

Package: tiledbsoma (via r-universe)

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Type Package

Title 'TileDB' Stack of Matrices, Annotated ('SOMA')

Description Interface for working with 'TileDB'-based Stack of Matrices, Annotated ('SOMA'): an open data model for representing annotated matrices, like those commonly used for single cell data analysis. It is documented at <https://github.com/single-cell-data>; a formal specification available is at https://github.com/single-cell-data/SOMA/blob/main/abstract_specification.md.

Version 1.14.4

URL <https://github.com/single-cell-data/TileDB-SOMA>

BugReports <https://github.com/single-cell-data/TileDB-SOMA/issues>

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ConfigList	<i>A Configuration List</i>
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Description

An R6 mapping type for configuring various “parameters”. Essentially, serves as a nested map where the inner map is a [ScalarMap](#): {<param>: {<key>: <value>}}

Super class

`tilebsoma::MappingBase -> ConfigList`

Methods

Public methods:

- `ConfigList$get()`
- `ConfigList$set()`
- `ConfigList$setv()`
- `ConfigList$clone()`

Method get():

Usage:

`ConfigList$get(param, key = NULL, default = quote(expr =))`

Arguments:

param Outer key or “parameter” to fetch

key Inner key to fetch; pass NULL to return the [map](#) for param

default Default value to fetch if key is not found; defaults to NULL

Returns: The value of key for param in the map, or default if key is not found

Method set():

Usage:

`ConfigList$set(param, key, value)`

Arguments:

param Outer key or “parameter” to set

key Inner key to set

value Value to add for key, or NULL to remove the entry for key; optionally provide only param and value as a [ScalarMap](#) to update param with the keys and values from value

Returns: \[chainable\] Invisibly returns self with value added for key in param

Method setv():

Usage:

ConfigList\$setv(...)

Arguments:

... Ignored

Returns: Nothing; setv() is disabled for ConfigList objects

Method clone(): The objects of this class are cloneable with this method.

Usage:

ConfigList\$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

delete_metadata	<i>Delete metadata for given key</i>
-----------------	--------------------------------------

Description

Delete metadata for given key

Usage

delete_metadata(uri, key, is_array, ctxxp)

Arguments

uri	The array URI
key	The array metadata key
is_array	A boolean to indicate array or group
ctxxp	An external pointer to the SOMAContext wrapper

example-datasets *SOMA Example Datasets*

Description

Access example SOMA objects bundled with the tiledbsoma package.

Use `list_datasets()` to list the available datasets and `load_dataset()` to load a dataset into memory using the appropriate SOMA class. The `extract_dataset()` method returns the path to the extracted dataset without loading it into memory.

Usage

```
list_datasets()
```

```
extract_dataset(name, dir = tempdir())
```

```
load_dataset(name, dir = tempdir(), tiledbsoma_ctx = NULL)
```

Arguments

<code>name</code>	The name of the dataset.
<code>dir</code>	The directory where the dataset will be extracted to (default: <code>tempdir()</code>).
<code>tiledbsoma_ctx</code>	Optional TileDB ‘Context’ object, defaults to <code>NULL</code>

Details

The SOMA objects are stored as `tar.gz` files in the package’s `extdata` directory. Calling `load_dataset()` extracts the `tar.gz` file to the specified `dir`, inspects its metadata to determine the appropriate SOMA class to instantiate, and returns the SOMA object.

Value

- `list_datasets()` returns a character vector of the available datasets.
- `extract_dataset()` returns the path to the extracted dataset.
- `load_dataset()` returns a SOMA object.

Examples

```
soma_pbmc_small <- load_dataset("soma-exp-pbmc-small")
```

get_all_metadata	<i>Read all metadata (as named list)</i>
------------------	--

Description

This function currently supports metadata as either a string or an 'int64' (or 'int32'). It will error if a different datatype is encountered.

Usage

```
get_all_metadata(uri, is_array, ctxxp)
```

Arguments

uri	The array URI
is_array	A boolean to indicate array or group
ctxxp	An external pointer to the SOMAContext wrapper

get_metadata	<i>Read metadata (as a string)</i>
--------------	------------------------------------

Description

Read metadata (as a string)

Usage

```
get_metadata(uri, key, is_array, ctxxp)
```

Arguments

uri	The array URI
key	The array metadata key
is_array	A boolean to indicate array or group
ctxxp	An external pointer to the SOMAContext wrapper

get_metadata_num *Get number of metadata items*

Description

Get nnumber of metadata items

Usage

`get_metadata_num(uri, is_array, ctxxp)`

Arguments

<code>uri</code>	The array URI
<code>is_array</code>	A boolean to indicate array or group
<code>ctxxp</code>	An external pointer to the SOMAContext wrapper

has_metadata *Check for metadata given key*

Description

Check for metadata given key

Usage

`has_metadata(uri, key, is_array, ctxxp)`

Arguments

<code>uri</code>	The array URI
<code>key</code>	The array metadata key
<code>is_array</code>	A boolean to indicate array or group
<code>ctxxp</code>	An external pointer to the SOMAContext wrapper

Description

A re-indexer for unique integer indices

Methods**Public methods:**

- [IntIndexer\\$new\(\)](#)
- [IntIndexer\\$get_indexer\(\)](#)
- [IntIndexer\\$clone\(\)](#)

Method `new()`: Create a new re-indexer

Usage:

```
IntIndexer$new(data)
```

Arguments:

`data` Integer keys used to build the index (hash) table

Method `get_indexer()`: Get the underlying indices for the target data

Usage:

```
IntIndexer$get_indexer(target, nomatch_na = FALSE)
```

Arguments:

`target` Data to re-index

`nomatch_na` Set non-matches to NA instead of -1

Returns: A vector of 64-bit integers with target re-indexed

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
IntIndexer$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

matrixZeroBasedView *matrixZeroBasedView is a wrapper shim for a matrix or Matrix::sparseMatrix providing*

Description

matrixZeroBasedView is a class that allows elemental matrix access using zero-based indices.

Methods

Public methods:

- [matrixZeroBasedView\\$new\(\)](#)
- [matrixZeroBasedView\\$take\(\)](#)
- [matrixZeroBasedView\\$dim\(\)](#)
- [matrixZeroBasedView\\$nrow\(\)](#)
- [matrixZeroBasedView\\$ncol\(\)](#)
- [matrixZeroBasedView\\$get_one_based_matrix\(\)](#)
- [matrixZeroBasedView\\$sum\(\)](#)
- [matrixZeroBasedView\\$print\(\)](#)
- [matrixZeroBasedView\\$clone\(\)](#)

Method `new()`: Initialize (lifecycle: maturing)

Usage:

```
matrixZeroBasedView$new(x)
```

Arguments:

x [matrix](#) or [Matrix::sparseMatrix](#) or [Matrix::Matrix](#)

Method `take()`: Zero-based matrix element access

Usage:

```
matrixZeroBasedView$take(i = NULL, j = NULL)
```

Arguments:

i Row index (zero-based).

j Column index (zero-based).

Returns: The specified matrix slice as another [matrixZeroBasedView](#)

Method `dim()`: dim

Usage:

```
matrixZeroBasedView$dim()
```

Returns: The dimensions of the matrix.

Method `nrow()`: nrow

Usage:

`matrixZeroBasedView$nrow()`

Returns: Matrix row count.

Method `ncol(): ncol`

Usage:

`matrixZeroBasedView$ncol()`

Returns: Matrix column count.

Method `get_one_based_matrix():` Get the one-based R matrix with its original class

Usage:

`matrixZeroBasedView$get_one_based_matrix()`

Returns: One-based matrix

Method `sum():` Perform arithmetic sum between this [matrixZeroBasedView](#) and another [matrixZeroBasedView](#).

Usage:

`matrixZeroBasedView$sum(x)`

Arguments:

x the [matrixZeroBasedView](#) to sum.

Returns: The result of the sum as a [matrixZeroBasedView](#).

Method `print(): print`

Usage:

`matrixZeroBasedView$print()`

Method `clone():` The objects of this class are cloneable with this method.

