Package ‘spatialEco’

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Type Package

Title Spatial Analysis and Modelling Utilities

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Description Utilities to support spatial data manipulation, query, sampling and modelling. Functions include models for species population density, download utilities for climate and global deforestation spatial products, spatial smoothing, multivariate separability, point process model for creating pseudo-absences and sub-sampling, polygon and point-distance landscape metrics, auto-logistic model, sampling models, cluster optimization, statistical exploratory tools and raster-based metrics.

Depends R (>= 4.0)

Imports sp, sf, raster, spatstat.geom, spatstat.core, spdep, rgeos, MASS, methods

Suggests exactextractr, cluster, readr, RCurl, RANN, rms, yaImpute, SpatialPack (>= 0.3), mgcv, EnvStats, maptools, GeNetIt, gstat, RStoolbox, terra, tabularaster, stringr

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License GPL-3

URL https://github.com/jeffreyevans/spatialEco

BugReports https://github.com/jeffreyevans/spatialEco/issues

NeedsCompilation no

Repository CRAN

LazyData true

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R topics documented:

`annulus.matrix` *Annulus matrix*

Description

Creates a square matrix representing annulus position values of 1 and defined null

Usage

```
annulus.matrix(scale = 3, inner.scale = 0, outer.scale = 0, null.value = 0)
```

Arguments

`scale`	Number of rings (defines dimensions of matrix)
`inner.scale`	Number of inner rings to set to null.value
`outer.scale`	Number of outer rings to set to null.value
`null.value`	Value to set inner and outer scale(s) to

Value

A matrix object with defined null.value and 1, representing retained rings

Note

This function will return a matrix of 1 and defined null.value based on a specification of the scale, inner scale and outer scale. The scale defines how many rings will be represented in the matrix based on (2 * scale - 1). So, a scale of 3 will result in a 5x5 matrix. The inner.scale and outer.scale arguments represent the > and < rings that will be set to the defined null.value (see examples). The resulting matrix can be used as the specified window in a focal function.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
annulus.matrix(5)                  # 5 concentric rings
annulus.matrix(5, 3)               # 5 concentric rings with the 3 inner set to 0
annulus.matrix(5, 3, null.value=NA) # 5 concentric rings with the 3 inner set to NA
annulus.matrix(5, 3, 5)            # 5 rings with 3 inner and 5 outer set to 0
annulus.matrix(9, 3, 7)            # 9 rings with 3 inner and 7 outer set to 0
```

ants *Ant Biodiversity Data*

Description

Roth et al., (1994) Costa Rican ant diversity data

Format

A data.frame with 82 rows (species) and 5 columns (covertypes):

species Ant species (family)

Primary.Forest Primary forest type

Abandoned.cacao.plantations Abandoned cacao plantations type

Productive.cacao.plantations Active cacao plantations type

Banana.plantations Active banana plantations type

Source

`http://www.tiem.utk.edu/~gross/bioed/bealsmodules/shannonDI.html`

References

Roth, D. S., I. Perfecto, and B. Rathcke (1994) The effects of management systems on ground-foraging ant diversity in Costa Rica. Ecological Applications 4(3):423-436.

background *Background sample*

Description

Creates a point sample that can be used as a NULL for SDM's and other modeling approaches.

Usage

```
background(
  x,
  ext = NULL,
  p = 1000,
  known = NULL,
  d = NULL,
  type = c("regular", "random", "hexagon", "nonaligned")
)
```

Arguments

x	A polygon defining sample region
ext	Vector of extent coordinates (xmin, xmax, ymin, ymax)
p	Size of sample
known	SpatialPoints of known locations (same CSR as x)
d	Threshold distance for known proximity
type	Type of sample c("systematic", "random", "hexagon", "nonaligned")

Value

A SpatialPointsDataFrame or data.frame with x,y coordinates

Note

This function creates a background point sample based on an extent or polygon sampling region. The known argument can be used with d to remove sample points based on distance-based proximity to existing locations (eg., known species locations). The size (p) of the resulting sample will be dependent on the known locations and the influence of the distance threshold (d). As such, if the know and d arguments are provided the exact value provided in p will not be returned.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
library(raster)
library(rgeos)
  data(meuse)
  coordinates(meuse) <- ~x+y

# create "known" locations
locs <- meuse[sample(1:nrow(meuse), 5),]

# systematic sample using extent polygon
e <- as(extent(meuse), "SpatialPolygons")
s <- background(e, p=1000, known=locs, d=300)
  plot(s,pch=20)
    points(locs, pch=20, col="red")

# systematic sample using irregular polygon
data(meuse.grid)
  coordinates(meuse.grid) = c("x", "y")
  gridded(meuse.grid) = TRUE
meuse.poly = gUnaryUnion(as(meuse.grid, "SpatialPolygons"))

s <- background(meuse.poly, p=1000, known=locs, d=200)
  plot(s,pch=20)
```

```
    plot(meuse.poly, add=TRUE)
    points(locs, pch=20, col="red")

# random sample using irregular polygon
s <- background(meuse.poly, p=500, known=locs,
                d=200, type="random")
  plot(s,pch=20)
    plot(meuse.poly, add=TRUE)
    points(locs, pch=20, col="red")

# systematic sample using defined extent
extent(meuse)
s <- background(ext=c(178605, 181390, 329714, 333611),
                p=1000, known=locs, d=300)
  plot(s,pch=20)
    points(locs, pch=20, col="red")
```

`bearing.distance` *Bearing and Distance*

Description

Calculates a new point [X,Y] based on defined bearing and distance

Usage

```
bearing.distance(x, y, distance, azimuth, EastOfNorth = TRUE)
```

Arguments

`x`	x coordinate
`y`	y coordinate
`distance`	Distance to new point (in same units as x,y)
`azimuth`	Azimuth to new point
`EastOfNorth`	Specified surveying convention

Value

a new point representing location of baring and distance

Note

East of north is a surveying convention and defaults to true.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
pt <- cbind( x=480933, y=4479433)
bearing.distance(pt[1], pt[2], 1000, 40)
```

`breeding.density` *Breeding density areas (aka, core habitat areas)*

Description

Calculates breeding density areas base on population counts and spatial point density.

Usage

```
breeding.density(x, pop, p = 0.75, bw = 6400, b = 8500, self = TRUE)
```

Arguments

`x`	sp SpatialPointsDataFrame object
`pop`	Population count/density column in x@data
`p`	Target percent of population
`bw`	Bandwidth distance for the kernel estimate (default 8500)
`b`	Buffer distance (default 8500)
`self`	(TRUE/FALSE) Should source observations be included in density (default TRUE)

Value

A list object with:

- pop.pts sp point object with points identified within the specified p
- pop.area sp polygon object of buffered points specified by parameter b
- bandwidth Specified distance bandwidth used in identifying neighbor counts
- buffer Specified buffer distance used in buffering points for pop.area
- p Specified population percent

Note

The breeding density areas model identifies the Nth-percent population exhibiting the highest spatial density and counts/frequency. It then buffers these points by a specified distance to produce breeding area polygons. If you would like to recreate the results in Doherty et al., (2010), then define bw = 6400m and b[if p < 0.75 b = 6400m, | p >= 0.75 b = 8500m]

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Doherty, K.E., J.D. Tack, J.S. Evans, D.E. Naugle (2010) Mapping breeding densities of greater sage-grouse: A tool for range-wide conservation planning. Bureau of Land Management. Number L10PG00911

Examples

```
require(sp)
n=1500
bb <- rbind(c(-1281299,-761876.5),c(1915337,2566433.5))
  bb.mat <- cbind(c(bb[1,1], bb[1,2], bb[1,2], bb[1,1]),
                  c(bb[2,1], bb[2,1], bb[2,2], bb[2,2]))
    bbp <- Polygon(bb.mat)
     s <- spsample(bbp, n, type='random')
        pop <- SpatialPointsDataFrame(s, data.frame(ID=1:length(s),
                                 counts=runif(length(s), 1,250)))

    bd75 <- breeding.density(pop, pop='counts', p=0.75, b=8500, bw=6400)
     plot(bd75$pop.area, main='75% breeding density areas')
       plot(pop, pch=20, col='black', add=TRUE)
         plot(bd75$pop.pts, pch=20, col='red', add=TRUE)
```

`built.index` *built index*

Description

Remote sensing built-up index

This function calculates the built-up index. Three methods are available:

- Bouhennache is a new method that uses a larger portion of the VIR/NIR following OLI bands (((b3+b4+b7)-b6)/3) / (((b3+b4+b7)+b6)/3)
- Zha is the original band ratio method using TM5 ndbi = (b5 - b4) / (b5 + b4)
- Xu is a modification to eliminate noise using ETM+7 (ndbi-((savi-nndwi)/2) / (ndbi+((savi-nndwi)/2)

Generally water has the highest values where built-up areas will occur in the mid portion of the distribution. Since Bouhennache et al (2018) index exploits a larger portion of the visible (Vis) and infra red spectrum, vegetation will occur as the lowest values and barren will exhibit greater values than the vegetation and lower values than the built-up areas.

Band wavelength (nanometers) designations for landsat TM4, TM5 and ETM+7

- band-2 0.52-0.60 (green)
- band-3 0.63-0.69 (red)
- band-4 0.76-0.90 (NIR)
- band-5 1.55-1.75 (SWIR 1)

- band-7 2.09-2.35 (SWIR 2)

OLI (Landsat 8)

- band-3 0.53-0.59 (green)
- band-4 0.64-0.67 (red)
- band-5 0.85-0.88 (NIR)
- band-6 1.57-1.65 (SWIR 1)
- band-7 2.11-2.29 (SWIR 2)

Usage

```
built.index(
  green,
  red,
  nir,
  swir1,
  swir2,
  L = 0.5,
  method = c("Bouhennache", "Zha", "Xu")
)
```

Arguments

`green`	Green band (0.53 - 0.59mm), landsat 5&7 band 3, OLI (landsat 8) band 3
`red`	Red band (0.636 - 0.673mm), landsat 5&7 band 3, OLI (landsat 8) band 4
`nir`	Near infrared band (0.851 - 0.879mm) landsat 5&7 band 4, OLI (landsat 8) band 5
`swir1`	short-wave infrared band 1 (1.566 - 1.651mm), landsat 5&7 band 5, OLI (landsat 8) band 6
`swir2`	short-wave infrared band 2 (2.11 - 2.29mm), landsat 5&7 band 7, OLI (landsat 8) band 7
`L`	The L factor for the savi index
`method`	Method to use for index options are "Bouhennache", "Zha", "Xu"

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Bouhennache, R., T. Bouden, A. Taleb-Ahmed & A. Chaddad(2018) A new spectral index for the extraction of built-up land features from Landsat 8 satellite imagery, Geocarto International 34(14):1531-1551

Xu H. (2008) A new index for delineating built-up land features in satellite imagery. International Journal Remote Sensing 29(14):4269-4276.

Zha G.Y., J. Gao, & S. Ni (2003) Use of normalized difference built-up index in automatically mapping urban areas from TM imagery. International Journal of Remote Sensing 24(3):583-594

Examples

