

# Package: rxode2 (via r-universe)

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**Version** 3.0.1

**Title** Facilities for Simulating from ODE-Based Models

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**Depends** R (>= 4.0.0)

**Suggests** Matrix, DT, covr, crayon, curl, digest, dplyr (>= 0.8.0),  
ggrepel, gridExtra, htmltools, knitr, learnr, microbenchmark,  
nlme, remotes, rlang, rmarkdown, scales, shiny, stringi,  
symengine, testthat, tidyr, usethis, vdiff (>= 1.0), withr,  
xgxr, pillar, tibble, units (>= 0.6-0), rsconnect, devtools,  
patchwork, nlmixr2data, lifecycle, kableExtra

**Imports** PreciseSums (>= 0.7), Rcpp (>= 0.12.3), backports, cli (>= 2.0.0), checkmate, ggplot2 (>= 3.4.0), inline, lotri (>= 1.0.0), magrittr, memoise, methods, rex, sys, tools, utils, dparser (>= 1.3.1-12), rxode2ll (>= 2.0.9), data.table (>= 1.12.4), qs (>= 0.26.3)

**Description** Facilities for running simulations from ordinary differential equation ('ODE') models, such as pharmacometrics and other compartmental models. A compilation manager translates the ODE model into C, compiles it, and dynamically loads the object code into R for improved computational efficiency. An event table object facilitates the specification of complex dosing regimens (optional) and sampling schedules. NB: The use of this package requires both C and Fortran compilers, for details on their use with R please see Section 6.3, Appendix A, and Appendix D in the ``R Administration and Installation'' manual. Also the code is mostly released under GPL. The 'VODE' and 'LSODA' are in the public domain. The information is available in the inst/COPYRIGHTS.

**BugReports** <https://github.com/nlmixr2/rxode2/issues/>

**NeedsCompilation** yes

**VignetteBuilder** knitr

**License** GPL (>= 3)

**URL** <https://nlmixr2.github.io/rxode2/>,  
<https://github.com/nlmixr2/rxode2/>

**RoxygenNote** 7.3.2

**Biarch** true

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 RcppArmadillo (>= 0.9.300.2.0), BH, RcppParallel, RcppEigen (>= 0.3.3.9.2), StanHeaders (>= 2.21.0.7), dparser (>= 1.3.1-12)

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---

.cbindOme	<i>cbind Ome</i>
-----------	------------------

---

**Description**

cbind Ome

**Usage**

```
.cbindOme(et, mat, n)
```

**Arguments**

et	The theta data frame
mat	The full matrix simulation from omegas
n	number of subject simulated

**Value**

data frame with et combined with simulated omega matrix values

**Author(s)**

Matthew Fidler

---

.collectWarnings      *Collect warnings and just warn once.*

---

**Description**

Collect warnings and just warn once.

**Usage**

```
.collectWarnings(expr, lst = FALSE)
```

**Arguments**

expr	R expression
lst	When TRUE return a list with list(object,warnings) instead of issuing the warnings. Otherwise, when FALSE issue the warnings and return the object.

**Value**

The value of the expression or a list with the value of the expression and a list of warning messages

**Author(s)**

Matthew L. Fidler

---

.copyUi      *This copies the rxode2 UI object so it can be modified*

---

**Description**

This copies the rxode2 UI object so it can be modified

**Usage**

```
.copyUi(ui)
```

**Arguments**

ui	Original UI object
----	--------------------

**Value**

Copied UI object

**Author(s)**

Matthew L. Fidler

---

```
.handleSingleErrTypeNormOrTFoeciBase
```

*Handle the single error for normal or t distributions*

---

### Description

Handle the single error for normal or t distributions

### Usage

```
.handleSingleErrTypeNormOrTFoeciBase(
  env,
  pred1,
  errNum = 1L,
  rxPredLlik = TRUE
)
```

### Arguments

<code>env</code>	Environment for the parsed model
<code>pred1</code>	The data.frame of the current error
<code>errNum</code>	The number of the error specification in the nlmixr2 model
<code>rxPredLlik</code>	A boolean indicating if the log likelihood should be calculated for non-normal distributions. By default TRUE.

### Value

A list of the lines added. The lines will contain

- `rx_yj_` which is an integer that corresponds to the transformation type.
- `rx_lambda_` is the transformation lambda
- `rx_low_` The lower boundary of the transformation
- `rx_hi_` The upper boundary of the transformation
- `rx_pred_f_` The prediction function
- `rx_pred_` The transformed prediction function
- `rx_r_` The transformed variance

### Author(s)

Matthew Fidler



---

`.matchesLangTemplate` *Check if a language object matches a template language object*

---

### Description

- If `template == str2lang(".")`, it will match anything.
- If `template == str2lang(".name")`, it will match any name.
- If `template == str2lang(".call()")`, it will match any call.

### Usage

```
.matchesLangTemplate(x, template)
```

### Arguments

<code>x</code>	The object to check
<code>template</code>	The template object it should match

### Value

TRUE if it matches, FALSE, otherwise

### Examples

```
.matchesLangTemplate(str2lang("d/dt(foo)"), str2lang("d/dt(.name)"))  
.matchesLangTemplate(str2lang("d/dt(foo)"), str2lang("d/foo(.name)"))  
.matchesLangTemplate(str2lang("d/dt(foo)"), str2lang("d/."))
```

---

`.modelHandleModelLines`

*Handle model lines*

---

### Description

Handle model lines

### Usage

```
.modelHandleModelLines(  
  modelLines,  
  rxui,  
  modifyIni = FALSE,  
  append = NULL,  
  auto = getOption("rxode2.autoVarPiping", TRUE),  
  cov = NULL,  
  envir  
)
```

**Arguments**

modellines	The model lines that are being considered
rxui	The rxode2 UI object
modifyIni	Should the ini() be considered
append	This is a boolean to determine if the lines are appended in piping. The possible values for this is: <ul style="list-style-type: none"> <li>• TRUE which is when the lines are appended to the model instead of replaced</li> <li>• FALSE when the lines are replaced in the model (default)</li> <li>• NA is when the lines are pre-pended to the model instead of replaced</li> <li>• lhs expression, which will append the lines after the last observed line of the expression lhs</li> </ul>
auto	This boolean tells if piping automatically selects the parameters should be characterized as a population parameter, between subject variability, or a covariate. When TRUE this automatic selection occurs. When FALSE this automatic selection is turned off and everything is added as a covariate (which can be promoted to a parameter with the ini statement). By default this is TRUE, but it can be changed by options(rxode2.autoVarPiping=FALSE).
cov	is a character vector of variables that should be assumed to be covariates. This will override automatic promotion to a population parameter estimate (or an eta)
envir	Environment for evaluation

**Value**

New UI

**Author(s)**

Matthew L. Fidler

---

.quoteCallInfoLines *Returns quoted call information*

---

**Description**

Returns quoted call information

**Usage**

```
.quoteCallInfoLines(callInfo, envir = parent.frame(), iniDf = NULL)
```

**Arguments**

callInfo	Call information
envir	Environment for evaluation (if needed)
iniDf	The parent model iniDf when piping in a ini block (NULL otherwise)

**Value**

Quote call information. for name=expression, change to name<-expression in quoted call list. For expressions that are within brackets ie {}, unlist the brackets as if they were called in one single sequence.

**Author(s)**

Matthew L. Fidler

---

.rxLinCmtGen	<i>Internal function to generate the model variables for a linCmt() model</i>
--------------	---

---

**Description**

Internal function to generate the model variables for a linCmt() model

**Usage**

```
.rxLinCmtGen(lenState, vars)
```

**Arguments**

lenState	Length of the state
vars	Variables in the model

**Value**

Model variables of expanded linCmt model

**Author(s)**

Matthew L. Fidler

---

.rxode2ptrs	<i>Get the rxode2 function pointers</i>
-------------	---

---

**Description**

This function is used to get the function pointers for rxode2. This is used to allow rxode2 to have binary linkage to nlmixr2est.

**Usage**

```
.rxode2ptrs()
```

**Value**

a list of function pointers

**Author(s)**

Matthew L. Fidler

**Examples**

```
.rxode2ptrs()
```

---

`.rxWithOptions`

*Temporarily set options then restore them while running code*

---

**Description**

Temporarily set options then restore them while running code

**Usage**

```
.rxWithOptions(ops, code)
```

**Arguments**

<code>ops</code>	list of options that will be temporarily set for the code
<code>code</code>	The code to run during the sink

**Value**

value of code

**Examples**

```
.rxWithOptions(list(digits = 21), {  
  print(pi)  
})  
  
print(pi)
```

---

.rxWithWd                      *Temporarily set options then restore them while running code*

---

**Description**

Temporarily set options then restore them while running code

**Usage**

```
.rxWithWd(wd, code)
```

**Arguments**

wd	working directory to temporarily set the system to while evaluating the code
code	The code to run during the sink

**Value**

value of code

**Examples**

```
.rxWithWd(tempdir(), {  
  getwd()  
})  
  
getwd()
```

---

.toClassicEvid                      *This converts NONMEM-style EVIDs to classic RxODE events*

---

**Description**

This converts NONMEM-style EVIDs to classic RxODE events

**Usage**

```
.toClassicEvid(cmt = 1L, amt = 0, rate = 0, dur = 0, ii = 0, evid = 0L, ss = 0)
```

**Arguments**

cmt	compartment flag
amt	dose amount
rate	dose rate
dur	dose duration
ii	inter-dose interval
evid	event id
ss	steady state

**Value**

classic evids, excluding evids that are added (you need to add them manually) or simply use etTran. This is mostly for testing and really shouldn't be used directly.

**Author(s)**

Matthew L. Fidler

**Examples**

```
.toClassicEvid(cmt=10, amt=3, evid=1)
.toClassicEvid(cmt=10, amt=3, rate=2, evid=1)
.toClassicEvid(cmt=10, amt=3, rate=-1, evid=1)
.toClassicEvid(cmt=10, amt=3, rate=-2, evid=1)
.toClassicEvid(cmt=10, amt=3, dur=2, evid=1)
.toClassicEvid(cmt=304, amt=3, dur=2, evid=1)
.toClassicEvid(cmt=7, amt=0, rate=2, evid=1, ss=1)
.toClassicEvid(cmt=-10, amt=3, evid=1)
.toClassicEvid(cmt=10, amt=3, evid=5)
.toClassicEvid(cmt=6, amt=3, evid=6)
.toClassicEvid(cmt=6, amt=3, evid=7)
.toClassicEvid(evid=2)
.toClassicEvid(evid=4)
```

---

```
.vecDf
```

*Convert numeric vector to repeated data.frame*

---

**Description**

Convert numeric vector to repeated data.frame

**Usage**

```
.vecDf(vec, n)
```

**Arguments**

vec	Named input vector
n	Number of columns

**Value**

Data frame with repeated vec

**Author(s)**

Matthew Fidler

---

add.dosing	<i>Add dosing to eventTable</i>
------------	---------------------------------

---

**Description**

This adds a dosing event to the event table. This is provided for piping syntax through magrittr. It can also be accessed by eventTable\$add.dosing(...)

**Usage**

```
add.dosing(
  eventTable,
  dose,
  nbr.doses = 1L,
  dosing.interval = 24,
  dosing.to = 1L,
  rate = NULL,
  amount.units = NA_character_,
  start.time = 0,
  do.sampling = FALSE,
  time.units = NA_character_,
  ...
)
```

**Arguments**

eventTable	eventTable object; When accessed from object it would be eventTable\$
dose	numeric scalar, dose amount in amount.units;
nbr.doses	integer, number of doses;
dosing.interval	required numeric scalar, time between doses in time.units, defaults to 24 of time.units="hours";
dosing.to	integer, compartment the dose goes into (first compartment by default);

rate	for infusions, the rate of infusion (default is NULL, for bolus dosing;
amount.units	optional string indicating the dosing units. Defaults to NA to indicate as per the original EventTable definition.
start.time	required dosing start time;
do.sampling	logical, should observation sampling records be added at the dosing times? Defaults to FALSE.
time.units	optional string indicating the time units. Defaults to "hours" to indicate as per the original EventTable definition.
...	Other parameters passed to <code>et()</code> .

**Value**

eventTable with updated dosing (note the event table will be updated anyway)

**Author(s)**

Matthew L. Fidler

Matthew L Fidler, Wenping Wang

**References**

Wang W, Hallow K, James D (2015). "A Tutorial on rxode2: Simulating Differential Equation Pharmacometric Models in R." CPT: Pharmacometrics and Systems Pharmacology, 5(1), 3-10. ISSN 2163-8306

**See Also**

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

**Examples**

```
library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function

mod1 <-function(){
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
```



```

  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days
et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

plot(infusionQd, C2)

## 2wk-on, 1wk-off

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

```

```
plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

qd <-et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5,by=0.005),weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)
```

---

add.sampling

*Add sampling to eventTable*

---

### Description

This adds a dosing event to the event table. This is provided for piping syntax through magrittr. It can also be accessed by `eventTable$add.sampling()`

### Usage

```
add.sampling(eventTable, time, time.units = NA)
```

### Arguments

<code>eventTable</code>	An eventTable object. When accessed from object it would be <code>eventTable\$</code>
<code>time</code>	a vector of time values (in <code>time.units</code> ).
<code>time.units</code>	an optional string specifying the time units. Defaults to the units specified when the EventTable was initialized.

### Value

`eventTable` with updated sampling. (Note the event table will be updated even if you don't reassign the eventTable)

### Author(s)

Matthew L Fidler, Wenping Wang

### References

Wang W, Hallow K, James D (2015). "A Tutorial on rxode2: Simulating Differential Equation Pharmacometric Models in R." *CPT: Pharmacometrics and Systems Pharmacology*, 5(1), 3-10. ISSN 2163-8306

**See Also**

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

**Examples**

```

library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function

mod1 <-function(){
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days

et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

```

```
## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

plot(infusionQd, C2)

## 2wk-on, 1wk-off

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5,by=0.005),weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)
```

---

as.et

*Coerce object to data.frame*

---

## Description

Coerce object to data.frame

## Usage

as.et(x, ...)

```
## Default S3 method:
as.et(x, ...)
```

### Arguments

x	Object to coerce to et.
...	Other parameters

### Value

An event table

---

as.ini	<i>Turn into an ini block for initialization</i>
--------	--

---

### Description

Turn into an ini block for initialization

### Usage

```
as.ini(x)

## S3 method for class 'character'
as.ini(x)

## S3 method for class 'data.frame'
as.ini(x)

## S3 method for class 'call'
as.ini(x)

## S3 method for class 'lotriFix'
as.ini(x)

## S3 method for class 'matrix'
as.ini(x)

## Default S3 method:
as.ini(x)
```

### Arguments

x	Item to convert to a rxode2/nlmixr2 ui ini expression
---	---

**Value**

rxode2 ini expression

**Author(s)**

Matthew L. Fidler

**Examples**

```
ini <- quote(ini({
  tka <- log(1.57)
  tcl <- log(2.72)
  tv <- log(31.5)
  eta.ka ~ 0.6
  eta.cl ~ 0.3
  eta.v ~ 0.1
  add.sd <- 0.7
}))
```

```
as.ini(ini)
```

```
l <- quote(lotri({
  tka <- log(1.57)
  tcl <- log(2.72)
  tv <- log(31.5)
  eta.ka ~ 0.6
  eta.cl ~ 0.3
  eta.v ~ 0.1
  add.sd <- 0.7
}))
```

```
as.ini(l)
```

```
m <- lotri({
  eta.ka ~ 0.6
  eta.cl ~ 0.3
  eta.v ~ 0.1
})
```

```
as.ini(m)
```

```
one.compartment <- function() {
  ini({
    tka <- log(1.57)
    tcl <- log(2.72)
    tv <- log(31.5)
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
```

```

    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
    cp ~ add(add.sd)
  })
}

as.ini(one.compartment)

ui <- one.compartment()

as.ini(ui)

ui$iniDf

as.ini(ui$iniDf)

ini <- c("ini({",
        "tka <- log(1.57)",
        "tcl <- log(2.72)",
        "tv <- log(31.5)",
        "eta.ka ~ 0.6",
        "eta.cl ~ 0.3",
        "eta.v ~ 0.1",
        "add.sd <- 0.7",
        "})")

as.ini(ini)

ini <- paste(ini, collapse="\n")

as.ini(ini)

```

---

as.model

*Turn into a model expression*


---

### Description

Turn into a model expression

### Usage

```
as.model(x)
```

```
## S3 method for class 'character'
as.model(x)
```

```
## S3 method for class 'call'
as.model(x)

## S3 method for class 'list'
as.model(x)

## Default S3 method:
as.model(x)
```

### Arguments

x                    item to convert to a model({}) expression

### Value

model expression

### Author(s)

Matthew L. Fidler

### Examples

```
model <- quote(model({
  ka <- exp(tka + eta.ka)
  cl <- exp(tcl + eta.cl)
  v <- exp(tv + eta.v)
  d/dt(depot) = -ka * depot
  d/dt(center) = ka * depot - cl / v * center
  cp = center / v
  cp ~ add(add.sd)
}))

as.model(model)

one.compartment <- function() {
  ini({
    tka <- log(1.57)
    tcl <- log(2.72)
    tv <- log(31.5)
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
```



```

      cp = center / v
      cp ~ add(add.sd)
    })
  }

  as.model(one.compartment)

  ui <- one.compartment()

  as.model(ui)

  model <- c("model({",
            "ka <- exp(tka + eta.ka)",
            "cl <- exp(tcl + eta.cl)",
            "v <- exp(tv + eta.v)",
            "d/dt(depot) = -ka * depot",
            "d/dt(center) = ka * depot - cl / v * center",
            "cp = center / v",
            "cp ~ add(add.sd)",
            "})")

  as.model(model)

  model <- paste(model, collapse="\n")

  as.model(model)

```

---

as.rxUi

*As rxode2 ui*


---

## Description

As rxode2 ui

## Usage

```

as.rxUi(x)

## S3 method for class 'rxode2'
as.rxUi(x)

## S3 method for class 'rxode2tos'
as.rxUi(x)

## S3 method for class 'rxModelVars'
as.rxUi(x)

## S3 method for class '`function`'

```

```

as.rxUi(x)

## S3 method for class 'rxUi'
as.rxUi(x)

## Default S3 method:
as.rxUi(x)

```

### Arguments

x                    Object to convert to rxUi object

### Value

rxUi object (or error if it cannot be converted)

### Author(s)

Matthew L. Fidler

### Examples

```

mod1 <- function() {
  ini({
    # central
    KA=2.94E-01
    CL=1.86E+01
    V2=4.02E+01
    # peripheral
    Q=1.05E+01
    V3=2.97E+02
    # effects
    Kin=1
    Kout=1
    EC50=200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    eff(0) <- 1
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

as.rxUi(mod1)

```

---

`assertCompartmentExists`*Verify that the compartment exists in a model*

---

**Description**

Verify that the compartment exists in a model

**Usage**

```
assertCompartmentExists(ui, x)
```

```
testCompartmentExists(ui, x)
```

**Arguments**

`ui` is the model to test

`x` The value to test (can be a vector of strings)

**Value**

the value of the compartment that exists; if it is a vector returns the first item that matches

**Functions**

- `testCompartmentExists()`: Test if compartment exists

**Author(s)**

Matthew Fidler & Bill Denney

**See Also**

Other Assertions: [assertCompartmentName\(\)](#), [assertCompartmentNew\(\)](#), [assertRxUi\(\)](#), [assertVariableExists\(\)](#), [assertVariableNew\(\)](#), [testRxUnbounded\(\)](#)

---

assertCompartmentName *Verify that a value is a valid nlmixr2 compartment name*

---

**Description**

Verify that a value is a valid nlmixr2 compartment name

**Usage**

```
assertCompartmentName(x)
```

```
assertVariableName(x)
```

```
assertParameterValue(x)
```

```
assertExists(ui, x)
```

```
testExists(ui, x)
```

**Arguments**

x	The value to test
ui	when needed, this is the rxode2/nlmixr2 model

**Value**

The value or an error

**Functions**

- `assertVariableName()`: Verify that a value is a valid nlmixr2 variable name
- `assertParameterValue()`: Verify that a value is a valid nlmixr2 parameter value
- `assertExists()`: Assert compartment/variable exists
- `testExists()`: Test compartment/variable exists

**Author(s)**

Bill Denney

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentNew\(\)](#), [assertRxUi\(\)](#), [assertVariableExists\(\)](#), [assertVariableNew\(\)](#), [testRxUnbounded\(\)](#)

---

assertCompartmentNew    *Verify that a compartment would be new to the model*

---

**Description**

Verify that a compartment would be new to the model

**Usage**

```
assertCompartmentNew(ui, x)
```

**Arguments**

ui	is the model to test that a model paramet exists
x	The value to test

**Value**

The value or an error

**Author(s)**

Matthew Fidler & Bill Denney

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentName\(\)](#), [assertRxUi\(\)](#), [assertVariableExists\(\)](#), [assertVariableNew\(\)](#), [testRxUnbounded\(\)](#)

---

assertRxUi    *Assert properties of the rxUi models*

---

**Description**

Assert properties of the rxUi models

**Usage**

```
assertRxUi(ui, extra = "", .var.name = .vname(ui))  
  
assertRxUiPrediction(ui, extra = "", .var.name = .vname(ui))  
  
assertRxUiSingleEndpoint(ui, extra = "", .var.name = .vname(ui))  
  
assertRxUiTransformNormal(ui, extra = "", .var.name = .vname(ui))
```

```

assertRxUiNormal(ui, extra = "", .var.name = .vname(ui))
assertRxUiMuRefOnly(ui, extra = "", .var.name = .vname(ui))
assertRxUiEstimatedResiduals(ui, extra = "", .var.name = .vname(ui))
assertRxUiPopulationOnly(ui, extra = "", .var.name = .vname(ui))
assertRxUiMixedOnly(ui, extra = "", .var.name = .vname(ui))
assertRxUiRandomOnIdOnly(ui, extra = "", .var.name = .vname(ui))

```

### Arguments

<code>ui</code>	Model to check
<code>extra</code>	Extra text to append to the error message (like "for focei")
<code>.var.name</code>	[character(1)] Name of the checked object to print in assertions. Defaults to the heuristic implemented in <a href="#">vname</a> .

### Details

These functions have different types of assertions

- `assertRxUi` – Make sure this is a proper rxode2 model (if not throw error)
- `assertRxUiSingleEndpoint` – Make sure the rxode2 model is only a single endpoint model (if not throw error)
- `assertRxUiTransformNormal` – Make sure that the model residual distribution is normal or transformably normal
- `assertRxUiNormal` – Make sure that the model residual distribution is normal
- `assertRxUiEstimatedResiduals` – Make sure that the residual error parameters are estimated (not modeled).
- `assertRxUiPopulationOnly` – Make sure the model is the population only model (no mixed effects)
- `assertRxUiMixedOnly` – Make sure the model is a mixed effect model (not a population effect, only)
- `assertRxUiPrediction` – Make sure the model has predictions
- `assertRxUiMuRefOnly` – Make sure that all the parameters are mu-referenced
- `assertRxUiRandomOnIdOnly` – Make sure there are only random effects at the ID level

### Value

the rxUi model

### Author(s)

Matthew L. Fidler

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentName\(\)](#), [assertCompartmentNew\(\)](#), [assertVariableExists\(\)](#), [assertVariableNew\(\)](#), [testRxUnbounded\(\)](#)

**Examples**

```
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

assertRxUi(one.cmt)
# assertRxUi(rnorm) # will fail

assertRxUiSingleEndpoint(one.cmt)
```

---

assertVariableExists *Assert a variable exists in the model*

---

**Description**

Assert a variable exists in the model

**Usage**

```
assertVariableExists(ui, x)
```

```
testVariableExists(ui, x)
```

**Arguments**

ui	rxode2 ui model
x	does the x variable exist in the model. If it is a vector of variable check to see if any exists, but all must be valid nlmixr2 variable names

**Value**

variable that matches, in the case of multiple variables, the first that matches. If nothing matches return error

**Functions**

- `testVariableExists()`: Test if variable exists

**Author(s)**

Matthew L. Fidler

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentName\(\)](#), [assertCompartmentNew\(\)](#), [assertRxUi\(\)](#), [assertVariableNew\(\)](#), [testRxUnbounded\(\)](#)

---

`assertVariableNew`      *Assert a variable would be new to the model*

---

**Description**

Assert a variable would be new to the model

**Usage**

```
assertVariableNew(ui, x)
```

**Arguments**

<code>ui</code>	rxode2 ui model
<code>x</code>	would the variable x variable be new in the model

**Value**

nothing, but will error if x would not be new

**Author(s)**

Matthew L. Fidler

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentName\(\)](#), [assertCompartmentNew\(\)](#), [assertRxUi\(\)](#), [assertVariableExists\(\)](#), [testRxUnbounded\(\)](#)



---

binomProbs	<i>Calculate expected confidence bands with binomial sampling distribution</i>
------------	--

---

### Description

This is meant to perform in the same way as `quantile()` so it can be a drop in replacement for code using `quantile()` but using distributional assumptions.

### Usage

```
binomProbs(x, ...)

## Default S3 method:
binomProbs(
  x,
  probs = c(0.025, 0.05, 0.5, 0.95, 0.975),
  na.rm = FALSE,
  names = TRUE,
  onlyProbs = TRUE,
  n = 0L,
  m = 0L,
  pred = FALSE,
  piMethod = c("lim"),
  M = 5e+05,
  tol = .Machine$double.eps^0.25,
  ciMethod = c("wilson", "wilsonCorrect", "agrestiCoull", "wald", "wc", "ac"),
  ...
)
```

### Arguments

<code>x</code>	numeric vector whose mean and probability based confidence values are wanted, NA and NaN values are not allowed in numeric vectors unless <code>na.rm</code> is TRUE.
<code>...</code>	Arguments passed to default method, allows many different methods to be applied.
<code>probs</code>	numeric vector of probabilities with values in the interval 0 to 1, inclusive. When 0, it represents the maximum observed, when 1, it represents the maximum observed. When 0.5 it represents the expected probability (mean).
<code>na.rm</code>	logical; if true, any NA and NaN's are removed from <code>x</code> before the quantiles are computed.
<code>names</code>	logical; if true, the result has a <code>names</code> attribute.
<code>onlyProbs</code>	logical; if true, only return the probability based confidence interval/prediction interval estimates, otherwise return extra statistics.

n	integer/integerish; this is the n used to calculate the prediction or confidence interval. When n=0 (default) use the number of non-NA observations. When calculating the prediction interval, this represents the number of observations used in the input ("true") distribution.
m	integer. When using the prediction interval this represents the number of samples that will be observed in the future for the prediction interval.
pred	Use a prediction interval instead of a confidence interval. By default this is FALSE.
piMethod	gives the prediction interval method (currently only lim) from Lu 2020
M	number of simulations to run for the LIM PI.
tol	tolerance of root finding in the LIM prediction interval
ciMethod	gives the method for calculating the confidence interval. Can be: <ul style="list-style-type: none"> <li>• "argestiCoull" or "ac" – Agresti-Coull method. For a 95\ interval, this method does not use the concept of "adding 2 successes and 2 failures," but rather uses the formulas explicitly described in the following link: <a href="https://en.wikipedia.org/wiki/Binomial_proportion_confidence_interval#Agresti-Coull_Interval">https://en.wikipedia.org/wiki/Binomial_proportion_confidence_interval#Agresti-Coull_Interval</a>.</li> <li>• "wilson" – Wilson Method</li> <li>• "wilsonCorrect" or "wc" – Wilson method with continuity correction</li> <li>• "wald" – Wald confidence interval or standard z approximation.</li> </ul>

### Details

It is used for confidence intervals with rxode2 solved objects using `confint(mean="binom")`

### Value

By default the return has the probabilities as names (if named) with the points where the expected distribution are located given the sampling mean and standard deviation. If `onlyProbs=FALSE` then it would prepend mean, variance, standard deviation, minimum, maximum and number of non-NA observations.

### Author(s)

Matthew L. Fidler

### References

- Newcombe, R. G. (1998). "Two-sided confidence intervals for the single proportion: comparison of seven methods". *Statistics in Medicine*. 17 (8): 857–872. doi:10.1002/(SICI)1097-0258(19980430)17:8<857::AID-SIM777>3.0.CO;2-E. PMID 9595616.
- Hezhi Lu, Hua Jin, A new prediction interval for binomial random variable based on inferential models, *Journal of Statistical Planning and Inference*, Volume 205, 2020, Pages 156-174, ISSN 0378-3758, <https://doi.org/10.1016/j.jspi.2019.07.001>.

**Examples**

```
x<- rbinom(7001, p=0.375, size=1)
binomProbs(x)

# you can also use the prediction interval

binomProbs(x, pred=TRUE)

# Can get some extra statistics if you request onlyProbs=FALSE
binomProbs(x, onlyProbs=FALSE)

x[2] <- NA_real_

binomProbs(x, onlyProbs=FALSE)

binomProbs(x, na.rm=TRUE)
```

---

boxCox

*boxCox/yeoJohnson and inverse boxCox/yeoJohnson functions*

---

**Description**

boxCox/yeoJohnson and inverse boxCox/yeoJohnson functions

**Usage**

```
boxCox(x, lambda = 1)

boxCoxInv(x, lambda = 1)

yeoJohnson(x, lambda = 1)

yeoJohnsonInv(x, lambda = 1)
```

**Arguments**

x	input value(s) to transform
lambda	lambda value for the transformation

**Value**

values from boxCox and boxCoxInv

**Examples**

```
boxCox(10, 0.5)
```

```
boxCoxInv(4.32, 0.5)
```

```
yeoJohnson(10, 0.5)
```

```
yeoJohnsonInv(4.32, 0.5)
```

---

cvPost	<i>Sample a covariance Matrix from the Posterior Inverse Wishart distribution.</i>
--------	--

---

**Description**

Note this Inverse wishart rescaled to match the original scale of the covariance matrix.

**Usage**

```
cvPost(
  nu,
  omega,
  n = 1L,
  omegaIsChol = FALSE,
  returnChol = FALSE,
  type = c("invWishart", "lkj", "separation"),
  diagXformType = c("log", "identity", "variance", "nlmixrSqrt", "nlmixrLog",
    "nlmixrIdentity")
)
```

**Arguments**

nu	Degrees of Freedom (Number of Observations) for covariance matrix simulation.
omega	Either the estimate of covariance matrix or the estimated standard deviations in matrix form each row forming the standard deviation simulated values
n	Number of Matrices to sample. By default this is 1. This is only useful when omega is a matrix. Otherwise it is determined by the number of rows in the input omega matrix of standard deviations
omegaIsChol	is an indicator of if the omega matrix is in the Cholesky decomposition. This is only used when type="invWishart"
returnChol	Return the Cholesky decomposition of the covariance matrix sample. This is only used when type="invWishart"
type	The type of covariance posterior that is being simulated. This can be:

- `invWishart` The posterior is an inverse wishart; This allows for correlations between parameters to be modeled. All the uncertainty in the parameter is captured in the degrees of freedom parameter.
- `lkj` The posterior separates the standard deviation estimates (modeled outside and provided in the `omega` argument) and the correlation estimates. The correlation estimate is simulated with the `rLKJ1()`. This simulation uses the relationship  $\eta = (\nu - 1) / 2$ . This is relationship based on the proof of the relationship between the restricted LKJ-distribution and inverse wishart distribution (XXXXXX). Once the correlation posterior is calculated, the estimated standard deviations are then combined with the simulated correlation matrix to create the covariance matrix.
- `separation` Like the `lkj` option, this separates out the estimation of the correlation and standard deviation. Instead of using the LKJ distribution to simulate the correlation, it simulates the inverse wishart of the identity matrix and converts the result to a correlation matrix. This correlation matrix is then used with the standard deviation to calculate the simulated covariance matrix.

`diagXformType` Diagonal transformation type. These could be:

- `log` The standard deviations are log transformed, so the actual standard deviations are  $\exp(\omega)$
- `identity` The standard deviations are not transformed. The standard deviations are not transformed; They should be positive.
- `variance` The variances are specified in the `omega` matrix; They are transformed into standard deviations.
- `nlmixrSqrt` These standard deviations come from an `nlmixr` `omega` matrix where  $\text{diag}(\text{chol}(\text{inv}(\omega))) = x^2$
- `nlmixrLog` These standard deviations come from a `nlmixr` `omega` matrix where  $\text{diag}(\text{chol}(\text{solve}(\omega))) = \exp(x)$
- `nlmixrIdentity` These standard deviations come from a `nlmixr` `omega` matrix where  $\text{diag}(\text{chol}(\text{solve}(\omega))) = x$

The `nlmixr` transformations only make sense when there is no off-diagonal correlations modeled.

## Details

If your covariance matrix is a 1x1 matrix, this uses an scaled inverse chi-squared which is equivalent to the Inverse Wishart distribution in the uni-directional case.

In general, the separation strategy is preferred for diagonal matrices. If the dimension of the matrix is below 10, `lkj` is numerically faster than separation method. However, the `lkj` method has densities too close to zero (XXXX) when the dimension is above 10. In that case, though computationally more expensive separation method performs better.

For matrices with modeled covariances, the easiest method to use is the inverse Wishart which allows the simulation of correlation matrices (XXXX). This method is more well suited for well behaved matrices, that is the variance components are not too low or too high. When modeling non-linear mixed effects modeling matrices with too high or low variances are considered sub-optimal in describing a system. With these rules in mind, it is reasonable to use the inverse Wishart.

**Value**

a matrix (n=1) or a list of matrices (n > 1)

**Author(s)**

Matthew L.Fidler & Wenping Wang

**References**

Alvarez I, Niemi J and Simpson M. (2014) *Bayesian Inference for a Covariance Matrix*. Conference on Applied Statistics in Agriculture.

