

# Package: Andromeda (via r-universe)

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**Type** Package

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**Description** Storing very large data objects on a local drive, while still making it possible to manipulate the data in an efficient manner.

**License** Apache License 2.0

**VignetteBuilder** knitr

**URL** <https://github.com/OHDSI/Andromeda>

**BugReports** <https://github.com/OHDSI/Andromeda/issues>

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andromeda	<i>Create an Andromeda object</i>
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---

### Description

By default the Andromeda object is created in the systems temporary file location. You can override this by specifying a folder using `options(andromedaTempFolder = "c:/andromedaTemp")`, where "c:/andromedaTemp" is the folder to create the Andromeda objects in.

Although in general Andromeda is well-behaved in terms of memory usage, it can consume a lot of memory for specific operations such as sorting and aggregating. By default the memory usage is limited to 75% of the physical memory. However it is possible to set another limit by using `options(andromedaMemoryLimit = 2.5)`, where 2.5 is the number of GB to use at most. One GB is 1,000,000,000 bytes.

Similarly, by default Andromeda will use all available CPU cores when needed. The `andromedaThreads` option controls the maximum number of threads Andromeda is allowed to use.

### Usage

```
andromeda(..., options = list())
```

**Arguments**

- ... Named objects. See details for what objects are valid. If no objects are provided, an empty Andromeda is returned.
- options A named list of options. Currently the only supported option is 'threads' (see example). All other options are ignored.

**Details**

Valid objects are data frames, Andromeda tables, or any other dplyr table.

**Value**

Returns an [Andromeda](#) object.

**Examples**

```
andr <- andromeda(cars = cars, iris = iris)

names(andr)
# [1] 'cars' 'iris'

andr$cars %>% filter(speed > 10) %>% collect()
# # A tibble: 41 x 2
#   speed dist
#   <dbl> <dbl>
# 1 11 17
# ...

close(andr)

# Use multiple threads for queries
andr <- andromeda(cars = cars, iris = iris, options = list(threads = 8))
```

---

Andromeda-class

*The Andromeda class*


---

**Description**

The Andromeda class is an S4 object.

This class provides the ability to work with data objects in R that are too large to fit in memory. Instead, these objects are stored on disk. This is slower than working from memory, but may be the only viable option.

Show the names of the tables in an Andromeda object.

**Usage**

```
## S4 method for signature 'Andromeda'
show(object)

## S4 method for signature 'Andromeda'
x$name

## S4 replacement method for signature 'Andromeda'
x$name <- value

## S4 replacement method for signature 'Andromeda'
x[[i]] <- value

## S4 method for signature 'Andromeda'
x[[i]]

## S4 method for signature 'Andromeda'
names(x)

## S4 method for signature 'Andromeda'
length(x)

## S4 method for signature 'Andromeda'
close(con, ...)
```

**Arguments**

object	An <a href="#">Andromeda</a> object.
x	An <a href="#">Andromeda</a> object.
name	The name of a table in the <a href="#">Andromeda</a> object.
value	A data frame, <a href="#">Andromeda</a> table, or other 'DBI' table.
i	The name of a table in the <a href="#">Andromeda</a> object.
con	An <a href="#">Andromeda</a> object.
...	Included for compatibility with generic <code>close()</code> method.

**Value**

A vector of names.

**Tables**

An [Andromeda](#) object has zero, one or more tables. The list of table names can be retrieved using the `names()` method. Tables can be accessed using the dollar sign syntax, e.g. `andromeda$myTable`, or double-square-bracket syntax, e.g. `andromeda[["myTable"]]`

## Permanence

To mimic the behavior of in-memory objects, when working with data in Andromeda the data is stored in a temporary location on the disk. You can modify the data as you can see fit, and when needed can save the data to a permanent location. Later this data can be loaded to a temporary location again and be read and modified, while keeping the saved data as is.

## Inheritance

The Andromeda inherits directly from `duckdb_connection`. As such, it can be used as if it is a `duckdb_connection`. The `duckdb` package is an R wrapper around 'duckdb', a low-weight but powerful single-user SQL database that can run from a single file on the local file system.

## See Also

[andromeda\(\)](#)

## Examples

```
andr <- andromeda(cars = cars, iris = iris)

names(andr)
# [1] 'cars' 'iris'

close(andr)
```

---

appendToTable

*Append to an Andromeda table*

---

## Description

Append a data frame, Andromeda table, or result of a query on an [Andromeda](#) table to an existing [Andromeda](#) table.

