSV(csvresource)) |>
    attr("metadata") |>
    lapply(names)
```

TENxSpatialList-class   *A class to represent and import spatial Visium data*

Description

This class is a composed class of [TENxFileList](#), which can contain a list of [TENxFile](#) objects, and a [TENxSpatialList](#) object. It is meant to handle spatial Visium data from 10X Genomics.

Usage

```
TENxSpatialList(
  resources,
  sample_id = "sample01",
 images = c("lowres", "hires", "detected", "aligned", "aligned_fiducials", "cytassist"),
  jsonFile = .SCALE_JSON_FILE,
  tissuePattern = "tissue_positions.*",
  bin_size = character(0L),
  ...
)

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

Arguments

resources	A [TENxFileList](#) object or a file path to the tarball containing the matrix / assay data resources.
sample_id	character(1) A single string specifying the sample ID.
images	character() A vector specifying the images to be imported; can be one or multiple of "lowres", "hires", "detected", "aligned".
jsonFile	character(1) A single string specifying the name of the JSON file containing the scale factors.
tissuePattern	character(1) A single string specifying the pattern to match the tissue positions file.
bin_size	character(1) The bin size of the images to import. The default is 008. It corresponds to the directory name square_000um where 000 is the bin value.
...	Parameters to pass to the format-specific method.
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.

Details

Typically, the user will not create an object of this class directly but rather use the [TENxVisium()](#)
constructor function to create an object of this class.

Value

A SpatialExperiment object

Methods (by generic)

- import(con = TENxSpatialList, format = ANY, text = ANY): Import a TENxSpatialList
  object

Slots

images character() The image name(s) to use with grep and include in the list of files. Can
      be one of "lowres", "hires", "lowres", "hires", "detected", "aligned", "aligned_fiducials", or
      "cytassist".

scaleJSON character(1) The file name of the scale factors JSON file, defaults to 'scalefac-
      tors_json.json'.

tissuePos character(1) The file name of the tissue positions file; typically a .parquet or .csv
      file.

sampleId character(1) A scalar specifying the sample identifier.

binSize The bin size of the images to import. The default slot value is character(). It typically
      corresponds to the directory name square_000um where 000 is the bin value.

Examples

```
spatial_dir <- system.file(
    file.path("extdata", "10xVisium", "section1", "outs", "spatial"),
    package = "VisiumIO"
)

TENxSpatialList(resources = spatial_dir, images = "lowres")

TENxSpatialList(resources = spatial_dir, images = "lowres") |>
    metadata() |> lapply(names)
```

TENxSpatialParquet-class

Represent and import spatial Parquet data from 10X Genomics

Description

TENxSpatialParquet is a class to represent and import spatial Parquet files with specific column names. It is a composed class of [TENxIO::TENxFile](#) and contains additional slots for the column names and whether the Parquet is a list-type of file.

Usage

```
TENxSpatialParquet(resource, colnames = .TISSUE_POS_COLS)

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

Arguments

resource	character(1) The path to the file
colnames	character() A vector specifying the column names of the Parquet, defaults to c("barcode", "in_tissue", "array_row", "array_col", "pxl_row_in_fullres", "pxl_col_in_fullres").
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.
...	Additional inputs to the low level class generator functions

Details

Typically, the user will not create an object of this class directly but rather use the [TENxVisium()](#) constructor function to create an object of this class in the background. The column names are set to the default values of c("barcode", "in_tissue", "array_row", "array_col", "pxl_row_in_fullres", "pxl_col_in_fullres"). The column names can be changed by specifying the colnames argument in the constructor function.

Value

TENxSpatialParquet(): An object of class [TENxSpatialParquet](#)

import-method: A DataFrame object containing the data from the Parquet file

Slots

colnames character() A vector specifying the column names of the Parquet

Examples

