

Package ‘simecol’

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Description simecol is an object oriented framework to simulate ecological (and other) dynamic systems. It can be used for differential equations, individual-based (or agent-based) and other models as well. The package helps to organize scenarios (avoids copy and paste) and improves readability and usability of code.

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simecol-package

General Information about the 'simecol' Package

Description

The **simecol** package is intended to give users (scientists and students) an interactive environment to implement, distribute, simulate and document ecological and other dynamic models without the need to write long simulation programs. For this purpose, an object oriented approach using the S4 class system is proposed, which should provide a consistent but still flexible and extensible way to implement simulation models of different types, namely:

- ordinary differential equation (ODE) models (class `odeModel`),
- grid-oriented individual-based models (class `gridModel`), and
- particle diffusion-type models (class `rwalkModel`),
- individual-based models (class `indbasedModel`),
- other model types by deriving a user specified subclass from `simObj`.

Each simulation model is implemented as S4 object (superclass `simObj`) with the following slots:

- `main = function(time, init, parms, ...)`: a function holding the main equations of the model,
- `equations`: an optional non-nested list holding arbitrary sub-equations (sub-models) of the model. Sub-equations can be interdependent and can be called directly from within `main` or `initfunc`.
- `parms`: a list (or vector for some classes) with constant model parameters,
- `times`: vector of time steps or vector with three named values `from`, `to`, `by` specifying the simulation time steps. The `from-to-by` form can be edited with `fixParms`.
- `init`: initial state (start values) of the simulation. This is typically a named vector (state variables in `odeModels`) or matrix (e.g. initial grid of `gridModels`).
- `inputs`: time dependent or spatially resolved external inputs can be specified as data frame or matrix (more efficient). It is up to the user to evaluate the corresponding values within the main function. Performance optimized versions of `approx` (see [approxTime](#)) are available.
- `solver`: a function or a character string specifying the numerical algorithm used, e.g. `"lsoda"`, `"rk4"` or `"euler"` from package `deSolve`). In addition, solvers from package `"dodesolve"` can also be used. In contrast to `"euler"` that can be used for difference equations (i.e. `main` returns derivatives), `"iterator"` is intended for models where `main` returns the new state (i.e. for individual-based models). It is also possible to reference own algorithms (solvers) that are defined in the user workspace or to assign solver functions directly.
- `observer`: optional slot which determines the data stored during the simulation. A user-provided observer function can also be used to write logging information to the screen or to the hard-disk, to perform run-time visualisation, or statistical analysis during the simulation. Note that the observer-mechanism works only with [iteration](#) solvers. It is generally not available for `odeModels`.
- `out`: this slot holds the simulation results after a simulation run as data frame (if the return value of `main` is a vector) or as list (otherwise). The type of data stored in `out` can be manipulated by providing a user-defined observer function.
- `initfunc`: this slot can hold an optional function which is called automatically when a new object is created by `new` or when it is re-initialized by `initialize` or `sim`.

`simObj` model objects should be defined and created using the common S4 mechanisms ([new](#)).

In this way, a `simObj` object may contain all data, which are needed to run simulations simply by entering the model object via `source()` or `data()` and then to run and plot the model for example via `plot(sim(obj))`.

Accessor functions (with names identical to the slot names) are provided to get or set model parameters, time steps, initial values, inputs, the solver, the main and sub-equations or `initfunc` or to extract the model outputs. It is also possible to modify the components of the `simecol` objects directly, e.g. the model equations of a model `lv` with `lv@main`, but this is not recommended as there is no guarantee that this will work in a compatible way in future versions.

Models of different type are provided as data and some more in source code (see directory examples).

The examples are intended as a starting point to write your own `simObj` objects and to distribute them to whomever you wish.

The package is supplemented with several utility functions (e.g. [seedfill](#) or [neighbours](#)), which can be used independently from `simObj` objects.

Author(s)

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References

Petzoldt, T and K. Rinke (2007) **simecol**: An Object-Oriented Framework for Ecological Modeling in R. *Journal of Statistical Software*, **22**(9). URL <http://www.jstatsoft.org/v22/i09/>.

See Also

[CA](#), [chemostat](#), [conway](#), [diffusion](#), [lv](#), [lv3](#), [upca](#).

Examples

```
## (1) Quick Start Examples =====

data(lv)          # load basic Lotka-Volterra model

## Not run:
fixParms(lv)

## End(Not run)
parms(lv)
main(lv)
lv <- sim(lv)
plot(lv)
results <- out(lv)

## Not run:
data(conway)     # Conway's game of life
init(conway) <- matrix(0, 10, 10)
times(conway) <- 1:100
fixInit(conway) # enter some "1"
sim(conway, animate=TRUE, delay=100)

## End(Not run)

## (2) Define and run your own simecol model =====

lv <- new("odeModel",
  main = function (time, init, parms) {
    with(as.list(c(init, parms)), {
      dn1 <- k1 * N1 - k2 * N1 * N2
      dn2 <- - k3 * N2 + k2 * N1 * N2
      list(c(dn1, dn2))
    })
  },
  parms = c(k1 = 0.2, k2 = 0.2, k3 = 0.2),
  times = c(from = 0, to = 100, by = 0.5),
  init = c(N1 = 0.5, N2 = 1),
  solver = "lsoda"
)
```

```

lv <- sim(lv)
plot(lv)

## (3) The same in matrix notation; this allows generalization      =====
##     to multi-species interaction models with > 2 species.      =====

LVPP <- new("odeModel",
  main = function(t, n, parms) {
    with(parms, {
      dn <- r * n + n * (A %% n)
      list(c(dn))
    })
  },
  parms = list(
    # growth/death rates
    r = c(k1 = 0.2, k3 = -0.2),
    # interaction matrix
    A = matrix(c(0.0, -0.2,
                 0.2,  0.0),
              nrow = 2, ncol = 2, byrow=TRUE)
  ),
  times = c(from = 0, to = 100, by = 0.5),
  init   = c(N1 = 0.5, N2 = 1),
  solver = "lsoda"
)

plot(sim(LVPP))

## (4) Additional resources =====

## Not run:
## open the directory with source code of demo
browseURL(paste(system.file(package="simecol"), "/demo", sep=""))

## run demo
demo(jss)

## open the directory with R sourcecode examples
browseURL(paste(system.file(package="simecol"), "/doc/examples", sep=""))

## show package vignette with introductory article
vignette("simecol-introduction")
edit(vignette("simecol-introduction"))

## open the installation directory of simecol
## (NEWS, THANKS, FAQ, ToDo, WISHLIST, ...)
browseURL(paste(system.file(package="simecol"), "/", sep=""))

## Open Project Homepage
browseURL("http://www.simecol.de")

```

```
## End(Not run)

## How to cite package simecol in publications
citation("simecol")
```

addtoenv	<i>Add Functions from a Non-nested List of Named Functions to a Common Environment</i>
----------	--

Description

Create and set an environment where functions within a non-nested named list of functions see each other. This function is normally used within other functions.

Usage

```
addtoenv(L, p = parent.frame())
```

Arguments

L	a non-nested list of named functions.
p	the environment where the functions are assigned to. Defaults to the parent frame.

Details

This function is used by the ‘solver functions’ of `simecol`.

Value

The list of equations within a common environment.

Note

This is a very special function that uses environment manipulations. Its purpose is to ‘open’ the access to interdependent functions within a common list structure (function list).

See Also

[attach](#), [environment](#)

Examples

```

eq <- list(f1 = function(x, y) x + y,
          f2 = function(a, x, y) a * f1(x, y)
          )

fx <- function(eq) {
  eq <- addtoenv(eq)
  print(ls())
  print(environment(eq$f1))
  f1(3,4) + f2(1,2,3)
}

fx(eq)
## eq$f2(2,3,4)      # should give an error outside fx
environment(eq$f2)   # should return R_GlobalEnv again

```

approxTime

Linear Interpolation with Complete Matrices or Data Frames

Description

Return a data frame, matrix or vector which linearly interpolates data from a given matrix or data frame.

Usage

```

approxTime(x, xout, ...)
approxTime1(x, xout, rule = 1)

```

Arguments

x	a matrix or data frame with numerical values giving coordinates of points to be interpolated. The first column is interpreted as independent variable (e.g. time), the remaining columns as dependend variables.
xout	a vector (or single value for approxTime1) of independent values specifying where interpolation has to be done.
rule	an integer describing how interpolation is to take place outside the interval $[\min(x), \max(x)]$. If rule is 1 then NAs are returned for such points and if it is 2, the value at the closest data extreme is used.
...	optional parameters passed to approx.

Details

The functions can be used for linear interpolation with a complete matrix or data frame. This can be used for example in the main function of an odeModel to get input values at a specified time xout. The version approxTime1 is less flexible (only one single value for xout and only linear interpolation) but has increased performance. Both functions are faster if x is a matrix instead of a data frame.