If data from another [Andromeda](#) is appended, a batch-wise copy process is used, which will be slower than when appending data from within the same [Andromeda](#) object.

**Important:** columns are appended based on column name, not on column order. The column names should therefore be identical (but not necessarily in the same order).

## Usage

```
appendToTable(tbl, data)
```

## Arguments

`tbl` An [Andromeda](#) table. This must be a base table (i.e. it cannot be a query result).

`data` The data to append. This can be either a `data.frame` or another [Andromeda](#) table.

**Value**

Returns no value. Executed for the side-effect of appending the data to the table.

**Examples**

```
andr <- andromeda(cars = cars)
nrow(andr$cars)
# [1] 50

appendToTable(andr$cars, cars)
nrow(andr$cars)
# [1] 100

appendToTable(andr$cars, andr$cars %>% filter(speed > 10))
nrow(andr$cars)
# [1] 182

close(andr)
```

---

batchApply

*Apply a function to batches of data in an Andromeda table*


---

**Description**

Apply a function to batches of data in an Andromeda table

**Usage**

```
batchApply(tbl, fun, ..., batchSize = 1e+05, progressBar = FALSE, safe = FALSE)
```

**Arguments**

tbl	An <a href="#">Andromeda</a> table (or any other 'DBI' table).
fun	A function where the first argument is a data frame.
...	Additional parameters passed to fun.
batchSize	Number of rows to fetch at a time.
progressBar	Show a progress bar?
safe	Create a copy of tbl first? Allows writing to the same Andromeda as being read from.

**Details**

This function is similar to the [lapply\(\)](#) function, in that it applies a function to sets of data. In this case, the data is batches of data from an [Andromeda](#) table. Each batch will be presented to the function as a data frame.

**Value**

Invisibly returns a list of objects, where each object is the output of the user-supplied function applied to a batch

**See Also**

[groupBy\(\)](#)

**Examples**

```
andr <- andromeda(cars = cars)

fun <- function(x) {
  return(nrow(x))
}

result <- batchApply(andr$cars, fun, batchSize = 25)

result
# [[1]]
# [1] 25
#
# [[2]]
# [1] 25

close(andr)
```

---

batchTest	<i>Apply a boolean test to batches of data in an Andromeda table and terminate early</i>
-----------	--

---

**Description**

Apply a boolean test to batches of data in an Andromeda table and terminate early

**Usage**

```
batchTest(tbl, fun, ..., batchSize = 1e+05)
```

**Arguments**

tbl	An <a href="#">Andromeda</a> table (or any other 'DBI' table).
fun	A function where the first argument is a data frame and returns a logical value.
...	Additional parameters passed to fun.
batchSize	Number of rows to fetch at a time.

**Details**

This function applies a boolean test function to sets of data and terminates at the first FALSE.

**Value**

Returns FALSE if any of the calls to the user-supplied function returned FALSE, else returns TRUE.

**Examples**

```
andr <- andromeda(cars = cars)

fun <- function(x) {
  is.unsorted(x %>% select(speed) %>% collect())
}

result <- batchTest(andr$cars, fun, batchSize = 25)

result
# [1] FALSE

close(andr)
```

---

copyAndromeda

*Copy Andromeda*

---

**Description**

Creates a complete copy of an [Andromeda](#) object. Object attributes are not copied.

**Usage**

```
copyAndromeda(andromeda, options = list())
```

**Arguments**

andromeda	The <a href="#">Andromeda</a> object to copy.
options	A list containing Andromeda options. Currently the only supported option is 'threads'. Setting options = list(threads = 10) will set the database used by Andromeda to use 10 threads.

**Value**

The copied [Andromeda](#) object.

**Examples**

```
andr <- andromeda(cars = cars, iris = iris)

andr2 <- copyAndromeda(andr)

names(andr2)
# [1] 'cars' 'iris'

close(andr)
close(andr2)
```

---

createIndex	<i>Create an index on one or more columns in an Andromeda table</i>
-------------	---

---

**Description**

Create an index on one or more columns in an Andromeda table

**Usage**

```
createIndex(tbl, columnNames, unique = FALSE, indexName = NULL)
```

**Arguments**

tbl	An <a href="#">Andromeda</a> table (or any other 'DBI' table).
columnNames	A vector of column names (character) on which the index is to be created.
unique	Should values in the column(s) be enforced to be unique?
indexName	The name of the index. If not provided, a random name will be generated.