Wang1 Z, Wu Y, and Chu H. (2018) *On Equivalence of the LKJ distribution and the restricted Wishart distribution*. <doi:10.48550/arXiv.1809.047463

**Examples**

```
## Sample a single covariance.
draw1 <- cvPost(3, matrix(c(1, .3, .3, 1), 2, 2))

## Sample 3 covariances
set.seed(42)
draw3 <- cvPost(3, matrix(c(1, .3, .3, 1), 2, 2), n = 3)

## Sample 3 covariances, but return the cholesky decomposition
set.seed(42)
draw3c <- cvPost(3, matrix(c(1, .3, .3, 1), 2, 2), n = 3, returnChol = TRUE)

## Sample 3 covariances with lognormal standard deviations via LKJ
## correlation sample
cvPost(3, sapply(1:3, function(...) {
  rnorm(10)
}), type = "lkj")

## or return cholesky decomposition
cvPost(3, sapply(1:3, function(...) {
  rnorm(10)
}),
type = "lkj",
returnChol = TRUE
)

## Sample 3 covariances with lognormal standard deviations via separation
## strategy using inverse Wishart correlation sample
cvPost(3, sapply(1:3, function(...) {
  rnorm(10)
}), type = "separation")

## or returning the cholesky decomposition
cvPost(3, sapply(1:3, function(...) {
  rnorm(10)
}),
```

```

type = "separation",
returnChol = TRUE
)

```

---

dfWishart

*This uses simulations to match the rse*


---

## Description

This uses simulations to match the rse

## Usage

```
dfWishart(omega, n, rse, upper, totN = 1000, diag = TRUE, seed = 1234)
```

## Arguments

omega	represents the matrix for simulation
n	This represents the number of subjects/samples this comes from (used to calculate rse). When present it assumes the $rse = \sqrt{2}/\sqrt{n}$
rse	This is the rse that we try to match, if not specified, it is derived from n
upper	The upper boundary for root finding in terms of degrees of freedom. If not specified, it is $n*200$
totN	This represents the total number of simulated inverse wishart deviates
diag	When TRUE, represents the rse to match is the diagonals, otherwise it is the total matrix.
seed	to make the simulation reproducible, this represents the seed that is used for simulating the inverse Wishart distribution

## Value

output from `uniroot()` to find the right estimate

## Author(s)

Matthew L. Fidler

## Examples

```
dfWishart(lotri::lotri(a+b~c(1, 0.5, 1)), 100)
```

---

erf                      *Error function*

---

**Description**

Error function

**Usage**

erf(x)

**Arguments**

x                      vector or real values

**Value**

erf of x

**Author(s)**

Matthew L. Fidler

**Examples**

```
erf(1.0)
```

---

et                      *Event Table Function*

---

**Description**

Event Table Function

**Usage**

```
et(x, ..., envir = parent.frame())

## S3 method for class 'rxode2'
et(x, ..., envir = parent.frame())

## S3 method for class '`function`'
et(x, ..., envir = parent.frame())

## S3 method for class 'rxUi'
et(x, ..., envir = parent.frame())
```



```

## S3 method for class 'rxSolve'
et(x, ..., envir = parent.frame())

## S3 method for class 'rxParams'
et(x, ..., envir = parent.frame())

## Default S3 method:
et(
  x,
  ...,
  time,
  amt,
  evid,
  cmt,
  ii,
  addl,
  ss,
  rate,
  dur,
  until,
  id,
  amountUnits,
  timeUnits,
  addSampling,
  envir = parent.frame(),
  by = NULL,
  length.out = NULL
)

```

## Arguments

x	This is the first argument supplied to the event table. This is named to allow et to be used in a pipe-line with arbitrary objects.
...	Times or event tables. They can also be one of the named arguments below.
envir	the <a href="#">environment</a> in which expr is to be evaluated. May also be NULL, a list, a data frame, a pairlist or an integer as specified to <a href="#">sys.call</a> .
time	Time is the time of the dose or the sampling times. This can also be unspecified and is determined by the object type (list or numeric/integer).
amt	Amount of the dose. If specified, this assumes a dosing record, instead of a sampling record.
evid	Event ID; This can be:

Numeric Value	Description
0	An observation. This can also be specified as evid=obs
1	A dose observation. This can also be specified as evid=dose
2	A non-dose event. This can also be specified as evid=other

- 3 A reset event. This can also be specified as `evid=reset`.  
 4 Dose and reset event. This can also be specified as `evid=doseReset` or `evid=resetDose`

Note a reset event resets all the compartment values to zero and turns off all infusions.

`cmt` Compartment name or number. If a number, this is an integer starting at 1. Negative compartments turn off a compartment. If the compartment is a name, the compartment name is changed to the correct state/compartment number before running the simulation. For a compartment named "-cmt" the compartment is turned off.

Can also specify ``cmt`` as ``dosing.to``, ``dose.to``, ``doseTo``, ``dosingTo``, and ``state``.

`ii` When specifying a dose, this is the inter-dose interval for `ss`, `addl` and `until` options (described below).

`addl` The number of additional doses at a inter-dose interval after one dose.

`ss` Steady state flag; It can be one of:

Value	Description
0	This dose is not a steady state dose
1	This dose is a steady state dose with the between/inter-dose interval of <code>ii</code>
2	Superposition steady state

When `ss=2` the steady state dose that uses the super-position principle to allow more complex steady states, like 10 mg in the morning and 20 mg at night, or dosing at 8 am 12 pm and 8 pm instead of every 12 hours. Since it uses the super positioning principle, it only makes sense when you know the kinetics are linear.

All other values of `SS` are currently invalid.

`rate` When positive, this is the rate of infusion. Otherwise:

Value	Description
0	No infusion is on this record
-1	Modeled rate (in <code>rxode2:rate(cmt) =</code> ); Can be <code>et(rate=model)</code> .
-2	Modeled duration (in <code>rxode2: dur(cmt) =</code> ); Can be <code>et(dur=model)</code> or <code>et(rate=dur)</code> .

When a modeled bioavailability is applied to positive rates (`rate > 0`), the duration of infusion is changed. This is because the data specify the rate and amount, the only think that modeled bioavailability can affect is duration.

If instead you want the modeled bioavailability to increase the rate of infusion instead of the duration of infusion, specify the `dur` instead or model the duration with `rate=2`.

dur	Duration of infusion. When amt and dur are specified the rate is calculated from the two data items. When dur is specified instead of rate, the bioavailability changes will increase rate instead of duration.
until	This is the time until the dosing should end. It can be an easier way to figure out how many additional doses are needed over your sampling period.
id	A integer vector of IDs to add or remove from the event table. If the event table is identical for each ID, then you may expand it to include all the IDs in this vector. All the negative IDs in this vector will be removed.
amountUnits	The units for the dosing records (amt)
timeUnits	The units for the time records (time)
addSampling	This is a boolean indicating if a sampling time should be added at the same time as a dosing time. By default this is FALSE.
by	number: increment of the sequence.
length.out	desired length of the sequence. A non-negative number, which for seq and seq.int will be rounded up if fractional.

**Value**

A new event table

**Author(s)**

Matthew L Fidler, Wenping Wang

**References**

Wang W, Hallow K, James D (2015). "A Tutorial on rxode2: Simulating Differential Equation Pharmacometric Models in R." CPT: Pharmacometrics and Systems Pharmacology, 5(1), 3-10. ISSN 2163-8306

**See Also**

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

**Examples**

```
library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function

mod1 <-function(){
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
```

```

V2 <- 4.02E+01
Q <- 1.05E+01
V3 <- 2.97E+02
Kin <- 1
Kout <- 1
EC50 <- 200
})
model({
  C2 <- centr/V2
  C3 <- peri/V3
  d/dt(depot) <- -KA*depot
  d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
  d/dt(peri) <- Q*C2 - Q*C3
  d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
})
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days

et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

plot(infusionQd, C2)

## 2wk-on, 1wk-off

```

```
qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

qd <-et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5,by=0.005),weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)
```

---

etExpand

*Expand additional doses*

---

### **Description**

Expand additional doses

### **Usage**

```
etExpand(et)
```

### **Arguments**

et                    Event table to expand additional doses for.

### **Value**

New event table with addl doses expanded

### **Author(s)**

Matthew Fidler

**Examples**

```

ev <- et(amt = 3, ii = 24, until = 240)
print(ev)
etExpand(ev) # expands event table, but doesn't modify it

print(ev)

ev$expand() ## Expands the current event table and saves it in ev

```

---

etRbind

*Combining event tables*


---

**Description**

Combining event tables

**Usage**

```

etRbind(
  ...,
  samples = c("use", "clear"),
  waitII = c("smart", "+ii"),
  id = c("merge", "unique")
)

## S3 method for class 'rxEt'
rbind(..., deparse.level = 1)

```

**Arguments**

...	The event tables and optionally time between event tables, called waiting times in this help document.
samples	How to handle samples when repeating an event table. The options are: <ul style="list-style-type: none"> <li>• "clear" Clear sampling records before combining the datasets</li> <li>• "use" Use the sampling records when combining the datasets</li> </ul>
waitII	This determines how waiting times between events are handled. The options are: <ul style="list-style-type: none"> <li>• "smart" This "smart" handling of waiting times is the default option. In this case, if the waiting time is above the last observed inter-dose interval in the first combined event table, then the actual time between doses is given by the wait time. If it is smaller than the last observed inter-dose interval, the time between event tables is given by the inter-dose interval + the waiting time between event tables.</li> <li>• "+ii" In this case, the wait time is added to the inter-dose interval no matter the length of the wait time or inter-dose interval</li> </ul>

- `id` This is how `rbind` will handle IDs. There are two different types of options:
- merge with `id="merge"`, the IDs are merged together, overlapping IDs would be merged into a single event table.
  - unique with `id="unique"`, the IDs will be renumbered so that the IDs in all the event tables are not overlapping.
- `deparse.level` The `deparse.level` of a traditional `rbind` is ignored.

### Value

An event table

### Author(s)

Matthew L Fidler

Matthew L Fidler, Wenping Wang

### References

Wang W, Hallow K, James D (2015). "A Tutorial on `rxode2`: Simulating Differential Equation Pharmacometric Models in R." *CPT: Pharmacometrics and Systems Pharmacology*, 5(1), 3-10. ISSN 2163-8306

### See Also

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

### Examples

```
library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function

mod1 <-function(){
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
```

```

    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days

et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

plot(infusionQd, C2)

## 2wk-on, 1wk-off

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

```



```

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5, by=0.005), weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)

```

---

etRep

*Repeat an rxode2 event table*


---

### Description

Repeat an rxode2 event table

### Usage

```

etRep(
  x,
  times = 1,
  length.out = NA,
  each = NA,
  n = NULL,
  wait = 0,
  id = integer(0),
  samples = c("clear", "use"),
  waitII = c("smart", "+ii"),
  ii = 24
)

## S3 method for class 'rxEt'
rep(x, ...)

```

### Arguments

x	An rxode2 event table
times	Number of times to repeat the event table
length.out	Invalid with rxode2 event tables, will throw an error if used.
each	Invalid with rxode2 event tables, will throw an error if used.
n	The number of times to repeat the event table. Overrides times.
wait	Waiting time between each repeated event table. By default there is no waiting, or wait=0

id	A integer vector of IDs to add or remove from the event table. If the event table is identical for each ID, then you may expand it to include all the IDs in this vector. All the negative IDs in this vector will be removed.
samples	How to handle samples when repeating an event table. The options are: <ul style="list-style-type: none"> <li>• "clear" Clear sampling records before combining the datasets</li> <li>• "use" Use the sampling records when combining the datasets</li> </ul>
waitII	This determines how waiting times between events are handled. The options are: <ul style="list-style-type: none"> <li>• "smart" This "smart" handling of waiting times is the default option. In this case, if the waiting time is above the last observed inter-dose interval in the first combined event table, then the actual time between doses is given by the wait time. If it is smaller than the last observed inter-dose interval, the time between event tables is given by the inter-dose interval + the waiting time between event tables.</li> <li>• "+i i" In this case, the wait time is added to the inter-dose interval no matter the length of the wait time or inter-dose interval</li> </ul>
ii	When specifying a dose, this is the inter-dose interval for <code>ss</code> , <code>add1</code> and <code>until</code> options (described below).
...	Times or event tables. They can also be one of the named arguments below.

**Value**

An event table

**Author(s)**

Matthew L Fidler, Wenping Wang

**References**

Wang W, Hallow K, James D (2015). "A Tutorial on rxode2: Simulating Differential Equation Pharmacometric Models in R." *CPT: Pharmacometrics and Systems Pharmacology*, 5(1), 3-10. ISSN 2163-8306

**See Also**

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

**Examples**

```
library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function
```

```

mod1 <-function(){
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days
et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

```

```

plot(infusionQd, C2)

## 2wk-on, 1wk-off

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

qd <-et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5,by=0.005),weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)

```

---

etSeq

*Sequence of event tables*


---

## Description

This combines a sequence of event tables.

## Usage

```

etSeq(..., samples = c("clear", "use"), waitII = c("smart", "+ii"), ii = 24)

## S3 method for class 'rxEt'
seq(...)

```

## Arguments

...	The event tables and optionally time between event tables, called waiting times in this help document.
samples	How to handle samples when repeating an event table. The options are: <ul style="list-style-type: none"> <li>"clear" Clear sampling records before combining the datasets</li> <li>"use" Use the sampling records when combining the datasets</li> </ul>

waitII	This determines how waiting times between events are handled. The options are: <ul style="list-style-type: none"> <li>• "smart" This "smart" handling of waiting times is the default option. In this case, if the waiting time is above the last observed inter-dose interval in the first combined event table, then the actual time between doses is given by the wait time. If it is smaller than the last observed inter-dose interval, the time between event tables is given by the inter-dose interval + the waiting time between event tables.</li> <li>• "+ii" In this case, the wait time is added to the inter-dose interval no matter the length of the wait time or inter-dose interval</li> </ul>
ii	If there was no inter-dose intervals found in the event table, assume that the interdose interval is given by this ii value. By default this is 24.

### Details

This sequences all the event tables in added in the argument list . . . . By default when combining the event tables the offset is at least by the last inter-dose interval in the prior event table (or ii). If you separate any of the event tables by a number, the event tables will be separated at least the wait time defined by that number or the last inter-dose interval.

### Value

An event table

### Author(s)

Matthew L Fidler, Wenping Wang

### References

Wang W, Hallow K, James D (2015). "A Tutorial on rxode2: Simulating Differential Equation Pharmacometric Models in R." CPT: Pharmacometrics and Systems Pharmacology, 5(1), 3-10. ISSN 2163-8306

### See Also

[eventTable](#), [add.sampling](#), [add.dosing](#), [et](#), [etRep](#), [etRbind](#), [rxode2](#)

### Examples

```
library(rxode2)
library(units)

# Model from rxode2 tutorial
# Using a nlmixr2 style function

mod1 <-function(){
  ini({
```

```

    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}

## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days

et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et)

plot(bidQd, C2)

## Now Infusion for 5 days followed by oral for 5 days

## note you can dose to a named compartment instead of using the compartment number
infusion <- et(timeUnits = "hr") %>%
  et(amt=10000, rate=5000, ii=24, until=set_units(5, "days"), cmt="centr")

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(5, "days"), cmt="depot")

et <- seq(infusion,qd)

infusionQd <- rxSolve(mod1, et)

plot(infusionQd, C2)

```

```

## 2wk-on, 1wk-off

qd <- et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- seq(qd, set_units(1,"weeks"), qd) %>%
  add.sampling(set_units(seq(0, 5.5,by=0.005),weeks))

wkOnOff <- rxSolve(mod1, et)

plot(wkOnOff, C2)

## You can also repeat the cycle easily with the rep function

qd <-et(timeUnits = "hr") %>% et(amt=10000, ii=24, until=set_units(2, "weeks"), cmt="depot")

et <- etRep(qd, times=4, wait=set_units(1,"weeks")) %>%
  add.sampling(set_units(seq(0, 12.5,by=0.005),weeks))

repCycle4 <- rxSolve(mod1, et)

plot(repCycle4, C2)

```

---

eventTable

*Create an event table object*


---

## Description

Initializes an object of class ‘EventTable’ with methods for adding and querying dosing and observation records

## Usage

```
eventTable(amount.units = NA, time.units = NA)
```

## Arguments

**amount.units** string denoting the amount dosing units, e.g., “mg”, “ug”. Default to NA to denote unspecified units. It could also be a solved rxode2 object. In that case, eventTable(obj) returns the eventTable that was used to solve the rxode2 object.

**time.units** string denoting the time units, e.g., “hours”, “days”. Default to “hours”.

An eventTable is an object that consists of a data.frame storing ordered time-stamped events of an (unspecified) PK/PD dynamic system, units (strings) for dosing and time records, plus a list of functions to add and extract event records. Currently, events can be of two types: dosing events that represent inputs to the system and sampling time events that represent observations of the system with ‘amount.units’ and ‘time.units’, respectively.

**Value**

A modified data.frame with the following accessible functions:

- `get.EventTable()` returns the current event table
- `add.dosing()` adds dosing records to the event table.
- `get.dosing()` returns a data.frame of dosing records.
- `clear.dosing()` clears or deletes all dosing from event table
- `add.sampling()` adds sampling time observation records to the event table.
- `get.sampling()` returns a data.frame of sampled observation records.
- `clear.sampling()` removes all sampling from event table.
- `get.obs.rec()` returns a logical vector indicating whether each event record represents an observation or not.
- `get.nobs()` returns the number of observation (not dosing) records.
- `get.units()` returns a two-element character vector with the dosing and time units, respectively
- `copy()` makes a copy of the current event table. To create a copy of an event table object use `qd2 <- qd$copy()`
- `expand()` Expands the event table for multi-subject solving. This is done by `qd$expand(400)` for a 400 subject data expansion

**Author(s)**

Matthew Fidler, Melissa Hallow and Wenping Wang

**See Also**

[et\(\)](#)

**Examples**

```
# create dosing and observation (sampling) events
# QD 50mg dosing, 5 days followed by 25mg 5 days
#
qd <- eventTable(amount.units = "mg", time.units = "days")
#
qd$add.dosing(dose = 50, nbr.doses = 5, dosing.interval = 1, do.sampling = FALSE)
#
# sample the system's drug amounts hourly the first day, then every 12 hours
# for the next 4 days
qd$add.sampling(seq(from = 0, to = 1, by = 1 / 24))
qd$add.sampling(seq(from = 1, to = 5, by = 12 / 24))
#
# print(qd$get.dosing())      # table of dosing records
print(qd$get.nobs()) # number of observation (not dosing) records
#
# BID dosing, 5 days
bid <- eventTable("mg", "days") # only dosing
```



```

bid$add.dosing(
  dose = 10000, nbr.doses = 2 * 5,
  dosing.interval = 12, do.sampling = FALSE
)
#
# Use the copy() method to create a copy (clone) of an existing
# event table (simple assignments just create a new reference to
# the same event table object (closure)).
#
bid.ext <- bid$copy() # three-day extension for a 2nd cohort
bid.ext$add.dosing(
  dose = 5000, nbr.doses = 2 * 3,
  start.time = 120, dosing.interval = 12, do.sampling = FALSE
)

# You can also use the Piping operator to create a table

qd2 <- eventTable(amount.units = "mg", time.units = "days") %>%
  add.dosing(dose = 50, nbr.doses = 5, dosing.interval = 1, do.sampling = FALSE) %>%
  add.sampling(seq(from = 0, to = 1, by = 1 / 24)) %>%
  add.sampling(seq(from = 1, to = 5, by = 12 / 24))
# print(qd2$get.dosing()) # table of dosing records
print(qd2$get.nobs()) # number of observation (not dosing) records

# Note that piping with %>% will update the original table.

qd3 <- qd2 %>% add.sampling(seq(from = 5, to = 10, by = 6 / 24))
print(qd2$get.nobs())
print(qd3$get.nobs())

```

---

gammap

*Gammap: normalized lower incomplete gamma function*


---

## Description

This is the `gamma_p` from the `boost` library

## Usage

```
gammap(a, z)
```

## Arguments

<code>a</code>	The numeric 'a' parameter in the normalized lower incomplete gamma
<code>z</code>	The numeric 'z' parameter in the normalized lower incomplete gamma

## Details

The gamma p function is given by:

$$\text{gammap} = \text{lowergamma}(a, z) / \text{gamma}(a)$$

**Value**

gammap results

**Author(s)**

Matthew L. Fidler

**Examples**

```
gammap(1, 3)
gammap(1:3, 3)
gammap(1, 1:3)
```

---

gammapDer

*gammapDer: derivative of gammap*

---

**Description**

This is the gamma\_p\_derivative from the boost library

**Usage**

```
gammapDer(a, z)
```

**Arguments**

a	The numeric 'a' parameter in the upper incomplete gamma
z	The numeric 'z' parameter in the upper incomplete gamma

**Value**

lowergamma results

**Author(s)**

Matthew L. Fidler

**Examples**

```
gammapDer(1:3, 3)
gammapDer(1, 1:3)
```

---

gammapInv	<i>gammapInv and gammapInva: Inverses of normalized gammap function</i>
-----------	---

---

**Description**

gammapInv and gammapInva: Inverses of normalized gammap function

**Usage**

```
gammapInv(a, p)
```

```
gammapInva(x, p)
```

**Arguments**

a	The numeric 'a' parameter in the upper incomplete gamma
p	The numeric 'p' parameter in the upper incomplete gamma
x	The numeric 'x' parameter in the upper incomplete gamma

**Details**

With the equation:

$$p = \text{gammap}(a, x)$$

The 'gammapInv' function returns a value 'x' that satisfies the equation above

The 'gammapInva' function returns a value 'q' that satisfies the equation above

NOTE: gammapInva is slow

**Value**

inverse gammap results

**Author(s)**

Matthew L. Fidler

**Examples**

```
gammapInv(1:3, 0.5)
```

```
gammapInv(1, 1:3 / 3.1)
```

```
gammapInv(1:3, 1:3 / 3.1)
```

```
gammapInva(1:3, 1:3 / 3.1)
```

---

 gammaq

*Gammaq: normalized upper incomplete gamma function*


---

**Description**

This is the gamma\_q from the boost library

**Usage**

```
gammaq(a, z)
```

**Arguments**

a	The numeric 'a' parameter in the normalized upper incomplete gamma
z	The numeric 'z' parameter in the normalized upper incomplete gamma

**Details**

The gamma q function is given by:

$$\text{gammaq} = \text{uppergamma}(a, z) / \text{gamma}(a)$$
**Value**

gammaq results

**Author(s)**

Matthew L. Fidler

**Examples**

```
gammaq(1, 3)
gammaq(1:3, 3)
gammaq(1, 1:3)
```

---

 gammaqInv

*gammaqInv and gammaqInva: Inverses of normalized gammaq function*


---

**Description**

gammaqInv and gammaqInva: Inverses of normalized gammaq function

**Usage**

```
gammaqInv(a, q)
```

```
gammaqInva(x, q)
```

**Arguments**

a	The numeric 'a' parameter in the upper incomplete gamma
q	The numeric 'q' parameter in the upper incomplete gamma
x	The numeric 'x' parameter in the upper incomplete gamma

**Details**

With the equation:

```
q = gammaq(a, x)
```

The 'gammaqInv' function returns a value 'x' that satisfies the equation above

The 'gammaqInva' function returns a value 'a' that satisfies the equation above

NOTE: gammaqInva is slow

**Value**

inverse gammaq results

**Author(s)**

Matthew L. Fidler

**Examples**

```
gammaqInv(1:3, 0.5)
```

```
gammaqInv(1, 1:3 / 3)
```

```
gammaqInv(1:3, 1:3 / 3.1)
```

```
gammaqInva(1:3, 1:3 / 3.1)
```

---

genShinyApp.template *Generate an example (template) of a dosing regimen shiny app*

---

**Description**

Create a complete shiny application for exploring dosing regimens given a (hardcoded) PK/PD model.

**Usage**

```
genShinyApp.template(
  appDir = "shinyExample",
  verbose = TRUE,
  ODE.config = list(ode = "model", params = c(KA = 0.294), inits = c(eff = 1), method =
    "lsoda", atol = 1e-08, rtol = 1e-06)
)

write.template.server(appDir)

write.template.ui(appDir, statevars)
```

**Arguments**

appDir	a string with a directory where to store the shiny app, by default is "shinyExample". The directory appDir will be created if it does not exist.
verbose	logical specifying whether to write messages as the shiny app is generated. Defaults to TRUE.
ODE.config	model name compiled and list of parameters sent to <code>rxSolve()</code> .
statevars	List of statevars passed to to the <code>write.template.ui()</code> function. This usually isn't called directly. A PK/PD model is defined using <code>rxode2()</code> , and a set of parameters and initial values are defined. Then the appropriate R scripts for the shiny's user interface <code>ui.R</code> and the server logic <code>server.R</code> are created in the directory <code>appDir</code> . The function evaluates the following PK/PD model by default:

```
C2 = centr/V2;
C3 = peri/V3;
d/dt(depot) = -KA*depot;
d/dt(centr) = KA*depot - CL*C2 - Q*C2 + Q*C3;
d/dt(peri) = Q*C2 - Q*C3;
d/dt(eff) = Kin - Kout*(1-C2/(EC50+C2))*eff;
```

This can be changed by the `ODE.config` parameter.

To launch the shiny app, simply issue the `runApp(appDir)` R command.

**Value**

None, these functions are used for their side effects.

**Note**

These functions create a simple, but working example of a dosing regimen simulation web application. Users may want to modify the code to experiment creating shiny applications for their specific `rxode2` models.

**See Also**

`rxode2()`, `eventTable()`, and the package **shiny** (<https://shiny.posit.co>).

**Examples**

```
# remove myapp when the example is complete
on.exit(unlink("myapp", recursive = TRUE, force = TRUE))
# create the shiny app example (template)
genShinyApp.template(appDir = "myapp")
# run the shiny app
if (requireNamespace("shiny", quietly=TRUE)) {
  library(shiny)
  # runApp("myapp") # Won't launch in environments without browsers
}
```

---

getRxThreads

*Get/Set the number of threads that rxode2 uses*


---

**Description**

Get/Set the number of threads that rxode2 uses

**Usage**

```
getRxThreads(verbose = FALSE)
```

```
setRxThreads(threads = NULL, percent = NULL, throttle = NULL)
```

```
rxCores(verbose = FALSE)
```

**Arguments**

verbose	Display the value of relevant OpenMP settings
threads	NULL (default) rereads environment variables. 0 means to use all logical CPUs available. Otherwise a number $\geq 1$
percent	If provided it should be a number between 2 and 100; the percentage of logical CPUs to use. By default on startup, 50 percent.
throttle	2 (default) means that, roughly speaking, a single thread will be used when number subjects solved for is $\leq 2$ , 2 threads when the number of all points is $\leq 4$ , etc. The throttle is to speed up small data tasks (especially when repeated many times) by not incurring the overhead of managing multiple threads. The throttle will also suppress sorting which ID will be solved first when there are $(n_{\text{subject solved}}) * \text{throttle} \leq n_{\text{threads}}$ . In rxode2 this sorting occurs to minimize the time for waiting for another thread to finish. If the last item solved is has a long solving time, all the other solving have to wait for that last costly solving to occur. If the items which are likely to take more time are solved first, this wait is less likely to have an impact on the overall solving time. In rxode2 the IDs are sorted by the individual number of solving points (largest first). It also has a C interface that allows these IDs to be resorted by total time

spent solving the equation. This allows packages like nlmixr to sort by solving time if needed.

Overall the the number of threads is throttled (restricted) for small tasks and sorting for IDs are suppressed.

## Value

number of threads that rxode2 uses

---

ini.rxUi	<i>Ini block for rxode2/nlmixr models</i>
----------	---

---

## Description

The ini block controls initial conditions for 'theta' (fixed effects), 'omega' (random effects), and 'sigma' (residual error) elements of the model.

## Usage

```
## S3 method for class 'rxUi'
ini(x, ..., envir = parent.frame(), append = NULL)

## Default S3 method:
ini(x, ..., envir = parent.frame(), append = NULL)

ini(x, ..., envir = parent.frame(), append = NULL)
```

## Arguments

x	expression
...	Other expressions for ini() function
envir	the environment in which unevaluated model expressions is to be evaluated. May also be NULL, a list, a data frame, a pairlist or an integer as specified to sys.call.
append	Reorder theta parameters. NULL means no change to parameter order. A parameter name (as a character string) means to put the new parameter after the named parameter. A number less than or equal to zero means to put the parameter at the beginning of the list. A number greater than the last parameter number means to put the parameter at the end of the list.

## Details

The ini() function is used in two different ways. The main way that it is used is to set the initial conditions and associated attributes (described below) in a model. The other way that it is used is for updating the initial conditions in a model, often using the pipe operator.

'theta' and 'sigma' can be set using either <- or = such as tvCL <- 1 or equivalently tvCL = 1. 'omega' can be set with a ~ such as etaCL ~ 0.1.



Parameters can be named or unnamed (though named parameters are preferred). A named parameter is set using the name on the left of the assignment while unnamed parameters are set without an assignment operator. `tvCL <- 1` would set a named parameter of `tvCL` to 1. Unnamed parameters are set using just the value, such as 1.

For some estimation methods, lower and upper bounds can be set for 'theta' and 'sigma' values. To set a lower and/or upper bound, use a vector of values. The vector is `c(lower, estimate, upper)`. The vector may be given with just the estimate (`estimate`), the lower bound and estimate (`c(lower, estimate)`), or all three (`c(lower, estimate, upper)`). To set an estimate and upper bound without a lower bound, set the lower bound to `-Inf`, `c(-Inf, estimate, upper)`. When an estimation method does not support bounds, the bounds will be ignored with a warning.

'omega' values can be set as a single value or as the values of a lower-triangular matrix. The values may be set as either a variance-covariance matrix (the default) or as a correlation matrix for the off-diagonals with the standard deviations on the diagonals. Names may be set on the left side of the `~`. To set a variance-covariance matrix with variance values of 2 and 3 and a covariance of -2.5 use `~c(2, 2.5, 3)`. To set the same matrix with names of `iivKa` and `iivCL`, use `iivKa + iivCL~c(2, 2.5, 3)`. To set a correlation matrix with standard deviations on the diagonal, use `cor()` like `iivKa + iivCL~cor(2, -0.5, 3)`. As of `rxode2` 3.0 you can also use `iivKa ~ 2, iivCL ~ c(2.5, 3)` for covariance matrices as well.

Values may be fixed (and therefore not estimated) using either the name `fixed` at the end of the assignment or by calling `fixed()` as a function for the value to fix. For 'theta' and 'sigma', either the estimate or the full definition (including lower and upper bounds) may be included in the fixed setting. For example, the following are all effectively equivalent to set a 'theta' or 'sigma' to a fixed value (because the lower and upper bounds are ignored for a fixed value): `tvCL <- fixed(1)`, `tvCL <- fixed(0, 1)`, `tvCL <- fixed(0, 1, 2)`, `tvCL <- c(0, fixed(1), 2)`, or `tvCL <- c(0, 1, fixed)`. For 'omega' assignment, the full block or none of the block must be set as fixed. Examples of setting an 'omega' value as fixed are: `iivKa~fixed(1)`, `iivKa + iivCL~fixed(1, 2, 3)`, or `iivKa + iivCL~c(1, 2, 3, fixed)`. Anywhere that `fixed` is used, `FIX`, `FIXED`, or `fix` may be used equivalently.

For any value, standard mathematical operators or functions may be used to define the value. For example, `log(2)` and `24*30` may be used to define a value anywhere that a number can be used (e.g. lower bound, estimate, upper bound, variance, etc.).

Values may be labeled using the `label()` function after the assignment. Labels are used to make reporting easier by giving a human-readable description of the parameter, but the labels do not have any effect on estimation. The typical way to set a label so that the parameter `tvCL` has a label of "Typical Value of Clearance (L/hr)" is `tvCL <- 1; label("Typical Value of Clearance (L/hr)")`.

Off diagonal values of 'omega' can be set to zero using the `diag()` to remove all off-diagonals can be removed with `ini(diag())`. To remove covariances of 'omega' item with `iivKa`, you can use `%>% ini(diag(iivKa))`. Or to remove covariances that contain either `iivKa` or `iivCL` you can use `%>% ini(diag(iivKa, iivCL))`. For finer control you can remove the covariance between two items (like `iivKa` and `iivCL`) by `%>% ini(-cov(iivKa, iivCL))`

`rxode2/nlmixr2` will attempt to determine some back-transformations for the user. For example, `CL <- exp(tvCL)` will detect that `tvCL` must be back-transformed by `exp()` for easier interpretation. When you want to control the back-transformation, you can specify the back-transformation using `backTransform()` after the assignment. For example, to set the back-transformation to `exp()`, you can use `tvCL <- 1; backTransform(exp())`.

**Value**

ini block

**Author(s)**

Matthew Fidler

**See Also**

Other Initial conditions: [zeroRe\(\)](#)

**Examples**

```
# Set the ini() block in a model
one.compartment <- function() {
  ini({
    tka <- log(1.57); label("Ka")
    tc1 <- log(2.72); label("Cl")
    tv <- log(31.5); label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tc1 + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
    cp ~ add(add.sd)
  })
}

# Use piping to update initial conditions
one.compartment %>% ini(tka <- log(2))
one.compartment %>% ini(tka <- label("Absorption rate, Ka (1/hr)"))
# Move the tka parameter to be just below the tv parameter (affects parameter
# summary table, only)
one.compartment %>% ini(tka <- label("Absorption rate, Ka (1/hr)", append = "tv")
# When programming with rxode2/nlmixr2, it may be easier to pass strings in
# to modify the ini
one.compartment %>% ini("tka <- log(2)")
```

**Description**

Assign the ini block in the rxode2 related object

**Usage**

```
ini(x, envir = environment(x)) <- value
```

**Arguments**

x	rxode2 related object
envir	Environment where assignment occurs
value	Value of the object

**Value**

rxode2 related object

**Author(s)**

Matthew L. Fidler

---

is.rxStackData	<i>Return if the object can be stacked</i>
----------------	--

---

**Description**

Return if the object can be stacked

**Usage**

```
is.rxStackData(object)
```

**Arguments**

object	object to test if it can be stacked
--------	-------------------------------------

**Value**

boolean to tell if an object can be stacked using rxode2

**Author(s)**

Matthew L. Fidler

**Examples**

```
is.rxStackData(NULL)
```

---

llikBeta	<i>Calculate the log likelihood of the binomial function (and its derivatives)</i>
----------	--

---

### Description

Calculate the log likelihood of the binomial function (and its derivatives)

### Usage

```
llikBeta(x, shape1, shape2, full = FALSE)
```

### Arguments

x	Observation
shape1, shape2	non-negative parameters of the Beta distribution.
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

### Details

In an `rxode2()` model, you can use `llikBeta()` but you have to use all arguments. You can also get the derivative of shape1 and shape2 with `llikBetaDshape1()` and `llikBetaDshape2()`.

