

# Package ‘scidb’

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**Type** Package

**Title** An R Interface to SciDB

**Version** 3.0.0

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**Copyright** Paradigm4, Inc.

**Description** An R interface to the 'SciDB' array database <<https://www.paradigm4.com>>.

**BugReports** <https://github.com/Paradigm4/SciDBR/issues>

**URL** <https://paradigm4.github.io/SciDBR/>

**VignetteBuilder** knitr

**Depends** R (>= 3.0.0), bit64

**Imports** curl, data.table, digest, methods, openssl

**Suggests** Matrix, rmarkdown, knitr (>= 1.8)

**License** AGPL-3

**LazyLoad** yes

**RoxygenNote** 7.1.1

**NeedsCompilation** yes

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scidb-package	<i>SciDB/R Interface</i>
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---

**Description**

Package options

**Package options**

```
options(scidb.prefix=NULL)
# Default shim port and host.
options(scidb.default_shim_port=8080L)
options(scidb.default_shim_host="localhost")
```

```
# How to download arrays and their coordinates. Set scidb.unpack=FALSE # to use apply, which
can be faster in some cases when used with aio.
```

```
options(scidb.unpack=FALSE)
```

```
# Disable SSL certificate host name checking by default. This is important mostly # for Amazon
EC2 where hostnames rarely match their DNS names. If you enable this # then the shim SSL
certificate CN entry *must* match the server host name for the # encrypted session to work. Set
this TRUE for stronger security (help avoid MTM) # in SSL connections.
```

```
options(scidb.verifyhost=FALSE)
```

```
# List of special DDL operators
```

```
options(scidb.ddl=c("create_array", "remove", "rename"))
```

### See Also

[scidb, iquery](#)

---

.attsplitter

*Internal function for processing SciDB attribute schema*

---

### Description

Internal function for processing SciDB attribute schema

### Usage

```
.attsplitter(x)
```

### Arguments

x                    a scidb object or schema string

### Value

a data frame with parsed attribute data

---

.dimsplitter	<i>Internal function for processing SciDB dimension schema</i>
--------------	--

---

**Description**

Internal function for processing SciDB dimension schema

**Usage**

```
.dimsplitter(x)
```

**Arguments**

x	a scidb object or schema string
---	---------------------------------

**Value**

a data frame with parsed dimension data

---

.scidbeval	<i>An important internal convenience function that returns a scidb object. If eval=TRUE, a new SciDB array is created the returned scidb object refers to that. Otherwise, the returned scidb object represents a SciDB array promise.</i>
------------	--

---

**Description**

An important internal convenience function that returns a scidb object. If eval=TRUE, a new SciDB array is created the returned scidb object refers to that. Otherwise, the returned scidb object represents a SciDB array promise.

**Usage**

```
.scidbeval(db, expr, eval = FALSE, name, gc = TRUE, depend, schema, temp)
```

**Arguments**

db	scidb connection object
expr	(character) A SciDB expression or array name
eval	(logical) If TRUE evaluate expression and assign to new SciDB array. If FALSE, infer output schema but don't evaluate.
name	(optional character) If supplied, name for stored array when eval=TRUE
gc	(optional logical) If TRUE, tie SciDB object to garbage collector.
depend	(optional list) An optional list of other scidb objects that this expression depends on (preventing their garbage collection if other references to them go away).
schema	(optional) used to create SciDB temp arrays (requires scidb >= 14.8)
temp	(optional) used to create SciDB temp arrays (requires scidb >= 14.8)

**Value**

A scidb array object

**Note**

Only AFL supported.

