

# Package: rolog (via r-universe)

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**Type** Package

**Title** Query 'SWI'-'Prolog' from R

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**Description** This R package connects to SWI-Prolog,  
<<https://www.swi-prolog.org/>>, so that R can send deterministic  
and non-deterministic queries to prolog (consult, query/submit,  
once, findall).

**License** FreeBSD

**Imports** Rcpp (>= 1.0.7), methods, utils

**Depends** R (>= 4.2)

**URL** <https://github.com/mgondan/rolog>

**BugReports** <https://github.com/mgondan/rolog/issues>

**LinkingTo** Rcpp, rswipl

**RoxygenNote** 7.2.3

**Encoding** UTF-8

**SystemRequirements** GNU Make, swi-prolog (>= 10.1.5)

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**Config/testthat/edition** 3

**VignetteBuilder** knitr, rmarkdown

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as.rolog	<i>Translate simplified to canonical representation</i>
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### Description

Translate simplified to canonical representation

### Usage

```
as.rolog(query = quote(member(.X, "[a, "b", 3L, 4, (pi), TRUE, .Y])))
```

### Arguments

query	an R call representing a Prolog query with prolog-like syntax, e.g., ‘member(.X, "[a, b, .Y]’ for use in [query()], [once()], and [findall()]. The argument is translated to Rolog’s representation, with R calls corresponding to Prolog terms and R expressions corresponding to Prolog variables. Variables and expressions in parentheses are evaluated.
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### See Also

[query()], [once()], [findall()]

**Examples**

```
q <- quote(member(.X, "[a, \"b\", 3L, 4, pi, (pi), TRUE, .Y]"))
as.rolog(q)
```

```
q <- quote(member(.X, "[a, \"b\", 3L, 4, pi, (pi), TRUE, .Y]"))
findall(as.rolog(q))
```

---

clear	<i>Clear current query</i>
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---

**Description**

Clear current query

**Usage**

```
clear()
```

**Value**

TRUE (invisible)

**See Also**

[query\(\)](#) for a opening a query.

[submit\(\)](#) for a submitting a query.

[once\(\)](#) for a opening a query, submitting it, and clearing it again.

[findall\(\)](#) for a opening a query, collecting all solutions, and clearing it again.

**Examples**

```
query(call("member", expression(X), list(quote(a), "b", 3L, 4)))
submit() # X = a
submit() # X = "b"
clear()
```

---

consult	<i>Consult a prolog database</i>
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**Description**

Consult a prolog database

**Usage**

```
consult(fname = system.file(file.path("pl", "family.pl"), package = "rolog"))
```

**Arguments**

fname	file name of database
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**Value**

TRUE on success

**See Also**

[once\(\)](#), [findall\(\)](#), and [query\(\)/submit\(\)/clear\(\)](#) for executing queries

**Examples**

```
consult(fname=system.file(file.path("pl", "family.pl"), package="rolog"))
findall(call("ancestor", quote(pam), expression(X)))
```

---

findall	<i>Invoke a query several times</i>
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---

**Description**

Invoke a query several times

**Usage**

```
findall(
  query = call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y))),
  options = list(portray = FALSE),
  env = globalenv()
)
```

**Arguments**

query	an R call. The R call consists of symbols, integers and real numbers, character strings, boolean values, expressions, lists, and other calls. Vectors of booleans, integers, floating point numbers, and strings with length $N > 1$ are translated to prolog compounds <code>!/N</code> , <code>%/N</code> , <code>#/N</code> and <code>\$\$/N</code> , respectively. The names can be modified with the options below.
options	This is a list of options controlling translation from and to prolog. <ul style="list-style-type: none"> <li>• <i>boolvec</i> (see option <code>rolog.boolvec</code>, default is <code>!</code>) is the name of the prolog compound for vectors of booleans.</li> <li>• <i>intvec</i>, <i>realvec</i>, <i>charvec</i> define the compound names for vectors of integers, doubles and strings, respectively (defaults are <code>%</code>, <code>#</code> and <code>\$\$</code>).</li> <li>• If <i>scalar</i> is <code>TRUE</code> (default), vectors of length 1 are translated to scalar prolog elements. If <i>scalar</i> is <code>FALSE</code>, vectors of length 1 are also translated to compounds.</li> </ul>
env	The R environment in which the query is run (default: <code>globalenv()</code> ). This is mostly relevant for <code>r_eval/2</code> .