```
sample_dir <- system.file(
    file.path("extdata", "binned_outputs", "square_002um", "spatial"),
    package = "VisiumIO"
)
spatial_dir <- Filter(
  function(x) endsWith(x, "spatial"), list.dirs(sample_dir)
)
parquetres <- file.path(spatial_dir, "tissue_positions.parquet")
TENxSpatialParquet(parquetres)
import(TENxSpatialParquet(parquetres))

## metadata in attributes
import(TENxSpatialParquet(parquetres)) |>
    attr("metadata") |>
    lapply(names)
```

TENxVisium-class   *A class to represent and import a single Visium Sample*

Description

This class is a composed class of [TENxFileList](#) which can contain a list of [TENxFile](#) objects and a [TENxSpatialList](#) object. It is meant to handle a single Visium sample from 10X Genomics.

Usage

```
TENxVisium(
  resources,
  spatialResource,
  spacerangerOut,
  sample_id = "sample01",
  processing = c("filtered", "raw"),
  format = c("mtx", "h5"),
  images = c("lowres", "hires", "detected", "aligned", "cytassist"),
  jsonFile = .SCALE_JSON_FILE,
  tissuePattern = "tissue_positions.*\\.csv",
  spatialCoordsNames = c("pxl_col_in_fullres", "pxl_row_in_fullres"),
  ...
)

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

Arguments

resources	A [TENxFileList](#) object or a file path to the tarball containing the matrix / assay data resources.
spatialResource	
	A [TENxSpatialList](#) object or a file path to the tarball containing the spatial data.
spacerangerOut	character(1) A single string specifying the path to the directory where the output of spaceranger count is located; typically (but not necessarily), this is the outs directory. The directory must contain the (processing)_feature_bc_matrix and spatial sub directories.
sample_id	character(1) A single string specifying the sample ID.
processing	character(1) A single string indicating the processing folder available e.g., "filtered_feature_barcode_matrix" in the spacerangerOut folder. It can be either "filtered" or "raw" (default "filtered"). Only used when spacerangerOut is specified.
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](#).
images	character() A vector specifying the images to be imported; can be one or multiple of "lowres", "hires", "detected", "aligned".
jsonFile	character(1) A single string specifying the name of the JSON file containing the scale factors.
tissuePattern	character(1) A single string specifying the pattern to match the tissue positions file.
spatialCoordsNames	
	character() A vector of strings specifying the names of the columns in the spatial data containing the spatial coordinates.
...	In the constructor, additional arguments passed to [TENxFileList](#); otherwise, 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.
text	If con is missing, this can be a character vector directly providing the string data to import.

Details

Typically, the user will not create an object of this class directly but rather use [TENxVisiumList](#) constructor function for multiple samples. Note that the images, jsonFile, tissuePattern, and spatialCoordsNames arguments are only considered when the spacerangerOut argument or both the resources and spatialResource arguments are paths to files.

Value

A [SpatialExperiment](#) object

Functions

- import(con = TENxVisium, format = ANY, text = ANY): Import Visium data

Slots

resources A TENxFileList or TENxH5 object containing the Visium data.

spatialList A TENxSpatialList object containing the spatial

coordNames character() A vector specifying the names of the columns in the spatial data containing the spatial coordinates.

sampleId character(1) A scalar specifying the sample identifier.

See Also

https://support.10xgenomics.com/spatial-gene-expression/software/pipelines/latest/output/overview

Examples

```
outs_dir <- system.file(
    file.path("extdata", "10xVisium", "section1", "outs"),
    package = "VisiumIO"
)

## using spacerangerOut folder
tv <- TENxVisium(
    spacerangerOut = outs_dir, processing = "raw", images = "lowres"
)

import(tv)

## with TENxFileList spacerangerOut input
tvfl <- TENxVisium(
    spacerangerOut = TENxFileList(outs_dir),
    format = "mtx",
    processing = "raw",
    images = "lowres"
)

import(tvfl)

## check metadata of the object
import(tvfl) |>
    metadata() |>
    lapply(names)

## importing h5 format
tvfl <- TENxVisium(
    spacerangerOut = outs_dir,
    format = "h5",
    processing = "raw",
    images = "lowres"
)

import(tvfl)
```

```
rffolder <- file.path(outs_dir, "raw_feature_bc_matrix")
## using resources and spatialResource inputs
tvfl <- TENxVisium(
    resources = rffolder,
    spatialResource = file.path(dirname(rffolder), "spatial"),
    format = "mtx",
    processing = "raw",
    images = "lowres"
)

import(tvfl)
```