```
## Not run:
library(raster)
library(RStoolbox)

data(lsat)
lsat <- radCor(lsat, metaData = readMeta(system.file(
               "external/landsat/LT52240631988227CUB02_MTL.txt",
                package="RStoolbox")), method = "apref")
   plotRGB(lsat, r=3, g=2, b=1, scale=1.0, stretch="lin")


# Using Bouhennache et al., (2018) method (needs green, red, swir1 and swir2)
( bouh <- built.index(red = lsat[[3]], green = lsat[[4]], swir1 = lsat[[5]],
                     swir2 = lsat[[7]]) )
   plotRGB(lsat, r=6,g=5,b=2, scale=1, stretch="lin")
     plot(bouh, legend=FALSE, col=rev(terrain.colors(100, alpha=0.35)),
       add=TRUE )

# Using simple Zha et al., (2003) method (needs nir and swir1)
( zha <- built.index(nir = lsat[[4]], swir1 = lsat[[5]], method = "Zha") )
  plotRGB(lsat, r=6,g=5,b=2, scale=1, stretch="lin")
    plot(zha, legend=FALSE, col=rev(terrain.colors(100, alpha=0.35)), add=TRUE )

# Using Xu (2008) normalized modification of Zha (needs green, red, nir and swir1)
( xu <- built.index(green= lsat[[3]], red = lsat[[3]], nir = lsat[[4]],
                    swir1 = lsat[[5]], , method = "Xu") )
  plotRGB(lsat, r=6,g=5,b=2, scale=1, stretch="lin")
    plot(xu, legend=FALSE, col=rev(terrain.colors(100, alpha=0.35)), add=TRUE )


## End(Not run)
```

---

cgls_urls *Provide URL's for Copernicus Global Land Service datasets*

Description

Returns URL's of a product/version/resolution

Usage

```
cgls_urls(
  dates = NULL,
  resolution = c(1000, 300),
  product = c("fapar", "fcover", "lai", "ndvi"),
  ver = c("newest", "v1", "v2", "v3")
)
```

Arguments

`dates`	Dates to subset default is NULL, returns all products
`resolution`	The product resolution c("1km", "300m"),
`product`	Which product to query options are "fapar",
`ver`	Product version options are "newest", "v1", "v2", "v3"

Details

Provides a query of the ESA's Copernicus Global Land Service global The query is performed on the manifest files and return URL's however, to download data you will need login credentials which, can be acquired from: http://land.copernicus.eu

If provided, dates need to be in a "YYYY-MM-DD" format. The dates are an explicit search string and can contain dates that are not in the imagery. As such, the user should generate a daily date string representing the range of the desired download as not to have to guess the available dates. Also note that multiple processing versions of a given image are retained in the manifest. This means that if you download a previous processing version, it could be an invalid image. It is highly recommended that you do not change the default ver="newest" argument unless there is a specific reason to.

Available products

- fapar Fraction of photosynthetically active radiation absorbed by the vegetation
- fcover Fraction of green vegetation cover
- lai Leaf Area index
- ndvi Normalized Difference Vegetation Index

Not yet implemented; Soil Water Index, Surface Soil Moisture, Copernicus product details: http://land.copernicus.eu/global/p

Value

A vector of download URL's for the products

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
# Create date string for query
d <- seq(as.Date("2020/05/01"), as.Date("2020-09-01"), by="day")

# Search for 300m (333m) LAI within specified date range
all.urls <- cgls_urls(dates = d, resolution = 300,
                        product = "lai")
# Search for 1000m LAI within specified date range
all.urls <- cgls_urls(dates = d, resolution = 1000,
                        product = "lai")

# Return all 300m LAI
```

```
lai <- cgls_urls(resolution = 300, product = "lai")
    head( basename(lai) )


## Example of downloading URL's
## You need to define your login credentials to download data
# username = "xxxx"
# password = "xxxx"
#
#   for(i in 1:length(all.urls)){
#     if(i > 1){ Sys.sleep(3) }
#     file.url <- paste0("https://", paste(username, password, sep=":"), "@",
#                        sub(".*//", "", all.urls[i]))
#     download.file(file.url, file.path(getwd(),
#                   basename(all.urls[i])), mode = 'wb')
#   }
```

chae *Canine-Human Age Equivalent*

Description

Calculates canines equivalent human age (for fun)

Usage

```
chae(x)
```

Arguments

x	numeric vector, dog age

Value

numeric vector, equivalent human age

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Wang, T., J. M, A.N. Hogan, S. Fong, K. Licon et al. (2020) quantitative translation of dog-to-human aging by conserved remodeling of epigenetic networks

Examples

```
dat <- data.frame(DogAge = seq(0,18,0.25),
             HumanAge=chae(seq(0,18,0.25)))[-1,]

plot(dat$DogAge, dat$HumanAge, "l",
     main="Canine-Human Age Equivalence",
 ylab="Human Age", xlab="Dog Age")
  points( 12, chae(12), col="red", pch=19, cex=1.5)
  points( 7, chae(7), col="blue", pch=19, cex=1.5)
  points( 0.5, chae(0.5), col="black", pch=19, cex=1.5)
legend("bottomright", legend=c("Camas (12-YO)", "Kele (7-YO)", "Aster (0.5-YO)"),
      pch=c(19,19,19), cex=c(1.5,1.5,1.5),
     col=c("red","blue","black"))
```

---

chen *Cross-correlation data from Chen (2015)*

Description

Urbanization and economic development data from Chen (2015) compiled from, National Bureau of Statistics of China http://www.stats.gov.cn/tjsj/ndsj/

Format

A list object with 3 elements:

X per capita GRP(yuan)

Y Level of urbanization percent

M Railway Distance (km) matrix of 29 Chinese regions

Source

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0126158

References

Chen, Y.G. (2012) On the four types of weight functions for spatial contiguity matrix. Letters in Spatial and Resource Sciences 5(2):65-72

Chen, Y.G. (2013) New approaches for calculating Moran's index of spatial autocorrelation. PLoS ONE 8(7):e68336

Chen, Y.G. (2015) A New Methodology of Spatial Cross-Correlation Analysis. PLoS One 10(5):e0126158. doi:10.1371/journal.pone.0126158

`class.comparison` *Class comparison between two nominal rasters*

Description

Compares two categorical rasters using Cohen's Kappa (d) or paired t-test statistic(s)

Usage

```
class.comparison(
  x,
  y,
  x.idx = 1,
  y.idx = 1,
  d = "AUTO",
  stat = "kappa",
  sub.sample = FALSE,
  type = "hexagon",
  p = 0.1,
  size = NULL
)
```

Arguments

`x`	First raster for comparison, SpatialPixelsDataFrame or SpatialGridDataFrame object
`y`	Second raster for comparison, SpatialPixelsDataFrame or SpatialGridDataFrame object
`x.idx`	Index for the column in the x raster object
`y.idx`	Index for the column in the y raster object
`d`	Distance for finding neighbors, the default "AUTO" will derive a distance
`stat`	Statistic to use in comparison ("kappa", "t.test", "both")
`sub.sample`	Should a subsampling approach be employed (FALSE/TRUE)
`type`	If sub.sample = TRUE, what type of sample ("random" or "hexagon")
`p`	If sub.sample = TRUE, what proportion of population should be sampled
`size`	If sub.sample = TRUE, alternate to proportion of population (p), using fixed sample size

Value

A SpatialPixelsDataFrame or SpatialPointsDataFrame with the following attributes:

- x x variable used to derive Kappa (d)
- y y variable used to derive Kappa (d)

- kappa Kappa (d) statistic
- t.test Paired t.test statistic (if stat = "t.test" or "both")
- p.value p-value of the paired t.test statistic (if stat = "t.test" or "both")

Note

This function provides a Cohen's Kappa or paired t-test to compare two classified maps. Point based subsampling is provided for computation tractability. The hexagon sampling is recommended as it it good at capturing spatial process that includes nonstationarity and anisotropy.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Cohen, J. (1960). A coefficient of agreement for nominal scales. Educational and Psychological Measurement, 20:37-46

Examples

```
 library(sp)
 library(raster)

 data(meuse.grid)
 r1 <- sp::SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
                                  data = meuse.grid)
   r1@data$class1 <- round(runif(nrow(r1), 1,5),0)
 r2 <- sp::SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
                                  data = meuse.grid)
r2@data$class2 <- round(runif(nrow(r2), 1,5),0)

 d <- class.comparison(r1, r2, x.idx = 8, y.idx = 8, stat="both")
 opar <- par(no.readonly=TRUE)
   par(mfrow=c(2,2))
     plot(raster(d, layer=3), main="Kappa")
    plot(raster(d, layer=4), main="t.test")
    plot(raster(d, layer=5), main="t.test p-value")
 par(opar)
 # Hexagonal sampling
 d.hex <- class.comparison(r1, r2, x.idx = 8, y.idx = 8, stat = "both",
                           sub.sample = TRUE, d = 500, size = 1000)
   sp::bubble(d.hex, "kappa")
    d.hex <- sp.na.omit(d.hex, col.name = "t.test")
  sp::bubble(d.hex, "t.test")
```

classBreaks *Class breaks*

Description

Finds class breaks in a distribution

Usage

```
classBreaks(x, n, type = c("equal", "quantile", "std", "geometric"))
```

Arguments

`x`	A vector to find breaks for
`n`	Number of breaks
`type`	Statistic used to find breaks c("equal", "quantile", "std", "geometric")

Value

A vector containing class break values the length is n+1 to allow for specification of ranges

Note

The robust std method uses sqrt(sum(x^2)/(n-1)) to center the data before deriving "pretty" breaks.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 y <- rnbinom(100, 10, 0.5)
   classBreaks(y, 10)
   classBreaks(y, 10, type="quantile")

opar <- par(no.readonly=TRUE)
   par(mfrow=c(2,2))
     d <- density(y)
     plot(d, type="n", main="Equal Area breaks")
       polygon(d, col="cyan")
       abline(v=classBreaks(y, 10))
     plot(d, type="n", main="Quantile breaks")
       polygon(d, col="cyan")
       abline(v=classBreaks(y, 10, type="quantile"))
     plot(d, type="n", main="Robust Standard Deviation breaks")
       polygon(d, col="cyan")
       abline(v=classBreaks(y, 10, type="std"))
     plot(d, type="n", main="Geometric interval breaks")
       polygon(d, col="cyan")
```

```
      abline(v=classBreaks(y, 10, type="geometric"))
par(opar)

