

Package: OceanView (via r-universe)

September 3, 2024

Version 1.0.7

Title Visualisation of Oceanographic Data and Model Output

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Depends plot3D, plot3Drgl, R (>= 3.2)

Imports methods, graphics, grDevices, stats, rgl, shape

Description Functions for transforming and viewing 2-D and 3-D (oceanographic) data and model output.

License GPL (>= 3.0)

LazyData yes

NeedsCompilation yes

Date/Publication 2024-02-06 13:30:06 UTC

Repository <https://karlines.r-universe.dev>

RemoteUrl <https://github.com/cran/OceanView>

RemoteRef HEAD

RemoteSha a8d5b07156770a329f4ecb841f40269841f45e66

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OceanView-package *Functions for visualising oceanic data sets and model output.*

Description

Visualisation of oceanic data.

Author(s)

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References

<https://www.rforscience.com/oceanview.html>

See Also

[db2cross](#), converts a dataset from database format to cross table.

[flowpath](#), plots velocities as trajectory plot.

[remap](#), [transect](#), [extract](#), [mapsigma](#), [transectsigma](#), mapping and extracting from 2-D or 3-D data.

[Mcommon](#), [Mplot](#), [Msplit](#), functions for plotting matrices.

[quiver2D](#), velocities plotted as arrows.

[vectorplot](#), vector velocity plot.

Chesapeake data set *Particle transport in Chesapeake Bay*

Description

Chesapeake is a list with the bathymetry of Chesapeake Bay, Mid-Atlantic Bight and the initial position of the particles.

Ltrans is an array with output of the Lagrangian Transport model (Ltrans v.2) from Chesapeake Bay mouth, at 37 dgN in the Mid-Atlantic Bight (Schlag and North, 2012).

Usage

```
data(Chesapeake)
data(Ltrans)
```

Format

- Chesapeake is a list with the bathymetry of the area. There are 154 x-values, at 77 y-values. It contains:
 - lon, the longitude, (154 x 77), dg East.
 - lat, the latitude, (154 x 77), dg North.
 - depth, the bathymetry (154 x 77), metres.
 - init, the initial condition of the particles, a (608 x 4) matrix with (lon, lat, depth, source) values.
- Ltrans contains output of the Lagrangian particle transport model, in the Chesapeake mouth area. 608 particles were released in two square regions, and their positions followed over 108 output steps. It is an array of dimension (608 x 4 x 108), and which contains for each of the 608 particles, and at each of the 108 output steps the following:
 - lon, the longitude of each particle.
 - lat, the latitude of each particle.
 - depth, the depth of each particle.
 - source, the square region of release, either 1 or 2.

Author(s)

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References

Schlag, Z. R., and E. W. North. 2012. Lagrangian TRANSport model (LTRANS v.2) User's Guide. University of Maryland Center for Environmental Science, Horn Point Laboratory. Cambridge, MD. 183 pp.

North, E. W., E. E. Adams, S. Schlag, C. R. Sherwood, R. He, S. Socolofsky. 2011. Simulating oil droplet dispersal from the Deepwater Horizon spill with a Lagrangian approach. AGU Book Series: Monitoring and Modeling the Deepwater Horizon Oil Spill: A Record Breaking Enterprise.

See Also

[Sylt3D](#) for output of a 3-D hydrodynamical model, GETM.

[Oxsat](#) for a 3-D data set, package plot3D.

[tracers2D](#) for plotting time series of tracer distributions in 2D

[tracers3D](#) for plotting time series of tracer distributions in 3D

Examples

```
# save plotting parameters
pm <- par("mfrow")
mar <- par("mar")

## =====
## Show bathymetry and initial distribution of particles
## =====
```

```

par(mfrow = c(1, 1))

lon <- Chesapeake$lon
lat <- Chesapeake$lat
depth <- Chesapeake$depth
init <- Chesapeake$init

image2D(z = depth, x = lon, y = lat, clab = c("depth", "m"),
        xlab = "lon", ylab = "lat")

# position of particles
with (init, scatter2D(lon, lat, colvar = source, pch = 16, cex = 0.5,
                    col = c("green", "orange"), add = TRUE, colkey = FALSE))

par (mar = c(2, 2, 2, 2))
# same, as persp plot
persp3D(x = lon, y = lat, z = -depth, scale = FALSE,
        expand = 0.02, main = "initial particle distribution",
        plot = FALSE)

points3D(x = init$lon, y = init$lat, z = -init$depth,
        colvar = init$source, col = c("green", "orange"),
        pch = 16, cex = 0.5,
        add = TRUE, colkey = FALSE, plot = FALSE)

## Not run:
plotdev(lightning = TRUE, lphi = 45)

## End(Not run)
plotrgl(lightning = TRUE, smooth = TRUE)

## =====
## Tracer output in 3D, traditional device
## =====
## Not run:
par(mfrow = c(2, 1), mar = c(2, 2, 2, 2))
for (i in c(50, 100))
  tracers3D(Ltrans[, 1, i], Ltrans[, 2, i], Ltrans[, 3, i],
           colvar = Ltrans[, 4, i], col = c("green", "orange"),
           pch = 16, cex = 0.5,
           surf = list(x = lon, y = lat, z = -depth, scale = FALSE,
                      expand = 0.02, colkey = FALSE, shade = 0.3,
                      colvar = depth), colkey = FALSE,
           main = paste("time ", i))

## End(Not run)

## =====
## Tracer output in 3D, using rgl
## =====

persp3D(x = lon, y = lat, z = -depth, colvar = depth, scale = FALSE,

```

```

    expand = 0.02, main = "particle distribution", plot = FALSE)

plotrgl(lighting = TRUE, smooth = TRUE)

# you may zoom to the relevant region, or cut a region
# cutrgl()
for (i in seq(1, 108, by = 4)) {
  tracers3Drgl(Ltrans[, 1, i], Ltrans[, 2, i], Ltrans[, 3, i],
              colvar = Ltrans[, 4, i], col = c("green", "orange"),
              main = paste("time ", i))
# remove # to slow down
# Sys.sleep(0.1)
}

# using function moviepoints3D
## Not run:
persp3Drgl(x = lon, y = lat, z = -depth, colvar = depth, scale = FALSE,
           expand = 0.02, main = "particle distribution",
           lighting = TRUE, smooth = TRUE)

nt <- dim(Ltrans)[3] # number of time points
np <- dim(Ltrans)[1] # number of particles

times <- rep(1:nt, each = np)

moviepoints3D(x = Ltrans[, 1, ], y = Ltrans[, 2, ], z = Ltrans[, 3, ],
             t = times, colvar = Ltrans[, 4, ], col = c("green", "orange"),
             cex = 5, ask = TRUE)

## End(Not run)
## =====
## Tracer output in 2D, traditional device
## =====

par(mfrow = c(2, 2))
for (i in seq(10, 106, length.out = 4))
  tracers2D(Ltrans[, 1, i], Ltrans[, 2, i],
           colvar = Ltrans[, 4, i], col = c("green", "orange"),
           pch = 16, cex = 0.5,
           image = list(x = lon, y = lat, z = depth), colkey = FALSE,
           main = paste("time ", i))

## =====
## Tracer output in 2D, rgl
## =====

image2Drgl (x = lon, y = lat, z = depth)
for (i in seq(1, 108, by = 3)) {
  tracers2Drgl(Ltrans[, 1, i], Ltrans[, 2, i],
              colvar = Ltrans[, 4, i], col = c("green", "orange"))
# remove # to slow down
# Sys.sleep(0.1)
}

```

```

}

# reset plotting parameters
par(mar = mar)
par(mfrow = pm)

```

Map and extract data *Functions for remapping, changing the resolution, and extracting from 2-D or 3-D data.*

Description

S3 functions `remap` maps a variable (`var`) (a matrix or array) with `x`, `y` (and `z`) coordinates to a matrix or array with coordinates given by `xto`, `yto` (and `zto`). `x`, `y`, `z`, `xto`, `yto` and `zto` are all vectors. The functions interpolate to all combinations of `xto`, `yto` and `zto`. Simple 2-D linear interpolation is used. Result is a matrix or array.

Function `changeres` changes the resolution of a variable (`var`) (a matrix or array) with `x`, `y` (and `z`) coordinates. If `var` is a matrix, then `x`, `y` can be either a vector or a matrix; if `var` is an array, then `x`, `y`, `z` should all be vectors. Simple 2-D linear interpolation is used. Result is a matrix or array.

S3-functions `extract` map a variable (`var`) from a matrix with `(x, y)` coordinates or from an array with `(x, y, z)` coordinates to the `xy` coordinate *pair* `xyto` or `xyz` coordinate *triplets* `xyzto` by linear interpolation. Result is a vector.

`transect` takes a cross section across an array (`var`). Result is a matrix.

`mapsigma` maps a matrix or array `var` containing values defined at `(x, sigma)` (or `(x, y, sigma)`) coordinates to `(x, depth)` (or `(x, y, depth)`) coordinates. The depths corresponding to the `sigma` values in `var` are in an input matrix or array called `sigma` with same dimensions as `var`. The result is a matrix or array which will contain NAs where the depth-coordinates extend beyond the `sigma` values.

Usage

```

remap      (var, ...)

## S3 method for class 'matrix'
remap(var, x, y, xto = NULL, yto = NULL,
      na.rm = TRUE, ...)

## S3 method for class 'array'
remap(var, x, y, z, xto = NULL, yto = NULL, zto = NULL,
      na.rm = TRUE, ...)

changeres  (var, ...)

## S3 method for class 'matrix'
changeres(var, x, y, resfac, na.rm = TRUE, ...)

```

```

## S3 method for class 'array'
changeres(var, x, y, z, resfac, na.rm = TRUE, ...)

extract    (var, ...)

## S3 method for class 'matrix'
extract(var, x, y, xyto, ...)

## S3 method for class 'array'
extract(var, x, y, z, xyzto, ...)

transect(var, x, y, z, to, margin = "xy", ...)

mapsigma   (var, ...)

## S3 method for class 'matrix'
mapsigma(var = NULL, sigma, signr = 2, x = NULL,
         depth = NULL, numdepth = NULL, xto = NULL, resfac = 1, ...)

## S3 method for class 'array'
mapsigma(var = NULL, sigma, signr = 3, x = NULL, y = NULL,
         depth = NULL, numdepth = NULL, xto = NULL, yto = NULL,
         resfac = 1, ...)

transectsigma(var = NULL, sigma, x, y, to, depth = NULL,
             numdepth = NULL, resfac = 1, ...)