Value

approxTime returns a matrix resp. data frame of the same structure as x containing data which interpolate the given data with respect to xout. approxTime1 is a performance optimized special version with less options than the original approx function. It returns an interpolated vector.

See Also

[approxfun](#)

Examples

```
inputs <- data.frame(time = 1:10, y1 = rnorm(10), y2 = rnorm(10, mean = 50))
input  <- approxTime(inputs, c(2.5, 3), rule = 2)
```

as.simObj

Coerce simObj Objects to Lists and Vice-Versa

Description

These functions can be used to coerce (i.e. convert) **simecol** model objects (simObj objects) to ordinary lists.

Usage

```
## S4 method for signature 'list'
as.simObj(x, ...)
## S4 method for signature 'simObj'
as.list(x, ...)
## alternative usage:
# as(x, "list")
# as(x, "simObj")
```

Arguments

```
x          object to be coerced
...        for compatibility
```

Details

Function as.list converts a simObj model to an ordinary list with an additional element 'class' storing the class name of the original object.

Function as.simObj converts in the opposite direction where the type of the object to be created is determined by a class name stored in the list element 'class'. If it is missing or contains a non-existing class name, an error message is printed. Additional list elements which are not slot names of the corresponding S4 object are omitted.

See Also

[odeModel](#), [new](#), [as](#), [as.list](#), [simecol-package](#)

Examples

```
data(lv3)
llv3 <- as(lv3, "list")
olv3 <- as(llv3, "simObj")

llv3 <- as.list(lv3)
olv3 <- as.simObj(llv3)

dput(as.list(lv3), control="useSource")
## Not run:
## save human readable object representation
dput(as.list(lv3), file="lv3.R", control=c("all"))
## read it back and test it
l_lv3 <- dget("lv3.R")
o_lv3 <- as.simObj(l_lv3)
plot(sim(o_lv3))

## End(Not run)
```

Description

simecol example: This model simulates a stochastic cellular automaton.

Usage

```
data(conway)
```

Format

An S4 object according to the [gridModel](#) specification. The object contains the following slots:

main functions with the state transition rules of Coway's Game of Life.

parms a list with two vector elements:

pbirth probability of birth,

pdeath death probability, dependend on neighbors.

times number of time steps to be simulated.

init a matrix, giving the initial state of the cellular grid (default: rectangle in the middle of the grid).

Details

To see all details, please have a look into the implementation below.

See Also

[sim](#), [parms](#), [init](#), [times](#).

Examples

```
#####
## Basic Usage:
##   work with the example
#####
data(CA)
times(CA)["to"] <- 10
plot(sim(CA))

set.seed(345)
times(CA)["to"] <- 50
CA <- sim(CA)

library(lattice)
tcol <- (terrain.colors(13))[-13]
x <- out(CA, last=TRUE)
x <- ifelse(x == 0, NA, x)
levelplot(x,
  cuts = 11,
  col.regions = tcol,
  colorkey = list(at = seq(0, 55, 5))
)

#####
## Implementation:
##   The code of the CA model
#####
CA <- new("gridModel",
  main = function(time, init, parms) {
    z <- init
    nb <- eightneighbors(z)
    pgen <- 1 - (1 - parms$pbirth)^nb
    zgen <- ifelse(z == 0 &
      runif(z) < pgen, 1, 0)
    zsurv <- ifelse(z >= 1 &
      runif(z) < (1 - parms$pdeath),
      z + 1, 0)
    zgen + zsurv
  },
  parms = list(pbirth = 0.02, pdeath = 0.01),
  times = c(from = 1, to = 50, by = 1),
  init = matrix(0, nrow = 40, ncol = 40),
  solver = "iteration"
)
```

```
init(CA)[18:22,18:22] <- 1
##=====
```

chemostat *Chemostat Model*

Description

simecol example: Model of continuous culture of microorganisms (chemostat).

Usage

```
data(chemostat)
```

Format

An S4 object according to the [odeModel](#) specification. The object contains the following slots:

main the differential equations for substrate (S) and cells (X).

parms a vector with the named parameters of the model:

vm maximum growth rate of the cells,

km half saturation constant,

Y yield coefficient (conversion factor of substrate into cells).

D dilution rate,

S0 substrate concentration in the inflow.

times simulation time and integration interval.

init vector with start values for substrate (S) and cells (X).

To see all details, please have a look into the implementation below.

See Also

[simecol-package](#), [sim](#), [parms](#), [init](#), [times](#).

Examples

```
##=====
## Basic Usage:
## work with the example
##=====
data(chemostat)
plot(sim(chemostat))

parms(chemostat)["D"] <- 0.9
plot(sim(chemostat))
```

```

#####
## Implementation:
## The code of the chemostat model
#####
chemostat <- new("odeModel",
  main = function(time, init, parms, inputs = NULL) {
    with(as.list(c(init, parms)), {
      mu <- vm * S/(km + S)          # Monod equation
      dx1 <- mu * X - D * X         # cells, e.g. algae
      dx2 <- D *(S0 - S) - 1/Y * mu * X # substrate, e.g. phosphorus
      list(c(dx1, dx2))
    })
  },
  parms = c(
    vm = 1.0,          # max growth rate, 1/d
    km = 2.0,          # half saturation constant, mumol / L
    Y = 100,           # cells /mumol Substrate
    D = 0.5,           # dilution rate, 1/d
    S0 = 10            # substrate in inflow, mumol / L
  ),
  times = c(from=0, to=40, by=.5),
  init = c(X=10, S=10), # cells / L; Substrate umol / L
  solver = "lsoda"
)

```

 conway

The Classical Conway's Game of Life

Description

simecol example: This model simulates a deterministic cellular automaton.

Usage

```
data(conway)
```

Format

An S4 object according to the [gridModel](#) specification. The object contains the following slots:

main functions with the state transition rules.

parms A list with two vector elements:

srv number of neighbours, necessary to survive,

gen number of neighbours, necessary to generate a new cell.

times number of time steps to be simulated,

init matrix with the initial state of the cellular grid (default: random).

Details

To see all details, please have a look into the implementation below.

References

Gardner, Martin (1970) The Fantastic Combinations of John Conway's New Solitaire Game 'Life.' *Scientific American*, October 1970.

See Also

[sim](#), [parms](#), [init](#), [times](#).

Examples

```
##=====
## Basic Usage:
##   explore the example
##=====
data(conway)
plot(sim(conway))

## more interesting start conditions
m <- matrix(0, 40, 40)
m[5:35, 19:21] <- 1
init(conway) <- m
plot(sim(conway), col=c("white", "green"), axes = FALSE)

## change survival rules
parms(conway) <- list(srv = c(3,4), gen = c(3, 4))
plot(sim(conway), col = c("white", "green"), axes = FALSE)
## Not run:
init(conway) <- matrix(0, 10, 10)
fixInit(conway) # enter some "1"
sim(conway, animate = TRUE, delay = 100)

##=====
## Implementation:
##   The code of Conways Game of Life
##=====
conway <- new("gridModel",
  main = function(time, init, parms) {
    x <- init
    nb <- eightneighbours(x)
    surviv <- (x > 0 & (nb
    gener <- (x == 0 & (nb
    x <- (surviv + gener) > 0
    return(x)
  },
  parms = list(srv = c(2, 3), gen = 3),
  times = 1:17,
  init = matrix(round(runif(1000)), ncol = 40),
  solver = "iteration"
```

```
)
## End(Not run)
```

diffusion

A Random Walk Particle Diffusion Model

Description

simecol example: This is a random walk (basic particle diffusion) model.

Usage

```
data(diffusion)
```

Format

An S4 object according to the [rwalkModel](#) specification. The object contains the following slots:

main A function with the movement rules for the particles.

parms A list with the following components:

ninds number of simulated particles,

speed speed of the particles,

area vector with 4 elements giving the coordinates (left, bottom, right, top) of the coordinate system.

times Simulation time (discrete time steps, by-argument ignored).

init Data frame holding the start properties (Cartesian coordinates x and y and movement angle a) of the particles.

Details

To see all details, please have a look into the implementation.

See Also

[sim](#), [parms](#), [init](#), [times](#).

