Package: nanoarrow (via r-universe)

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Title Interface to the 'nanoarrow' 'C' Library

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Description Provides an 'R' interface to the 'nanoarrow' 'C' library and the 'Apache Arrow' application binary interface. Functions to import and export 'ArrowArray', 'ArrowSchema', and 'ArrowArrayStream' 'C' structures to and from 'R' objects are provided alongside helpers to facilitate zero-copy data transfer among 'R' bindings to libraries implementing the 'Arrow' 'C' data interface.

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`array_stream_set_finalizer` *Register an array stream finalizer*

Description

In some cases, R functions that return a nanoarrow_array_stream may require that the scope of some other object outlive that of the array stream. If there is a need for that object to be released deterministically (e.g., to close open files), you can register a function to run after the stream's release callback is invoked from the R thread. Note that this finalizer will **not** be run if the stream's release callback is invoked from a **non**-R thread. In this case, the finalizer and its chain of environments will be garbage-collected when `nanoarrow:::preserved_empty()` is run.

Usage

```
array_stream_set_finalizer(array_stream, finalizer)
```

Arguments

`array_stream`	A nanoarrow_array_stream
`finalizer`	A function that will be called with zero arguments.

Value

A newly allocated `array_stream` whose release callback will call the supplied finalizer.

Examples

```
stream <- array_stream_set_finalizer(
  basic_array_stream(list(1:5)),
  function() message("All done!")
)
stream$release()
```

`as_nanoarrow_array` *Convert an object to a nanoarrow array*

Description

In nanoarrow an 'array' refers to the `struct ArrowArray` definition in the Arrow C data interface. At the R level, we attach a schema such that functionally the nanoarrow_array class can be used in a similar way as an `arrow::Array`. Note that in nanoarrow an `arrow::RecordBatch` and a non-nullable `arrow::StructArray` are represented identically.

Usage

```
as_nanoarrow_array(x, ..., schema = NULL)
```

Arguments

`x`	An object to convert to a array
`...`	Passed to S3 methods
`schema`	An optional schema used to enforce conversion to a particular type. Defaults to `infer_nanoarrow_schema()`.

Value

An object of class 'nanoarrow_array'

Examples

```
(array <- as_nanoarrow_array(1:5))
as.vector(array)

(array <- as_nanoarrow_array(data.frame(x = 1:5)))
as.data.frame(array)
```

`as_nanoarrow_array_stream` *Convert an object to a nanoarrow array_stream*

Description

In nanoarrow, an 'array stream' corresponds to the `struct ArrowArrayStream` as defined in the Arrow C Stream interface. This object is used to represent a stream of arrays with a common schema. This is similar to an arrow::RecordBatchReader except it can be used to represent a stream of any type (not just record batches). Note that a stream of record batches and a stream of non-nullable struct arrays are represented identically. Also note that array streams are mutable objects and are passed by reference and not by value.

Usage

```
as_nanoarrow_array_stream(x, ..., schema = NULL)
```

Arguments

`x`	An object to convert to a array_stream
`...`	Passed to S3 methods
`schema`	An optional schema used to enforce conversion to a particular type. Defaults to `infer_nanoarrow_schema()`.

Value

An object of class 'nanoarrow_array_stream'

Examples

```
(stream <- as_nanoarrow_array_stream(data.frame(x = 1:5)))
stream$get_schema()
stream$get_next()

# The last batch is returned as NULL
stream$get_next()

# Release the stream
stream$release()
```

as_nanoarrow_buffer *Convert an object to a nanoarrow buffer*

Description

Convert an object to a nanoarrow buffer

Usage

```
as_nanoarrow_buffer(x, ...)
```

Arguments

x	An object to convert to a buffer
...	Passed to S3 methods

Value

An object of class 'nanoarrow_buffer'

Examples

```
array <- as_nanoarrow_array(c(NA, 1:4))
array$buffers
as.raw(array$buffers[[1]])
as.raw(array$buffers[[2]])
convert_buffer(array$buffers[[1]])
convert_buffer(array$buffers[[2]])
```

as_nanoarrow_schema *Convert an object to a nanoarrow schema*

Description

In nanoarrow a 'schema' refers to a `struct ArrowSchema` as defined in the Arrow C Data interface. This data structure can be used to represent an `arrow::schema()`, an `arrow::field()`, or an `arrow::DataType`. Note that in nanoarrow, an `arrow::schema()` and a non-nullable `arrow::struct()` are represented identically.