```

Arguments

var	Matrix or array with values to be mapped to other coordinates (remap), or to lower or higher resolution (changeres), or whose values have to be extracted (extract, transect), or which has to be mapped from sigma to depth coordinates (mapsigma). For transect and transectsigma, var has to be an array.
x	Vector with original x-coordinates of the matrix or array var to be mapped. Length should be = first dimension of var.
y	Vector with original y-coordinates of the matrix or array var to be mapped. Length should be = second dimension of var.
z	Vector with original z-coordinates of the array var to be mapped. Length should be = third dimension of var.
xto	Vector with x-coordinates to which var should be mapped. The elements in xto should be embraced by the elements in x (it is not allowed to extrapolate outside of the region). If NULL then the range of x is covered, with the same number of points.
yto	Vector with y-coordinates to which var should be mapped. The elements in yto should be embraced by the elements in y (it is not allowed to extrapolate outside

	of the region). If NULL then the range of y is covered, with the same number of points.
zto	Vector with z-coordinates to which var should be mapped. The elements in zto should be embraced by the elements in z (it is not allowed to extrapolate outside of the region). If NULL then the range of z is covered, with the same number of points.
xyto	Two-columned matrix, with first and second column specifying the x- respectively y-coordinates to which the matrix var should be mapped. The elements should be embraced by the elements in x (first column) and y (second column) (it is not allowed to extrapolate outside of the region).
xyzto	Three-columned matrix, specifying the x-, y- and z-coordinates to which the array var should be mapped. The elements should be embraced by the elements in x, y and z (it is not allowed to extrapolate outside of the region).
to	Two-columned matrix, specifying the values along the margin coordinates of the transect to be taken on the array var. The elements should be embraced by the elements in x, y and z (it is not allowed to extrapolate outside of the region).
margin	String with the names of the coordinates in the matrix to, and along which the transect is to be taken on the array var. One of "xy", "xz", "yz". If "xy", then the first and second column in input to represent x and y values respectively, and the transect will select all z values corresponding with these inputs.
sigma	The sigma coordinates, a matrix or array with the same dimension as var. The sigma coordinates should refer to the column as defined by signr.
signr	The position of the sigma coordinates, in the matrix or array. The default is the second or third dimension in var for a matrix and array respectively.
depth	The depth (often referred to as 'z') coordinates to which matrix var has to be mapped. If NULL then seq(min(sigma), max(sigma), length.out = numdepth).
numdepth	Only used when depth= NULL, the length of the depth vector to which the matrix var has to be mapped. If NULL then the length will be equal to ncol(var) (if var is a matrix), or dim(var)[3] in case var is an array.
resfac	Resolution factor, one value or a vector of two or three numbers, for the x, y- and z- values respectively. A value > 1 will increase the resolution. For instance, if resfac equals 3 then for each adjacent pair of x- and y- values, var will be interpolated to two intermediary points. This uses simple linear interpolation. If resfac is one number then the resolution will be increased similarly in x, y- and z-direction. In case of mapsigma, resfac is overruled if xto, yto or zto is specified.
na.rm	How to treat NAs in the matrix or array var. If TRUE, they are ignored while interpolating; this will make the size of NA regions smaller; if FALSE, the size of the NA region will increase.
...	any other arguments.

Details

S3-function remap can be used to increase or decrease the resolution of a matrix or array var, or to zoom in on a certain area. It returns an object of the same class as var (i.e. a matrix or array).

S3-function `transect` takes a slice from an array; it returns a matrix.

S3-function `extract` returns a vector with one value corresponding to each row in `xyto` or `xyzto`.

`mapsigma` should be used to make images from data that are in sigma coordinates.

Value

`remap.matrix`:

`var` The higher or lower resolution matrix with dimension = $c(\text{length}(xto), \text{length}(yto))$.
`x` The x coordinates, corresponding to first dimension of `var` (input argument `xto`).
`y` The y coordinates, corresponding to second dimension of `var` (input argument `yto`).

`remap.array`:

`var` The higher or lower resolution array, with dimension = $c(\text{length}(xto), \text{length}(yto), \text{length}(zto))$.
`x` The x coordinates, corresponding to first dimension of `var` (input argument `xto`).
`y` The y coordinates, corresponding to second dimension of `var` (input argument `yto`).
`z` The z coordinates, corresponding to third dimension of `var` (input argument `zto`).

`extract.matrix`:

`var` The higher or lower resolution object, with dimension = $c(\text{nrow}(xyto), \text{dim}(var)[3])$.
`xy` The pairs of (x,y) coordinates (input argument `xyto`).

`extract.array`:

`var` The higher or lower resolution object, with dimension = $c(\text{nrow}(xyzto), \text{dim}(var)[3])$.
`xyz` The triplets of (x,y,z) coordinates (input argument `xyzto`).

`mapsigma`:

`var` A matrix with columns in depth-coordinates.
`depth` The depth-coordinates, also known as 'z'-coordinates, referring to the dimension of `var` as specified by `signr`.
`x` The 'x'-coordinates referring to the first dimension of `var`, except for the depth.
`y` Only if `var` is an array, the 'y'-coordinates referring to the second dimension of `var`, except for the depth.

See Also

[Sylt3D](#) for other examples of mapping.

Examples

```

# save plotting parameters
pm <- par("mfrow")

## =====
## Simple examples
## =====
M <- matrix(nrow = 2, data = 1:4)
remap(M, x = 1:2, y = 1:2,
      xto = seq(1, 2, length.out = 3), yto = 1:2)

changeres(M, x = 1:2, y = 1:2, resfac = c(2, 1))
changeres(M, x = 1:2, y = 1:2, resfac = 2)

# x and or y are a matrix.
changeres(var = M, x = M, y = 1:2, resfac = c(2, 1))
changeres(M, x = M, y = 1:2, resfac = 2)

## =====
## Use remap to add more detail to a slice3D plot
## =====

par(mfrow = c(1, 1))
x <- y <- z <- seq(-4, 4, by = 0.5)
M <- mesh(x, y, z)

R <- with (M, sqrt(x^2 + y^2 + z^2))
p <- sin(2*R) / (R+1e-3)

slice3D(x, y, z, ys = seq(-4, 4, by = 2), theta = 85,
        colvar = p, pch = ".", clim = range(p))

xto <- yto <- zto <- seq(-1.2, 1.2, 0.3)
Res <- remap (p, x, y, z, xto, yto, zto)

# expand grid for scatterplot
Mt <- mesh(Res$x, Res$y, Res$z)

scatter3D(x = Mt$x, y = Mt$y, z = Mt$z, colvar = Res$var,
          pch = ".", add = TRUE, cex = 3, clim = range(p))

# same in rgl:
## Not run:
plotrgl()

## End(Not run)

# extract specific values from 3-D data
xyzto <- matrix(nrow = 2, ncol = 3, data = c(1,1,1,2,2,2), byrow = TRUE)
extract(var = p, x, y, z, xyzto = xyzto)

```

```

# a transect
to <- cbind(seq(-4, 4, length.out = 20), seq(-4, 4, length.out = 20))
image2D( transect(p, x, y, z, to = to)$var)

## =====
## change the resolution of a 2-D image
## =====

par(mfrow = c(2, 2))
nr <- nrow(volcano)
nc <- ncol(volcano)

x <- 1 : nr
y <- 1 : nc
image2D(x = x, y = y, volcano, main = "original")

# increasing the resolution
x2 <- seq(from = 1, to = nr, by = 0.5)
y2 <- seq(from = 1, to = nc, by = 0.5)

VOLC1 <- remap(volcano, x = x, y = y, xto = x2, yto = y2)$var
image2D(x = x2, y = y2, z = VOLC1, main = "high resolution")

# low resolution
xb <- seq(from = 1, to = nr, by = 2)
yb <- seq(from = 1, to = nc, by = 3)
VOLC2 <- remap(volcano, x, y, xb, yb)$var
image2D(VOLC2, main = "low resolution")

# zooming in high resolution
xc <- seq(10, 40, 0.1)
yc <- seq(10, 40, 0.1)

VOLC3 <- remap(volcano,x, y, xc, yc)$var
image2D(VOLC3, main = "zoom")

# Get one value or a grid of values
remap(volcano, x, y, xto = 2.5, yto = 5)
remap(volcano, x, y, xto = c(2, 5), yto = c(5, 10))

# Specific values
extract(volcano, x, y, xyto = cbind(c(2, 5), c(5, 10)))

## =====
## take a cross section or transect of volcano
## =====

par(mfrow = c(2, 1))
image2D(volcano, x = 1:nr, y = 1:nc)
xyto <- cbind(seq(from = 1, to = nr, length.out = 20),
              seq(from = 20, to = nc, length.out = 20))
points(xyto[,1], xyto[,2], pch = 16)

```

```

(Crossection <- extract (volcano, x = 1:nr, y = 1:nc,
                        xyto = xyto))

scatter2D(xyto[, 1], Crossection$var, colvar = Crossection$var,
          type = "b", cex = 2, pch = 16)

## =====
## mapsigma: changing from sigma coordinates into depth-coordinates
## =====

par(mfrow = c(2, 2))
var <- t(matrix(nrow = 10, ncol = 10, data = rep(1:10, times = 10)))
image2D(var, ylab = "sigma", main = "values in sigma coordinates",
        clab = "var")

# The depth at each 'column'
Depth <- approx(x = 1:5, y = c(10, 4, 5, 6, 4),
               xout = seq(1,5, length.out = 10))$y
Depth <- rep(Depth, times = 10)

# Sigma coordinates
sigma <- t(matrix(nrow = 10, ncol = 10, data = Depth, byrow = TRUE) *
           seq(from = 0, to = 1, length = 10))
matplot(sigma, type = "l", main = "sigma coordinates",
        xlab = "sigma", ylab = "depth", ylim = c(10, 0))

# Mapping to the default depth coordinates
varz <- mapsigma(var = var, sigma = sigma)
image2D(varz$var, y = varz$depth, NAcol = "black", ylim = c(10, 0),
        clab = "var", ylab = "depth",
        main = "depth-coord, low resolution")

# Mapping at higher resolution of depth coordinates
varz <- mapsigma(var, sigma = sigma, resfac = 10)
image2D(varz$var, y = varz$depth, NAcol = "black", ylim = c(10, 0),
        clab = "var", ylab = "depth",
        main = "depth-coord, high resolution")

## =====
## mapsigma: mapping to depth for data Sylttran (x, sigma, time)
## =====

# depth values
D <- seq(-1, 20, by = 0.5)
dim(Sylttran$visc)

# sigma coordinates are the second dimension (signr)
# resolution is increased for 'x' and decreased for 'time'

visc <- mapsigma(Sylttran$visc, x = Sylttran$x, y = Sylttran$time,
                sigma = Sylttran$sigma, signr = 2, depth = D, resfac = c(2, 1, 0.4))

# changed dimensions

```

```

dim(visc$var)

image2D(visc$var, x = visc$x, y = -visc$depth, ylim = c(-20, 1),
  main = paste("eddy visc,", format(visc$y, digits = 2), " hr"),
  ylab = "m", xlab = "x", clab = c("", "m2/s"),
  clim = range(visc$var, na.rm = TRUE))

par(mfrow = c(1, 1))
# make depth the last dimension
cv <- aperm(visc$var, c(1, 3, 2))

# visualise as slices
slice3D(colvar = cv, x = visc$x, y = visc$y, z = -visc$depth,
  phi = 10, theta = 60, ylab = "time",
  xs = NULL, zs = NULL, ys = visc$y, NAcot = "transparent")

# restore plotting parameters
par(mfrow = pm)

```

Matrix plotting	<i>Functions for plotting matrices, or for splitting them and for maing suitable summaries</i>
-----------------	--

Description

Mplot plots data from (a list of) matrices.

Msplit splits a matrix in a list according to factors (or unique values).

Mcommon creates a list of matrices that have only common variables.

Msummary and Mdescribe create suitable summaries of all columns of a matrix or list.