Examples

```
##=====
## Basic Usage:
##   explore the example
##=====
## Not run:
data(diffusion)
## (1) minimal example
plot(sim(diffusion))
```

```

## show "grid of environmental conditions"
image(inputs(diffusion))

## (2) scenario
##   with homogeneous environment (no "refuge" in the middle)
no_refuge <- diffusion # Cloning of the whole model object
inputs(no_refuge) <- matrix(1, 100, 100)
plot(sim(no_refuge))

##=====
## Advanced Usage:
##   Assign a function to the observer-slot.
##=====
observer(diffusion) <- function(state, ...) {
  ## numerical output to the screen
  cat("mean x=", mean(state$x),
      ", mean y=", mean(state$y),
      ", sd   x=", sd(state$x),
      ", sd   y=", sd(state$y), "\n")
  ## animation
  par(mfrow=c(2,2))
  plot(state$x, state$y, xlab="x", ylab="y", pch=16, col="red", xlim=c(0, 100))
  hist(state$y)
  hist(state$x)
  ## default case: return the state --> iteration stores it in "out"
  state
}

sim(diffusion)

## remove the observer and restore original behavior
observer(diffusion) <- NULL
diffusion <- sim(diffusion)

## End(Not run)

##=====
## Implementation:
##   The code of the diffusion model.
##   Note the use of the "initfunc"-slot.
##=====
diffusion <- rwalkModel(
  main = function(time, init, parms, inputs = NULL) {
    speed <- parms$speed
    xleft <- parms$area[1]
    xright <- parms$area[2]
    ybottom <- parms$area[3]
    ytop <- parms$area[4]

    x <- init$x # x coordinate
    y <- init$y # y coordinate
    a <- init$a # angle (in radians)
    n <- length(a)

```

```

## Rule 1: respect environment (grid as given in "inputs")
## 1a) identify location on "environmental 2D grid" for each individual
i.j <- array(c(pmax(1, ceiling(x)), pmax(1, ceiling(y))), dim=c(n, 2))

## 1b) speed dependend on "environmental conditions"
speed <- speed * inputs[i.j]

## Rule 2: Random Walk
a <- (a + 2 * pi / runif(a))
dx <- speed * cos(a)
dy <- speed * sin(a)
x <- x + dx
y <- y + dy

## Rule 3: Wrap Around
x <- ifelse(x > xright, xleft, x)
y <- ifelse(y > ytop, ybottom, y)
x <- ifelse(x < xleft, xright, x)
y <- ifelse(y < ybottom, ytop, y)
data.frame(x=x, y=y, a=a)
},
times = c(from=0, to=100, by=1),
parms = list(ninds=50, speed = 1, area = c(0, 100, 0, 100)),
solver = "iteration",
initfunc = function(obj) {
  ninds <- obj@parms$ninds
  xleft <- obj@parms$area[1]
  xright <- obj@parms$area[2]
  ybottom <- obj@parms$area[3]
  ytop <- obj@parms$area[4]
  obj@init <- data.frame(x = runif(ninds) * (xright - xleft) + xleft,
                        y = runif(ninds) * (ytop - ybottom) + ybottom,
                        a = runif(ninds) * 2 * pi)
  inp <- matrix(1, nrow=100, ncol=100)
  inp[, 45:55] <- 0.2
  inputs(obj) <- inp
  obj
}
)

```

eightneighbours

Count Number of Neighbours in a Rectangular Cellular Grid.

Description

This function returns the sum of the eight neighbours of a cell within a matrix. It can be used to simulate simple cellular automata, e.g. Conway's Game of Life.

Usage

```
eightneighbours(x)
eightneighbors(x)
```

Arguments

`x` The cellular grid, which typically contains integer values of zero (dead cell) or one (living cell).

Value

A matrix with the same structure as `x`, but with the sum of the neighbouring cells of each cell.

See Also

[seedfill](#), [neighbours](#), [conway](#)

Examples

```
n <- 80; m <- 80
x <- matrix(rep(0, m*n), nrow = n)
x[round(runif(1500, 1, m*n))] <- 1
## uncomment this for another figure
#x[40, 20:60] <- 1

image(x, col=c("wheat", "grey", "red"))
x2 <- x
for (i in 2:10){
  nb <- eightneighbours(x)

  ## survive with 2 or 3 neighbours
  xsurv <- ifelse(x > 0 & (nb == 2 | nb ==3), 1, 0)

  ## generate for empty cells with 3 neighbours
  xgen <- ifelse(x == 0 & nb == 3, 1, 0)

  x <- ((xgen + xsurv)>0)
  x2 <- ifelse(x2>1, 1, x2)
  x2 <- ifelse(x>0, 2, x2)

  image(x2, col=c("wheat", "grey", "red"), add=TRUE)
}
```

Description

Fit parameters of `odeModel` objects to measured data.

Usage

```
fitOdeModel(simObj, whichpar = names(params(simObj)), obstime, yobs,
  sd.yobs = as.numeric(lapply(yobs, sd)), initialize = TRUE,
  weights = NULL, debuglevel = 0, fn = ssqOdeModel,
  method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", "PORT"),
  lower = -Inf, upper = Inf, scale.par = 1,
  control = list(), ...)
```

Arguments

simObj	a valid object of class <code>odeModel</code> ,
whichpar	character vector with names of parameters which are to be optimized (subset of parameter names of the <code>simObj</code>),
obstime	vector with time steps for which observational data are available,
yobs	data frame with observational data for all or a subset of state variables. Their names must correspond exactly with existing names of state variables in the <code>odeModel</code> ,
sd.yobs	vector of given standard deviations (or scale) for all observational variables given in <code>yobs</code> . If no standard deviations (resp. scales) are given, these are estimated from <code>yobs</code> ,
initialize	optional boolean value whether the <code>simObj</code> should be re-initialized after the assignment of new parameter values. This can be necessary in certain models to assign consistent values to initial state variables if they depend on parameters.
weights	optional weights to be used in the fitting process. See cost function (currently only <code>ssqOdeModel</code>) for details.
debuglevel	a positive number that specifies the amount of debugging information printed,
fn	objective function, i.e. function that returns the quality criterium that is minimized, defaults to <code>ssqOdeModel</code> ,
method	optimization method, see <code>nlminb</code> for the PORT algorithm and <code>optim</code> for all other methods,
lower, upper	bounds of the parameters for method L-BFGS-B, see <code>optim</code> and for method PORT see <code>nlminb</code> . The bounds are also respected by other optimizers by means of an internal transformation of the parameter space (see <code>p.constrain</code>). In this case, <i>named vectors</i> are required.
scale.par	scaling of parameters for method PORT see <code>nlminb</code> . In many cases, automatic scaling (<code>scale.par = 1</code>) does well, but sometimes (e.g. if parameter ranges differ several orders of magnitude) manual adjustment is required. Often you get a reasonable choice if you set <code>scale.par = 1/upper</code> . The parameter is ignored by all other methods. For "Nelder-Mead", "BFGS", "CG" and "SANN" parameter scaling occurs as a side effect of parameter transformation with <code>p.constrain</code> .
control	a list of control parameters for <code>optim</code> resp. <code>nlminb</code> ,
...	additional parameters passed to the solver method (e.g. to <code>lsoda</code>).

Details

This function works currently only with `odeModel` objects where `parms` is a vector, not a list.

Note also that the control parameters of the PORT algorithm are different from the control parameters of the other optimizers.

Value

A list with the optimized parameters and other information, see `optim` resp. `nlminb` for details.

Note

The interface to the PORT algorithm will change for future R versions.

References

Gay, D. M. (1990) Usage Summary for Selected Optimization Routines. Computing Science Technical Report No. 153. AT&T Bell Laboratories, Murray Hill, NJ. <http://netlib.bell-labs.com/cm/cs/cstr/153.pdf>

See Also

`ssqOdeModel`, `optim`

Note also that package **FME** function `modFit` has even more flexible means to fit model parameters.

Examples are given in the package vignettes.

Examples

```
## ===== load example model =====
data(chemostat)

#source("chemostat.R")

## derive scenarios
cs1 <- cs2 <- chemostat

## generate some noisy data
parms(cs1)[c("vm", "km")] <- c(2, 10)
times(cs1) <- c(from=0, to=20, by=2)
yobs <- out(sim(cs1))
obstime <- yobs$time
yobs$time <- NULL
yobs$S <- yobs$S + rnorm(yobs$S, sd= 0.1 * sd(yobs$S))*2
yobs$X <- yobs$X + rnorm(yobs$X, sd= 0.1 * sd(yobs$X))

## ===== optimize it! =====

## time steps for simulation, either small for rk4 fixed step
# times(cs2)["by"] <- 0.1
# solver(cs2) <- "rk4"
```

```

## or, faster: use lsoda and return only required steps that are in the data
times(cs2) <- obstime
solver(cs2) <- "lsoda"

## Nelder-Mead (default)
whichpar <- c("vm", "km")

res <- fitOdeModel(cs2, whichpar=whichpar, obstime, yobs,
  debuglevel=0,
  control=list(trace=TRUE))

res$par
## assign fitted parameters to the model, i.e. as start values for next step
parms(cs2)[whichpar] <- res$par

## alternatively, L-BFGS-B (allows lower and upper bounds for parameters)
res <- fitOdeModel(cs2, whichpar=c("vm", "km"), obstime, yobs,
  debuglevel=0, fn = ssqOdeModel,
  method = "L-BFGS-B", lower = 0,
  control=list(trace=TRUE),
  atol=1e-4, rtol=1e-4)

res$par

## alternative 2, transform parameters to constrain unconstrained method
## Note: lower and upper are *named* vectors
res <- fitOdeModel(cs2, whichpar=c("vm", "km"), obstime, yobs,
  debuglevel=0, fn = ssqOdeModel,
  method = "BFGS", lower = c(vm=0, km=0), upper=c(vm=4, km=20),
  control=list(trace=TRUE),
  atol=1e-4, rtol=1e-4)

res$par

## alternative 3a, use PORT algorithm
## Note: lower and upper are *named* vectors
parms(cs2)[whichpar] <- c(vm=1, km=2)

lower <- c(vm=0, km=0)
upper <- c(vm=4, km=20)

res <- fitOdeModel(cs2, whichpar=c("vm", "km"), obstime, yobs,
  debuglevel=0, fn = ssqOdeModel,
  method = "PORT", lower = lower, upper = upper,
  control=list(trace=TRUE),
  atol=1e-4, rtol=1e-4)

res$par

## alternative 3b, PORT algorithm with manual parameter scaling
## Note: lower and upper are *named* vectors