Usage

```
as_nanoarrow_schema(x, ...)

infer_nanoarrow_schema(x, ...)

nanoarrow_schema_parse(x, recursive = FALSE)

nanoarrow_schema_modify(x, new_values, validate = TRUE)
```

Arguments

x	An object to convert to a schema
...	Passed to S3 methods
recursive	Use TRUE to include a children member when parsing schemas.
new_values	New schema component to assign
validate	Use FALSE to skip schema validation

Value

An object of class 'nanoarrow_schema'

Examples

```
infer_nanoarrow_schema(integer())
infer_nanoarrow_schema(data.frame(x = integer()))
```

---

as_nanoarrow_schema.python.builtin.object

Python integration via reticulate

Description

These functions enable Python wrapper objects created via reticulate to be used with any function that uses `as_nanoarrow_array()` or `as_nanoarrow_array_stream()` to accept generic "arrow-able" input. Implementations for `reticulate::py_to_r()` and `reticulate::r_to_py()` are also included such that nanoarrow's array/schema/array stream objects can be passed as arguments to Python functions that would otherwise accept an object implementing the Arrow PyCapsule protocol.

Usage

```
## S3 method for class 'python.builtin.object'
as_nanoarrow_schema(x, ...)

## S3 method for class 'python.builtin.object'
as_nanoarrow_array(x, ..., schema = NULL)

## S3 method for class 'python.builtin.object'
as_nanoarrow_array_stream(x, ..., schema = NULL)

test_reticulate_with_nanoarrow()
```

Arguments

x	An Python object to convert
...	Unused
schema	A requested schema, which may or may not be honoured depending on the capabilities of the producer

Details

This implementation uses the Arrow PyCapsule protocol to interpret an arbitrary Python object as an Arrow array/schema/array stream and produces Python objects that implement this protocol. This is currently implemented using the nanoarrow Python package which provides similar primitives for facilitating interchange in Python.

Value

- `as_nanoarrow_schema()` returns an object of class nanoarrow_schema
- `as_nanoarrow_array()` returns an object of class nanoarrow_array
- `as_nanoarrow_array_stream()` returns an object of class nanoarrow_array_stream.

Examples

```
library(reticulate)

py_require("nanoarrow")

na <- import("nanoarrow", convert = FALSE)
python_arrayish_thing <- na$Array(1:3, na_int32())
as_nanoarrow_array(python_arrayish_thing)

r_to_py(as_nanoarrow_array(1:3))
```

`as_nanoarrow_vctr` *Experimental Arrow encoded arrays as R vectors*

Description

This experimental vctr class allows zero or more Arrow arrays to present as an R vector without converting them. This is useful for arrays with types that do not have a non-lossy R equivalent, and helps provide an intermediary object type where the default conversion is prohibitively expensive (e.g., a nested list of data frames). These objects will not survive many vctr transformations; however, they can be sliced without copying the underlying arrays.

Usage

```
as_nanoarrow_vctr(x, ..., schema = NULL, subclass = character())

nanoarrow_vctr(schema = NULL, subclass = character())
```

Arguments

`x`	An object that works with `as_nanoarrow_array_stream()`.
`...`	Passed to `as_nanoarrow_array_stream()`
`schema`	An optional `schema`
`subclass`	An optional subclass of nanoarrow_vctr to prepend to the final class name.

Details

The nanoarrow_vctr is currently implemented similarly to `factor()`: its storage type is an `integer()` that is a sequence along the total length of the vctr and there are attributes that are required to resolve these indices to an array + offset. Sequences typically have a very compact representation in recent versions of R such that this has a cheap storage footprint even for large arrays. The attributes are currently:

- `schema`: The nanoarrow_schema shared by each chunk.
- `chunks`: A `list()` of `nanoarrow_array`.
- `offsets`: An `integer()` vector beginning with `0` and followed by the cumulative length of each chunk. This allows the chunk index + offset to be resolved from a logical index with `log(n)` complexity.

This implementation is preliminary and may change; however, the result of `as_nanoarrow_array_stream(some_vctr[begi` should remain stable.