Usage

```

Mplot (M, ..., x = 1, select = NULL, which = select,
  subset = NULL, ask = NULL,
  legend = list(x = "center"), pos.legend = NULL,
  xyswap = FALSE, rev = "")

```

```

Msummary (M, ...,
  select = NULL, which = select,
  subset = NULL)

```

```

Mdescribe (M, ...,
  select = NULL, which = select,
  subset = NULL)

```

```

Msplit (M, split = 1, subset = NULL)

```

```

Mcommon (M, ..., verbose = FALSE)

```

Arguments

<code>M</code>	Matrix or <code>data.frame</code> to be plotted, or treated. For <code>Mplot</code> , <code>M</code> can be a list with matrices or <code>data.frames</code> .
<code>x</code>	Name or number of the column to be used as the x-values.
<code>select</code>	Which variable/columns to be selected. This is added for consistency with the R-function <code>subset</code> .
<code>which</code>	The name(s) or the index to the variables that should be plotted or selected. Default = all variables, except <code>time</code> .
<code>subset</code>	Logical expression indicating elements or rows to keep in <code>select</code> : missing values are taken as <code>FALSE</code>
<code>ask</code>	Logical; if <code>TRUE</code> , the user is <i>asked</i> before each plot, if <code>NULL</code> the user is only asked if more than one page of plots is necessary and the current graphics device is set interactive, see <code>par(ask)</code> and dev.interactive .
<code>legend</code>	A list with parameters for the legend to be added. If <code>FALSE</code> , then no legend will be drawn.
<code>pos.legend</code>	The position of the legend, a number. The default is to put the legend in the last figure. Also allowed is <code>pos.legend = 0</code> , which will create a new figure with only the legend.
<code>xyswap</code>	If <code>TRUE</code> , then the x- and y-values will be swapped.
<code>rev</code>	a character string which contains "x" if the x axis is to be reversed, "y" if the y axis is to be reversed and "xy" or "yx" if both axes are to be reversed.
<code>split</code>	The name or number of the column with the factor according to which the matrix will be split.
<code>verbose</code>	If <code>TRUE</code> will write output to the screen.
<code>...</code>	Additional arguments passed to the methods. For <code>Mplot</code> : can also be extra matrices to plot. The arguments after <code>...</code> must be matched exactly.

Value

Function `Msplit` returns a list with the matrices, split according to the factors; the names of the elements is set by the factor's name. It is similar to the R-function [split](#).

Function `Mcommon` returns a list with the matrices, which only have the common variables.

Function `Msummary` returns a `data.frame` with summary values (minimum, first quantile, median, mean, 3rd quantile, maximum) for each column of the input (variable). If there are more than one object to be summarised, or if `M` is a list of objects, the name of the object is in the second column.

Function `Mdescribe` returns a `data.frame` with summary values (number of data, number of missing values, number of unique values, mean value, the standard deviation, the minimum, the $p = 0.05, 0.1, 0.5, 0.9, 0.95$ quantiles, and the maximum) for each column of the input (variable). If there are more than one object to be summarised, or if `M` is a list of objects, the name of the object is in the second column.

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

Examples

```
# save plotting parameters
pm <- par("mfrow")

## =====
## Create three dummy matrices
## =====

M1 <- matrix(nrow = 10, ncol = 5, data = 1:50)
colnames(M1) <- LETTERS[1:5]

M2 <- M1[, c(1, 3, 4, 5, 2)]
M2[, -1] <- M2[, -1] / 2
colnames(M2)[3] <- "CC" # Different name

M3 <- matrix(nrow = 5, ncol = 4, data = runif(20)*10)
M3[, 1] <- sort(M3[, 1])
colnames(M3) <- colnames(M1)[-3]

# show them
head(M1); head(M2); head(M3)
Msummary(M1)
Msummary(M1, M2, M3)

# plot all columns of M3 - will change mfrow
Mplot(M3, type = "b", pch = 18, col = "red")

# plot results of all three data sets
Mplot(M1, M2, M3, lwd = 2, mtext = "All variables versus 1st column",
      legend = list(x = "top", legend = c("M1", "M2", "M3")))

## =====
## Plot a selection or only common elements
## =====

Mplot(M1, M2, M3, x = "B", select = c("A", "E"), pch = c(NA, 16, 1),
      type = c("l", "p", "b"), col = c("black", "red", "blue"),
      legend = list(x = "right", legend = c("M1", "M2", "M3")))

Mplot(Mcommon(M1, M2, M3), lwd = 2, mtext = "common variables",
      legend = list(x = "top", legend = c("M1", "M2", "M3")))

Mdescribe(Mcommon(M1, M2, M3))

## =====
## The iris and Orange data set
## =====
```

```

# Split the matrix according to the species
Irislist <- Msplit(iris, split = "Species")
names(Irislist)

Mdescribe(Irislist, which = "Sepal.Length")
Mdescribe(iris, which = "Sepal.Length", subset = Species == "setosa")

# legend in a separate plot
Mplot(Irislist, type = "p", pos.legend = 0,
      legend = list(x = "center", title = "species"))

Mplot(Msplit(Orange,1), lwd = 2,
      legend = list(x = "topleft", title = "tree nr"))
Msummary(Msplit(Orange,1))

# reset plotting parameters
par(mfrow = pm)

```

Moving slices in 3D *Plotting volumetric data as moving slices in 3D using rgl*

Description

`movieslice3D` plots 3D volumetric data as slices moving in one direction in open-GL graphics. It is based on the `plot3Drgl` function [slice3Drgl](#).

Usage

```

movieslice3D (x, y, z, colvar = NULL, xs = NULL,
             ys = NULL, zs = NULL, along = NULL,
             col = jet.col(100), NAcol = "white", breaks = NULL,
             colkey = FALSE, clim = NULL, clab = NULL,
             wait = NULL, ask = FALSE, add = FALSE, basename = NULL, ...)

```

Arguments

<code>x, y, z</code>	Vectors with x, y and z-values. They should be of length equal to the first, second and third dimension of <code>colvar</code> respectively.
<code>colvar</code>	The variable used for coloring. It should be an array of dimension equal to <code>c(length(x), length(y), length(z))</code> . It must be present.
<code>col</code>	Colors to be used for coloring the <code>colvar</code> variable. If <code>col</code> is NULL then a red-yellow-blue colorscheme (jet.col) will be used.
<code>NAcol</code>	Colors to be used for <code>colvar</code> values that are NA.
<code>breaks</code>	a set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.

<code>colkey</code>	A logical, NULL (default), or a list with parameters for the color key (legend). If <code>colkey = NULL</code> then a color key will be added only if <code>col</code> is a vector. Setting <code>colkey = list(plot = FALSE)</code> will create room for the color key without drawing it. if <code>colkey = FALSE</code> , no color key legend will be added.
<code>clim</code>	Only if <code>colvar</code> is specified, the range of the color variable values. Values of <code>colvar</code> that extend the range will be put to NA and colored as specified with <code>NAcol</code> .
<code>clab</code>	Only if <code>colkey</code> is not NULL or FALSE, the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, <code>clab</code> can be made a vector, with the first values empty strings.
<code>xs, ys, zs</code>	Vectors specify the positions in x, y or z where the slices (planes) are to be drawn consecutively. The movie will loop over the slices, each time projecting the values of <code>colvar</code> on them. If all <code>xs, ys, zs</code> are NULL, then <code>xs</code> will be taken equal to x.
<code>along</code>	A number 1, 2, 3 denoting the dimension over which the slices are to be moved. If NULL, then the dimension will be the one corresponding to the longest vector <code>xs, ys, zs</code> .
<code>add</code>	Logical. If TRUE, then the slices will be added to the current plot. If FALSE a new plot is started.
<code>ask</code>	Logical. If TRUE, then the new slice will only be drawn after a key has been struck. If FALSE, redrawing will depend on <code>wait</code>
<code>wait</code>	The time interval inbetween drawing of a new slice, in seconds. If NULL, the drawing will not be suspended.
<code>basename</code>	The base name of a png file to be produced for each movieframe.
<code>...</code>	additional arguments passed to slice3D from package <code>plot3D</code> or to <code>plotrgl</code> from package <code>plot3Drgl</code> .

Value

returns nothing

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

See Also

[Sylt3D](#) for a data set that can be displayed with `movieslice3D`
[moviepoints3D](#) for plotting moving points in 3D

Examples

```
x <- y <- z <- seq(-1, 1, by = 0.1)
grid <- mesh(x, y, z)
colvar <- with(grid, x*exp(-x^2 - y^2 - z^2))

movieslice3D (x, y, z, colvar = colvar, ticktype = "detailed")
```

 Moving surfaces in 3D *Plotting moving surfaces in 3D using rgl*

Description

moviepersp3D plots moving perspective plots of a surface in open-GL.

It is based on the plot3Drgl function [persp3Drgl](#).

Usage

```
moviepersp3D (z, x = NULL, y = NULL, t = NULL, colvar = z, tdim = 1,
  col = jet.col(100), NAcol = "white", breaks = NULL,
  colkey = FALSE, clim = NULL, clab = NULL,
  wait = NULL, ask = FALSE, add = FALSE, basename = NULL, ... )
```

Arguments

x, y, t	Vectors with x, y and t-values. Their position in the z-array depends on tdim.
z	Three-dimensional array with the z-values to be plotted.
tdim	Index to where the time variable (over which the plot will loop) is to be found in z and colvar. The default is the first position, so that z and colvar are of dimension (length(t), length(x), (length(y)).
colvar	The variable used for coloring. It should be an array of dimension equal to the dimension of z. It need not be present.
col	Colors to be used for coloring the colvar variable. If col is NULL then a red-yellow-blue colorscheme (jet.col) will be used.
NAcol	Colors to be used for colvar values that are NA.
breaks	A set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.
colkey	A logical, NULL (default), or a list with parameters for the color key (legend). If colkey = NULL then a color key will be added only if col is a vector. Setting colkey = list(plot = FALSE) will create room for the color key without drawing it. if colkey = FALSE, no color key legend will be added.
clim	Only if colvar is specified, the range of the color variable values. Values of colvar that extend the range will be put to NA and colored as specified with NAcol.
clab	Only if colkey is not NULL or FALSE, the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, clab can be made a vector, with the first values empty strings.
add	Logical. If TRUE, then the slices will be added to the current plot. If FALSE a new plot is started.
ask	Logical. If TRUE, then the new slice will only be drawn after a key has been struck. If FALSE, redrawing will depend on wait

<code>wait</code>	The time interval inbetween drawing of a new slice, in seconds. If NULL, the drawing will not be suspended.
<code>basename</code>	The base name of a png file to be produced for each movieframe.
<code>...</code>	additional arguments passed to persp3Drgl from package <code>plot3Drgl</code> .

Value

returns nothing

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

See Also

[Sylt3D](#) for a data set that can be displayed with `moviepersp3D`

[moviepoints3D](#) for plotting moving points in 3D

[movieslice3D](#) for plotting moving slices in 3D

Examples

```
x <- y <- t <- seq(-1, 1, by = 0.1)
grid <- mesh(x, y, t)
z <- with(grid, x*exp(-x^2 - y^2 - z^2))

moviepersp3D (x, y, z = z, colvar = z, colkey = TRUE,
             ticktype = "detailed", wait = 0.1, main = "t = ")

## Not run:
moviepersp3D (x, y, z = z, colvar = z, colkey = TRUE,
             aspect = TRUE, bty = "n", ask = FALSE, main = "t = ")

## End(Not run)
```

NIOZ Westerschelde monitoring

NIOZ monitoring data of Westerschelde estuary.

Description

Part of the long-term monitoring data of the Westerschelde estuary, from 1996 till 2004.

A total of 17 stations were monitored on a monthly basis.

The dataset `WSnioz` is in long format and contains the following variables: oxygen, temperature, salinity, nitrate, ammonium, nitrite, phosphate, silicate and chlorophyll.

The dataset `WSnioz.table` is in tabular format.

The full dataset can be downloaded from: <https://www.nioz.nl/monitoring-data-downloads>

Usage

```
data(WSnioz)
data(WSnioz.table)
```

Format

WSnioz is a data.frame with the following columns:

- `SamplingDateTime`, a string with the date and time of sampling.
- `SamplingDateTimeREAL`, a numeric value with day as per 1900.
- `Station`, the station number.
- `Latitude`, `Longitude`, the station position.
- `VariableName`, the variable acronym.
- `VariableDesc`, description of the variable.
- `VariableUnits`, units of measurement.
- `DataValue`, the actual measurement.