Usage:

`matrixZeroBasedView$clone(deep = FALSE)`

Arguments:

deep Whether to make a deep clone.

PlatformConfig

Platform Configuration

Description

An R6 mapping type for configuring various “parameters” for multiple “platforms”, essentially serves a multi-nested map where the inner map is a [ScalarMap](#) contained within a [ConfigList](#) (middle map): `{platform: {param: {key: value}}}`

Super class

[tiledbsoma::MappingBase](#) -> PlatformConfig

Methods

Public methods:

- [PlatformConfig\\$platforms\(\)](#)
- [PlatformConfig\\$params\(\)](#)
- [PlatformConfig\\$get\(\)](#)
- [PlatformConfig\\$get_params\(\)](#)
- [PlatformConfig\\$set\(\)](#)
- [PlatformConfig\\$setv\(\)](#)
- [PlatformConfig\\$clone\(\)](#)

Method `platforms()`:

Usage:

```
PlatformConfig$platforms()
```

Returns: The names of the “platforms” (outer keys)

Method `params()`:

Usage:

```
PlatformConfig$params(platform = NULL)
```

Arguments:

`platform` The “platform” to pull parameter names (middle keys) for; pass TRUE to return all possible parameter names

Returns: The parameter names (middle keys) for platform

Method `get()`:

Usage:

```
PlatformConfig$get(  
  platform,  
  param = NULL,  
  key = NULL,  
  default = quote(expr = )  
)
```

Arguments:

`platform` The name of the “platform” (outer key) to fetch

`param` The name of the “parameters” of platform to fetch; if NULL, returns the [configuration](#) for platform

`key` The “key” (inner key) for param in platform to fetch; if NULL and param is passed, returns the [map](#) for param in platform

`default` Default value to fetch if key is not found; defaults to null

Returns: The value of key for param in platform in the map, or default if key is not found

Method `get_params()`:

Usage:

```
PlatformConfig$get_params(platform)
```

Arguments:

platform The name of the “platform” (outer key) to fetch

Returns: The [ConfigList](#) for platform

Method set():*Usage:*

```
PlatformConfig$set(platform, param, key, value)
```

Arguments:

platform The name of the “platform” (outer key) to set

param Name of the “parameter” (middle key) in platform to set

key Inner key to set

value Value to add for key, or NULL to remove the entry for key; optionally provide only platform, param, and value as a [ScalarMap](#) to update param for platform with the keys and values from value

Returns: `\[chainable\]` Invisibly returns self with value added for key in param for platform

Method setv():*Usage:*

```
PlatformConfig$setv(...)
```

Arguments:

... Ignored

Returns: Nothing; setv() is disabled for PlatformConfig objects

Method clone(): The objects of this class are cloneable with this method.*Usage:*

```
PlatformConfig$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

 set_log_level

Set the logging level for the R package and underlying C++ library

Description

Set the logging level for the R package and underlying C++ library

Usage

```
set_log_level(level)
```

Arguments

level A character value with logging level understood by ‘spdlog’ such as “trace”, “debug”, “info”, or “warn”.

Value

Nothing is returned as the function is invoked for the side-effect.

set_metadata	<i>Set metadata (as a string)</i>
--------------	-----------------------------------

Description

Set metadata (as a string)

Usage

```
set_metadata(uri, key, valuesxp, type, is_array, ctxxp, tsvec = NULL)
```

Arguments

uri	The array URI
key	The array metadata key
valuesxp	The metadata value
type	The datatype
is_array	A boolean to indicate array or group
ctxxp	An external pointer to the SOMAContext wrapper
tsvec	An optional two-element datetime vector

show_package_versions	<i>Display package versions</i>
-----------------------	---------------------------------

Description

Print version information for **tiledb** (R package), libtiledbsoma, and TileDB embedded, suitable for assisting with bug reports.

Usage

```
show_package_versions()
```

SOMAAxisQuery

*SOMA Axis Query***Description**

Construct a single-axis query object with a combination of coordinates and/or value filters for use with [SOMAExperimentAxisQuery](#). (lifecycle: maturing)

Per dimension, the SOMAAxisQuery can have value of:

- None (i.e., coords = NULL and value_filter = NULL) - read all values
- Coordinates - a set of coordinates on the axis dataframe index, expressed in any type or format supported by [SOMADataFrame](#)'s read() method.
- A SOMA value_filter across columns in the axis dataframe, expressed as string
- Or, a combination of coordinates and value filter.

Public fields

coords The coordinates for the query.

value_filter The value filter for the query.

Methods**Public methods:**

- [SOMAAxisQuery\\$new\(\)](#)
- [SOMAAxisQuery\\$clone\(\)](#)

Method new(): Create a new SOMAAxisQuery object.

Usage:

```
SOMAAxisQuery$new(value_filter = NULL, coords = NULL)
```

Arguments:

value_filter Optional string containing a logical expression that is used to filter the returned values.

coords Optional indices specifying the rows to read: either a vector of the appropriate type or a named list of vectors corresponding to each dimension.

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
SOMAAxisQuery$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[tiledb::parse_query_condition\(\)](#) for more information about valid value filters.

SOMAAxisQueryResult SOMAExperiment *Axis Query Result*

Description

Access [SOMAExperimentAxisQuery](#) results.

Active bindings

obs [arrow::Table](#) containing obs query slice.

var [arrow::Table](#) containing var query slice. measurement_name.

X_layers named list of [arrow::Tables](#) for each X layer.

Methods

Public methods:

- [SOMAAxisQueryResult\\$new\(\)](#)
- [SOMAAxisQueryResult\\$clone\(\)](#)

Method `new()`: Create a new `SOMAAxisQueryResult` object.

Usage:

```
SOMAAxisQueryResult$new(obs, var, X_layers)
```

Arguments:

obs, var [arrow::Table](#) containing obs or var query slice.

X_layers named list of [arrow::Tables](#), one for each X layer.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMAAxisQueryResult$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

SOMACollection *SOMA Collection*

Description

Contains a key-value mapping where the keys are string names and the values are any SOMA-defined foundational or composed type, including [SOMACollection](#), [SOMADataFrame](#), [SOMADenseNDArray](#), [SOMASparseNDArray](#), or [SOMAExperiment](#). (lifecycle: maturing)

Super classes

```

tiledbsoma::TiledDBObject -> tiledbsoma::TiledBGroup -> tiledbsoma::SOMACollectionBase
-> SOMACollection

```

Methods

Public methods:

- [SOMACollection\\$clone\(\)](#)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMACollection$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

SOMACollectionCreate *Create SOMA Collection*

Description

Factory function to create a SOMADataFrame for writing, (lifecycle: maturing)

Usage

```

SOMACollectionCreate(
  uri,
  ingest_mode = c("write", "resume"),
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)

```


Arguments

uri	URI for the TileDB object
ingest_mode	Ingestion mode when creating the TileDB object; choose from: <ul style="list-style-type: none"> • “write”: create a new TileDB object and error if it already exists • “resume”: attempt to create a new TileDB object; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp

SOMACollectionOpen	<i>Open SOMA Collection</i>
--------------------	-----------------------------

Description

Factory function to open a SOMACollection for reading, (lifecycle: maturing)

Usage

```
SOMACollectionOpen(
  uri,
  mode = "READ",
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

uri	URI for the TileDB object
mode	One of "READ" or "WRITE"
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMADataFrame

*SOMADataFrame***Description**

SOMADataFrame is a multi-column table that must contain a column called `soma_joinid` of type `int64`, which contains a unique value for each row and is intended to act as a join key for other objects, such as [SOMASparseNDArray](#). (lifecycle: maturing)

Super classes

```

tiledbsoma::TileDBObject -> tiledbsoma::TileDBArray -> tiledbsoma::SOMAArrayBase -
> SOMADataFrame

```

Methods**Public methods:**

- [SOMADataFrame\\$create\(\)](#)
- [SOMADataFrame\\$write\(\)](#)
- [SOMADataFrame\\$read\(\)](#)
- [SOMADataFrame\\$update\(\)](#)
- [SOMADataFrame\\$shape\(\)](#)
- [SOMADataFrame\\$maxshape\(\)](#)
- [SOMADataFrame\\$tiledbsoma_has_upgraded_domain\(\)](#)
- [SOMADataFrame\\$clone\(\)](#)

Method `create()`: Create (lifecycle: maturing)

Usage:

```

SOMADataFrame$create(
  schema,
  index_column_names = c("soma_joinid"),
  platform_config = NULL,
  internal_use_only = NULL
)

```

Arguments:

`schema` an [arrow::schema](#).