**Details**

Indices can speed up subsequent queries that use the indexed columns, but can take time to create, and will take additional space on the drive.

**Value**

Invisibly returns the input table.

**See Also**

[listIndices\(\)](#), [removeIndex\(\)](#)

### Examples

```
andr <- andromeda(cars = cars)

createIndex(andr$cars, "speed")

# Will be faster now that speed is indexed:
andr$cars %>%
  filter(speed == 10) %>%
  collect()

close(andr)
```

---

flushAndromeda	<i>Flush changes to disk</i>
----------------	------------------------------

---

### Description

Flush all changes to disk. This only affects the data in the Andromeda temp folder.

This function is for advanced users, who wish to share the same underlying object with other processes, which is very dangerous if you don't know what you're doing.

### Usage

```
flushAndromeda(andromeda, evictCache = TRUE)
```

### Arguments

andromeda	An <a href="#">Andromeda</a> object.
evictCache	If TRUE, will also evict the cache to free up memory.

### Value

This function does not return anything, but is executed for its side-effect.

### Examples

```
andr <- andromeda()
andr$cars <- cars

flushAndromeda(andr)
# The database in andromeda temp is now fully up-to-date.

close(andr)
```

---

`getAndromedaTempDiskSpace`*Get the available disk space in Andromeda temp*

---

### Description

Attempts to determine how much disk space is still available in the Andromeda temp folder. This function uses Java, so will only work if the rJava package is installed.

By default the Andromeda temp folder is located in the system temp space, but the location can be altered using `options(AndromedaTempFolder = "c:/andromedaTemp")`, where "c:/andromedaTemp" is the folder to create the Andromeda objects in.

### Usage

```
getAndromedaTempDiskSpace(Andromeda = NULL)
```

### Arguments

`Andromeda` Optional: provide an [Andromeda](#) object for which to get the available disk space. Normally all [Andromeda](#) objects use the same temp folder, but the user could have altered it.

### Value

The number of bytes of available disk space in the Andromeda temp folder. Returns NA if unable to determine the amount of available disk space, for example because rJava is not installed, or because the user doesn't have the rights to query the available disk space.

### Examples

```
# Get the number of available gigabytes:  
getAndromedaTempDiskSpace() / 1024^3  
#123.456
```

---

`groupApply`*Apply a function to groups of data in an Andromeda table*

---

### Description

Apply a function to groups of data in an Andromeda table

**Usage**

```
groupApply(
  tbl,
  groupVariable,
  fun,
  ...,
  batchSize = 1e+05,
  progressBar = FALSE,
  safe = FALSE
)
```

**Arguments**

tbl	An <a href="#">Andromeda</a> table (or any other 'DBI' table).
groupVariable	The variable to group by
fun	A function where the first argument is a data frame.
...	Additional parameters passed to fun.
batchSize	Number of rows fetched from the table at a time. This is not the number of rows to which the function will be applied. Included mostly for testing purposes.
progressBar	Show a progress bar?
safe	Create a copy of tbl first? Allows writing to the same Andromeda as being read from.

**Details**

This function applies a function to groups of data. The groups are identified by unique values of the `groupVariable`, which must be a variable in the table.

**Value**

Invisibly returns a list of objects, where each object is the output of the user-supplied function applied to a group.

**See Also**

[batchApply\(\)](#)

**Examples**

```
andr <- andromeda(cars = cars)

fun <- function(x) {
  return(tibble::tibble(speed = x$speed[1], meanDist = mean(x$dist)))
}

result <- groupApply(andr$cars, "speed", fun)
result <- bind_rows(result)
result
```

```
# # A tibble: 19 x 2
# speed meanDist
# <dbl> <dbl>
# 1 4 6
# 2 7 13
# 3 8 16
# ...

close(andr)
```

---

isAndromeda	<i>Check whether an object is an Andromeda object</i>
-------------	---

---

### Description

Check whether an object is an Andromeda object

### Usage

```
isAndromeda(x)
```

### Arguments

x                   The object to check.

### Details

Checks whether an object is an Andromeda object.

### Value

A logical value.

---

isAndromedaTable	<i>Is the object an Andromeda table?</i>
------------------	--

---

### Description

Is the object an Andromeda table?