Value

A vctr of class 'nanoarrow_vctr'

Examples

```
array <- as_nanoarrow_array(1:5)
as_nanoarrow_vctr(array)
```

`basic_array_stream` *Create ArrayStreams from batches*

Description

Create ArrayStreams from batches

Usage

```
basic_array_stream(batches, schema = NULL, validate = TRUE)
```

Arguments

`batches`	A `list()` of nanoarrow_array objects or objects that can be coerced via `as_nanoarrow_array()`.
`schema`	A nanoarrow_schema or `NULL` to guess based on the first schema.
`validate`	Use `FALSE` to skip the validation step (i.e., if you know that the arrays are valid).

Value

An nanoarrow_array_stream

Examples

```
(stream <- basic_array_stream(list(data.frame(a = 1, b = 2))))
as.data.frame(stream$get_next())
stream$get_next()
```

`convert_array` *Convert an Array into an R vector*

Description

Converts `array` to the type specified by `to`. This is a low-level interface; most users should use `as.data.frame()` or `as.vector()` unless finer-grained control is needed over the conversion. This function is an S3 generic dispatching on `to`: developers may implement their own S3 methods for custom vector types.

Usage

```
convert_array(array, to = NULL, ...)
```

Arguments

array	A nanoarrow_array.
to	A target prototype object describing the type to which array should be converted, or NULL to use the default conversion as returned by infer_nanoarrow_ptype(). Alternatively, a function can be passed to perform an alternative calculation of the default ptype as a function of array and the default inference of the prototype.
...	Passed to S3 methods

Details

Note that unregistered extension types will by default issue a warning. Use options(nanoarrow.warn_unregistered_exte = FALSE) to disable this behaviour.

Conversions are implemented for the following R vector types:

- logical(): Any numeric type can be converted to logical() in addition to the bool type. For numeric types, any non-zero value is considered TRUE.
- integer(): Any numeric type can be converted to integer(); however, a warning will be signaled if the any value is outside the range of the 32-bit integer.
- double(): Any numeric type can be converted to double(). This conversion currently does not warn for values that may not roundtrip through a floating-point double (e.g., very large uint64 and int64 values).
- character(): String and large string types can be converted to character(). The conversion does not check for valid UTF-8: if you need finer-grained control over encodings, use to = blob::blob().
- base::factor(): Dictionary-encoded arrays of strings can be converted to factor(); however, this must be specified explicitly (i.e., convert_array(array, factor())) because arrays arriving in chunks can have dictionaries that contain different levels. Use convert_array(array, factor(levels = c(...))) to materialize an array into a vector with known levels.
- Date: Only the date32 type can be converted to an R Date vector.
- hms::hms(): Time32 and time64 types can be converted to hms::hms().
- difftime(): Time32, time64, and duration types can be converted to R difftime() vectors. The value is converted to match the units() attribute of to.
- blob::blob(): String, large string, binary, and large binary types can be converted to blob::blob().
- vctrs::list_of(): List, large list, and fixed-size list types can be converted to vctrs::list_of().
- base::matrix(): Fixed-size list types can be converted to matrix(ptype, ncol = fixed_size).
- data.frame(): Struct types can be converted to data.frame().
- vctrs::unspecified(): Any type can be converted to vctrs::unspecified(); however, a warning will be raised if any non-null values are encountered.

In addition to the above conversions, a null array may be converted to any target prototype except data.frame(). Extension arrays are currently converted as their storage type.

Value

An R vector of type to.

Examples

```
array <- as_nanoarrow_array(data.frame(x = 1:5))
str(convert_array(array))
str(convert_array(array, to = data.frame(x = double())))
```

---

convert_array_stream *Convert an Array Stream into an R vector*

Description

Converts array_stream to the type specified by to. This is a low-level interface; most users should use as.data.frame() or as.vector() unless finer-grained control is needed over the conversion. See convert_array() for details of the conversion process; see infer_nanoarrow_ptype() for default inferences of to.