**Value**

If the query fails, an empty list is returned. If the query succeeds  $N \geq 1$  times, a list of length  $N$  is returned, each element being a list of conditions for each solution, see [once\(\)](#).

**See Also**

[once\(\)](#) for a single query

[query\(\)](#), [submit\(\)](#), and [clear\(\)](#) for fine-grained control over non-deterministic queries

[rolog\\_options\(\)](#)

**Examples**

```
# This query returns a list stating that it works if X = a, "b", ...
findall(call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, NULL, NA)))

# Continued
findall(call("member", expression(X), list(call("sin", call("/", quote(pi), 2)), expression(Y))))

# The same using simplified syntax
q <- quote(member(.X, "[a, "b", 3L, 4, TRUE, NULL, NA, sin(pi/2), .Y]))
findall(as.rolog(q))
```

---

once

*Invoke a query once*

---

### Description

Invoke a query once

### Usage

```
once(  
  query = call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y))),  
  options = list(portray = FALSE),  
  env = globalenv()  
)
```

### Arguments

query	an R call. The R call consists of symbols, integers and real numbers, character strings, boolean values, expressions, lists, and other calls. Vectors of booleans, integers, floating point numbers, and strings with length $N > 1$ are translated to prolog compounds $!/N$ , $%/N$ , $#/N$ and $$$/N$ , respectively. The names can be modified with the options below.
options	This is a list of options controlling translation from and to prolog. <ul style="list-style-type: none"><li>• <i>boolvec</i> (see option <code>rolog.boolvec</code>, default is <code>!</code>) is the name of the prolog compound for vectors of booleans.</li><li>• <i>intvec</i>, <i>realvec</i>, <i>charvec</i> define the compound names for vectors of integers, doubles and strings, respectively (defaults are <code>%</code>, <code>#</code> and <code>\$\$</code>).</li><li>• If <i>scalar</i> is <code>TRUE</code> (default), vectors of length 1 are translated to scalar prolog elements. If <i>scalar</i> is <code>FALSE</code>, vectors of length 1 are also translated to compounds.</li></ul>
env	The R environment in which the query is run (default: <code>globalenv()</code> ). This is mostly relevant for <code>r_eval/2</code> .

### Value

If the query fails, `FALSE` is returned. If the query succeeds, a (possibly empty) list is returned that includes the bindings required to satisfy the query.

### See Also

[findall\(\)](#) for querying all solutions

[query\(\)](#), [submit\(\)](#), and [clear\(\)](#) for fine-grained control over non-deterministic queries

[rolog\\_options\(\)](#) for options controlling R to prolog translation

### Examples

```
# This query returns FALSE
once(call("member", 1, list(quote(a), quote(b), quote(c))))

# This query returns an empty list meaning yes, it works
once(call("member", 3, list(1, 2, 3)))

# This query returns a list stating that it works if X = 1
once(call("member", 1, list(quote(a), expression(X))))

# The same query using simplified syntax
q = quote(member(1, "[a, .X]"))
once(as.olog(q))

# This query returns a list stating that X = 1 and Z = expression(Y)
once(call("=", list(expression(X), expression(Y)), list(1, expression(Z))))

# This works for X = [1 | _]; i.e. something like [1](1, expression(_6330))
once(call("member", 1, expression(X)))

# This returns S = '1.0' (scalar)
once(call("format", call("string", expression(S)), "~w", list(1)), options=list(scalar=TRUE))

# This returns S = '#(1.0)' (vector), because the 1 is translated to #(1.0).
# To prevent "~w" from being translated to $$("~w"), it is given as an atom.
once(call("format", call("string", expression(S)), as.symbol("~w"), list(1)),
options=list(scalar=FALSE))
```

---

portray

*Translate an R call to a prolog compound and pretty print it*

---

### Description

Translate an R call to a prolog compound and pretty print it

### Usage

```
portray(
  query = call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y))),
  options = NULL
)
```

### Arguments

query            an R call. The R call consists of symbols, integers and real numbers, character strings, boolean values, expressions and lists, and other calls. Vectors of booleans, integers, floating point numbers, and strings with length  $N > 1$  are translated to prolog compounds  $!N$ ,  $%N$ ,  $\#N$  and  $$$N$ , respectively. The names can be modified with the options below.