`index_column_names` A vector of column names to use as user-defined index columns. All named columns must exist in the schema, and at least one index column name is required.

`platform_config` A [platform configuration](#) object

`internal_use_only` Character value to signal this is a 'permitted' call, as `create()` is considered internal and should not be called directly.

Method `write()`: Write (lifecycle: maturing)

Usage:

```
SOMADataFrame$write(values)
```

Arguments:

values An [arrow::Table](#) or [arrow::RecordBatch](#) containing all columns, including any index columns. The schema for values must match the schema for the SOMADataFrame.

Method read(): Read (lifecycle: maturing) Read a user-defined subset of data, addressed by the dataframe indexing column, and optionally filtered.

Usage:

```
SOMADataFrame$read(
  coords = NULL,
  column_names = NULL,
  value_filter = NULL,
  result_order = "auto",
  iterated = FALSE,
  log_level = "auto"
)
```

Arguments:

coords Optional named list of indices specifying the rows to read; each (named) list element corresponds to a dimension of the same name.

column_names Optional character vector of column names to return.

value_filter Optional string containing a logical expression that is used to filter the returned values. See [tiledb::parse_query_condition](#) for more information.

result_order Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

iterated Option boolean indicated whether data is read in call (when FALSE, the default value) or in several iterated steps.

log_level Optional logging level with default value of "warn".

Returns: [arrow::Table](#) or [TableReader](#)

Method update(): Update (lifecycle: maturing)

Usage:

```
SOMADataFrame$update(values, row_index_name = NULL)
```

Arguments:

values A data.frame, [arrow::Table](#), or [arrow::RecordBatch](#).

row_index_name An optional scalar character. If provided, and if the values argument is a data.frame with row names, then the row names will be extracted and added as a new column to the data.frame prior to performing the update. The name of this new column will be set to the value specified by row_index_name.

Details: Update the existing SOMADataFrame to add or remove columns based on the input:

- columns present in the current the SOMADataFrame but absent from the new values will be dropped
- columns absent in current SOMADataFrame but present in the new values will be added
- any columns present in both will be left alone, with the exception that if values has a different type for the column, the entire update will fail because attribute types cannot be changed.

Furthermore, values must contain the same number of rows as the current SOMADataFrame.

Method `shape()`: Retrieve the shape; as SOMADataFrames are shapeless, simply raises an error

Usage:

`SOMADataFrame$shape()`

Returns: None, instead a `.NotYetImplemented()` error is raised

Method `maxshape()`: Retrieve the maxshape; as SOMADataFrames are shapeless, simply raises an error

Usage:

`SOMADataFrame$maxshape()`

Returns: None, instead a `.NotYetImplemented()` error is raised

Method `tiledbsoma_has_upgraded_domain()`: Returns TRUE if the array has the upgraded resizeable domain feature from TileDB-SOMA 1.15: the array was created with this support, or it has had `upgrade_domain` applied to it. (lifecycle: maturing)

Usage:

`SOMADataFrame$tiledbsoma_has_upgraded_domain()`

Returns: Logical

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

`SOMADataFrame$clone(deep = FALSE)`

Arguments:

`deep` Whether to make a deep clone.

SOMADataFrameCreate *Create SOMA DataFrame*

Description

Factory function to create a SOMADataFrame for writing, (lifecycle: maturing)

Usage

```
SOMADataFrameCreate(
  uri,
  schema,
  index_column_names = c("soma_joinid"),
  ingest_mode = c("write", "resume"),
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL,
  soma_context = NULL
)
```

Arguments

uri	URI for the TileDB object
schema	Arrow schema argument for the SOMA dataframe
index_column_names	A vector of column names to use as user-defined index columns; all named columns must exist in the schema, and at least one index column name is required
ingest_mode	Ingestion mode when creating the TileDB object; choose from: <ul style="list-style-type: none"> • “write”: create a new TileDB object and error if it already exists • “resume”: attempt to create a new TileDB object; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp

SOMADataFrameOpen *Open SOMA DataFrame*

Description

Factory function to open a SOMADataFrame for reading, (lifecycle: maturing)

Usage

```
SOMADataFrameOpen(
  uri,
  mode = "READ",
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL,
  soma_context = NULL
)
```

Arguments

uri	URI for the TileDB object
mode	One of "READ" or "WRITE"
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMADenseNDArray	<i>SOMADenseNDArray</i>
------------------	-------------------------

Description

SOMADenseNDArray is a dense, N-dimensional array of primitive type, with offset (zero-based) int64 integer indexing on each dimension with domain $[0, \text{maxInt64})$. The SOMADenseNDArray has a user-defined schema, which includes:

- **type**: a primitive type, expressed as an Arrow type (e.g., int64, float32, etc), indicating the type of data contained within the array
- **shape**: the shape of the array, i.e., number and length of each dimension

All dimensions must have a positive, non-zero length, and there must be 1 or more dimensions.

The default "fill" value for SOMADenseNDArray is the zero or null value of the array type (e.g., Arrow.float32 defaults to 0.0).

The write method is currently limited to writing from 2-d matrices. (lifecycle: maturing)

Super classes

```

 tiledbsoma::TileDBObject -> tiledbsoma::TileDBArray -> tiledbsoma::SOMAArrayBase -
 > tiledbsoma::SOMANDArrayBase -> SOMADenseNDArray

```

Methods

Public methods:

- SOMADenseNDArray\$read_arrow_table()
- SOMADenseNDArray\$read_dense_matrix()
- SOMADenseNDArray\$write()
- SOMADenseNDArray\$clone()

Method read_arrow_table(): Read as an 'arrow::Table' (lifecycle: maturing)

Usage:

```

SOMADenseNDArray$read_arrow_table(
  coords = NULL,
  result_order = "auto",
  log_level = "warn"
)

```

Arguments:

coords Optional list of integer vectors, one for each dimension, with a length equal to the number of values to read. If NULL, all values are read. List elements can be named when specifying a subset of dimensions.

result_order Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

`result_order` Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

`log_level` Optional logging level with default value of "warn".

Returns: An `arrow::Table`.

Method `read_dense_matrix()`: Read as a dense matrix (lifecycle: maturing)

Usage:

```
SOMADenseNDArray$read_dense_matrix(
  coords = NULL,
  result_order = "ROW_MAJOR",
  log_level = "warn"
)
```

Arguments:

`coords` Optional list of integer vectors, one for each dimension, with a length equal to the number of values to read. If NULL, all values are read. List elements can be named when specifying a subset of dimensions.

`result_order` Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

`result_order` Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

`log_level` Optional logging level with default value of "warn".

Returns: A matrix object

Method `write()`: Write matrix data to the array. (lifecycle: maturing)

More general write methods for higher-dimensional array could be added.

Usage:

```
SOMADenseNDArray$write(values, coords = NULL)
```

Arguments:

`values` A matrix. Character dimension names are ignored because SOMANDArray's use integer indexing.