( y.breaks <- classBreaks(y, 10) )
cut(y, y.breaks, include.lowest = TRUE, labels = 1:10)
```

`collinear` *Collinearity test*

Description

Test for linear or nonlinear collinearity/correlation in data

Test for linear or nonlinear collinearity/correlation in data

Usage

```
collinear(x, p = 0.85, nonlinear = FALSE, p.value = 0.001)
```

```
collinear(x, p = 0.85, nonlinear = FALSE, p.value = 0.001)
```

Arguments

`x`	A data.frame or matrix containing continuous data
`p`	The correlation cutoff (default is 0.85)
`nonlinear`	A boolean flag for calculating nonlinear correlations (FALSE/TRUE)
`p.value`	If nonlinear is TRUE, the p value to accept as the significance of the correlation

Details

Evaluation of the pairwise linear correlated variables to remove is accomplished through calculating the mean correlations of each variable and selecting the variable with higher mean.

Evaluation of the pairwise linear correlated variables to remove is accomplished through calculating the mean correlations of each variable and selecting the variable with higher mean. If nonlinear = TRUE, pairwise nonlinear correlations are evaluated by fitting y as a semi-parametrically estimated function of x using a generalized additive model and testing whether or not that functional estimate is constant, which would indicate no relationship between y and x thus, avoiding potentially arbitrary decisions regarding the order in a polynomial regression.

Value

Messages and a vector of correlated variables

Messages and a vector of correlated variables

Author(s)

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Examples

```
data(cor.data)

# Evaluate linear correlations on linear data
head( dat <- cor.data[[4]] )
pairs(dat, pch=20)
  ( cor.vars <- collinear( dat ) )

# Remove identified variable(s)
head( dat[,-which(names(dat) %in% cor.vars)] )

# Evaluate linear correlations on nonlinear data
#   using nonlinear correlation function
plot(cor.data[[1]], pch=20)
  collinear(cor.data[[1]], p=0.80, nonlinear = TRUE )

data(cor.data)

# Evaluate linear correlations on linear dataCollinearity between
head( dat <- cor.data[[4]] )
pairs(dat, pch=20)
  ( cor.vars <- collinear( dat ) )

# Remove identified variable(s)
head( dat[,-which(names(dat) %in% cor.vars)] )

# Evaluate linear correlations on nonlinear data
#   using nonlinear correlation function
plot(cor.data[[1]], pch=20)
  collinear(cor.data[[1]], p=0.80, nonlinear = TRUE )
```

---

combine *raster combine*

Description

Combines rasters into all unique combinations of inputs

Usage

```
combine(x, rnames = NULL, sp = FALSE)
```

Arguments

`x`	raster stack/brick or SpatialPixelsDataFrame object
`rnames`	Column names to combine in raster stack or sp object
`sp`	(FALSE/TRUE) output SpatialPixelsDataFrame

Details

Please note that this is not a memory safe function that utilizes rasters out of memory in the manner that the raster package does.

If sp = TRUE the object will be a list with "combine", containing the SpatialPixelsDataFrame with the value attribute containing the unique combinations, and "summary" with the summary table of collapsed combinations and associated attributes.

If sp = FALSE the a single ratified rasterLayer class object is returned with the summary table as the raster attribute table, this is most similar to the ESRI format resulting from their combine function.

Value

A ratified rasterLayer or a list containing a SpatialPixelsDataFrame and a data.frame of unique combinations.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)

r1 <- raster(nrows=100, ncol=100)
  r1[] <- round(runif(ncell(r1), 1,4),0)
r2 <- raster(nrows=100, ncol=100)
  r2[] <- round(runif(ncell(r2), 2,6),0)
r3 <- raster(nrows=100, ncol=100)
  r3[] <- round(runif(ncell(r3), 2,6),0)
r <- stack(r1,r2,r3)
  names(r) <- c("LC1","LC2","LC3")

# Combine rasters in stack
( cr <- combine(r) )
  levels(cr)

# Combine rasters in stack, using specific rasters
( cr <- combine(r, rnames=c("LC1","LC3")) )

# Combine rasters in stack, output SpatialPixelsDataFrame
cr.sp <- combine(r, sp = TRUE)
  head(cr.sp$summary)
  class(cr.sp$combine)

# Input SpatialPixelsDataFrame
```

```
r.sp <- as(r, "SpatialPixelsDataFrame")
cr.sp <- combine(r.sp, sp = TRUE)
```

concordance — *Concordance test for binomial models*

Description

Performs a concordance/disconcordance (C-statistic) test on binomial models.

Usage

```
concordance(y, p)
```

Arguments

y	vector of binomial response variable used in model
p	estimated probabilities from fit binomial model

Value

list object with: concordance, discordance, tied and pairs

Note

Test of binomial regression for the hypothesis that probabilities of all positives [1], are greater than the probabilities of the nulls [0]. The concordance would be 100 inverse of concordance, representing the null. The C-statistic has been show to be comparable to the area under an ROC

Results are: concordance - percent of positives that are greater than probabilities of nulls. discordance - concordance inverse of concordance representing the null class, tied - number of tied probabilities and pairs - number of pairs compared

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Austin, P.C. & E.W. Steyerberg (2012) Interpreting the concordance statistic of a logistic regression model: relation to the variance and odds ratio of a continuous explanatory variable. BMC Medical Research Methodology, 12:82

Harrell, F.E. (2001) Regression modelling strategies. Springer, New York, NY.

Royston, P. & D.G. Altman (2010) Visualizing and assessing discrimination in the logistic regression model. Statistics in Medicine 29(24):2508-2520

Examples

```
data(mtcars)
dat <- subset(mtcars, select=c(mpg, am, vs))
glm.reg <- glm(vs ~ mpg, data = dat, family = binomial)
concordance(dat$vs, predict(glm.reg, type = "response"))
```

`conf.interval` *Confidence interval for mean or median*

Description

Calculates confidence interval for the mean or median of a distribution with unknown population variance

Usage

```
conf.interval(x, cl = 0.95, stat = "mean", std.error = TRUE)
```

Arguments

`x`	Vector to calculate confidence interval for
`cl`	Percent confidence level (default = 0.95)
`stat`	Statistic (mean or median)
`std.error`	Return standard error (TRUE/FALSE)

Value

lci Lower confidence interval value

uci Upper confidence interval value

mean If stat = "mean", mean value of distribution

mean Value of the mean or median

conf.level Confidence level used for confidence interval

std.error If std.error = TRUE standard error of distribution

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
x <- runif(100)
cr <- conf.interval(x, cl = 0.97)
print(cr)

d <- density(x)
plot(d, type="n", main = "PDF with mean and 0.97 confidence interval")
  polygon(d, col="cyan3")
  abline(v=mean(x, na.rm = TRUE), lty = 2)
  segments( x0=cr[["lci"]], y0=mean(d$y), x1=cr[["uci"]],
            y1=mean(d$y), lwd = 2.5,
            col = "black")
 legend("topright", legend = c("mean", "CI"),
        lty = c(2,1), lwd = c(1,2.5))
```

`cor.data` *Various correlation structures*

Description

linear and nonlinear correlated data examples

A list object with various linear and nonlinear correlation structures

Format

A list object with 4 elements containing data.frames:

example 1 two columns with nonlinear wave function relationship

example 2 two columns with simple nonlinear relationship

example 3 two columns with nonlinear multi-level wave function relationship

example 4 4 columns with first two having linear relationship

---

`correlogram` *Correlogram*

Description

Calculates and plots a correlogram

Usage

```
correlogram(x, v, dist = 5000, dmatrix = FALSE, ns = 99, latlong = FALSE, ...)
```

Arguments

`x`	SpatialPointsDataFrame object
`v`	Test variable in x@data
`dist`	Distance of correlation lags, if latlong=TRUE units are in kilometers
`dmatrix`	Should the distance matrix be include in output (TRUE/FALSE)
`ns`	Number of simulations to derive simulation envelope
`latlong`	Coordinates are in latlong (TRUE/FALSE)
`...`	Arguments passed to cor ('pearson', 'kendall' or 'spearman')

Value

A list object containing:

- autocorrelation is a data.frame object with the following components
- autocorrelation - Autocorrelation value for each distance lag
- dist - Value of distance lag
- lci - Lower confidence interval (p=0.025)
- uci - Upper confidence interval (p=0.975)
- CorrPlot recordedplot object to recall plot
- dmatrix Distance matrix (if dmatrix=TRUE)

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

Examples

```
library(sp)
  data(meuse)
coordinates(meuse) = ~x+y
zinc.cg <- correlogram(x = meuse, v = meuse@data[,'zinc'], dist = 250, ns = 9)
```

`cross.tab` *Class comparison between two nominal rasters*

Description

Creates a labeled cross tabulation between two nominal rasters

Usage

```
cross.tab(x, y, values = NULL, labs = NULL, pct = FALSE, ...)
```

Arguments

`x`	rasterLayer class object
`y`	rasterLayer class object to compare to x
`values`	Expected values in both rasters
`labs`	Labels associated with values argument
`pct`	(TRUE/FALSE) return proportions rather than counts
`...`	Additional arguments

Value

a table with the cross tabulated counts

Note

This function returns a cross tabulation between two nominal rasters. Arguments allow for labeling the results and returning proportions rather than counts. It also accounts for asymmetrical classes between the two rasters

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Pontius Jr, R.G., Shusas, E., McEachern, M. (2004). Detecting important categorical land changes while accounting for persistence. Agriculture, Ecosystems & Environment 101(2):251-268.

See Also

`raster::crosstab`

Examples

```
library(sp)
library(raster)
  data(meuse.grid)

r1 <- sp::SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
                                 data = meuse.grid)
lulc2010 <- raster(r1)
  na.idx <- which(!is.na(lulc2010[]))
    lulc2010[na.idx] <- sample(1:5, length(na.idx), replace=TRUE)

lulc2020 <- raster(lulc2010)
  lulc2020[na.idx] <- sample(1:5, length(na.idx), replace=TRUE)

( v = sort(unique(c(lulc2010[], lulc2020[]))) )
l = c("water","urban","forest",
      "ag","barren")
```

```
 cross.tab(lulc2010, lulc2020)
 cross.tab(lulc2010, lulc2020, values = v, labs = l)
 cross.tab(lulc2010, lulc2020, values = v, labs = l, pct=TRUE)

# Create asymmetrical classes
lulc2020[na.idx] <- sample(c(1,2,4,5), length(na.idx), replace=TRUE)

cross.tab(lulc2010, lulc2020, values = v, labs = l, pct=TRUE)
```

crossCorrelation *Spatial cross correlation*

Description

Calculates univariate or bivariate spatial cross-correlation using local Moran's-I (LISA), following Chen (2015)

Usage