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

References

Soetaert, K., Middelburg, JJ, Heip, C, Meire, P., Van Damme, S., Maris, T., 2006. Long-term change in dissolved inorganic nutrients in the heterotrophic Scheldt estuary (Belgium, the Netherlands). *Limnology and Oceanography* 51: 409-423. DOI: 10.4319/lo.2006.51.1_part_2.0409
http://aslo.org/lo/toc/vol_51/issue_1_part_2/0409.pdf

See Also

[image2D](#) for plotting images, package `plot3D`.
[ImageOcean](#) for an image of the ocean's bathymetry, package `plot3D`.
[scatter2D](#) for making scatterplots, package `plot3D`.
[Oxsat](#) for a 3-D data set, package `plot3D`.

Examples

```
# save plotting parameters
pm <- par("mfrow")
mar <- par("mar")

## =====
## Show stations and measured variables
## =====
unique(WSnioz[,c("Station", "Latitude", "Longitude")])
unique(WSnioz[,c("VariableName", "VariableDesc")])
```

```

## =====
## An image for Nitrate:
## =====

# 1. use db2cross to make a cross table of the nitrate data
# assume that samples that were taken within 5 days belong to the same
# monitoring campaign (df.row).

N03 <- db2cross(WSnioz, row = "SamplingDateTimeREAL",
               col = "Station", val = "DataValue",
               subset = (VariableName == "WNO3"), df.row = 5)

# 2. plot the list using image2D; increase resolution
image2D(N03, resfac = 3)

## =====
## All timeseries for one station
## =====

st1 <- db2cross(WSnioz, row = "SamplingDateTimeREAL",
               col = "VariableName", val = "DataValue",
               subset = (WSnioz$Station == 1), df.row = 5)

Mplot(cbind(st1$x/365+1900,st1$z))

## =====
## All timeseries for multiple stations
## =====

dat <- NULL
for (st in 1:17) {
  dd <- db2cross(WSnioz, row = "SamplingDateTimeREAL",
                col = "VariableName", val = "DataValue",
                subset = (WSnioz$Station == st), df.row = 5)
  dat <- rbind(dat, cbind(st, time = dd$x/365+1900, dd$z))
}

# select data for station 1, 17
dat2 <- Msplit(dat, split = "st", subset = st %in% c(1, 17))
names(dat2)

Mplot(dat2, lty = 1)

## =====
## tabular format of the same data
## =====

head(WSnioz.table)

# plot all data from station 1:
Mplot(WSnioz.table, select = 3:11, subset = Station == 1, legend = FALSE)

Mplot(Msplit(WSnioz.table, "Station", subset = Station %in% c(1, 13)) ,
      select = c("WNO3", "WNO2", "WNH4", "WO2"), lty = 1, lwd = 2,

```

```
xlab = "Daynr", log = c("y", "y", "y", ""),
legend = list(x = "left", title = "Station")

# reset plotting parameters
par(mar = mar)
par(mfrow = pm)
```

Profile data set *Temperature profiles made along a ship track.*

Description

Profiles of temperature made along a ship track, originally made available by US NOAA NODC.

The data were merged from 29 input files named `gtspp_103799_xb_111.nc` till `gtspp_103827_xb_111.nc`.

These data were acquired from the US NOAA National Oceanographic Data Center (NODC) on 9/06/2012 from <https://www.nodc.noaa.gov/gtspp/>.

Usage

```
data(TrackProf)
```

Format

list with

- `meta`, a `data.frame` with the metadata, containing for each of the 29 profiles the following:
 - `station`, the number of the station (part of the original filename).
 - `filename`, the original name of the NetCDF file.
 - `date`, the date of sampling.
 - `time`, the time of sampling, a number relative to 1-1-1900 0 hours.
 - `longitude`, dg E.
 - `latitutde`, dg N.
- `temp`, the seawater temperature, at the depth of the measurement in dg C. A matrix of dimension (29, 93) for the 29 profiles and (at most) 93 depth values; NA means no measurement.
- `depth`, the depth of the measurement in `temp`, in metres, positive downward. A matrix of dimension (29, 93) for the 29 profiles and (at most) 93 depth values; NA means no measurement.

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

References

<https://www.nodc.noaa.gov/gtspp/>

U.S. National Oceanographic Data Center: Global Temperature-Salinity Profile Programme. June 2006. U.S. Department of Commerce, National Oceanic and Atmosphere Administration, National Oceanographic Data Center, Silver Spring, Maryland, 20910. Date of Access: 9/06/2012.

See Also

[image2D](#) for plotting images, package `plot3D`.

[ImageOcean](#) for an image of the ocean bathymetry, package `plot3D`.

[scatter2D](#) for making scatterplots, package `plot3D`.

[Oxsat](#) for a 3-D data set, package `plot3D`.

Examples

```
# save plotting parameters
pm <- par(mfrow = c(2, 2))
mar <- par("mar")

## =====
## show the metadata
## =====
print(TrackProf$meta)

## =====
## display the cruisetrack on the Ocean Bathymetry data
## =====
# 1. plots the ocean's bathymetry and add sampling positions
ImageOcean(xlim = c(-50, 50), ylim = c(-50, 50),
           main = "cruise track")
points(TrackProf$meta$longitude, TrackProf$meta$latitude, pch = "+")

# mark starting point
points(TrackProf$meta$longitude[1], TrackProf$meta$latitude[1],
      pch = 18, cex = 2, col = "purple")

## =====
## image plots of raw data
## =====

image2D(z = TrackProf$depth, main = "raw depth values",
       xlab = "station nr", ylab = "sample nr", clab = "depth")
image2D(z = TrackProf$temp, main = "raw temperature values",
       xlab = "station nr", ylab = "sample nr", clab = "dgC")

## =====
## image plots of temperatures at correct depth
## =====

# water depths to which data set is interpolated
```

```

depth <- 0 : 809

# map from "sigma" to "depth" coordinates
Temp_Depth <- mapsigma (TrackProf$temp, sigma = TrackProf$depth,
  depth = depth)$var

# image with depth increasing downward and increased resolution (resfac)
image2D(z = Temp_Depth, main = "Temperature-depth",
  ylim = c(809, 0), y = depth, NAcol = "black", resfac = 2,
  xlab = "station nr", ylab = "depth, m", clab = "dgC")

## =====
## scatterplot of surface values on ocean bathymetry
## =====

par(mar = mar + c(0, 0, 0, 2))
par(mfrow = c(1, 1))

# No colors, but add contours
ImageOcean(xlim = c(-30, 30), ylim = c(-40, 40),
  main = "cruise track", col = "white", contour = TRUE)

# use data set TrackProf to add measured temperature, with color key
with (TrackProf,
  scatter2D(colvar = temp[,1], x = meta[ ,"longitude"],
    y = meta[ ,"latitude"], clab = "temp",
    add = TRUE, pch = 18, cex = 2))

# reset plotting parameters
par(mar = mar)
par(mfrow = pm)

```

Quiver and flow paths *Plots velocities as arrows or as trajectory plots.*

Description

Function `quiver2D` displays velocity vectors as arrows, using ordinary graphics.

Function `quiver2Drgl` displays velocity vectors as arrows using `rgl`.

Function `flowpath` displays the flow paths of particles, based on velocity vectors.

Usage

```
quiver2D(u, ...)
```

```
## S3 method for class 'matrix'
quiver2D(u, v, x = NULL, y = NULL,
  colvar = NULL, ...,
  scale = 1, arr.max = 0.2, arr.min = 0, speed.max = NULL,
```

```

    by = NULL, type = "triangle", col = NULL, NAcol = "white",
    breaks = NULL, colkey = NULL, mask = NULL,
    image = FALSE, contour = FALSE,
    clim = NULL, clab = NULL,
    add = FALSE, plot = TRUE)

## S3 method for class 'array'
  quiver2D(u, v, margin = c(1, 2), subset, ask = NULL, ...)

quiver2Drgl (u, v, x = NULL, y = NULL, colvar = NULL, ...,
  scale = 1, arr.max = 0.2, arr.min = 0, speed.max = NULL,
  by = NULL, type = "triangle",
  col = NULL, NAcol = "white", breaks = NULL,
  mask = NULL, image = FALSE, contour = FALSE,
  colkey = NULL, clim = NULL, clab = NULL, add = FALSE, plot = TRUE)

flowpath(u, v, x = NULL, y = NULL, startx = NULL, starty = NULL, ...,
  scale = 1, numarr = 0, arr.length = 0.2, maxstep = 1000,
  add = FALSE, plot = TRUE)

```

Arguments

u	A matrix (quiver2D) or array (quiver2D.array) with velocities in x-direction. For quiver2D the number of rows should be = Nx or Nx+1 (Nx = length(x), if x given), the number of columns should be = Ny or Ny+1 (Ny = length(y), if y given).
v	A matrix (quiver2D) or array (quiver2D.array) with velocities in y-direction. For quiver2D the number of rows should be = Nx or Nx+1, the number of columns should be = Ny or Ny+1.
x	Vector with x-coordinates of the velocities. If NULL, it is taken to be a sequence between (0, 1), and with length = nrow(u).
y	Vector with y-coordinates of the velocities. If NULL, it is taken to be a sequence between (0, 1), and with length = ncol(v).
startx	Vector with the start position in x-direction of the flow paths. Length >=1. If not specified, then all combinations of x and y at the outer margins will be used as starting point.
starty	Vector with start position in y-direction of flow paths. Length = length of startx.
colvar	The variable used for coloring. It need not be present, but if specified, it should be a vector of dimension equal to c(nrow(u), ncol(v)). Values of NULL, NA, or FALSE will toggle off coloration according to colvar.
col	Colors to be used for coloring the arrows as specified by the colvar variable. If col is NULL and colvar is specified, then a red-yellow-blue colorscheme (jet.col) will be used. If col is NULL and colvar is not specified, then col will be "black".
NAcol	Colors to be used for colvar values that are NA.

