

# Package ‘Andromeda’

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**Type** Package

**Title** Asynchronous Disk-Based Representation of Massive Data

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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://ohdsi.github.io/Andromeda/>,  
<https://github.com/OHDSI/Andromeda>

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

**Depends** dplyr

**Imports** RSQLite, DBI, zip, methods, dbplyr, tidyselect, cli, pillar

**Suggests** testthat, knitr, rmarkdown, rlang, tibble, rJava

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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.

### Usage

```
andromeda(...)
```

### Arguments

... Named objects. See details for what objects are valid. If no objects are provided, an empty Andromeda is returned.

### 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)
```

---

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 [SQLiteConnection](#). As such, it can be used as if it is a [SQLiteConnection](#). [RSQLite](#) is an R wrapper around 'SQLite', a low-weight but very 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	<i>Append to an Andromeda table</i>
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### 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 <a href="#">Andromeda</a> 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 <a href="#">Andromeda</a> 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

### 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	<i>Copy Andromeda</i>
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**Description**

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

**Usage**

```
copyAndromeda(andromeda)
```

**Arguments**

andromeda      The [Andromeda](#) object to copy.

**Value**

The copied [Andromeda](#) object.

**Examples**

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

andr2 <- copyAndromeda(andr)

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

close(andr)
close(andr2)
```

---

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
```

---

<code>groupApply</code>	<i>Apply a function to groups of data in an Andromeda table</i>
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---

**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 [Andromeda](#) 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.

### 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

*Check whether an object is an Andromeda object*

---

### 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.

---

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

**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
```

---

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

### Description

Load Andromeda from file

### Usage

```
loadAndromeda(fileName)
```

### Arguments

fileName      The path where the object was saved using [saveAndromeda\(\)](#).

### 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)
```

---

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

**Description**

Restores dates that were converted by Andromeda to numeric values back to dates.

**Usage**

```
restoreDate(x)
```

**Arguments**

x                    A numeric vector representing dates.

**Value**

A vector of type Date.

**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**

Restores dates that were converted by Andromeda to numeric values back to dates.

**Usage**

```
restorePosixct(x)
```

**Arguments**

x                    A numeric vector representing timestamps

**Value**

A vector of type POSIXct.

**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

*Save Andromeda to file*

---

**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 ('SQLite'). 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**

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