```

```

res <- fitOdeModel(cs2, whichpar=c("vm", "km"), obstime, yobs,
  debuglevel=0, fn = ssqOdeModel,
  method = "PORT", lower = lower, upper = upper, scale.par = 1/upper,
  control=list(trace=TRUE),
  atol=1e-4, rtol=1e-4)

res$par

## set model parameters to fitted values and simulate again
parms(cs2)[whichpar] <- res$par
times(cs2) <- c(from=0, to=20, by=1)
ysim <- out(sim(cs2))

## plot results
par(mfrow=c(2,1))
plot(obstime, yobs$X, ylim = range(yobs$X, ysim$X))
lines(ysim$time, ysim$X, col="red")
plot(obstime, yobs$S, ylim= range(yobs$S, ysim$S))
lines(ysim$time, ysim$S, col="red")

```

fixParms

Fix 'parms', 'init' or 'times' Slot of 'simecol' Objects

Description

The functions invoke an editor dialog for parameters, initial values or time steps of `simObj` objects and then assign the new (edited) version of `x` in the user's workspace. A **Tcl/Tk** version or spreadsheet editor is displayed if possible, depending on the structure of the respective slot.

Usage

```

fixParms(x)
fixTimes(x)
fixInit(x)

```

Arguments

`x` A valid instance of the `simObj` class.

See Also

[sEdit](#), [simObj](#), [parms](#), [times](#), [init](#), [fix](#)

Examples

```
## Not run:
data(lv)      # load basic Lotka-Volterra model
fixParms(lv)
plot(sim(lv))

data(conway)  # Conway's game of life
init(conway) <- matrix(0, 10, 10)
fixInit(conway) # enter some "1"
sim(conway, animate = TRUE, delay = 100)

## End(Not run)
```

fromtoby

Create Regular Sequence from 'from-to-by' Vector

Description

This function creates a sequence from named vectors with the names from, to and by.

Usage

```
fromtoby(times)
```

Arguments

times A named vector with the names from, to and by.

Details

Named vectors with from, to and by can be used in **simecol** to specify time steps.

Value

The appropriate vector with a sequence, generated by seq.

See Also

[seq](#)

Examples

```
times <- c(from=1, to=5, by=0.1)
fromtoby(times)
```

initialize-methods *Methods for Function 'initialize' in Package 'simecol'*

Description

This function is used to initialize objects derived from the `simObj` superclass, it is by default automatically called during object creation and by `sim`.

Usage

```
## S4 method for signature 'simObj'
initialize(.Object, ...)
```

Arguments

`.Object` `simObj` instance which is to be re-initialized.
`...` provided for compatibility with the default method of `initialize`, or slots of the object which is to be created (in case of `new`).

Methods

.Object = "ANY" Generic function: see `new`.

.Object = "simObj" The `initialize` function is normally called implicitly by `new` to create new objects. It may also be called explicitly to return a cloned and re-initialized object.

The **simecol** version of `initialize` provides an additional mechanism to call a user specified function provided in the `initfunc` slot of a `simObj` instance that can perform computations during the object creation process. The `initfunc` must have `obj` as its only argument and must return the modified version of this `obj`, see examples below. As a side effect end to ensure consistency, `initialize` clears outputs stored in slot `out` from former simulations.

See Also

`simObj`, `new`

Examples

```
## Note: new calls initialize and initialize calls initfunc(obj)
lv_efr <- new("odeModel",
  main = function (time, init, parms, ...) {
    x <- init
    p <- parms
    S <- approxTime1(inputs, time, rule=2)["s.in"]
    dx1 <- S * p["k1"] * x[1] - p["k2"] * x[1] * x[2]
    dx2 <- - p["k3"] * x[2] + p["k2"] * x[1] * x[2]
    list(c(dx1, dx2))
  },
  parms = c(k1=0.2, k2=0.2, k3=0.2),
  times = c(from=0, to=100, by=0.5),
```

```

init = c(pre=0.5, predator=1),
solver = "lsoda",
initfunc = function(obj) {
  tt <- fromtoby(times(obj))
  inputs(obj) <- as.matrix(data.frame(
    time = tt,
    s.in = pmax(rnorm(tt, mean=1, sd=0.5), 0)
  ))
  obj
}
)
plot(sim(lv_efr)) # initialize called automatically
plot(sim(lv_efr)) # automatic initialization, different figure

lv_efr<- initialize(lv_efr) # re-initialize manually
plot(sim(lv_efr, initialize = FALSE)) # simulation with that configuration

```

iteration

Discrete Simulation

Description

Solver function to simulate discrete ecological (or other) dynamic models. It is normally called indirectly from `sim`.

Usage

```
iteration(y, times=FALSE, func=FALSE, parms=FALSE, animate = FALSE, ...)
```

Arguments

<code>y</code>	the initial values for the system. If <code>y</code> has a <code>names</code> attribute, the names will be used to label the output matrix.
<code>times</code>	times at which explicit estimates for <code>y</code> are desired. The first value in <code>times</code> must be the initial time.
<code>func</code>	<p>a user-supplied function that computes the values of the <i>next time step</i> (not the derivatives !!!) in the system (the <i>model definition</i>) at time <code>t</code>. The user-supplied function <code>func</code> must be called as: <code>yprime = func(t, y, parms)</code>. <code>t</code> is the current time point in the integration, <code>y</code> is the current estimate of the variables in the ode system, and <code>parms</code> is a vector of parameters (which may have a <code>names</code> attribute, desirable in a large system).</p> <p>The return value of <code>func</code> should be a list, whose first element is a vector containing the derivatives of <code>y</code> with respect to time, and whose second element is a vector (possibly with a <code>names</code> attribute) of global values that are required at each point in <code>times</code>.</p>

parms	vector or list holding the parameters used in func that should be modifiable without rewriting the function.
animate	Animation during the simulation (if available for the specified class.
...	optional arguments passed to the plot function if animate=TRUE.

Details

The solver method `iteration` is used to simulate discrete event models. Normally, this function is run indirectly from `sim`.

In contrast to differential equation solvers, the main function of the model must not return the first derivative but instead and explicitly the new state at the specified times.

The actual value of time is available in the main function as `time` and the current increment as `parms["DELTAT"]` or `parms$DELTAT`. It is element of a vector if `parms` is a vector and it is a list if `parms` is a list.

If `iteration` is used for difference equations (see example `dlogist` below), it is mandatory to multiply the incremental part with `DELTAT` to ensure that variable time steps are correctly respected and that the first row of the simulation outputs contains the states at t_0 .

The default `iteration` method of class `simObj` supports the observer mechanism. This means that a function stored in slot `observer` is called during each iteration step with the return value of `main` as its first argument. You can use this to control the amount of data stored during each iteration step (e.g. whole population or only mean values for individual based models), to do run-time animation or to write log files.

Value

A list of the model outputs (states ...) for each timestep.

See Also

[sim](#), [observer](#), [parms](#), [lsoda](#), [rk4](#), [euler](#).

Examples

```
data(conway)
## plot after simulation:
plot(sim(conway), delay=100)

## plot during simulation
sim(conway, animate=TRUE, delay=100)

## discrete version of logistic growth equation
## Note: function main returns the *new value*, not the derivative

dlogist <- new("odeModel",
  main = function (time, init, parms, ...) {
    x <- init
    with(as.list(parms), {
      x <- x + r * x * (1 - x / K) * DELTAT
      #   ^^^ add to old value          ^^^^^^ special parameter with time step
```

```

        list(c(x))
      })
    },
    parms = c(r=0.1, K=10),
    times = seq(0, 100, 1),
    init = c(population=0.1),
    solver = "iteration" #!!!
  )

plot(sim(dlogist))

## alternative with function that returns the derivative
## discrete steps are realized with the euler method

dlogist <- new("odeModel",
  main = function (time, init, parms, ...) {
    x <- init
    with(as.list(parms), {
      x <- r * x * (1 - x / K)
      list(c(x))
    })
  },
  parms = c(r=0.1, K=10),
  times = seq(0, 100, 1),
  init = c(population=0.1),
  solver = "euler"
)

plot(sim(dlogist))

```

listOrNULL-class

Helpful Union Classes

Description

Classes representing either list or NULL (i.e. empty), function or NULL, function or character vector, numeric vector or list, or list or data.frame.