TENxVisiumHD-class   *A class to represent and import multiple Visium HD samples*

Description

This class contains a `SimpleList` of [TENxVisiumHD](#) objects each corresponding to one sample.
The provided `spacerangerOut` folder should contain a `binned_outputs` folder where multiple
`bin_size` subfolders are present, e.g., `square_002um`.

Usage

```
TENxVisiumHD(
  resources,
  spatialResource,
  spacerangerOut,
  segmented_outputs,
  sample_id = "sample01",
  processing = c("filtered", "raw"),
  format = c("mtx", "h5"),
  images = c("lowres", "hires", "detected", "aligned_fiducials"),
  bin_size = c("008", "016", "002"),
  jsonFile = .SCALE_JSON_FILE,
  tissuePattern = "tissue_positions\\.parquet",
  spatialCoordsNames = c("pxl_col_in_fullres", "pxl_row_in_fullres"),
  ...
)

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

Arguments

resources	A [TENxFileList](#) object or a file path to the tarball containing the matrix / assay data resources.
spatialResource	
	A [TENxSpatialList](#) object or a file path to the tarball containing the spatial data.
spacerangerOut	character(1) A single string specifying the path to the directory where the output of `spaceranger count` is located; typically (but not necessarily), this is the `outs` directory. The directory must contain the `(processing)_feature_bc_matrix` and `spatial` sub directories.

segmented_outputs

                 `character(1)` The path to the `segmented_outputs` directory

sample_id   `character(1)` A single string specifying the sample ID.

processing   `character(1)` A single string indicating the processing folder available e.g., "filtered_feature_barcode_matrix" in the `spacerangerOut` folder. It can be either "filtered" or "raw" (default "filtered"). Only used when `spacerangerOut` is specified.

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](#).

images   `character()` A vector specifying the images to be imported; can be one or multiple of "lowres", "hires", "detected", "aligned".

bin_size   `character(1)` The bin size of the images to import. The default is `008`. It corresponds to the directory name `square_000um` where `000` is the bin value.

jsonFile   `character(1)` A single string specifying the name of the JSON file containing the scale factors.

tissuePattern   `character(1)` A single string specifying the pattern to match the tissue positions file.

spatialCoordsNames

                 `character()` A vector of strings specifying the names of the columns in the spatial data containing the spatial coordinates.

...   In the constructor, additional arguments passed to [TENxFileList](#); otherwise, 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.

text   If con is missing, this can be a character vector directly providing the string data to import.

Details

Typically, the user will provide a path to a directory containing the output of the `spaceranger count` command. The `spaceranger count` command outputs a folder containing the "raw" or "filtered" `()_feature_bc_matrix`.

Value

A [SpatialExperiment](#) object

Functions

- `import(con = TENxVisiumHD, format = ANY, text = ANY)`: Import Visium HD data from multiple bin sizes

Author(s)

E. Y. Dong, M. Ramos

Examples

```
vdir <- system.file(
    "extdata", package = "VisiumIO", mustWork = TRUE
)

## with spacerangerOut folder
TENxVisiumHD(spacerangerOut = vdir, bin_size = "002", images = "lowres")

TENxVisiumHD(spacerangerOut = vdir, bin_size = "002", images = "lowres") |>
    import()

## indicate h5 format
TENxVisiumHD(
    spacerangerOut = vdir, bin_size = "002",
    images = "lowres", format = "h5"
)

TENxVisiumHD(
    spacerangerOut = vdir, bin_size = "002",
    images = "lowres", format = "h5"
) |>
    import()