`coords` A list of integer vectors, one for each dimension, with a length equal to the number of values to write. If NULL, the default, the values are taken from the row and column names of values.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMADenseNDArray$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

SOMADenseNDArrayCreate

Create SOMA Dense Nd Array

Description

Factory function to create a SOMADenseNDArray for writing, (lifecycle: maturing)

Usage

```
SOMADenseNDArrayCreate(
  uri,
  type,
  shape,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

uri	URI for the TileDB object
type	An Arrow type defining the type of each element in the array.
shape	A vector of integers defining the shape of the array.
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp

SOMADenseNDArrayOpen *Open SOMA Dense Nd Array*

Description

Factory function to open a SOMADenseNDArray for reading, (lifecycle: maturing)

Usage

```
SOMADenseNDArrayOpen(
  uri,
  mode = "READ",
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```


Arguments

uri	URI for the TileDB object
mode	One of "READ" or "WRITE"
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMAExperiment

SOMA Experiment

Description

SOMAExperiment is a specialized [SOMACollection](#), representing one or more modes of measurement across a single collection of cells (aka a "multimodal dataset") with pre-defined fields: obs and ms (see *Active Bindings* below for details). (lifecycle: maturing)

Adding new objects to a collection

The [SOMAExperiment](#) class provides a number of type-specific methods for adding new a object to the collection, such as `add_new_sparse_ndarray()` and `add_new_dataframe()`. These methods will create the new object and add it as member of the SOMAExperiment. The new object will always inherit the parent context (see [SOMATileDBContext](#)) and, by default, its platform configuration (see [PlatformConfig](#)). However, the user can override the default platform configuration by passing a custom configuration to the `platform_config` argument.

Super classes

```
tiledbsoma::TileDBObject -> tiledbsoma::TileDBGroup -> tiledbsoma::SOMACollectionBase
-> SOMAExperiment
```

Active bindings

obs a [SOMADataFrame](#) containing primary annotations on the observation axis. The contents of the `soma_joinid` column define the observation index domain, `obs_id`. All observations for the SOMAExperiment must be defined in this dataframe.

ms a [SOMACollection](#) of named [SOMAMeasurements](#).

Methods

Public methods:

- [SOMAEperiment\\$axis_query\(\)](#)
- [SOMAEperiment\\$update_obs\(\)](#)
- [SOMAEperiment\\$update_var\(\)](#)
- [SOMAEperiment\\$clone\(\)](#)

Method [axis_query\(\)](#): Subset and extract data from a [SOMAMeasurement](#) by querying the obs/var axes.

Usage:

```
SOMAEperiment$axis_query(measurement_name, obs_query = NULL, var_query = NULL)
```

Arguments:

`measurement_name` The name of the measurement to query.

`obs_query`, `var_query` An [SOMAAxisQuery](#) object for the obs/var axis.

Returns: A [SOMAEperimentAxisQuery](#) object.

Method [update_obs\(\)](#): Update the obs [SOMADataFrame](#) to add or remove columns. See [SOMADataFrame\\$update\(\)](#) for details.

Usage:

```
SOMAEperiment$update_obs(values, row_index_name = NULL)
```

Arguments:

`values` A `data.frame`, [arrow::Table](#), or [arrow::RecordBatch](#).

`row_index_name` An optional scalar character. If provided, and if the `values` argument is a `data.frame` with row names, then the row names will be extracted and added as a new column to the `data.frame` prior to performing the update. The name of this new column will be set to the value specified by `row_index_name`.

Method [update_var\(\)](#): Update the var [SOMADataFrame](#) to add or remove columns. See [SOMADataFrame\\$update\(\)](#) for details.

Usage:

```
SOMAEperiment$update_var(values, measurement_name, row_index_name = NULL)
```

Arguments:

`values` A `data.frame`, [arrow::Table](#), or [arrow::RecordBatch](#).

`measurement_name` The name of the [SOMAMeasurement](#) whose var will be updated.

`row_index_name` An optional scalar character. If provided, and if the `values` argument is a `data.frame` with row names, then the row names will be extracted and added as a new column to the `data.frame` prior to performing the update. The name of this new column will be set to the value specified by `row_index_name`.

Method [clone\(\)](#): The objects of this class are cloneable with this method.

Usage:

```
SOMAEperiment$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

SOMAXperimentAxisQuery

SOMAXperiment *Axis Query*

Description

Perform an axis-based query against a [SOMAXperiment](#).

SOMAXperimentAxisQuery allows easy selection and extraction of data from a single [SOMAMeasurement](#) in a [SOMAXperiment](#), by obs/var (axis) coordinates and/or value filter. The primary use for this class is slicing [SOMAXperiment](#) X layers by obs or var value and/or coordinates. (lifecycle: maturing)

X Layer Support:

Slicing on [SOMASparseNDArray](#) X matrices is supported; slicing on [SOMADenseNDArray](#) is not supported at this time.

Result Size:

SOMAXperimentAxisQuery query class assumes it can store the full result of both axis dataframe queries in memory, and only provides incremental access to the underlying X NDArray. Accessors such as `n_obs` and `n_vars` codify this in the class.

Active bindings

`experiment` The parent [SOMAXperiment](#) object.

`indexer` The [SOMAAxisIndexer](#) object.

`obs_query` The obs [SOMAAxisQuery](#) object.

`var_query` The var [SOMAAxisQuery](#) object.

`n_obs` The number of obs axis query results.

`n_vars` The number of var axis query results.

`obs_df` The obs [SOMADataFrame](#) object.

`var_df` The var [SOMADataFrame](#) object for the specified `measurement_name`.

`ms` The [SOMAMeasurement](#) object for the specified `measurement_name`.

Methods

Public methods:

- [SOMAXperimentAxisQuery\\$new\(\)](#)
- [SOMAXperimentAxisQuery\\$obs\(\)](#)
- [SOMAXperimentAxisQuery\\$var\(\)](#)
- [SOMAXperimentAxisQuery\\$obs_joinids\(\)](#)
- [SOMAXperimentAxisQuery\\$var_joinids\(\)](#)
- [SOMAXperimentAxisQuery\\$X\(\)](#)
- [SOMAXperimentAxisQuery\\$obsm\(\)](#)

- `SOMAExperimentAxisQuery$varm()`
- `SOMAExperimentAxisQuery$obsp()`
- `SOMAExperimentAxisQuery$varp()`
- `SOMAExperimentAxisQuery$read()`
- `SOMAExperimentAxisQuery$to_sparse_matrix()`
- `SOMAExperimentAxisQuery$to_seurat()`
- `SOMAExperimentAxisQuery$to_seurat_assay()`
- `SOMAExperimentAxisQuery$to_seurat_reduction()`
- `SOMAExperimentAxisQuery$to_seurat_graph()`
- `SOMAExperimentAxisQuery$to_single_cell_experiment()`
- `SOMAExperimentAxisQuery$clone()`

Method `new()`: Create a new `SOMAExperimentAxisQuery` object.

Usage:

```
SOMAExperimentAxisQuery$new(
  experiment,
  measurement_name,
  obs_query = NULL,
  var_query = NULL
)
```

Arguments:

`experiment` A `SOMAExperiment` object.

`measurement_name` The name of the measurement to query.

`obs_query`, `var_query` An `SOMAAxisQuery` object for the obs/var axis.

Method `obs()`: Retrieve obs `TableReadIter`

Usage:

```
SOMAExperimentAxisQuery$obs(column_names = NULL)
```

Arguments:

`column_names` A character vector of column names to retrieve

Method `var()`: Retrieve var `arrow::Table`

Usage:

```
SOMAExperimentAxisQuery$var(column_names = NULL)
```

Arguments:

`column_names` A character vector of column names to retrieve

Method `obs_joinids()`: Retrieve `soma_joinids` as an `arrow::Array` for obs.

Usage:

```
SOMAExperimentAxisQuery$obs_joinids()
```

Method `var_joinids()`: Retrieve `soma_joinids` as an `arrow::Array` for var.

Usage:

```
SOMAExperimentAxisQuery$var_joinids()
```

Method X(): Retrieves an X layer as a [SOMASparseNDArrayRead](#)

Usage:

```
SOMAEperimentAxisQuery$X(layer_name)
```

Arguments:

layer_name The name of the layer to retrieve.

Method obsm(): Retrieves an obsm layer as a [SOMASparseNDArrayRead](#)

Usage:

```
SOMAEperimentAxisQuery$obsm(layer_name)
```

Arguments:

layer_name The name of the layer to retrieve

Method varm(): Retrieves a varm layer as a [SOMASparseNDArrayRead](#)

Usage:

```
SOMAEperimentAxisQuery$varm(layer_name)
```

Arguments:

layer_name The name of the layer to retrieve

Method obsp(): Retrieves an obsp layer as a [SOMASparseNDArrayRead](#)

Usage:

```
SOMAEperimentAxisQuery$obsp(layer_name)
```

Arguments:

layer_name The name of the layer to retrieve

Method varp(): Retrieves a varp layer as a [SOMASparseNDArrayRead](#)

Usage:

```
SOMAEperimentAxisQuery$varp(layer_name)
```

Arguments:

layer_name The name of the layer to retrieve

Method read(): Reads the entire query result as a list of [arrow::Tables](#). This is a low-level routine intended to be used by loaders for other in-core formats, such as Seurat, which can be created from the resulting Tables.

Usage:

```
SOMAEperimentAxisQuery$read(
  X_layers = NULL,
  obs_column_names = NULL,
  var_column_names = NULL
)
```

Arguments:

X_layers The name(s) of the X layer(s) to read and return.

obs_column_names, var_column_names Specify which column names in var and obs dataframes to read and return.

Method `to_sparse_matrix()`: Retrieve a collection layer as a sparse matrix with named dimensions.

Load any layer from the X, obsm, varm, obsp, or varp collections as a [sparse matrix](#).

By default the matrix dimensions are named using the `soma_joinid` values in the specified layer's dimensions (e.g., `soma_dim_0`). However, dimensions can be named using values from any obs or var column that uniquely identifies each record by specifying the `obs_index` and `var_index` arguments.

For layers in obsm or varm, the column axis (the axis not indexed by "obs" or "var") is set to the range of values present in "soma_dim_1"; this ensures that gaps in this axis are preserved (eg. when a query for "obs" that results in selecting entries that are all zero for a given PC)

Usage:

```
SOMAExperimentAxisQuery$to_sparse_matrix(
  collection,
  layer_name,
  obs_index = NULL,
  var_index = NULL
)
```

Arguments:

`collection` The [SOMACollection](#) containing the layer of interest, either: "X", "obsm", "varm", "obsp", or "varp".

`layer_name` Name of the layer to retrieve from the collection.

`obs_index`, `var_index` Name of the column in obs or var (`var_index`) containing values that should be used as dimension labels in the resulting matrix. Whether the values are used as row or column labels depends on the selected collection:

Collection	obs_index	var_index
X	row names	column names
obsm	row names	ignored
varm	ignored	row names
obsp	row and column names	ignored
varp	ignored	row and column names

Returns: A [Matrix::sparseMatrix](#)

Method `to_seurat()`: Loads the query as a [Seurat](#) object

Usage:

```
SOMAExperimentAxisQuery$to_seurat(
  X_layers = c(counts = "counts", data = "logcounts"),
  obs_index = NULL,
  var_index = NULL,
  obs_column_names = NULL,
  var_column_names = NULL,
  obsm_layers = NULL,
  varm_layers = NULL,
  obsp_layers = NULL,
  drop_levels = FALSE
)
```

Arguments:

`X_layers` A named character of X layers to add to the Seurat assay where the names are the names of Seurat slots and the values are the names of layers within X; names should be one of:

- “counts” to add the layer as counts
- “data” to add the layer as data
- “scale.data” to add the layer as scale.data

At least one of “counts” or “data” is required

`obs_index` Name of column in obs to add as cell names; uses `paste0("cell", obs_joinids())` by default

`var_index` Name of column in var to add as feature names; uses `paste0("feature", var_joinids())` by default

`obs_column_names` Names of columns in obs to add as cell-level meta data; by default, loads all columns

`var_column_names` Names of columns in var to add as feature-level meta data; by default, loads all columns

`obsm_layers` Names of arrays in obsm to add as the cell embeddings; pass FALSE to suppress loading in any dimensional reductions; by default, loads all dimensional reduction information

`varm_layers` Named vector of arrays in varm to load in as the feature loadings; names must be names of arrays in obsm (eg. `varm_layers = c(X_pca = "PCs")`); pass FALSE to suppress loading in any feature loadings; will try to determine `varm_layers` from `obsm_layers`

`obsp_layers` Names of arrays in obsp to load in as [Graphs](#); by default, loads all graphs

`drop_levels` Drop unused levels from obs and var factor columns

Returns: A [Seurat](#) object

Method `to_seurat_assay()`: Loads the query as a Seurat [Assay](#)

Usage:

```
SOMAExperimentAxisQuery$to_seurat_assay(
  X_layers = c(counts = "counts", data = "logcounts"),
  obs_index = NULL,
  var_index = NULL,
  var_column_names = NULL,
  drop_levels = FALSE
)
```

Arguments:

`X_layers` A named character of X layers to add to the Seurat assay where the names are the names of Seurat slots and the values are the names of layers within X; names should be one of:

- “counts” to add the layer as counts
- “data” to add the layer as data
- “scale.data” to add the layer as scale.data

At least one of “counts” or “data” is required

`obs_index` Name of column in obs to add as cell names; uses `paste0("cell", obs_joinids())` by default

var_index Name of column in var to add as feature names; uses paste0("feature", var_joinids()) by default
var_column_names Names of columns in var to add as feature-level meta data; by default, loads all columns
drop_levels Drop unused levels from var factor columns
Returns: An [Assay](#) object

Method to_seurat_reduction(): Loads the query as a Seurat [dimensional reduction](#)

Usage:

```
SOMAExperimentAxisQuery$to_seurat_reduction(
  obsm_layer,
  varm_layer = NULL,
  obs_index = NULL,
  var_index = NULL
)
```

Arguments:

obsm_layer Name of array in obsm to load as the cell embeddings
varm_layer Name of the array in varm to load as the feature loadings; by default, will try to determine varm_layer from obsm_layer
obs_index Name of column in obs to add as cell names; uses paste0("cell", obs_joinids()) by default
var_index Name of column in var to add as feature names; uses paste0("feature", var_joinids()) by default

Returns: A [DimReduc](#) object

Method to_seurat_graph(): Loads the query as a Seurat [graph](#)

Usage:

```
SOMAExperimentAxisQuery$to_seurat_graph(obsp_layer, obs_index = NULL)
```

Arguments:

obsp_layer Name of array in obsp to load as the graph
obs_index Name of column in obs to add as cell names; uses paste0("cell", obs_joinids()) by default

Returns: A [Graph](#) object

Method to_single_cell_experiment(): Loads the query as a [SingleCellExperiment](#) object

Usage:

```
SOMAExperimentAxisQuery$to_single_cell_experiment(
  X_layers = NULL,
  obs_index = NULL,
  var_index = NULL,
  obs_column_names = NULL,
  var_column_names = NULL,
  obsm_layers = NULL,
  obsp_layers = NULL,
  varp_layers = NULL,
  drop_levels = FALSE
)
```


Arguments:

`X_layers` A character vector of X layers to add as assays in the main experiment; may optionally be named to set the name of the resulting assay (eg. `X_layers = c(counts = "raw")` will load in X layer "raw" as assay "counts"); by default, loads in all X layers

`obs_index` Name of column in obs to add as cell names; uses `paste0("cell", obs_joinids())` by default

`var_index` Name of column in var to add as feature names; uses `paste0("feature", var_joinids())` by default

`obs_column_names` Names of columns in obs to add as colData; by default, loads all columns

`var_column_names` Names of columns in var to add as rowData; by default, loads all columns

`obsm_layers` Names of arrays in obsm to add as the reduced dimensions; pass FALSE to suppress loading in any reduced dimensions; by default, loads all reduced dimensions

`obsp_layers` Names of arrays in obsp to load in as [SelfHits](#); by default, loads all graphs

`varp_layers` Names of arrays in varp to load in as [SelfHits](#); by default, loads all networks

`drop_levels` Drop unused levels from obs and var factor columns

Returns: A [SingleCellExperiment](#) object

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMAExperimentAxisQuery$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

SOMAExperimentCreate *Create SOMA Experiment*

Description

Factory function to create a SOMADataFrame for writing, (lifecycle: maturing)

Usage