breaks	a set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.
scale	Scaling factor for the arrows. When <code>scale = 1</code> , the longest arrow will fill a grid cell in x- and y- direction. When <code>scale = 2</code> , it will be twice as long.
arr.max	Maximal size of the arrowhead, in cm (approximately). The arrows are scaled according to the velocity ($\sqrt{u^2 + v^2}$). <code>arr.max</code> is associated with the maximal velocity.
arr.min	Minimal size of the arrowhead, in cm (approximately). Set <code>arr.min = arr.max</code> for constant size.
speed.max	Speed that corresponds to <code>arr.max</code> . Everything with speed larger than <code>speed.max</code> will be depicted with size equal to <code>arr.max</code> . If unspecified ($\max(\sqrt{u^2 + v^2})$).
by	Number increment for plotting the vectors; one value or two (x, y) values. For example, setting <code>by = 2</code> will plot every second velocity value in x and in y direction. Setting <code>by = c(1, 2)</code> will plot all vectors in x and every second vector in y. Useful if the vector density is too high.
colkey	A logical, NULL (default), or a list with parameters for the color key (legend). List parameters should be one of <code>side</code> , <code>plot</code> , <code>length</code> , <code>width</code> , <code>dist</code> , <code>shift</code> , <code>addlines</code> , <code>col.clab</code> , <code>cex.clab</code> , <code>side.clab</code> , <code>line.clab</code> , <code>adj.clab</code> , <code>font.clab</code> and the axis parameters <code>at</code> , <code>labels</code> , <code>tick</code> , <code>line</code> , <code>pos</code> , <code>outer</code> , <code>font</code> , <code>lty</code> , <code>lwd</code> , <code>lwd.ticks</code> , <code>col.box</code> , <code>col.axis</code> , <code>col.ticks</code> , <code>hadj</code> , <code>padj</code> , <code>cex.axis</code> , <code>mgp</code> , <code>tck</code> , <code>tcl</code> , <code>las</code> . The defaults for the parameters are <code>side = 4</code> , <code>plot = TRUE</code> , <code>length = 1</code> , <code>width = 1</code> , <code>dist = 0</code> , <code>shift = 0</code> , <code>addlines = FALSE</code> , <code>col.clab = NULL</code> , <code>cex.clab = par("cex.lab")</code> , <code>side.clab = NULL</code> , <code>line.clab = NULL</code> , <code>adj.clab = NULL</code> , <code>font.clab = NULL</code>) See colkey from package <code>plot3D</code> . The default is to draw the color key on <code>side = 4</code> , i.e. in the right margin. If <code>colkey = NULL</code> then a color key will be added only if <code>col</code> is a vector. Setting <code>colkey = list(plot = FALSE)</code> will create room for the color key without drawing it. if <code>colkey = FALSE</code> , no color key legend will be added.
type	The type of the arrow head, one of "triangle" (the default) or "simple", which uses R-function arrows .
contour, image	If present, then a contour2D or image2D plot will be added to the quiver plot. They should be a list with arguments for the contour2D or image2D function.
clim	Only if <code>colvar</code> is specified, the range of the colors, used for the color key.
clab	Only if <code>colkey</code> is not NULL or FALSE, the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, <code>clab</code> can be made a vector, with the first values empty strings.
margin	A vector giving the subscripts which the plotting function will be applied over. The plotting function will loop over the index that is not in <code>margin</code> . For instance, <code>c(1, 2)</code> , indicates to plot rows(x) and columns(y) and to loop over index 3; <code>c(2, 1)</code> will do the same but transposed. <code>margin</code> should be a vector with two numbers inbetween 1, and 3.
ask	A logical; if TRUE, the user is asked before each plot, if NULL the user is only asked if more than one page of plots is necessary and the current graphics device is set interactive, see par(ask) and dev.interactive .

<code>add</code>	If TRUE, will add to current plot. Else will start a new plot. Note: to use this in a consistent way, the previous plot should have been done with one of the <code>plot3D</code> functions.
<code>mask</code>	A matrix or list defining the grid cells outside the domain as NA. Use a list with argument <code>NAcol</code> to specify the color that the masked cells (that are NA) should get; the default is "black". The unmasked cells are left "white". If <code>x</code> and <code>y</code> are a vector, then <code>mask</code> can be a matrix with dimension equal to <code>length(x)</code> , <code>length(y)</code> . If either <code>x</code> or <code>y</code> is itself a matrix, then <code>mask</code> should be a list that contains the <code>x</code> , <code>y</code> , and <code>z</code> values (and that are named 'x', 'y', 'z'). A mask cannot be combined with <code>add = TRUE</code> .
<code>plot</code>	If FALSE, will not plot the flow paths, but will return the matrix with path values instead.
<code>numarr</code>	The number of arrows added on the flow paths.
<code>arr.length</code>	Constant size of the arrowhead, in cm (approximately).
<code>maxstep</code>	Maximum number of steps for calculating the flow paths.
<code>...</code>	Additional arguments passed to the plotting methods (arrows2D). The arguments after <code>...</code> must be matched exactly.
<code>subset</code>	A logical expression indicating over which elements to loop; missing values are taken as FALSE.

Details

S3 function `quiver2D` plots vectors specified by `u`, `v` at the coordinates `x`, `y`.

`flowpath` uses the velocities `u`, `v` at the coordinates `x`, `y` to create trajectories, starting at points `startx`, `starty`. It can also be used to return the flow path points by setting `plot` equal to FALSE. It uses very simple Euler integration and may not be very accurate.

Value

`flowpath` returns (as invisible) a 2-column matrix with the x-y coordinates of the flow paths. Separate flow paths are separated with NA.

`quiver2D` returns (as invisible) a list containing the coordinates of the arrows (`x0`, `x1`, `y0`, `y1`), the color of each arrow (`col`), the length of the arrowhead (`length`) and the maximal speed corresponding to `arr.max` (`speed.max`). This output can be used e.g. with function [arrows](#).

Note

There was a slight error in the scaling of the arrows in versions previous to 1.0.3, which has been corrected. See last example.

See Also

[arrows3D](#) for an arrows function from package `plot3D`.

[vectorplot](#) for plotting velocity vectors as spikes.

[Arrows](#) for the arrow function from package `shape` on which `quiver2D` is based.

Examples

```

## =====
## EXAMPLE 1:
## =====
pm <- par("mfrow")
par(mfrow = c(2, 2))

# generate velocities
x <- seq(-1, 1, by = 0.2)
y <- seq(-1, 1, by = 0.2)
dx <- outer(x, y, function(x, y) -y)
dy <- outer(x, y, function(x, y) x)

# velocity plot, with legend
F <- quiver2D(u = dx, v = dy, x = x, y = y)
legend("topright", bg = "white",
      legend = paste("max = ", format(F$speed.max, digits = 2)))

# different color for up/downward pointing arrows
quiver2D(u = dx, v = dy, x = x, y = y, colvar = dx > 0,
        col = c("red", "blue"), colkey = FALSE,
        arr.max = 0.4, arr.min = 0.1)

# different scale
quiver2D(u = dx, v = dy, x = x, y = y, by = 2, scale = 2)

# three flow paths
flowpath(u = dx, v = dy, x = x, y = y, startx = 0.1, starty = 0.1)
flowpath(u = dx, v = dy, x = x, y = y,
        startx = c(0.9, -0.9), starty = c(0.0, 0.0), col = "red",
        numarr = 2, add = TRUE)

## =====
## EXAMPLE 2: note: has changed in version 1.0.3 - uses contour2D!
## =====
par(mfrow = c(1, 1))
x <- seq(-2, 2, by = 0.2)
y <- seq(-1, 1, by = 0.2)
z <- outer(x, y, function(x, y) x^3 - 3*x - 2*y^2)
contour2D(x, y, z = z, col = jet.col(10))

# gradients in x- and y-direction (analytical)
dX <- outer(x, y, function(x,y) 3*x^2 - 3)
dY <- outer(x, y, function(x,y) -4*y)

quiver2D(u = dX, v = dY, x = x, y = y, scale = 1, add = TRUE, by = 1)
flowpath(u = dX, v = dY, x = x, y = y, startx = c(-2, 1.1),
        starty = c(-1, -1), add = TRUE, arr.length = 0.5,
        col = "darkgreen", lwd = 3, numarr = 1)

## =====
## EXAMPLE 3:

```

```

## =====
x <- y <- 1:20
u <- outer (x, y, function (x, y) cos(2*pi*y/10))
v <- outer (x, y, function (x, y) cos(2*pi*x/10))

quiver2D(x = x, y = y, u = u, v = v, col = "grey")

# flowpaths using all combinations of x and y at edges
flowpath(x = x, y = y, u = u, v = v, add = TRUE,
         lwd = 2, col = "orange")

## =====
## EXAMPLE 4: quiver of an array..
## =====

x <- y <- 1:20
u2 <- outer (x, y, function (x, y) sin(2*pi*y/10))
v2 <- outer (x, y, function (x, y) sin(2*pi*x/10))

# merge u, u2 and v, v2 to create an "array"
U <- array(dim = c(dim(u2), 2), data = c(u, u2))
V <- array(dim = c(dim(v2), 2), data = c(v, v2))

quiver2D(u = U, v = V, x = x, y = y, main = c("time 1", "time 2"))

# quiver over x and time, for a subset of y-values:
quiver2D(u = U, v = V, x = x, y = 1:2,
        margin = c(1, 3), main = paste("y ", y),
        subset = y <= 4)

## Not run:
quiver2D(u = U, v = V, x = x, y = y, ask = TRUE,
        mfrow = c(1, 1))

quiver2D(u = U, v = V, x = x, y = 1:2, ask = TRUE,
        margin = c(1, 3), main = paste("y ", y),
        mfrow = c(1, 1))

## End(Not run)

## =====
## EXAMPLE 5:
## =====

par(mfrow = c(1, 1))

image2D(x = 1:nrow(volcano), y = 1:ncol(volcano),
        z = volcano, contour = TRUE)

# Assume these are streamfunctions, we calculate the velocity field as:
dx <- dy <- 1
v <- (volcano[-1, ] - volcano[-nrow(volcano), ])/dx

```

```

u <- - (volcano[, -1] - volcano[ , -ncol(volcano)] )/dy

quiver2D(x = 1:nrow(u), y = 1:ncol(v),
         u = u, v = v, add = TRUE, by = 3)

flowpath(x = 1:nrow(u), y = 1:ncol(v), numarr = 10,
         u = u, v = v, add = TRUE, lwd = 2, col = "grey",
         startx = 20, starty = 30)

## =====
## EXAMPLE 6: boundary mask, images, contours
## =====
par (mfrow = c(2, 2))

mask <- volcano; mask[volcano < 120] <- NA
quiver2D(by = c(3, 2), u = u, v = v, mask = mask)

quiver2D(by = c(3, 2), u = u, v = v,
         image = list(z = mask, NAcol = "black"))

quiver2D(by = c(4, 3), u = u, v = v,
         contour = list(z = volcano, lwd = 2))

quiver2D(by = c(4, 3), u = u, v = v,
         contour = list(z = volcano, col = "black"),
         image = list(z = volcano, NAcol = "black"))

## =====
## Same in rgl
## =====
## Not run:
quiver2Drgl(by = c(3, 2), u = u, v = v, mask = mask, NAcol = "black")

quiver2Drgl(by = c(3, 2), u = u, v = v,
            image = list(z = volcano, NAcol = "black"))

quiver2Drgl(by = c(4, 3), u = u, v = v, scale = 2,
            contour = list(z = volcano, lwd = 2))

quiver2Drgl(by = c(4, 3), u = u, v = v,
            contour = list(z = volcano, col = "black"),
            image = list(z = volcano, NAcol = "black"))
cutrgl()
uncutrgl()

## End(Not run)

## =====
## 2-D Data set SyltSurf
## =====

par(mfrow = c(1, 1))
with (Syltsurf,

```

```

    quiver2D(x = x, y = y, u = u[ , ,2], v = v[ , ,2],
             xlim = c(5, 20), ylim = c(10, 25), by = 3,
             main = paste(formatC(time[1]), " hr"), scale = 1.5,
             image = list(z = depth, x = x, y = y, NAcol = "black",
                          colkey = TRUE),
             contour = list(z = depth, x = x, y = y, col = "black",
                             drawlabels = FALSE)
    )
)

## =====
## 2-D Data set SyltSurf, several time points
## =====

# now for an array (first and 4th time point only)
ii <- c(1, 4)
with (Syltsurf,
      quiver2D(x = x, y = y, u = u[ , ,ii], v = v[ , ,ii],
               xlim = c(5, 20), ylim = c(10, 25), by = 4,
               mask = list(z = depth, x = x, y = y, NAcol = "blue"),
               main = paste(formatC(time[ii]), " hr"), scale = 1.5,
               contour = list(z = depth, x = x, y = y, drawlabels = FALSE)
      )
)

## =====
## Adding quivers ...
## =====
x <- 1:2
y <- 1:3
u <- matrix(data = 1:6, nrow = 2, ncol = 3)
v <- matrix(data = 6:1, nrow = 2, ncol = 3)

par(mfrow = c(1, 1))
A <- quiver2D(x = x, y = y, u = u, v = v)
B <- quiver2D(x = x, y = y[-1], u = u[,-1], v = v[,-1], col = 2, add = TRUE)
C <- quiver2D(x = x, y = y[-3], u = u[,-3], v = v[,-3], col = 3, add = TRUE)

# restore parameter settings
par(mfrow = pm)

```

Reshaping to a crosstable

Converts a dataset from database-format to a cross table

Description

Reshapes data arranged in 3 columns to a “crosstable” matrix.

