

# Package ‘alabaster.spatial’

June 1, 2023

**Title** Save and Load Spatial 'Omics Data to/from File

**Description** Save SpatialExperiment objects and their images into file artifacts, and load them back into memory.

This is a more portable alternative to serialization of such objects into RDS files. Each artifact is associated with metadata for further interpretation; downstream applications can enrich this metadata with context-specific properties.

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**Suggests** testthat, knitr, rmarkdown, BiocStyle, magick, png, digest

**VignetteBuilder** knitr

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**biocViews** DataImport, DataRepresentation

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loadSpatialExperiment *Load a spatial experiment*

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## Description

Load a [SpatialExperiment](#) object from its constituent files in DataSetDB.

## Usage

```
loadSpatialExperiment(exp.info, project)
```

## Arguments

exp.info	Named list of metadata for a spatial 'omics experiment.
project	Any argument accepted by the acquisition functions, see <a href="#">?acquireFile</a> . By default, this should be a string containing the path to a staging directory.

## Value

A [SpatialExperiment](#) object.

## Author(s)

Aaron Lun

## Examples

```
library(SpatialExperiment)
example(read10xVisium, echo=FALSE)
colnames(spe) <- make.unique(colnames(spe)) # forcing unique column names.

tmp <- tempfile()
dir.create(tmp)
meta <- stageObject(spe, tmp, "experiment-1")

meta$path <- "experiment-1/experiment.json"
loadSpatialExperiment(meta, tmp)
```

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loadSpatialImage	<i>Load a spatial image</i>
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**Description**

Load an image as a [SpatialImage](#) or subclass thereof.

**Usage**

```
loadSpatialImage(img.info, project)
```

**Arguments**

img.info	Named list containing the metadata for this assay.
project	Any argument accepted by the acquisition functions, see <a href="#">?acquireFile</a> . By default, this should be a string containing the path to a staging directory.

**Value**

A [SpatialImage](#) containing the image data (or a reference to it).

**Author(s)**

Aaron Lun

**Examples**

```
example(read10xVisium, echo=FALSE)
img <- imgData(spe)$data[[1]]

tmp <- tempfile()
dir.create(tmp)
meta <- stageObject(img, tmp, "whee")

out <- loadSpatialImage(meta, tmp)
```

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stageObject, SpatialExperiment-method
<i>Stage a spatial experiment</i>

---

**Description**

Stage a [SpatialExperiment](#) object.

**Usage**

```
## S4 method for signature 'SpatialExperiment'
stageObject(x, dir, path, child = FALSE, ...)
```

**Arguments**

x	A <a href="#">SpatialExperiment</a> object.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
...	Further arguments to pass to specific methods.

**Value**

A named list of the same form as that returned by the [stageObject](#) method for a [SingleCellExperiment](#), but containing additional fields for the spatial data. A directory is created at path inside dir and is populated with the contents of x.

**Author(s)**

Aaron Lun

**Examples**

```
library(SpatialExperiment)
example(read10xVisium, echo=FALSE)
colnames(spe) <- make.unique(colnames(spe)) # forcing unique column names.

tmp <- tempfile()
dir.create(tmp)
stageObject(spe, tmp, "experiment-1")
list.files(tmp, recursive=TRUE)
```

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stageSpatialImage

*Stage images for upload to DataSetDB*


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**Description**

Stage images from a variety of sources in preparation for upload to DataSetDB.

## Usage

```
## S4 method for signature 'VirtualSpatialImage'
stageObject(x, dir, path, child = FALSE, ...)

## S4 method for signature 'StoredSpatialImage'
stageObject(x, dir, path, child = FALSE, ...)

## S4 method for signature 'RemoteSpatialImage'
stageObject(x, dir, path, child = FALSE, ...)
```

## Arguments

x	A <a href="#">SpatialImage</a> object.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
...	Further arguments to pass to specific methods.

## Details

Each of the different methods will take advantage of any existing files to avoid an actual save. For example, the [RemoteSpatialImage](#) method will download the file directly to path, while the [StoredSpatialImage](#) method will create a link or copy the file. The [SpatialImage](#) method will fall back to saving the raster directly as a PNG.

## Value

An image file is created at `file.path(dir, path)`, possibly after appending an appropriate file extension.

The return value should be a named list containing at least:

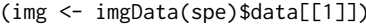
- `$schema`, a string specifying the schema to use to validate the metadata. This may have a `package` attribute to specify the package where the schema lives (in its `inst/schemas` directory).
- `path`, a string containing the path to the file containing the assay contents. This should start with the input path but can be followed by any necessary file extensions.
- `child`, whether this is a child resource of a larger object.

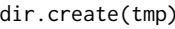
Other fields can be provided and will be included in the metadata, provided that they are recognized by the specified schema.

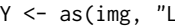
## Author(s)

Aaron Lun

**Examples**

```
example(read10xVisium, echo=FALSE)
 <- imgData(spe)$data[[1]])

# Doing a local run:
tmp <- tempfile()
dir.create(tmp)
stageObject, tmp, "whee")

# Forcing a re-save:
Y <- as, "LoadedSpatialImage")
stageObject(Y, tmp, "foo")
```

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