```
crossCorrelation(
  x,
  y = NULL,
  coords = NULL,
  w = NULL,
  type = c("LSCI", "GSCI"),
  k = 999,
  dist.function = c("inv.power", "neg.exponent", "none"),
  scale.xy = TRUE,
  scale.partial = FALSE,
  scale.matrix = FALSE,
  alpha = 0.05,
  clust = TRUE,
  return.sims = FALSE
)
```

Arguments

x	Vector of x response variables
y	Vector of y response variables, if not specified the univariate statistic is returned
coords	A matrix of coordinates corresponding to (x,y), only used if w = NULL. Can also be an sp object with relevant x,y coordinate slot (ie., points or polygons)
w	Spatial neighbors/weights in matrix format. Dimensions must match (n(x),n(y)) and be symmetrical. If w is not defined then a default method is used.
type	c("LSCI","GSCI") Return Local Spatial Cross-correlation Index (LSCI) or Global Spatial cross-correlation Index (GSCI)

`k`	Number of simulations for calculating permutation distribution under the null hypothesis of no spatial autocorrelation
`dist.function`	("inv.power", "neg.exponent", "none") If w = NULL, the default method for deriving spatial weights matrix, options are: inverse power or negative exponent, none is for use with a provided matrix
`scale.xy`	(TRUE/FALSE) scale the x,y vectors, if FALSE it is assumed that they are already scaled following Chen (2015)
`scale.partial`	(FALSE/TRUE) rescale partial spatial autocorrelation statistics
`scale.matrix`	(FALSE/TRUE) If a neighbor/distance matrix is passed, should it be scaled using (w/sum(w))
`alpha`	= 0.05 confidence interval (default is 95 pct)
`clust`	(FALSE/TRUE) Return approximated lisa clusters
`return.sims`	(FALSE/TRUE) Return randomizations vector n = k

Details

In specifying a distance matrix, you can pass a coordinates matrix or spatial object to coords or alternately, pass a distance or spatial weights matrix to the w argument. If the w matrix represents spatial weights dist.function="none" should be specified. Otherwise, w is assumed to represent distance and will be converted to spatial weights using inv.power or neg.exponent. The w distances can represent an alternate distance hypothesis (eg., road, stream, network distance) Here are example argument usages for defining a matrix.

- IF coords=x, w=NULL, dist.function= c("inv.power", "neg.exponent") A distance matrix is derived using the data passed to coords then spatial weights derived using one of the dist.function options
- IF cords=NULL, w=x, dist.function= c("inv.power", "neg.exponent") It is expected that the distance matrix specified with w represent some form of distance then the spatial weights are derived using one of the dist.function options
- IF cords=NULL, w=x, dist.function="none" It is assumed that the matrix passed to w already represents the spatial weights

Value

When not simulated k=0, a list containing:

- I Global autocorrelation statistic
- SCI A data.frame with two columns representing the xy and yx autocorrelation
- nsim value of NULL to represent p values were derived from observed data (k=0)
- p Probability based observations above/below confidence interval
- t.test Probability based on t-test
- clusters If "clust" argument TRUE, vector representing LISA clusters

when simulated (k>0), a list containing:

- I Global autocorrelation statistic

- SCI A data.frame with two columns representing the xy and yx autocorrelation
- nsim value representing number of simulations
- global.p p-value of global autocorrelation statistic
- local.p Probability based simulated data using successful rejection of t-test
- range.p Probability based on range of probabilities resulting from paired t-test
- clusters If "clust" argument TRUE, vector representing lisa clusters

References

Chen, Y.G. (2012) On the four types of weight functions for spatial contiguity matrix. Letters in Spatial and Resource Sciences 5(2):65-72

Chen, Y.G. (2013) New approaches for calculating Moran's index of spatial autocorrelation. PLoS ONE 8(7):e68336

Chen, Y.G. (2015) A New Methodology of Spatial Cross-Correlation Analysis. PLoS One 10(5):e0126158. doi:10.1371/journal.pone.0126158

Examples

```
# replicate Chen (2015)
 data(chen)
( r <- crossCorrelation(x=chen[["X"]], y=chen[["Y"]], w = chen[["M"]],
                        clust=TRUE, type = "LSCI", k=0,
                        dist.function = "inv.power") )


  library(sp)
  library(spdep)

  data(meuse)
    coordinates(meuse) <- ~x+y

  #### Using a default spatial weights matrix method (inverse power function)
  ( I <- crossCorrelation(meuse$zinc, meuse$copper,
             coords = coordinates(meuse), k=99) )
    meuse$lisa <- I$SCI[,"lsci.xy"]
      spplot(meuse, "lisa")

  #### Providing a distance matrix
   Wij <- spDists(meuse)
   ( I <- crossCorrelation(meuse$zinc, meuse$copper, w = Wij, k=99) )

  #### Providing an inverse power function weights matrix
   Wij <- spDists(meuse)
     Wij <- 1 / Wij
           diag(Wij) <- 0
         Wij <- Wij / sum(Wij)
   diag(Wij) <- 0
   ( I <- crossCorrelation(meuse$zinc, meuse$copper, w = Wij,
                          dist.function = "none", k=99) )
```

csi *Cosine Similarity Index*

Description

Calculates the cosine similarity and angular similarity on two vectors or a matrix

Usage

```
csi(x, y = NULL)
```

Arguments

x	A vector or matrix object
y	If x is a vector, then a vector object

Value

If x is a matrix, a list object with: similarity and angular.similarity matrices or, if x and y are vectors, a vector of similarity and angular.similarity

Note

The cosine similarity index is a measure of similarity between two vectors of an inner product space. This index is bested suited for high-dimensional positive variable space. One useful application of the index is to measure separability of clusters derived from algorithmic approaches (e.g., k-means). It is a good common practice to center the data before calculating the index. It should be noted that the cosine similarity index is mathematically, and often numerically, equivalent to the Pearson's correlation coefficient

The cosine similarity index is derived: s(xy) = x * y / ||x|| * ||y||, where the expected is 1.0 (perfect similarity) to -1.0 (perfect dissimilarity). A normalized angle between the vectors can be used as a bounded similarity function within [0,1] angular similarity = 1 - (cos(s)^-1/pi)

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
# Compare two vectors (centered using scale)
  x=runif(100)
  y=runif(100)^2
  csi(as.vector(scale(x)),as.vector(scale(y)))

  #' # Compare columns (vectors) in a matrix (centered using scale)
  x <- matrix(round(runif(100),0),nrow=20,ncol=5)
  ( s <- csi(scale(x)) )

# Compare vector (x) to each column in a matrix (y)
y <- matrix(round(runif(500),3),nrow=100,ncol=5)
x=runif(100)
csi(as.vector(scale(x)),scale(y))
```

curvature *Surface curvature*

Description

Calculates Zevenbergen & Thorne, McNab's or Bolstad's curvature

Usage

```
curvature(x, type = c("planform", "profile", "total", "mcnab", "bolstad"), ...)
```

Arguments

x	rasterLayer object
type	Method used c("planform", "profile", "total", "mcnab", "bolstad")
...	Additional arguments passed to writeRaster

Value

raster class object of surface curvature

Note

The planform and profile curvatures are the second derivative(s) of the elevation surface, or the slope of the slope. Profile curvature is in the direction of the maximum slope, and the planform curvature is perpendicular to the direction of the maximum slope. Negative values in the profile curvature indicate the surface is upwardly convex whereas, positive values indicate that the surface is upwardly concave. Positive values in the planform curvature indicate an that the surface is laterally convex whereas, negative values indicate that the surface is laterally concave.

Total curvature is the sigma of the profile and planform curvatures. A value of 0 in profile, planform or total curvature, indicates the surface is flat. The planform, profile and total curvatures are derived using Zevenbergen & Thorne (1987) via a quadratic equation fit to eight neighbors as such, the s (focal window size) argument is ignored.

McNab's and Bolstad's variants of the surface curvature (concavity/convexity) index (McNab 1993; Bolstad & Lillesand 1992; McNab 1989). The index is based on features that confine the view from the center of a 3x3 window. In the Bolstad equation, edge correction is addressed by dividing by the radius distance to the outermost cell (36.2m).

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Bolstad, P.V., and T.M. Lillesand (1992). Improved classification of forest vegetation in northern Wisconsin through a rule-based combination of soils, terrain, and Landsat TM data. Forest Science. 38(1):5-20.

Florinsky, I.V. (1998). Accuracy of Local Topographic Variables Derived from Digital Elevation Models. International Journal of Geographical Information Science, 12(1):47-62.

McNab, H.W. (1989). Terrain shape index: quantifying effect of minor landforms on tree height. Forest Science. 35(1):91-104.

McNab, H.W. (1993). A topographic index to quantify the effect of mesoscale landform on site productivity. Canadian Journal of Forest Research. 23:1100-1107.

Zevenbergen, L.W. & C.R. Thorne (1987). Quantitative Analysis of Land Surface Topography. Earth Surface Processes and Landforms, 12:47-56.

See Also

`writeRaster` For additional ... arguments passed to writeRaster

Examples

```
  library(raster)
  library(spatialEco)
  data(elev)
  elev <- projectRaster(elev, crs="+proj=robin +datum=WGS84",
                        res=1000, method='bilinear')
curvature(elev, type="planform")
  mcnab.crv <- curvature(elev, type="mcnab")
      plot(mcnab.crv, main="McNab's curvature")
```

dahi *Diurnal Anisotropic Heat Index*

Description

Simple approximation of the anisotropic diurnal heat (Ha) distribution

The Diurnal Anisotropic Heat Index is based on this equation. Ha = cos(amax - a) * arctan(b) Where; amax defines the aspect with the maximum total heat surplus, a is the aspect and b is the slope angle.