### Value

data frame with `fx` for the log pdf value of with `dShape1` and `dShape2` that has the derivatives with respect to the parameters at the observation time-point

### Author(s)

Matthew L. Fidler

### Examples

```
x <- seq(1e-4, 1 - 1e-4, length.out = 21)

llikBeta(x, 0.5, 0.5)

llikBeta(x, 1, 3, TRUE)

et <- et(seq(1e-4, 1-1e-4, length.out=21))
et$shape1 <- 0.5
et$shape2 <- 1.5

model <- function() {
  model({
```

```

    fx <- llikBeta(time, shape1, shape2)
    dShape1 <- llikBetaDshape1(time, shape1, shape2)
    dShape2 <- llikBetaDshape2(time, shape1, shape2)
  })
}

rxSolve(model, et)

```

---

llikBinom	<i>Calculate the log likelihood of the binomial function (and its derivatives)</i>
-----------	--

---

### Description

Calculate the log likelihood of the binomial function (and its derivatives)

### Usage

```
llikBinom(x, size, prob, full = FALSE)
```

### Arguments

x	Number of successes
size	Size of trial
prob	probability of success
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

### Details

In an `rxode2()` model, you can use `llikBinom()` but you have to use all arguments. You can also get the derivative of prob with `llikBinomDprob()`

### Value

data frame with fx for the pdf value of with dProb that has the derivatives with respect to the parameters at the observation time-point

### Author(s)

Matthew L. Fidler

**Examples**

```

llikBinom(46:54, 100, 0.5)

llikBinom(46:54, 100, 0.5, TRUE)

# In rxode2 you can use:

et <- et(46:54)
et$size <- 100
et$prob <- 0.5

model <- function() {
  model({
    fx <- llikBinom(time, size, prob)
    dProb <- llikBinomDprob(time, size, prob)
  })
}

rxSolve(model, et)

```

---

llikCauchy

*log likelihood of Cauchy distribution and it's derivatives (from stan)*


---

**Description**

log likelihood of Cauchy distribution and it's derivatives (from stan)

**Usage**

```
llikCauchy(x, location = 0, scale = 1, full = FALSE)
```

**Arguments**

x	Observation
location, scale	location and scale parameters.
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an rxode2() model, you can use llikCauchy() but you have to use all arguments. You can also get the derivative of location and scale with llikCauchyDlocation() and llikCauchyDscale().

**Value**

data frame with fx for the log pdf value of with dLocation and dScale that has the derivatives with respect to the parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
x <- seq(-3, 3, length.out = 21)

llikCauchy(x, 0, 1)

llikCauchy(x, 3, 1, full=TRUE)

et <- et(-3, 3, length.out=10)
et$location <- 0
et$scale <- 1

model <- function() {
  model({
    fx <- llikCauchy(time, location, scale)
    dLocation <- llikCauchyDlocation(time, location, scale)
    dScale <- llikCauchyDscale(time, location, scale)
  })
}

rxSolve(model, et)
```

---

llikChisq

*log likelihood and derivatives for chi-squared distribution*


---

**Description**

log likelihood and derivatives for chi-squared distribution

**Usage**

```
llikChisq(x, df, full = FALSE)
```

**Arguments**

x	variable that is distributed by chi-squared distribution
df	degrees of freedom (non-negative, but can be non-integer).
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikChisq()` but you have to use the `x` and `df` arguments. You can also get the derivative of `df` with `llikChisqDdf()`.

**Value**

data frame with `fx` for the log pdf value of with `dDf` that has the derivatives with respect to the `df` parameter the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikChisq(1, df = 1:3, full=TRUE)

llikChisq(1, df = 6:9)

et <- et(1:3)
et$x <- 1

model <- function() {
  model({
    fx <- llikChisq(x, time)
    dDf <- llikChisqDdf(x, time)
  })
}

rxSolve(model, et)
```

---

llikExp

*log likelihood and derivatives for exponential distribution*


---

**Description**

log likelihood and derivatives for exponential distribution

**Usage**

```
llikExp(x, rate, full = FALSE)
```

**Arguments**

<code>x</code>	variable that is distributed by exponential distribution
<code>rate</code>	vector of rates.
<code>full</code>	Add the data frame showing <code>x</code> , mean, sd as well as the <code>fx</code> and derivatives

**Details**

In an `rxode2()` model, you can use `llikExp()` but you have to use the `x` and `rate` arguments. You can also get the derivative of rate with `llikExpDrate()`.



**Value**

data frame with `fx` for the log pdf value of with `dRate` that has the derivatives with respect to the rate parameter the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikExp(1, 1:3)

llikExp(1, 1:3, full=TRUE)

# You can use rxode2 for these too:

et <- et(1:3)
et$x <- 1

model <- function() {
  model({
    fx <- llikExp(x, time)
    dRate <- llikExpDrate(x, time)
  })
}

rxSolve(model, et)
```

---

llikF

*log likelihood and derivatives for F distribution*


---

**Description**

log likelihood and derivatives for F distribution

**Usage**

```
llikF(x, df1, df2, full = FALSE)
```

**Arguments**

<code>x</code>	variable that is distributed by f distribution
<code>df1, df2</code>	degrees of freedom. Inf is allowed.
<code>full</code>	Add the data frame showing <code>x</code> , mean, sd as well as the <code>fx</code> and derivatives

**Details**

In an `rxode2()` model, you can use `llikF()` but you have to use the `x` and `rate` arguments. You can also get the derivative of `df1` and `df2` with `llikFDdf1()` and `llikFDdf2()`.

**Value**

data frame with `fx` for the log pdf value of with `dDf1` and `dDf2` that has the derivatives with respect to the `df1/df2` parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
x <- seq(0.001, 5, length.out = 100)

llikF(x^2, 1, 5)

model <- function(){
  model({
    fx <- llikF(time, df1, df2)
    dMean <- llikFDdf1(time, df1, df2)
    dSd <- llikFDdf2(time, df1, df2)
  })
}

et <- et(x)
et$df1 <- 1
et$df2 <- 5

rxSolve(model, et)
```

---

llikGamma

*log likelihood and derivatives for Gamma distribution*

---

**Description**

log likelihood and derivatives for Gamma distribution

**Usage**

```
llikGamma(x, shape, rate, full = FALSE)
```

**Arguments**

x	variable that is distributed by gamma distribution
shape	this is the distribution's shape parameter. Must be positive.
rate	this is the distribution's rate parameters. Must be positive.
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikGamma()` but you have to use the `x` and `rate` arguments. You can also get the derivative of shape or rate with `llikGammaDshape()` and `llikGammaDrate()`.

**Value**

data frame with `fx` for the log pdf value of with `dProb` that has the derivatives with respect to the prob parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikGamma(1, 1, 10)

# You can use this in `rxode2` too:

et <- et(seq(0.001, 1, length.out=10))
et$shape <- 1
et$rate <- 10

model <- function() {
  model({
    fx <- llikGamma(time, shape, rate)
    dShape <- llikGammaDshape(time, shape, rate)
    dRate <- llikGammaDrate(time, shape, rate)
  })
}

rxSolve(model, et)
```

---

llikGeom *log likelihood and derivatives for Geom distribution*

---

**Description**

log likelihood and derivatives for Geom distribution

**Usage**

```
llikGeom(x, prob, full = FALSE)
```

**Arguments**

x	variable distributed by a geom distribution
prob	probability of success in each trial. $0 < \text{prob} \leq 1$ .
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikGeom()` but you have to use the `x` and `rate` arguments. You can also get the derivative of `prob` with `llikGeomDprob()`.

**Value**

data frame with `fx` for the log pdf value of with `dProb` that has the derivatives with respect to the `prob` parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikGeom(1:10, 0.2)

et <- et(1:10)
et$prob <- 0.2

model <- function() {
  model({
    fx <- llikGeom(time, prob)
    dProb <- llikGeomDprob(time, prob)
  })
}

rxSolve(model, et)
```

---

llikNbinom	<i>Calculate the log likelihood of the negative binomial function (and its derivatives)</i>
------------	---

---

**Description**

Calculate the log likelihood of the negative binomial function (and its derivatives)

**Usage**

```
llikNbinom(x, size, prob, full = FALSE)
```

**Arguments**

x	Number of successes
size	Size of trial
prob	probability of success
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikNbinom()` but you have to use all arguments. You can also get the derivative of prob with `llikNbinomDprob()`

**Value**

data frame with `fx` for the pdf value of with `dProb` that has the derivatives with respect to the parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikNbinom(46:54, 100, 0.5)

llikNbinom(46:54, 100, 0.5, TRUE)

# In rxode2 you can use:

et <- et(46:54)
et$size <- 100
et$prob <- 0.5

model <- function() {
  model({
    fx <- llikNbinom(time, size, prob)
  })
}
```

```

      dProb <- llikNbinomDprob(time, size, prob)
    })
  }

  rxSolve(model, et)

```

---

llikNbinomMu	<i>Calculate the log likelihood of the negative binomial function (and its derivatives)</i>
--------------	---

---

### Description

Calculate the log likelihood of the negative binomial function (and its derivatives)

### Usage

```
llikNbinomMu(x, size, mu, full = FALSE)
```

### Arguments

x	Number of successes
size	Size of trial
mu	mu parameter for negative binomial
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

### Details

In an `rxode2()` model, you can use `llikNbinomMu()` but you have to use all arguments. You can also get the derivative of mu with `llikNbinomMuDmu()`

### Value

data frame with `fx` for the pdf value of with `dProb` that has the derivatives with respect to the parameters at the observation time-point

### Author(s)

Matthew L. Fidler

**Examples**

```

llikNbinomMu(46:54, 100, 40)

llikNbinomMu(46:54, 100, 40, TRUE)

et <- et(46:54)
et$size <- 100
et$mu <- 40

model <- function() {
  model({
    fx <- llikNbinomMu(time, size, mu)
    dProb <- llikNbinomMuDmu(time, size, mu)
  })
}

rxSolve(model, et)

```

---

llikNorm

*Log likelihood for normal distribution*


---

**Description**

Log likelihood for normal distribution

**Usage**

```
llikNorm(x, mean = 0, sd = 1, full = FALSE)
```

**Arguments**

x	Observation
mean	Mean for the likelihood
sd	Standard deviation for the likelihood
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikNorm()` but you have to use all arguments. You can also get the derivatives with `llikNormDmean()` and `llikNormDsd()`

**Value**

data frame with `fx` for the pdf value of with `dMean` and `dSd` that has the derivatives with respect to the parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```

llikNorm(0)

llikNorm(seq(-2,2,length.out=10), full=TRUE)

# With rxode2 you can use:

et <- et(-3, 3, length.out=10)
et$mu <- 0
et$sigma <- 1

model <- function(){
  model({
    fx <- llikNorm(time, mu, sigma)
    dMean <- llikNormDmean(time, mu, sigma)
    dSd <- llikNormDsd(time, mu, sigma)
  })
}

ret <- rxSolve(model, et)
ret

```

---

llikPois

*log-likelihood for the Poisson distribution*


---

**Description**

log-likelihood for the Poisson distribution

**Usage**

```
llikPois(x, lambda, full = FALSE)
```

**Arguments**

x	non negative integers
lambda	non-negative means
full	Add the data frame showing x, mean, sd as well as the fx and derivatives



**Details**

In an rxode2() model, you can use llikPois() but you have to use all arguments. You can also get the derivatives with llikPoisDlambda()

**Value**

data frame with fx for the pdf value of with dLambda that has the derivatives with respect to the parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
llikPois(0:7, lambda = 1)

llikPois(0:7, lambda = 4, full=TRUE)

# In rxode2 you can use:

et <- et(0:10)
et$lambda <- 0.5

model <- function() {
  model({
    fx <- llikPois(time, lambda)
    dLambda <- llikPoisDlambda(time, lambda)
  })
}

rxSolve(model, et)
```

---

llikT

*Log likelihood of T and it's derivatives (from stan)*

---

**Description**

Log likelihood of T and it's derivatives (from stan)

**Usage**

```
llikT(x, df, mean = 0, sd = 1, full = FALSE)
```

**Arguments**

x	Observation
df	degrees of freedom ( $> 0$ , maybe non-integer). $df = Inf$ is allowed.
mean	Mean for the likelihood
sd	Standard deviation for the likelihood
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

**Details**

In an `rxode2()` model, you can use `llikT()` but you have to use all arguments. You can also get the derivative of `df`, `mean` and `sd` with `llikTDdf()`, `llikTDmean()` and `llikTDsd()`.

**Value**

data frame with `fx` for the log pdf value of with `dDf` `dMean` and `dSd` that has the derivatives with respect to the parameters at the observation time-point

**Author(s)**

Matthew L. Fidler

**Examples**

```
x <- seq(-3, 3, length.out = 21)

llikT(x, 7, 0, 1)

llikT(x, 15, 0, 1, full=TRUE)

et <- et(-3, 3, length.out=10)
et$nu <- 7
et$mean <- 0
et$sd <- 1

model <- function() {
  model({
    fx <- llikT(time, nu, mean, sd)
    dDf <- llikTDdf(time, nu, mean, sd)
    dMean <- llikTDmean(time, nu, mean, sd)
    dSd <- llikTDsd(time, nu, mean, sd)
  })
}

rxSolve(model, et)
```

---

llikUnif *log likelihood and derivatives for Unif distribution*

---

### Description

log likelihood and derivatives for Unif distribution

### Usage

```
llikUnif(x, alpha, beta, full = FALSE)
```

### Arguments

x	variable distributed by a uniform distribution
alpha	is the lower limit of the uniform distribution
beta	is the upper limit of the distribution
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

### Details

In an `rxode2()` model, you can use `llikUnif()` but you have to use the `x` and `rate` arguments. You can also get the derivative of `alpha` or `beta` with `llikUnifDalpha()` and `llikUnifDbeta()`.

### Value

data frame with `fx` for the log pdf value of with `dProb` that has the derivatives with respect to the prob parameters at the observation time-point

### Author(s)

Matthew L. Fidler

### Examples

```
llikUnif(1, -2, 2)

et <- et(seq(1,1, length.out=4))
et$alpha <- -2
et$beta <- 2

model <- function() {
  model({
    fx <- llikUnif(time, alpha, beta)
    dAlpha <- llikUnifDalpha(time, alpha, beta)
    dBeta <- llikUnifDbeta(time, alpha, beta)
  })
}
```

```

}
rxSolve(model, et)

```

---

llikWeibull *log likelihood and derivatives for Weibull distribution*

---

### Description

log likelihood and derivatives for Weibull distribution

### Usage

```
llikWeibull(x, shape, scale, full = FALSE)
```

### Arguments

x	variable distributed by a Weibull distribution
shape, scale	shape and scale parameters, the latter defaulting to 1.
full	Add the data frame showing x, mean, sd as well as the fx and derivatives

### Details

In an rxode2() model, you can use llikWeibull() but you have to use the x and rate arguments. You can also get the derivative of shape or scale with llikWeibullDshape() and llikWeibullDscale().

### Value

data frame with fx for the log pdf value of with dProb that has the derivatives with respect to the prob parameters at the observation time-point

### Author(s)

Matthew L. Fidler

### Examples

```

llikWeibull(1, 1, 10)

# rxode2 can use this too:

et <- et(seq(0.001, 1, length.out=10))
et$shape <- 1
et$scale <- 10

model <- function() {
  model({
    fx <- llikWeibull(time, shape, scale)

```

```

    dShape<- llikWeibullDshape(time, shape, scale)
    dScale <- llikWeibullDscale(time, shape, scale)
  })
}

rxSolve(model, et)

```

---

logit

*logit and inverse logit (expit) functions*


---

### Description

logit and inverse logit (expit) functions

### Usage

```
logit(x, low = 0, high = 1)
```

```
expit(alpha, low = 0, high = 1)
```

```
logitNormInfo(mean = 0, sd = 1, low = 0, high = 1, abs.tol = 1e-06, ...)
```

```
probitNormInfo(mean = 0, sd = 1, low = 0, high = 1, abs.tol = 1e-06, ...)
```

### Arguments

x	Input value(s) in range [low,high] to translate -Inf to Inf
low	Lowest value in the range
high	Highest value in the range
alpha	Infinite value(s) to translate to range of [low, high]
mean	logit-scale mean
sd	logit-scale standard deviation
abs.tol	absolute accuracy requested.
...	other parameters passed to integrate()

### Details

logit is given by:

$$\text{logit}(p) = -\log(1/p-1)$$

where:

$$p = x-\text{low}/\text{high}-\text{low}$$

expit is given by:

$$\text{expit}(p, \text{low}, \text{high}) = (\text{high}-\text{low})/(1+\exp(-\alpha)) + \text{low}$$

The `logitNormInfo()` gives the mean, variance and coefficient of variability on the untransformed scale.

**Value**

values from logit and expit

**Examples**

```
logit(0.25)
```

```
expit(-1.09)
```

```
logitNormInfo(logit(0.25), sd = 0.1)
```

```
logitNormInfo(logit(1, 0, 10), sd = 1, low = 0, high = 10)
```

---

lowergamma

*lowergamma: upper incomplete gamma function*

---

**Description**

This is the `tgamma_lower` from the boost library

**Usage**

```
lowergamma(a, z)
```

**Arguments**

`a` The numeric 'a' parameter in the upper incomplete gamma

`z` The numeric 'z' parameter in the upper incomplete gamma

**Details**

The lowergamma function is given by:

$$\text{lowergamma}(a, z) = \int_0^z t^{a-1} \cdot e^{-t} dt$$

**Value**

lowergamma results

**Author(s)**

Matthew L. Fidler

**Examples**

```
lowergamma(1, 3)
lowergamma(1:3, 3)
lowergamma(1, 1:3)
```

---

meanProbs	<i>Calculate expected confidence bands or prediction interval with normal or t sampling distribution</i>
-----------	--

---

**Description**

The generic function meanProbs produces expected confidence bands under either the t distribution or the normal sampling distribution. This uses qnorm() or qt() with the mean and standard deviation.

**Usage**

```
meanProbs(x, ...)

## Default S3 method:
meanProbs(
  x,
  probs = seq(0, 1, 0.25),
  na.rm = FALSE,
  names = TRUE,
  useT = TRUE,
  onlyProbs = TRUE,
  pred = FALSE,
  n = 0L,
  ...
)
```

**Arguments**

x	numeric vector whose mean and probability based confidence values are wanted, NA and NaN values are not allowed in numeric vectors unless 'na.rm' is 'TRUE'.
...	Arguments passed to default method, allows many different methods to be applied.
probs	numeric vector of probabilities with values in the interval from 0 to 1 .
na.rm	logical; if true, any NA and NaN's are removed from x before the quantiles are computed.
names	logical; if true, the result has a names attribute.
useT	logical; if true, use the t-distribution to calculate the confidence-based estimates. If false use the normal distribution to calculate the confidence based estimates.

onlyProbs	logical; if true, only return the probability based confidence interval estimates, otherwise return
pred	logical; if true use the prediction interval instead of the confidence interval
n	integer/integerish; this is the n used to calculate the prediction or confidence interval. When n=0 (default) use the number of non-NA observations.

### Details

For a single probability, p, it uses either:

$\text{mean} + \text{qt}(p, \text{df}=n) * \text{sd} / \text{sqrt}(n)$

or

$\text{mean} + \text{qnorm}(p) * \text{sd} / \text{sqrt}(n)$

The smallest observation corresponds to a probability of 0 and the largest to a probability of 1 and the mean corresponds to 0.5.

The mean and standard deviation of the sample is calculated based on Welford's method for a single pass.

This is meant to perform in the same way as `quantile()` so it can be a drop in replacement for code using `quantile()` but using distributional assumptions.

### Value

By default the return has the probabilities as names (if named) with the points where the expected distribution are located given the sampling mean and standard deviation. If `onlyProbs=FALSE` then it would prepend mean, variance, standard deviation, minimum, maximum and number of non-NA observations.

### Author(s)

Matthew L. Fidler

### Examples

```
quantile(x<- rnorm(1001))
meanProbs(x)

# Can get some extra statistics if you request onlyProbs=FALSE
meanProbs(x, onlyProbs=FALSE)

x[2] <- NA_real_

meanProbs(x, onlyProbs=FALSE)

quantile(x<- rnorm(42))

meanProbs(x)

meanProbs(x, useT=FALSE)
```



---

model.function	<i>Model block for rxode2/nlmixr models</i>
----------------	---

---

**Description**

Model block for rxode2/nlmixr models

**Usage**

```
## S3 method for class ``function``  
model(  
  x,  
  ...,  
  append = NULL,  
  auto = getOption("rxode2.autoVarPiping", TRUE),  
  cov = NULL,  
  envir = parent.frame()  
)
```

```
## S3 method for class 'rxUi'  
model(  
  x,  
  ...,  
  append = NULL,  
  auto = getOption("rxode2.autoVarPiping", TRUE),  
  cov = NULL,  
  envir = parent.frame()  
)
```

```
## S3 method for class 'rxode2'  
model(  
  x,  
  ...,  
  append = NULL,  
  auto = getOption("rxode2.autoVarPiping", TRUE),  
  cov = NULL,  
  envir = parent.frame()  
)
```

```
## S3 method for class 'rxModelVars'  
model(  
  x,  
  ...,  
  append = NULL,  
  auto = getOption("rxode2.autoVarPiping", TRUE),  
  cov = NULL,  
  envir = parent.frame()  
)
```

```

)

model(
  x,
  ...,
  append = FALSE,
  auto = getOption("rxode2.autoVarPiping", TRUE),
  cov = NULL,
  envir = parent.frame()
)

## Default S3 method:
model(x, ..., append = FALSE, cov = NULL, envir = parent.frame())

```

### Arguments

x	model expression
...	Other arguments
append	This is a boolean to determine if the lines are appended in piping. The possible values for this is: <ul style="list-style-type: none"> <li>• TRUE which is when the lines are appended to the model instead of replaced</li> <li>• FALSE when the lines are replaced in the model (default)</li> <li>• NA is when the lines are pre-pended to the model instead of replaced</li> <li>• lhs expression, which will append the lines after the last observed line of the expression lhs</li> </ul>
auto	This boolean tells if piping automatically selects the parameters should be characterized as a population parameter, between subject variability, or a covariate. When TRUE this automatic selection occurs. When FALSE this automatic selection is turned off and everything is added as a covariate (which can be promoted to a parameter with the ini statement). By default this is TRUE, but it can be changed by <code>options(rxode2.autoVarPiping=FALSE)</code> .
cov	is a character vector of variables that should be assumed to be covariates. This will override automatic promotion to a population parameter estimate (or an eta)
envir	the environment in which unevaluated model expressions is to be evaluated. May also be NULL, a list, a data frame, a pairlist or an integer as specified to <code>sys.call</code> .

### Value

Model block with ini information included. ini must be called before model block

### Author(s)

Matthew Fidler

---

model<-                    *Assign the model block in the rxode2 related object*

---

**Description**

Assign the model block in the rxode2 related object

**Usage**

```
model(x, envir = environment(x)) <- value
```

**Arguments**

x	rxode2 related object
envir	Environment where assignment occurs
value	Value of the object

**Value**

rxode2 related object

**Author(s)**

Matthew L. Fidler

---

modelExtract                *Extract model lines from a rxui model*

---

**Description**

Extract model lines from a rxui model

**Usage**

```
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)  
  
## S3 method for class ``function``  
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)
```

```
x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)  
  
## S3 method for class 'rxUi'  
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)  
  
## S3 method for class 'rxode2'  
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)  
  
## S3 method for class 'rxModelVars'  
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)  
  
## Default S3 method:  
modelExtract(  
  x,  
  ...,  
  expression = FALSE,  
  endpoint = FALSE,  
  lines = FALSE,  
  envir = parent.frame()  
)
```

**Arguments**

x	model to extract lines from
...	variables to extract. When it is missing, it will extract the entire model (conditioned on the endpoint option below)
expression	return expressions (if TRUE) or strings (if FALSE)
endpoint	include endpoint. This can be: <ul style="list-style-type: none"> <li>• NA – Missing means include both the endpoint and non-endpoint lines</li> <li>• TRUE – Only include endpoint lines</li> <li>• FALSE – Only include non-endpoint lines</li> </ul>
lines	is a boolean. When TRUE this will add the lines as an attribute to the output value ie attr("lines")
envir	Environment for evaluating variables

**Value**

expressions or strings of extracted lines. Note if there is a duplicated lhs expression in the line, it will return both lines

**Author(s)**

Matthew L. Fidler

**Examples**

```
one.compartment <- function() {
  ini({
    tka <- 0.45 # Log Ka
    tc1 <- 1 # Log Cl
    tv <- 3.45 # Log V
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tc1 + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) <- -ka * depot
    d/dt(center) <- ka * depot - cl / v * center
    cp <- center / v
    cp ~ add(add.sd)
  })
}

f <- one.compartment()

modelExtract(f, cp)
```

```

modelExtract(one.compartment, d/dt(depot))

# from variable
var <- "d/dt(depot)"

modelExtract(one.compartment, var)

modelExtract(f, endpoint=NA, lines=TRUE, expression=TRUE)

```

---

odeMethodToInt	<i>Conversion between character and integer ODE integration methods for rxode2</i>
----------------	--

---

### Description

If NULL is given as the method, all choices are returned as a named vector.

### Usage

```
odeMethodToInt(method = c("liblsoda", "lsoda", "dop853", "indLin"))
```

### Arguments

method	<p>The method for solving ODEs. Currently this supports:</p> <ul style="list-style-type: none"> <li>• "liblsoda" thread safe lsoda. This supports parallel thread-based solving, and ignores user Jacobian specification.</li> <li>• "lsoda" – LSODA solver. Does not support parallel thread-based solving, but allows user Jacobian specification.</li> <li>• "dop853" – DOP853 solver. Does not support parallel thread-based solving nor user Jacobian specification</li> <li>• "indLin" – Solving through inductive linearization. The rxode2 dll must be setup specially to use this solving routine.</li> </ul>
--------	--

### Value

An integer for the method (unless the input is NULL, in which case, see the details)

---

phi	<i>Cumulative distribution of standard normal</i>
-----	---

---

**Description**

Cumulative distribution of standard normal

**Usage**

phi(q)

**Arguments**

q                    vector of quantiles

**Value**

cumulative distribution of standard normal distribution

**Author(s)**

Matthew Fidler

**Examples**

```
# phi is equivalent to pnorm(x)
phi(3)

# See
pnorm(3)

# This is provided for NONMEM-like compatibility in rxode2 models
```

---

plot.rxSolve	<i>Plot rxode2 objects</i>
--------------	----------------------------

---

**Description**

Plot rxode2 objects

**Usage**

```
## S3 method for class 'rxSolve'
plot(x, y, ..., log = "", xlab = "Time", ylab = "")

## S3 method for class 'rxSolveConfint1'
plot(x, y, ..., xlab = "Time", ylab = "", log = "")

## S3 method for class 'rxSolveConfint2'
plot(x, y, ..., xlab = "Time", ylab = "", log = "")
```

**Arguments**

x	rxode2 object to plot
y	Compartments or left-hand-side values to plot either as a bare name or as a character vector
...	Ignored
log	Should "" (neither x nor y), "x", "y", or "xy" (or "yx") be log-scale?
xlab, ylab	The x and y axis labels

**Value**

A ggplot2 object

**See Also**

Other rxode2 plotting: [rxTheme\(\)](#)

---

print.rxModelVars      *Print Values*

---

**Description**

print prints its argument and returns it *invisibly* (via [invisible\(x\)](#)). It is a generic function which means that new printing methods can be easily added for new [classes](#).

**Usage**

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

**Arguments**

x	an object used to select a method.
...	further arguments passed to or from other methods.



## Details

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the `print` generic.

`print.factor` allows some customization and is used for printing `ordered` factors as well.

`print.table` for printing `tables` allows other customization. As of R 3.0.0, it only prints a description in case of a table with 0-extents (this can happen if a classifier has no valid data).

See `noquote` as an example of a class whose main purpose is a specific `print` method.

## Value

This returns invisibly the model variables object

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

The default method `print.default`, and help for the methods above; further `options`, `noquote`.

For more customizable (but cumbersome) printing, see `cat`, `format` or also `write`. For a simple prototypical `print` method, see `.print.via.format` in package `tools`.

## Examples

```
require(stats)

ts(1:20) #-- print is the "Default function" --> print.ts(.) is called
for(i in 1:3) print(1:i)

## Printing of factors
attenu$station ## 117 levels -> 'max.levels' depending on width

## ordered factors: levels "l1 < l2 < .."
esoph$agegp[1:12]
esoph$alcgp[1:12]

## Printing of sparse (contingency) tables
set.seed(521)
t1 <- round(abs(rt(200, df = 1.8)))
t2 <- round(abs(rt(200, df = 1.4)))
table(t1, t2) # simple
print(table(t1, t2), zero.print = ".") # nicer to read

## same for non-integer "table":
T <- table(t2,t1)
T <- T * (1+round(rlnorm(length(T)))/4)
print(T, zero.print = ".") # quite nicer,
print.table(T[,2:8] * 1e9, digits=3, zero.print = ".")
## still slightly inferior to Matrix::Matrix(T) for larger T
```

```
## Corner cases with empty extents:  
table(1, NA) # < table of extent 1 x 0 >
```

---

probit	<i>probit and inverse probit functions</i>
--------	--

---

### Description

probit and inverse probit functions

### Usage

```
probit(x, low = 0, high = 1)
```

```
probitInv(x, low = 0, high = 1)
```

### Arguments

x	Input value(s) in range [low,high] to translate -Inf to Inf
low	Lowest value in the range
high	Highest value in the range

### Value

values from probit, probitInv and probitNormInfo

### Examples

```
probit(0.25)
```

```
probitInv(-0.674)
```

```
probitNormInfo(probit(0.25), sd = 0.1)
```

```
probitNormInfo(probit(1, 0, 10), sd = 1, low = 0, high = 10)
```

---

rinvchisq	<i>Scaled Inverse Chi Squared distribution</i>
-----------	--

---

**Description**

Scaled Inverse Chi Squared distribution

**Usage**

```
rinvchisq(n = 1L, nu = 1, scale = 1)
```

**Arguments**

n	Number of random samples
nu	degrees of freedom of inverse chi square
scale	Scale of inverse chi squared distribution (default is 1).

**Value**

a vector of inverse chi squared deviates.

**Examples**

```
rinvchisq(3, 4, 1) ## Scale = 1, degrees of freedom = 4
rinvchisq(2, 4, 2) ## Scale = 2, degrees of freedom = 4
```

---

rxAllowUnload	<i>Allow unloading of dlls</i>
---------------	--------------------------------

---

**Description**

Allow unloading of dlls

**Usage**

```
rxAllowUnload(allow)
```

**Arguments**

allow	boolean indicating if garbage collection will unload of rxode2 dlls.
-------	--

**Value**

Boolean allow; called for side effects

**Author(s)**

Matthew Fidler

**Examples**

```
# Garbage collection will not unload un-used rxode2 dlls
rxAllowUnload(FALSE);

# Garbage collection will unload unused rxode2 dlls
rxAllowUnload(TRUE);
```

---

rxAppendModel	<i>Append two rxui models together</i>
---------------	--

---

**Description**

Append two rxui models together

**Usage**

```
rxAppendModel(..., common = TRUE)
```

**Arguments**

...	models to append together
common	boolean that determines if you need a common value to bind

**Value**

New model with both models appended together

**Author(s)**

Matthew L. Fidler

**Examples**

```
ocmt <- function() {
  ini({
    tka <- exp(0.45) # Ka
    tcl <- exp(1) # Cl
    tv <- exp(3.45); # log V
    ## the label("Label name") works with all models
    add.sd <- 0.7
  })
  model({
    ka <- tka
```

```

    cl <- tcl
    v <- tv
    d/dt(depot) <- -ka * depot
    d/dt(center) <- ka * depot - cl / v * center
    cp <- center / v
    cp ~ add(add.sd)
  })
}

idr <- function() {
  ini({
    tkin <- log(1)
    tkout <- log(1)
    tic50 <- log(10)
    gamma <- fix(1)
    idr.sd <- 1
  })
  model({
    kin <- exp(tkin)
    kout <- exp(tkout)
    ic50 <- exp(tic50)
    d/dt(eff) <- kin - kout*(1-ceff^gamma/(ic50^gamma+ceff^gamma))
    eff ~ add(idr.sd)
  })
}

rxAppendModel(ocmt %>% model(ceff=cp,append=TRUE), idr)

```

---

rxAssignControlValue    *Assign Control Variable*

---

### Description

Assign Control Variable

### Usage

```
rxAssignControlValue(ui, option, value)
```

### Arguments

ui	rxode2 ui function
option	Option name in the control to modify
value	Value of control to modify

**Value**

Nothing; called for the side effects

**Author(s)**

Matthew L. Fidler

---

rxAssignPtr

*Assign pointer based on model variables*

---

**Description**

Assign pointer based on model variables

**Usage**

```
rxAssignPtr(object = NULL)
```

**Arguments**

object            rxode2 family of objects

**Value**

nothing, called for side effects

---

rxbeta

*Simulate beta variable from threefry generator*

---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxbeta(shape1, shape2, n = 1L, ncores = 1L)
```

**Arguments**

shape1, shape2	non-negative parameters of the Beta distribution.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation <code>rxnorm</code> simulates using the threefry sitmo generator. <code>rxnormV</code> used to simulate with the vandercompt simulator, but since it didn't satisfy the normal properties it was changed to simply be an alias of <code>rxnorm</code> . It is no longer supported in <code>rxode2({})</code> blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the `rxode2` environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the `rxode2` engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

beta random deviates

**Examples**

```
## Use threefry engine

rxbeta(0.5, 0.5, n = 10) # with rxbeta you have to explicitly state n
rxbeta(5, 1, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxbeta(1, 3)

## This example uses `rxbeta` directly in the model

rx <- function() {
  model({
    a <- rxbeta(2, 2)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

 rxbinom

*Simulate Binomial variable from threefry generator*


---

### Description

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

### Usage

```
rxbinom(size, prob, n = 1L, ncores = 1L)
```

### Arguments

size	number of trials (zero or more).
prob	probability of success on each trial.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in <code>rxode2({})</code> blocks

### Details

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the `rxode2` environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the `rxode2` engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

### Value

binomial random deviates



**Examples**

```
## Use threefry engine

rxbinom(10, 0.9, n = 10) # with rxbinom you have to explicitly state n
rxbinom(3, 0.5, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxbinom(4, 0.7)

## This example uses `rxbinom` directly in the model

rx <- function() {
  model({
    a <- rxbinom(1, 0.5)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

 rxcauchy

*Simulate Cauchy variable from threefry generator*


---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxcauchy(location = 0, scale = 1, n = 1L, ncores = 1L)
```

**Arguments**

location, scale	location and scale parameters.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simply be an alias of rxnorm. It is no longer supported in <code>rxode2({})</code> blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with rxSetSeed()

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

Cauchy random deviates

**Examples**

```
## Use threefry engine

rxcauchy(0, 1, n = 10) # with rxcauchy you have to explicitly state n
rxcauchy(0.5, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxcauchy(3)

## This example uses `rxcauchy` directly in the model

rx <- function() {
  model({
    a <- rxcauchy(2)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

rxCbindStudyIndividual

*Bind the study parameters and individual parameters*

---

**Description**

Bind the study parameters and individual parameters

**Usage**

```
rxCbindStudyIndividual(studyParameters, individualParameters)
```

**Arguments**

`studyParameters`

These are the study parameters, often can be generated by sampling from a population. This can be either a matrix or a data frame

`individualParameters`

A data frame of individual parameters

**Value**

Data frame that can be used in rxode2 simulations

**Author(s)**

Matthew Fidler

**Examples**

```
# Function for converting coefficient of covariance into a variance
lognCv <- function(x){log((x/100)^2+1)}

set.seed(32)

nSub <- 100
nStud <- 10

#define theta
theta <- c(lka=log(0.5), # log ka
          lCl=log(5), # log Cl
          lV=log(300) # log V
          )

#define theta Matrix
thetaMat <- lotri(lCl ~ lognCv(5),
                 lV ~ lognCv(5),
                 lka ~ lognCv(5))

nev <- nSub*nStud

ev1 <- data.frame(COV1=rnorm(nev, 50, 30), COV2=rnorm(nev, 75, 10),
                 COV3=sample(c(1.0, 2.0), nev, replace=TRUE))

tmat <- rxRmvn(nStud, theta[dimnames(thetaMat)[[1]]], thetaMat)

rxCbindStudyIndividual(tmat, ev1)
```

rxchisq

*Simulate chi-squared variable from threefry generator***Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxchisq(df, n = 1L, ncores = 1L)
```

**Arguments**

df	degrees of freedom (non-negative, but can be non-integer).
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

chi squared random deviates

**Examples**

```
## Use threefry engine
rxchisq(0.5, n = 10) # with rxchisq you have to explicitly state n
```

```
rxchisq(5, n = 10, ncores = 2) # You can parallelize the simulation using openMP
rxchisq(1)

## This example uses `rxchisq` directly in the model

rx <- function() {
  model({
    a <- rxchisq(2)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

rxClean

*Cleanup anonymous DLLs by unloading them*

---

### Description

This cleans up any rxode2 loaded DLLs

### Usage

```
rxClean(wd)
```

### Arguments

wd	What directory should be cleaned; (DEPRECATED), this no longer does anything. This unloads all rxode2 anonymous dlls.
----	--

### Value

TRUE if successful

### Author(s)

Matthew L. Fidler

---

`rxCompile`*Compile a model if needed*

---

**Description**

This is the compilation workhorse creating the rxode2 model DLL files.