---

aflhelp

*Display SciDB AFL operator documentation*

---

**Description**

Display SciDB AFL operator documentation

**Usage**

```
aflhelp(topic, db)
```

**Arguments**

topic	an afl object from a SciDB database connection, or optionally a character string name
db	optional database connection from <a href="#">scidbconnect</a> (only needed when topic is a character string)

**Value**

displays help

**Examples**

```
## Not run:  
d <- scidbconnect()  
aflhelp("list", d)      # explicitly look up a character string  
help(d$list)           # same thing via R's \code{help} function  
  
## End(Not run)
```

---

`as.R`*Download SciDB data to R*

---

**Description**

Download SciDB data to R

**Usage**

```
as.R(x, only_attributes = FALSE, binary = TRUE)
```

**Arguments**

<code>x</code>	a <code>scidb</code> object (a SciDB array or expression)
<code>only_attributes</code>	optional logical argument, if TRUE do not download SciDB dimensions (see note)
<code>binary</code>	optional logical value, set to FALSE to download data using text format (useful for some unsupported SciDB types)

**Value**

An R `data.frame`

**Note**

This convenience function is equivalent to running `iquery(db,x,return=TRUE)` for a SciDB connection object `db`.

The `only_attributes=TRUE` option only works with binary transfers, and if specified will set `binary=TRUE`. Beware of the `only_attributes=TRUE` setting—SciDB may return data in arbitrary order.

SciDB values are always returned as R data frames. SciDB scalar types are converted to corresponding R types as follows:

- double -> double
- int64 -> integer64
- uint64 -> double
- uint32 -> double
- int32 -> integer
- int16 -> integer
- unit16 -> integer
- int8 -> integer
- uint8 -> integer
- bool -> logical

- string -> character
- char -> character
- binary -> raw
- datetime -> Date

### See Also

[as.scidb](#)

### Examples

```
## Not run:
db <- scidbconnect()
x <- scidb(db, "build(<v:double>[i=1:5], sin(i))")
as.R(x)
## i          v
## 1  0.8414710
## 2  0.9092974
## 3  0.1411200
## 4 -0.7568025
## 5 -0.9589243

as.R(x, only_attributes=TRUE)
##          v
## 0.8414710
## 0.9092974
## 0.1411200
## -0.7568025
## -0.9589243

## End(Not run)
```

---

as.scidb

*Upload R data to SciDB*

---

### Description

Upload R data to SciDB

### Usage

```
as.scidb(db, x, name, start, gc = TRUE, ...)
```

**Arguments**

db	a scidb database connection returned from <a href="#">scidbconnect</a>
x	an R data frame, raw value, Matrix, matrix, or vector object
name	a SciDB array name to use
start	starting SciDB integer coordinate index (does not apply to data frames)
gc	set to FALSE to disconnect the SciDB array from R's garbage collector
...	other options, see <a href="#">df2scidb</a>

**Value**

A scidb object

**Note**

Supported R objects include data frames, scalars, vectors, dense matrices, and double-precision sparse matrices of class `CsparseMatrix`. Supported R scalar types and their resulting SciDB types are:

- integer -> int32
- logical -> int32
- character -> string
- double -> double
- integer64 -> int64
- raw -> binary
- Date -> datetime

R factor values are converted to their corresponding character levels.

**See Also**

[as.R](#)

---

at_least	<i>Returns TRUE if version string x is greater than or equal to than version y</i>
----------	--

---

**Description**

Returns TRUE if version string x is greater than or equal to than version y

**Usage**

```
at_least(x, y)
```



**Arguments**

x                    version string like "12.1", "15.12", etc. (non-numeric ignored)  
y                    version string like "12.1", "15.12", etc. (non-numeric ignored)

**Value**

logical TRUE if x is greater than or equal to y

---

cov,scidb-method	<i>Covariance matrix This function is more limited than R's default cov function. It can only compute a covariance matrix from a data matrix without any missing value handling by the procedure (in R notation) <math>S_0 \leftarrow \text{sweep}(x, 2, \text{colMeans}(x))</math>, <math>\text{crossprod}(S_0) / (\text{nrow}(S_0) - 1)</math> # (covariance matrix result)</i>
------------------	---

---

**Description**

Covariance matrix This function is more limited than R's default cov function. It can only compute a covariance matrix from a data matrix without any missing value handling by the procedure (in R notation)  $S_0 \leftarrow \text{sweep}(x, 2, \text{colMeans}(x))$ ,  $\text{crossprod}(S_0) / (\text{nrow}(S_0) - 1)$  # (covariance matrix result)