Usage

```
convert_array_stream(array_stream, to = NULL, size = NULL, n = Inf)

collect_array_stream(array_stream, n = Inf, schema = NULL, validate = TRUE)
```

Arguments

array_stream	A nanoarrow_array_stream.
to	A target prototype object describing the type to which array should be converted, or NULL to use the default conversion as returned by infer_nanoarrow_ptype(). Alternatively, a function can be passed to perform an alternative calculation of the default ptype as a function of array and the default inference of the prototype.
size	The exact size of the output, if known. If specified, slightly more efficient implementation may be used to collect the output.
n	The maximum number of batches to pull from the array stream.
schema	A nanoarrow_schema or NULL to guess based on the first schema.
validate	Use FALSE to skip the validation step (i.e., if you know that the arrays are valid).

Value

- convert_array_stream(): An R vector of type to.
- collect_array_stream(): A list() of nanoarrow_array

Examples

```
stream <- as_nanoarrow_array_stream(data.frame(x = 1:5))
str(convert_array_stream(stream))
str(convert_array_stream(stream, to = data.frame(x = double())))

stream <- as_nanoarrow_array_stream(data.frame(x = 1:5))
collect_array_stream(stream)
```

`example_ipc_stream` *Example Arrow IPC Data*

Description

An example stream that can be used for testing or examples.

Usage

```
example_ipc_stream(compression = c("none", "zstd", "lz4"))
```

Arguments

`compression`	One of "none", "zstd", or "lz4"

Value

A raw vector that can be passed to `read_nanoarrow()`

Examples

```
as.data.frame(read_nanoarrow(example_ipc_stream()))
```

`function_array_stream` *Create an array stream from an R function*

Description

The function is called once for each requested array. It should return an object coercible by `as_nanoarrow_array()`, or `NULL` to indicate end of stream. The schema is required because it is available before the first array is requested. Neither construction nor schema access calls `fun`. After `NULL` or an error is returned, the callback is not called again.

Usage

```
function_array_stream(fun, schema, validate = TRUE)
```

Arguments

fun	A function called with no arguments to produce each array.
schema	A schema coercible by as_nanoarrow_schema(), used to coerce and validate each result.
validate	A single TRUE or FALSE. Use FALSE to skip validation within the callback. The stream's get_next() method can validate the returned array independently.

Details

Errors and interrupts raised by fun are converted to stream errors. Evaluation is also isolated in a top-level R context so other non-local exits (for example, invoking an abort restart) cannot escape through the C stream interface. Calling handlers in the caller are therefore not applied to callback evaluation. The callback is evaluated only on R's main thread. Warnings are handled in this isolated context, unless handled within fun. fun must not release the stream (or call its methods) while it is being evaluated. The stream retains fun until it is released; explicitly release streams when fun or its environment refers to the stream itself.

Value

An nanoarrow_array_stream

Examples

```
i <- 0L
stream <- function_array_stream(
  function() {
    i <<- i + 1L
    if (i > 2L) NULL else mtcars[i, , drop = FALSE]
  },
  infer_nanoarrow_schema(mtcars)
)
as.data.frame(stream$get_next())
as.data.frame(stream$get_next())
stream$get_next()
stream$release()
```

---

infer_nanoarrow_ptype *Infer an R vector prototype*

Description

Resolves the default to value to use in convert_array() and convert_array_stream(). The default conversions are:

Usage

```
infer_nanoarrow_ptype(x)
```

Arguments

x	A nanoarrow_schema, nanoarrow_array, or nanoarrow_array_stream.

Details

- null to `vctrs::unspecified()`
- boolean to `logical()`
- int8, uint8, int16, uint16, and int13 to `integer()`
- uint32, int64, uint64, float, and double to `double()`
- string and large string to `character()`
- struct to `data.frame()`
- binary and large binary to `blob::blob()`
- list, large_list, and fixed_size_list to `vctrs::list_of()`
- time32 and time64 to `hms::hms()`
- duration to `difftime()`
- date32 to `as.Date()`
- timestamp to `as.POSIXct()`

Additional conversions are possible by specifying an explicit value for `to`. For details of each conversion, see `convert_array()`.

Value

An R vector of zero size describing the target into which the array should be materialized.

