Package: tiledbsoma (via r-universe)

August 29, 2024

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 1.8.1

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

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

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Encoding UTF-8

Depends R (>= 4.0.0)

Imports R6, methods, Matrix, stats, bit64, tiledb (>= 0.24.0), tiledb (<= 0.24.99), arrow, utils, fs, glue, urltools, Rcpp, data.table, spdl, rlang, tools, tibble

LinkingTo Rcpp, RcppSpdlog, RcppInt64

Additional_repositories https://ghrr.github.io/drat

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Suggests rmarkdown, knitr, withr, testthat (>= 3.0.0), pbmc3k.tiledb, pbmc3k.sce, SeuratObject (>= 4.1.0), datasets, SingleCellExperiment (>= 1.20.0), SummarizedExperiment (>= 1.28.0), S4Vectors, jsonlite

VignetteBuilder knitr

Config/testthat/edition 2

OS_type unix

SystemRequirements cmake, git

Repository https://mojaveazure.r-universe.dev

RemoteUrl https://github.com/single-cell-data/TileDB-SOMA

RemoteRef ph/test/doublepin

RemoteSha 9f8ed9555a0dec364887dc5d4fe54931aa47728d

Contents

ConfigList *A Configuration List*

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

tiledbsoma::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.

`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

`name`	The name of the dataset.
`dir`	The directory where the dataset will be extracted to (default: `tempdir()`).
`tiledbsoma_ctx`	Optional TileDB 'Context' object, defaults to `NULL`

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")
```

`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 indeces.

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: experimental)

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 linkmatrixZeroBasedView and another linkmatrixZeroBasedView.

Usage:

```
matrixZeroBasedView$sum(x)
```

Arguments:

`x` the linkmatrixZeroBasedView 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 "paramters" 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 `platfomr`, `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.

show_package_versions *Display package versions*

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: experimental)

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: experimental)

Super classes

tiledbsoma::TileDBObject -> 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: experimental)

Usage

```
SOMACollectionCreate(
  uri,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

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

---

SOMACollectionOpen *Open SOMA Collection*

Description

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

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: experimental)

Super classes

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

Methods

Public methods:

- SOMADataFrame$create()
- SOMADataFrame$write()
- SOMADataFrame$read()
- SOMADataFrame$update()
- SOMADataFrame$clone()

Method `create()`**:** Create (lifecycle: experimental)

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: experimental)

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: experimental) 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 TableReadIter

Method `update()`**:** Update (lifecycle: experimental)

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 `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: experimental)

Usage

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

Arguments

`uri`	URI for the TileDB object
`schema`	schema Arrow schema argument passed on to DataFrame$create()
`index_column_names`	Index column names passed on to DataFrame$create()
`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: experimental)

Usage

```
SOMADataFrameOpen(
  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

SOMADenseNDArray *SOMADenseNDArray*

Description

SOMADenseNDArray is a dense, N-dimensional array of primitive type, with offset (zero-based) int64 integer indexing on each dimension with domain [0, 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: experimental)

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: experimental)

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: experimental)

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: experimental)

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: experimental)

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: experimental)

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

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: experimental)

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:

- SOMAExperiment$axis_query()
- SOMAExperiment$update_obs()
- SOMAExperiment$update_var()
- SOMAExperiment$clone()

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

Usage:

```
SOMAExperiment$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 SOMAExperimentAxisQuery object.

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

Usage:

```
SOMAExperiment$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:

```
SOMAExperiment$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:

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

Arguments:

`deep` Whether to make a deep clone.

`SOMAExperimentAxisQuery`

`SOMAExperiment` *Axis Query*

Description

Perform an axis-based query against a SOMAExperiment.

`SOMAExperimentAxisQuery` allows easy selection and extraction of data from a single SOMAMeasurement in a SOMAExperiment, by `obs`/`var` (axis) coordinates and/or value filter. The primary use for this class is slicing SOMAExperiment `X` layers by `obs` or `var` value and/or coordinates. (lifecycle: experimental)

X Layer Support:

Slicing on SOMASparseNDArray X matrices is supported; slicing on SOMADenseNDArray is not supported at this time.