Objects from the Class

These classes are virtual: No objects may be created from it.

Methods

No methods exist for these classes.

See Also

[simObj](#)

 lv *Lotka-Volterra Predator-Prey Model*

Description

simecol example: basic Lotka-Volterra predator prey-model.

Usage

data(lv)

Format

An S4 object according to the [odeModel](#) specification. The object contains the following slots:

main Lotka-Volterra equations for predator and prey.

parms Vector with the named parameters of the model:

 k1 growth rate of the prey population,

 k2 encounter rate of predator and prey,

 k3 death rate of the predator population.

times Simulation time and integration interval.

init Vector with start values for predator and prey.

Details

To see all details, please have a look into the implementation.

References

Lotka, A. J. 1925. *Elements of physical biology*. Williams and Wilkins, Baltimore.

Volterra, V. (1926). *Variazione e fluttuazioni del numero d'individui in specie animali conviventi*. *Mem. Acad.Lincei*, **2**, 31-113.

See Also

[simecol-package](#), [sim](#), [parms](#), [init](#), [times](#).

Examples

```
##=====
## Basic Usage:
##   explore the example
##=====
data(lv)
print(lv)
plot(sim(lv))
```

```

parms(lv) <- c(k1=0.5, k2=0.5, k3=0.5)
plot(sim(lv))

##=====
## Implementation:
## The code of the Lotka-Volterra-model
##=====
lv <- new("odeModel",
  main = function (time, init, parms) {
    x <- init
    p <- parms
    dx1 <- p["k1"] * x[1] - p["k2"] * x[1] * x[2]
    dx2 <- - p["k3"] * x[2] + p["k2"] * x[1] * x[2]
    list(c(dx1, dx2))
  },
  parms = c(k1=0.2, k2=0.2, k3=0.2),
  times = c(from=0, to=100, by=0.5),
  init = c(pre=0.5, predator=1),
  solver = "rk4"
)

```

Description

simecol example: predator prey-model with three equations: predator, prey and resource (e.g. nutrients, grassland).

Usage

```
data(lv3)
```

Format

A valid S4 object according to the `odeModel` specification. The object contains the following slots:

main Lotka-Volterra equations for predator prey and resource.

parms Vector with named parameters of the model:

- c growth rate of the prey population,
- d encounter rate of predator and prey,
- e yield factor (allows conversion with respect to d),
- f death rate of the predator population,
- g recycling parameter.

inputs Time series specifying external delivery of resource.

times Simulation time and integration interval.

init Vector with start values for s, p and k.
 s Resource (e.g. grassland or phosphorus).
 p Producer (prey).
 k Consumer (predator).
 solver Character string specifying the integration method.

See Also

[simecol-package](#), [sim](#), [parms](#), [init](#), [times](#).

Examples

```

##=====
## Basic Usage:
##  explore the example
##=====
data(lv3)
plot(sim(lv3))
times(lv3)["by"] <- 5  # set maximum external time step to a large value
plot(sim(lv3))         # wrong! automatic time step overlooks internal inputs
plot(sim(lv3, hmax = 1)) # integration with correct maximum internal time step

##=====
## Implementation:
##  The code of the model
##=====
lv3 <- new("odeModel",
  main = function(time, init, parms, inputs) {
    s.in <- approxTime1(inputs, time, rule = 2)["s.in"]
    with(as.list(c(init, parms)),{
      ds <- s.in - b*s*p + g*k
      dp <- c*s*p - d*k*p
      dk <- e*p*k - f*k
      list(c(ds, dp, dk), s.in = s.in)
    })
  },
  parms = c(b = 0.1, c = 0.1, d = 0.1, e = 0.1, f = 0.1, g = 0),
  times = c(from = 0, to = 200, by = 1),
  inputs = as.matrix(
    data.frame(
      time = c(0, 99, 100, 101, 200),
      s.in = c(0.1, 0.1, 0.5, 0.1, 0.1)
    )
  ),
  init = c(s = 1, p = 1, k = 1), # substrate, producer, consumer
  solver = "lsoda"
)

```

 mixNamedVec

Mix Two Named Vectors, Resolving Name Conflicts

Description

The function mixes two named vectors. The resulting vectors contains all elements with unique name and only one of the two versions of the elements which have the same name in both vectors.

Usage

```
mixNamedVec(x, y, resolve.conflicts = c("x", "y"), warn = TRUE)
```

Arguments

x	first named vector,
y	second named vector,
resolve.conflicts	name of the vector from which all elements are taken,
warn	an indicator if a warning should be given if elements are not unique. This argument should usually set to FALSE, but the default is TRUE to be on the safe side.

Value

a vector with all elements from one vector and only these elements of the second, that have a unique name not contained in the other vector.

Author(s)

Thomas Petzoldt

See Also

[which](#)

Examples

```
x <- c(a=1, b=2, c=3)
y <- c(a=1, b=3, d=3)

mixNamedVec(x, y)
mixNamedVec(x, y, resolve.conflicts="x")

mixNamedVec(x, y, resolve.conflicts="x", warn=FALSE)
mixNamedVec(x, y, resolve.conflicts="y", warn=FALSE)

## without names, returns vector named in "resolve conflicts"
x <- as.vector(x)
```

```

y <- as.vector(y)
mixNamedVec(x, y)
mixNamedVec(x, y, resolve.conflicts="y")

## names partly
x <- c(4, a=1, b=2, c=3, 4, 9)
y <- c(a=1, 6, b=3, d=3, 8)

mixNamedVec(x, y)
mixNamedVec(x, y, resolve.conflicts="y")

```

neighbours

*Count Number of Neighbours on a Rectangular Grid.***Description**

This is the base function for the simulation of deterministic and stochastic cellular automata on rectangular grids.

Usage

```

neighbours(x, state = NULL, wdist = NULL, tol = 1e-4, bounds = 0)
neighbors(x, state = NULL, wdist = NULL, tol = 1e-4, bounds = 0)

```

Arguments

x	Matrix. The cellular grid, in which each cell can have a specific state value, e.g. zero (dead cell) or one (living cell) or the age of an individual.
state	A value, whose existence is checked within the neighbourhood of each cell.
wdist	The neighbourhood weight matrix. It has to be a square matrix with an odd number of rows and columns).
tol	Tolerance value for the comparison of state with the state of each cell. If tol is a large value, then more than one state can be checked simultaneously.
bounds	A vector with either one or four values specifying the type of boundaries, where 0 means open boundaries and 1 torus-like boundaries. The values are specified in the order bottom, left, top, right.

Details

The performance of the function depends on the size of the matrices and the type of the boundaries, where open boundaries are faster than torus like boundaries. Function [eightneighbours](#) is even faster.

Value

A matrix with the same structure as x with the weighted sum of the neighbours with values between $state - tol$ and $state + tol$.

See Also

[seedfill](#), [eightneighbours](#), [conway](#)