Usage

```
dahi(x, amax = 202.5)
```

Arguments

`x`	An elevation raster of class RasterLayer, SpatRaster or SpatialPixelsDataFrame
`amax`	The Alpha Max (amax) parameter in degrees defined as: minimum = 0, maximum = 360 with the default = 202.500

Value

RasterLayer class object Diurnal Anisotropic Heat Index

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Boehner, J., and Antonic, O. (2009) Land-surface parameters specific to topo-climatology. In: Hengl, T., & Reuter, H. (Eds.), Geomorphometry - Concepts, Software, Applications. Developments in Soil Science, 33:195-226

Examples

```
library(raster)
data(elev)
Ha <- dahi(elev)
  plot(Ha)
```

`date_seq` *date sequence*

Description

creates date sequence given start and stop dates

Usage

```
date_seq(
  start,
  end,
  step = c("day", "week", "month", "quarter", "year", "minute"),
  rm.leap = FALSE
)
```

Arguments

`start`	Start date in "yyyy/mm/dd" character format
`end`	End date in "yyyy/mm/dd" character format
`step`	Time step, options are c("day", "week", "month", "quarter", "year", "minute")
`rm.leap`	Remove extra days in leap years

Value

A date vector of class POSIXct for minute and Date for other options

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
# monthly steps 1990/01/01 - 2019/12/31
d <- date_seq("1990/01/01", "2019/12/31", step="month")

# daily steps 1990/01/01 - 2019/12/31
d <- date_seq("1990/01/01", "2019/12/31", step="day")

# daily steps 1990/01/01 - 2019/12/31 with leap days removed
d <- date_seq("1990/01/01", "2019/12/31", step="day", rm.leap=TRUE)

# daily step 2008/12/29 - 2008/12/31, 2008 is leap year
d <- date_seq("2008/12/29", "2008/12/31")

# minutes step 2008/12/29 - 2008/12/31, 2008 is leap year
d <- date_seq("2008/12/29", "2008/12/31", step="minute")
```

`daymet.point` *DAYMET point values*

Description

Downloads DAYMET climate variables for specified point and time-period

Usage

```
daymet.point(
  lat,
  long,
  start.year,
  end.year,
  site = NULL,
  files = FALSE,
  echo = FALSE
)
```

Arguments

`lat`	latitude of point (decimal degrees WGS84)
`long`	longitude pf point (decimal degrees WGS84)
`start.year`	First year of data
`end.year`	Last year of data
`site`	Unique identification value that is appended to data
`files`	(TRUE/FALSE) Write file to disk
`echo`	(TRUE/FALSE) Echo progress

Value

A data.frame with climate results

Note

data is available for Long -131.0 W and -53.0 W; lat 52.0 N and 14.5 N Function uses the Single Pixel Extraction tool and returns year, yday, dayl(s), prcp (mm/day), srad (W/m^2), swe (kg/m^2), tmax (deg c), tmin (deg c), vp (Pa) Metadata for DAYMET single pixel extraction: https://daymet.ornl.gov/files/UserGuides/current/readme_singlepointextraction.pdf

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
( d <- daymet.point(lat = 36.0133, long = -84.2625, start.year = 2013,
                    end.year=2014, site = "1", files = FALSE, echo = FALSE) )
```

`daymet.tiles` *DAYMET Tile ID's*

Description

Returns a vector of DAYMET tile id's within a specified extent

Usage

```
daymet.tiles(...)
```

Arguments

`...`	ignored

Value

Vector of DAYMET tile IDS or if sp = TRUE a sp class SpatialPolygonsDataFrame

Note

Function accepts sp, raster or extent class object or bounding coordinates. All input must be in the same projection as the tile index SpatialPolygonsDataFrame. The library includes the DAYMAT tile index "DAYMET_tiles" which can be add using data(), see examples.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

`DAYMET_tiles` *DAYMET climate tile index*

Description

Polygon tile index for DAYMET climate data

Format

An sp SpatialPolygonsDataFrame with 404 features (rows) and 6 columns (columns):

Id Tile Index Identification

Area Area of each tile

XMin Minimum x geographic decimal degree coordinate

XMax Maximum x geographic decimal degree coordinate

YMin Minimum y geographic decimal degree coordinate

yMax Maximum y geographic decimal degree coordinate

Source

`https://daymet.ornl.gov/`

`dispersion` *Dispersion (H-prime)*

Description

Calculates the dispersion ("rarity") of targets associated with planning units

Usage

```
dispersion(x)
```

Arguments

`x`	data.frame object of target values

Value

data.frame with columns H values for each target, H , sH, sHmax

Note

The dispersion index (H-prime) is calculated H = sum(sqrt(p) / sqrt(a)) where; P = [sum of target in planning unit / sum of target across all planning units] and a = [count of planning units containing target / number of planning units]

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Evans, J.S., S.R. Schill, G.T. Raber (2015) A Systematic Framework for Spatial Conservation Planning and Ecological Priority Design in St. Lucia, Eastern Caribbean. Chapter 26 in Central American Biodiversity : Conservation, Ecology and a Sustainable Future. F. Huettman (eds). Springer, NY.

Examples

```
library(sp)
  data(pu)

d <- dispersion(pu@data[,2:ncol(pu)])
p <- d[,"H"]
clr <- c("#3288BD", "#99D594", "#E6F598", "#FEE08B",
         "#FC8D59", "#D53E4F")
clrs <- ifelse(p < 0.5524462, clr[1],
          ifelse(p >= 0.5524462 & p < 1.223523, clr[2],
            ifelse(p >= 1.223523 & p < 2.465613, clr[3],
           ifelse(p >= 2.465613 & p < 4.76429, clr[4],
             ifelse(p >= 4.76429 & p < 8.817699, clr[5],
               ifelse(p >= 8.817699, clr[6], NA))))))
plot(pu, col=clrs, border=NA)
  legend("topleft", legend=rev(c("Very Rare","Rare","Moderately Rare",
         "Somewhat Common","Common","Over Dispersed")),
         fill=clr, cex=0.6, bty="n")
  box()
```

`dissection` *Dissection*

Description

Calculates the Evans (1972) Martonne's modified dissection

Usage

```
dissection(x, s = 5, ...)
```

Arguments

`x`	raster object
`s`	Focal window size
`...`	Additional arguments passed to raster::calc

Value

raster class object of Martonne's modified dissection

Note

Dissection is calculated as: (z(s) - min(z(s))) / (max(z(s)) - min(z(s)))

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)
data(elev)
d <- dissection(elev, s=3)
  plot(d, main="dissection")
```

`divergence` *divergence*

Description

Kullback-Leibler Divergence (Cross-entropy)

Usage

```
divergence(x, y, type = c("Kullback-Leibler", "cross-entropy"))
```

Arguments

`x`	a vector of integer values, defining observed
`y`	a vector of integer values, defining estimates
`type`	Type of divergence statistic c("Kullback-Leibler", "cross-entropy")

Value

single value vector with divergence statistic

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
x <- round(runif(10,1,4),0)
y <- round(runif(10,1,4),0)

divergence(x, y)
divergence(x, y, type = "cross-entropy")
```

`download.daymet` *Download DAYMET*

Description

Batch download of daily gridded DAYMET climate data

Usage

```
download.daymet(...)
```

Arguments

`...`	ignored

Details

DAYMET website: http://daymet.ornl.gov, path structure: /year/tile_year/file.nc

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Thornton P.E., S.W. Running and M.A. White (1997) Generating surfaces of daily meteorological variables over large regions of complex terrain. Journal of Hydrology 190: 214-251.

Thornton, P.E. and S.W. Running (1999) An improved algorithm for estimating incident daily solar radiation from measurements of temperature, humidity, and precipitation. Agriculture and Forest Meteorology. 93:211-228.

Thornton, P.E., H. Hasenauer and M.A. White (2000) Simultaneous estimation of daily solar radiation and humidity from observed temperature and precipitation: An application over complex terrain in Austria. Agricultural and Forest Meteorology 104:255-271.

`download.hansen` *Download Hansen Forest 2000-2013 Change*

Description

Download of Hansen Global Forest Change 2000-2013

Usage

```
download.hansen(
  tile,
  data.type = c("loss"),
  download.folder = c("current", "temp")
)
```

Arguments

`tile`	Granule index (See project URL for granule grid index)
`data.type`	Type of data to download options: ’treecover2000’, ’loss’, ’gain’, ’lossyear’, datamask’, ’first’, ’last’
`download.folder`	Destination folder

Details

Available products: treecover2000, loss, gain, lossyear, datamask, first, or last

- treecover2000 - (Tree canopy cover for year 2000) - Tree cover in the year 2000, defined as canopy closure for all vegetation taller than 5m in height. Encoded as a percentage per output grid cell, in the range 0-100.
- loss - (Global forest cover loss 2000-2013) - Forest loss during the period 2000-2013, defined as a stand-replacement disturbance, or a change from a forest to non-forest state. Encoded as either 1 (loss) or 0 (no loss).
- gain - (Global forest cover gain 2000-2012) - Forest gain during the period 2000-2012, defined as the inverse of loss, or a non-forest to forest change entirely within the study period. Encoded as either 1 (gain) or 0 (no gain).
- lossyear - (Year of gross forest cover loss event) - A disaggregation of total forest loss to annual time scales. Encoded as either 0 (no loss) or else a value in the range 1-13, representing loss detected primarily in the year 2001-2013.
- datamask - (Data mask) - Three values representing areas of no data (0), mapped land surface (1), and permanent water bodies (2).
- first - (Circa year 2000 Landsat 7 cloud-free image composite) - Reference multispectral imagery from the first available year, typically 2000. If no cloud-free observations were available for year 2000, imagery was taken from the closest year with cloud-free data, within the range 1999-2012.
- last - (Circa year 2013 Landsat cloud-free image composite) - Reference multispectral imagery from the last available year, typically 2013. If no cloud-free observations were available for year 2013, imagery was taken from the closest year with cloud-free data, within the range 2010-2012.

Project website with 10x10 degree granule index: `http://earthenginepartners.appspot.com/science-2013-global-forest/download_v1.1.html`

Value

Downloaded Hansen forest loss tif files

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Hansen, M. C., P. V. Potapov, R. Moore, M. Hancher, S. A. Turubanova, A. Tyukavina, D. Thau, S. V. Stehman, S. J. Goetz, T. R. Loveland, A. Kommareddy, A. Egorov, L. Chini, C. O. Justice, and J. R. G. Townshend. (2013) High-Resolution Global Maps of 21st-Century Forest Cover Change. Science 342:850-53.

Examples

```
## Not run:
# Download single tile
 download.hansen(tile=c('00N', '130E'), data.type=c('loss', 'lossyear'),
                 download.folder=getwd())

# Batch download of multiple tiles
tiles <- list(c('00N', '140E'), c('00N', '130E'))
  for( j in 1:length(tiles)){
    download.hansen(tile=tiles[[j]], data.type=c('loss'))
  }


## End(Not run)
```

---

download.prism *Download PRISM*

Description

Batch download of monthly gridded PRISM climate data

Usage

```
download.prism(...)
```

Arguments

`...`	Nonexistent parameters

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

---

effect.size *Cohen's-d effect size*

Description

Cohen's-d effect size with pooled sd for a control and experimental group

Usage

```
effect.size(y, x, pooled = TRUE, conf.level = 0.95)
```

Arguments

`y`	A character or factor vector
`x`	A numeric vector, same length as y
`pooled`	Pooled or population standard deviation (TRUE/FALSE)
`conf.level`	Specified confidence interval. Default is 0.95

Value

An effect.size class object with x, y and a data.frame with columns for effect size, lower confidence interval, lower confidence interval. The row names of the data frame represent the levels in y

Note

This implementation will iterate through each class in y and treating a given class as the experimental group and all other classes as a control case. Each class had d and the confidence interval derived. A negative d indicate directionality with same magnitude. The expected range for d is 0 - 3 d is derived; (mean(experimental group) - mean(control group)) / sigma(p) pooled standard deviation is derived; sqrt(((Ne - 1) * sigma(e)^2 + (Nc - 1) * sigma(c)^2) / (Ne + Nc - 2)) where; Ne, Nc = n of experimental and control groups.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Cohen, J., (1988) Statistical Power Analysis for the Behavioral Sciences (second ed.). Lawrence Erlbaum Associates.