Result Size:

SOMAExperimentAxisQuery 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 SOMAExperiment 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:

- SOMAExperimentAxisQuery$new()
- SOMAExperimentAxisQuery$obs()
- SOMAExperimentAxisQuery$var()
- SOMAExperimentAxisQuery$obs_joinids()
- SOMAExperimentAxisQuery$var_joinids()
- SOMAExperimentAxisQuery$X()
- 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 linkSOMASparseNDArrayRead

Usage:

```
SOMAExperimentAxisQuery$X(layer_name)
```

Arguments:

`layer_name` The name of the layer to retrieve.

Method `read()`**:** Reads the entire query result as a list of `arrow::Table`s. 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:

```
SOMAExperimentAxisQuery$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
)
```

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 `Graph`s; by default, loads all graphs

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
)
```

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

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
)
```

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

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: experimental)

Usage

```
SOMAExperimentCreate(
  uri,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

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

---

SOMAExperimentOpen *Open SOMA Experiment*

Description

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

Usage

```
SOMAExperimentOpen(
  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.

SOMAMeasurement *SOMA Measurement*

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: experimental)

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: experimental)

Usage

```
SOMAMeasurementCreate(
  uri,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL
)
```

Arguments

`uri`	URI for the TileDB object
`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: experimental)

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: experimental)

Usage

```
SOMAOpen(
  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) 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 *SOMASparseNDArray*

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 an 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: experimental)

Super classes

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

Methods

Public methods:

- SOMASparseNDArray$read()
- SOMASparseNDArray$write()
- SOMASparseNDArray$nnz()
- SOMASparseNDArray$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: experimental)

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`.

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

Usage:

```
SOMASparseNDArray$nnz()
```

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

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: experimental)

Usage

```
SOMASparseNDArrayCreate(
  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

---

SOMASparseNDArrayOpen *Open SOMA Sparse Nd Array*

Description

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

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

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.

SparseReadIter *SparseReadIter*

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: experimental)

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: experimental)

Active bindings

platform_config Platform configuration

tiledbsoma_ctx SOMATileDBContext

uri The URI of the TileDB object.

Methods

Public methods:

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

Usage:

```
TileDBObject$new(
  uri,
  platform_config = NULL,
  tiledbsoma_ctx = NULL,
  tiledb_timestamp = NULL,
  internal_use_only = 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 `print()`**:** Print-friendly representation of the object.

Usage:

```
TileDBObject$print()
```

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

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.

`tiledbsoma_stats` *TileDB SOMA statistics*

Description

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

Usage

```
tiledbsoma_stats_enable()

tiledbsoma_stats_disable()

tiledbsoma_stats_reset()

tiledbsoma_stats_dump()

tiledbsoma_stats_show()
```

Details

- `tiledbsoma_stats_enable()`/`tiledbsoma_stats_disable()`: Enable and disable TileDB's internal statistics.
- `tiledbsoma_stats_reset()`: Reset all statistics to 0.
- `tiledbsoma_stats_dump()`: Dump all statistics to a JSON string.
- `tiledbsoma_stats_show()`: Print all statistics to the console.

write_soma *Write a SOMA Object from an R Object*

Description

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

Usage

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

Arguments

x	An object
uri	URI for resulting SOMA object
...	Arguments passed to other methods
platform_config	Optional platform configuration
tiledbsoma_ctx	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 *Write a Seurat object to a SOMA*

Description

Write a Seurat object to a SOMA

Usage

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

Arguments

x	A Seurat object
uri	URI for resulting SOMA object
...	Arguments passed to other methods
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 "obsp" 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,
  ...,
  platform_config = NULL,
  tiledbsoma_ctx = NULL
)
```

Arguments

`x`	An object
`uri`	URI for resulting SOMA object
`ms_name`	Name for resulting measurement; defaults to `mainExpName(x)`
`...`	Arguments passed to other methods
`platform_config`	Optional platform configuration
`tiledbsoma_ctx`	Optional `SOMATileDBContext`

Value

The URI to the resulting `SOMAExperiment` 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, ..., platform_config = NULL, tiledbsoma_ctx = NULL)
```

Arguments

`x`	An object
`uri`	URI for resulting SOMA object
`ms_name`	Name for resulting measurement
`...`	Arguments passed to other methods
`platform_config`	Optional platform configuration
`tiledbsoma_ctx`	Optional `SOMATileDBContext`

Value

The URI to the resulting `SOMAExperiment` 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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