**Usage**

```
rxCompile(  
  model,  
  dir,  
  prefix,  
  force = FALSE,  
  modName = NULL,  
  package = NULL,  
  ...  
)  
  
## S3 method for class 'rxModelVars'  
rxCompile(  
  model,  
  dir = NULL,  
  prefix = NULL,  
  force = FALSE,  
  modName = NULL,  
  package = NULL,  
  ...  
)  
  
## S3 method for class 'character'  
rxCompile(  
  model,  
  dir = NULL,  
  prefix = NULL,  
  force = FALSE,  
  modName = NULL,  
  package = NULL,  
  ...  
)  
  
## S3 method for class 'rxDll'  
rxCompile(model, ...)  
  
## S3 method for class 'rxode2'  
rxCompile(model, ...)
```

**Arguments**

model	<p>This is the ODE model specification. It can be:</p> <ul style="list-style-type: none"> <li>• a string containing the set of ordinary differential equations (ODE) and other expressions defining the changes in the dynamic system.</li> <li>• a file name where the ODE system equation is contained</li> </ul> <p>An ODE expression enclosed in <code>\{\}</code> (see also the filename argument). For details, see the sections “Details” and <code>rxode2</code> Syntax below.</p>
dir	<p>This is the model directory where the C file will be stored for compiling.</p> <p>If unspecified, the C code is stored in a temporary directory, then the model is compiled and moved to the current directory. Afterwards the C code is removed.</p> <p>If specified, the C code is stored in the specified directory and then compiled in that directory. The C code is not removed after the DLL is created in the same directory. This can be useful to debug the c-code outputs.</p>
prefix	is a string indicating the prefix to use in the C based functions. If missing, it is calculated based on file name, or md5 of parsed model.
force	is a boolean stating if the (re)compile should be forced if <code>rxode2</code> detects that the models are the same as already generated.
modName	a string to be used as the model name. This string is used for naming various aspects of the computations, including generating C symbol names, dynamic libraries, etc. Therefore, it is necessary that <code>modName</code> consists of simple ASCII alphanumeric characters starting with a letter.
package	Package name for pre-compiled binaries.
...	Other arguments sent to the <code>rxTrans()</code> function.

**Value**

An `rxDll` object that has the following components

- `dll` DLL path
- `model` model specification
- `.c` A function to call C code in the correct context from the DLL using the `.C()` function.
- `.call` A function to call C code in the correct context from the DLL using the `.Call()` function.
- `args` A list of the arguments used to create the `rxDll` object.

**Author(s)**

Matthew L.Fidler

**See Also**

[rxode2\(\)](#)

---

rxControlUpdateSens    *This updates the tolerances based on the sensitivity equations*

---

### Description

This assumes the normal ODE equations are the first equations and the ODE is expanded by the forward sensitivities or other type of sensitivity (like adjoint)

### Usage

```
rxControlUpdateSens(rxControl, sensCmt = NULL, ncmt = NULL)
```

### Arguments

rxControl	Input list or rxControl type of list
sensCmt	Number of sensitivity compartments
ncmt	Number of compartments

### Value

Updated rxControl where \$atol, \$rtol, \$ssAtol \$ssRtol are updated with different sensitivities for the normal ODEs (first) and a different sensitivity for the larger compartments (sensitivities).

### Author(s)

Matthew L. Fidler

### Examples

```
tmp <- rxControl()

tmp2 <- rxControlUpdateSens(tmp, 3, 6)

tmp2$atol
tmp2$rtol
tmp2$ssAtol
tmp2$ssRtol
```



---

rxCreateCache	<i>This will create the cache directory for rxode2 to save between sessions</i>
---------------	---

---

**Description**

When run, if the R\_user\_dir for rxode2's cache isn't present, create the cache

**Usage**

```
rxCreateCache()
```

**Value**

nothing

**Author(s)**

Matthew Fidler

---

rxD	<i>Add to rxode2's derivative tables</i>
-----	--

---

**Description**

Add to rxode2's derivative tables

**Usage**

```
rxD(name, derivatives)
```

**Arguments**

name	Function Name
derivatives	A list of functions. Each function takes the same number of arguments as the original function. The first function will construct the derivative with respect to the first argument; The second function will construct the derivative with respect to the second argument, and so on.

**Value**

nothing

**Author(s)**

Matthew Fidler

**Examples**

```
## Add an arbitrary list of derivative functions
## In this case the fun(x,y) is assumed to be 0.5*x^2+0.5*y^2

rxD("fun", list(
  function(x, y) {
    return(x)
  },
  function(x, y) {
    return(y)
  }
))
```

---

 rxDelete

*Delete the DLL for the model*


---

**Description**

This function deletes the DLL, but doesn't delete the model information in the object.

**Usage**

```
rxDelete(obj)
```

**Arguments**

obj                    rxode2 family of objects

**Value**

A boolean stating if the operation was successful.

**Author(s)**

Matthew L.Fidler

---

 rxDerived

*Calculate derived parameters for the 1-, 2-, and 3- compartment linear models.*


---

**Description**

This calculates the derived parameters based on what is provided in a data frame or arguments

**Usage**

```
rxDerived(..., verbose = FALSE, digits = 0)
```

**Arguments**

...	The input can be: <ul style="list-style-type: none"> <li>• A data frame with PK parameters in it; This should ideally be a data frame with one pk parameter per row since it will output a data frame with one PK parameter per row.</li> <li>• PK parameters as either a vector or a scalar</li> </ul>
verbose	boolean that when TRUE provides a message about the detected pk parameters and the detected compartmental model. By default this is FALSE.
digits	represents the number of significant digits for the output; If the number is zero or below (default), do not round.

**Value**

Return a data.frame of derived PK parameters for a 1-, 2-, or 3-compartment linear model given provided clearances and volumes based on the inferred model type.

The model parameters that will be provided in the data frame are:

- vc: Central Volume (for 1-, 2- and 3- compartment models)
- kel: First-order elimination rate (for 1-, 2-, and 3-compartment models)
- k12: First-order rate of transfer from central to first peripheral compartment; (for 2- and 3-compartment models)
- k21: First-order rate of transfer from first peripheral to central compartment, (for 2- and 3-compartment models)
- k13: First-order rate of transfer from central to second peripheral compartment; (3-compartment model)
- k31: First-order rate of transfer from second peripheral to central compartment (3-compartment model)
- vp: Peripheral Volume (for 2- and 3- compartment models)
- vp2: Peripheral Volume for 3rd compartment (3- compartment model)
- vss: Volume of distribution at steady state; (1-, 2-, and 3-compartment models)
- t12alpha:  $t_{1/2,\alpha}$ ; (1-, 2-, and 3-compartment models)
- t12beta:  $t_{1/2,\beta}$ ; (2- and 3-compartment models)
- t12gamma:  $t_{1/2,\gamma}$ ; (3-compartment model)
- alpha:  $\alpha$ ; (1-, 2-, and 3-compartment models)
- beta:  $\beta$ ; (2- and 3-compartment models)
- gamma:  $\beta$ ; (3-compartment model)
- A: true A; (1-, 2-, and 3-compartment models)
- B: true B; (2- and 3-compartment models)
- C: true C; (3-compartment model)
- fracA: fractional A; (1-, 2-, and 3-compartment models)
- fracB: fractional B; (2- and 3-compartment models)
- fracC: fractional C; (3-compartment model)

**Author(s)**

Matthew Fidler and documentation from Justin Wilkins, <justin.wilkins@occams.com>

**References**

Shafer S. L. CONVERT.XLS

Rowland M, Tozer TN. Clinical Pharmacokinetics and Pharmacodynamics: Concepts and Applications (4th). Clipping Williams & Wilkins, Philadelphia, 2010.

**Examples**

```
## Note that rxode2 parses the names to figure out the best PK parameter
params <- rxDerived(cl = 29.4, v = 23.4, Vp = 114, vp2 = 4614, q = 270, q2 = 73)

## That is why this gives the same results as the value before
params <- rxDerived(CL = 29.4, V1 = 23.4, V2 = 114, V3 = 4614, Q2 = 270, Q3 = 73)

## You may also use micro-constants alpha/beta etc.
params <- rxDerived(k12 = 0.1, k21 = 0.2, k13 = 0.3, k31 = 0.4, kel = 10, v = 10)

## or you can mix vectors and scalars
params <- rxDerived(CL = 29.4, V = 1:3)

## If you want, you can round to a number of significant digits
## with the `digits` argument:
params <- rxDerived(CL = 29.4, V = 1:3, digits = 2)
```

---

 rxDfdy

*Jacobian and parameter derivatives*


---

**Description**

Return Jacobain and parameter derivatives

**Usage**

```
rxDfdy(obj)
```

**Arguments**

obj                    rxode2 family of objects

**Value**

A list of the jacobian parameters defined in this rxode2 object.

**Author(s)**

Matthew L. Fidler

**See Also**

Other Query model information: [rxInits\(\)](#), [rxLhs\(\)](#), [rxModelVars\(\)](#), [rxParams\(\)](#), [rxState\(\)](#)

---

rxEtDispatchSolve      *Dispatch solve to 'rxode2' solve*

---

**Description**

Dispatch solve to 'rxode2' solve

**Usage**

```
rxEtDispatchSolve(x, ...)
```

```
## Default S3 method:  
rxEtDispatchSolve(x, ...)
```

**Arguments**

x	rxode2 solve dispatch object
...	other arguments

**Value**

if 'rxode2' is loaded, a solved object, otherwise an error

**Author(s)**

Matthew L. Fidler

---

`rxEvid`*EVID formatting for tibble and other places.*

---

**Description**

This is to make an EVID more readable by non pharmacometricians. It displays what each means and allows it to be displayed in a tibble.

**Usage**

```
rxEvid(x)

as.rxEvid(x)

## S3 method for class 'rxEvid'
c(x, ...)

## S3 method for class 'rxEvid'
x[...]

## S3 method for class 'rxEvid'
as.character(x, ...)

## S3 method for class 'rxEvid'
x[[...]]

## S3 method for class 'rxRateDur'
c(x, ...)

## S3 method for class 'rxEvid'
format(x, ...)

## S3 method for class 'rxRateDur'
format(x, ...)

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

**Arguments**

<code>x</code>	Item to be converted to a rxode2 EVID specification.
<code>...</code>	Other parameters

**Value**

rxEvid specification

**Examples**

```
rxEvid(1:7)
```

---

```
rxexp
```

*Simulate exponential variable from threefry generator*

---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxexp(rate, n = 1L, ncores = 1L)
```

**Arguments**

rate	vector of rates.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

exponential random deviates

## Examples

```
## Use threefry engine

rxexp(0.5, n = 10) # with rxexp you have to explicitly state n
rxexp(5, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxexp(1)

## This example uses `rxexp` directly in the model

rx <- function() {
  model({
    a <- rxexp(2)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

rxf

---

*Simulate F variable from threefry generator*


---

## Description

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

## Usage

```
rxf(df1, df2, n = 1L, ncores = 1L)
```

## Arguments

df1, df2	degrees of freedom. Inf is allowed.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation <code>rxnorm</code> simulates using the threefry sitmo generator. <code>rxnormV</code> used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of <code>rxnorm</code> . It is no longer supported in <code>rxode2({})</code> blocks



**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with rxSetSeed()

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

f random deviates

**Examples**

```
## Use threefry engine

rxf(0.5, 0.5, n = 10) # with rxf you have to explicitly state n
rxf(5, 1, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxf(1, 3)

## This example uses `rxf` directly in the model

rx <- function() {
  model({
    a <- rxf(2, 2)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

 rxFixPop

*Apply the fixed population estimated parameters*


---

**Description**

Apply the fixed population estimated parameters

**Usage**

```
rxFixPop(ui, returnNull = FALSE)
```

**Arguments**

ui	rxode2 ui function
returnNull	boolean for if unchanged values should return the original ui (FALSE) or null (TRUE)

**Value**

when returnNull is TRUE, NULL if nothing was changed, or the changed model ui. When returnNull is FALSE, return a ui no matter if it is changed or not.

**Author(s)**

Matthew L. Fidler

**Examples**

```
One.comp.transit.allo <- function() {
  ini({
    # Where initial conditions/variables are specified
    lktr <- log(1.15) #log k transit (/h)
    lcl <- log(0.15) #log Cl (L/hr)
    lv <- log(7) #log V (L)
    ALLC <- fix(0.75) #allometric exponent cl
    ALLV <- fix(1.00) #allometric exponent v
    prop.err <- 0.15 #proportional error (SD/mean)
    add.err <- 0.6 #additive error (mg/L)
    eta.ktr ~ 0.5
    eta.cl ~ 0.1
    eta.v ~ 0.1
  })
  model({
    #Allometric scaling on weight
    cl <- exp(lcl + eta.cl + ALLC * logWT70)
    v <- exp(lv + eta.v + ALLV * logWT70)
    ktr <- exp(lktr + eta.ktr)
    # RxODE-style differential equations are supported
    d/dt(depot) = -ktr * depot
    d/dt(central) = ktr * trans - (cl/v) * central
    d/dt(trans) = ktr * depot - ktr * trans
    ## Concentration is calculated
    cp = central/v
    # And is assumed to follow proportional and additive error
    cp ~ prop(prop.err) + add(add.err)
  })
}

m <- rxFixPop(One.comp.transit.allo)
m

# now everything is already fixed, so calling again will do nothing
```

```

rxFixPop(m)

# if you call it with returnNull=TRUE when no changes have been
# performed, the function will return NULL

rxFixPop(m, returnNull=TRUE)

```

---

 rxFun

---

*Add/Create C functions for use in rxode2*


---

## Description

Add/Create C functions for use in rxode2

## Usage

```

rxFun(name, args, cCode)

rxRmFun(name)

```

## Arguments

name	This can either give the name of the user function or be a simple R function that you wish to convert to C. If you have rxode2 convert the R function to C, the name of the function will match the function name provided and the number of arguments will match the R function provided. Hence, if you are providing an R function for conversion to C, the rest of the arguments are implied.
args	This gives the arguments of the user function
cCode	This is the C-code for the new function

## Examples

```

# Right now rxode2 is not aware of the function fun
# Therefore it cannot translate it to symengine or
# Compile a model with it.

try(rxode2("a=fun(a,b,c)"))

# Note for this approach to work, it cannot interfere with C
# function names or reserved rxode2 special terms. Therefore
# f(x) would not work since f is an alias for bioavailability.

fun <- "
double fun(double a, double b, double c) {
  return a*a+b*a+c;
}
" # C-code for function

```

```

rxFun("fun", c("a", "b", "c"), fun) ## Added function

# Now rxode2 knows how to translate this function to symengine

rxToSE("fun(a,b,c)")

# And will take a central difference when calculating derivatives

rxFromSE("Derivative(fun(a,b,c),a)")

## Of course, you could specify the derivative table manually
rxD("fun", list(
  function(a, b, c) {
    paste0("2*", a, "+", b)
  },
  function(a, b, c) {
    return(a)
  },
  function(a, b, c) {
    return("0.0")
  }
))

rxFromSE("Derivative(fun(a,b,c),a)")

# You can also remove the functions by `rxRmFun`

rxRmFun("fun")

# you can also use R functions directly in rxode2

gg <- function(x, y) {
  x + y
}

f <- rxode2({
  z = gg(x, y)
})

e <- et(1:10) |> as.data.frame()

e$x <- 1:10
e$y <- 21:30

rxSolve(f, e)

# Note that since it touches R, it can only run single-threaded.
# There are also requirements for the function:
#
# 1. It accepts one value per argument (numeric)
#

```

```
# 2. It returns one numeric value

# If it is a simple function (like gg) you can also convert it to C
# using rxFun and load it into rxode2

rxFun(gg)

rxSolve(f, e)

# to stop the recompile simply reassign the function
f <- rxode2(f)

rxSolve(f, e)

rxRmFun("gg")
rm(gg)
rm(f)

# You can also automatically convert a R function to R code (and
# calculate first derivatives)

fun <- function(a, b, c) {
  a^2+b*a+c
}

rxFun(fun)

# You can see the R code if you want with rxC

message(rxC("fun"))

# you can also remove both the function and the
# derivatives with rxRmFun("fun")

rxRmFun("fun")
```

---

rxgamma

*Simulate gamma variable from threefry generator*

---

## Description

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxgamma(shape, rate = 1, n = 1L, ncores = 1L)
```

**Arguments**

shape	The shape of the gamma random variable
rate	an alternative way to specify the scale.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation <code>rxnorm</code> simulates using the threefry sitmo generator. <code>rxnormV</code> used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simply be an alias of <code>rxnorm</code> . It is no longer supported in <code>rxode2({})</code> blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the `rxode2` environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the `rxode2` engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

gamma random deviates

**Examples**

```
## Use threefry engine

rxgamma(0.5, n = 10) # with rxgamma you have to explicitly state n
rxgamma(5, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxgamma(1)

## This example uses `rxbeta` directly in the model

rx <- function() {
  model({
    a <- rxgamma(2)
  })
}
```

```

}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)

```

---

 rxgeom

*Simulate geometric variable from threefry generator*


---

### Description

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

### Usage

```
rxgeom(prob, n = 1L, ncores = 1L)
```

### Arguments

prob	probability of success in each trial. $0 < \text{prob} \leq 1$ .
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

### Details

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with rxSetSeed()

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

### Value

geometric random deviates

## Examples

```
## Use threefry engine

rxgeom(0.5, n = 10) # with rxgeom you have to explicitly state n
rxgeom(0.25, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxgeom(0.75)

## This example uses `rxgeom` directly in the model

rx <- function() {
  model({
    a <- rxgeom(0.24)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

rxGetControl

*rxGetControl option from ui*

---

## Description

rxGetControl option from ui

## Usage

```
rxGetControl(ui, option, default)
```

## Arguments

ui	rxode2 ui object
option	Option to get
default	Default value

## Value

Option (if present) or default value

## Author(s)

Matthew L. Fidler



---

rxGetLin	<i>Get the linear compartment model true function</i>
----------	---

---

**Description**

Get the linear compartment model true function

**Usage**

```
rxGetLin(
  model,
  linCmtSens = c("linCmtA", "linCmtB", "linCmtC"),
  verbose = FALSE
)
```

**Arguments**

model	<p>This is the ODE model specification. It can be:</p> <ul style="list-style-type: none"> <li>• a string containing the set of ordinary differential equations (ODE) and other expressions defining the changes in the dynamic system.</li> <li>• a file name where the ODE system equation is contained</li> </ul> <p>An ODE expression enclosed in <code>\{\}</code> (see also the <code>filename</code> argument). For details, see the sections “Details” and <code>rxode2</code> Syntax below.</p>
linCmtSens	The method to calculate the <code>linCmt()</code> solutions
verbose	When TRUE be verbose with the linear compartmental model

**Value**

model with `linCmt()` replaced with `linCmtA()`

**Author(s)**

Matthew Fidler

---

rxGetrxode2	<i>Get rxode2 model from object</i>
-------------	-------------------------------------

---

**Description**

Get rxode2 model from object

**Usage**

```
rxGetrxode2(obj)
```

**Arguments**

obj                    rxode2 family of objects

**Value**

rxode2 model

---

rxGetSeed	<i>Get the rxode2 seed</i>
-----------	----------------------------

---

**Description**

Get the rxode2 seed

**Usage**

```
rxGetSeed()
```

**Value**

rxode2 seed state or -1 when the seed isn't set

**See Also**

rxSetSeed, rxWithSeed, rxWithPreserveSeed

**Examples**

```
# without setting seed

rxGetSeed()
# Now set the seed
rxSetSeed(42)

rxGetSeed()

rxnorm()

rxGetSeed()

# don't use the rxode2 seed again

rxSetSeed(-1)

rxGetSeed()

rxnorm()

rxGetSeed()
```

---

rxHtml	<i>Format rxSolve and related objects as html.</i>
--------	--

---

**Description**

Format rxSolve and related objects as html.

**Usage**

```
rxHtml(x, ...)
```

```
## S3 method for class 'rxSolve'
```

```
rxHtml(x, ...)
```

**Arguments**

x	rxode2 object
...	Extra arguments sent to kable

**Value**

html code for rxSolve object

**Author(s)**

Matthew L. Fidler

---

rxIndLinState	<i>Set the preferred factoring by state</i>
---------------	---

---

**Description**

Set the preferred factoring by state

**Usage**

```
rxIndLinState(preferred = NULL)
```

**Arguments**

preferred	A list of each state's preferred factorization
-----------	--

**Value**

Nothing

**Author(s)**

Matthew Fidler

---

rxIndLinStrategy	<i>This sets the inductive linearization strategy for matrix building</i>
------------------	---

---

**Description**

When there is more than one state in a ODE that cannot be separated this specifies how it is incorporated into the matrix exponential.

**Usage**

```
rxIndLinStrategy(strategy = c("curState", "split"))
```

**Arguments**

strategy	The strategy for inductive linearization matrix building
----------	--

- `curState` Prefer parameterizing in terms of the current state, followed by the first state observed in the term.
- `split` Split the parameterization between all states in the term by dividing each by the number of states in the term and then adding a matrix term for each state.

**Value**

Nothing

**Author(s)**

Matthew L. Fidler

---

rxInv	<i>Invert matrix using RcppArmadillo.</i>
-------	---

---

**Description**

Invert matrix using RcppArmadillo.

**Usage**

```
rxInv(matrix)
```

**Arguments**

matrix	matrix to be inverted.
--------	------------------------

**Value**

inverse or pseudo inverse of matrix.

---

rxIsCurrent	<i>Checks if the rxode2 object was built with the current build</i>
-------------	---

---

**Description**

Checks if the rxode2 object was built with the current build

**Usage**

```
rxIsCurrent(obj)
```

**Arguments**

obj                    rxode2 family of objects

**Value**

boolean indicating if this was built with current rxode2

---

rxLhs	<i>Left handed Variables</i>
-------	------------------------------

---

**Description**

This returns the model calculated variables

**Usage**

```
rxLhs(obj)
```

**Arguments**

obj                    rxode2 family of objects

**Value**

a character vector listing the calculated parameters

**Author(s)**

Matthew L.Fidler

**See Also**[rxode2](#)Other Query model information: [rxDfdy\(\)](#), [rxInits\(\)](#), [rxModelVars\(\)](#), [rxParams\(\)](#), [rxState\(\)](#)

---

`rxLock`*Lock/unlocking of rxode2 dll file*

---

**Description**

Lock/unlocking of rxode2 dll file

**Usage**`rxLock(obj)``rxUnlock(obj)`**Arguments**`obj` A rxode2 family of objects**Value**

nothing; called for side effects

---

`rxnbinom`*Simulate Binomial variable from threefry generator*

---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**`rxnbinom(size, prob, n = 1L, ncores = 1L)``rxnbinomMu(size, mu, n = 1L, ncores = 1L)`

**Arguments**

size	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
prob	probability of success in each trial. $0 < \text{prob} \leq 1$ .
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks
mu	alternative parametrization via mean: see 'Details'.

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

negative binomial random deviates. Note that rxbinom2 uses the mu parameterization an the rxbinom uses the prob parameterization ( $\text{mu} = \text{size} / (\text{prob} + \text{size})$ )

**Examples**

```
## Use threefry engine

rxnbinom(10, 0.9, n = 10) # with rxbinom you have to explicitly state n
rxnbinom(3, 0.5, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxnbinom(4, 0.7)

# use mu parameter
rxnbinomMu(40, 40, n=10)

## This example uses `rxbinom` directly in the model

rx <- function() {
  model({
    a <- rxnbinom(10, 0.5)
  })
}
```

```
}  
  
et <- et(1, id = 1:100)  
  
s <- rxSolve(rx, et)  
  
rx <- function() {  
  model({  
    a <- rxnbinomMu(10, 40)  
  })  
}  
  
s <- rxSolve(rx, et)
```

---

rxNorm

*Get the normalized model*

---

### Description

This get the syntax preferred model for processing

### Usage

```
rxNorm(obj, condition = NULL, removeInis, removeJac, removeSens)
```

### Arguments

obj	rxode2 family of objects
condition	Character string of a logical condition to use for subsetting the normalized model. When missing, and a condition is not set via rxCondition, return the whole code with all the conditional settings intact. When a condition is set with rxCondition, use that condition.
removeInis	A boolean indicating if parameter initialization will be removed from the model
removeJac	A boolean indicating if the Jacobians will be removed.
removeSens	A boolean indicating if the sensitivities will be removed.

### Value

Normalized Normal syntax (no comments)

### Author(s)

Matthew L. Fidler



---

rxnormV	<i>Simulate random normal variable from threefry generator</i>
---------	--

---

**Description**

Simulate random normal variable from threefry generator

**Usage**

```
rxnormV(mean = 0, sd = 1, n = 1L, ncores = 1L)
```

```
rxnorm(mean = 0, sd = 1, n = 1L, ncores = 1L)
```

**Arguments**

mean	vector of means.
sd	vector of standard deviations.
n	number of observations
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

**Value**

normal random number deviates

**Examples**

```
## Use threefry engine

rxnorm(n = 10) # with rxnorm you have to explicitly state n
rxnorm(n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxnorm(2, 3) ## The first 2 arguments are the mean and standard deviation

## This example uses `rxnorm` directly in the model

rx <- function() {
  model({
    a <- rxnorm()
  })
}

et <- et(1, id = 1:2)
```

```
s <- rxSolve(rx, et)
```

---

rxode2

*Create an ODE-based model specification*

---

## Description

Create a dynamic ODE-based model object suitably for translation into fast C code

## Usage

```
rxode2(  
  model,  
  modName = basename(wd),  
  wd = getwd(),  
  filename = NULL,  
  extraC = NULL,  
  debug = FALSE,  
  calcJac = NULL,  
  calcSens = NULL,  
  collapseModel = FALSE,  
  package = NULL,  
  ...,  
  linCmtSens = c("linCmtA", "linCmtB", "linCmtC"),  
  indLin = FALSE,  
  verbose = FALSE,  
  fullPrint = getOption("rxode2.fullPrint", FALSE),  
  envir = parent.frame()  
)
```

```
RxODE(  
  model,  
  modName = basename(wd),  
  wd = getwd(),  
  filename = NULL,  
  extraC = NULL,  
  debug = FALSE,  
  calcJac = NULL,  
  calcSens = NULL,  
  collapseModel = FALSE,  
  package = NULL,  
  ...,  
  linCmtSens = c("linCmtA", "linCmtB", "linCmtC"),  
  indLin = FALSE,  
  verbose = FALSE,
```

```

    fullPrint = getOption("rxode2.fullPrint", FALSE),
    envir = parent.frame()
)

rxode(
  model,
  modName = basename(wd),
  wd = getwd(),
  filename = NULL,
  extraC = NULL,
  debug = FALSE,
  calcJac = NULL,
  calcSens = NULL,
  collapseModel = FALSE,
  package = NULL,
  ...,
  linCmtSens = c("linCmtA", "linCmtB", "linCmtC"),
  indLin = FALSE,
  verbose = FALSE,
  fullPrint = getOption("rxode2.fullPrint", FALSE),
  envir = parent.frame()
)

```

## Arguments

model	<p>This is the ODE model specification. It can be:</p> <ul style="list-style-type: none"> <li>• a string containing the set of ordinary differential equations (ODE) and other expressions defining the changes in the dynamic system.</li> <li>• a file name where the ODE system equation is contained</li> </ul> <p>An ODE expression enclosed in <code>{\}</code> (see also the filename argument). For details, see the sections “Details” and rxode2 Syntax below.</p>
modName	a string to be used as the model name. This string is used for naming various aspects of the computations, including generating C symbol names, dynamic libraries, etc. Therefore, it is necessary that modName consists of simple ASCII alphanumeric characters starting with a letter.
wd	character string with a working directory where to create a subdirectory according to modName. When specified, a subdirectory named after the “modName.d” will be created and populated with a C file, a dynamic loading library, plus various other working files. If missing, the files are created (and removed) in the temporary directory, and the rxode2 DLL for the model is created in the current directory named rx_????_platform, for example rx_129f8f97fb94a87ca49ca8daf691e1e_i386.dl
filename	A file name or connection object where the ODE-based model specification resides. Only one of model or filename may be specified.
extraC	Extra c code to include in the model. This can be useful to specify functions in the model. These C functions should usually take double precision arguments, and return double precision values.

debug	is a boolean indicating if the executable should be compiled with verbose debugging information turned on.
calcJac	boolean indicating if rxode2 will calculate the Jacobian according to the specified ODEs.
calcSens	boolean indicating if rxode2 will calculate the sensitivities according to the specified ODEs.
collapseModel	boolean indicating if rxode2 will remove all LHS variables when calculating sensitivities.
package	Package name for pre-compiled binaries.
...	ignored arguments.
linCmtSens	The method to calculate the linCmt() solutions
indLin	Calculate inductive linearization matrices and compile with inductive linearization support.
verbose	When TRUE be verbose with the linear compartmental model
fullPrint	When using printf within the model, if TRUE print on every step (except ME/indLin), otherwise when FALSE print only when calculating the d/dt
envir	is the environment to look for R user functions (defaults to parent environment)

## Details

The Rx in the name rxode2 is meant to suggest the abbreviation *Rx* for a medical prescription, and thus to suggest the package emphasis on pharmacometrics modeling, including pharmacokinetics (PK), pharmacodynamics (PD), disease progression, drug-disease modeling, etc.

The ODE-based model specification may be coded inside four places:

- Inside a rxode2({}) block statements:

```
library(rxode2)
mod <- rxode2({
  # simple assignment
  C2 <- centr/V2

  # time-derivative assignment
  d/dt(centr) <- F*KA*depot - CL*C2 - Q*C2 + Q*C3;
})

## using C compiler: 'gcc (Ubuntu 11.4.0-1ubuntu1~22.04) 11.4.0'
```

- Inside a rxode2("") string statement:

```
mod <- rxode2("
  # simple assignment
  C2 <- centr/V2

  # time-derivative assignment
  d/dt(centr) <- F*KA*depot - CL*C2 - Q*C2 + Q*C3;
")
```

```
## using C compiler: 'gcc (Ubuntu 11.4.0-1ubuntu1~22.04) 11.4.0'
```

- In a file name to be loaded by rxode2:

```
writelnLines("
# simple assignment
C2 <- centr/V2

# time-derivative assignment
d/dt(centr) <- F*Ka*depot - CL*C2 - Q*C2 + Q*C3;
", "modelFile.rxode2")
mod <- rxode2(filename='modelFile.rxode2')
unlink("modelFile.rxode2")
```

- In a model function which can be parsed by rxode2:

```
mod <- function() {
  model({
    # simple assignment
    C2 <- centr/V2

    # time-derivative assignment
    d/dt(centr) <- F*Ka*depot - CL*C2 - Q*C2 + Q*C3;
  })
}
```

```
mod <- rxode2(mod) # or simply mod() if the model is at the end of the function
```

```
# These model functions often have residual components and initial
# (`ini({})`) conditions attached as well. For example the
# theophylline model can be written as:
```

```
one.compartment <- function() {
  ini({
    tka <- 0.45 # Log Ka
    tcl <- 1 # Log Cl
    tv <- 3.45 # Log V
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
  })
}
```

```

    cp ~ add(add.sd)
  })
}

# after parsing the model
mod <- one.compartment()

```

For the block statement, character string or text file an internal rxode2 compilation manager translates the ODE system into C, compiles it and loads it into the R session. The call to rxode2 produces an object of class rxode2 which consists of a list-like structure (environment) with various member functions.

For the last type of model (a model function), a call to rxode2 creates a parsed rxode2 ui that can be translated to the rxode2 compilation model.

```

mod$simulationModel

## using C compiler: 'gcc (Ubuntu 11.4.0-1ubuntu1~22.04) 11.4.0'

## rxode2 3.0.0 model named rx_632db1954a006dfe249974d0974ba18b model (ready).
## x$state: depot, center
## x$stateExtra: cp
## x$params: tka, tcl, tv, add.sd, eta.ka, eta.cl, eta.v, rxerr.cp
## x$lhs: ka, cl, v, cp, ipredSim, sim

# or
mod$simulationIniModel

## using C compiler: 'gcc (Ubuntu 11.4.0-1ubuntu1~22.04) 11.4.0'

## rxode2 3.0.0 model named rx_7e1fb9007822c2542d741c71c9c37dd4 model (ready).
## x$state: depot, center
## x$stateExtra: cp
## x$params: tka, tcl, tv, add.sd, eta.ka, eta.cl, eta.v, rxerr.cp
## x$lhs: ka, cl, v, cp, ipredSim, sim

```

This is the same type of function required for nlmixr2 estimation and can be extended and modified by model piping. For this reason will be focused on in the documentation.