Cohen, J (1992) A power primer. Psychological Bulletin 112(1):155-159

Examples

```
 ( es <- effect.size(iris$Species, iris$Sepal.Length) )
   plot(es)
```

`elev` *Elevation raster*

Description

elevation raster of Switzerland

Format

A raster RasterLayer class object:

resoultion	5 arc-minute 0.00833 (10000m)
nrow	264
ncol	564
ncell	148896
xmin	5.9
xmax	10.6
ymin	45.7
ymax	47.9
proj4string	+proj=longlat +ellps=WGS84

Source

`http://www.diva-gis.org/Data`

`erase.point` *Erase points*

Description

Removes points intersecting a polygon feature class

Usage

```
erase.point(y, x, inside = TRUE)
```

Arguments

`y`	A SpatialPoints or SpatialPointsDataFrame
`x`	A SpatialPolygons or SpatialPolygonsDataFrame
`inside`	(TRUE/FALSE) Remove points inside polygon, else outside polygon

Value

A SpatialPoints or SpatialPointsDataFrame

Note

Used to erase points that intersect polygon(s). If inside=FALSE then the function results in an intersection operation where points that intersect the polygon are retained. This function effectively duplicates the ESRI ArcGIS Erase Point tool.

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

Examples

```
library(sp)
library(raster)
library(rgeos)
  data(meuse)
  coordinates(meuse) = ~x+y

# Create systematic sample and polygons
s <- spsample(x=as(extent(meuse), "SpatialPolygons"), n=1000,
              type="regular")
b <- rgeos::gBuffer(s[sample(1:length(s),5),],
                    byid = FALSE, width = 300)

# Erase points based on polygons
s.erase <- erase.point(s, b)

 opar <- par(no.readonly=TRUE)
 par(mfrow=c(2,2))
   plot(s, pch=20, main="original data")
   plot(b, main="erased data")
     points(s.erase, pch=20)
   plot(b, main="erased data using inside=FALSE")
     points(erase.point(s, b, inside=FALSE), pch=20)
 par(opar)
```

`explode` *Explodes multipart features*

Description

Explodes multipart features into single part

Usage

```
explode(x, sp = FALSE)
```

Arguments

x	sp or sf multipart (MULTIPOLYGON, MULTIPOINT, MULTILINE) object
sp	(FALSE/TRUE) output as sp class object, else is sf class

Value

A single part sp or sf object (polygons or points)

Note

Multipart geometries are a data structure where a single attribute shares multiple features (polygons, points, lines). This function dissaggregates the data into a one-to-one match.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sf)
library(sp)

dim( p.sf <- st_read(system.file("shapes/sids.shp", package = "spData")[1]) )
dim( p.sf <- explode(p.sf) )
```

`extract.vertices` *Extract vertices for polygons or lines*

Description

Extracts [x,y] vertices from an sp line or polygon object

Usage

```
extract.vertices(x, as.sp = FALSE, rm.duplicates = FALSE, join = FALSE)
```

Arguments

`x`	An sp class SpatialPolygonsDataFrame, SpatialPolygons, SpatialLinesDataFrame or SpatialLines object
`as.sp`	(FALSE/TRUE) Output as sp SpatialPointsDataFrame
`rm.duplicates`	(FALSE/TRUE) remove duplicate (x,y) coordinates
`join`	(FALSE/TRUE) Joint attributes from original object

Value

A SpatialPointsDataFrame or data.frame with id, x, y and merged attributes

Note

This function returns the vertices of a line or polygon object, as opposed to the polygon centroids or line start/stop coordinates available in the @coords slot. This requires accessing the coordinates located in the x@polygons@Polygons or x@lines@Lines slots

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
library(raster)
library(sf)

# For polygons
r <- raster(xmn=-11.69, xmx=2988.31, ymn=-749.97, ymx=1650.03,
            resolution=c(100,100))
  r[] <- runif(ncell(r))
    names(r) <- "random_process"

polys <- as(r, "SpatialPolygonsDataFrame")
  polys <- polys[sample(1:nrow(polys),10),]

extract.vertices(polys, join=TRUE, rm.duplicates=TRUE)

v <- extract.vertices(polys, as.sp=TRUE, join=TRUE)
  head(v@data)

  plot(polys)
    points(v, pch=20, cex=2, col="red")

# For lines
nc <- sf::st_read(system.file("shape/nc.shp", package="sf"))
  nc <- sf::st_cast(sf::st_cast(nc, "POLYGON"), "LINESTRING")
    nc <- as(nc, "Spatial")

extract.vertices(nc)
extract.vertices(nc, join=TRUE, rm.duplicates=TRUE)

v <- extract.vertices(nc, as.sp=TRUE, join=TRUE)
  head(v@data)

  plot(nc)
    points(v, pch=20, cex=2, col="red")
```

`focal.lmetrics` *Focal landscape metrics*

Description

Calculates a variety of landscape metrics on integer rasters using focal approach

Usage

```
focal.lmetrics(...)
```

Arguments

`...`	Parameters to be passed to the modern version of the function

Examples

```
## Not run:
library(landscapemetrics)
library(raster)

data(landscape)

s <- matrix(1, nrow = 3, ncol = 3)
( result <- do.call(stack, window_lsm(landscape, window = s,
                  what = c("lsm_l_pr", "lsm_l_joinent"))) )
  plot(result)

## End(Not run)
```

`fuzzySum` *Fuzzy Sum*

Description

Calculates the fuzzy sum of a vector

Usage

```
fuzzySum(x)
```

Arguments

`x`	Vector of values to apply fuzzy sum

Value

Value of fuzzy sum

Note

The fuzzy sum is an increasing linear combination of values. This can be used to sum probabilities or results of multiple density functions.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
p = c(0.8,0.76,0.87)
  fuzzySum(p)
  sum(p)

p = c(0.3,0.2,0.1)
  fuzzySum(p)
  sum(p)
```

`gaussian.kernel` *Gaussian Kernel*

Description

Creates a Gaussian Kernel of specified size and sigma

Usage

```
gaussian.kernel(sigma = 2, n = 5)
```

Arguments

`sigma`	sigma (standard deviation) of kernel (defaults 2)
`n`	size of symmetrical kernel (defaults to 5x5)

Value

Symmetrical (NxN) matrix of a Gaussian distribution

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
  par(mfrow=c(2,2))
  persp(gaussian.kernel(sigma=1, n=27), theta = 135,
        phi = 30, col = "grey", ltheta = -120, shade = 0.6,
        border=NA )
  persp(gaussian.kernel(sigma=2, n=27), theta = 135, phi = 30,
        col = "grey", ltheta = -120, shade = 0.6, border=NA )
  persp(gaussian.kernel(sigma=3, n=27), theta = 135, phi = 30,
        col = "grey", ltheta = -120, shade = 0.6, border=NA )
  persp(gaussian.kernel(sigma=4, n=27), theta = 135, phi = 30,
        col = "grey", ltheta = -120, shade = 0.6, border=NA )
```

geo.buffer *Buffer geographic data*

Description

Buffers data in geographic (Latitude/Longitude) projection

Usage

```
geo.buffer(x, r, sf = FALSE, ...)
```

Arguments

`x`	A sf or sp vector class object
`r`	Buffer radius in meters
`sf`	(FALSE/TRUE) Output sf class object else sp
`...`	Additional arguments passed to gBuffer

Value

an sp or sf polygon class object representing buffer for each feature

Note

Projects (Latitude/Longitude) data in decimal-degree geographic projection using an on-the-fly azimuthal equidistant projection in meters centered on

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

See Also

`gBuffer` for gBuffer ... arguments

Examples

```
library(sp)
library(raster)

s <- spsample(as(extent(61.87125, 76.64458, 23.90153, 37.27042),
              "SpatialPolygons"), n=100, type="random")
  proj4string(s) <- '+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs'

b <- geo.buffer(x=s, r=1000, quadsegs=100)
  plot(b[1,])
    points(s[1,], pch=20,cex=2)
```

group.pdf *Probability density plot by group*

Description

Creates a probability density plot of y for each group of x

Usage

```
group.pdf(
  x,
  y,
  col = NULL,
  lty = NULL,
  lwd = NULL,
  lx = "topleft",
  ly = NULL,
  ...
)
```

Arguments

`x`	Numeric, character or factorial vector of grouping variable (must be same length as y)
`y`	Numeric vector (density variable)
`col`	Optional line colors (see par, col)
`lty`	Optional line types (see par, lty)
`lwd`	Optional line widths (see par, lwd)
`lx`	Position of legend (x coordinate or 'topright', 'topleft', 'bottomright', 'bottomleft')
`ly`	Position of legend (y coordinate)
`...`	Additional arguments passed to plot

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

References

Simonoff, J. S. (1996). Smoothing Methods in Statistics. Springer-Verlag, New York.

Examples

```
y=dnorm(runif(100))
x=rep(c(1,2,3), length.out=length(y))
group.pdf(x=as.factor(x), y=y, main='Probability Density of y by group(x)',
ylab='PDF', xlab='Y', lty=c(1,2,3))
```

---

hexagons *Hexagons*

Description

Create hexagon polygons

Usage

```
hexagons(x, res = 100, ...)
```

Arguments

x	sp SpatialDataFrame class object
res	Area of resulting hexagons
...	Additional arguments passed to spsample

Value

SpatialPolygonsDataFrame OBJECT

Note

depends: sp

Examples

```
require(sp)
  data(meuse)
    coordinates(meuse) <- ~x+y

hex.polys <- hexagons(meuse, res=100)
  plot(hex.polys)
    plot(meuse,pch=20,add=TRUE)

# Points intersecting hexagons
hex.pts <- na.omit(over(meuse,hex.polys))
(hex.pts <- data.frame(PTID=rownames(hex.pts), hex.pts))
```

hli *Heat Load Index*

Description

Calculates the McCune & Keon (2002) Heat Load Index

Usage

```
hli(x, check = TRUE, force.hemisphere = c("none", "southern", "northern"))
```

Arguments

`x`	rasterLayer class object
`check`	(TRUE/FALSE) check for projection integrity and calculate central latitude for non-geographic projections
`force.hemisphere`	If country is split at the equator, force southern or northern hemisphere equation c("southern", "northern")

Value

raster class object of McCune & Keon (2002) Heat Load Index

Note

Describes A southwest facing slope should have warmer temperatures than a southeast facing slope, even though the amount of solar radiation they receive is equivalent. The McCune and Keon (2002) method accounts for this by "folding" the aspect so that the highest values are southwest and the lowest values are northeast. Additionally, this method account for steepness of slope, which is not addressed in most other aspect rescaling equations. HLI values range from 0 (coolest) to 1 (hottest).