### Usage

```
isAndromedaTable(tbl)
```

### Arguments

tbl                   A reference to an Andromeda table

**Value**

TRUE or FALSE

**Examples**

```
## Not run:  
andr <- andromeda(cars = cars)  
isValidAndromedaTable(andr$cars)  
close(andr)  
  
## End(Not run)
```

---

isValidAndromeda	<i>Check whether an Andromeda object is still valid</i>
------------------	---

---

**Description**

Check whether an Andromeda object is still valid

**Usage**

```
isValidAndromeda(x)
```

**Arguments**

x                    The Andromeda object to check.

**Details**

Checks whether an Andromeda object is still valid, or whether it has been closed.

**Value**

A logical value.

**Examples**

```
andr <- andromeda(cars = cars, iris = iris)  
  
isValidAndromeda(andr)  
# TRUE  
  
close(andr)  
  
isValidAndromeda(andr)  
# FALSE
```

---

listIndices	<i>List all indices on an Andromeda table</i>
-------------	---

---

**Description**

List all indices on an Andromeda table

**Usage**

```
listIndices(tbl)
```

**Arguments**

tbl                    An [Andromeda](#) table (or any other 'DBI' table).

**Details**

Lists any indices that may have been created using the [createIndex\(\)](#) function.

**Value**

Returns a tibble listing the indices, indexed columns, and whether the index is unique.

**See Also**

[createIndex\(\)](#), [removeIndex\(\)](#)

**Examples**

```
andr <- andromeda(cars = cars)

createIndex(andr$cars, "speed")

listIndices(andr$cars)
# # A tibble: 1 x 5
#   indexSequenceId indexName      unique columnSequenceId columnName
#   <int> <chr>                <lgl>      <int> <chr>
#1       0 idx_ocy8we9j2i7ld0rshgb4 FALSE          0 speed

close(andr)
```

---

loadAndromeda	<i>Load Andromeda from file</i>
---------------	---------------------------------

---

### Description

Load Andromeda from file

### Usage

```
loadAndromeda(fileName, options = list())
```

### Arguments

fileName	The path where the object was saved using <a href="#">saveAndromeda()</a> .
options	A list containing Andromeda options. Currently the only supported option is 'threads'. Setting <code>options = list(threads = 10)</code> will set the database used by Andromeda to use 10 threads.

### Value

An [Andromeda](#) object.

### See Also

[saveAndromeda\(\)](#)

### Examples

```
# For this example we create an Andromeda object and save it to
# a temporary file locationL
fileName <- tempfile()
andr <- andromeda(cars = cars)
saveAndromeda(andr, fileName)

# Using loadAndromeda to load the object back:
andr <- loadAndromeda(fileName)

# Don't forget to close Andromeda when you are done:
close(andr)

# Cleaning up the file used in this example:
unlink(fileName)
```

---

names.tbl\_Andromeda    *Get the column names of an Andromeda table*

---

**Description**

Get the column names of an Andromeda table

**Usage**

```
## S3 method for class 'tbl_Andromeda'  
names(x)
```

**Arguments**

x                      An table in an Andromeda object

**Value**

A character vector of column names

**Examples**

```
andr <- andromeda(cars = cars)  
names(andr$cars)  
# [1] "speed" "dist"  
close(andr)
```

---

names<- ,Andromeda-method

*Set table names in an Andromeda object*

---

**Description**

names(andromedaObject) must be set to a character vector with length equal to the number of tables in the andromeda object (i.e. length(andromedaObject)). The user is responsible for setting valid table names (e.g. not using SQL keywords or numbers as names) This function treats Andromeda table names as case insensitive so if the only difference between the new names and old names is the case then the names will not be changed.

**Usage**

```
## S4 replacement method for signature 'Andromeda'  
names(x) <- value
```

**Arguments**

x	An Andromeda object
value	A character vector with the same length as the number of tables in x

**Examples**

```
andr <- andromeda(cars = cars, iris = iris)
names(andr) <- c("CARS", "IRIS")
names(andr)
# [1] "CARS" "IRIS"
close(andr)
```

---

names<-tbl\_Andromeda *Set column names of an Andromeda table*

---

**Description**

Set column names of an Andromeda table

**Usage**

```
## S3 replacement method for class 'tbl_Andromeda'
names(x) <- value
```

**Arguments**

x	A reference to a table in an andromeda object. (see examples)
value	A character vector of new names that must have length equal to the number of columns in the table.