This basic model specification consists of one or more statements optionally terminated by semicolons ; and optional comments (comments are delimited by # and an end-of-line).

A block of statements is a set of statements delimited by curly braces, { ... }.

Statements can be either assignments, conditional if/else if/else, while loops (can be exited by break), special statements, or printing statements (for debugging/testing).

Assignment statements can be:

- **simple** assignments, where the left hand is an identifier (i.e., variable). This includes string assignments

- special **time-derivative** assignments, where the left hand specifies the change of the amount in the corresponding state variable (compartment) with respect to time e.g.,  $d/dt(\text{depot})$ :
- special **initial-condition** assignments where the left hand specifies the compartment of the initial condition being specified, e.g.  $\text{depot}(0) = 0$
- special model event changes including **bioavailability** ( $f(\text{depot})=1$ ), **lag time** ( $\text{alag}(\text{depot})=0$ ), **modeled rate** ( $\text{rate}(\text{depot})=2$ ) and **modeled duration** ( $\text{dur}(\text{depot})=2$ ). An example of these model features and the event specification for the modeled infusions the rxode2 data specification is found in [rxode2 events vignette](#).
- special **change point syntax, or model times**. These model times are specified by  $\text{mtime}(\text{var})=\text{time}$
- special **Jacobian-derivative** assignments, where the left hand specifies the change in the compartment ode with respect to a variable. For example, if  $d/dt(y) = dy$ , then a Jacobian for this compartment can be specified as  $df(y)/dy(dy) = 1$ . There may be some advantage to obtaining the solution or specifying the Jacobian for very stiff ODE systems. However, for the few stiff systems we tried with LSODA, this actually slightly slowed down the solving.
- Special **string value declarations** which tell what values a string variable will take within a rxode2 solving structure. These values will then cause a factor to be created for this variable on solving the rxode2 model. As such, they are declared in much the same way as R, that is: `labels(a) <- c("a1", "a2")`.

Note that assignment can be done by `=`, `<-` or `~`.

When assigning with the `~` operator, the **simple assignments** and **time-derivative** assignments will not be output. Note that with the rxode2 model functions assignment with `~` can also be overloaded with a residual distribution specification.

Special statements can be:

- **Compartment declaration statements**, which can change the default dosing compartment and the assumed compartment number(s) as well as add extra compartment names at the end (useful for multiple-endpoint nlmixr models); These are specified by `cmt(compartmentName)`
- **Parameter declaration statements**, which can make sure the input parameters are in a certain order instead of ordering the parameters by the order they are parsed. This is useful for keeping the parameter order the same when using 2 different ODE models. These are specified by `param(par1, par2, ...)`
- **Variable interpolation statements**, which tells the interpolation for specific covariates. These include `locf(cov1, cov2, ...)` for last observation carried forward, `nocb(cov1, cov2, ...)` for next observation carried backward, `linear(cov1, cov2, ...)` for linear interpolation and `midpoint(cov1, cov2, ...)` for midpoint interpolation.

An example model is shown below:

```
# simple assignment
C2 <- centr/V2

# time-derivative assignment
d/dt(centr) <- F*Ka*depot - CL*C2 - Q*C2 + Q*C3;
```

Expressions in assignment and `if` statements can be numeric or logical.

Numeric expressions can include the following numeric operators  $+$ ,  $-$ ,  $*$ ,  $/$ ,  $^$  and those mathematical functions defined in the C or the R math libraries (e.g., `fabs`, `exp`, `log`, `sin`, `abs`).

You may also access the R's functions in the **R math libraries**, like `lgammafn` for the log gamma function.

The `rxode2` syntax is case-sensitive, i.e., `ABC` is different than `abc`, `Abc`, `ABc`, etc.

### Identifiers:

Like R, Identifiers (variable names) may consist of one or more alphanumeric, underscore `_` or period `.` characters, but the first character cannot be a digit or underscore `_`.

Identifiers in a model specification can refer to:

- State variables in the dynamic system (e.g., compartments in a pharmacokinetics model).
- Implied input variable, `t` (time), `tlast` (last time point), and `podo` (oral dose, in the undocumented case of absorption transit models).
- Special constants like `pi` or **R's predefined constants**.
- Model parameters (e.g., `ka` rate of absorption, `CL` clearance, etc.)
- Others, as created by assignments as part of the model specification; these are referred as *LHS* (left-hand side) variable.

Currently, the `rxode2` modeling language only recognizes system state variables and “parameters”, thus, any values that need to be passed from R to the ODE model (e.g., `age`) should be either passed in the `params` argument of the integrator function `rxSolve()` or be in the supplied event data-set.

There are certain variable names that are in the `rxode2` event tables. To avoid confusion, the following event table-related items cannot be assigned, or used as a state but can be accessed in the `rxode2` code:

- `cmt`
- `dvid`
- `addl`
- `ss`
- `amt`
- `dur`
- `rate`
- `Rprintf`
- `print`
- `printf`
- `id`

However the following variables are cannot be used in a model specification:

- `evid`
- `ii`

Sometimes `rxode2` generates variables that are fed back to `rxode2`. Similarly, `nlmixr2` generates some variables that are used in `nlmixr` estimation and simulation. These variables start with the either the `rx` or `nlmixr` prefixes. To avoid any problems, it is suggested to not use these variables starting with either the `rx` or `nlmixr` prefixes.



**Logical Operators:**

Logical operators support the standard R operators `==`, `!=`, `>=`, `<=`, `>` and `<`. Like R these can be in `if()` or `while()` statements, `ifelse()` expressions. Additionally they can be in a standard assignment. For instance, the following is valid:

```
cov1 = covm*(sexf == "female") + covm*(sexf != "female")
```

Notice that you can also use character expressions in comparisons. This convenience comes at a cost since character comparisons are slower than numeric expressions. Unlike R, `as.numeric` or `as.integer` for these logical statements is not only not needed, but will cause a syntax error if you try to use the function.

**Supported functions:**

All the supported functions in rxode2 can be seen with the `rxSupportedFuns()`.

A brief description of the built-in functions are in the following table:

Function	Description
<code>gamma(x)</code>	The Gamma function
<code>lgamma(x)</code>	Natural logarithm of absolute value of gamma function
<code>digamma(x)</code>	First derivative of lgamma
<code>trigamma(x)</code>	Second derivative of lgamma
<code>tetragamma(x)</code>	Third derivative of lgamma
<code>pentagamma(x)</code>	Fourth derivative of lgamma
<code>psigamma(x, deriv)</code>	n-th derivative of Psi, the digamma function, which is the derivative of lgammafn. In other words, $\psi^{(n)}(x)$ .
<code>cospi(x)</code>	$\cos(\pi*x)$
<code>sinpi(x)</code>	$\sin(\pi*x)$
<code>tanpi(x)</code>	$\tan(\pi*x)$
<code>beta(a, b)</code>	Beta function
<code>lbeta(a, b)</code>	log Beta function
<code>bessel_i(x, nu, expo)</code>	Bessel function type I with index nu
<code>bessel_j(x, nu)</code>	Bessel function type J with index nu
<code>bessel_k(x, ku, expo)</code>	Bessel function type K with index nu
<code>bessel_y(x, nu)</code>	Bessel function type Y with index nu
<code>R_pow(x, y)</code>	$x^y$
<code>R_pow_di(x, I)</code>	$x^y$
<code>log1pmx</code>	$\log(1+x) - x$
<code>log1pexp</code>	$\log(1+\exp(x))$
<code>expm1(x)</code>	$\exp(x)-1$
<code>lgamma1p(x)</code>	$\log(\text{gamma}(x+1))$
<code>sign(x)</code>	Compute the signum function where $\text{sign}(x)$ is 1, 0 -1
<code>fsign(x, y)</code>	$\text{abs}(x)*\text{sign}(y)$
<code>fprec(x, digits)</code>	x rounded to digits (after the decimal point, used by <code>signif()</code> )
<code>fround(x, digits)</code>	Round, used by R's <code>round()</code>
<code>ftrunc(x)</code>	Truncated towards zero
<code>abs(x)</code>	absolute value of x
<code>sin(x)</code>	sine of x
<code>cos(x)</code>	cos of x
<code>tan(x)</code>	tan of x
<code>factorial(x)</code>	factorial of x

lfactorial(x)	log(factorial(x))
log10(x)	log base 10
log2(x)	log base 2
pnorm(x)	Normal CDF of x
qnorm(x)	Normal pdf of x
probit(x, low=0, hi=1)	Probit (normal pdf) of x transforming into a range
probitInv(q, low=0, hi=1)	Inverse probit of x transforming into a range
acos(x)	Inverse cosine
asin(x)	Inverse sine
atan(x)	Inverse tangent
atan2(a, b)	Four quadrant inverse tangent
sinh(x)	Hyperbolic sine
cosh(x)	Hyperbolic cosine
tanh(x)	Hyperbolic tangent
floor(x)	Downward rounding
ceil(x)	Upward rounding
logit(x, low=0, hi=1)	Logit transformation of x transforming into a range
expit(x, low=0, hi=1)	expit transofmrtn in range
gammaq(a, z)	Normalized incomplete gamma from boost
gammaqInv(a, q)	Normalized incomplete gamma inverse from boost
ifelse(cond, trueValue, falseValue)	if else function
gammap(a, z)	Normalized lower incomplete gamma from boost
gammapInv(a, p)	Inverse of Normalized lower incomplete gamma from boost
gammapInva(x, p)	Inverse of Normalized lower incomplete gamma from boost
rxnorm(x)	Generate one deviate of from a normal distribution for each observation scale
rxnormV(x)	Generate one deviate from low discrepancy normal for each observation
rxcauchy	Generate one deviate from the cauchy distribution for each observation
rxchisq	Generate one deviate from the chisq distribution for each observation
rxexp	Generate one deviate from the exponential distribution for each observation
rxf	Generate one deviate from low discrepancy normal for each observation
rxgamma	Generate one deviate from the gamma distribution for each observation
rxbeta	Generate one deviate from the beta distribution for each observation
rxgeom	Generate one deviate from the geometric distribution for each observation
rxpois	Generate one deviate from the poission distribution for each observation
rxrt	Generate one deviate from the t distribuion for each observation
tad() or tad(x)	Time after dose (tad()) or time after dose for a compartment tad(cmt); no dose=NA
tad0() or tad0(x)	Time after dose (tad0()) or time after dose for a compartment tad0(cmt); no dose=0
tafd() or tafd(x)	Time after first dose (tafd()) or time after first dose for a compartment tafd(cmt); no dose=NA
tafd0() or tafd0(x)	Time after first dose (tafd()) or time after first dose for a compartment tafd(cmt); no dose=0
dosenum()	Dose Number
tlast() or tlast(cmt)	Time of Last dose; This takes into consideration any lag time, so if there is a dose at time
tlast0() or tlast0(cmt)	Time of Last dose; This takes into consideration any lag time, so if there is a dose at time
tfirst() or tfirst(cmt)	Time since first dose or time since first dose of a compartment; no dose=NA
tfirst0() or tfirst0(cmt)	Time since first dose or time since first dose of a compartment; no dose=0
prod(...)	product of terms; This uses PreciseSums so the product will not have as much floating po
sum(...)	sum of terms; This uses PreciseSums so the product will not have as much floating point
max(...)	maximum of a group of numbers
min(...)	Min of a group of numbers

lag(parameter, number=1)	Get the lag of an input parameter; You can specify a number of lagged observations
lead(parameter, number=2)	Get the lead of an input parameter; You can specify a number of lead observation
diff(par, number=1)	Get the difference between the current parameter and the last parameter; Can change the
first(par)	Get the first value of an input parameter
last(par)	Get the last value of an input parameter
transit()	The transit compartment psuedo function
is.na()	Determine if a value is NA
is.nan()	Determine if a value is NaN
is.infinite()	Check to see if the value is infinite
rinorm(x)	Generate one deviate of from a normal distribution for each individual
rinormV(x)	Generate one deviate from low discrepancy normal for each individual
ricauchy	Generate one deviate from the cauchy distribution for each individual
richisq	Generate one deviate from the chisq distribution for each individual
riexp	Generate one deviate from the exponential distribution for each individual
rif	Generate one deviate from low discrepancy normal for each individual
rigamma	Generate one deviate from the gamma distribution for each individual
ribeta	Generate one deviate from the beta distribution for each individual
rigeom	Generate one deviate from the geometric distribution for each individual
ropois	Generate one deviate from the poission distribution for each individual
rit	Generate one deviate from the t distribtuion for each individual
simeps	Simulate EPS from possibly truncated sigma matrix. Will take sigma matrix from the cu
simeta	Simulate ETA from possibly truncated omega matrix. Will take the omega matrix from th

Note that `lag(cmt) =` is equivalent to `alag(cmt) =` and not the same as `= lag(wt)`

### Reserved keywords:

There are a few reserved keywords in a rxode2 model. They are in the following table:

Reserved Name	Meaning
time	solver time
pod0	In Transit compartment models, last dose amount
tlast	Time of Last dose
M_E	Exp(1)
M_LOG2E	log <sub>2</sub> (e)
M_LOG10E	log <sub>10</sub> (e)
M_LN2	log(2)
M_LN10	log(10)
M_PI	pi
M_PI_2	pi/2
M_PI_4	pi/4
M_1_PI	1/pi
M_2_PI	2/pi
M_2_SQRTPI	2/sqrt(pi)
M_SQRT2	sqrt(2)
M_SQRT1_2	1/sqrt(2)
M_SQRT_3	sqrt(3)
M_SQRT_32	sqrt(32)

M_LOG10_2	Log10(2)
M_2PI	2*pi
M_SQRT_PI	sqrt(pi)
M_1_SQRT_2PI	1/(sqrt(2*pi))
M_LN_SQRT_PI	log(sqrt(pi))
M_LN_SQRT_2PI	log(sqrt(2*pi))
M_LN_SQRT_PId2	log(sqrt(pi/2))
pi	pi
NA	R's NA value
NaN	Not a Number Value
Inf	Infinite Value
newind	1: First record of individual; 2: Subsequent record of individual
rxFlag	Flag for what part of the rxode2 model is being run; 1: ddt; 2: jac; 3: ini; 4: F; 5: lag; 6: rate; 7: dur; 8:

Note that rxFlag will always output 11 or calc\_lhs since that is where the final variables are calculated, though you can tweak or test certain parts of rxode2 by using this flag.

#### Residual functions when using rxode2 functions:

In addition to ~ hiding output for certain types of output, it also is used to specify a residual output or endpoint when the input is an rxode2 model function (that includes the residual in the model({}) block).

These specifications are of the form:

```
var ~ add(add.sd)
```

Indicating the variable var is the variable that represents the individual central tendencies of the model and it also represents the compartment specification in the data-set.

You can also change the compartment name using the | syntax, that is:

```
var ~ add(add.sd) | cmt
```

In the above case var represents the central tendency and cmt represents the compartment or divid specification.

#### Transformations:

For normal and related distributions, you can apply the transformation on both sides by using some keywords/functions to apply these transformations.

Transformation	rxode2/nlmixr2 code
Box-Cox	+boxCox(lambda)
Yeo-Johnson	+yeoJohnson(lambda)
logit-normal	+logitNorm(logit.sd, low, hi)
probit-normal	+probitNorm(probid.sd, low, hi)
log-normal	+lnorm(lnorm.sd)

By default for the likelihood for all of these transformations is calculated on the **untransformed** scale.

For bounded variables like logit-normal or probit-normal the low and high values are defaulted to 0 and 1 if missing.

For models where you wish to have a proportional model on one of these transformation you can replace the standard deviation with NA

To allow for more transformations, `lnorm()`, `probitNorm()` and `logitNorm()` can be combined the variance stabilizing `yeoJohnson()` transformation.

*Normal and t-related distributions:*

For the normal and t-related distributions, we wanted to keep the ability to use skewed distributions additive and proportional in the `t/cauchy-space`, so these distributions are specified differently in comparison to the other supported distributions within `nlmixr2`:

Distribution	How to Add	Example
Normal (log-likelihood)	<code>+dnorm()</code>	<code>cc ~ add(add.sd) + dnorm()</code>
T-distribution	<code>+dt(df)</code>	<code>cc ~ a dd(add.sd) + dt(df)</code>
Cauchy (t with <code>df=1</code> )	<code>+dcauchy()</code>	<code>cc ~ add(add.sd) + dcauchy()</code>

Note that with the normal and t-related distributions `nlmixr2` will calculate `cwres` and `npde` under the normal assumption to help assess the goodness of the fit of the model.

Also note that the `+dnorm()` is mostly for testing purposes and will slow down the estimation procedure in `nlmixr2`. We suggest not adding it (except for explicit testing). When there are multiple endpoint models that mix non-normal and normal distributions, the whole problem is shifted to a log-likelihood method for estimation in `nlmixr2`.

*Notes on additive + proportional models:*

There are two different ways to specify additive and proportional models, which we will call **combined1** and **combined2**, the same way that Monolix calls the two distributions (to avoid between software differences in naming).

The first, **combined1**, assumes that the additive and proportional differences are on the standard deviation scale, or:

$$y=f+(a+b \cdot f^c) \cdot \text{err}$$

The second, **combined2**, assumes that the additive and proportional differences are combined on a variance scale:

$$y=f+[\text{sqrt}(a^2+b^2 \cdot f^{2c})] \cdot \text{err}$$

The default in `nlmixr2/rxode2` if not otherwise specified is **combined2** since it mirrors how adding 2 normal distributions in statistics will add their variances (not the standard deviations). However, the **combined1** can describe the data possibly even better than **combined2** so both are possible options in `rxode2/nlmixr2`.

*Distributions of known likelihoods:*

For residuals that are not related to normal, t-distribution or cauchy, often the residual specification is of the form:

$$\text{cmt} \sim \text{dbeta}(\text{alpha}, \text{beta})$$

Where the compartment specification is on the left handed side of the specification.

For generalized likelihood you can specify:

$$\text{ll}(\text{cmt}) \sim \text{llik specification}$$

*Ordinal likelihoods:*

Finally, ordinal likelihoods/simulations can be specified in 2 ways. The first is:

$$\text{err} \sim \text{c}(p_0, p_1, p_2)$$

Here `err` represents the compartment and  $p_0$  is the probability of being in a specific category:

Category	Probability
1	$p_0$
2	$p_1$
3	$p_2$
4	$1-p_0-p_1-p_2$

It is up to the model to ensure that the sum of the  $p$  values are less than 1. Additionally you can write an arbitrary number of categories in the ordinal model described above.

It seems a little off that  $p_0$  is the probability for category 1 and sometimes scores are in non-whole numbers. This can be modeled as follows:

```
err ~ c(p0=0, p1=1, p2=2, 3)
```

Here the numeric categories are specified explicitly, and the probabilities remain the same:

Category	Probability
0	$p_0$
1	$p_1$
2	$p_2$
3	$1-p_0-p_1-p_2$

*General table of supported residual distributions:*

In general all the that are supported are in the following table (available in `rxode2::rxResidualError`)

Error model	Functional Form	Transformation	code
constant		None	<code>var ~ add(add.sd)</code>
proportional		None	<code>var ~ prop(prop.sd)</code>
power		None	<code>var ~ pow(pow.sd, exponent)</code>
additive+proportional	combined1	None	<code>var ~ add(add.sd) + prop(prop.sd) + combined1()</code>
additive+proportional	combined2	None	<code>var ~ add(add.sd) + prop(prop.sd) + combined2()</code>
additive+power	combined1	None	<code>var ~ add(add.sd) + pow(pow.sd, exponent) + combined1()</code>
additive+power	combined2	None	<code>var ~ add(add.sd) + pow(pow.sd, exponent) + combined2()</code>
constant		log	<code>var ~ lnorm(add.sd)</code>
proportional		log	<code>var ~ lnorm(NA) + prop(prop.sd)</code>
power		log	<code>var ~ lnorm(NA) + pow(pow.sd, exponent)</code>
additive+proportional	combined1	log	<code>var ~ lnorm(add.sd) + prop(prop.sd) + combined1()</code>
additive+proportional	combined2	log	<code>var ~ lnorm(add.sd) + prop(prop.sd) + combined2()</code>
additive+power	combined1	log	<code>var ~ lnorm(add.sd) + pow(pow.sd, exponent) + combined1()</code>
additive+power	combined2	log	<code>var ~ lnorm(add.sd) + pow(pow.sd, exponent) + combined2()</code>
constant		boxCox	<code>var ~ boxCox(lambda) + add(add.sd)</code>
proportional		boxCox	<code>var ~ boxCox(lambda) + prop(prop.sd)</code>
power		boxCox	<code>var ~ boxCox(lambda) + pow(pow.sd, exponent)</code>
additive+proportional	combined1	boxCox	<code>var ~ boxCox(lambda) + add(add.sd) + prop(prop.sd)</code>
additive+proportional	combined2	boxCox	<code>var ~ boxCox(lambda) + add(add.sd) + prop(prop.sd)</code>
additive+power	combined1	boxCox	<code>var ~ boxCox(lambda) + add(add.sd) + pow(pow.sd, exponent)</code>
additive+power	combined2	boxCox	<code>var ~ boxCox(lambda) + add(add.sd) + pow(pow.sd, exponent)</code>

constant		yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd)
proportional		yeoJohnson	var ~ yeoJohnson(lambda) + prop(prop.sd)
power		yeoJohnson	var ~ yeoJohnson(lambda) + pow(pow.sd, exponen
additive+proportional	combined1	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + prop(p
additive+proportional	combined2	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + prop(p
additive+power	combined1	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + pow(p
additive+power	combined2	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + pow(p
constant		logit	var ~ logitNorm(logit.sd)
proportional		logit	var ~ logitNorm(NA) + prop(prop.sd)
power		logit	var ~ logitNorm(NA) + pow(pow.sd, exponent)
additive+proportional	combined1	logit	var ~ logitNorm(logit.sd) + prop(prop.sd)
additive+proportional	combined2	logit	var ~ logitNorm(logit.sd) + prop(prop.sd)
additive+power	combined1	logit	var ~ logitNorm(logit.sd) + pow(pow.sd, exponen
additive+power	combined2	logit	var ~ logitNorm(logit.sd) + pow(pow.sd, exponen
additive		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
proportional		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(NA) + pr
power		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(NA) + po
additive+proportional	combined1	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+proportional	combined2	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+power	combined1	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+power	combined2	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
constant		logit	var ~ probitNorm(probit.sd)
proportional		probit	var ~ probitNorm(NA) + prop(prop.sd)
power		probit	var ~ probitNorm(NA) + pow(pow.sd, exponent)
additive+proportional	combined1	probit	var ~ probitNorm(probit.sd) + prop(prop.sd) + co
additive+proportional	combined2	probit	var ~ probitNorm(probit.sd) + prop(prop.sd) + co
additive+power	combined1	probit	var ~ probitNorm(probit.sd) + pow(pow.sd, expon
additive+power	combined2	probit	var ~ probitNorm(probit.sd) + pow(pow.sd, expon
additive		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
proportional		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(NA) + p
power		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(NA) + p
additive+proportional	combined1	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+proportional	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power	combined1	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
constant+t		None	var ~ add(add.sd) + dt(df)
proportional+t		None	var ~ prop(prop.sd) + dt(df)
power+t		None	var ~ pow(pow.sd, exponent) + dt(df)
additive+proportional+t	combined1	None	var ~ add(add.sd) + prop(prop.sd) + dt(df) + com
additive+proportional+t	combined2	None	var ~ add(add.sd) + prop(prop.sd) + dt(df) + com
additive+power+t	combined1	None	var ~ add(add.sd) + pow(pow.sd, exponent) + dt(d
additive+power+t	combined2	None	var ~ add(add.sd) + pow(pow.sd, exponent) + dt(d
constant+t		log	var ~ lnorm(add.sd) + dt(df)
proportional+t		log	var ~ lnorm(NA) + prop(prop.sd) + dt(df)
power+t		log	var ~ lnorm(NA) + pow(pow.sd, exponent) + dt(d
additive+proportional+t	combined1	log	var ~ lnorm(add.sd) + prop(prop.sd) + dt(df) + cor
additive+proportional+t	combined2	log	var ~ lnorm(add.sd) + prop(prop.sd) + dt(df) + co
additive+power+t	combined1	log	var ~ lnorm(add.sd) + pow(pow.sd, exponent) + d

additive+power+t	combined2	log	var ~ lnorm(add.sd) + pow(pow.sd, exponent) + d
constant+t		boxCox	var ~ boxCox(lambda) + add(add.sd)+dt(df)
proportional+t		boxCox	var ~ boxCox(lambda) + prop(prop.sd)+dt(df)
power+t		boxCox	var ~ boxCox(lambda) + pow(pow.sd, exponent)+
additive+proportional+t	combined1	boxCox	var ~ boxCox(lambda) + add(add.sd) + prop(prop
additive+proportional+t	combined2	boxCox	var ~ boxCox(lambda) + add(add.sd) + prop(prop
additive+power+t	combined1	boxCox	var ~ boxCox(lambda) + add(add.sd) + pow(pop.
additive+power+t	combined2	boxCox	var ~ boxCox(lambda) + add(add.sd) + pow(pop.
constant+t		yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + dt(df)
proportional+t		yeoJohnson	var ~ yeoJohnson(lambda) + prop(prop.sd) + dt(d
power+t		yeoJohnson	var ~ yeoJohnson(lambda) + pow(pow.sd, expone
additive+proportional+t	combined1	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + prop(p
additive+proportional+t	combined2	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + prop(p
additive+power+t	combined1	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + pow(p
additive+power+t	combined2	yeoJohnson	var ~ yeoJohnson(lambda) + add(add.sd) + pow(p
constant+t		logit	var ~ logitNorm(logit.sd)+dt(df)
proportional+t		logit	var ~ logitNorm(NA) + prop(prop.sd)+dt(df)
power+t		logit	var ~ logitNorm(NA) + pow(pow.sd, exponent) +
additive+proportional+t	combined1	logit	var ~ logitNorm(logit.sd) + prop(prop.sd) + dt(df)
additive+proportional+t	combined2	logit	var ~ logitNorm(logit.sd) + prop(prop.sd) + dt(df)
additive+power+t	combined1	logit	var ~ logitNorm(logit.sd) + pow(pow.sd, exponen
additive+power+t	combined2	logit	var ~ logitNorm(logit.sd) + pow(pow.sd, exponen
additive+t		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
proportional+t		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(NA) + pr
power+t		yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(NA) + po
additive+proportional+t	combined1	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+proportional+t	combined2	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+power+t	combined1	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
additive+power+t	combined2	yeoJohnson(logit())	var ~ yeoJohnson(lambda) + logitNorm(logit.sd)
constant+t		logit	var ~ probitNorm(probit.sd) + dt(df)
proportional+t		probit	var ~ probitNorm(NA) + prop(prop.sd) + dt(df)
power+t		probit	var ~ probitNorm(NA) + pow(pow.sd, exponent)
additive+proportional+t	combined1	probit	var ~ probitNorm(probit.sd) + prop(prop.sd) + dt
additive+proportional+t	combined2	probit	var ~ probitNorm(probit.sd) + prop(prop.sd) + dt
additive+power+t	combined1	probit	var ~ probitNorm(probit.sd) + pow(pow.sd, expon
additive+power+t	combined2	probit	var ~ probitNorm(probit.sd) + pow(pow.sd, expon
additive+t		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
proportional+t		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(NA) + p
power+t		yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(NA) + p
additive+proportional+t	combined1	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+proportional+t	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power+t	combined1	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power+t	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
constant+cauchy		None	var ~ add(add.sd) + dcauchy()
proportional+cauchy		None	var ~ prop(prop.sd) + dcauchy()
power+cauchy		None	var ~ pow(pow.sd, exponent) + dcauchy()
additive+proportional+cauchy	combined1	None	var ~ add(add.sd) + prop(prop.sd) + dcauchy() +
additive+proportional+cauchy	combined2	None	var ~ add(add.sd) + prop(prop.sd) + dcauchy() +





additive+proportional+cauchy	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power+cauchy	combined1	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
additive+power+cauchy	combined2	yeoJohnson(probit())	var ~ yeoJohnson(lambda) + probitNorm(probit.s
poission		none	cmt ~ dpois(lambda)
binomial		none	cmt ~ dbinom(n, p)
beta		none	cmt ~ dbeta(alpha, beta)
chisq		none	cmt ~ dchisq(nu)
exponential		none	cmt ~ dexp(r)
uniform		none	cmt ~ dunif(a, b)
weibull		none	cmt ~ dweibull(a, b)
gamma		none	cmt ~ dgamma(a, b)
geometric		none	cmt ~ dgeom(a)
negative binomial form #1		none	cmt ~ dnbinom(n, p)
negative binomial form #2		none	cmt ~ dnbinomMu(size, mu)
ordinal probability		none	cmt ~ c(p0=0, p1=1, p2=2, 3)
log-likelihood		none	ll(cmt) ~ log likelihood expression

## Value

An object (environment) of class `rxode2` (see Chambers and Temple Lang (2001)) consisting of the following list of strings and functions:

- \* ``model`` a character string holding the source model specification.
  - \* ``get.modelVars`` a function that returns a list with 3 character vectors, ``params``, ``state``, and ``lhs`` of variable names used in the model specification. These will be output when the model is computed (i.e., the ODE solved by integration).
  - \* ``solve``{this function solves (integrates) the ODE. This is done by passing the code to `[rxSolve()]`. This is as if you called ``rxSolve(rxode2object, ...)``, but returns a matrix instead of a `rxSolve` object.
- ``params``: a numeric named vector with values for every parameter in the ODE system; the names must correspond to the parameter identifiers used in the ODE specification;
- ``events``: an ``eventTable`` object describing the input (e.g., doses) to the dynamic system and observation sampling time points (see `[eventTable()]`);
- ``inits``: a vector of initial values of the state variables (e.g., amounts in each compartment), and the order in this vector must be the same as the state variables (e.g., PK/PD compartments);
- ``stiff``: a logical (``TRUE`` by default) indicating whether the ODE system is stiff or not.

For stiff ODE systems (``stiff = TRUE``), ``rxode2`` uses the LSODA (Livermore Solver for Ordinary Differential Equations) Fortran package, which implements an automatic method switching for stiff and non-stiff problems along the integration interval, authored by Hindmarsh and Petzold (2003).

For non-stiff systems (``stiff = FALSE``), ``rxode2`` uses ``DOP853``, an explicit Runge-Kutta method of order 8(5, 3) of Dormand and Prince as implemented in C by Hairer and Wanner (1993).

``trans_abs``: a logical (``FALSE`` by default) indicating whether to fit a transit absorption term (TODO: need further documentation and example);

``atol``: a numeric absolute tolerance (1e-08 by default);

``rtol``: a numeric relative tolerance (1e-06 by default).

The output of `\dQuote{solve}` is a matrix with as many rows as there are sampled time points and as many columns as system variables (as defined by the ODEs and additional assignments in the `rxode2` model code).}

- \* ``isValid`` a function that (naively) checks for model validity, namely that the C object code reflects the latest model specification.
- \* ``version`` a string with the version of the ``rxode2`` object (not the package).
- \* ``dynLoad`` a function with one ``force = FALSE`` argument that dynamically loads the object code if needed.
- \* ``dynUnload`` a function with no argument that unloads the model object code.
- \* ``delete`` removes all created model files, including C and DLL files. The model object is no longer valid and should be removed, e.g., ``rm(m1)``.
- \* ``run`` deprecated, use ``solve``.
- \* ``get.index`` deprecated.
- \* ``getObj`` internal (not user callable) function.

## Creating rxode2 models

NA

## Note on strings in rxode2

Strings are converted to double values inside of `rxode2`, hence you can refer to them as an integer corresponding to the string value or the string value itself. For covariates these are calculated on the fly based on your data and you should likely not try this, though you should be aware. For strings defined in the model, this is fixed and both could be used.

For example:

```
if (APGAR == 10 || APGAR == 8 || APGAR == 9) {
  tAPGAR <- "High"
} else if (APGAR == 1 || APGAR == 2 || APGAR == 3) {
  tAPGAR <- "Low"
} else if (APGAR == 4 || APGAR == 5 || APGAR == 6 || APGAR == 7) {
  tAPGAR <- "Med"
} else {
  tAPGAR<- "Med"
}
```

Could also be replaced by:

```
if (APGAR == 10 || APGAR == 8 || APGAR == 9) {
  tAPGAR <- "High"
} else if (APGAR == 1 || APGAR == 2 || APGAR == 3) {
  tAPGAR <- "Low"
} else if (APGAR == 4 || APGAR == 5 || APGAR == 6 || APGAR == 7) {
  tAPGAR <- "Med"
} else {
  tAPGAR<- 3
}
```

Since "Med" is already defined

If you wanted you can pre-declare what levels it has (and the order) to give you better control of this:

```
levels(tAPGAR) <- c("Med", "Low", "High")
if (APGAR == 10 || APGAR == 8 || APGAR == 9) {
  tAPGAR <- 3
} else if (APGAR == 1 || APGAR == 2 || APGAR == 3) {
  tAPGAR <- 2
} else if (APGAR == 4 || APGAR == 5 || APGAR == 6 || APGAR == 7) {
  tAPGAR <- 1
} else {
  tAPGAR<- 1
}
```

You can see that the number changed since the declaration change the numbers in each variable for tAPGAR. These levels() statements need to be declared before the variable occurs to ensure the numbering is consistent with what is declared.

### Author(s)

Melissa Hallow, Wenping Wang and Matthew Fidler

## References

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- Petzold, L. R. *Automatic Selection of Methods for Solving Stiff and Nonstiff Systems of Ordinary Differential Equations*. Siam J. Sci. Stat. Comput. 4 (1983), pp. 136-148.
- Hairer, E., Norsett, S. P., and Wanner, G. *Solving ordinary differential equations I, nonstiff problems*. 2nd edition, Springer Series in Computational Mathematics, Springer-Verlag (1993).
- Plevyak, J. dparser, <https://dparser.sourceforge.net/>. Web. 12 Oct. 2015.