- options      This is a list of options controlling translation from and to prolog.
- *boolvec* (see option `rolog.boolvec`, default is `!`) is the name of the prolog compound for vectors of booleans.
  - *intvec*, *realvec*, *charvec* define the compound names for vectors of integers, doubles and strings, respectively (defaults are `%`, `#` and `$$`).
  - If *scalar* is TRUE (default), vectors of length 1 are translated to scalar prolog elements. If *scalar* is FALSE, vectors of length 1 are also translated to compounds.

### Details

The R elements are translated to the following prolog citizens:

- numeric -> real (vectors of size  $N$  ->  $\#/N$ )
- integer -> integer (vectors ->  $\%/N$ )
- character -> string (vectors ->  $$$/N$ )
- symbol/name -> atom
- expression -> variable
- call/language -> compound
- boolean -> true, false (atoms)
- list -> list

### Value

character string with the prolog syntax of the call

### See Also

[rolog\\_options\(\)](#) for fine-grained control over the translation

---

postproc	<i>Default hook for postprocessing</i>
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---

### Description

Default hook for postprocessing

### Usage

```
postproc(constraint = call("=<", 1, 2))
```

### Arguments

constraint      the R call representing constraints of the Prolog query.

**Value**

The default hook translates the inequality and smaller-than-or-equal-to back from Prolog ( $\backslash=$ ,  $=<$ ) to R ( $\neq$ ,  $<=$ ).

**See Also**

[`rolog_options()`] for fine-grained control over the translation

---

preproc	<i>Default hook for preprocessing</i>
---------	---------------------------------------

---

**Description**

Default hook for preprocessing

**Usage**

```
preproc(query = quote(1 <= sin))
```

**Arguments**

query            the R call representing the Prolog query.

**Value**

The default hook translates the inequality and smaller-than-or-equal-to from R ( $\neq$ ,  $<=$ ) to Prolog ( $\backslash=$ ,  $=<$ ). Moreover, primitive functions are converted to regular functions.

**See Also**

[`rolog_options()`] for fine-grained control over the translation

---

query	<i>Create a query</i>
-------	-----------------------

---

**Description**

Create a query

**Usage**

```
query(
  query = call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y))),
  options = NULL,
  env = globalenv()
)
```

**Arguments**

query	an R call. The R call consists of symbols, integers and real numbers, character strings, boolean values, expressions, lists, and other calls. Vectors of booleans, integers, floating point numbers, and strings with length $N > 1$ are translated to prolog compounds <code>!/N</code> , <code>%/N</code> , <code>#/N</code> and <code>\$\$/N</code> , respectively. The names can be modified with the options below.
options	This is a list of options controlling translation from and to prolog. <ul style="list-style-type: none"> <li>• <i>boolvec</i> (see option <code>rolog.boolvec</code>, default is <code>!</code>) is the name of the prolog compound for vectors of booleans.</li> <li>• <i>intvec</i>, <i>realvec</i>, <i>charvec</i> define the compound names for vectors of integers, doubles and strings, respectively (defaults are <code>%</code>, <code>#</code> and <code>\$\$</code>).</li> <li>• If <i>scalar</i> is <code>TRUE</code> (default), vectors of length 1 are translated to scalar prolog elements. If <i>scalar</i> is <code>FALSE</code>, vectors of length 1 are also translated to compounds.</li> </ul>
env	The R environment in which the query is run (default: <code>globalenv()</code> ). This is mostly relevant for <code>r_eval/2</code> .