The equations follow McCune (2007) and support northern and southern hemisphere calculations. The folded aspect for northern hemispheres use (180 - (Aspect – 225)) and for Southern hemisphere (180 - (Aspect – 315)). If a country is split at the equator you can use the force.hemisphere argument to choose which equation to use. Valid values for this argument are "southern" and "northern" with the default "none".

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

McCune, B., and D. Keon (2002) Equations for potential annual direct incident radiation and heat load index. Journal of Vegetation Science. 13:603-606.

McCune, B. (2007). Improved estimates of incident radiation and heat load using non-parametric regression against topographic variables. Journal of Vegetation Science 18:751-754.

Examples

```
library(raster)
data(elev)
heat.load <- hli(elev)
  plot(heat.load, main="Heat Load Index")
```

`hsp` *Hierarchical Slope Position*

Description

Calculates a hierarchical scale decomposition of topographic position index

Usage

```
hsp(
  x,
  min.scale = 3,
  max.scale = 27,
  inc = 4,
  win = "rectangle",
  normalize = FALSE
)
```

Arguments

`x`	Object of class raster (requires integer raster)
`min.scale`	Minimum scale (window size)
`max.scale`	Maximum scale (window size)
`inc`	Increment to increase scales
`win`	Window type, options are "rectangle" or "circle"
`normalize`	Normalize results to 0-1 scale (FALSE | TRUE)

Value

raster class object

Note

if win = "circle" units are distance, if win = "rectangle" units are number of cells

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Murphy M.A., J.S. Evans, and A.S. Storfer (2010) Quantify Bufo boreas connectivity in Yellowstone National Park with landscape genetics. Ecology 91:252-261

Examples

```
library(raster)
data(elev)
hsp27 <- hsp(elev, 3, 27, 4, normalize = TRUE)
plot(hsp27)
```

`hybrid.kmeans` *Hybrid K-means*

Description

Hybrid K-means clustering using hierarchical clustering to define cluster-centers

Usage

```
hybrid.kmeans(x, k = 2, hmethod = "ward.D", stat = mean, ...)
```

Arguments

`x`	A data.frame or matrix with data to be clustered
`k`	Number of clusters
`hmethod`	The agglomeration method used in hclust
`stat`	The statistic to aggregate class centers (mean or median)
`...`	Additional arguments passed to `kmeans`

Details

This method uses hierarchical clustering to define the cluster-centers in the K-means clustering algorithm. This mitigates some of the know convergence issues in K-means.

Value

returns an object of class "kmeans" which has a print and a fitted method

Note

options for hmethod are: "ward.D", "ward.D2", "single", "complete", "average", mcquitty", "median", "centroid"

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Singh, H., & K. Kaur (2013) New Method for Finding Initial Cluster Centroids in K-means Algorithm. International Journal of Computer Application. 74(6):27-30

Ward, J.H., (1963) Hierarchical grouping to optimize an objective function. Journal of the American Statistical Association. 58:236-24

See Also

`kmeans` for available ... arguments and function details

`hclust` for details on hierarchical clustering

Examples

```
x <- rbind(matrix(rnorm(100, sd = 0.3), ncol = 2),
           matrix(rnorm(100, mean = 1, sd = 0.3), ncol = 2))

# Compare k-means to hybrid k-means with k=4
km <- kmeans(x, 4)
hkm <- hybrid.kmeans(x,k=4)

opar <- par(no.readonly=TRUE)
par(mfrow=c(1,2))
  plot(x[,1],x[,2], col=km$cluster,pch=19, main="K-means")
  plot(x[,1],x[,2], col=hkm$cluster,pch=19, main="Hybrid K-means")
par(opar)
```

`idw.smoothing` *Inverse Distance Weighted smoothing*

Description

Distance weighted smoothing of a variable in a spatial point object

Usage

```
idw.smoothing(x, y, d, k)
```

Arguments

x	Object of class SpatialPointsDataFrame
y	Numeric data in x@data
d	Distance constraint
k	Maximum number of k-nearest neighbors within d

Value

A vector, same length as nrow(x), of adjusted y values

Note

Smoothing is conducted with a weighted-mean where; weights represent inverse standardized distance lags Distance-based or neighbour-based smoothing can be specified by setting the desired neighbour smoothing method to a specified value then the other parameter to the potential maximum. For example; a constraint distance, including all neighbors within 1000 (d=1000) would require k to equal all of the potential neighbors (n-1 or k=nrow(x)-1).

Examples

```
 library(sp)
  data(meuse)
  coordinates(meuse) <- ~x+y

# Calculate distance weighted mean on cadmium variable in meuse data
  cadmium.idw <- idw.smoothing(meuse, 'cadmium', k=nrow(meuse), d = 1000)
  meuse@data$cadmium.wm <- cadmium.idw

  opar <- par(no.readonly=TRUE)
    par(mfrow=c(2,1))
      plot(density(meuse@data$cadmium), main='Cadmium')
      plot(density(meuse@data$cadmium.wm), main='IDW Cadmium')
  par(opar)
```

`impute.loess` *Impute loess*

Description

Imputes missing data or smooths using Loess regression

Usage

```
impute.loess(y, s = 0.2, smooth = FALSE)
```

Arguments

y	A vector to impute
s	Smoothing parameter ()
smooth	(FALSE/TRUE) Smooth data, else only replace NA’s

Details

Performs a local polynomial regression to smooth data or to impute NA values. The minimal number of non-NA observations to reliably impute/smooth values is 6. There is not a reliably way to impute NA's on the tails of the distributions so if the missing data is in the first or last position of the vector it will remain NA. Please note that smooth needs to be TRUE to return a smoothed vector, else only NA's will be imputed.

Value

a vector the same length as x with NA values filled or the data smoothed (or both)..

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

Examples

```
data(cor.data)
d <- cor.data[[1]][,2]
  plot(d, type="l")
  lines(impute.loess(d, s=0.3, smooth=TRUE), lwd=2, col="red")

# add some NA's
d <- d[1:100]
  d[sample(30:70, 5)] <- NA
  d

impute.loess(d, s=0.2)
```

`insert` *Insert a row or column into a data.frame*

Description

Inserts a new row or column into a data.frame at a specified location

Usage

```
insert(x, MARGIN = 1, value = NULL, idx, name = NULL)
```

Arguments

`x`	Existing data.frame
`MARGIN`	Insert a 1 = row or 2 = column
`value`	A vector of values equal to the length of MARGIN, if nothing specified values with be NA
`idx`	Index position to insert row or column
`name`	Name of new column (not used for rows, MARGIN=1)

Value

A data.frame with the new row or column inserted

Note

Where there are methods to easily add a row/column to the end or beginning of a data.frame, it is not straight forward to insert data at a specific location within the data.frame. This function allows for inserting a vector at a specific location eg., between columns or rows 1 and 2 where row/column 2 is moved to the 3rd position and a new vector of values is inserted into the 2nd position.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
d <- data.frame(ID=1:10, y=runif(10))

# insert row
insert(d, idx=2)
insert(d, value=c(20,0), idx=2)

# insert column
insert(d, MARGIN=2, idx=2)
insert(d, MARGIN = 2, value = rep(0,10), idx=2, name="x")
```

`insert.values` *Insert Values*

Description

Inserts new values into a vector at specified positions

This function inserts new values at specified positions in a vector. It does not replace existing values. If a single value is provided for y and l represents multiple positions y will be replicated for the length of l. In this way you can insert the same value at multiple locations.

Usage

```
insert.values(x, value, index)
```

Arguments

`x`	A vector to insert values
`value`	Values to insert into x
`index`	Index position(s) to insert y values into x

Value

A vector with values of y inserted into x and the position(s) defined by the index

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
(x=1:10)

# Insert single value in one location
insert.values(x, 100, 2)

# Insert multiple values in multiple locations
insert.values(x, c(100,200), c(2,8))

# Insert single value in multiple locations
insert.values(x, NA, c(2,8))
```

`is.empty` *is.empty*

Description

evaluates empty elements in a vector

This function evaluates if an element in a vector is empty the na.empty argument allows for evaluating NA values (TRUE if NA) and all.na returns a TRUE if all elements are NA. The trim argument trims a character string to account for the fact that c(" ") is not empty but, a vector with c("") is empty. Using trim = TRUE will force both to return TRUE

Usage

```
is.empty(x, all.na = FALSE, na.empty = TRUE, trim = TRUE)
```

Arguments

`x`	A vector to evaluate elements
`all.na`	(FALSE / TRUE) Return a TRUE if all elements are NA
`na.empty`	(TRUE / FALSE) Return TRUE if element is NA
`trim`	(TRUE / FALSE) Trim empty strings

Value

A Boolean indicating empty elements in a vector, if all.na = FALSE a TRUE/FALSE value will be returned for each element in the vector

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
is.empty( c("") )
is.empty( c(" ") )
is.empty( c(" "), trim=FALSE )

is.empty( c("",NA,1) )
is.empty( c("",NA,1), na.empty=FALSE)

is.empty( c(NA,NA,NA) )
is.empty( c(NA,NA,NA), all.na=TRUE )
is.empty( c(NA,2,NA), all.na=TRUE )

any( is.empty( c("",2,3) ) )
any( is.empty( c(1,2,3) ) )
```

`is.whole` *is.whole*

Description

Boolean for evaluating whole numbers

Usage

```
is.whole(a, tol = 0.0000001)
```

Arguments

`a`	A numeric vector to evaluate, only first element will be evaluated
`tol`	numeric >= 0, differences smaller than tolerance are not reported

Value

A Boolean indicating if number is whole or float

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
is.whole( 1 )
is.whole( 1.5 )
is.whole( 0.5 )
```

kde.2D — *2-dimensional kernel density estimate*

Description

Calculates 2-dimensional kernel density estimate over specified extent

Usage

```
kde.2D(...)
```

Arguments

`...`	Parameters to be passed to the modern version of the function

kendall — *Kendall tau trend with continuity correction for time-series*

Description

Calculates a nonparametric statistic for a monotonic trend based on the Kendall tau statistic and the Theil-Sen slope modification

Usage

```
kendall(
  y,
  tau = TRUE,
  p.value = TRUE,
  z.value = TRUE,
  confidence = TRUE,
  intercept = TRUE,
  prewhiten = FALSE,
  na.rm,
  ...
)
```

Arguments

`y`	A vector representing a timeseries with >= 8 obs
`tau`	(FALSE/TRUE) return tau values
`p.value`	(FALSE/TRUE) return p.values
`z.value`	(FALSE/TRUE) return z values
`confidence`	(FALSE/TRUE) return 95 pct confidence levels

`intercept`	(FALSE/TRUE) return intercept values
`prewhiten`	(FALSE/TRUE) Apply autocorrelation correction using pre-whitening
`na.rm`	(FALSE/TRUE) Remove NA values
`...`	Not used

Details

This function implements Kendall's nonparametric test for a monotonic trend using the Theil-Sen (Theil 1950; Sen 1968; Siegel 1982) method to estimate the slope and related confidence intervals. Critical values are Z > 1.96 representing a significant increasing trend and a Z < -1.96 a significant decreasing trend (p < 0.05). The null hypothesis can be rejected if Tau = 0. There is also an option for autocorrelation correction using the method proposed in Yue & Wang (2002).