```
SOMAExperimentCreate(
  uri,
  ingest_mode = c("write", "resume"),
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

<code>uri</code>	URI for the TileDB object
<code>ingest_mode</code>	Ingestion mode when creating the TileDB object; choose from: <ul style="list-style-type: none"> • “write”: create a new TileDB object and error if it already exists • “resume”: attempt to create a new TileDB object; if it already exists, simply open it for writing
<code>platform_config</code>	Optional platform configuration
<code>tiledbsoma_ctx</code>	Optional SOMATileDBContext
<code>tiledb_timestamp</code>	Optional Datetime (POSIXct) for TileDB timestamp

SOMAExperimentOpen	<i>Open SOMA Experiment</i>
--------------------	-----------------------------

Description

Factory function to open a SOMAExperiment for reading, (lifecycle: maturing)

Usage

```
SOMAExperimentOpen(
  uri,
  mode = "READ",
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

<code>uri</code>	URI for the TileDB object
<code>mode</code>	One of "READ" or "WRITE"
<code>platform_config</code>	Optional platform configuration
<code>tiledbsoma_ctx</code>	Optional SOMATileDBContext
<code>tiledb_timestamp</code>	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMAMeasurement	<i>SOMA Measurement</i>
-----------------	-------------------------

Description

A `SOMAMeasurement` is a sub-element of a `SOMAExperiment`, and is otherwise a specialized `SOMACollection` with pre-defined fields: `X`, `var`, `obsm/varm`, and `obsp/varp` (see *Active Bindings* below for details). (lifecycle: maturing)

Adding new objects to a collection

The `SOMAMeasurement` class provides a number of type-specific methods for adding new a object to the collection, such as `add_new_sparse_ndarray()` and `add_new_dataframe()`. These methods will create the new object and add it as member of the `SOMAMeasurement`. The new object will always inherit the parent context (see `SOMATileDBContext`) and, by default, its platform configuration (see `PlatformConfig`). However, the user can override the default platform configuration by passing a custom configuration to the `platform_config` argument.

Super classes

```

tiledbsoma::TileDBObject -> tiledbsoma::TileDBGroup -> tiledbsoma::SOMACollectionBase
-> SOMAMeasurement

```

Active bindings

`var` a `SOMADataFrame` containing primary annotations on the variable axis, for variables in this measurement (i.e., annotates columns of `X`). The contents of the `soma_joinid` column define the variable index domain, `var_id`. All variables for this measurement must be defined in this dataframe.

`X` a `SOMACollection` of `SOMASparseNDArrays`, each contains measured feature values indexed by `[obsid, varid]`.

`obsm` a `SOMACollection` of `SOMADenseNDArrays` containing annotations on the observation axis. Each array is indexed by `obsid` and has the same shape as `obs`.

`obsp` a `SOMACollection` of `SOMASparseNDArrays` containing pairwise annotations on the observation axis and indexed with `[obsid_1, obsid_2]`.

`varm` a `SOMACollection` of `SOMADenseNDArrays` containing annotations on the variable axis. Each array is indexed by `varid` and has the same shape as `var`.

`varp` a `SOMACollection` of `SOMASparseNDArrays` containing pairwise annotations on the variable axis and indexed with `[varid_1, varid_2]`.

Methods

Public methods:

- `SOMAMeasurement$clone()`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMAMeasurement$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

SOMAMeasurementCreate *Create SOMA Measurement*

Description

Factory function to create a SOMAMeasurement for writing, (lifecycle: maturing)

Usage

```
SOMAMeasurementCreate(
  uri,
  ingest_mode = c("write", "resume"),
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

uri	URI for the TileDB object
ingest_mode	Ingestion mode when creating the TileDB object; choose from: <ul style="list-style-type: none"> • “write”: create a new TileDB object and error if it already exists • “resume”: attempt to create a new TileDB object; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp

SOMAMeasurementOpen *Open SOMA Measurement*

Description

Factory function to open a SOMAMeasurement for reading, (lifecycle: maturing)

Usage

```
SOMAMeasurementOpen(
    uri,
    mode = "READ",
    platform_config = NULL,
    tiledbsoma_ctx = NULL,
    tiledb_timestamp = NULL
)
```

Arguments

uri	URI for the TileDB object
mode	One of "READ" or "WRITE"
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMAOpen *Open a SOMA Object*

Description

Utility function to open the corresponding SOMA Object given a URI, (lifecycle: maturing)

Usage

```
SOMAOpen(
    uri,
    mode = "READ",
    platform_config = NULL,
    tiledbsoma_ctx = NULL,
    tiledb_timestamp = NULL
)
```

Arguments

<code>uri</code>	URI for the TileDB object
<code>mode</code>	One of "READ" or "WRITE"
<code>platform_config</code>	Optional platform configuration
<code>tiledb_soma_ctx</code>	Optional SOMATileDBContext
<code>tiledb_timestamp</code>	Optional Datetime (POSIXct) with TileDB timestamp. For SOMACollections, all accessed members inherit the collection opening timestamp, and in READ mode the collection timestamp defaults to the time of opening.

SOMASparseNDArray	<i>SOMASparseNDArray</i>
-------------------	--------------------------

Description

SOMASparseNDArray is a sparse, N-dimensional array with offset (zero-based) integer indexing on each dimension. The SOMASparseNDArray has a user-defined schema, which includes:

- `type` - a primitive type, expressed as an Arrow type (e.g., `int64`, `float32`, etc)
- `shape` - the shape of the array, i.e., number and length of each dimension

All dimensions must have a positive, non-zero length.

Note - on TileDB this is a sparse array with N `int64` dimensions of domain `[0, maxInt64)`, and a single attribute.

Duplicate writes:

As duplicate index values are not allowed, index values already present in the object are overwritten and new index values are added. (lifecycle: maturing)

Super classes

```
tiledb_soma::TileDBObject -> tiledb_soma::TileDBArray -> tiledb_soma::SOMAArrayBase -
> tiledb_soma::SOMANDArrayBase -> SOMASparseNDArray
```

Methods**Public methods:**

- `SOMASparseNDArray$read()`
- `SOMASparseNDArray$write()`
- `SOMASparseNDArray$nnz()`
- `SOMASparseNDArray$resize()`
- `SOMASparseNDArray$tiledb_soma_upgrade_shape()`
- `SOMASparseNDArray$.write_coordinates()`
- `SOMASparseNDArray$clone()`

Method `read()`: Reads a user-defined slice of the SOMASparseNDArray

Usage:

```
SOMASparseNDArray$read(
  coords = NULL,
  result_order = "auto",
  log_level = "auto"
)
```

Arguments:

`coords` Optional list of integer vectors, one for each dimension, with a length equal to the number of values to read. If NULL, all values are read. List elements can be named when specifying a subset of dimensions.

`result_order` Optional order of read results. This can be one of either "ROW_MAJOR", "COL_MAJOR", or "auto" (default).

`log_level` Optional logging level with default value of "warn".

`iterated` Option boolean indicated whether data is read in call (when FALSE, the default value) or in several iterated steps.

Returns: [SOMASparseNDArrayRead](#)

Method `write()`: Write matrix-like data to the array. (lifecycle: maturing)

Usage:

```
SOMASparseNDArray$write(values, bbox = NULL)
```

Arguments:

`values` Any matrix-like object coercible to a [TsparseMatrix](#). Character dimension names are ignored because SOMANDArray's use integer indexing.

`bbox` A vector of integers describing the upper bounds of each dimension of values. Generally should be NULL.

Returns: Invisibly returns self

Method `nnz()`: Retrieve number of non-zero elements (lifecycle: maturing)

Usage:

```
SOMASparseNDArray$nnz()
```

Returns: A scalar with the number of non-zero elements

Method `resize()`: Increases the shape of the array as specified. Raises an error if the new shape is less than the current shape in any dimension. Raises an error if the new shape exceeds maxshape in any dimension. Raises an error if the array doesn't already have a shape: in that case please call `tiledb_soma_upgrade_shape`.

Usage:

```
SOMASparseNDArray$resize(new_shape)
```

Arguments:

`new_shape` A vector of integerish, of the same length as the array's `ndim`.