**Details**

SWI-Prolog does not allow multiple open queries. If another query is open, it is closed and a warning is shown.

**Value**

If the creation of the query succeeds, `TRUE`.

**See Also**

[once\(\)](#) for a query that is submitted only a single time.

[findall\(\)](#) for a query that is submitted until it fails.

**Examples**

```
query(call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y))))
submit() # X = a
submit() # X = "b"
clear()

query(call("member", expression(X), list(quote(a), "b", 3L, 4, TRUE, expression(Y),
  NA, NaN, Inf, NULL, function(x) {y <- sin(x); y^2}))))
submit() # X = a
submit() # X = "b"
submit() # X = 3L
submit() # X = 4.0
submit() # X = TRUE
submit() # X = expression(Y) or Y = expression(X)
submit() # X = NA
submit() # X = NaN
submit() # X = Inf
```

```

submit() # X = NULL
submit() # X = function(x) {y <- sin(x); y^2})
submit() # FALSE (no more results)
submit() # warning that no query is open

query(call("member", expression(X), list(quote(a), "b", 3L, 4)))
query(call("member", expression(X), list(TRUE, expression(Y)))) # warning that another query is open
clear()

```

---

rolog_done	<i>Clean up when detaching the library</i>
------------	--

---

**Description**

Clean up when detaching the library

**Usage**

```
rolog_done()
```

**Value**

‘TRUE’ on success

---

rolog_init	<i>Start prolog</i>
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---

**Description**

Start prolog

**Usage**

```
rolog_init(argv1 = commandArgs()[1])
```

**Arguments**

argv1            file name of the R executable

**Details**

SWI-prolog is automatically initialized when the rolog library is loaded, so this function is normally not directly invoked.

**Value**

‘TRUE’ on success

---

rolog_ok	<i>Check if rolog is properly loaded</i>
----------	--

---

**Description**

Check if rolog is properly loaded

**Usage**

```
rolog_ok(warn = FALSE, stop = FALSE)
```

**Arguments**

warn	raise a warning if problems occurred
stop	raise an error if problems occurred

**Value**

TRUE if rolog is properly loaded

---

rolog_options	<i>Quick access the package options</i>
---------------	---

---

**Description**

Quick access the package options

**Usage**

```
rolog_options()
```

**Details**

Translation from R to Prolog

- numeric vector of size N -> *realvec/N* (default is ##)
- integer vector of size N -> *intvec/N* (default is %%)
- boolean vector of size N -> *boolvec/N* (default is !!)
- character vector of size N -> *charvec/N* (default is \$\$)
- *scalar*: if TRUE (default), translate R vectors of length 1 to scalars
- *portray*: if TRUE (default) whether to return the prolog translation as an attribute to the return value of [once\(\)](#), [query\(\)](#) and [findall\(\)](#)

**Value**

list with some options for translating R expressions to prolog

---

submit

---

*Submit a query that has been opened with `query()` before.*


---

**Description**

Submit a query that has been opened with `query()` before.

**Usage**

```
submit(options = NULL)
```

**Arguments**

`options` This is a list of options controlling translation from and to Prolog. Here, only *postproc* is relevant.

**Value**

If the query fails, FALSE is returned. If the query succeeds, a (possibly empty) list is returned that includes the bindings required to satisfy the query.

**See Also**

`query()` for a opening a query.

`rolog_options()` for fine-grained control on the translation from R to Prolog and back.

`clear()` for a clearing a query.

`once()` for a opening a query, submitting it, and clearing it again.

`findall()` for a opening a query, collecting all solutions, and clearing it again.

**Examples**

```
query(call("member", expression(X), list(quote(a), "b", 3L, 4, expression(Y))))
submit() # X = 3L
submit() # X = 4.0
submit() # X = TRUE
submit() # X = expression(Y) or Y = expression(X)
submit() # FALSE
submit() # warning that no query is open
```

```
query(call("member", expression(X), list(quote(a), "b", 3L, 4)))
submit() # X = a
submit() # X = "b"
clear()
```

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