

# Package: XeniumIO (via r-universe)

May 22, 2026

**Type** Package

**Title** Import and represent Xenium data from the 10X Xenium Analyzer

**Version** 1.5.0

**Description** The package allows users to readily import spatial data obtained from the 10X Xenium Analyzer pipeline. Supported formats include 'parquet', 'h5', and 'mtx' files. The package mainly represents data as SpatialExperiment objects.

**License** Artistic-2.0

**Depends** TEnxIO, R (>= 4.5.0)

**Imports** BiocBaseUtils, BiocGenerics, BiocIO, jsonlite, methods, S4Vectors, SingleCellExperiment, SpatialExperiment, SummarizedExperiment, VisiumIO (>= 1.7.5)

**Suggests** arrow, BiocFileCache, BiocStyle, knitr, rmarkdown, tinytest

**biocViews** Software, Infrastructure, DataImport, SingleCell, Spatial

**VignetteBuilder** knitr

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**BugReports** <https://github.com/waldronlab/XeniumIO/issues>

**URL** <https://github.com/waldronlab/XeniumIO>

**Collate** 'XeniumFile.R' 'TEnxXenium-class.R' 'XeniumIO-package.R' 'utilities.R'

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**Repository** <https://waldronlab.r-universe.dev>

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XeniumIO-package	<i>XeniumIO: Import and represent Xenium data from the 10X Xenium Analyzer</i>
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## Description

The package allows users to readily import spatial data obtained from the 10X Xenium Analyzer pipeline. Supported formats include 'parquet', 'h5', and 'mtx' files. The package mainly represents data as SpatialExperiment objects.

## Author(s)

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## See Also

Useful links:

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

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TENxXenium-class	<i>A class to represent Xenium output data</i>
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## Description

This class is a composed class of [TENxFileList](#) which can contain a list of [TENxFile](#) objects for the cell-feature matrix. It is meant to handle a single Xenium sample from 10X Genomics.

**Usage**

```
TENxXenium(
  resources,
  xeniumOut,
  sample_id = "sample01",
  format = c("mtx", "h5"),
  boundaries_format = c("parquet", "csv.gz"),
  spatialCoordsNames = c("x_centroid", "y_centroid"),
  ...
)

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

**Arguments**

resources	A <a href="#">TENxFileList</a> object or a file path to the tarball containing the matrix / assay data resources.
xeniumOut	character(1) The path to the Xenium output directory.
sample_id	character(1) A single string specifying the sample ID.
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 <a href="#">BiocFile</a> .
boundaries_format	character(1) Either "parquet" or "csv.gz" to specify the file extension of the boundaries file. Default is "parquet".
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 <a href="#">TENxFileList</a> ; 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 <a href="#">BiocFile</a> 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**

Note that one can provide a ref argument to import method which will get passed to the internal splitAltExps operation. This allows one to set a mainExpName in the output object.

**Value**

A [SpatialExperiment](#) object

**Functions**

- `import(con = TENxXenium, format = ANY, text = ANY)`: Import Xenium Analyzer data

**Slots**

`resources` A [TENxFileList](#) or [TENxH5](#) object containing the cell feature matrix.

`boundaries` Either a [TENxSpatialParquet](#) or [TENxSpatialCSV](#) object containing the spatial boundaries data.

`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.

`colData` [TENxSpatialParquet](#) A [TENxSpatialParquet](#) object containing the spatial coordinates data.

`metadata` [XeniumFile](#) A [XeniumFile](#) object containing the metadata information.

**See Also**

<https://www.10xgenomics.com/support/software/xenium-onboard-analysis/latest/analysis/xoa-output-understanding-outputs>

**Examples**

```
showClass("TENxXenium")

zipfile <- paste0(
  "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenDemo/",
  "Xenium_Prime_MultiCellSeg_Mouse_Ileum_tiny_outs.zip"
)
destfile <- XeniumIO:::.cache_url_file(zipfile)
outfold <- file.path(
  tempdir(), tools::file_path_sans_ext(basename(zipfile))
)
if (!dir.exists(outfold))
  dir.create(outfold, recursive = TRUE)
unzip(
  zipfile = destfile, exdir = outfold, overwrite = FALSE
)
TENxXenium(xeniumOut = outfold) |>
  import(ref = "Gene Expression")
```

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XeniumFile-class

*A minimal class to represent Xenium metadata*

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**Description**

This class is a minimal class to represent Xenium metadata. It is dedicated to importing `experiment.xenium` metadata files. It uses the `jsonlite` package to import the metadata.

**Usage**

```
XeniumFile(resource)

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

**Arguments**

resource	character(1) The path to the Xenium metadata 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 <a href="#">BiocFile</a> 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 <a href="#">BiocFile</a> .
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.

**Value**

A [XeniumFile](#) object

**Functions**

- `import(con = XeniumFile, format = ANY, text = ANY)`: Import Xenium metadata

**Examples**

```
showClass("XeniumFile")
```

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