**Usage**

```
## S4 method for signature 'scidb'
cov(x, y = NULL, use = "everything", method = c("pearson", "kendall", "spearman"))
```

**Arguments**

x                    a 2-d scidb array with a single numeric attribute  
y                    UNUSED, limited to correlation matrix in the SciDB case  
use                  UNUSED, limited to "everything" in the SciDB case  
method              UNUSED, limited to "pearson" in the SciDB case

**Value**

covariance matrix of x (as a SciDB array)

dimnames.scidb      *Names of array dimensions*

---

**Description**

Names of array dimensions

**Usage**

```
## S3 method for class 'scidb'  
dimnames(x)
```

**Arguments**

x                    scidb array object

**Value**

a vector of SciDB array dimension names

---

getpwd                    *Simple utility to interactively enter a password without showing it on the screen*

---

**Description**

Simple utility to interactively enter a password without showing it on the screen

**Usage**

```
getpwd(prompt = "Password:")
```

**Arguments**

prompt                a text prompt to display, defaults to "Password:"

---

help,operator-method *AFL operator help*

---

**Description**

AFL operator help

**Usage**

```
## S4 method for signature 'operator'
help(topic)
```

**Arguments**

topic                    afl operator

**Value**

help summary

---

iquery                    *Run a SciDB query, optionally returning the result.*

---

**Description**

Run a SciDB query, optionally returning the result.

**Usage**

```
iquery(db, query, return = FALSE, binary = TRUE, ...)
```

**Arguments**

db	a scidb database connection from <a href="#">scidbconnect</a>
query	a single SciDB query string or scidb array object
return	if TRUE, return the result
binary	set to FALSE to read result from SciDB in text form
...	additional options passed to <code>read.table</code> when <code>binary=FALSE</code> , or optional result schema when <code>binary=TRUE</code> (see note below).

**Note**

When query is an arbitrary AFL query string and binary=TRUE, optionally specify schema with a valid result array schema to skip an extra metadata lookup query (see [scidb](#)).

Setting return=TRUE wraps the AFL query expression with a SciDB save operator, saving the data on the SciDB server in either binary or text format depending on the value of the binary parameter. Please note that some AFL expressions may not be "saved" using the AFL save operator, including for instance the AFL create\_array operator. Trying to return the result of such a SciDB expression will result in a run-time error.

**See Also**

[scidb as.R](#)

**Examples**

```
## Not run:
db <- scidbconnect()
iquery(db, "build(<v:double>[i=1:5], sin(i))", return=TRUE)
## i          v
## 1  0.8414710
## 2  0.9092974
## 3  0.1411200
## 4 -0.7568025
## 5 -0.9589243

# Use binary=FALSE and additional options to read.table function:
iquery(db, "build(<val:string>[i=1:3], '[(01),(02),(03)]', true)",xi
      return=TRUE, binary=FALSE, colClasses=c("integer", "character"))
## i val
## 1 1  01
## 2 2  02
## 3 3  03

## End(Not run)
```

---

ls,afl-method

---

*List contents of a SciDB database*


---

**Description**

List contents of a SciDB database

**Usage**

```
## S4 method for signature 'afl'
ls(name)
```

**Arguments**

name                   af1 SciDB connection object from [scidbconnect](#)

**Value**

a data.frame listing the contents of the database

---

names.scidb	<i>SciDB dimension and attribute names</i>
-------------	--

---

**Description**

SciDB dimension and attribute names

**Usage**

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

**Arguments**

x                       scidb array object

**Value**

Character vector of names

---

operators	<i>Base SciDB operators</i>
-----------	-----------------------------

---

**Description**

Base SciDB operators as of SciDB version 16.9

**Usage**

```
data(operators)
```

**Format**

A data frame with 4 variables, name, signature, help.