## use resources and spatialResource arguments as file paths
TENxVisiumHD(
    resources = file.path(
        vdir, "binned_outputs", "square_002um",
        "filtered_feature_bc_matrix.h5"
    ),
    spatialResource = file.path(
        vdir, "binned_outputs", "square_002um",
        "spatial"
    ),
    bin_size = "002", processing = "filtered",
    images = "lowres", format = "h5"
) |>
    import()

## provide the spatialResource argument as a TENxFileList
TENxVisiumHD(
    resources = file.path(
        vdir, "binned_outputs", "square_002um",
        "filtered_feature_bc_matrix.h5"
    ),
    spatialResource = TENxFileList(
        file.path(
            vdir, "binned_outputs", "square_002um",
            "spatial"
        )
    ),
    bin_size = "002", images = "lowres", format = "h5"
) |>
    import()

seg_outs <- system.file(
    "extdata", "segmented_outputs", package = "VisiumIO", mustWork = TRUE
```

```
)
TENxVisiumHD(
    segmented_outputs = seg_outs,
    format = "h5",
    images = "lowres"
) |>
    import()
```

TENxVisiumList-class   *A class to represent and import multiple Visium samples*

Description

This class contains a `SimpleList` of [TENxVisium](#) objects each corresponding to one sample.

Usage

```
TENxVisiumList(
  sampleFolders,
  sample_ids,
  processing = c("filtered", "raw"),
  images = c("lowres", "hires", "detected", "aligned"),
  format = c("mtx", "h5"),
  jsonFile = .SCALE_JSON_FILE,
  tissuePattern = "tissue_positions.*\\.csv",
  spatialCoordsNames = c("pxl_col_in_fullres", "pxl_row_in_fullres"),
  ...
)

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

Arguments

sampleFolders	character() A vector of strings specifying the directories containing the output of the `spaceranger count` command.
sample_ids	character() A vector of strings specifying the sample IDs. If not provided, the sample IDs will be the names of the `sampleFolders`. Therefore, the `sample_ids` must be the same length as `sampleFolders`.
processing	character(1) A single string indicating the processing folder available e.g., "filtered_feature_barcode_matrix" in the `spacerangerOut` folder. It can be either "filtered" or "raw" (default "filtered"). Only used when `spacerangerOut` is specified.
images	character() A vector specifying the images to be imported; can be one or multiple of "lowres", "hires", "detected", "aligned".
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](#).
jsonFile	character(1) A single string specifying the name of the JSON file containing the scale factors.

tissuePattern   character(1) A single string specifying the pattern to match the tissue posi-
                 tions file.

spatialCoordsNames

                 character() A vector of strings specifying the names of the columns in the
                 spatial data containing the spatial coordinates.

...   In the constructor, additional arguments passed to [TENxFileList](); otherwise, 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.

text   If con is missing, this can be a character vector directly providing the string data
                 to import.

Details

Typically, the user will provide a path to a directory containing the output of the spaceranger count
command. The spaceranger count command outputs a folder containing the "raw" or "filtered"
()_feature_bc_matrix.

Value

A [SpatialExperiment]() object

Functions

- import(con = TENxVisiumList, format = ANY, text = ANY): Import multiple Visium sam-
  ples

See Also

[https://support.10xgenomics.com/spatial-gene-expression/software/pipelines/latest/](https://support.10xgenomics.com/spatial-gene-expression/software/pipelines/latest/output/overview)
[output/overview](https://support.10xgenomics.com/spatial-gene-expression/software/pipelines/latest/output/overview)

Examples

```
sample_dirs <- list.dirs(
    system.file(
        file.path("extdata", "10xVisium"),
        package = "VisiumIO"
    ),
    recursive = FALSE, full.names = TRUE
)

tvl <- TENxVisiumList(
    sampleFolders = sample_dirs,
    sample_ids = c("sample01", "sample02"),
    processing = "raw",
    images = "lowres",
    format = "mtx"
)
```

```
import(tvl)
```

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