Usage

```
db2cross (input, row = 1, col = 2, value = 3, subset = NULL,
         df.row = NA, df.col = NA, out.row = NA, out.col = NA,
         full.out = FALSE)
```

Arguments

<code>input</code>	A matrix in <i>database</i> format, (x,y,z) .
<code>row</code>	Number or name of the column in <code>input</code> , to be used as rows in the result.
<code>col</code>	Number or name of the column in <code>input</code> , to be used as columns in the result.
<code>value</code>	Number or name of the column in <code>input</code> , to be used as values in the result.
<code>subset</code>	Logical expression indicating elements or rows to keep; missing values are taken as FALSE
<code>df.row, df.col</code>	Maximal distance in row and column values that should be considered the same. The default is to use each unique row or column value in <code>input</code> as a row or column value in the crosstable. Overruled when <code>out.row</code> or <code>out.col</code> are defined.
<code>out.row, out.col</code>	Values of rows and columns to be used in the cross table. The default is to use each unique row or column value in <code>input</code> as a row or column value in the crosstable. Each value in <code>input</code> is mapped to <code>out.row</code> and <code>out.col</code> to which it is closest. Overrules <code>df.row</code> or <code>df.col</code> .
<code>full.out</code>	If TRUE, will also output how the input values were mapped to the output values. This is only relevant if either of <code>df.row</code> , <code>df.col</code> , <code>out.row</code> or <code>out.col</code> is not NULL.

Details

Uses a simple fortran function.

rows and columns are generated by the unique values in each x- and y-column.

Value

a list containing:

<code>x</code>	The values of the <i>rows</i> .
<code>y</code>	The values of the <i>columns</i> .
<code>z</code>	The crosstable, a matrix.

and if `full.out = TRUE` also

<code>map</code>	The mapping of the <code>x</code> and <code>y</code> values, consisting of <code>var.input</code> , <code>factor</code> , <code>var.output</code> , with the original values, how they are mapped, and the resulting values respectively.
------------------	---

Author(s)

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See Also

[reshape](#), the official (slow) R-function

[remap](#) to remap a matrix or array to higher or lower resolution

Examples

```
## =====
## test the function on a small data set
## =====

df3 <- data.frame(school = rep(c("a","b","c"), each = 4),
                  class = rep(9:10, 6),
                  time = rep(c(1,1,2,2), 3),
                  score = rnorm(12))

head(df3)
db2cross(df3, val = 4)

## =====
## Defining the output rows
## =====
Samples <- data.frame(time = c(1, 1.1, 1.2, 2, 2.1, 2.2, 4, 4.1, 4.2),
                      var = rep(c("O2", "NO3", "NH3"), 3),
                      val = 1:9)

Samples

db2cross(Samples)
db2cross(Samples, df.row = 0.5)
db2cross(Samples, out.row = c(1, 2, 4))
db2cross(Samples, out.row = 1:4)

## =====
## A larger dataset; requires OceanView.Data
## =====
## Not run:
data (pp.aug2009.db)
crosstab <- db2cross(pp.aug2009.db)
crosstab$z[crosstab$z>1000] <- 1000
crosstab$z[crosstab$z<0] <- NA

image2D(z = crosstab$z, x = crosstab$x, y = crosstab$y,
        main = "primary production august 2009 mgC/m2/d",
        NAcol = "black")

## End(Not run)
```

Description

3D Sylt-tidal simulation model output generated by the GETM model version 2.2.2.

The Sylt-Romo bight is a Wadden Sea embayment in the North Sea, between the Danish island Romo and the German island Sylt at about 55 dg N and 8 dg E, an area of approximately 300 km².

- `Sylttran` contains (x, sigma, time) data from an E-W transect.
- `Syltsurf` contains 2-D surface data, at 5 time intervals.
- `Sylt3D` contains 3-D (x, y, z) data, at 2 time intervals.

Usage

```
data(Sylttran)
data(Syltsurf)
data(Sylt3D)
```

Format

- `Sylttran` is a `data.frame` with (x, sigma, time) data from an E-W transect (8.1 - 17.9 km) taken at km 18.5. There are 50 x-values, 21 sigma levels and 21 model output times.

It contains:

- x, y, the positions in km, of length 50 and 1 respectively.
- time, the model output time in hours, of length 21.
- visc, the viscosity (getm variable num), (50 x 21 x 21), m²/s.
- tke, the turbulent kinetic energy (getm variable tke), (50 x 21 x 21), m²/s².
- u, v, the zonal and meridional velocity, (50 x 21 x 21), m/s.
- sigma, the depth of the sigma coordinates (50 x 21 x 21), metres.
- `Syltsurf` contains 2-D surface data of the entire model domain, at 5 time intervals (hour 24.7 to 37.1). It is a `data.frame` with:
 - x, y, the positions in km, of length 135 and 160 respectively.
 - time, the output time in hours, of length 5.
 - u, v, the vertically averaged zonal and meridional velocity (135 x 160 x 5), m/s.
 - elev, tidal elevation (135 x 160 x 5), metres.
 - depth, the bathymetry (135 x 160), metres.
- `Sylt3D` contains 3-D (x, y, z) data, at 2 time intervals (hour 0 and 9.94). The box extends from x inbetween [12.1, 14.9] and from y inbetween [12.7 - 16.3]; there are 21 sigma levels.

It is a `data.frame` with:

- x, y, the positions in km, of length 15 and 19 respectively.
- time, the output time in hours, of length 2.
- visc, the viscosity (getm model variable num), (55 x 19 x 21 x 2), m²/s.
- sigma, the sigma depth levels, (55 x 19 x 21 x 2), m²/s. metres.
- depth, the bathymetry (15 x 19), metres.

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

References

Hans Burchard and Karsten Bolding, 2002. GETM, A General Estuarine Transport Model, Scientific Documentation. EUR 20253 EN.

<https://getm.eu>

See Also

[image2D](#) for plotting images, package `plot3D`.

[ImageOcean](#) for an image of the ocean's bathymetry, package `plot3D`.

[scatter2D](#) for making scatterplots, package `plot3D`.

[Oxsat](#) for a 3-D data set, package `plot3D`.

Examples

```
# save plotting parameters
pm <- par("mfrow")
mar <- par("mar")

## =====
## Show position of transect and 3D box in bathymetry
## =====

par(mfrow = c(2, 2))
par(mar = c(4, 4, 4, 4))

x <- Syltsurf$x ; y <- Syltsurf$y ; depth <- Syltsurf$depth
image2D(z = depth, x = x, y = y, clab = c("depth", "m"))

# position of transect
with(Sylttran, points(x, rep(y, length(x)),
  pch = 16, col = "grey"))
# position of 3-D area
with(Sylt3D, rect(x[1], y[1], x[length(x)], y[length(y)], lwd = 3))

image2D(z = depth, x = x, y = y, clab = c("depth", "m"), log = "z")

# sigma coordinates of the transect (at time = 10)
matplot(Sylttran$x, Sylttran$sigma[,10], type = "l",
  main = "sigma", ylim = c(25, -2), col = "black", lty = 1)

# perspective view - reduce resolution for speed
ix <- seq(1, length(x), by = 3)
iy <- seq(1, length(y), by = 3)

par(mar = c(1, 1, 1, 2))
persp3D(z = -depth[ix, iy], x = x[ix], y = y[iy],
  scale = FALSE, expand = 0.2, ticktype = "detailed",
  col = "grey", shade = 0.6, bty = "f",
  plot = FALSE)
```

```

# add 3-D region; small amount added to z so that it is visible in rgl
persp3D(z = -Sylt3D$depth + 1e-3, x = Sylt3D$x, y = Sylt3D$y,
  col = alpha.col("red", alpha = 0.4), add = TRUE,
  plot = FALSE)

# transect
with (Sylttran, points3D(x = x, y = rep(y, length(x)),
  z = rep(0, length(x)), pch = 16, add = TRUE, colkey = FALSE))

## Not run:
plotrgl()
plotrgl(lightning = TRUE, new = FALSE, smooth = TRUE)

## End(Not run)

## =====
## Data Syltsurf: Surface elevation
## =====

par(mfrow = c(2, 2), mar = c(0, 0, 1, 0))
# reduce resolution for speed
ix <- seq(1, length(x), by = 3)
iy <- seq(1, length(y), by = 3)

clim <- range(Syltsurf$elev, na.rm = TRUE)
for (i in 1:3)
  persp3D(z = -depth[ix, iy], colvar = Syltsurf$elev[ix,iy,i],
    x = x[ix], y = y[iy], clim = clim, inttype = 2, d = 2,
    scale = FALSE, expand = 0.1, colkey = FALSE, shade = 0.5,
    main = paste(format(Syltsurf$time[i], digits = 3), " hr"))
par(mar = c(3, 3, 3, 3))
colkey(clim = clim, clab = c("elevation", "m"))

# can also be done using shaded image2D plots, faster
par(mfrow = c(2, 2), mar = c(3, 3, 3, 3))
clim <- range(Syltsurf$elev, na.rm = TRUE)
for (i in 1:3)
  image2D(z = -depth[ix, iy], colvar = Syltsurf$elev[ix,iy,i],
    x = x[ix], y = y[iy], clim = clim,
    colkey = FALSE, shade = 0.3, resfac = 2,
    main = paste(format(Syltsurf$time[i], digits = 3), " hr"))
colkey(clim = clim, clab = c("elevation", "m"))

## =====
## Data Syltsurf: Surface currents
## =====

par(mfrow = c(1, 1))
Speed <- sqrt(Syltsurf$u[,2]^2 + Syltsurf$v[,2]^2)

with (Syltsurf,
  quiver2D(x = x, y = y, u = u[,2], v = v[,2], col = gg.col(100),
    xlim = c(5, 20), ylim = c(10, 25), by = 3,

```

```

        colvar = Speed, clab = c("speed", "m/s"),
        main = paste(formatC(time[1]), " hr"), scale = 1.5,
        image = list(z = depth, x = x, y = y, col = "white", #background
                    NAcol = "darkblue"),
        contour = list(z = depth, x = x, y = y, col = "black", #depth
                      lwd = 2)
    )
)

## =====
## Data Sylttran: plot a transect
## =====

par(mfrow = c(1, 1), mar = c(4, 4, 4, 2))
D <- seq(-1, 20, by = 0.02)

visc <- mapsigma (Sylttran$visc [ , ,1], x = Sylttran$x,
                 sigma = Sylttran$sigma[ , ,1], depth = D, resfac = 2)

image2D(visc$var, x = visc$x, y = -visc$depth, ylim = c(-20, 1),
        main = "eddy viscosity", ylab = "m", xlab = "hour",
        clab = "m2/s")

# show position of timeseries in next example
abline(v = visc$x[45])

## =====
## Data Sylttran: plot a time-series
## =====

par(mfrow = c(1, 1), mar = c(5, 4, 4, 3))
ix <- 45

visct <- Sylttran$visc [ix, ,]
sig <- Sylttran$sigma [ix, ,]

# sigma coordinates are first dimension (signr)
visc <- mapsigma(visct, sigma = sig, signr = 1,
                x = Sylttran$time, numdepth = 100, resfac = 3)
D <- -visc$depth

image2D(t(visc$var), x = visc$x, y = D, NAcol = "black",
        ylim = range(D), main = "eddy viscosity",
        ylab = "m", xlab = "hour", clab = "m2/s")

## =====
## Data Sylt3D: increase resolution and map from sigma to depth
## =====

# select a time series point
it <- 1
par(mfrow = c(1, 1))
sigma <- Sylt3D$sigma[, , it]