Examples

```
infer_nanoarrow_ptype(as_nanoarrow_array(1:10))
```

---

infer_nanoarrow_ptype_extension

Implement Arrow extension types

Description

Implement Arrow extension types

Usage

```
infer_nanoarrow_ptype_extension(
  extension_spec,
  x,
  ...,
  warn_unregistered = TRUE
)

convert_array_extension(
  extension_spec,
  array,
  to,
  ...,
  warn_unregistered = TRUE
)

as_nanoarrow_array_extension(extension_spec, x, ..., schema = NULL)
```

Arguments

`extension_spec`	An extension specification inheriting from 'nanoarrow_extension_spec'.
`x`, `array`, `to`, `schema`, `...`	Passed from `infer_nanoarrow_ptype()`, `convert_array()`, `as_nanoarrow_array()`, and/or `as_nanoarrow_array_stream()`.
`warn_unregistered`	Use `FALSE` to infer/convert based on the storage type without a warning.

Value

- `infer_nanoarrow_ptype_extension()`: The R vector prototype to be used as the default conversion target.
- `convert_array_extension()`: An R vector of type `to`.
- `as_nanoarrow_array_extension()`: A nanoarrow_array of type `schema`.

---

na_type *Create type objects*

Description

In nanoarrow, types, fields, and schemas are all represented by a nanoarrow_schema. These functions are convenience constructors to create these objects in a readable way. Use `na_type()` to construct types based on the constructor name, which is also the name that prints/is returned by `nanoarrow_schema_parse()`.

Usage

```
na_type(
  type_name,
  byte_width = NULL,
  unit = NULL,
  timezone = NULL,
  precision = NULL,
  scale = NULL,
  column_types = NULL,
  item_type = NULL,
  key_type = NULL,
  value_type = NULL,
  index_type = NULL,
  ordered = NULL,
  list_size = NULL,
  keys_sorted = NULL,
  storage_type = NULL,
  extension_name = NULL,
  extension_metadata = NULL,
  nullable = NULL
)

na_na(nullable = TRUE)

na_bool(nullable = TRUE)

na_int8(nullable = TRUE)

na_uint8(nullable = TRUE)

na_int16(nullable = TRUE)

na_uint16(nullable = TRUE)

na_int32(nullable = TRUE)

na_uint32(nullable = TRUE)

na_int64(nullable = TRUE)

na_uint64(nullable = TRUE)

na_half_float(nullable = TRUE)

na_float(nullable = TRUE)

na_double(nullable = TRUE)
```

```
na_string(nullable = TRUE)

na_large_string(nullable = TRUE)

na_string_view(nullable = TRUE)

na_binary(nullable = TRUE)

na_large_binary(nullable = TRUE)

na_fixed_size_binary(byte_width, nullable = TRUE)

na_binary_view(nullable = TRUE)

na_date32(nullable = TRUE)

na_date64(nullable = TRUE)

na_time32(unit = c("ms", "s"), nullable = TRUE)

na_time64(unit = c("us", "ns"), nullable = TRUE)

na_duration(unit = c("ms", "s", "us", "ns"), nullable = TRUE)

na_interval_months(nullable = TRUE)

na_interval_day_time(nullable = TRUE)

na_interval_month_day_nano(nullable = TRUE)

na_timestamp(unit = c("us", "ns", "s", "ms"), timezone = "", nullable = TRUE)

na_decimal32(precision, scale, nullable = TRUE)

na_decimal64(precision, scale, nullable = TRUE)

na_decimal128(precision, scale, nullable = TRUE)

na_decimal256(precision, scale, nullable = TRUE)

na_struct(column_types = list(), nullable = FALSE)

na_sparse_union(column_types = list())

na_dense_union(column_types = list())

na_list(item_type, nullable = TRUE)
```

```
na_large_list(item_type, nullable = TRUE)

na_list_view(item_type, nullable = TRUE)

na_large_list_view(item_type, nullable = TRUE)

na_fixed_size_list(item_type, list_size, nullable = TRUE)

na_map(key_type, item_type, keys_sorted = FALSE, nullable = TRUE)

na_dictionary(value_type, index_type = na_int32(), ordered = FALSE)

na_extension(storage_type, extension_name, extension_metadata = "")
```