Returns: No return value

Method `tiledb_soma_upgrade_shape()`: Allows the array to have a resizable shape as described in the TileDB-SOMA 1.15 release notes. Raises an error if the shape exceeds `maxshape` in any dimension. Raises an error if the array already has a shape.

Usage:

```
SOMASparseNDArray$tiledb_soma_upgrade_shape(shape)
```

Arguments:

`shape` A vector of integers, of the same length as the array's `ndim`.

Returns: No return value

Method `.write_coordinates()`: Write a COO table to the array

Usage:

```
SOMASparseNDArray$.write_coordinates(values)
```

Arguments:

`values` A data frame or [Arrow::Table](#) with data in COO format; must be named with the dimension and attribute labels of the array

Returns: Invisibly returns `self`

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SOMASparseNDArray$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

SOMASparseNDArrayCreate

Create SOMA Sparse Nd Array

Description

Factory function to create a `SOMASparseNDArray` for writing, (lifecycle: maturing)

Usage

```
SOMASparseNDArrayCreate(
  uri,
  type,
  shape,
  ingest_mode = c("write", "resume"),
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```


Arguments

uri	URI for the TileDB object
type	An Arrow type defining the type of each element in the array.
shape	A vector of integers defining the shape of the array.
ingest_mode	Ingestion mode when creating the TileDB object; choose from: <ul style="list-style-type: none"> • “write”: create a new TileDB object and error if it already exists • “resume”: attempt to create a new TileDB object; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp

SOMASparseNDArrayOpen *Open SOMA Sparse Nd Array*

Description

Factory function to open a SOMASparseNDArray for reading, (lifecycle: maturing)

Usage

```
SOMASparseNDArrayOpen(
  uri,
  mode = "READ",
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

uri	URI for the TileDB object
mode	One of "READ" or "WRITE"
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext
tiledb_timestamp	Optional Datetime (POSIXct) for TileDB timestamp. In READ mode, defaults to the current time. If non-NULL, then all members accessed through the collection object inherit the timestamp.

SOMATileDBContext *SOMA TileDB Context*

Description

Context map for TileDB-backed SOMA objects

Super classes

`tiledbsoma::MappingBase -> tiledbsoma::ScalarMap -> tiledbsoma::SOMAContextBase -> SOMATileDBContext`

Methods

Public methods:

- `SOMATileDBContext$new()`
- `SOMATileDBContext$keys()`
- `SOMATileDBContext$items()`
- `SOMATileDBContext$length()`
- `SOMATileDBContext$get()`
- `SOMATileDBContext$set()`
- `SOMATileDBContext$to_tiledb_context()`
- `SOMATileDBContext$context()`
- `SOMATileDBContext$clone()`

Method `new()`:

Usage:

`SOMATileDBContext$new(config = NULL, cached = TRUE)`

Arguments:

`config` ...

`cached` Force new creation

Returns: An instantiated SOMATileDBContext object

Method `keys()`:

Usage:

`SOMATileDBContext$keys()`

Returns: The keys of the map

Method `items()`:

Usage:

`SOMATileDBContext$items()`

Returns: Return the items of the map as a list

Method length():

Usage:

SOMATileDBContext\$length()

Returns: The number of items in the map

Method get():

Usage:

SOMATileDBContext\$get(key, default = quote(expr =))

Arguments:

key Key to fetch

default Default value to fetch if key is not found; defaults to NULL

Returns: The value of key in the map, or default if key is not found

Method set():

Usage:

SOMATileDBContext\$set(key, value)

Arguments:

key Key to set

value Value to add for key, or NULL to remove the entry for key

Returns: [chainable] Invisibly returns self with value added as key

Method to_tiledb_context():

Usage:

SOMATileDBContext\$to_tiledb_context()

Returns: A `tiledb_ctx` object, dynamically constructed. Most useful for the constructor of this class.

Method context():

Usage:

SOMATileDBContext\$context()

Returns: A `tiledb_ctx` object, which is a stored (and long-lived) result from `to_tiledb_context`.

Method clone(): The objects of this class are cloneable with this method.

Usage:

SOMATileDBContext\$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

soma_context	<i>Create and cache a SOMA Context Object</i>
--------------	---

Description

Create and cache a SOMA Context Object

Usage

```
soma_context(config)
```

Arguments

config	A named character vector with ‘key’ and ‘value’ pairs defining the configuration setting
--------	--

Value

An external pointer object containing a shared pointer instance of SOMAContext

Examples

```
cfgvec <- as.vector(tiledb::tiledb_config()) # TileDB Config in vector form
sctx <- soma_context(cfgvec)
```

SparseReadIter	<i>SparseReadIter</i>
----------------	-----------------------

Description

SparseReadIter is a class that allows for iteration over a reads on [SOMASparseNDArray](#). Iteration chunks are retrieved as 0-based Views [matrixZeroBasedView](#) of [Matrix::sparseMatrix](#).

Super class

```
tiledbsoma::ReadIter -> SparseReadIter
```

Methods**Public methods:**

- [SparseReadIter\\$new\(\)](#)
- [SparseReadIter\\$concat\(\)](#)
- [SparseReadIter\\$clone\(\)](#)

Method new(): Create (lifecycle: maturing)

Usage:

```
SparseReadIter$new(sr, shape, zero_based = FALSE)
```

Arguments:

sr Soma reader pointer

shape Shape of the full matrix

zero_based Logical, if TRUE will make iterator for [Matrix::dgTMatrix-class](#) otherwise [matrixZeroBasedView](#).

Method `concat()`: Concatenate remainder of iterator.

Usage:

```
SparseReadIter$concat()
```

Returns: [matrixZeroBasedView](#) of [Matrix::sparseMatrix](#)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SparseReadIter$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

TableReadIter

*SOMA Read Iterator over Arrow Table***Description**

TableReadIter is a class that allows for iteration over a reads on [SOMASparseNDArray](#) and [SOMADataFrame](#). Iteration chunks are retrieved as [arrow::Table](#)

Super class

[tiledbsoma::ReadIter](#) -> TableReadIter

Methods**Public methods:**

- [TableReadIter\\$concat\(\)](#)
- [TableReadIter\\$clone\(\)](#)

Method `concat()`: Concatenate remainder of iterator.

Usage:

```
TableReadIter$concat()
```

Returns: [arrow::Table](#)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
TableReadIter$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

TileDBObject

*TileDB Object Base Class***Description**

Base class to implement shared functionality across the TileDBArray and TileDBGroup classes. (lifecycle: maturing)

Active bindings

platform_config Platform configuration
 tiledbsoma_ctx SOMATileDBContext
 tiledb_timestamp Time that object was opened at
 uri The URI of the TileDB object.
 .tiledb_timestamp_range Time range for libtiledbsoma

Methods**Public methods:**

- [TileDBObject\\$new\(\)](#)
- [TileDBObject\\$class\(\)](#)
- [TileDBObject\\$is_open\(\)](#)
- [TileDBObject\\$mode\(\)](#)
- [TileDBObject\\$reopen\(\)](#)
- [TileDBObject\\$print\(\)](#)
- [TileDBObject\\$exists\(\)](#)
- [TileDBObject\\$clone\(\)](#)

Method `new()`: Create a new TileDB object. (lifecycle: maturing)

Usage:

```
TileDBObject$new(
  uri,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL,
  internal_use_only = NULL,
  soma_context = NULL
)
```

Arguments:

uri URI for the TileDB object
 platform_config Optional platform configuration
 tiledbsoma_ctx Optional SOMATileDBContext
 tiledb_timestamp Optional Datetime (POSIXct) with TileDB timestamp

`internal_use_only` Character value to signal this is a 'permitted' call, as `new()` is considered internal and should not be called directly.

Method `class()`: Print the name of the R6 class.