```

```

visc <- Sylt3D$visc [,,it]
(D <- dim(sigma))    # x, y, z

# remap the data from sigma coordinates to depth coordinates
# depth from max in first box to max in last box
depth <- seq(max(sigma[,D[3]], na.rm = TRUE),
             max(sigma[,1 ], na.rm = TRUE), length.out = 20)

# Step-bystep mapping, increasing the resolution
z <- 1:21
x <- Sylt3D$x
y <- Sylt3D$y

xto <- seq(min(x), max(x), length.out = 30)
yto <- seq(min(y), max(y), length.out = 30)

# higher resolution
Sigma <- remap(sigma, x, y, z, xto, yto, zto = z)$var
Visc <- remap(visc, x, y, z, xto, yto, zto = z)$var

# viscosity in sigma coordinates
visc_sig <- mapsigma(Visc, sigma = Sigma, depth = depth)

## =====
## The 3-D data set - plotted as slices
## =====

slice3D(xto, yto, -visc_sig$depth, colvar = visc_sig$var,
        scale = FALSE, expand = 0.1, NAcol = "transparent",
        ys = yto[seq(1, length(yto), length.out = 10)], plot = FALSE,
        colkey = list(side = 1))
persp3D(x = x, y = y, z = -Sylt3D$depth, add = TRUE,
        border = "black", facets = NA, colkey = FALSE)

# visualise it in rgl window
plotrgl()

## the same, as a movie

persp3Drgl(x = x, y = y, z = -Sylt3D$depth, smooth = TRUE,
           col = "grey", lighting = TRUE)

movieslice3D(xto, yto, -visc_sig$depth, colvar = visc_sig$var,
            add = TRUE, ys = yto)

# in order to wait inbetween slice drawings until a key is hit:
## Not run:
persp3Drgl(x = x, y = y, z = -Sylt3D$depth, smooth = TRUE,
           col = "grey", lighting = TRUE)
movieslice3D(xto, yto, -visc_sig$depth, colvar = visc_sig$var, add = TRUE,
            ask = TRUE, ys = yto)

## End(Not run)

```

```

## =====
## The 3-D data set - plotted as isosurfaces
## =====

isosurf3D(xto, yto, -visc_sig$depth, colvar = visc_sig$var,
  level = c(0.005, 0.01, 0.015), col = c("red", "blue", "green"),
  scale = FALSE, expand = 0.1, ticktype = "detailed",
  main = "viscosity", clab = "m2/s",
  plot = FALSE, colkey = list(side = 1))
persp3D(x = x, y = y, z = -Sylt3D$depth, border = "black",
  col = "white", add = TRUE, plot = FALSE)

## Not run:
plotdev(alpha = 0.3, phi = 30)      # this is slow

## End(Not run)
plotrgl(alpha = 0.3)

# reset plotting parameters
par(mar = mar)
par(mfrow = pm)

```

Tracers in 2D

Plots tracer distributions in 2-D.

Description

tracers2D plots a tracer distribution using traditional R graphics. The topography can be defined when calling this function.

tracers2Drgl plots a tracer distribution in open-GL graphics. A suitable topography has to be created before calling this function.

Usage

```
tracers2D(x, y, colvar = NULL, ...,
  col = NULL, NAcot = "white", colkey = NULL,
  mask = NULL, image = FALSE, contour = FALSE,
  clim = NULL, clab = NULL)
```

```
tracers2Drgl(x, y, colvar = NULL, ...,
  col = NULL, NAcot = "white", breaks = NULL,
  colkey = FALSE, clim = NULL, clab = NULL)
```

Arguments

x, y Vectors with x- and y-coordinates of the tracers. Should be of equal length.

colvar	The variable used for coloring. It need not be present, but if specified, it should be a vector of dimension equal to x . Values of NULL, NA, or FALSE will toggle off coloration according to colvar.
col	Colors to be used for coloring each individual point (if colvar not specified) or that define the colors as specified by the colvar variable. If col is NULL and colvar is specified, then a red-yellow-blue colorscheme (<code>jet.col</code>) will be used. If col is NULL and colvar is not specified, then col will be "black".
NAcol	Colors to be used for colvar values that are NA.
breaks	a set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.
colkey	A logical, NULL (default), or a list with parameters for the color key (legend). List parameters should be one of <code>side</code> , <code>plot</code> , <code>length</code> , <code>width</code> , <code>dist</code> , <code>shift</code> , <code>addlines</code> , <code>col.clab</code> , <code>cex.clab</code> , <code>side.clab</code> , <code>line.clab</code> , <code>adj.clab</code> , <code>font.clab</code> and the axis parameters <code>at</code> , <code>labels</code> , <code>tick</code> , <code>line</code> , <code>pos</code> , <code>outer</code> , <code>font</code> , <code>lty</code> , <code>lwd</code> , <code>lwd.ticks</code> , <code>col.box</code> , <code>col.axis</code> , <code>col.ticks</code> , <code>hadj</code> , <code>padj</code> , <code>cex.axis</code> , <code>mgp</code> , <code>tck</code> , <code>tcl</code> , <code>las</code> . The defaults for the parameters are <code>side = 4</code> , <code>plot = TRUE</code> , <code>length = 1</code> , <code>width = 1</code> , <code>dist = 0</code> , <code>shift = 0</code> , <code>addlines = FALSE</code> , <code>col.clab = NULL</code> , <code>cex.clab = par("cex.lab")</code> , <code>side.clab = NULL</code> , <code>line.clab = NULL</code> , <code>adj.clab = NULL</code> , <code>font.clab = NULL</code>) See <code>colkey</code> from package <code>plot3D</code> . The default is to draw the color key on <code>side = 4</code> , i.e. in the right margin. If <code>colkey = NULL</code> then a color key will be added only if <code>col</code> is a vector. Setting <code>colkey = list(plot = FALSE)</code> will create room for the color key without drawing it. if <code>colkey = FALSE</code> , no color key legend will be added.
contour, image	If TRUE, then a <code>contour2D</code> or <code>image2D</code> plot will be added to the quiver plot. Also allowed is to pass a list with arguments for the <code>contour2D</code> or <code>image2D</code> function.
clim	Only if colvar is specified, the range of the colors, used for the color key.
clab	Only if colkey is not NULL or FALSE, the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, clab can be made a vector, with the first values empty strings.
mask	A list defining the grid cells outside the domain as NA. Use a list with argument <code>NAcol</code> to specify the color that the masked cells (that are NA) should get; the default is "black". The unmasked cells are left "white". mask should be a list that contains the <code>x</code> , <code>y</code> , and <code>z</code> values (and that are named <code>'x'</code> , <code>'y'</code> , <code>'z'</code>). A mask cannot be combined with <code>add = TRUE</code> .
...	additional arguments passed to the plotting method <code>scatter2D</code> . The arguments after ... must be matched exactly.

Value

returns nothing

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

See Also

[tracers3D](#) for plotting time series of tracer distributions in 3D

[Ltrans](#) for the output of a particle tracking model

Examples

```
# save plotting parameters
pm <- par("mfrow")

## =====
## Create topography, data
## =====

# The topographic surface
x <- seq(-pi, pi, by = 0.2)
y <- seq(0, pi, by = 0.1)
M <- mesh(x, y)
z <- with(M, sin(x)*sin(y))

# Initial condition
xi <- c(0.125 * rnorm(100) - pi/2, 0.125 * rnorm(100) - pi/4)
yi <- 0.25 * rnorm(200) + pi/2

# the species
species <- c(rep(1, 100), rep(2, 100))

# set initial conditions
xp <- xi; yp <- yi

## =====
## using a mask and contour
## =====

Z <- z; Z[abs(Z) < 0.1] <- NA
par(mfrow = c(2, 2))

for (i in 1:4) {
  # update tracer distribution
  xp <- xp + 0.25 * rnorm(200)
  yp <- yp + 0.025 * rnorm(200)

  # plot new tracer distribution
  tracers2D(xp, yp, colvar = species, pch = ".", cex = 5,
    main = paste("timestep ", i), col = c("orange", "blue"),
    colkey = list(side = 1, length = 0.5, labels = c("sp1", "sp2"),
    at = c(1.25, 1.75), dist = 0.075), NAcol = "black",
    mask = list(x = x, y = y, z = Z),
    contour = list(x = x, y = y, z = Z) )
}

## =====
## using image and contour
```

```

## =====
for (i in 1:4) {
  # update tracer distribution
  xp <- xp + 0.25 * rnorm(200)
  yp <- yp + 0.025 * rnorm(200)

  # plot new tracer distribution
  tracers2D(xp, yp, colvar = species, pch = ".", cex = 5,
    main = paste("timestep ", i), col = c("orange", "blue"),
    colkey = list(side = 1, length = 0.5, labels = c("sp1", "sp2")),
    at = c(1.25, 1.75), dist = 0.075), NAcol = "black",
    contour = list(x = x, y = y, z = z),
    image = list(x = x, y = y, z = z, colkey = TRUE))
}

## =====
## rgl tracer plot
## =====

# here the image has to be drawn first
image2Drgl(x = x, y = y, z = z)

# set initial conditions
xp <- xi; yp <- yi
nstep <- 40
for (i in 1:nstep) {
  # update tracer distribution
  xp <- xp + 0.25 * rnorm(200)
  yp <- yp + 0.025 * rnorm(200)

  # plot new tracer distribution
  tracers2Drgl(xp, yp, colvar = species, cex = 1,
    main = paste("timestep ", i), col = c("orange", "blue"))
}

# reset plotting parameters
par(mfrow = pm)

```

Description

tracers3D plots 3D tracer distributions in traditional graphics. The topography can be defined when calling this function or created before calling this function.

tracers3Drgl plots 3D tracer distributions in open-GL graphics. A suitable topography has to be created before calling this function. It does not create a movie.

moviepoints3D creates a movie of tracer distributions in open-GL graphics.

It is based on the plot3Drgl function [points3Drgl](#).