Arguments

type_name	The name of the type (e.g., "int32"). This form of the constructor is useful for writing tests that loop over many types.
byte_width	For na_fixed_size_binary(), the number of bytes occupied by each item.
unit	One of 's' (seconds), 'ms' (milliseconds), 'us' (microseconds), or 'ns' (nanoseconds).
timezone	A string representing a timezone name. The empty string "" represents a naive point in time (i.e., one that has no associated timezone).
precision	The total number of digits representable by the decimal type
scale	The number of digits after the decimal point in a decimal type
column_types	A list() of nanoarrow_schemas.
item_type	For na_list(), na_large_list(), na_fixed_size_list(), and na_map(), the nanoarrow_schema representing the item type.
key_type	The nanoarrow_schema representing the na_map() key type.
value_type	The nanoarrow_schema representing the na_dictionary() or na_map() value type.
index_type	The nanoarrow_schema representing the na_dictionary() index type.
ordered	Use TRUE to assert that the order of values in the dictionary are meaningful.
list_size	The number of elements in each item in a na_fixed_size_list().
keys_sorted	Use TRUE to assert that keys are sorted.
storage_type	For na_extension(), the underlying value type.
extension_name	For na_extension(), the extension name. This is typically namespaced separated by dots (e.g., nanoarrow.r.vctrs).
extension_metadata	A string or raw vector defining extension metadata. Most Arrow extension types define extension metadata as a JSON object.
nullable	Use FALSE to assert that this field cannot contain null values.

Value

A nanoarrow_schema

Examples

```
na_int32()
na_struct(list(col1 = na_int32()))
```

---

na_vctrs *Vctrs extension type*

Description

The Arrow format provides a rich type system that can handle most R vector types; however, many R vector types do not roundtrip perfectly through Arrow memory. The vctrs extension type uses `vctrs::vec_data()`, `vctrs::vec_restore()`, and `vctrs::vec_ptype()` in calls to `as_nanoarrow_array()` and `convert_array()` to ensure roundtrip fidelity.

Usage

```
na_vctrs(ptype, storage_type = NULL)
```

Arguments

ptype	A vctrs prototype as returned by `vctrs::vec_ptype()`. The prototype can be of arbitrary size, but a zero-size vector is sufficient here.
storage_type	For `na_extension()`, the underlying value type.

Value

A nanoarrow_schema.

Examples

```
vctr <- as.POSIXlt("2000-01-02 03:45", tz = "UTC")
array <- as_nanoarrow_array(vctr, schema = na_vctrs(vctr))
infer_nanoarrow_ptype(array)
convert_array(array)
```

`nanoarrow_array_init` *Modify nanoarrow arrays*

Description

Create a new array or from an existing array, modify one or more parameters. When importing an array from elsewhere, `nanoarrow_array_set_schema()` is useful to attach the data type information to the array (without this information there is little that nanoarrow can do with the array since its content cannot be otherwise interpreted). `nanoarrow_array_modify()` can create a shallow copy and modify various parameters to create a new array, including setting children and buffers recursively. These functions power the `$<-` operator, which can modify one parameter at a time.

Usage

```
nanoarrow_array_init(schema)

nanoarrow_array_set_schema(array, schema, validate = TRUE)

nanoarrow_array_modify(array, new_values, validate = TRUE)
```

Arguments

`schema`	A nanoarrow_schema to attach to this `array`.
`array`	A nanoarrow_array.
`validate`	Use `FALSE` to skip validation. Skipping validation may result in creating an array that will crash R.
`new_values`	A named `list()` of values to replace.

Value

- `nanoarrow_array_init()` returns a possibly invalid but initialized array with a given `schema`.
- `nanoarrow_array_set_schema()` returns `array`, invisibly. Note that `array` is modified in place by reference.
- `nanoarrow_array_modify()` returns a shallow copy of `array` with the modified parameters such that the original array remains valid.

Examples

```
nanoarrow_array_init(na_string())

# Modify an array using $ and <-
array <- as_nanoarrow_array(1:5)
array$length <- 4
as.vector(array)

# Modify potentially more than one component at a time
```

```
array <- as_nanoarrow_array(1:5)
as.vector(nanoarrow_array_modify(array, list(length = 4)))

# Attach a schema to an array
array <- as_nanoarrow_array(-1L)
nanoarrow_array_set_schema(array, na_uint32())
as.vector(array)
```

`nanoarrow_buffer_init` *Create and modify nanoarrow buffers*

Description

Create and modify nanoarrow buffers

Usage

```
nanoarrow_buffer_init()

nanoarrow_buffer_append(buffer, new_buffer)

convert_buffer(buffer, to = NULL)
```

Arguments

`buffer`, `new_buffer`	nanoarrow_buffers.
`to`	A target prototype object describing the type to which `array` should be converted, or `NULL` to use the default conversion as returned by `infer_nanoarrow_ptype()`. Alternatively, a function can be passed to perform an alternative calculation of the default ptype as a function of `array` and the default inference of the prototype.