Examples

```
## =====
## Demonstration of the neighborhood function alone
## =====

## weight matrix for neighbourhood determination
wdist <- matrix(c(0.5,0.5,0.5,0.5,0.5,
                 0.5,1.0,1.0,1.0,0.5,
                 0.5,1.0,1.0,1.0,0.5,
                 0.5,1.0,1.0,1.0,0.5,
                 0.5,0.5,0.5,0.5,0.5), nrow=5)

## state matrix
n <- 20; m <- 20
x <- matrix(rep(0, m * n), nrow = n)

## set state of some cells to 1
x[10, 10] <- 1
x[1, 5] <- 1
x[n, 15] <- 1
x[5, 2] <- 1
x[15, m] <- 1
#x[n, 1] <- 1 # corner

opar <- par(mfrow = c(2, 2))
## start population
image(x)
## open boundaries
image(matrix(neighbours(x, wdist = wdist, bounds = 0), nrow = n))
## torus (donut like)
image(matrix(neighbours(x, wdist = wdist, bounds = 1), nrow = n))
## cylinder (left and right boundaries connected)
image(matrix(neighbours(x, wdist = wdist, bounds = c(0, 1, 0, 1)), nrow = n))
par(opar) # reset graphics area

## =====
## The following example demonstrates a "plain implementation" of a
## stochastic cellular automaton i.e. without the simecol structure.
##
## A simecol implementation of this can be found in
## the example directory of this package (file: stoch_ca.R).
## =====
mycolors <- function(n) {
  col <- c("wheat", "darkgreen")
  if (n>2) col <- c(col, heat.colors(n - 2))
  col
}
```

```

pj <- 0.99 # survival probability of juveniles
pa <- 0.99 # survival probability of adults
ps <- 0.1  # survival probability of senescent
ci <- 1.0  # "seeding constant"
adult <- 5 # age of adolescence
old   <- 10 # age of senescence

## Define a start population
n <- 80
m <- 80
x <- rep(0, m*n)

## stochastic seed
## x[round(runif(20,1,m*n))] <- adult
dim(x) <- c(n, m)

## rectangular seed in the middle
x[38:42, 38:42] <- 5

## plot the start population
image(x, col = mycolors(2))

## -----
## Simulation loop (hint: increase loop count)
## -----
for (i in 1:10){

  ## rule 1: reproduction
  ## 1.1 which cells are adult? (only adults can generate)
  ad <- ifelse(x >= adult & x < old, x, 0)

  ## 1.2 how much (weighted) adult neighbours has each cell?
  nb <- neighbours(ad, wdist = wdist)

  ## 1.3 a proportion of the seeds develops juveniles
  ## simplified version, you can also use probabilities
  genprob <- nb * runif(nb) * ci
  xgen <- ifelse(x == 0 & genprob >= 1, 1, 0)

  ## rule 2: growth and survival of juveniles
  xsurvj <- ifelse(x >= 1 & x < adult & runif(x) <= pj, x+1, 0)
  ## rule 2: growth and survival of adults
  xsurva <- ifelse(x >= adult & x < old & runif(x) <= pa, x+1, 0)
  ## rule 2: growth and survival of senescent
  xsurvs <- ifelse(x >= old & runif(x) <= ps, x+1, 0)

  ## make resulting grid of complete population
  x <- xgen + xsurvj + xsurva + xsurvs

  ## plot resulting grid
  image(x, col = mycolors(max(x) + 1), add = TRUE)
  if (max(x) == 0) stop("extinction", call. = FALSE)
}

```

```
## modifications: pa<-pj<-0.9

## additional statistics of population structure
## with table, hist, mean, sd, ...
```

observer *Get or Set an Observer Functions to an 'simObj' Object*

Description

Get or set a user-defined observer to enable user-specified storage of simulation results, visualisation or logging.

Usage

```
observer(obj, ...)
observer(obj) <- value
```

Arguments

obj	A valid <code>simObj</code> instance.
value	A function specifying an observer, see Details.
...	Reserved for method consistency.

Details

The observer can be used with solver `iteration` or a user-defined solver function. It does not work with differential equations solvers.

The observer is a function with the following arguments:

```
function(state)
```

or:

```
function(state, time, i, out, y)
```

Where `state` is the actual state of the system, `time` and `i` are the simulation time and the index of the time step respectively, `out` is the output of the actual simulation collected so far. The original object used in the simulation is passed via `y` and can be used to get access on parameter values or model equations.

If available, the observer function is called for every time step in the iteration. It can be used for calculations “on the fly” to reduce memory of saved data, for user-specified animation or for logging purposes.

If the value returned by observer is a vector, than resulting out will be a `data.frame`, otherwise it will be a list of all states.

Value

The observer function either modifies `obj` or it returns the assigned observer function or `NULL` (the default).

See Also

[iteration](#) for the iteration solver,
[parms](#) for accessor and replacement functions of other slots,
[simecol-package](#) for an overview of the package.

Examples

```
## load model "diffusion"
data(diffusion)

solver(diffusion) # solver is iteration, supports observer

### == Example 1 =====

## assign an observer for visualisation
observer(diffusion) <- function(state) {
  ## numerical output to the screen
  cat("mean x=", mean(state$x),
      ", mean y=", mean(state$y),
      ", sd  x=", sd(state$x),
      ", sd  y=", sd(state$y), "\n")
  ## animation
  par(mfrow = c(2, 2))
  plot(state$x, state$y, xlab = "x", ylab = "y", pch = 16,
       col = "red", xlim = c(0, 100))
  hist(state$y)
  hist(state$x)

  ## default case:
  ## return the state --> iteration stores full state in "out"
  state
}

sim(diffusion)

### == Example 2 =====

## an extended observer with full argument list
observer(diffusion) <- function(state, time, i, out, y) {
  ## numerical output to the screen
  cat("index =", i,
      ", time =", time,
      ", sd  x=", sd(state$x),
      ", sd  y=", sd(state$y), "\n")
  ## animation
```

```

par(mfrow = c(2, 2))
plot(state$x, state$y, xlab = "x", ylab = "y", pch = 16,
     col = "red", xlim = c(0, 100))
hist(state$y)
hist(state$x)
if (is.matrix(out)) # important because out may be NULL for the first call
  matplot(out[,1], out[,-1]) # dynamic graph of sd in both directions

## return a vector with summary information
c(times = time, sdx=sd(state$x), sdy=sd(state$y))
}

diffusion <- sim(diffusion)

### == Restore default =====

observer(diffusion) <- NULL # delete observer
diffusion <- sim(diffusion)

```

odeModel

*Generating-functions (Constructors) to Create Objects of Classes
'odeModel', 'rwalkModel' and 'gridModel'.*

Description

These functions can be used to create `simObj` instances without using `new` explicitly.

Usage

```

odeModel(obj = NULL, main = NULL,
         equations = NULL, times = c(from = 0, to = 10, by = 1),
         init = numeric(0), parms = numeric(0),
         inputs = NULL, solver = "rk4", initfunc = NULL)

gridModel(obj = NULL, main = NULL,
          equations = NULL, times = c(from=0, to=10, by=1),
          init = matrix(0), parms = list(),
          inputs = NULL, solver = "iteration", initfunc = NULL)

rwalkModel(obj = NULL, main = NULL,
           equations = NULL, times = c(from = 0, to = 10, by = 1),
           init = NULL, parms = list(),
           inputs = NULL, solver = "iteration", initfunc = NULL)

indbasedModel(obj = NULL, main = NULL,
              equations = NULL, times = c(from = 0, to = 10, by = 1),
              init = NULL, parms = list(),
              inputs = NULL, solver = "iteration", initfunc = NULL)

```

Arguments

obj	Unnamed arguments are regarded as objects of the corresponding class. If obj is omitted, the new object is created from scratch.
main	The main equations of the model.
equations	The sub-models (sub-equations and of the model).
times	A vector of time steps or a vector with three named values from, to, by specifying the simulation time steps. The 'from-to-by' form can be edited with fixParms.
init	Initial values (start values) of the state variable given as named vector.
parms	A vector or list (depending on the respective class) of constant parameters.
inputs	Optional time-dependent input variables (matrix or data frame).
solver	The solver used to integrate the model.
initfunc	The function is called by the initialize mechanism and allows direct access and manipulation of all slots of the object in creation

Details

These functions provide an alternative way to create simObj instances in addition to the standard S4 new mechanism. The functions are provided mainly for compatibility with older versions of **simecol**.

See [simecol-package](#) and the examples for details about the slots.

Value

The function returns an S4 object of type odeModel, rwalkModel, gridModel

See Also

[new](#), [simecol-package](#)

Examples

```
## (1) Define and run your own simecol model with new =====
lv <- new("odeModel",
  main = function (time, init, parms) {
    with(as.list(c(init, parms)), {
      dn1 <- k1 * N1 - k2 * N1 * N2
      dn2 <- - k3 * N2 + k2 * N1 * N2
      list(c(dn1, dn2))
    })
  },
  parms = c(k1 = 0.2, k2 = 0.2, k3 = 0.2),
  times = c(from = 0, to = 100, by = 0.5),
  init = c(N1 = 0.5, N2 = 1),
  solver = "lsoda"
)
```

```

## ... or use the generating function -----

lv <- odeModel(
  main = function (time, init, parms) {
    with(as.list(c(init, parms)), {
      dn1 <- k1 * N1 - k2 * N1 * N2
      dn2 <- - k3 * N2 + k2 * N1 * N2
      list(c(dn1, dn2))
    })
  },
  parms = c(k1 = 0.2, k2 = 0.2, k3 = 0.2),
  times = c(from = 0, to = 100, by = 0.5),
  init = c(N1 = 0.5, N2 = 1),
  solver = "lsoda"
)

lv <- sim(lv)
plot(lv)

## (2) Conway's Game of Life =====

set.seed(23) # to make it reproducible

conway <- new("gridModel",
  main = function(time, x, parms) {
    nb <- eightneighbours(x)
    surviv <- (x > 0 & (nb %in% parms$srv))
    gener <- (x == 0 & (nb %in% parms$gen))
    x <- (surviv + gener) > 0
    return(x)
  },
  parms = list(srv = c(2, 3), gen = 3),
  times = 1:17,
  init = matrix(round(runif(1000)), ncol=40),
  solver = "iteration"
)

sim(conway, animate=TRUE)

```

Description

These functions can be used to transform a vector of data or parameters between unconstrained $[-\text{Inf}, \text{Inf}]$ and box-constrained representation (interval $[\text{lower}, \text{upper}]$).