## See Also

[eventTable\(\)](#), [et\(\)](#), [add.sampling\(\)](#), [add.dosing\(\)](#)

## Examples

```
mod <- function() {
  ini({
    KA <- .291
    CL <- 18.6
    V2 <- 40.2
    Q <- 10.5
    V3 <- 297.0
    Kin <- 1.0
    Kout <- 1.0
    EC50 <- 200.0
  })
  model({
    # A 4-compartment model, 3 PK and a PD (effect) compartment
    # (notice state variable names 'depot', 'centr', 'peri', 'eff')
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot;
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3;
    d/dt(peri) <- Q*C2 - Q*C3;
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff;
    eff(0) <- 1
  })
}

m1 <- rxode2(mod)
print(m1)

# Step 2 - Create the model input as an EventTable,
# including dosing and observation (sampling) events

# QD (once daily) dosing for 5 days.
```

```

qd <- et(amountUnits = "ug", timeUnits = "hours") %>%
  et(amt = 10000, addl = 4, ii = 24)

# Sample the system hourly during the first day, every 8 hours
# then after
qd <- qd %>% et(0:24) %>%
  et(from = 24 + 8, to = 5 * 24, by = 8)

# Step 3 - solve the system

qd.cp <- rxSolve(m1, qd)

head(qd.cp)

```

---

```

rxode2<-          Set the function body of an rxUi object while retaining other object
                  information (like data)

```

---

### Description

Set the function body of an rxUi object while retaining other object information (like data)

### Usage

```

rxode2(x, envir = environment(x)) <- value

## S3 replacement method for class ``function``
rxode2(x, envir = environment(x)) <- value

## Default S3 replacement method:
rxode2(x, envir = environment(x)) <- value

rxode(x, envir = environment(x)) <- value

RxODE(x, envir = environment(x)) <- value

```

### Arguments

x	The rxUi object
envir	environment where the assignment occurs
value	the value that will be assigned

### Value

The rxode2 ui/function

**Examples**

```

one.compartment <- function() {
  ini({
    tka <- log(1.57); label("Ka")
    tc1 <- log(2.72); label("Cl")
    tv <- log(31.5); label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tc1 + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
    cp ~ add(add.sd)
  })
}

two.compartment <- function() {
  ini({
    lka <- 0.45 ; label("Absorption rate (Ka)")
    lcl <- 1 ; label("Clearance (CL)")
    lvc <- 3 ; label("Central volume of distribution (V)")
    lvp <- 5 ; label("Peripheral volume of distribution (Vp)")
    lq <- 0.1 ; label("Intercompartmental clearance (Q)")
    propSd <- 0.5 ; label("Proportional residual error (fraction)")
  })
  model({
    ka <- exp(lka)
    cl <- exp(lcl)
    vc <- exp(lvc)
    vp <- exp(lvp)
    q <- exp(lq)
    kel <- cl/vc
    k12 <- q/vc
    k21 <- q/vp
    d/dt(depot) <- -ka*depot
    d/dt(central) <- ka*depot - kel*central - k12*central + k21*peripheral1
    d/dt(peripheral1) <- k12*central - k21*peripheral1
    cp <- central / vc
    cp ~ prop(propSd)
  })
}

ui <- rxode2(one.compartment)

rxode2(ui) <- two.compartment

```

---

`rxode2parse`*Internal translation to get model variables list*

---

**Description**

Internal translation to get model variables list

**Usage**

```
rxode2parse(  
  model,  
  linear = FALSE,  
  linCmtSens = c("linCmtA", "linCmtB", "linCmtC"),  
  verbose = FALSE,  
  code = NULL,  
  envir = parent.frame()  
)
```

**Arguments**

<code>model</code>	Model (either file name or string)
<code>linear</code>	boolean indicating if linear compartment model should be generated from <code>linCmt()</code> (default FALSE)
<code>linCmtSens</code>	Linear compartment model sensitivity type
<code>verbose</code>	is a boolean indicating the type of model detected with <code>linCmt()</code> parsing
<code>code</code>	is a file name where the c code is written to (for testing purposes mostly, it needs <code>rxode2</code> to do anything fancy)
<code>envir</code>	is the environment to look for R user functions (defaults to parent environment)

**Value**

A `rxModelVars` object that has the model variables of a `rxode2` syntax expression

**Examples**

```
rxode2parse("a=3")
```



---

`rxode2parseAssignTranslation`*This assigns the c level linkages for a roxde2 model*

---

**Description**

This assigns the c level linkages for a roxde2 model

**Usage**

```
rxode2parseAssignTranslation(df)
```

**Arguments**

`df` data frame containing the character column names `rxFun`, `fun`, `type`, `package`, `packageFun` and the integer column names `argMin` and `argMax`

**Value**

Nothing called for side effects

**Author(s)**

Matthew L. Fidler

**Examples**

```
rxode2parseAssignTranslation(rxode2parseGetTranslation())
```

---

`rxode2parseD`*This gives the derivative table for rxode2*

---

**Description**

This will help allow registration of functions in rxode2

**Usage**

```
rxode2parseD()
```

**Details**

This environment is a derivative table;

For example:

```
Derivative(f(a,b,c), a) = fa() Derivative(f(a,b,c), b) = fb() Derivative(f(a,b,c), c) = fc()
```

Then the derivative table for f would be:

```
assign("f", list(fa(a,b,c), fb(a,b,c), fc(a,b,c)), rxode2parseD())
```

fa translates the arguments to the derivative with respect to a fb translates the arguments to the derivative with respect to b

If any of the list is NULL then rxode2 won't know how to take a derivative with respect to the argument.

If the list is shorter than the length of the arguments then the argument then the derivative of arguments that are not specified cannot be taken.

**Value**

Derivative table environment for rxode2

**Author(s)**

Matthew L. Fidler

---

rxode2parseGetPackagesToLoad

*Control the packages that are loaded when a rxode2 model dll is loaded*

---

**Description**

Control the packages that are loaded when a rxode2 model dll is loaded

**Usage**

```
rxode2parseGetPackagesToLoad()
```

```
rxode2parseAssignPackagesToLoad(pkgs = rxode2parseGetPackagesToLoad())
```

**Arguments**

pkgs                    The packages to make sure are loaded every time you load an rxode2 model.

**Value**

List of packages to load

**Author(s)**

Matthew Fidler

**Examples**

```
rxode2parseGetPackagesToLoad()
```

```
rxode2parseAssignPackagesToLoad(rxode2parseGetPackagesToLoad())
```

---

rxode2parseGetPointerAssignment

*This function gets the currently assigned function pointer assignments*

---

**Description**

This function gets the currently assigned function pointer assignments

**Usage**

```
rxode2parseGetPointerAssignment()
```

**Value**

The currently assigned pointer assignments

**Author(s)**

Matthew L. Fidler

**Examples**

```
rxode2parseGetTranslation()
```

---

rxode2parseGetTranslation

*This function gets the currently assigned translations*

---

**Description**

This function gets the currently assigned translations

**Usage**

```
rxode2parseGetTranslation()
```

**Value**

The currently assigned translations

**Author(s)**

Matthew L. Fidler

**Examples**

```
rxode2parseGetTranslation()
```

---

rxOptExpr

*Optimize rxode2 for computer evaluation*

---

**Description**

This optimizes rxode2 code for computer evaluation by only calculating redundant expressions once.

**Usage**

```
rxOptExpr(x, msg = "model")
```

**Arguments**

x	rxode2 model that can be accessed by rxNorm
msg	This is the name of type of object that rxode2 is optimizing that will in the message when optimizing. For example "model" will produce the following message while optimizing the model: finding duplicate expressions in model...

**Value**

Optimized rxode2 model text. The order and type lhs and state variables is maintained while the evaluation is sped up. While parameters names are maintained, their order may be modified.

**Author(s)**

Matthew L. Fidler

---

rxord	<i>Simulate ordinal value</i>
-------	-------------------------------

---

**Description**

Simulate ordinal value

**Usage**

```
rxord(...)
```

**Arguments**

... the probabilities to be simulated. These should sum up to a number below one.

**Details**

The values entered into the 'rxord' simulation will simulate the probability of falling each group. If it falls outside of the specified probabilities, it will simulate the group (number of probabilities specified + 1)

**Value**

A number from 1 to the (number of probabilities specified + 1)

**Author(s)**

Matthew L. Fidler

**Examples**

```
# This will give values 1, and 2
rxord(0.5)
rxord(0.5)
rxord(0.5)
rxord(0.5)

# This will give values 1, 2 and 3
rxord(0.3, 0.3)
rxord(0.3, 0.3)
rxord(0.3, 0.3)
```

---

`rxParams`*Parameters specified by the model*

---

**Description**

This returns the model's parameters that are required to solve the ODE system, and can be used to pipe parameters into an `rxode2` solve

**Usage**

```
rxParams(obj, ...)  
  
## S3 method for class 'rxode2'  
rxParams(  
  obj,  
  constants = TRUE,  
  ...,  
  params = NULL,  
  inits = NULL,  
  iCov = NULL,  
  keep = NULL,  
  thetaMat = NULL,  
  omega = NULL,  
  dfSub = NULL,  
  sigma = NULL,  
  dfObs = NULL,  
  nSub = NULL,  
  nStud = NULL  
)  
  
## S3 method for class 'rxSolve'  
rxParams(  
  obj,  
  constants = TRUE,  
  ...,  
  params = NULL,  
  inits = NULL,  
  iCov = NULL,  
  keep = NULL,  
  thetaMat = NULL,  
  omega = NULL,  
  dfSub = NULL,  
  sigma = NULL,  
  dfObs = NULL,  
  nSub = NULL,  
  nStud = NULL  
)
```

```
## S3 method for class 'rxEt'
rxParams(
  obj,
  ...,
  params = NULL,
  inits = NULL,
  iCov = NULL,
  keep = NULL,
  thetaMat = NULL,
  omega = NULL,
  dfSub = NULL,
  sigma = NULL,
  dfObs = NULL,
  nSub = NULL,
  nStud = NULL
)

rxParam(obj, ...)
```

### Arguments

obj	rxode2 family of objects
...	Other arguments including scaling factors for each compartment. This includes S# = numeric will scale a compartment # by a dividing the compartment amount by the scale factor, like NONMEM.
constants	is a boolean indicting if constants should be included in the list of parameters. Currently rxode2 parses constants into variables in case you wish to change them without recompiling the rxode2 model.
params	a numeric named vector with values for every parameter in the ODE system; the names must correspond to the parameter identifiers used in the ODE specification;
inits	a vector of initial values of the state variables (e.g., amounts in each compartment), and the order in this vector must be the same as the state variables (e.g., PK/PD compartments);
iCov	A data frame of individual non-time varying covariates to combine with the events dataset. The iCov dataset has one covariate per ID and should match the event table
keep	Columns to keep from either the input dataset or the iCov dataset. With the iCov dataset, the column is kept once per line. For the input dataset, if any records are added to the data LOCF (Last Observation Carried forward) imputation is performed.
thetaMat	Named theta matrix.
omega	Estimate of Covariance matrix. When omega is a list, assume it is a block matrix and convert it to a full matrix for simulations. When omega is NA and you are using it with a rxode2 ui model, the between subject variability described by the omega matrix are set to zero.

dfSub	Degrees of freedom to sample the between subject variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
sigma	Named sigma covariance or Cholesky decomposition of a covariance matrix. The names of the columns indicate parameters that are simulated. These are simulated for every observation in the solved system. When sigma is NA and you are using it with a rxode2 ui model, the unexplained variability described by the sigma matrix are set to zero.
dfObs	Degrees of freedom to sample the unexplained variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
nSub	Number between subject variabilities (ETAs) simulated for every realization of the parameters.
nStud	Number virtual studies to characterize uncertainty in estimated parameters.

**Value**

When extracting the parameters from an rxode2 model, a character vector listing the parameters in the model.

**Author(s)**

Matthew L.Fidler

**See Also**

Other Query model information: [rxDfdy\(\)](#), [rxInits\(\)](#), [rxLhs\(\)](#), [rxModelVars\(\)](#), [rxState\(\)](#)

---

rxParseSuppressMsg      *Respect suppress messages*

---

**Description**

This turns on the silent REprintf in C when suppressMessages() is turned on. This makes the REprintf act like messages in R, they can be suppressed with suppressMessages()

**Usage**

```
rxParseSuppressMsg()
```

**Value**

Nothing

**Author(s)**

Matthew Fidler



**Examples**

```

# rxParseSuppressMsg() is called with rxode2()

# Note the errors are output to the console

try(rxode2parse("d/dt(matt)=/3"), silent = TRUE)

# When using suppressMessages, the output is suppressed

suppressMessages(try(rxode2parse("d/dt(matt)=/3"), silent = TRUE))

# In rxode2, we use Rprintf so that interrupted threads do not crash R
# if there is a user interrupt. This isn't captured by R's messages, but
# This interface allows the `suppressMessages()` to suppress the C printing
# as well

# If you want to suppress messages from rxode2 in other packages, you can use
# this function

```

---

rxPkg

*Creates a package from compiled rxode2 models*


---

**Description**

Creates a package from compiled rxode2 models

**Usage**

```

rxPkg(
  ...,
  package,
  wd = getwd(),
  action = c("install", "build", "binary", "create"),
  license = c("gpl3", "lgpl", "mit", "agpl3"),
  name = "Firstname Lastname",
  fields = list()
)

```

**Arguments**

...	Models to build a package from
package	String of the package name to create
wd	character string with a working directory where to create a subdirectory according to modName. When specified, a subdirectory named after the “modName.d” will be created and populated with a C file, a dynamic loading library, plus various other working files. If missing, the files are created (and removed) in the temporary directory, and the rxode2 DLL for the model is created in the current directory named rx_????_platform, for example rx_129f8f97fb94a87ca49ca8dafe691e1e_i386.dl

action	Type of action to take after package is created
license	is the type of license for the package.
name	Full name of author
fields	A named list of fields to add to DESCRIPTION, potentially overriding default values. See <a href="#">use_description()</a> for how you can set personalized defaults using package options.

**Value**

this function returns nothing and is used for its side effects

**Author(s)**

Matthew Fidler

---

 rxpois

---

*Simulate random Poisson variable from threefry generator*


---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxpois(lambda, n = 1L, ncores = 1L)
```

**Arguments**

lambda	vector of (non-negative) means.
n	number of random values to return.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

## Details

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with rxSetSeed()

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

## Value

poission random number deviates

## Examples

```
## Use threefry engine

rxpois(lambda = 3, n = 10) # with rxpois you have to explicitly state n
rxpois(lambda = 3, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxpois(4) ## The first arguments are the lambda parameter

## This example uses `rxpois` directly in the model

rx <- function() {
  model({
    a <- rxpois(3)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

 rxPp

---

*Simulate a from a Poisson process*


---

## Description

Simulate a from a Poisson process

**Usage**

```
rxPp(
  n,
  lambda,
  gamma = 1,
  prob = NULL,
  t0 = 0,
  tmax = Inf,
  randomOrder = FALSE
)
```

**Arguments**

n	Number of time points to simulate in the Poisson process
lambda	Rate of Poisson process
gamma	Asymmetry rate of Poisson process. When gamma=1.0, this simulates a homogenous Poisson process. When gamma<1.0, the Poisson process has more events early, when gamma > 1.0, the Poisson process has more events late in the process. When gamma is non-zero, the tmax should not be infinite but indicate the end of the Poisson process to be simulated. In most pharamcometric cases, this will be the end of the study. Internally this uses a rate of: $l(t) = \text{lambda} \gamma (t/t_{\text{max}})^{\gamma-1}$
prob	When specified, this is a probability function with one argument, time, that gives the probability that a Poisson time t is accepted as a rejection time.
t0	the starting time of the Poisson process
tmax	the maximum time of the Poisson process
randomOrder	when TRUE randomize the order of the Poisson events. By default (FALSE) it returns the Poisson process is in order of how the events occurred.

**Value**

This returns a vector of the Poisson process times; If the dropout is  $\geq$  tmax, then all the rest of the times are = tmax to indicate the dropout is equal to or after tmax.

**Author(s)**

Matthew Fidler

**Examples**

```
## Sample homogenous Poisson process of rate 1/10
rxPp(10, 1 / 10)

## Sample inhomogenous Poisson rate of 1/10
rxPp(10, 1 / 10, gamma = 2, tmax = 100)
```

```
## Typically the Poisson process times are in a sequential order,  
## using randomOrder gives the Poisson process in random order  
  
rxPp(10, 1 / 10, gamma = 2, tmax = 10, randomOrder = TRUE)  
  
## This uses an arbitrary function to sample a non-homogenous Poisson process  
  
rxPp(10, 1 / 10, prob = function(x) {  
  1/(1+abs(x))  
})
```

---

rxPreferredDistributionName

*Change distribution name to the preferred distribution name term*

---

### Description

This is determined by the internal preferred condition name list `.errIdenticalDists`

### Usage

```
rxPreferredDistributionName(dist)
```

### Arguments

`dist` This is the input distribution

### Value

Preferred distribution term

### Author(s)

Matthew Fidler

### Examples

```
rxPreferredDistributionName("dt")  
  
rxPreferredDistributionName("add")  
  
# can be vectorized  
  
rxPreferredDistributionName(c("add", "dt"))
```

---

rxProgress                      *rxode2 progress bar functions*

---

### Description

rxProgress sets up the progress bar

### Usage

```
rxProgress(num, core = 0L)

rxTick()

rxProgressStop(clear = TRUE)

rxProgressAbort(error = "Aborted calculation")
```

### Arguments

num	Tot number of operations to track
core	Number of cores to show. If below 1, don't show number of cores
clear	Boolean telling if you should clear the progress bar after completion (as if it wasn't displayed). By default this is TRUE
error	With rxProgressAbort this is the error that is displayed

### Details

rxTick is a progress bar tick  
rxProgressStop stop progress bar  
rxProgressAbort shows an abort if rxProgressStop wasn't called.

### Value

All return NULL invisibly.

### Author(s)

Matthew L. Fidler

### Examples

```
f <- function() {
  on.exit({
    rxProgressAbort()
  })
  rxProgress(100)
  for (i in 1:100) {
```

```
    rxTick()
    Sys.sleep(1 / 100)
  }
  rxProgressStop()
}

f()
```

---

rxRateDur	<i>Creates a rxRateDur object</i>
-----------	-----------------------------------

---

## Description

This is primarily to display information about rate

## Usage

```
rxRateDur(x)

## S3 method for class 'rxRateDur'
x[...]

as.rxRateDur(x)

## S3 method for class 'rxRateDur'
as.character(x, ...)

## S3 method for class 'rxRateDur'
x[[...]]
```

## Arguments

x	rxRateDur data
...	Other parameters

## Value

rxRateDur object

---

rxRemoveControl	<i>rxRemoveControl options for UI object</i>
-----------------	--

---

**Description**

rxRemoveControl options for UI object

**Usage**

```
rxRemoveControl(ui)
```

**Arguments**

ui                    rxode2 ui object

**Value**

Nothing, called for side effects

**Author(s)**

Matthew L. Fidler

---

rxRename	<i>Rename items inside of a rxode2 ui model</i>
----------	---

---

**Description**

rxRename() changes the names of individual variables, lhs, and ode states using new\_name = old\_name syntax

**Usage**

```
rxRename(.data, ..., envir = parent.frame())
.rxRename(.data, ..., envir = parent.frame())
rename.rxUi(.data, ...)
rename.function(.data, ...)

## S3 method for class 'rxUi'
rxRename(.data, ...)

## S3 method for class '`function`'
rxRename(.data, ...)
```



```
## Default S3 method:
rxRename(.data, ...)
```

### Arguments

.data	rxode2 ui function, named data to be consistent with <code>dplyr::rename()</code>
...	rename items
envir	Environment for evaluation

### Details

This is similar to `dplyr`'s `rename()` function. When `dplyr` is loaded, the `s3` methods work for the `ui` objects.

Note that the `.rxRename()` is the internal function that is called when renaming and is likely not what you need to call unless you are writing your own extension of the function

### Value

New model with items renamed

### Author(s)

Matthew L. Fidler

### Examples

```
ocmt <- function() {
  ini({
    tka <- exp(0.45) # Ka
    tcl <- exp(1) # Cl
    ## This works with interactive models
    ## You may also label the preceding line with label("label text")
    tv <- exp(3.45) # log V
    ## the label("Label name") works with all models
    add.sd <- 0.7
  })
  model({
    ka <- tka
    cl <- tcl
    v <- tv
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
    cp ~ add(add.sd)
  })
}

ocmt %>% rxRename(cpParent=cp)
```

---

rxReservedKeywords      *A list and description of rxode2 supported reserved keywords*

---

**Description**

A list and description of rxode2 supported reserved keywords

**Usage**

rxReservedKeywords

**Format**

A data frame with 3 columns and 31 rows

**Reserved Name** Reserved Keyword Name

**Meaning** Reserved Keyword Meaning

**Alias** Keyword Alias

---

rxResidualError      *A description of Rode2 supported residual errors*

---

**Description**

A description of Rode2 supported residual errors

**Usage**

rxResidualError

**Format**

A data frame with 6 columns and 181 rows

**Error model** A description of the type of residual error

**Functional Form** For additive and proportional what functional form is used

**Transformation** The type of transformation that is done on the DV and the prediction

**code** Example code for the residual error type

**addProp** The type of add+prop residual error default that would be equivalent

**lhs** what the left handed side of the specification represents, either a response variable, or a compartment specification

rxRmvn

*Simulate from a (truncated) multivariate normal***Description**

This is simulated with the fast, thread-safe threefry simulator and can use multiple cores to generate the random deviates.

**Usage**

```
rxRmvn(
  n,
  mu = NULL,
  sigma,
  lower = -Inf,
  upper = Inf,
  ncores = 1,
  isChol = FALSE,
  keepNames = TRUE,
  a = 0.4,
  tol = 2.05,
  nlTol = 1e-10,
  nlMaxiter = 100L
)
```

**Arguments**

n	Number of random row vectors to be simulated OR the matrix to use for simulation (faster).
mu	mean vector
sigma	Covariance matrix for multivariate normal or a list of covariance matrices. If a list of covariance matrix, each matrix will simulate n matrices and combine them to a full matrix
lower	is a vector of the lower bound for the truncated multivariate norm
upper	is a vector of the upper bound for the truncated multivariate norm
ncores	Number of cores used in the simulation
isChol	A boolean indicating if sigma is a cholesky decomposition of the covariance matrix.
keepNames	Keep the names from either the mean or covariance matrix.
a	threshold for switching between methods; They can be tuned for maximum speed; There are three cases that are considered: case 1: $a < l < u$ case 2: $l < u < -a$ case 3: otherwise where $l$ =lower and $u$ = upper

tol	When case 3 is used from the above possibilities, the tol value controls the acceptance rejection and inverse-transformation; When $\text{abs}(u-l) > \text{tol}$ , uses accept-reject from randn
n1Tol	Tolerance for newton line-search
n1Maxiter	Maximum iterations for newton line-search

**Value**

If `n==integer` (default) the output is an  $(n \times d)$  matrix where the  $i$ -th row is the  $i$ -th simulated vector.

If `is.matrix(n)` then the random vector are store in `n`, which is provided by the user, and the function returns NULL invisibly.

**Author(s)**

Matthew Fidler, Zdravko Botev and some from Matteo Fasiolo

**References**

John K. Salmon, Mark A. Moraes, Ron O. Dror, and David E. Shaw (2011). Parallel Random Numbers: As Easy as 1, 2, 3. D. E. Shaw Research, New York, NY 10036, USA.

The thread safe multivariate normal was inspired from the mvnfast package by Matteo Fasiolo <https://CRAN.R-project.org/package=mvnfast>

The concept of the truncated multivariate normal was taken from Zdravko Botev Botev (2017) [doi:10.1111/rssb.12162](https://doi.org/10.1111/rssb.12162) and Botev and L'Ecuyer (2015) [doi:10.1109/WSC.2015.7408180](https://doi.org/10.1109/WSC.2015.7408180) and converted to thread safe simulation;

**Examples**

```
## From mvnfast
## Unlike mvnfast, uses threefry simulation

d <- 5
mu <- 1:d

# Creating covariance matrix
tmp <- matrix(rnorm(d^2), d, d)
mcov <- tcrossprod(tmp, tmp)

set.seed(414)
rxRmvn(4, 1:d, mcov)

set.seed(414)
rxRmvn(4, 1:d, mcov)

set.seed(414)
rxRmvn(4, 1:d, mcov, ncores = 2) # r.v. generated on the second core are different
```

```
##### Here we create the matrix that will hold the simulated
# random variables upfront.
A <- matrix(NA, 4, d)
class(A) <- "numeric" # This is important. We need the elements of A to be of class "numeric".

set.seed(414)
rxRmvn(A, 1:d, mcov, ncores = 2) # This returns NULL ...
A # ... but the result is here

## You can also simulate from a truncated normal:

rxRmvn(10, 1:d, mcov, lower = 1:d - 1, upper = 1:d + 1)

# You can also simulate from different matrices (if they match
# dimensions) by using a list of matrices.

matL <- lapply(1:4, function(...) {
  tmp <- matrix(rnorm(d^2), d, d)
  tcrossprod(tmp, tmp)
})

rxRmvn(4, setNames(1:d, paste0("a", 1:d)), matL)
```

---

 rxS

*Load a model into a symengine environment*


---

## Description

Load a model into a symengine environment

## Usage

```
rxS(x, doConst = TRUE, promoteLinSens = FALSE, envir = parent.frame())
```

## Arguments

x	rxode2 object
doConst	Load constants into the environment as well.
promoteLinSens	Promote solved linear compartment systems to sensitivity-based solutions.
envir	default is NULL; Environment to put symengine variables in.

## Value

rxode2/symengine environment

## Author(s)

Matthew Fidler

---

rxSetControl                    *rxSetControl options for UI object*

---

**Description**

rxSetControl options for UI object

**Usage**

```
rxSetControl(ui, control)
```

**Arguments**

ui	rxode2 ui object
control	Default value

**Value**

Nothing, called for side effects

**Author(s)**

Matthew L. Fidler

---

rxSetCovariateNamesForPiping  
*Assign covariates for piping*

---

**Description**

Assign covariates for piping

**Usage**

```
rxSetCovariateNamesForPiping(covariates = NULL)
```

**Arguments**

covariates	NULL (for no covariates), or the list of covariates. nlmixr uses this function to set covariates if you pipe from a nlmixr fit.
------------	---

**Value**

Nothing, called for side effects

**Author(s)**

Matthew L. Fidler

**Examples**

```

# First set the name of known covariates
# Note this is case sensitive

rxSetCovariateNamesForPiping(c("WT", "HT", "TC"))

one.compartment <- function() {
  ini({
    tka <- 0.45 ; label("Log Ka")
    tcl <- 1 ; label("Log Cl")
    tv <- 3.45 ; label("Log V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.err <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    d / dt(depot) <- -ka * depot
    d/dt(depot) <- -ka * depot
    d / dt(center) <- ka * depot - cl / v * center
    cp <- center / v
    cp ~ add(add.err)
  })
}

# now TC is detected as a covariate instead of a population parameter

one.compartment %>%
  model({ka <- exp(tka + eta.ka + TC * cov_C)})

# You can turn it off by simply adding it back

rxSetCovariateNamesForPiping()

one.compartment %>%
  model({ka <- exp(tka + eta.ka + TC * cov_C)})

# The covariates you set with `rxSetCovariateNamesForPiping()`
# are turned off every time you solve (or fit in nlmixr)

```

**Description**

Set Initial conditions to time zero instead of the first observed/dosed time

**Usage**

```
rxSetIni0(ini0 = TRUE)
```

**Arguments**

`ini0` When TRUE (default), set initial conditions to time zero. Otherwise the initial conditions are the first observed time.

**Value**

the boolean `ini0`, though this is called for its side effects

---

<code>rxSetPipingAuto</code>	<i>Set the variables for the model piping automatic covarite selection</i>
------------------------------	--

---

**Description**

Set the variables for the model piping automatic covarite selection

**Usage**

```
rxSetPipingAuto(
  thetamodelVars = rex::rex(or("tv", "t", "pop", "POP", "Pop", "TV", "T", "cov", "err",
    "eff")),
  covariateExceptions = rex::rex(start, or("wt", "sex", "crcl", "kout"), end),
  etaParts = c("eta", "ETA", "Eta", "ppv", "PPV", "Ppv", "iiv", "Iiv", "bsv", "Bsv",
    "BSV", "bpv", "Bpv", "BPV", "psv", "PSV", "Psv")
)
```

**Arguments**

`tethamodelVars` This is the prefixes for the theta model variables in a regular expression

`covariateExceptions` This is a regular expression of covariates that should always be covariates

`etaParts` This is the list of eta prefixes/post-fixes that identify a variable as a between subject variability

**Details**

This is called once at startup to set the defaults, though you can change this if you wish so that piping can work differently for your individual setup



**Value**

Nothing, called for side effects

**Author(s)**

Matthew L. Fidler

---

rxSetProd	<i>Defunct setting of product</i>
-----------	-----------------------------------

---

**Description**

Defunct setting of product

**Usage**

```
rxSetProd(type = c("long double", "double", "logify"))
```

**Arguments**

type	used to be type of product
------	----------------------------

**Value**

nothing

---

rxSetProgressBar	<i>Set timing for progress bar</i>
------------------	------------------------------------

---

**Description**

Set timing for progress bar

**Usage**

```
rxSetProgressBar(seconds = 1)
```

**Arguments**

seconds	This sets the number of seconds that need to elapse before drawing the next segment of the progress bar. When this is zero or below this turns off the progress bar.
---------	--

**Value**

nothing, used for side effects

**Author(s)**

Matthew Fidler

---

`rxSetSeed`*Set the parallel seed for rxode2 random number generation*

---

**Description**

This sets the seed for the rxode2 parallel random number generation. If set, then whenever a seed is set for the threefry or vandercorput simulation engine, it will use this seed, increment for the number of seeds and continue with the sequence the next time the random number generator is called.

**Usage**`rxSetSeed(seed)`**Arguments**

<code>seed</code>	An integer that represents the rxode2 parallel and internal random number generator seed. When positive, use this seed for random number generation and increment and reseed any parallel or new engines that are being called. When negative, turn off the rxode2 seed and generate a seed from the R's uniform random number generator. Best practice is to set this seed.
-------------------	--

**Details**

In contrast, when this is not called, the time that the vandercorput or threefry simulation engines are seeded it comes from a uniform random number generated from the standard R random seed. This may cause a duplicate seed based on the R seed state. This means that there could be correlations between simulations that do not exist. This will avoid the birthday problem picking exactly the same seed using the seed state of the R random number generator. The more times the seed is called, the more likely this becomes.

**Value**

Nothing, called for its side effects

**Author(s)**

Matthew Fidler

**References**

JD Cook. (2016). Random number generator seed mistakes. <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>

**See Also**

rxGetSeed, rxWithSeed, rxWithPreserveSeed

**Examples**

```
rxSetSeed(42)

# seed with generator 42
rxnorm()

# Use R's random number generator
rnorm(1)

rxSetSeed(42)

# reproduces the same number
rxnorm()

# But R's random number is not the same
rnorm(1)

# If we reset this to use the R's seed
# (internally rxode2 uses a uniform random number to span seeds)
# This can lead to duplicate sequences and seeds

rxSetSeed(-1)

# Now set seed works for both.

# This is not recommended, but illustrates the different types of
# seeds that can be generated.

set.seed(42)

rxnorm()

rnorm(1)

set.seed(42)

rxnorm()

rnorm(1)
```

**Description**

Defunct setting of sum

**Usage**

```
rxSetSum(type = c("pairwise", "fsum", "kahan", "neumaier", "c"))
```

**Arguments**

type                    used to be type of product

**Value**

nothing

---

 rxShiny

*Use Shiny to help develop an rxode2 model*


---

**Description**

Use Shiny to help develop an rxode2 model

**Usage**

```
rxShiny(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  data = data.frame()
)

## S3 method for class 'rxSolve'
rxShiny(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  data = data.frame()
)

## Default S3 method:
rxShiny(
  object = NULL,
  params = NULL,
```

```

    events = NULL,
    inits = NULL,
    ...,
    data = data.frame()
  )

```

### Arguments

object	A rxode2 family of objects. If not supplied a 2-compartment indirect effect model is used. If it is supplied, use the model associated with the rxode2 object for the model exploration.
params	Initial parameters for model
events	Event information (currently ignored)
inits	Initial estimates for model
...	Other arguments passed to rxShiny. Currently doesn't do anything.
data	Any data that you would like to plot. If the data has a time variable as well as a compartment or calculated variable that matches the rxode2 model, the data will be added to the plot of a specific compartment or calculated variable.