Value

- `nanoarrow_buffer_init()`: An object of class 'nanoarrow_buffer'
- `nanoarrow_buffer_append()`: Returns `buffer`, invisibly. Note that `buffer` is modified in place by reference.

Examples

```
buffer <- nanoarrow_buffer_init()
nanoarrow_buffer_append(buffer, 1:5)

array <- nanoarrow_array_modify(
  nanoarrow_array_init(na_int32()),
  list(length = 5, buffers = list(NULL, buffer))
```

```
)
as.vector(array)
```

`nanoarrow_extension_array` *Create Arrow extension arrays*

Description

Create Arrow extension arrays

Usage

```
nanoarrow_extension_array(
  storage_array,
  extension_name,
  extension_metadata = NULL
)
```

Arguments

`storage_array`	A nanoarrow_array.
`extension_name`	For `na_extension()`, the extension name. This is typically namespaced separated by dots (e.g., nanoarrow.r.vctrs).
`extension_metadata`	A string or raw vector defining extension metadata. Most Arrow extension types define extension metadata as a JSON object.

Value

A nanoarrow_array with attached extension schema.

Examples

```
nanoarrow_extension_array(1:10, "some_ext", '{"key": "value"}')
```

nanoarrow_extension_spec *Register Arrow extension types*

Description

Register Arrow extension types

Usage

```
nanoarrow_extension_spec(data = list(), subclass = character())

register_nanoarrow_extension(extension_name, extension_spec)

unregister_nanoarrow_extension(extension_name)

resolve_nanoarrow_extension(extension_name)
```

Arguments

data	Optional data to include in the extension type specification
subclass	A subclass for the extension type specification. Extension methods will dispatch on this object.
extension_name	An Arrow extension type name (e.g., nanoarrow.r.vctrs)
extension_spec	An extension specification inheriting from 'nanoarrow_extension_spec'.

Value

- `nanoarrow_extension_spec()` returns an object of class 'nanoarrow_extension_spec'.
- `register_nanoarrow_extension()` returns `extension_spec`, invisibly.
- `unregister_nanoarrow_extension()` returns `extension_name`, invisibly.
- `resolve_nanoarrow_extension()` returns an object of class 'nanoarrow_extension_spec' or NULL if the extension type was not registered.

Examples

```
nanoarrow_extension_spec("mynamespace.mytype", subclass = "mypackage_mytype_spec")
```

`nanoarrow_pointer_is_valid` *Danger zone: low-level pointer operations*

Description

The nanoarrow_schema, nanoarrow_array, and nanoarrow_array_stream classes are represented in R as external pointers (`EXTPTRSXP`). When these objects go out of scope (i.e., when they are garbage collected or shortly thereafter), the underlying object's `release()` callback is called if the underlying pointer is non-null and if the `release()` callback is non-null.

Usage

```
nanoarrow_pointer_is_valid(ptr)

nanoarrow_pointer_addr_dbl(ptr)

nanoarrow_pointer_addr_chr(ptr)

nanoarrow_pointer_addr_pretty(ptr)

nanoarrow_pointer_release(ptr)

nanoarrow_pointer_move(ptr_src, ptr_dst)

nanoarrow_pointer_export(ptr_src, ptr_dst)

nanoarrow_allocate_schema()

nanoarrow_allocate_array()

nanoarrow_allocate_array_stream()

nanoarrow_pointer_set_protected(ptr_src, protected)
```

Arguments

`ptr`, `ptr_src`, `ptr_dst`	An external pointer to a `struct ArrowSchema`, `struct ArrowArray`, or `struct ArrowArrayStream`.
`protected`	An object whose scope must outlive that of `ptr`. This is useful for array streams since at least two specifications involving the array stream specify that the stream is only valid for the lifecycle of another object (e.g., an AdbcStatement or OGRDataset).