Usage

```
p.constrain(p, lower = -Inf, upper = Inf, f = 1)
p.unconstrain(p, lower = -Inf, upper = Inf, f = 1)
```

Arguments

`p` vector of data (e.g. model parameters),
`lower`, `upper` vectors with lower resp. upper bounds used for transformation,
`f` optional scaling factor.

Details

These functions are employed by `fitOdeModel` `ssqOdeModel` in order to be able to use the unconstrained optimizers of `optim` for constrained optimization.

The transformation functions are

$$p' = \tan(\pi/2 \cdot (2p - upper - lower)/(upper - lower)) \cdot 1/f$$

and its inverse

$$p = (upper + lower)/2 + (upper - lower) \cdot \arctan(f \cdot p')/\pi$$

Value

vector with transformed (resp. back-transformed) values.

References

This trick seems to be quite common, but in most cases it is preferred to apply optimizers that can handle constraints internally.

Reichert, T. (1998) AQUASIM 2.0 User Manual. Computer Program for the Identification and Simulation of Aquatic Systems. Swiss Federal Institute for Environmental Science and Technology (EAWAG), CH - 8600 Duebendorf Switzerland, http://www.aquasim.eawag.ch/e_aquasim_manual.html

See Also

[fitOdeModel](#), [ssqOdeModel](#)

Examples

```
xx <- seq(-100, 100, 2)
plot(xx, yy<-p.constrain(xx, -20, 45), type="l")
points(p.unconstrain(yy, -20, 45), yy, col="red")
```

parms

Accessor Functions for 'simObj' Objects

Description

Get or set simulation model parameters, main or sub-equations, initial values, time steps or solvers and extract simulation results.

Usage

```
parms(obj, ...)
parms(obj) <- value

main(obj, ...)
main(obj) <- value

equations(obj, ...)
equations(obj) <- value

init(obj, ...)
init(obj) <- value

inputs(obj, ...)
inputs(obj) <- value

times(obj, ...)
times(obj) <- value

solver(obj, ...)
solver(obj) <- value

#observer(obj, ...)
#observer(obj) <- value

initfunc(obj, ...)
initfunc(obj) <- value

out(obj, ...)
out(obj) <- value
```

Arguments

obj	A valid simObj instance.
value	Named list, vector, function or other data structure (depending on the slot and model class) with the same structure as the value returned by parms. Either all or a subset of values (e.g. single elements of vectors or lists) can be changed at once.

... Reserved for method consistency.

Details

These are the accessing functions for parms, times etc.

Please take care of the semantics of your model when changing slots. All, element names, data structure and values have to correspond to you model object definition. For example in `init` the applied names must exactly correspond to the names and number (!) of state variables. The restrictions of parms or equations are less strict (additional values for “future use” are allowed).

The function `times` allows either to assign or to modify a special vector with three elements named `from`, `to` and `by` or to overwrite `times` with an un-named sequence (e.g. `seq(1, 100, 0.1)`).

To ensure object consistency function `out` cannot assign arbitrary values. It can only extract or delete the contents (by assigning `NULL`) of the `out`-slot.

Value

A list, named vector, matrix or function (for main slot) or list of functions (equation slot) or other appropriate data structure depending on the class of the model object.

See Also

General explanation of the slots can be found in [simecol-package](#).

Usage of the observer slot is found in the special help file [observer](#).

Examples

```
data(lv)
parms(lv)
parms(lv) <- c(k1 = 0.2, k2 = 0.5, k3 = 0.3)
parms(lv)["k2"] <- 0.5

data(conway)
parms(conway)
parms(conway)$srv <- c(2, 2)
parms(conway)

## add a new named parameter value
parms(lv)["dummy"] <- 1
## remove dummy parameter
parms(lv) <- parms(lv)[names(parms(lv)) != "dummy"]

## simulation and extraction of outputs
lv <- sim(lv)
o <- out(lv)

## remove outputs from object
out(lv) <- NULL

## store object persistently to the disk
save(lv, file = "lv.Rdata") # in binary form
```

```
dput(as.list(lv), file = "lv-list.R") # in text form
```

pcuseries

Generate Plackett Bivariate Random Numbers

Description

Generate bivariate uniform random numbers according to the Plackett distribution.

Usage

```
pcu(x, alpha = rho2alpha(rho), rho)
pcuseries(n, alpha = rho2alpha(rho), rho, min = 0, max = 1)
alpha2rho(alpha)
rho2alpha(rho)
```

Arguments

n	number of observations.
x	vector of uniformly [0, 1] distributed real numbers.
alpha	association coefficient of the Plackett distribution.
rho	Pearson correlation coefficient.
min, max	lower and upper limits of the distribution. Must be finite.

Details

The functions can be used to generate bivariate distributions with uniform marginals. Function `pcu` generates a vector of uniform random values of `length(x)` which are correlated to the corresponding vector `x`, `pcuseries` generates an auto-correlated series, and `alphatorho` resp. `rho2alpha` convert between the usual correlation coefficient and the association measure of the Plackett distribution.

References

Johnson, M., Wang, C., & Ramberg, J. (1984). Generation of multivariate distributions for statistical applications. *American Journal of Mathematical and Management Sciences*, **4**, 225-248.

Nelsen, R. B. (2006). *An Introduction to Copulas*. Springer, New York.

See Also

[runif](#)

Examples

```
x <- runif(100)
y <- pcu(x, rho = 0.8)
plot(x, y)
cor(x, y)

x <- pcuseries(1000, rho=0.8)
plot(x, type="l")
acf(x)
pacf(x)
```

peaks

Find Peaks Within xy-Data

Description

The function returns maxima (values which have only smaller neighbours) and minima (values which have only larger neighbours).

Usage

```
peaks(x, y=NULL, mode="maxmin")
```

Arguments

x, y	the coordinates of given points.
mode	specifies if both maxima and minima (mode="maxmin") or only maxima (mode="max") or minima (mode="min") are requested.

Value

A list with x and y coordinates of all peaks.

See Also

[approx](#), [upca](#)

Examples

```
x <- sin(seq(0, 10, 0.1))
plot(x)
points(peaks(x), col="red", pch=15)
```

Description

Methods for function plot in package **simecol**.

Usage

```

## S4 method for signature 'simObj,missing'
plot(x, y, ...)
## S4 method for signature 'odeModel,missing'
plot(x, y, ...)
## S4 method for signature 'odeModel,odeModel'
plot(x, y, ...)
## S4 method for signature 'gridModel,missing'
plot(x, y, index=1:length(x@out), delay=0, ...)
## S4 method for signature 'rwalkModel,missing'
plot(x, y, index=1:length(x@out), delay=0, ...)

```

Arguments

x	an object of class <code>simObj</code> ,
y	either a second <code>odeModel</code> object or ignored,
index	index of time steps to be plotted,
delay	delay (in ms) between consecutive images (for <code>gridModels</code>) or xy-plots (for <code>rwalkModels</code>),
...	optional plotting parameters.

Methods

x = "ANY", y = "ANY" Generic function: see [plot](#).

x = "simObj", ... template function, does nothing and only issues a warning.

x = "odeModel", ... plots time series of the state variables where one or more `odeModel` objects can be supplied. Optional plotting parameters are possible, too. See [plot.deSolve](#) for details.

x = "gridModel", ... displays a series of images for the simulated grid.

x = "rwalkModel", ... displays a series of x-y plots of the simulated individuals.

print-methods	<i>Methods for Function 'print' in Package 'simecol'</i>
---------------	--

Description

Methods for function print in Package **simecol**.

Usage

```
## S4 method for signature 'simObj'
print(x, all = FALSE, ...)
```

Arguments

x	an object of class <code>simObj</code> or one of its subclasses.
all	specifies whether all slots are printed. Default is that only not-empty slots are printed and the contents of out are suppressed.
...	optional parameters passed to print.

Methods

x = "ANY" generic function: see [print](#).

x = "simObj" prints the contents (slots) of the `simObj` object.

sEdit	<i>Simple editing</i>
-------	-----------------------

Description

Simple Editing of Vectors, Lists of Vectors and Other Objects.

Usage

```
sEdit(x, title = "Please enter values:")
```

Arguments

x	A named object that you want to edit.
title	A title for the dialog box.

Details

If called with a vector or list of vectors and if **Tcl/Tk** is installed, a dialog box is shown in which data can be entered. If the x is not of type vector or list of vectors, a default editing method is called.

Value

An object with the same type like x.

See Also

[edit fixParms](#)

Examples

```
## Not run:
## named vector
vec <- c(a = 1, b = 20, c = 0.03)
new <- sEdit(vec)
## unnamed vector
sEdit(numeric(10))
## list of vectors
lst <- list(vec = vec, test = 1:10)
sEdit(lst)
## list with numeric and character vectors mixed
lst <- list(vec = vec, test = c("a", "b", "c"))
sEdit(lst)

## End(Not run)
```

seedfill

Color Fill Algorithm

Description

Fills a bounded area within a numeric matrix with a given number (color).