### Value

Nothing; Starts a shiny server

### Author(s)

Zufar Mulyukov and Matthew L. Fidler

---

 rxSimThetaOmega

*Simulate Parameters from a Theta/Omega specification*

---

### Description

Simulate Parameters from a Theta/Omega specification

### Usage

```

rxSimThetaOmega(
  params = NULL,
  omega = NULL,
  omegaDf = NULL,
  omegaLower = as.numeric(c(R_NegInf)),
  omegaUpper = as.numeric(c(R_PosInf)),
  omegaIsChol = FALSE,
  omegaSeparation = "auto",
  omegaXform = 1L,
  nSub = 1L,

```

```

thetaMat = NULL,
thetaLower = as.numeric(c(R_NegInf)),
thetaUpper = as.numeric(c(R_PosInf)),
thetaDf = NULL,
thetaIsChol = FALSE,
nStud = 1L,
sigma = NULL,
sigmaLower = as.numeric(c(R_NegInf)),
sigmaUpper = as.numeric(c(R_PosInf)),
sigmaDf = NULL,
sigmaIsChol = FALSE,
sigmaSeparation = "auto",
sigmaXform = 1L,
nCoresRV = 1L,
nObs = 1L,
dfSub = 0,
dfObs = 0,
simSubjects = TRUE,
simVariability = as.logical(c(NA_LOGICAL))
)

```

### Arguments

params	Named Vector of rxode2 model parameters
omega	Estimate of Covariance matrix. When omega is a list, assume it is a block matrix and convert it to a full matrix for simulations. When omega is NA and you are using it with a rxode2 ui model, the between subject variability described by the omega matrix are set to zero.
omegaDf	The degrees of freedom of a t-distribution for simulation. By default this is NULL which is equivalent to Inf degrees, or to simulate from a normal distribution instead of a t-distribution.
omegaLower	Lower bounds for simulated ETAs (by default -Inf)
omegaUpper	Upper bounds for simulated ETAs (by default Inf)
omegaIsChol	Indicates if the omega supplied is a Cholesky decomposed matrix instead of the traditional symmetric matrix.
omegaSeparation	<p>Omega separation strategy</p> <p>Tells the type of separation strategy when simulating covariance with parameter uncertainty with standard deviations modeled in the thetaMat matrix.</p> <ul style="list-style-type: none"> <li>• "lkj" simulates the correlation matrix from the rLKJ1 matrix with the distribution parameter eta equal to the degrees of freedom nu by (nu-1)/2</li> <li>• "separation" simulates from the identity inverse Wishart covariance matrix with nu degrees of freedom. This is then converted to a covariance matrix and augmented with the modeled standard deviations. While computationally more complex than the "lkj" prior, it performs better when the covariance matrix size is greater or equal to 10</li> </ul>

	<ul style="list-style-type: none"> <li>• "auto" chooses "lkj" when the dimension of the matrix is less than 10 and "separation" when greater than equal to 10.</li> </ul>
omegaXform	<p>When taking omega values from the thetaMat simulations (using the separation strategy for covariance simulation), how should the thetaMat values be turned into standard deviation values:</p> <ul style="list-style-type: none"> <li>• identity This is when standard deviation values are directly modeled by the params and thetaMat matrix</li> <li>• variance This is when the params and thetaMat simulates the variance that are directly modeled by the thetaMat matrix</li> <li>• log This is when the params and thetaMat simulates <math>\log(sd)</math></li> <li>• nlmixrSqrt This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>x^2</math> modeled along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrLog This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>\exp(x^2)</math> along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrIdentity This is when the params and thetaMat simulates the inverse cholesky decomposed matrix. This only works with a diagonal matrix.</li> </ul>
nSub	Number between subject variabilities (ETAs) simulated for every realization of the parameters.
thetaMat	Named theta matrix.
thetaLower	Lower bounds for simulated population parameter variability (by default -Inf)
thetaUpper	Upper bounds for simulated population unexplained variability (by default Inf)
thetaDf	The degrees of freedom of a t-distribution for simulation. By default this is NULL which is equivalent to Inf degrees, or to simulate from a normal distribution instead of a t-distribution.
thetaIsChol	Indicates if the theta supplied is a Cholesky decomposed matrix instead of the traditional symmetric matrix.
nStud	Number virtual studies to characterize uncertainty in estimated parameters.
sigma	Named sigma covariance or Cholesky decomposition of a covariance matrix. The names of the columns indicate parameters that are simulated. These are simulated for every observation in the solved system. When sigma is NA and you are using it with a rxode2 ui model, the unexplained variability described by the sigma matrix are set to zero.
sigmaLower	Lower bounds for simulated unexplained variability (by default -Inf)
sigmaUpper	Upper bounds for simulated unexplained variability (by default Inf)
sigmaDf	Degrees of freedom of the sigma t-distribution. By default it is equivalent to Inf, or a normal distribution.
sigmaIsChol	Boolean indicating if the sigma is in the Cholesky decomposition instead of a symmetric covariance
sigmaSeparation	<p>separation strategy for sigma;</p> <p>Tells the type of separation strategy when simulating covariance with parameter uncertainty with standard deviations modeled in the thetaMat matrix.</p>

	<ul style="list-style-type: none"> <li>• "lkj" simulates the correlation matrix from the rLKJ1 matrix with the distribution parameter eta equal to the degrees of freedom nu by (nu-1)/2</li> <li>• "separation" simulates from the identity inverse Wishart covariance matrix with nu degrees of freedom. This is then converted to a covariance matrix and augmented with the modeled standard deviations. While computationally more complex than the "lkj" prior, it performs better when the covariance matrix size is greater or equal to 10</li> <li>• "auto" chooses "lkj" when the dimension of the matrix is less than 10 and "separation" when greater than equal to 10.</li> </ul>
sigmaXform	<p>When taking sigma values from the thetaMat simulations (using the separation strategy for covariance simulation), how should the thetaMat values be turned into standard deviation values:</p> <ul style="list-style-type: none"> <li>• identity This is when standard deviation values are directly modeled by the params and thetaMat matrix</li> <li>• variance This is when the params and thetaMat simulates the variance that are directly modeled by the thetaMat matrix</li> <li>• log This is when the params and thetaMat simulates log(sd)</li> <li>• nlmixrSqrt This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>x^2</math> modeled along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrLog This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>\exp(x^2)</math> along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrIdentity This is when the params and thetaMat simulates the inverse cholesky decomposed matrix. This only works with a diagonal matrix.</li> </ul>
nCoresRV	Number of cores used for the simulation of the sigma variables. By default this is 1. To reproduce the results you need to run on the same platform with the same number of cores. This is the reason this is set to be one, regardless of what the number of cores are used in threaded ODE solving.
nObs	Number of observations to simulate (with sigma matrix)
dfSub	Degrees of freedom to sample the between subject variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
dfObs	Degrees of freedom to sample the unexplained variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
simSubjects	boolean indicated rxode2 should simulate subjects in studies (TRUE, default) or studies (FALSE)
simVariability	determines if the variability is simulated. When NA (default) this is determined by the solver.

**Value**

a data frame with the simulated subjects

**Author(s)**

Matthew L.Fidler



**Description**

This uses rxode2 family of objects, file, or model specification to solve a ODE system. There are many options for a solved rxode2 model, the first are the required object, and events with the some-times optional params and inits.

**Usage**

```
rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  scale = NULL,
  method = c("liblsoda", "lsoda", "dop853", "indLin"),
  sigdig = NULL,
  atol = 1e-08,
  rtol = 1e-06,
  maxsteps = 70000L,
  hmin = 0,
  hmax = NA_real_,
  hmaxSd = 0,
  hini = 0,
  maxordn = 12L,
  maxords = 5L,
  ...,
  cores,
  covsInterpolation = c("locf", "linear", "nocb", "midpoint"),
  naInterpolation = c("locf", "nocb"),
  keepInterpolation = c("na", "locf", "nocb"),
  addCov = TRUE,
  sigma = NULL,
  sigmaDf = NULL,
  sigmaLower = -Inf,
  sigmaUpper = Inf,
  nCoresRV = 1L,
  sigmaIsChol = FALSE,
  sigmaSeparation = c("auto", "lkj", "separation"),
  sigmaXform = c("identity", "variance", "log", "nlmixrSqrt", "nlmixrLog",
    "nlmixrIdentity"),
  nDisplayProgress = 10000L,
  amountUnits = NA_character_,
  timeUnits = "hours",
  theta = NULL,
```

```
thetaLower = -Inf,
thetaUpper = Inf,
eta = NULL,
addDosing = FALSE,
stateTrim = Inf,
updateObject = FALSE,
omega = NULL,
omegaDf = NULL,
omegaIsChol = FALSE,
omegaSeparation = c("auto", "lkj", "separation"),
omegaXform = c("variance", "identity", "log", "nlmixrSqrt", "nlmixrLog",
  "nlmixrIdentity"),
omegaLower = -Inf,
omegaUpper = Inf,
nSub = 1L,
thetaMat = NULL,
thetaDf = NULL,
thetaIsChol = FALSE,
nStud = 1L,
dfSub = 0,
dfObs = 0,
returnType = c("rxSolve", "matrix", "data.frame", "data.frame.TBS", "data.table",
  "tbl", "tibble"),
seed = NULL,
nsim = NULL,
minSS = 10L,
maxSS = 1000L,
infSSstep = 12,
strictSS = TRUE,
istateReset = TRUE,
subsetNonmem = TRUE,
maxAtoIRtolFactor = 0.1,
from = NULL,
to = NULL,
by = NULL,
length.out = NULL,
iCov = NULL,
keep = NULL,
indLinPhiTol = 1e-07,
indLinPhiM = 0L,
indLinMatExpType = c("expokit", "Al-Mohy", "arma"),
indLinMatExpOrder = 6L,
drop = NULL,
idFactor = TRUE,
mxhnil = 0,
hmxi = 0,
warnIdSort = TRUE,
warnDrop = TRUE,
```

```

    ssAtol = 1e-08,
    ssRtol = 1e-06,
    safeZero = TRUE,
    safeLog = TRUE,
    safePow = TRUE,
    sumType = c("pairwise", "fsum", "kahan", "neumaier", "c"),
    prodType = c("long double", "double", "logify"),
    sensType = c("advan", "autodiff", "forward", "central"),
    linDiff = c(tlag = 1.5e-05, f = 1.5e-05, rate = 1.5e-05, dur = 1.5e-05, tlag2 =
      1.5e-05, f2 = 1.5e-05, rate2 = 1.5e-05, dur2 = 1.5e-05),
    linDiffCentral = c(tlag = TRUE, f = TRUE, rate = TRUE, dur = TRUE, tlag2 = TRUE, f2 =
      TRUE, rate2 = TRUE, dur2 = TRUE),
    resample = NULL,
    resampleID = TRUE,
    maxwhile = 1e+05,
    atolSens = 1e-08,
    rtolSens = 1e-06,
    ssAtolSens = 1e-08,
    ssRtolSens = 1e-06,
    simVariability = NA,
    nLlikAlloc = NULL,
    useStdPow = FALSE,
    naTimeHandle = c("ignore", "warn", "error"),
    addlKeepsCov = FALSE,
    addlDropSs = TRUE,
    ssAtDoseTime = TRUE,
    ss2cancelAllPending = FALSE,
    envir = parent.frame()
  )

```

```
## S3 method for class 'function'
```

```

rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  theta = NULL,
  eta = NULL,
  envir = parent.frame()
)

```

```
## S3 method for class 'rxUi'
```

```

rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,

```

```
    ...,
    theta = NULL,
    eta = NULL,
    envir = parent.frame()
)

## S3 method for class 'rxode2tos'
rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  theta = NULL,
  eta = NULL,
  envir = parent.frame()
)

## S3 method for class 'nlmixr2FitData'
rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  theta = NULL,
  eta = NULL,
  envir = parent.frame()
)

## S3 method for class 'nlmixr2FitCore'
rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
  ...,
  theta = NULL,
  eta = NULL,
  envir = parent.frame()
)

## Default S3 method:
rxSolve(
  object,
  params = NULL,
  events = NULL,
  inits = NULL,
```

```
    ...,
    theta = NULL,
    eta = NULL,
    envir = parent.frame()
)

## S3 method for class 'rxSolve'
update(object, ...)

## S3 method for class 'rxode2'
predict(object, ...)

## S3 method for class ``function``
predict(object, ...)

## S3 method for class 'rxUi'
predict(object, ...)

## S3 method for class 'rxSolve'
predict(object, ...)

## S3 method for class 'rxEt'
predict(object, ...)

## S3 method for class 'rxParams'
predict(object, ...)

## S3 method for class 'rxode2'
simulate(object, nsim = 1L, seed = NULL, ...)

## S3 method for class 'rxSolve'
simulate(object, nsim = 1L, seed = NULL, ...)

## S3 method for class 'rxParams'
simulate(object, nsim = 1L, seed = NULL, ...)

## S3 method for class 'rxSolve'
solve(a, b, ...)

## S3 method for class 'rxUi'
solve(a, b, ...)

## S3 method for class ``function``
solve(a, b, ...)

## S3 method for class 'rxode2'
solve(a, b, ...)
```

```

## S3 method for class 'rxParams'
solve(a, b, ...)

## S3 method for class 'rxEt'
solve(a, b, ...)

rxControl(
  ...,
  params = NULL,
  events = NULL,
  inits = NULL,
  envir = parent.frame()
)

```

### Arguments

object	is a either a rxode2 family of objects, or a file-name with a rxode2 model specification, or a string with a rxode2 model specification.
params	a numeric named vector with values for every parameter in the ODE system; the names must correspond to the parameter identifiers used in the ODE specification;
events	an eventTable object describing the input (e.g., doses) to the dynamic system and observation sampling time points (see <a href="#">eventTable()</a> );
inits	a vector of initial values of the state variables (e.g., amounts in each compartment), and the order in this vector must be the same as the state variables (e.g., PK/PD compartments);
scale	a numeric named vector with scaling for ode parameters of the system. The names must correspond to the parameter identifiers in the ODE specification. Each of the ODE variables will be divided by the scaling factor. For example <code>scale=c(center=2)</code> will divide the center ODE variable by 2.
method	The method for solving ODEs. Currently this supports: <ul style="list-style-type: none"> <li>• "liblsoda" thread safe lsoda. This supports parallel thread-based solving, and ignores user Jacobian specification.</li> <li>• "lsoda" – LSODA solver. Does not support parallel thread-based solving, but allows user Jacobian specification.</li> <li>• "dop853" – DOP853 solver. Does not support parallel thread-based solving nor user Jacobian specification</li> <li>• "indLin" – Solving through inductive linearization. The rxode2 dll must be setup specially to use this solving routine.</li> </ul>
sigdig	Specifies the "significant digits" that the ode solving requests. When specified this controls the relative and absolute tolerances of the ODE solvers. By default the tolerance is $0.5 \times 10^{-(\text{sigdig}-2)}$ for regular ODEs. For the sensitivity equations the default is $0.5 \times 10^{-(\text{sigdig}-1.5)}$ (sensitivity changes only applicable for liblsoda). This also controls the <code>atol/rtol</code> of the steady state solutions. The <code>ssAtol/ssRtol</code> is $0.5 \times 10^{-(\text{sigdig})}$ and for the sensitivities $0.5 \times 10^{-(\text{sigdig}+0.625)}$ . By default this is unspecified (NULL) and uses the standard <code>atol/rtol</code> .

atol	a numeric absolute tolerance (1e-8 by default) used by the ODE solver to determine if a good solution has been achieved; This is also used in the solved linear model to check if prior doses do not add anything to the solution.
rtol	a numeric relative tolerance (1e-6 by default) used by the ODE solver to determine if a good solution has been achieved. This is also used in the solved linear model to check if prior doses do not add anything to the solution.
maxsteps	maximum number of (internally defined) steps allowed during one call to the solver. (5000 by default)
hmin	The minimum absolute step size allowed. The default value is 0.
hmax	The maximum absolute step size allowed. When hmax=NA (default), uses the average difference + hmaxSd*sd in times and sampling events. The hmaxSd is a user specified parameter and which defaults to zero. When hmax=NULL rxode2 uses the maximum difference in times in your sampling and events. The value 0 is equivalent to infinite maximum absolute step size.
hmaxSd	The number of standard deviations of the time difference to add to hmax. The default is 0
hini	The step size to be attempted on the first step. The default value is determined by the solver (when hini = 0)
maxordn	The maximum order to be allowed for the nonstiff (Adams) method. The default is 12. It can be between 1 and 12.
maxords	The maximum order to be allowed for the stiff (BDF) method. The default value is 5. This can be between 1 and 5.
...	Other arguments including scaling factors for each compartment. This includes S# = numeric will scale a compartment # by a dividing the compartment amount by the scale factor, like NONMEM.
cores	Number of cores used in parallel ODE solving. This is equivalent to calling <a href="#">setRxThreads()</a>
covsInterpolation	<p>specifies the interpolation method for time-varying covariates. When solving ODEs it often samples times outside the sampling time specified in events. When this happens, the time varying covariates are interpolated. Currently this can be:</p> <ul style="list-style-type: none"> <li>• "linear" interpolation, which interpolates the covariate by solving the line between the observed covariates and extrapolating the new covariate value.</li> <li>• "locf" – Last observation carried forward (the default).</li> <li>• "nocb" – Next Observation Carried Backward. This is the same method that NONMEM uses.</li> <li>• "midpoint" Last observation carried forward to midpoint; Next observation carried backward to midpoint.</li> </ul> <p>For time-varying covariates where a missing value is present, the interpolation method will use either "locf" or "nocb" throughout if they are the type of covariate interpolation that is selected.</p> <p>When using the linear or midpoint interpolation, the lower point in the interpolation will use locf to interpolate missing covariates and the upper point will use the nocb to interpolate missing covariates.</p>

<code>naInterpolation</code>	<p>specifies the interpolation method for time-varying covariates when the instantaneous value is NA (not during an explicit interpolation) and the <code>covsInterpolation</code> is either "midpoint" or "linear". This can be:</p> <ul style="list-style-type: none"> <li>• "locf" – last observation carried forward (default)</li> <li>• "nocb" – next observation carried backward.</li> </ul> <p>This will look for the prior value (backwards/locf) when instantaneously missing, or the next value when instantaneously missing. If all the covariates are missing and you find the end/beginning of the individual record, switch direction. If all are really missing, then return missing.</p>
<code>keepInterpolation</code>	<p>specifies the interpolation method for variables in the keep column. When <code>nlmixr2</code> creates <code>mtime</code>, <code>addl</code> doses etc, these items were not originally in the dataset. The interpolation methods you can choose are:</p> <ul style="list-style-type: none"> <li>• "locf" – last observation carried forward (default)</li> <li>• "nocb" – next observation carried backward.</li> <li>• "na" – no interpolation, simply put NA for the interpolated keep covariates.</li> </ul>
<code>addCov</code>	A boolean indicating if covariates should be added to the output matrix or data frame. By default this is disabled.
<code>sigma</code>	Named sigma covariance or Cholesky decomposition of a covariance matrix. The names of the columns indicate parameters that are simulated. These are simulated for every observation in the solved system. When <code>sigma</code> is NA and you are using it with a <code>rxode2</code> ui model, the unexplained variability described by the <code>sigma</code> matrix are set to zero.
<code>sigmaDf</code>	Degrees of freedom of the sigma t-distribution. By default it is equivalent to Inf, or a normal distribution.
<code>sigmaLower</code>	Lower bounds for simulated unexplained variability (by default -Inf)
<code>sigmaUpper</code>	Upper bounds for simulated unexplained variability (by default Inf)
<code>nCoresRV</code>	Number of cores used for the simulation of the sigma variables. By default this is 1. To reproduce the results you need to run on the same platform with the same number of cores. This is the reason this is set to be one, regardless of what the number of cores are used in threaded ODE solving.
<code>sigmaIsChol</code>	Boolean indicating if the sigma is in the Cholesky decomposition instead of a symmetric covariance
<code>sigmaSeparation</code>	<p>separation strategy for sigma;</p> <p>Tells the type of separation strategy when simulating covariance with parameter uncertainty with standard deviations modeled in the <code>thetaMat</code> matrix.</p> <ul style="list-style-type: none"> <li>• "lkj" simulates the correlation matrix from the <code>rLKJ1</code> matrix with the distribution parameter <math>\eta</math> equal to the degrees of freedom <math>\nu</math> by <math>(\nu-1)/2</math></li> <li>• "separation" simulates from the identity inverse Wishart covariance matrix with <math>\nu</math> degrees of freedom. This is then converted to a covariance matrix and augmented with the modeled standard deviations. While computationally more complex than the "lkj" prior, it performs better when the covariance matrix size is greater or equal to 10</li> </ul>



	<ul style="list-style-type: none"> <li>• "auto" chooses "lkj" when the dimension of the matrix is less than 10 and "separation" when greater than equal to 10.</li> </ul>
sigmaXform	<p>When taking sigma values from the thetaMat simulations (using the separation strategy for covariance simulation), how should the thetaMat values be turned into standard deviation values:</p> <ul style="list-style-type: none"> <li>• identity This is when standard deviation values are directly modeled by the params and thetaMat matrix</li> <li>• variance This is when the params and thetaMat simulates the variance that are directly modeled by the thetaMat matrix</li> <li>• log This is when the params and thetaMat simulates log(sd)</li> <li>• nlmixrSqrt This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>x^2</math> modeled along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrLog This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>\exp(x^2)</math> along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrIdentity This is when the params and thetaMat simulates the inverse cholesky decomposed matrix. This only works with a diagonal matrix.</li> </ul>
nDisplayProgress	An integer indicating the minimum number of c-based solves before a progress bar is shown. By default this is 10,000.
amountUnits	This supplies the dose units of a data frame supplied instead of an event table. This is for importing the data as an rxode2 event table.
timeUnits	This supplies the time units of a data frame supplied instead of an event table. This is for importing the data as an rxode2 event table.
theta	A vector of parameters that will be named THETA[#] and added to parameters
thetaLower	Lower bounds for simulated population parameter variability (by default -Inf)
thetaUpper	Upper bounds for simulated population unexplained variability (by default Inf)
eta	A vector of parameters that will be named ETA[#] and added to parameters
addDosing	<p>Boolean indicating if the solve should add rxode2 EVID and related columns. This will also include dosing information and estimates at the doses. By default, rxode2 only includes estimates at the observations. (default FALSE). When addDosing is NULL, only include EVID=0 on solve and exclude any model-times or EVID=2. If addDosing is NA the classic rxode2 EVID events are returned. When addDosing is TRUE add the event information in NONMEM-style format; If subsetNonmem=FALSE rxode2 will also include extra event types (EVID) for ending infusion and modeled times:</p> <ul style="list-style-type: none"> <li>• EVID=-1 when the modeled rate infusions are turned off (matches rate=-1)</li> <li>• EVID=-2 When the modeled duration infusions are turned off (matches rate=-2)</li> <li>• EVID=-10 When the specified rate infusions are turned off (matches rate&gt;0)</li> <li>• EVID=-20 When the specified dur infusions are turned off (matches dur&gt;0)</li> <li>• EVID=101, 102, 103, ... Modeled time where 101 is the first model time, 102 is the second etc.</li> </ul>

stateTrim	When amounts/concentrations in one of the states are above this value, trim them to be this value. By default Inf. Also trims to -stateTrim for large negative amounts/concentrations. If you want to trim between a range say $c(0, 2000000)$ you may specify 2 values with a lower and upper range to make sure all state values are in the reasonable range.
updateObject	This is an internally used flag to update the rxode2 solved object (when supplying an rxode2 solved object) as well as returning a new object. You probably should not modify it's FALSE default unless you are willing to have unexpected results.
omega	Estimate of Covariance matrix. When omega is a list, assume it is a block matrix and convert it to a full matrix for simulations. When omega is NA and you are using it with a rxode2 ui model, the between subject variability described by the omega matrix are set to zero.
omegaDf	The degrees of freedom of a t-distribution for simulation. By default this is NULL which is equivalent to Inf degrees, or to simulate from a normal distribution instead of a t-distribution.
omegaIsChol	Indicates if the omega supplied is a Cholesky decomposed matrix instead of the traditional symmetric matrix.
omegaSeparation	<p>Omega separation strategy</p> <p>Tells the type of separation strategy when simulating covariance with parameter uncertainty with standard deviations modeled in the thetaMat matrix.</p> <ul style="list-style-type: none"> <li>• "lkj" simulates the correlation matrix from the rLKJ1 matrix with the distribution parameter eta equal to the degrees of freedom nu by <math>(nu-1)/2</math></li> <li>• "separation" simulates from the identity inverse Wishart covariance matrix with nu degrees of freedom. This is then converted to a covariance matrix and augmented with the modeled standard deviations. While computationally more complex than the "lkj" prior, it performs better when the covariance matrix size is greater or equal to 10</li> <li>• "auto" chooses "lkj" when the dimension of the matrix is less than 10 and "separation" when greater than equal to 10.</li> </ul>
omegaXform	<p>When taking omega values from the thetaMat simulations (using the separation strategy for covariance simulation), how should the thetaMat values be turned into standard deviation values:</p> <ul style="list-style-type: none"> <li>• identity This is when standard deviation values are directly modeled by the params and thetaMat matrix</li> <li>• variance This is when the params and thetaMat simulates the variance that are directly modeled by the thetaMat matrix</li> <li>• log This is when the params and thetaMat simulates <math>\log(sd)</math></li> <li>• nlmixrSqrt This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>x^2</math> modeled along the diagonal. This only works with a diagonal matrix.</li> <li>• nlmixrLog This is when the params and thetaMat simulates the inverse cholesky decomposed matrix with the <math>\exp(x^2)</math> along the diagonal. This only works with a diagonal matrix.</li> </ul>

	<ul style="list-style-type: none"> <li>• <code>nlmixrIdentity</code> This is when the <code>params</code> and <code>thetaMat</code> simulates the inverse cholesky decomposed matrix. This only works with a diagonal matrix.</li> </ul>
<code>omegaLower</code>	Lower bounds for simulated ETAs (by default -Inf)
<code>omegaUpper</code>	Upper bounds for simulated ETAs (by default Inf)
<code>nSub</code>	Number between subject variabilities (ETAs) simulated for every realization of the parameters.
<code>thetaMat</code>	Named theta matrix.
<code>thetaDf</code>	The degrees of freedom of a t-distribution for simulation. By default this is NULL which is equivalent to Inf degrees, or to simulate from a normal distribution instead of a t-distribution.
<code>thetaIsChol</code>	Indicates if the theta supplied is a Cholesky decomposed matrix instead of the traditional symmetric matrix.
<code>nStud</code>	Number virtual studies to characterize uncertainty in estimated parameters.
<code>dfSub</code>	Degrees of freedom to sample the between subject variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
<code>dfObs</code>	Degrees of freedom to sample the unexplained variability matrix from the inverse Wishart distribution (scaled) or scaled inverse chi squared distribution.
<code>returnType</code>	<p>This tells what type of object is returned. The currently supported types are:</p> <ul style="list-style-type: none"> <li>• <code>"rxSolve"</code> (default) will return a reactive data frame that can change easily change different pieces of the solve and update the data frame. This is the currently standard solving method in rxode2, is used for <code>rxSolve(object, ...)</code>, <code>solve(object, ...)</code>,</li> <li>• <code>"data.frame"</code> – returns a plain, non-reactive data frame; Currently very slightly faster than <code>returnType="matrix"</code></li> <li>• <code>"matrix"</code> – returns a plain matrix with column names attached to the solved object. This is what is used <code>object\$run</code> as well as <code>object\$solve</code></li> <li>• <code>"data.table"</code> – returns a <code>data.table</code>; The <code>data.table</code> is created by reference (ie <code>setDt()</code>), which should be fast.</li> <li>• <code>"tbl"</code> or <code>"tibble"</code> returns a tibble format.</li> </ul>
<code>seed</code>	an object specifying if and how the random number generator should be initialized
<code>nsim</code>	represents the number of simulations. For rxode2, if you supply single subject event tables (created with <code>[eventTable()]</code> )
<code>minSS</code>	Minimum number of iterations for a steady-state dose
<code>maxSS</code>	Maximum number of iterations for a steady-state dose
<code>infSSstep</code>	Step size for determining if a constant infusion has reached steady state. By default this is large value, 12.
<code>strictSS</code>	Boolean indicating if a strict steady-state is required. If a strict steady-state is (TRUE) required then at least <code>minSS</code> doses are administered and the total number of steady states doses will continue until <code>maxSS</code> is reached, or <code>atol</code> and <code>rtol</code> for every compartment have been reached. However, if ODE solving problems occur after the <code>minSS</code> has been reached the whole subject is considered an invalid

	solve. If <code>strictSS</code> is FALSE then as long as <code>minSS</code> has been reached the last good solve before ODE solving problems occur is considered the steady state, even though either <code>atol</code> , <code>rto1</code> or <code>maxSS</code> have not been achieved.
<code>istateReset</code>	When TRUE, reset the ISTATE variable to 1 for <code>lsoda</code> and <code>liblsoda</code> with doses, like <code>deSolve</code> ; When FALSE, do not reset the ISTATE variable with doses.
<code>subsetNonmem</code>	subset to NONMEM compatible EVIDs only. By default TRUE.
<code>maxAtolRtolFactor</code>	The maximum <code>atol/rto1</code> that FOCEi and other routines may adjust to. By default 0.1
<code>from</code>	When there is no observations in the event table, start observations at this value. By default this is zero.
<code>to</code>	When there is no observations in the event table, end observations at this value. By default this is 24 + maximum dose time.
<code>by</code>	When there are no observations in the event table, this is the amount to increment for the observations between <code>from</code> and <code>to</code> .
<code>length.out</code>	The number of observations to create if there isn't any observations in the event table. By default this is 200.
<code>iCov</code>	A data frame of individual non-time varying covariates to combine with the events dataset. The <code>iCov</code> dataset has one covariate per ID and should match the event table
<code>keep</code>	Columns to keep from either the input dataset or the <code>iCov</code> dataset. With the <code>iCov</code> dataset, the column is kept once per line. For the input dataset, if any records are added to the data LOCF (Last Observation Carried forward) imputation is performed.
<code>indLinPhiTol</code>	the requested accuracy tolerance on exponential matrix.
<code>indLinPhiM</code>	the maximum size for the Krylov basis
<code>indLinMatExpType</code>	This is them matrix exponential type that is use for <code>rxode2</code> . Currently the following are supported: <ul style="list-style-type: none"> <li>• <code>A1-Mohy</code> Uses the exponential matrix method of Al-Mohy Higham (2009)</li> <li>• <code>arma</code> Use the exponential matrix from <code>RcppArmadillo</code></li> <li>• <code>expokit</code> Use the exponential matrix from Roger B. Sidje (1998)</li> </ul>
<code>indLinMatExpOrder</code>	an integer, the order of approximation to be used, for the <code>A1-Mohy</code> and <code>expokit</code> values. The best value for this depends on machine precision (and slightly on the matrix). We use 6 as a default.
<code>drop</code>	Columns to drop from the output
<code>idFactor</code>	This boolean indicates if original ID values should be maintained. This changes the default sequentially ordered ID to a factor with the original ID values in the original dataset. By default this is enabled.
<code>mxhnil</code>	maximum number of messages printed (per problem) warning that $T + H = T$ on a step ( $H =$ step size). This must be positive to result in a non-default value. The default value is 0 (or infinite).

hmxi	inverse of the maximum absolute value of H to be used. hmxi = 0.0 is allowed and corresponds to an infinite hmax1 (default). hminandhmximay be changed at any time, but wi
warnIdSort	Warn if the ID is not present and rxode2 assumes the order of the parameters/iCov are the same as the order of the parameters in the input dataset.
warnDrop	Warn if column(s) were supposed to be dropped, but were not present.
ssAtol	Steady state atol convergence factor. Can be a vector based on each state.
ssRtol	Steady state rtol convergence factor. Can be a vector based on each state.
safeZero	Use safe zero divide. By default this is turned on but you may turn it off if you wish.
safeLog	Use safe log. When enabled if your value that you are taking log() of is negative or zero, this will return log(machine epsilon). By default this is turned on.
safePow	Use safe powers. When enabled if your power is negative and your base is zero, this will return the machine epsilon^(negative power). By default this is turned on.
sumType	Sum type to use for sum() in rxode2 code blocks. pairwise uses the pairwise sum (fast, default) fsum uses the PreciseSum package's fsum function (most accurate) kahan uses Kahan correction neumaier uses Neumaier correction c uses no correction: default/native summing
prodType	Product to use for prod() in rxode2 blocks long double converts to long double, performs the multiplication and then converts back. double uses the standard double scale for multiplication.
sensType	Sensitivity type for linCmt() model: advan Use the direct advan solutions autodiff Use the autodiff advan solutions forward Use forward difference solutions central Use central differences
linDiff	This gives the linear difference amount for all the types of linear compartment model parameters where sensitivities are not calculated. The named components of this numeric vector are: <ul style="list-style-type: none"> <li>• "lag" Central compartment lag</li> <li>• "f" Central compartment bioavailability</li> <li>• "rate" Central compartment modeled rate</li> <li>• "dur" Central compartment modeled duration</li> <li>• "lag2" Depot compartment lag</li> <li>• "f2" Depot compartment bioavailability</li> <li>• "rate2" Depot compartment modeled rate</li> <li>• "dur2" Depot compartment modeled duration</li> </ul>
linDiffCentral	This gives the which parameters use central differences for the linear compartment model parameters. The are the same components as linDiff

resample	A character vector of model variables to resample from the input dataset; This sampling is done with replacement. When NULL or FALSE no resampling is done. When TRUE resampling is done on all covariates in the input dataset
resampleID	boolean representing if the resampling should be done on an individual basis TRUE (ie. a whole patient is selected) or each covariate is resampled independent of the subject identifier FALSE. When resampleID=TRUE correlations of parameters are retained, where as when resampleID=FALSE ignores patient covariate correlations. Hence the default is resampleID=TRUE.
maxwhile	represents the maximum times a while loop is evaluated before exiting. By default this is 100000
atolSens	Sensitivity atol, can be different than atol with liblsoda. This allows a less accurate solve for gradients (if desired)
rtolSens	Sensitivity rtol, can be different than rtol with liblsoda. This allows a less accurate solve for gradients (if desired)
ssAtolSens	Sensitivity absolute tolerance (atol) for calculating if steady state has been achieved for sensitivity compartments.
ssRtolSens	Sensitivity relative tolerance (rtol) for calculating if steady state has been achieved for sensitivity compartments.
simVariability	determines if the variability is simulated. When NA (default) this is determined by the solver.
nLlikAlloc	The number of log likelihood endpoints that are used in the model. This allows independent log likelihood per endpoint in focei for nlmixr2. It likely shouldn't be set, though it won't hurt anything if you do (just may take up more memory for larger allocations).
useStdPow	This uses C's pow for exponentiation instead of R's R_pow or R_pow_di. By default this is FALSE
naTimeHandle	Determines what time of handling happens when the time becomes NA: current options are: <ul style="list-style-type: none"> <li>• ignore this ignores the NA time input and passes it through.</li> <li>• warn (default) this will produce a warning at the end of the solve, but continues solving passing through the NA time</li> <li>• error this will stop this solve if this is not a parallel solved ODE (otherwise stopping can crash R)</li> </ul>
addlKeepsCov	This determines if the additional dosing items repeats the dose only (FALSE) or keeps the covariates at the record of the dose (TRUE)
addlDropSs	When there are steady state doses with an addl specification the steady state flag is dropped with repeated doses (when TRUE) or retained (when FALSE)
ssAtDoseTime	Boolean that when TRUE back calculates the steady concentration at the actual time of dose, otherwise when FALSE the doses are shifted
ss2cancelAllPending	When TRUE the SS=2 event type cancels all pending doses like SS=1. When FALSE the pending doses not canceled with SS=2 (the infusions started before SS=2 occurred are canceled, though).
envir	is the environment to look for R user functions (defaults to parent environment)

- a when using `solve()`, this is equivalent to the `object` argument. If you specify `object` later in the argument list it overwrites this parameter.
- b when using `solve()`, this is equivalent to the `params` argument. If you specify `params` as a named argument, this overwrites the output

### Details

The rest of the document focus on the different ODE solving methods, followed by the core solving method's options, rxode2 event handling options, rxode2's numerical stability options, rxode2's output options, and finally internal rxode2 options or compatibility options.

### Value

An "rxSolve" solve object that stores the solved value in a special data.frame or other type as determined by `returnType`. By default this has as many rows as there are sampled time points and as many columns as system variables (as defined by the ODEs and additional assignments in the rxode2 model code). It also stores information about the call to allow dynamic updating of the solved object.

The operations for the object are similar to a data-frame, but expand the `$` and `[[ "" ]]` access operators and assignment operators to resolve based on different parameter values, initial conditions, solver parameters, or events (by updating the `time` variable).

You can call the `eventTable()` methods on the solved object to update the event table and resolve the system of equations.