Details

When interacting with other C Data Interface implementations, it is important to keep in mind that the R object wrapping these pointers is always passed by reference (because it is an external pointer) and may be referred to by another R object (e.g., an element in a `list()` or as a variable assigned in a user's environment). When importing a schema, array, or array stream into nanoarrow this is not a problem: the R object takes ownership of the lifecycle and memory is released when the R object is garbage collected. In this case, one can use `nanoarrow_pointer_move()` where `ptr_dst` was created using `nanoarrow_allocate_*()`.

The case of exporting is more complicated and as such has a dedicated function, `nanoarrow_pointer_export()`, that implements different logic schemas, arrays, and array streams:

- Schema objects are (deep) copied such that a fresh copy of the schema is exported and made the responsibility of some other C data interface implementation.
- Array objects are exported as a shell around the original array that preserves a reference to the R object. This ensures that the buffers and children pointed to by the array are not copied and that any references to the original array are not invalidated.
- Array stream objects are moved: the responsibility for the object is transferred to the other C data interface implementation and any references to the original R object are invalidated. Because these objects are mutable, this is typically what you want (i.e., you should not be pulling arrays from a stream accidentally from two places).

If you know the lifecycle of your object (i.e., you created the R object yourself and never passed references to it elsewhere), you can slightly more efficiently call `nanoarrow_pointer_move()` for all three pointer types.

Value

- `nanoarrow_pointer_is_valid()` returns TRUE if the pointer is non-null and has a non-null release callback.
- `nanoarrow_pointer_addr_dbl()` and `nanoarrow_pointer_addr_chr()` return pointer representations that may be helpful to facilitate moving or exporting nanoarrow objects to other libraries.
- `nanoarrow_pointer_addr_pretty()` gives a pointer representation suitable for printing or error messages.
- `nanoarrow_pointer_release()` returns `ptr`, invisibly.
- `nanoarrow_pointer_move()` and `nanoarrow_pointer_export()` reeturn `ptr_dst`, invisibly.
- `nanoarrow_allocate_array()`, `nanoarrow_allocate_schema()`, and `nanoarrow_allocate_array_stream()` return an array, a schema, and an array stream, respectively.

nanoarrow_version *Underlying 'nanoarrow' C library build*

Description

Underlying 'nanoarrow' C library build

Usage

```
nanoarrow_version(runtime = TRUE)

nanoarrow_with_zstd()

nanoarrow_with_lz4()
```

Arguments

runtime	Compare TRUE and FALSE values to detect a possible ABI mismatch.

Value

A string identifying the version of nanoarrow this package was compiled against.

Examples

```
nanoarrow_version()
nanoarrow_with_zstd()
nanoarrow_with_lz4()
```

read_nanoarrow *Read/write serialized streams of Arrow data*

Description

Reads/writes connections, file paths, URLs, or raw vectors from/to serialized Arrow data. Arrow documentation typically refers to this format as "Arrow IPC", since its origin was as a means to transmit tables between processes (e.g., multiple R sessions). This format can also be written to and read from files or URLs and is essentially a high performance equivalent of a CSV file that does a better job maintaining types.

Usage

```
read_nanoarrow(x, ..., lazy = FALSE)

write_nanoarrow(data, x, ...)
```

Arguments

x	A raw() vector, connection, or file path from which to read binary data. Common extensions indicating compression (.gz, .bz2, .zip) are automatically uncompressed.
...	Currently unused.
lazy	By default, read_nanoarrow() will read and discard a copy of the reader's schema to ensure that invalid streams are discovered as soon as possible. Use lazy = TRUE to defer this check until the reader is actually consumed.
data	An object to write as an Arrow IPC stream, converted using as_nanoarrow_array_stream(). Notably, this includes a data.frame().

Details

The nanoarrow package implements an IPC writer; however, you can also use arrow::write_ipc_stream() to write data from R, or use the equivalent writer from another Arrow implementation in Python, C++, Rust, JavaScript, Julia, C#, and beyond.

The media type of an Arrow stream is application/vnd.apache.arrow.stream and the recommended file extension is .arrows.

Value

A nanoarrow_array_stream

Examples

```
as.data.frame(read_nanoarrow(example_ipc_stream()))
```

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