Usage

```
seedfill(z, x=1, y=1, fcol=0, bcol=1, tol=1e-6)
```

Arguments

z	a matrix containing an image (double precision values are possible).
x, y	start coordinates of the filled area.
fcol	numeric value of the fill color.
bcol	numeric value of the border value.
tol	numeric value of border color tolerance.

Details

The function implements a basic color fill algorithm for use in image manipulation or cellular automata.

Value

A matrix with the same structure as z.

See Also

[neighbours](#)

Examples

```
# define a matrix
z<-matrix(0, nrow=20, ncol=20)

# draw some lines
z[10,]<-z[,10] <- 1
z[5,] <-z[,5] <- 3

# plot matrix and filled variants
par(mfrow=c(2, 2))
image(z)
image(seedfill(z))
image(seedfill(z ,x=15, y=15, fcol=1, bcol=3))
image(seedfill(z, x=7, y=7, fcol=3, bcol=1))
```

 sim-methods

Simulation of 'simObj' model objects

Description

This function provides the core functionality of the 'simecol' package. Several methods depending on the class of the model are available.

Usage

```
sim(obj, initialize=TRUE, ...)
# sim(obj, animation=FALSE, delay=0, ...)
```

Arguments

obj	an object of class <code>simObj</code> or one of its subclasses.
initialize	re-initialize the object if the object contains a user-defined initializing function (<code>initfunc</code>). Setting <code>initialize</code> to <code>FALSE</code> can be useful to avoid time-consuming computations during initialization or to reproduce simulations of models which assign random values during the initialization process.
animation	logical value to switch animation on (for classes <code>gridModel</code> and <code>rwalkModel</code>).
delay	delay (in ms and in addition to the time needed for the simulation) between consecutive images (for <code>gridModels</code>) or xy-plots (for <code>rwalkModels</code>).
...	optional parameters passed to the solver function (e.g. <code>hmax</code> for <code>lsoda</code>).

Details

sim re-initializes the model object (if initialize==TRUE and calls the appropriate solver, specified in the solver-slot. Objects of class rwalkModel and indbasedModel are simulated by the default simObj method. If you derive own subclasses from simObj it may be necessary to write an appropriate sim method and/or solver function.

Value

The function returns the complete simObj instance with the simulation results in the out slot.

Methods

obj = "simObj" simulates the respective model object with optional animation.

obj = "odeModel" simulates the respective model object.

obj = "indbasedModel" simulates the respective model object with optional animation.

obj = "gridModel" simulates the respective model object with optional animation.

Examples

```
data(lv)
plot(sim(lv))

lv2 <- lv
parms(lv2)["k1"] <- 0.5
lv2 <- sim(lv2)
plot(out(lv2))
```

ssqOdeModel

Sum of Squares Between odeModel and Data

Description

Compute the sum of squares between a given data and an odeModel object.

Usage

```
ssqOdeModel(p, simObj, obstime, yobs,
  sd.yobs = as.numeric(lapply(yobs, sd)),
  initialize = TRUE, lower. = -Inf, upper. = Inf, weights = NULL,
  debuglevel = 0, ..., pnames = NULL)
```

Arguments

<code>p</code>	vector of named parameter values of the model (can be a subset),
<code>simObj</code>	a valid object of class <code>odeModel</code> ,
<code>obstime</code>	vector with time steps for which observational data are available,
<code>yobs</code>	data frame with observational data for all or a subset of state variables. Their names must correspond exactly with existing names of state variables in the <code>odeModel</code> .
<code>sd.yobs</code>	vector of given standard deviations for all observational variables given in <code>yobs</code> . If no standard deviations are given, these are estimated from <code>yobs</code> .
<code>initialize</code>	optional boolean value whether the <code>simObj</code> should be re-initialized after the assignment of new parameter values. This can be necessary in certain models to assign consistent values to initial state variables if they depend on parameters.
<code>lower.</code> , <code>upper.</code>	named vectors with lower and upper bounds used in the optimisation,
<code>weights</code>	optional weights to be used in the fitting process. Should be <code>NULL</code> or a data frame with the same structure as <code>yobs</code> . If non- <code>NULL</code> , weighted least squares is used with <code>weights</code> (that is, minimizing $\sum(w \cdot e^2)$); otherwise ordinary least squares is used.
<code>debuglevel</code>	a positive number that specifies the amount of debugging information printed,
<code>...</code>	additional parameters passed to the solver method (e.g. <code>lsoda</code>),
<code>pnames</code>	names of the parameters, optionally passed from <code>fitOdeModel</code> . This argument is a workaround for R versions below 2.8.1. It may be removed in future versions of <code>simecol</code> .

Details

This is the default function called by function `fitOdeModel`. The source code of this function can be used as a starting point to develop user-defined optimization criteria (cost functions).

Value

The sum of squared differences between `yobs` and simulation, by default weighted by the inverse of the standard deviations of the respective variables.

See Also

[fitOdeModel](#), [optim](#), [p.constrain](#)

Examples

```
data(chemostat)
cs1 <- chemostat

## generate some noisy data
parms(cs1)[c("vm", "km")] <- c(2, 10)
times(cs1) <- c(from = 0, to = 20, by = 2)
yobs <- out(sim(cs1))
```

```

obstime <- yobs$time
yobs$time <- NULL
yobs$S <- yobs$S + rnorm(yobs$S, sd = 0.1 * sd(yobs$S))*2
yobs$X <- yobs$X + rnorm(yobs$X, sd = 0.1 * sd(yobs$X))

## SSQ between model and data
ssqOdeModel(NULL, cs1, obstime, yobs)

## SSQ between model and data, different parameter set
ssqOdeModel(p=c(v=1, km=2), cs1, obstime, yobs)

## SSQ between model and data, downweight second observation
## (both variables)
weights <- data.frame(X=rep(1, nrow(yobs)), S = rep(1, nrow(yobs)))
ssqOdeModel(p=c(v=1, km=2), cs1, obstime, yobs, weights=weights)

## downweight 3rd data set (row)
weights[3,] <- 0.1
ssqOdeModel(p=c(v=1, km=2), cs1, obstime, yobs, weights=weights)

## give one value double weight (e.g. 4th value of S)
weights$S[4] <- 2
ssqOdeModel(p=c(v=1, km=2), cs1, obstime, yobs, weights=weights)

```

upca

The Uniform Period Chaotic Amplitude Model

Description

simecol example: resource-predator-prey model, which is able to exhibit chaotic behaviour.

Usage

```
data(upca)
```

Format

S4 object according to the [odeModel](#) specification. The object contains the following slots:

main The differential equations for predator prey and resource with:

- u resource (e.g. grassland or phosphorus),
- v producer (prey),
- w consumer (predator).

equations Two alternative (and switchable) equations for the functional response.

parms Vector with the named parameters of the model, see references for details.

times Simulation time and integration interval.

init Vector with start values for u, v and w.

solver Character string with the integration method.

Details

To see all details, please have a look into the implementation below and the original publications.

References

Blasius, B., Huppert, A., and Stone, L. (1999) Complex dynamics and phase synchronization in spatially extended ecological systems. *Nature*, **399** 354–359.

Blasius, B. and Stone, L. (2000) Chaos and phase synchronization in ecological systems. *International Journal of Bifurcation and Chaos*, **10** 2361–2380.

See Also

[sim](#), [parms](#), [init](#), [times](#).

Examples

```
##=====
## Basic Usage:
##   explore the example
##=====
data(upca)
plot(sim(upca))

# omit stabilizing parameter wstar
parms(upca)["wstar"] <- 0
plot(sim(upca))

# change functional response from
# Holling II (default) to Lotka-Volterra
equations(upca)$f <- function(x, y, k) x * y
plot(sim(upca))

##=====
## Implementation:
##   The code of the UPCA model
##=====
upca <- new("odeModel",
  main = function(time, init, parms) {
    u   <- init[1]
    v   <- init[2]
    w   <- init[3]
    with(as.list(parms), {
      du <- a * u           - alpha1 * f(u, v, k1)
      dv <- -b * v          + alpha1 * f(u, v, k1) +
      - alpha2 * f(v, w, k2)
      dw <- -c * (w - wstar) + alpha2 * f(v, w, k2)
      list(c(du, dv, dw))
    })
  },
  equations = list(
    f1 = function(x, y, k){x*y},          # Lotka-Volterra
```

```
    f2 = function(x, y, k){x*y / (1+k*x)} # Holling II
  ),
  times = c(from=0, to=100, by=0.1),
  parms = c(a=1, b=1, c=10, alpha1=0.2, alpha2=1,
    k1=0.05, k2=0, wstar=0.006),
  init = c(u=10, v=5, w=0.1),
  solver = "lsoda"
)

equations(upca)$f <- equations(upca)$f2
```

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