**Source**

Paradigm4 <https://www.paradigm4.com>

---

`print,af1-method`      *Print a summary of a af1 SciDB database connection object*

---

**Description**

Print a summary of a af1 SciDB database connection object

**Usage**

```
## S4 method for signature 'af1'  
print(x)
```

**Arguments**

x                      af1 object

**Value**

printed object summary

---

`print,scidb-method`      *Print a summary of a scidb object*

---

**Description**

Print a summary of a scidb object

**Usage**

```
## S4 method for signature 'scidb'  
print(x)
```

**Arguments**

x                      a scidb object

**Value**

printed object summary

---

print.af1	<i>Print a summary of a af1 SciDB database connection object</i>
-----------	--

---

**Description**

Print a summary of a af1 SciDB database connection object

**Usage**

```
## S3 method for class 'af1'
print(x, ...)
```

**Arguments**

x	af1 object
...	optional arguments (not used)

**Value**

printed object summary

---

schema	<i>SciDB array schema</i>
--------	---------------------------

---

**Description**

SciDB array schema

**Usage**

```
schema(x, what = c("schema", "attributes", "dimensions"))
```

**Arguments**

x	a <a href="#">scidb</a> array object
what	optional schema subset (subsets are returned in data frames; partial argument matching is supported)

**Value**

character-valued SciDB array schema

**Examples**

```
## Not run:
s <- scidbconnect()
x <- scidb(s, "build(<v:double>[i=1:10,2,0,j=0:19,1,0],0)")
schema(x)
# [1] "<v:double> [i=1:10:0:2; j=0:19:0:1]"
schema(x, "attributes")
# name type nullable
#1 v double TRUE
schema(x, "dimensions")
  name start end chunk overlap
#1 i 1 10 2 j
#2 0 0 19 1 0

## End(Not run)
```

---

scidb

---

*Create an R reference to a SciDB array or expression.*


---

**Description**

Create an R reference to a SciDB array or expression.

**Usage**

```
scidb(db, name, gc = FALSE, schema)
```

**Arguments**

db	scidb connection object from <a href="#">scidbconnect</a>
name	a character string name of a stored SciDB array or a valid SciDB AFL expression
gc	a logical value, TRUE means connect the SciDB array to R's garbage collector
schema	optional SciDB array schema, if specified avoid an extra metadata query to determine array schema. Use this option with care, the schema must exactly match the SciDB array result.

**Value**

a scidb object



---

scidbconnect	<i>Connect to a SciDB database</i>
--------------	------------------------------------

---

## Description

Connect to a SciDB database

## Usage

```
scidbconnect(
  host = getOption("scidb.default_shim_host", "127.0.0.1"),
  port = getOption("scidb.default_shim_port", 8080L),
  username,
  password,
  auth_type = c("scidb", "digest"),
  protocol = c("http", "https"),
  admin = FALSE,
  int64 = FALSE,
  doc
)
```

## Arguments

host	optional host name or I.P. address of a SciDB shim service to connect to
port	optional port number of a SciDB shim service to connect to. For connecting to Shim when the Shim port is forwarded, use port=NULL (see detailed note below).
username	optional authentication username
password	optional authentication password
auth_type	optional SciDB authentication type
protocol	optional shim protocol type
admin	Set to TRUE to open a higher-priority session. This is identical with the --admin flag for the iquery SciDB client (default FALSE)
int64	logical value, if TRUE then preserve signed 64-bit SciDB integers as R integer64 values from the bit64 package. Otherwise, 64-bit integers from SciDB are converted to R double values, possibly losing precision.
doc	optional AFL operator/macro documentation (see notes)

## Value

A scidb connection object. Use \$ to access AFL operators and macros, ls() on the returned object to list SciDB arrays, and names() on the returned object to list all available AFL operators and macros.

**Note**

Use the optional username and password arguments with `auth_type` set to "digest" to use HTTP digest authentication (see the shim documentation to configure this). Digest authentication may use either "http" or "https" selected by the protocol setting. Set `auth_type = "scidb"` to use SciDB authentication, which only works over "https".

Use the returned SciDB connection object (of class `af1`) with other package functions to interact with SciDB arrays. Apply R's `ls` function on the returned value to see a list of arrays. The returned value contains a list of available SciDB AFL language operators and macro names. Use the dollar-sign function to access those functions.

The optional `doc` argument may be a three-column data frame with character-valued columns `name`, `signature`, and `help` containing AFL operator names, function signatures, and help strings, respectively. See `'data("operators", package="scidb")'` for an example.