**Examples**

```
andr <- andromeda(cars = cars)
names(andr$cars) <- toupper(names(andr$cars))
names(andr$cars)
# [1] "SPEED" "DIST"
close(andr)
```

---

removeIndex	<i>Removes an index from an Andromeda table</i>
-------------	---

---

### Description

Removes an index from an Andromeda table

### Usage

```
removeIndex(tbl, columnNames = NULL, indexName = NULL)
```

### Arguments

tbl	An <a href="#">Andromeda</a> table (or any other 'DBI' table).
columnNames	A vector of column names (character) on which the index was created. If not provided, then the <code>indexName</code> argument must be provided.
indexName	The name of the index. If not provided, the <code>columnNames</code> argument must be provided.

### Details

Remove an index created using the [createIndex\(\)](#) function. Either the index name or the column names on which the index was created must be provided.

### Value

Invisibly returns the input table.

### See Also

[createIndex\(\)](#), [listIndices\(\)](#)

### Examples

```
andr <- andromeda(cars = cars)

createIndex(andr$cars, "speed")

# Will be faster now that speed is indexed:
andr$cars %>%
  filter(speed == 10) %>%
  collect()

removeIndex(andr$cars, "speed")

close(andr)
```

---

restoreDate	<i>Restore dates</i>
-------------	----------------------

---

### Description

This function has been deprecated since Andromeda v0.5 preserves dates.

### Usage

```
restoreDate(x)
```

### Arguments

x                    A numeric vector representing dates.

### Value

A vector of type Date.

### See Also

[restorePosixct\(\)](#)

### Examples

```
myData <- data.frame(startDate = as.Date(c("2000-01-01", "2001-01-31", "2004-12-31")))
andr <- andromeda(myData = myData)

andr$myData %>%
  collect() %>%
  mutate(startDate = restoreDate(startDate))
# # A tibble: 3 x 1
#   startDate
#   <date>
# 1 2000-01-01
# 2 2001-01-31
# 3 2004-12-31

close(andr)
```

---

restorePosixct	<i>Restore timestamps</i>
----------------	---------------------------

---

## Description

This function has been deprecated since Andromeda v0.5 preserves POSIXct datetimes.

## Usage

```
restorePosixct(x)
```

## Arguments

x                    A numeric vector representing timestamps

## Value

A vector of type POSIXct.

## See Also

[restoreDate\(\)](#)

## Examples

```
myData <- data.frame(startTime = as.POSIXct(c("2000-01-01 10:00",
                                             "2001-01-31 11:00",
                                             "2004-12-31 12:00")))

andr <- andromeda(myData = myData)

andr$myData %>%
  collect() %>%
  mutate(startTime = restorePosixct(startTime))
## A tibble: 3 x 1
## startTime
## <dtm>
## 1 2000-01-01 10:00:00
## 2 2001-01-31 11:00:00
## 3 2004-12-31 12:00:00

close(andr)
```

---

saveAndromeda	<i>Save Andromeda to file</i>
---------------	-------------------------------

---

### Description

Saves the [Andromeda](#) object in a zipped file. Note that by default the [Andromeda](#) object is automatically closed by saving it to disk. This is due to a limitation of the underlying technology ('duckdb'). To keep the connection open, use `maintainConnection = TRUE`. This will first create a temporary copy of the [Andromeda](#) object. Note that this can be substantially slower.

### Usage

```
saveAndromeda(  
  andromeda,  
  fileName,  
  maintainConnection = FALSE,  
  overwrite = TRUE  
)
```

### Arguments

<code>andromeda</code>	An object of class <a href="#">Andromeda</a> .
<code>fileName</code>	The path where the object will be written.
<code>maintainConnection</code>	Should the connection be maintained after saving? If <code>FALSE</code> , the <a href="#">Andromeda</a> object will be invalid after this operation, but saving will be faster.
<code>overwrite</code>	If the file exists, should it be overwritten? If <code>FALSE</code> and the file exists, an error will be thrown.

### Value

Returns no value. Executed for the side-effect of saving the object to disk.

### See Also

[loadAndromeda](#)  
[loadAndromeda\(\)](#)

### Examples

```
andr <- andromeda(cars = cars)  
  
# For this example we'll use a temporary file location:  
fileName <- tempfile()  
  
saveAndromeda(andr, fileName)
```

```
# Cleaning up the file used in this example:  
unlink(fileName)
```

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