Usage

```
tracers3D (x, y, z, colvar = NULL, ...,
          col = NULL, NAcot = "white", breaks = NULL,
          colkey = FALSE, clim = NULL, clab = NULL, surf = NULL)
```

```
tracers3Drgl (x, y, z, colvar = NULL, ...,
             col = NULL, NAcot = "white", breaks = NULL,
             colkey = FALSE, clim = NULL, clab = NULL)
```

```
moviepoints3D (x, y, z, colvar, t, by = 1,
              col = jet.col(100), NAcot = "white", breaks = NULL,
              clim = NULL, wait = NULL, ask = FALSE, add = FALSE,
              basename = NULL, ...)
```

Arguments

x, y, z	Vectors with (x, y, z) positions of tracers. Should be of equal length.
colvar	The variable used for coloring. It need not be present, but if specified, it should be a vector of dimension equal to x, y, z. Values of NULL, NA, or FALSE will toggle off coloration according to colvar.
t	Vectors with time points of tracers. Should be of length equal to length of x, y, z, colvar.
by	Number increment of the time sequence.
col	Colors to be used for coloring each individual point (if colvar not specified) or that define the colors as specified by the colvar variable. If col is NULL and colvar is specified, then a red-yellow-blue colorscheme (jet.col) will be used. If col is NULL and colvar is not specified, then col will be "black".
NAcol	Colors to be used for colvar values that are NA.
breaks	a set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.
colkey	A logical, NULL (default), or a list with parameters for the color key (legend). List parameters should be one of side, plot, length, width, dist, shift, addlines, col.clab, cex.clab, side.clab, line.clab, adj.clab, font.clab and the axis parameters at, labels, tick, line, pos, outer, font, lty, lwd, lwd.ticks, col.box, col.axis, col.ticks, hadj, padj, cex.axis, mgp, tck, tcl, las. The defaults for the parameters are side = 4, plot = TRUE, length = 1, width = 1, dist = 0, shift = 0, addlines = FALSE, col.clab = NULL, cex.clab = par("cex.lab"), side.clab = NULL, line.clab = NULL, adj.clab = NULL, font.clab = NULL) See colkey from package plot3D. The default is to draw the color key on side = 4, i.e. in the right margin. If colkey = NULL then a color key will be added only if col is a vector. Setting

	<code>colkey = list(plot = FALSE)</code> will create room for the color key without drawing it. if <code>colkey = FALSE</code> , no color key legend will be added.
<code>clim</code>	Only if <code>colvar</code> is specified, the range of the colors, used for the color key.
<code>clab</code>	Only if <code>colkey</code> is not <code>NULL</code> or <code>FALSE</code> , the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, <code>clab</code> can be made a vector, with the first values empty strings.
<code>surf</code>	If not <code>NULL</code> , a list specifying a surface to be added on the scatterplot. They should include at least <code>x</code> , <code>y</code> , <code>z</code> , equal sized matrices, and optional: <code>colvar</code> , <code>col</code> , <code>NACol</code> , <code>border</code> , <code>facets</code> , <code>lwd</code> , <code>resfac</code> , <code>clim</code> , <code>ltheta</code> , <code>lphi</code> , <code>shade</code> , <code>lighting</code> . Note that the default is that <code>colvar</code> is not specified.
<code>add</code>	Logical. If <code>TRUE</code> , then the points will be added to the current plot. If <code>FALSE</code> a new plot is started.
<code>ask</code>	Logical. If <code>TRUE</code> , then new points will only be drawn after a key has been struck. If <code>FALSE</code> , redrawing will depend on <code>wait</code>
<code>wait</code>	The time interval inbetween drawing of a set of new points, in seconds. If <code>NULL</code> , the drawing will not be suspended.
<code>basename</code>	The base name of a png file to be produced for each movieframe.
<code>...</code>	additional arguments passed to <code>scatter3D</code> from package <code>plot3D</code> . Typical arguments are <code>cex</code> , <code>main</code> (both functions), and <code>pch</code> , <code>...</code> for <code>tracers3D</code> .

Value

returns nothing

Author(s)

Karline Soetaert <karline.soetaert@nioz.nl>

See Also

[tracers2D](#) for plotting time series of tracer distributions in 2D

[movieslice3D](#) for plotting slices in 3D

[Ltrans](#) for 3-D output of a particle tracking model

Examples

```
# save plotting parameters
pm <- par("mfrow")

## =====
## Create topography, data
## =====

# The topographic surface
x <- seq(-pi, pi, by = 0.2)
y <- seq(0, pi, by = 0.1)
M <- mesh(x, y)
```

```

z <- with(M, sin(x)*sin(y))

# Initial condition
xi <- c(0.25 * rnorm(100) - pi/2, 0.25 * rnorm(100) - pi/4)
yi <- 0.25 * rnorm(200) + pi/2
zi <- 0.005*rnorm(200) + 0.5

# the species
species <- c(rep(1, 100), rep(2, 100))

# set initial conditions
xp <- xi; yp <- yi; zp <- zi

## =====
## Traditional graphics
## =====

par(mfrow = c(2, 2))

# Topography is defined by argument surf
for (i in 1:4) {
  # update tracer distribution
  xp <- xp + 0.25 * rnorm(200)
  yp <- yp + 0.025 * rnorm(200)
  zp <- zp + 0.25 * rnorm(200)

  # plot new tracer distribution
  tracers3D(xp, yp, zp, colvar = species, pch = ".", cex = 5,
    main = paste("timestep ", i), col = c("orange", "blue"),
    surf = list(x, y, z = z, theta = 0, facets = FALSE),
    colkey = list(side = 1, length = 0.5, labels = c("sp1", "sp2"),
      at = c(1.25, 1.75), dist = 0.075))
}

# same, but creating topography first
## Not run:
# create the topography on which to add points
persp3D(x, y, z = z, theta = 0, facets = FALSE, plot = FALSE)

for (i in 1:4) {
  # update tracer distribution
  xp <- xp + 0.25 * rnorm(200)
  yp <- yp + 0.025 * rnorm(200)
  zp <- zp + 0.25 * rnorm(200)

  # plot new tracer distribution
  tracers3D(xp, yp, zp, colvar = species, pch = ".", cex = 5,
    main = paste("timestep ", i), col = c("orange", "blue"),
    colkey = list(side = 1, length = 0.5, labels = c("sp1", "sp2"),
      at = c(1.25, 1.75), dist = 0.075))
}

## End(Not run)

```

```

## =====
## rgl graphics
## =====

# pause <- 0.05
# create a suitable topography
persp3D(x, y, z = z, theta = 0, facets = NA, plot = FALSE)

plotrgl( )
xp <- xi; yp <- yi; zp <- zi

nstep <- 10
for (i in 1:nstep) {
  xp <- xp + 0.05 * rnorm(200) + 0.05
  yp <- yp + 0.0025 * (rnorm(200) + 0.0025)
  zp <- zp + 0.05 * rnorm(200)

# tracers3Drgl(xp, yp, zp, col = c(rep("orange", 100), rep("blue", 100)),
#   main = paste("timestep ", i))
# or:
  tracers3Drgl(xp, yp, zp, colvar = species, col = c("orange", "blue"),
    main = paste("timestep ", i))
# Sys.sleep(pause)
# or: readline("hit enter for next")
}

# using function moviepoints3D

## Not run:
# first create the data in matrices
xp <- matrix(nrow = 200, ncol = nstep, data = rep(xi, times=nstep))
yp <- matrix(nrow = 200, ncol = nstep, data = rep(yi, times=nstep))
zp <- matrix(nrow = 200, ncol = nstep, data = rep(zi, times=nstep))
tp <- matrix(nrow = 200, ncol = nstep, data = 0)
cv <- matrix(nrow = 200, ncol = nstep, data = rep(species, times=nstep))
nstep <- 10
for (i in 2:nstep) {
  xp[,i] <- xp[,i-1] + 0.05 * rnorm(200) + 0.05
  yp[,i] <- yp[,i-1] + 0.0025 * (rnorm(200) + 0.0025)
  zp[,i] <- zp[,i-1] + 0.05 * rnorm(200)
  tp[,i] <- i
}
# create the topography
persp3Drgl(x, y, z = z, theta = 0, lighting = TRUE, smooth = TRUE)

# add moviepoints:
moviepoints3D (xp, yp, zp, colvar = cv, t = tp,
  wait = 0.05, cex = 10, col = c("red", "orange"))

## End(Not run)

```

```
# reset plotting parameters
par(mfrow = pm)
```

vector plots	<i>Vector velocity plot.</i>
--------------	------------------------------

Description

Displays (velocity) vectors as segments.

Usage

```
vectorplot(u, v, x = 0, y = 0, colvar = NULL, ...,
           col = NULL, NAcol = "white", breaks = NULL, colkey = NULL,
           by = 1, arr = FALSE, xfac = NULL,
           clim = NULL, clab = NULL, add = FALSE)
```

Arguments

u	A vector with quantities (velocities) in x-direction.
v	A vector with quantities (velocities) in y-direction. Should have the same length as u
x	A vector with x-axis values. If 0, everything will be radiating from the origin. Usually x will be equal to time.
y	The y-axis value. One number, or a vector of length = u.
colvar	The variable used for coloring. It need not be present, but if specified, it should be a vector of dimension equal to $c(nrow(u), ncol(v))$. Values of NULL, NA, or FALSE will toggle off coloration according to colvar.
col	Colors to be used for coloring the arrows as specified by the colvar variable. If col is NULL and colvar is specified, then a red-yellow-blue colorscheme (jet.col) will be used. If col is NULL and colvar is not specified, then col will be "black".
NAcol	Colors to be used for colvar values that are NA.
breaks	a set of finite numeric breakpoints for the colors; must have one more breakpoint than color and be in increasing order. Unsorted vectors will be sorted, with a warning.
colkey	A logical, NULL (default), or a list with parameters for the color key (legend). List parameters should be one of side, plot, length, width, dist, shift, addlines, col.clab, cex.clab, side.clab, line.clab, adj.clab, font.clab and the axis parameters at, labels, tick, line, pos, outer, font, lty, lwd, lwd.ticks, col.box, col.axis, col.ticks, hadj, padj, cex.axis, mgp, tck, tcl, las. The defaults for the parameters are side = 4, plot = TRUE, length = 1, width = 1, dist = 0, shift = 0, addlines = FALSE, col.clab = NULL, cex.clab = par("cex.lab"), side.clab = NULL, line.clab = NULL, adj.clab = NULL, font.clab = NULL) See colkey from package plot3D.

	The default is to draw the color key on side = 4, i.e. in the right margin. If colkey = NULL then a color key will be added only if col is a vector. Setting colkey = list(plot = FALSE) will create room for the color key without drawing it. if colkey = FALSE, no color key legend will be added.
clim	Only if colvar is specified, the range of the colors, used for the color key.
clab	Only if colkey is not NULL or FALSE, the label to be written on top of the color key. The label will be written at the same level as the main title. To lower it, clab can be made a vector, with the first values empty strings.
by	Number increment for plotting vectors. Set this to an integer > 1 if the vector density is too high.
xfac	Only for x not NULL, the proportionality factor with which the vectors on the x-axis must be drawn. A value of 1 means that the distance of one will be drawn as one x-unit on the x-axis. For a value of 2 a distance of 1 will appear as 2 x-units on the x-axis. if NULL, the range on the y-axis is used. In that case, it may be necessary to manually set the xlim of the figure.
arr	If TRUE, then Arrows will be drawn; if FALSE, segments will be drawn.
add	If TRUE, will add to the current plot.
...	additional arguments passed to the plotting methods.

Value

none

See Also[quiver2D](#), [flowpath](#), for other functions to plot velocities.**Examples**

```
# save plotting parameters
mf <- par("mfrow")

## =====
## EXAMPLE 1:
## =====

par(mfrow = c(2, 2))

u <- cos(seq(0, 2*pi, 0.1))
v <- sin(seq(0, 2*pi, 0.1)+ 1)

vectorplot(u = u, v = v)
vectorplot(u = u, v = v, col = 1:10)

x <- seq(0, 1, length.out = length(u))
vectorplot(u = u, v = v, x = x, xfac = 3)
points(x, rep(0, length(u)), pch = "+", col = "red")

vectorplot(u = u, v = v, x = 1:length(u), xfac = 10)
```

```
## =====  
## EXAMPLE 2: adding to a plot  
## =====  
  
par(mfrow = c(2, 2))  
x <- 1:length(u)  
plot(x, u)  
vectorplot(u = u, v = v, x = x, xfac = 10,  
           add = TRUE, col = "red")  
  
vectorplot(u = u, v = v, x = x, xfac = 10,  
           colvar = sqrt(u^2+v^2), clab = "m/s")  
  
vectorplot(u = u, v = v, x = x, xfac = 10,  
           colvar = sqrt(u^2+v^2), clab = "m/s", log = "c")  
  
# reset plotting parameters  
par(mfrow = mf)
```

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