**Forwarded Shim port:** Shim usually runs on a selected port e.g. 8080 or 8083 (for secure communication) and those ports need to be opened up to clients. In other situations, the admin might decide to not open the Shim port and instead forward the Shim port to a URL like `https://hostname/shim/`. In this case, we do not need to supply the port number during `scidbconnect()`; instead one should use `port = NULL` and `host=HOSTNAME/FORWARDED-PATH/`.

All arguments support partial matching.

**See Also**

[scidb\\_prefix](#)

**Examples**

```
## Not run:
db <- scidbconnect()

# SciDB 15.12 authentication example (using shim's default HTTPS port 8083)
db <- scidbconnect(user="root", password="Paradigm4",
                  auth_type="scidb", port=8083, protocol="https")

# List available AFL operators
names(db)

# List arrays
ls(db)

# Explicitly upload an R matrix to SciDB:
x <- as.scidb(db, matrix(rnorm(20), 5))
# Implicitly do the same as part of an AFL expression
y <- db$join(x, as.scidb(matrix(1:20, 5)))
print(y)

as.R(y) # Download a SciDB array to R.

## End(Not run)
```

---

scidb_prefix	<i>Register an AFL prefix expression</i>
--------------	--

---

## Description

SciDB AFL statements are normally executed in a stateless query context. Use `scidb_prefix` to create compound AFL expressions useful in some circumstances.

## Usage

```
scidb_prefix(db, expression = NULL)
```

## Arguments

<code>db</code>	a scidb database connection returned from <a href="#">scidbconnect</a>
<code>expression</code>	a valid AFL expression to be issued prior to, and in the same context as all subsequent query expressions issued to the database corresponding to <code>db</code> . Set <code>expression=NULL</code> to remove the prefix expression.

## Value

A new SciDB database connection object with the prefix set.

## Note

This is mostly useful for setting namespaces, see the examples.

## Examples

```
## Not run:
library(scidb)
db <- scidbconnect()
ls(db)
new_db <- scidb_prefix(db, "set_role('functionary')")
ls(new_db)

## End(Not run)
```

---

show, afl-method      *Print a summary of a afl object*

---

**Description**

Print a summary of a afl object

**Usage**

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

**Arguments**

object              afl object

**Value**

printed object summary

---

show, scidb-method      *Print a summary of a scidb object*

---

**Description**

Print a summary of a scidb object

**Usage**

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

**Arguments**

object              a scidb object

**Value**

printed object summary

---

store	<i>Evaluate an expression to scidb or scidb objects</i>
-------	---

---

**Description**

Force evaluation of an expression that yields a scidb or scidb object, storing the result to a SciDB array when eval=TRUE.

**Usage**

```
store(db, expr, name, eval = TRUE, gc = TRUE, temp = FALSE)
```

**Arguments**

db	scidb connection object from <a href="#">scidbconnect</a>
expr	a quoted SciDB expression scidb object
name	(character) optional SciDB array name to store result to
eval	FALSE do not evaluate the expression in SciDB (leave as a view)
gc	(logical) optional, when TRUE tie result to R garbage collector
temp	(logical, optional), when TRUE store as a SciDB temp array

---

%as%,scidb-method	<i>AFL array aliasing</i>
-------------------	---------------------------

---

**Description**

AFL array aliasing

**Usage**

```
## S4 method for signature 'scidb'
x %as% y
```

**Arguments**

x	an object of class <a href="#">scidb</a> (a scidb array or expression)
y	alias name

**Value**

a [scidb](#) object

**Note**

Use the %as% operator in place of the native AFL "as" operator in AFL expressions written in R.

**Examples**

```
## Not run:  
db <- scidbconnect()  
x <- scidb(db, "build(<v:double>[i=1:2,1,0], i)")  
x %as% y  
  
## End(Not run)
```

---

%as%

*AFL array aliasing*

---

**Description**

AFL array aliasing

**Usage**

```
x %as% y
```

**Arguments**

x	an object of class <code>scidb</code> (a <code>scidb</code> array or expression)
y	alias name

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