Usage:

```
TileDBObject$class()
```

Method `is_open()`: Determine if the object is open for reading or writing

Usage:

```
TileDBObject$is_open()
```

Returns: TRUE if the object is open, otherwise FALSE

Method `mode()`: Get the mode of the object

Usage:

```
TileDBObject$mode()
```

Returns: If the object is closed, returns "CLOSED"; otherwise returns the mode (eg. "READ") of the object

Method `reopen()`: Close and reopen the TileDB object in a new mode

Usage:

```
TileDBObject$reopen(mode, tiledb_timestamp = NULL)
```

Arguments:

`mode` New mode to open the object in; choose from:

- "READ"
- "WRITE"

`tiledb_timestamp` Optional Datetime (POSIXct) with TileDB timestamp

Returns: Invisibly returns `self` opened in mode

Method `print()`: Print-friendly representation of the object.

Usage:

```
TileDBObject$print()
```

Method `exists()`: Check if the object exists. (lifecycle: maturing)

Usage:

```
TileDBObject$exists()
```

Returns: TRUE if the object exists, FALSE otherwise.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
TileDBObject$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

tiledb_soma_stats	<i>TileDB SOMA statistics</i>
-------------------	-------------------------------

Description

These functions expose the TileDB Core functionality for performance measurements and statistics.

Usage

```
tiledb_soma_stats_enable()
tiledb_soma_stats_disable()
tiledb_soma_stats_reset()
tiledb_soma_stats_dump()
tiledb_soma_stats_show()
```

Details

- `tiledb_soma_stats_enable()/tiledb_soma_stats_disable()`: Enable and disable TileDB's internal statistics.
- `tiledb_soma_stats_reset()`: Reset all statistics to 0.
- `tiledb_soma_stats_dump()`: Dump all statistics to a JSON string.
- `tiledb_soma_stats_show()`: Print all statistics to the console.

write_soma	<i>Write a SOMA Object from an R Object</i>
------------	---

Description

Convert R objects to their appropriate SOMA counterpart function and methods can be written for it to provide a high-level $R \rightarrow$ SOMA interface

Usage

```
write_soma(x, uri, ..., platform_config = NULL, tiledb_soma_ctx = NULL)
```

Arguments

<code>x</code>	An object
<code>uri</code>	URI for resulting SOMA object
<code>...</code>	Arguments passed to other methods
<code>platform_config</code>	Optional platform configuration
<code>tiledb_soma_ctx</code>	Optional SOMATileDBContext

Value

The URI to the resulting [SOMAExperiment](#) generated from the data contained in x

Known methods

- [Writing Seurat objects](#)
- [Writing SummarizedExperiment objects](#)
- [Writing SingleCellExperiment objects](#)

write_soma.Seurat	<i>Write a Seurat object to a SOMA</i>
-------------------	--

Description

Write a [Seurat](#) object to a SOMA

Usage

```
## S3 method for class 'Seurat'
write_soma(
  x,
  uri,
  ...,
  ingest_mode = "write",
  platform_config = NULL,
  tiledbsoma_ctx = NULL
)
```

Arguments

x	A Seurat object
uri	URI for resulting SOMA object
...	Arguments passed to other methods
ingest_mode	Ingestion mode when creating the SOMA; choose from: <ul style="list-style-type: none"> • “write”: create a new SOMA and error if it already exists • “resume”: attempt to create a new SOMA; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext

Value

The URI to the resulting [SOMAExperiment](#) generated from the data contained in x

Writing Cell-Level Meta Data

Cell-level meta data is written out as a [data frame](#) called “obs” at the [experiment](#) level

Writing Assays

Seurat Assay objects are written out as individual [measurements](#):

- the “data” matrix is written out a [sparse matrix](#) called “data” within the “X” group
- the “counts” matrix, if not [empty](#), is written out a [sparse matrix](#) called “counts” within the “X” group
- the “scale.data” matrix, if not [empty](#), is written out a [sparse matrix](#) called “scale_data” within the “X” group
- feature-level meta data is written out as a [data frame](#) called “var”

Expression matrices are transposed (cells as rows) prior to writing. All other slots, including results from extended assays (eg. SCTAssay, ChromatinAssay) are lost

Writing DimReducs

Seurat DimReduc objects are written out to the “obsm” and “varm” groups of a [measurement](#):

- cell embeddings are written out as a [sparse matrix](#) in the “obsm” group
- feature loadings, if not [empty](#), are written out as a [sparse matrix](#) in the “varm” groups; loadings are padded with NAs to include all features

Dimensional reduction names are translated to AnnData-style names (eg. “pca” becomes X_pca for embeddings and “PCs” for loadings). All other slots, including projected feature loadings and jackstraw information, are lost

Writing Graphs

Seurat Graph objects are written out as [sparse matrices](#) to the “obs” group of a [measurement](#)

Writing SeuratCommands

Seurat command logs are written out as [data frames](#) to the “seurat_commands” group of a [collection](#)

```
write_soma.SingleCellExperiment
```

Write a [SingleCellExperiment](#) object to a SOMA

Description

Write a [SingleCellExperiment](#) object to a SOMA

Usage

```
## S3 method for class 'SingleCellExperiment'
write_soma(
  x,
  uri,
  ms_name = NULL,
  ...,
  ingest_mode = "write",
  platform_config = NULL,
  tiledbsoma_ctx = NULL
)
```

Arguments

x	An object
uri	URI for resulting SOMA object
ms_name	Name for resulting measurement; defaults to <code>mainExpName(x)</code>
...	Arguments passed to other methods
ingest_mode	Ingestion mode when creating the SOMA; choose from: <ul style="list-style-type: none"> • “write”: create a new SOMA and error if it already exists • “resume”: attempt to create a new SOMA; if it already exists, simply open it for writing
platform_config	Optional platform configuration
tiledbsoma_ctx	Optional SOMATileDBContext

Value

The URI to the resulting [SOMASingleCellExperiment](#) generated from the data contained in x

Writing Reduced Dimensions

Reduced dimensions are written out as [sparse matrices](#) within the obsm group of [measurement](#) names ms_name

Writing Column Pairs

Column-wise relationship matrices are written out as [sparse matrices](#) within the obsp group of [measurement](#) names ms_name

Writing Row Pairs

Row-wise relationship matrices are written out as [sparse matrices](#) within the varp group of [measurement](#) names ms_name

Writing colData

colData is written out as a [data frame](#) called “obs” at the [experiment](#) level

Writing Assay Matrices

Each [assay matrix](#) is written out as a [sparse matrix](#) within the X group of [measurement](#) names `ms_name`. Names for assay matrices within X are taken from the [assay names](#). Assay matrices are transposed (samples as rows) prior to writing

Writing rowData

`rowData` is written out as a [data frame](#) called “var” at the [measurement](#) level

```
write_soma.SummarizedExperiment
```

Write a [SummarizedExperiment](#) object to a SOMA

Description

Write a [SummarizedExperiment](#) object to a SOMA

Usage

```
## S3 method for class 'SummarizedExperiment'
write_soma(
  x,
  uri,
  ms_name,
  ...,
  ingest_mode = "write",
  platform_config = NULL,
  tiledbsoma_ctx = NULL
)
```

Arguments

<code>x</code>	An object
<code>uri</code>	URI for resulting SOMA object
<code>ms_name</code>	Name for resulting measurement
<code>...</code>	Arguments passed to other methods
<code>ingest_mode</code>	Ingestion mode when creating the SOMA; choose from: <ul style="list-style-type: none"> “write”: create a new SOMA and error if it already exists “resume”: attempt to create a new SOMA; if it already exists, simply open it for writing
<code>platform_config</code>	Optional platform configuration
<code>tiledbsoma_ctx</code>	Optional SOMATileDBContext

Value

The URI to the resulting [SOMAEperiment](#) generated from the data contained in `x`

Writing colData

`colData` is written out as a [data frame](#) called “obs” at the [experiment](#) level

Writing Assay Matrices

Each [assay matrix](#) is written out as a [sparse matrix](#) within the `X` group of [measurement](#) names `ms_name`. Names for assay matrices within `X` are taken from the [assay names](#). Assay matrices are transposed (samples as rows) prior to writing

Writing rowData

`rowData` is written out as a [data frame](#) called “var” at the [measurement](#) level

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