### Author(s)

Matthew Fidler, Melissa Hallow and Wenping Wang

### References

- "New Scaling and Squaring Algorithm for the Matrix Exponential", by Awad H. Al-Mohy and Nicholas J. Higham, August 2009
- Roger B. Sidje (1998). EXPOKIT: Software package for computing matrix exponentials. *ACM - Transactions on Mathematical Software* 24(1), 130-156.
- Hindmarsh, A. C. *ODEPACK, A Systematized Collection of ODE Solvers*. Scientific Computing, R. S. Stepleman et al. (Eds.), North-Holland, Amsterdam, 1983, pp. 55-64.
- Petzold, L. R. *Automatic Selection of Methods for Solving Stiff and Nonstiff Systems of Ordinary Differential Equations*. *Siam J. Sci. Stat. Comput.* 4 (1983), pp. 136-148.
- Hairer, E., Norsett, S. P., and Wanner, G. *Solving ordinary differential equations I, nonstiff problems*. 2nd edition, Springer Series in Computational Mathematics, Springer-Verlag (1993).

### See Also

[rxode2\(\)](#)

---

rxStack	<i>Stack a solved object for things like default ggplot2 plot</i>
---------	---

---

**Description**

Stack a solved object for things like default ggplot2 plot

**Usage**

```
rxStack(data, vars = NULL, doSim = TRUE)
```

**Arguments**

data	is a rxode2 object to be stacked.
vars	Variables to include in stacked data; By default this is all the variables when vars is NULL. When vars is sim and comes from a rxode2 ui simulation with multiple endpoints (ie it has a CMT in the simulation), it will rework the data as if it was stacked based the value based on the compartments in the multiple endpoint model. When the vars is sim.endpoint1 it will subset the stack to endpoint1, you can also have 'c("sim.endpoint1", "sim.endpoint2") and the "stack" will subset to endpoint1 and endpoint2. When you specify the sim type variables they have to be all prefixed with sim otherwise, the stack will not treat them differently.
doSim	boolean that determines if the "sim" variable in a rxSolve dataset is actually "stacking" based on the endpoint (TRUE) or simply treating sim as a variable.

**Value**

Stacked data with value and trt, where value is the values and trt is the state and lhs variables.

**Author(s)**

Matthew Fidler

---

rxState	<i>State variables</i>
---------	------------------------

---

**Description**

This returns the model's compartments or states.

**Usage**

```
rxState(obj = NULL, state = NULL)
```



**Arguments**

obj rxode2 family of objects  
 state is a string indicating the state or compartment that you would like to lookup.

**Value**

If state is missing, return a character vector of all the states.  
 If state is a string, return the compartment number of the named state.

**Author(s)**

Matthew L.Fidler

**See Also**

[rxode2\(\)](#)

Other Query model information: [rxDfdy\(\)](#), [rxInits\(\)](#), [rxLhs\(\)](#), [rxModelVars\(\)](#), [rxParams\(\)](#)

---

rxSumProdModel *Recast model in terms of sum/prod*

---

**Description**

Recast model in terms of sum/prod

**Usage**

```
rxSumProdModel(model, expand = FALSE, sum = TRUE, prod = TRUE)
```

**Arguments**

model rxode2 model  
 expand Boolean indicating if the expression is expanded.  
 sum Use sum(...)  
 prod Use prod(...)

**Value**

model string with prod(.) and sum(.) for all these operations.

**Author(s)**

Matthew L. Fidler

rxSupportedFuns      *Get list of supported functions*

---

**Description**

Get list of supported functions

**Usage**

```
rxSupportedFuns()
```

**Value**

list of supported functions in rxode2

**Examples**

```
rxSupportedFuns()
```

---

rxSuppressMsg      *Respect suppress messages*

---

**Description**

This turns on the silent REprintf in C when suppressMessages() is turned on. This makes the REprintf act like messages in R, they can be suppressed with suppressMessages()

**Usage**

```
rxSuppressMsg()
```

**Value**

Nothing

**Author(s)**

Matthew Fidler

**Examples**

```

# rxSupressMsg() is called with rxode2()

# Note the errors are output to the console

try(rxode2("d/dt(matt)=/3"), silent = TRUE)

# When using suppressMessages, the output is suppressed

suppressMessages(try(rxode2("d/dt(matt)=/3"), silent = TRUE))

# In rxode2, we use Rprintf so that interrupted threads do not crash R
# if there is a user interrupt. This isn't captured by R's messages, but
# This interface allows the `suppressMessages()` to suppress the C printing
# as well

# If you want to suppress messages from rxode2 in other packages, you can use
# this function

```

---

rxSymInvChol

*Get Omega<sup>-1</sup> and derivatives*


---

**Description**

Get Omega<sup>-1</sup> and derivatives

**Usage**

```

rxSymInvChol(
  invObjOrMatrix,
  theta = NULL,
  type = "cholOmegaInv",
  thetaNumber = 0L
)

```

**Arguments**

- |                |  |
|----------------|--|
| invObjOrMatrix | Object for inverse-type calculations. If this is a matrix, setup the object for inversion <code>rxSymInvCholCreate()</code> with the default arguments and return a reactive s3 object. Otherwise, use the inversion object to calculate the requested derivative/inverse. |
| theta          | Thetas to be used for calculation. If missing (NULL), a special s3 class is created and returned to access Omega <sup>-1</sup> objects as needed and cache them based on the theta that is used.   |
| type           | The type of object. Currently the following types are supported: <ul style="list-style-type: none"> <li>cholOmegaInv gives the Cholesky decomposition of the Omega Inverse matrix.</li> </ul>  |

- `omegaInv` gives the Omega Inverse matrix.
  - `d(omegaInv)` gives the  $d(\Omega^{-1})$  with respect to the theta parameter specified in `thetaNumber`.
  - `d(D)` gives the  $d(\text{diagonal}(\Omega^{-1}))$  with respect to the theta parameter specified in the `thetaNumber` parameter
- `thetaNumber` For types `d(omegaInv)` and `d(D)`, the theta number that the derivative is taken against. This must be positive from 1 to the number of thetas defining the Omega matrix.

**Value**

Matrix based on parameters or environment with all the matrixes calculated in variables `omega`, `omegaInv`, `dOmega`, `dOmegaInv`.

**Author(s)**

Matthew L. Fidler

---

`rxSyncOptions`      *Sync options with rxode2 variables*

---

**Description**

Accessing `rxode2` options via `getOption` slows down solving. This allows the options to be synced with variables.

**Usage**

```
rxSyncOptions(setDefaults = c("none", "permissive", "strict"))
```

**Arguments**

- `setDefaults` This will setup `rxode2`'s default solving options with the following options:
- "none" leave the options alone
  - "permissive" This is a permissive option set similar to R language specifications.
  - "strict" This is a strict option set similar to the original `rxode2()`. It requires semicolons at the end of lines and equals for assignment

**Value**

nothing; called for side effects

**Author(s)**

Matthew L. Fidler

---

rxSyntaxFunctions	<i>A list and description of Rode supported syntax functions</i>
-------------------	--

---

**Description**

A list and description of Rode supported syntax functions

**Usage**

```
rxSyntaxFunctions
```

**Format**

A data frame with 3 columns and 102 rows

**Function** Reserved function Name

**Description** Description of function

**Aliases** Function Aliases

---

rxt	<i>Simulate student t variable from threefry generator</i>
-----	--

---

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxt(df, n = 1L, ncores = 1L)
```

**Arguments**

df	degrees of freedom (> 0, maybe non-integer). df = Inf is allowed.
n	number of observations. If length(n) > 1, the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

### Details

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with rxSetSeed()

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

### Value

t-distribution random numbers

### Examples

```
## Use threefry engine
rxt(df = 3, n = 10) # with rxt you have to explicitly state n
rxt(df = 3, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxt(4) ## The first argument is the df parameter

## This example uses `rxt` directly in the model

rx <- function() {
  model({
    a <- rxt(3)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)
```

---

rxTempDir

*Get the rxode2 temporary directory*

---

### Description

Get the rxode2 temporary directory

### Usage

```
rxTempDir()
```

**Value**

rxode2 temporary directory.

---

rxTheme

*rxTheme is the ggplot2 theme for rxode2 plots*

---

**Description**

rxTheme is the ggplot2 theme for rxode2 plots

**Usage**

```
rxTheme(  
  base_size = 11,  
  base_family = "",  
  base_line_size = base_size/22,  
  base_rect_size = base_size/22,  
  grid = TRUE  
)
```

**Arguments**

base_size	base font size, given in pts.
base_family	base font family
base_line_size	base size for line elements
base_rect_size	base size for rect elements
grid	a Boolean indicating if the grid is on (TRUE) or off (FALSE). This could also be a character indicating x or y.

**Value**

ggplot2 theme used in rxode2

**See Also**

Other rxode2 plotting: [plot.rxSolve\(\)](#)

---

rxToSE                      *rxode2 to symengine environment*

---

## Description

rxode2 to symengine environment

## Usage

```
rxToSE(  
  x,  
  envir = NULL,  
  progress = FALSE,  
  promoteLinSens = TRUE,  
  parent = parent.frame()  
)  
  
.rxToSE(x, envir = NULL, progress = FALSE)  
  
rxFromSE(  
  x,  
  unknownDerivatives = c("forward", "central", "error"),  
  parent = parent.frame()  
)  
  
.rxFromSE(x)
```

## Arguments

x	expression
envir	default is NULL; Environment to put symengine variables in.
progress	shows progress bar if true.
promoteLinSens	Promote solved linear compartment systems to sensitivity-based solutions.
parent	is the parent environment to look for R-based user functions
unknownDerivatives	When handling derivatives from unknown functions, the translator will translate into different types of numeric derivatives. The currently supported methods are: <ul style="list-style-type: none"><li>- `forward` for forward differences</li><li>- `central` for central differences</li><li>- `error` for throwing an error for unknown derivatives</li></ul>

## Value

An rxode2 symengine environment



**Author(s)**

Matthew L. Fidler

---

`rxTrans`*Translate the model to C code if needed*

---

**Description**

This function translates the model to C code, if needed

**Usage**

```
rxTrans(  
  model,  
  modelPrefix = "",  
  md5 = "",  
  modName = NULL,  
  modVars = FALSE,  
  ...  
)  
  
## Default S3 method:  
rxTrans(  
  model,  
  modelPrefix = "",  
  md5 = "",  
  modName = NULL,  
  modVars = FALSE,  
  ...  
)  
  
## S3 method for class 'character'  
rxTrans(  
  model,  
  modelPrefix = "",  
  md5 = "",  
  modName = NULL,  
  modVars = FALSE,  
  ...  
)
```

**Arguments**

`model` This is the ODE model specification. It can be:

- a string containing the set of ordinary differential equations (ODE) and other expressions defining the changes in the dynamic system.

- a file name where the ODE system equation is contained

An ODE expression enclosed in `\{\}`

(see also the `filename` argument). For details, see the sections “Details” and `rxode2` Syntax below.

<code>modelPrefix</code>	Prefix of the model functions that will be compiled to make sure that multiple <code>rxode2</code> objects can coexist in the same R session.
<code>md5</code>	Is the md5 of the model before parsing, and is used to embed the md5 into DLL, and then provide for functions like <code>rxModelVars()</code> .
<code>modName</code>	a string to be used as the model name. This string is used for naming various aspects of the computations, including generating C symbol names, dynamic libraries, etc. Therefore, it is necessary that <code>modName</code> consists of simple ASCII alphanumeric characters starting with a letter.
<code>modVars</code>	returns the model variables instead of the named vector of translated properties.
<code>...</code>	Ignored parameters.

### Value

a named vector of translated model properties including what type of jacobian is specified, the C function prefixes, as well as the C functions names to be called through the compiled model.

### Author(s)

Matthew L.Fidler

### See Also

[rxode2\(\)](#), [rxCompile\(\)](#).

---

<code>rxUiDecompress</code>	<i>Compress/Decompress rxode2 ui</i>
-----------------------------	--------------------------------------

---

### Description

Compress/Decompress `rxode2 ui`

### Usage

```
rxUiDecompress(ui)
```

```
rxUiCompress(ui)
```

### Arguments

`ui` `rxode2 ui` object

**Value**

A compressed or decompressed rxui object

**Author(s)**

Matthew L. Fidler

**Examples**

```

one.cmt <- function() {
  ini({
    ## You may label each parameter with a comment
    tka <- 0.45 # Log Ka
    tcl <- log(c(0, 2.7, 100)) # Log Cl
    ## This works with interactive models
    ## You may also label the preceding line with label("label text")
    tv <- 3.45; label("log V")
    ## the label("Label name") works with all models
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd) | tmp
  })
}

f <- rxode2(one.cmt)
print(class(f))
print(is.environment(f))

f <- rxUiDecompress(f)
print(class(f))
print(is.environment(f))

f <- rxUiCompress(f)
print(class(f))
print(is.environment(f))

```

**Description**

This is a generic function for deparsing certain objects when printing out a rxode2 object. Currently it is used for any meta-information

```
rxUiDeparse.rxControl(rxControl(covsInterpolation="linear", method="dop853", naInterpolation="nocb",
keepInterpolation="nocb", sigmaXform="variance", omegaXform="variance", returnType="data.frame",
sumType="fsum", prodType="logify", sensType="central"), "ctl")
```

**Usage**

```
rxUiDeparse(object, var)

## S3 method for class 'lotriFix'
rxUiDeparse(object, var)

## Default S3 method:
rxUiDeparse(object, var)

## S3 method for class 'rxControl'
rxUiDeparse(object, var)
```

**Arguments**

object	object to be deparsed
var	variable name to be assigned

**Value**

parsed R expression that can be used for printing and as.function() calls.

**Author(s)**

Matthew L. Fidler

**Examples**

```
mat <- matrix(c(1, 0.1, 0.1, 1), 2, 2, dimnames=list(c("a", "b"), c("a", "b")))

rxUiDeparse(matrix(c(1, 0.1, 0.1, 1), 2, 2, dimnames=list(c("a", "b"), c("a", "b"))), "x")
```

---

rxUiGet.cmtLines

*S3 for getting information from UI model*

---

**Description**

S3 for getting information from UI model

**Usage**

```
## S3 method for class 'cmtLines'
rxUiGet(x, ...)

## S3 method for class 'dvidLine'
rxUiGet(x, ...)

## S3 method for class 'paramsLine'
rxUiGet(x, ...)

## S3 method for class 'interplines'
rxUiGet(x, ...)

## S3 method for class 'simulationSigma'
rxUiGet(x, ...)

## S3 method for class 'simulationModel'
rxUiGet(x, ...)

## S3 method for class 'symengineModelNoPrune'
rxUiGet(x, ...)

## S3 method for class 'symengineModelPrune'
rxUiGet(x, ...)

## S3 method for class 'simulationIniModel'
rxUiGet(x, ...)

rxUiGet(x, ...)

## S3 method for class 'levels'
rxUiGet(x, ...)

## S3 method for class 'state'
rxUiGet(x, ...)

## S3 method for class 'stateDf'
rxUiGet(x, ...)

## S3 method for class 'statePropDf'
rxUiGet(x, ...)

## S3 method for class 'props'
rxUiGet(x, ...)

## S3 method for class 'theta'
rxUiGet(x, ...)
```

```
## S3 method for class 'lstChr'  
rxUiGet(x, ...)  
  
## S3 method for class 'omega'  
rxUiGet(x, ...)  
  
## S3 method for class 'funTxt'  
rxUiGet(x, ...)  
  
## S3 method for class 'allCovs'  
rxUiGet(x, ...)  
  
## S3 method for class 'muRefTable'  
rxUiGet(x, ...)  
  
## S3 method for class 'multipleEndpoint'  
rxUiGet(x, ...)  
  
## S3 method for class 'funPrint'  
rxUiGet(x, ...)  
  
## S3 method for class 'fun'  
rxUiGet(x, ...)  
  
## S3 method for class 'md5'  
rxUiGet(x, ...)  
  
## S3 method for class 'ini'  
rxUiGet(x, ...)  
  
## S3 method for class 'iniFun'  
rxUiGet(x, ...)  
  
## S3 method for class 'modelFun'  
rxUiGet(x, ...)  
  
## S3 method for class 'model'  
rxUiGet(x, ...)  
  
## S3 method for class 'modelDesc'  
rxUiGet(x, ...)  
  
## S3 method for class 'thetaLower'  
rxUiGet(x, ...)  
  
## S3 method for class 'thetaUpper'  
rxUiGet(x, ...)
```

```
## S3 method for class 'lhsVar'  
rxUiGet(x, ...)  
  
## S3 method for class 'varLhs'  
rxUiGet(x, ...)  
  
## S3 method for class 'lhsEta'  
rxUiGet(x, ...)  
  
## S3 method for class 'lhsTheta'  
rxUiGet(x, ...)  
  
## S3 method for class 'lhsCov'  
rxUiGet(x, ...)  
  
## S3 method for class 'etaLhs'  
rxUiGet(x, ...)  
  
## S3 method for class 'thetaLhs'  
rxUiGet(x, ...)  
  
## S3 method for class 'covLhs'  
rxUiGet(x, ...)  
  
## Default S3 method:  
rxUiGet(x, ...)
```

### Arguments

x	list of (UIenvironment, exact). UI environment is the parsed function for rxode2. exact is a boolean that says if an exact match is required.
...	Other arguments

### Value

value that was requested from the UI object

### Author(s)

Matthew Fidler

**Description**

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

**Usage**

```
rxunif(min = 0, max = 1, n = 1L, ncores = 1L)
```

**Arguments**

min, max	lower and upper limits of the distribution. Must be finite.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in rxode2({}) blocks

**Details**

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the rxode2 environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the rxode2 engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

**Value**

uniform random numbers

**Examples**

```
## Use threefry engine

rxunif(min = 0, max = 4, n = 10) # with rxunif you have to explicitly state n
rxunif(min = 0, max = 4, n = 10, ncores = 2) # You can parallelize the simulation using openMP

rxunif()

## This example uses `rxunif` directly in the model
```



```
rx <- function() {  
  model({  
    a <- rxunif(0, 3)  
  })  
}  
  
et <- et(1, id = 1:2)  
  
s <- rxSolve(rx, et)
```

---

rxUnloadAll	<i>Unloads all rxode2 compiled DLLs</i>
-------------	---

---

**Description**

Unloads all rxode2 compiled DLLs

**Usage**

```
rxUnloadAll()
```

**Value**

List of rxode2 dlls still loaded

boolean of if all rxode2 dlls have been unloaded

**Examples**

```
print(rxUnloadAll())
```

---

rxUse	<i>Use model object in your package</i>
-------	---

---

**Description**

Use model object in your package

**Usage**

```
rxUse(obj, overwrite = TRUE, compress = "bzip2", internal = FALSE)
```

**Arguments**

obj	model to save.
overwrite	By default, use_data() will not overwrite existing files. If you really want to do so, set this to TRUE.
compress	Choose the type of compression used by save(). Should be one of "gzip", "bzip2", or "xz".
internal	If this is run internally. By default this is FALSE

**Value**

Nothing; This is used for its side effects and shouldn't be called by a user

---

rxValidate	<i>Validate rxode2 This allows easy validation/qualification of nlmixr by running the testing suite on your system.</i>
------------	---

---

**Description**

Validate rxode2 This allows easy validation/qualification of nlmixr by running the testing suite on your system.

**Usage**

```
rxValidate(type = NULL, skipOnCran = TRUE)
```

```
rxTest(type = NULL, skipOnCran = TRUE)
```

**Arguments**

type	Type of test or filter of test type, When this is an expression, evaluate the contents, respecting skipOnCran
skipOnCran	when TRUE skip the test on CRAN.

**Value**

nothing

**Author(s)**

Matthew L. Fidler

---

`rxweibull`*Simulate Weibull variable from threefry generator*

---

### Description

Care should be taken with this method not to encounter the birthday problem, described <https://www.johndcook.com/blog/2016/01/29/random-number-generator-seed-mistakes/>. Since the sitmo threefry, this currently generates one random deviate from the uniform distribution to seed the engine threefry and then run the code.

### Usage

```
rxweibull(shape, scale = 1, n = 1L, ncores = 1L)
```

### Arguments

shape, scale	shape and scale parameters, the latter defaulting to 1.
n	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
ncores	Number of cores for the simulation rxnorm simulates using the threefry sitmo generator. rxnormV used to simulate with the vandercorput simulator, but since it didn't satisfy the normal properties it was changed to simple be an alias of rxnorm. It is no longer supported in <code>rxode2({})</code> blocks

### Details

Therefore, a simple call to the random number generated followed by a second call to random number generated may have identical seeds. As the number of random number generator calls are increased the probability that the birthday problem will increase.

The key to avoid this problem is to either run all simulations in the `rxode2` environment once (therefore one seed or series of seeds for the whole simulation), pre-generate all random variables used for the simulation, or seed the `rxode2` engine with `rxSetSeed()`

Internally each ID is seeded with a unique number so that the results do not depend on the number of cores used.

### Value

Weibull random deviates

### Examples

```
## Use threefry engine  
  
# with rxweibull you have to explicitly state n
```

```

rxweibull(shape = 1, scale = 4, n = 10)

# You can parallelize the simulation using openMP
rxweibull(shape = 1, scale = 4, n = 10, ncores = 2)

rxweibull(3)

## This example uses `rxweibull` directly in the model

rx <- function() {
  model({
    a <- rxweibull(1, 3)
  })
}

et <- et(1, id = 1:2)

s <- rxSolve(rx, et)

```

---

 rxWithSeed

*Preserved seed and possibly set the seed*


---

### Description

Preserved seed and possibly set the seed

### Usage

```

rxWithSeed(
  seed,
  code,
  rxseed = rxGetSeed(),
  kind = "default",
  normal.kind = "default",
  sample.kind = "default"
)

rxWithPreserveSeed(code)

```

### Arguments

seed	R seed to use for the session
code	Is the code to evaluate
rxseed	is the rxode2 seed that is being preserved
kind	character or NULL. If kind is a character string, set R's RNG to the kind desired. Use "default" to return to the R default. See 'Details' for the interpretation of NULL.

normal.kind	character string or NULL. If it is a character string, set the method of Normal generation. Use "default" to return to the R default. NULL makes no change.
sample.kind	character string or NULL. If it is a character string, set the method of discrete uniform generation (used in <a href="#">sample</a> , for instance). Use "default" to return to the R default. NULL makes no change.

**Value**

returns whatever the code is returning

**See Also**

rxGetSeed, rxSetSeed

**Examples**

```
rxGetSeed()
rxWithSeed(1, {
  print(rxGetSeed())
  rxnorm()
  print(rxGetSeed())
  rxnorm()
}, rxseed=3)
```

---

stat\_amt

*Dosing/Amt geom/stat*


---

**Description**

This is a dosing geom that shows the vertical lines where a dose occurs

**Usage**

```
stat_amt(
  mapping = NULL,
  data = NULL,
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

```
geom_amt(
  mapping = NULL,
  data = NULL,
  position = "identity",
  show.legend = NA,
```

```

  inherit.aes = TRUE,
  ...
)

```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes()</a> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply <code>mapping</code> if there is no plot mapping.
data	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot()</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
position	<p>A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following:</p> <ul style="list-style-type: none"> <li>• The result of calling a position function, such as <a href="#">position_jitter()</a>. This method allows for passing extra arguments to the position.</li> <li>• A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <a href="#">position_jitter()</a>, give the position as "jitter".</li> <li>• For more information and other ways to specify the position, see the <a href="#">layer position</a> documentation.</li> </ul>
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If <code>FALSE</code> , overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders()</a> .
...	<p>Other arguments passed on to <a href="#">layer()</a>'s <code>params</code> argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the <code>position</code> argument, or aesthetics that are required can <i>not</i> be passed through ... Unknown arguments that are not part of the 4 categories below are ignored.</p> <ul style="list-style-type: none"> <li>• Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, <code>colour = "red"</code> or <code>linewidth = 3</code>. The <code>geom</code>'s documentation has an <b>Aesthetics</b> section that lists the available options. The 'required' aesthetics cannot be passed on to the <code>params</code>. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.</li> </ul>

- When constructing a layer using a `stat_*`() function, the `...` argument can be used to pass on parameters to the `geom` part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The `geom`'s documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*`() function, the `...` argument can be used to pass on parameters to the `stat` part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The `stat`'s documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through `...`. This can be one of the functions described as [key glyphs](#), to change the display of the layer in the legend.

### Details

Requires the following aesthetics:

- `x` representing the x values, usually time
- `amt` representing the dosing values; They are missing or zero when no dose is given

### Value

This returns a `stat_amt` in context of a `ggplot2` plot

### Examples

```
library(rxode2)
library(units)

## Model from RxODE tutorial
mod1 <- function() {
  ini({
    KA <- 2.94E-01
    CL <- 1.86E+01
    V2 <- 4.02E+01
    Q <- 1.05E+01
    V3 <- 2.97E+02
    Kin <- 1
    Kout <- 1
    EC50 <- 200
  })
  model({
    C2 <- centr/V2
    C3 <- peri/V3
    d/dt(depot) <- -KA*depot
    d/dt(centr) <- KA*depot - CL*C2 - Q*C2 + Q*C3
    d/dt(peri) <- Q*C2 - Q*C3
    d/dt(eff) <- Kin - Kout*(1-C2/(EC50+C2))*eff
  })
}
```

```
## These are making the more complex regimens of the rxode2 tutorial

## bid for 5 days
bid <- et(timeUnits="hr") %>%
  et(amt=10000,ii=12,until=set_units(5, "days"))

## qd for 5 days
qd <- et(timeUnits="hr") %>%
  et(amt=20000,ii=24,until=set_units(5, "days"))

## bid for 5 days followed by qd for 5 days

et <- seq(bid,qd) %>% et(seq(0,11*24,length.out=100))

bidQd <- rxSolve(mod1, et, addDosing=TRUE)

# by default dotted and under-stated
plot(bidQd, C2) + geom_amt(aes(amt=amt))

# of course you can make it a bit more visible

plot(bidQd, C2) + geom_amt(aes(amt=amt), col="red", lty=1, linewidth=1.2)
```

---

stat\_cens

*Censoring geom/stat*


---

## Description

This is a censoring geom that shows the left or right censoring specified in the nlmixr input data-set or fit

## Usage

```
stat_cens(
  mapping = NULL,
  data = NULL,
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  width = 0.01,
  ...
)
```

```
geom_cens(
  mapping = NULL,
  data = NULL,
```



```

    position = "identity",
    show.legend = NA,
    inherit.aes = TRUE,
    width = 0.01,
    ...
  )

```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes()</a> . If specified and <code>inherit.aes = TRUE</code> (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot()</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
position	<p>A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following:</p> <ul style="list-style-type: none"> <li>• The result of calling a position function, such as <a href="#">position_jitter()</a>. This method allows for passing extra arguments to the position.</li> <li>• A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <a href="#">position_jitter()</a>, give the position as "jitter".</li> <li>• For more information and other ways to specify the position, see the <a href="#">layer position</a> documentation.</li> </ul>
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If <code>FALSE</code> , overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <a href="#">borders()</a> .
width	represents the width (in \ censoring box
...	<p>Other arguments passed on to <a href="#">layer()</a>'s <code>params</code> argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the <code>position</code> argument, or aesthetics that are required can <i>not</i> be passed through ... Unknown arguments that are not part of the 4 categories below are ignored.</p> <ul style="list-style-type: none"> <li>• Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, <code>colour = "red"</code> or <code>linewidth = 3</code>. The <code>geom</code>'s documentation has an <b>Aesthetics</b> section that lists the available options. The 'required' aesthetics cannot be passed on to the</li> </ul>

params. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.

- When constructing a layer using a `stat_*()` function, the `...` argument can be used to pass on parameters to the geom part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the `...` argument can be used to pass on parameters to the stat part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through `...`. This can be one of the functions described as [key glyphs](#), to change the display of the layer in the legend.

## Details

Requires the following aesthetics:

- `x` Represents the independent variable, often the time scale
- `y` represents the dependent variable
- `CENS` for the censoring information; (-1 right censored, 0 no censoring or 1 left censoring)
- `LIMIT` which represents the corresponding limit ()

Will add boxes representing the areas of the fit that were censored.

## Value

This returns a ggplot2 stat

---

summary.rxode2

*Print expanded information about the rxode2 object.*

---

## Description

This prints the expanded information about the rxode2 object.

## Usage

```
## S3 method for class 'rxode2'
summary(object, ...)
```

## Arguments

object	rxode2 object
...	Ignored parameters

**Value**

object is returned

**Author(s)**

Matthew L.Fidler

---

swapMatListWithCube    *Swaps the matrix list with a cube*

---

**Description**

Swaps the matrix list with a cube

**Usage**

```
swapMatListWithCube(matrixListOrCube)
```

**Arguments**

matrixListOrCube

Either a list of 2-dimensional matrices or a cube of matrices

**Value**

A list or a cube (opposite format as input)

**Author(s)**

Matthew L. Fidler

**Examples**

```
# Create matrix list
matLst <- cvPost(10, lotri::lotri(a+b~c(1, 0.25, 1)), 3)
print(matLst)

# Convert to cube
matCube <- swapMatListWithCube(matLst)
print(matCube)

# Convert back to list
matLst2 <- swapMatListWithCube(matCube)
print(matLst2)
```

---

testRxLinCmt	<i>Test if rxode2 uses linear solved systems</i>
--------------	--

---

### Description

Test if rxode2 uses linear solved systems

### Usage

```
testRxLinCmt(ui, extra = "", .var.name = .vname(ui))
assertRxLinCmt(ui, extra = "", .var.name = .vname(ui))
```

### Arguments

ui	rxode2 model
extra	Extra text to append to the error message (like "for focci")
.var.name	[character(1)] Name of the checked object to print in assertions. Defaults to the heuristic implemented in <a href="#">vname</a> .

### Value

TRUE if the model uses linear solved systems, FALSE otherwise

### Functions

- `assertRxLinCmt()`: Assert that the rxode2 uses linear solved systems

### Author(s)

Matthew L. Fidler

### Examples

```
one.cmt <- function() {
  ini({
    ## You may label each parameter with a comment
    tka <- 0.45 # Log Ka
    tcl <- log(c(0, 2.7, 100)) # Log Cl
    ## This works with interactive models
    ## You may also label the preceding line with label("label text")
    tv <- 3.45; label("log V")
    ## the label("Label name") works with all models
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
}
```

```

  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

testRxLinCmt(one.cmt)

```

---

testRxUnbounded	<i>Test if the rxode2 model has any parameters with user defined boundaries</i>
-----------------	---

---

### Description

Test if the rxode2 model has any parameters with user defined boundaries

### Usage

```

testRxUnbounded(ui)

assertRxUnbounded(ui, extra = "", .var.name = .vname(ui))

warnRxBounded(ui, extra = "", .var.name = .vname(ui))

```

### Arguments

ui	rxode2 ui
extra	extra information to append to the error message
.var.name	variable name

### Value

boolean indicating if any parameters have user defined boundaries

### Functions

- `assertRxUnbounded()`: Assert that the rxode2 model has any parameters with user defined boundaries
- `warnRxBounded()`: Warn that the rxode2 model has any parameters with user defined boundaries

### Author(s)

Matthew L. Fidler

**See Also**

Other Assertions: [assertCompartmentExists\(\)](#), [assertCompartmentName\(\)](#), [assertCompartmentNew\(\)](#), [assertRxUi\(\)](#), [assertVariableExists\(\)](#), [assertVariableNew\(\)](#)

**Examples**

```
one.cmt <- function() {
  ini({
    tka <- 0.45; label("Ka")
    tcl <- log(c(0, 2.7, 100)); label("Cl")
    tv <- 3.45; label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    linCmt() ~ add(add.sd)
  })
}

testRxUnbounded(one.cmt)

try(assertRxUnbounded(one.cmt))

warnRxBounded(one.cmt)
```

---

toTrialDuration	<i>Convert event data to trial duration data A helper function to create a custom event table. The observation time will start from the first event time (baseline) and end at trial duration. The interval is the spacing between each observation.</i>
-----------------	--

---

**Description**

Convert event data to trial duration data A helper function to create a custom event table. The observation time will start from the first event time (baseline) and end at trial duration. The interval is the spacing between each observation.

**Usage**

```
toTrialDuration(ev, trialEnd, interval, writeDir = NULL)
```

**Arguments**

ev	event data
trialEnd	extend trial duration. Must be same time unit as event data
interval	observation interval. Must be same time unit as event data
writeDir	if not NULL, write the output to a csv file

**Author(s)**

Omar Elashkar

**Examples**

```
# Create event table with unique time for each ID
ev = et(data.frame(id = rep(1:10, 3), time = runif(min = 10, max = 20, n = 30)))

# select the duration and spacing interval (assuming time is in years)
toTrialDuration(ev, trialEnd = 1.5, interval = 0.2)
```

---

update.rxUi

*Update for rxUi*


---

**Description**

Update for rxUi

**Usage**

```
## S3 method for class 'rxUi'
update(object, ..., envir = parent.frame())
```

**Arguments**

object	rxode2 UI object
...	Lines to update
envir	Environment for evaluating ini() style calls

**Value**

a new rxode2 updated UI object

uppergamma

*uppergamma: upper incomplete gamma function*

---

**Description**

This is the tgamma from the boost library

**Usage**

```
uppergamma(a, z)
```

**Arguments**

a	The numeric 'a' parameter in the upper incomplete gamma
z	The numeric 'z' parameter in the upper incomplete gamma

**Details**

The uppergamma function is given by:

$$\text{uppergamma}(a, z) = \int_z^\infty t^{a-1} \cdot e^{-t} dt$$

**Value**

uppergamma results

**Author(s)**

Matthew L. Fidler

**Examples**

```
uppergamma(1, 3)
```

```
uppergamma(1:3, 3)
```

```
uppergamma(1, 1:3)
```



---

zeroRe	<i>Set random effects and residual error to zero</i>
--------	--

---

**Description**

Set random effects and residual error to zero

**Usage**

```
zeroRe(object, which = c("omega", "sigma"), fix = TRUE)
```

**Arguments**

object	The model to modify
which	The types of parameters to set to zero
fix	Should the parameters be fixed to the zero value?

**Value**

The object with some parameters set to zero

**Author(s)**

Bill Denney

**See Also**

Other Initial conditions: [ini.rxUi\(\)](#)

**Examples**

```
one.compartment <- function() {
  ini({
    tka <- log(1.57); label("Ka")
    tc1 <- log(2.72); label("Cl")
    tv <- log(31.5); label("V")
    eta.ka ~ 0.6
    eta.cl ~ 0.3
    eta.v ~ 0.1
    add.sd <- 0.7
  })
  model({
    ka <- exp(tka + eta.ka)
    cl <- exp(tc1 + eta.cl)
    v <- exp(tv + eta.v)
    d/dt(depot) = -ka * depot
    d/dt(center) = ka * depot - cl / v * center
    cp = center / v
    cp ~ add(add.sd)
  })
}
```

```
    })  
  }  
  zeroRe(one.compartment)
```

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