Value

Depending on arguments, a vector containing:

- value 1 Theil-Sen slope, always returned
- value 2 Kendall's tau two-sided test, if tau TRUE
- value 3 intercept for trend if intercept TRUE, not if prewhitened
- value 4 p value for trend fit if p.value TRUE
- value 5 Z value for trend fit if z.value TRUE
- value 6 lower confidence level at 95-pct if confidence TRUE, not if prewhitened
- value 7 upper confidence level at 95-pct if confidence TRUE, not if prewhitened

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Theil, H. (1950) A rank invariant method for linear and polynomial regression analysis. Nederl. Akad. Wetensch. Proc. Ser. A 53:386-392 (Part I), 53:521-525 (Part II), 53:1397-1412 (Part III).

Sen, P.K. (1968) Estimates of Regression Coefficient Based on Kendall's tau. Journal of the American Statistical Association. 63(324):1379-1389.

Siegel, A.F. (1982) Robust Regression Using Repeated Medians. Biometrika, 69(1):242-244

Yue, S., & Wang, C. Y. (2002). Applicability of prewhitening to eliminate the influence of serial correlation on the Mann-Kendall test. Water Resources Research, 38(6):41-47.

kl.divergence *Kullback-Leibler divergence (relative entropy)*

Description

Calculates the Kullback-Leibler divergence (relative entropy) between unweighted theoretical component distributions. Divergence is calculated as: int [f(x) (log f(x) - log g(x)) dx] for distributions with densities f() and g().

Usage

```
kl.divergence(object, eps = 10^-4, overlap = TRUE)
```

Arguments

`object`	Matrix or dataframe object with >=2 columns
`eps`	Probabilities below this threshold are replaced by this threshold for numerical stability.
`overlap`	Logical, do not determine the KL divergence for those pairs where for each point at least one of the densities has a value smaller than eps.

Value

pairwise Kullback-Leibler divergence index (matrix)

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Kullback S., and R. A. Leibler (1951) On information and sufficiency. The Annals of Mathematical Statistics 22(1):79-86

Examples

```
x <- seq(-3, 3, length=200)
y <- cbind(n=dnorm(x), t=dt(x, df=10))
  matplot(x, y, type='l')
    kl.divergence(y)

# extract value for last column
  kl.divergence(y[,1:2])[3:3]
```

knn — *Spatial K nearest neighbor*

Description

Find K nearest neighbors for two spatial objects

Finds nearest neighbor in x based on y and returns rownames, index and distance, If ids is NULL, rownames of x are returned. If coordinate matrix provided, columns need to be ordered [X,Y]. If a radius for d is specified than a maximum search radius is imposed. If no neighbor is found, a neighbor is not returned

You can specify weights to act as covariates for x and y. The vectors or matrices must match row dimensions with x and y as well as columns matching between weights. In other words, the covariates must match and be numeric.

Usage

```
knn(
  y,
  x,
  k = 1,
  d = NULL,
  ids = NULL,
  weights.y = NULL,
  weights.x = NULL,
  indexes = FALSE
)
```

Arguments

`y`	Spatial points or polygons object or coordinates matrix
`x`	Spatial points or polygons object or coordinates matrix
`k`	Number of neighbors
`d`	Optional search radius
`ids`	Optional column of ID's in x
`weights.y`	A vector or matrix representing covariates of y
`weights.x`	A vector or matrix representing covariates of x
`indexes`	(FALSE/TRUE) Return row indexes of x neighbors

Value

A data.frame with row indexes (optional), rownames, ids (optional) and distance of k

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

See Also

nn2 for details on search algorithm

Examples

```
 library(sp)
 data(meuse)
   coordinates(meuse) <- ~x+y

 idx <- sample(1:nrow(meuse), 10)
   pts <- meuse[idx,]
   meuse <- meuse[-idx,]
     meuse$IDS <- 1:nrow(meuse)

 # Find 2 neighbors in meuse
 ( nn <- knn(pts, meuse, k=2, ids = "IDS", indexes = TRUE) )
    plot(pts, pch=19, main="KNN")
      points(meuse[nn[,1],], pch=19, col="red")

# Using covariates (weights)
wx = as.matrix(meuse@data[,1:3])
wy = as.matrix(pts@data[,1:3])

( nn <- knn(pts, meuse, k=2, ids = "IDS", indexes = TRUE,
            weights.y=wy, weights.x=wx) )
    plot(pts, pch=19, main="KNN")
      points(meuse[nn[,1],], pch=19, col="red")

 # Using coordinate matrices
 y <- coordinates(pts)
 x <- coordinates(meuse)
 knn(y, x, k=2)
```

---

land.metrics *Landscape metrics for points and polygons*

Description

Calculates a variety of landscape metrics, on binary rasters, for polygons or points with a buffer distance

Usage

```
land.metrics(...)
```

Arguments

...	Parameters to be passed to the modern version of the function

Examples

```
## Not run:
library(landscapemetrics)
library(raster)

data(landscape)
points <- matrix(c(10, 5, 25, 15, 5, 25),
                 ncol = 2, byrow = TRUE)

sample_lsm(landscape, y = points, size = 10,
           level = "landscape", type = "diversity metric",
           classes_max = 3,
           verbose = FALSE)

## End(Not run)
```

`local.min.max` *Local minimum and maximum*

Description

Calculates the local minimums and maximums in a numeric vector, indicating inflection points in the distribution.

Usage

```
local.min.max(x, dev = mean, plot = TRUE, add.points = FALSE, ...)
```

Arguments

`x`	A numeric vector
`dev`	Deviation statistic (mean or median)
`plot`	plot the minimum and maximum values with the distribution (TRUE/FALSE)
`add.points`	Should all points of x be added to plot (TRUE/FALSE)
`...`	Arguments passed to plot

Value

A list object with:

- minima - minimum local values of x
- maxima - maximum local values of x
- mindev - Absolute deviation of minimum from specified deviation statistic (dev argument)
- maxdev - Absolute deviation of maximum from specified deviation statistic (dev argument)

Note

Useful function for identifying inflection or enveloping points in a distribution

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

Examples

```
x <- rnorm(100,mean=1500,sd=800)
( lmm <- local.min.max(x, dev=mean, add.points=TRUE,
                       main="Local Minima and Maxima") )

# return only local minimum values
   local.min.max(x)$minima
```

`loess.boot` *Loess Bootstrap*

Description

Bootstrap of a Local Polynomial Regression (loess)

The function fits a loess curve and then calculates a symmetric nonparametric bootstrap with a confidence region. Fitted curves are evaluated at a fixed number of equally-spaced x values, regardless of the number of x values in the data. Some replicates do not include the values at the lower and upper end of the range of x values. If the number of such replicates is too large, it becomes impossible to construct a confidence region that includes a fraction "confidence" of the bootstrap replicates. In such cases, the left and/or right portion of the confidence region is truncated.

Usage

```
loess.boot(x, y, nreps = 100, confidence = 0.95, ...)
```

Arguments

`x`	Independent variable
`y`	Dependent variable
`nreps`	Number of bootstrap replicates
`confidence`	Fraction of replicates contained in confidence region
`...`	Additional arguments passed to loess function

Value

list object containing

- nreps Number of bootstrap replicates
- confidence Confidence interval (region)
- span alpha (span) parameter used loess fit
- degree polynomial degree used in loess fit
- normalize Normalized data (TRUE/FALSE)
- family Family of statistic used in fit
- parametric Parametric approximation (TRUE/FALSE)
- surface Surface fit, see loess.control
- data data.frame of x,y used in model
- fit data.frame including:
    1. x - Equally-spaced x index (see NOTES)
    2. y.fit - loess fit
    3. up.lim - Upper confidence interval
    4. low.lim - Lower confidence interval
    5. stddev - Standard deviation of loess fit at each x value

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Cleveland, WS, (1979) Robust Locally Weighted Regression and Smoothing Plots Journal of the American Statistical Association 74:829-836

Efron, B., and R. Tibshirani (1993) An Introduction to the Bootstrap Chapman and Hall, New York

Hardle, W., (1989) Applied Nonparametric Regression Cambridge University Press, NY.

Tibshirani, R. (1988) Variance stabilization and the bootstrap. Biometrika 75(3):433-44.

Examples

```
n=1000
x <- seq(0, 4, length.out=n)
y <- sin(2*x)+ 0.5*x + rnorm(n, sd=0.5)
sb <- loess.boot(x, y, nreps=99, confidence=0.90, span=0.40)
plot(sb)
```

`loess.ci` *Loess with confidence intervals*

Description

Calculates a local polynomial regression fit with associated confidence intervals

Usage

```
loess.ci(y, x, p = 0.95, plot = FALSE, ...)
```

Arguments

`y`	Dependent variable, vector
`x`	Independent variable, vector
`p`	Percent confidence intervals (default is 0.95)
`plot`	Plot the fit and confidence intervals
`...`	Arguments passed to loess

Value

A list object with:

- loess Predicted values
- se Estimated standard error for each predicted value
- lci Lower confidence interval
- uci Upper confidence interval
- df Estimated degrees of freedom
- rs Residual scale of residuals used in computing the standard errors

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

W. S. Cleveland, E. Grosse and W. M. Shyu (1992) Local regression models. Chapter 8 of Statistical Models in S eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole.

Examples

```
 x <- seq(-20, 20, 0.1)
 y <- sin(x)/x + rnorm(length(x), sd=0.03)
 p <- which(y == "NaN")
   y <- y[-p]
   x <- x[-p]

opar <- par(no.readonly=TRUE)
  par(mfrow=c(2,2))
    lci <- loess.ci(y, x, plot=TRUE, span=0.10)
    lci <- loess.ci(y, x, plot=TRUE, span=0.30)
    lci <- loess.ci(y, x, plot=TRUE, span=0.50)
    lci <- loess.ci(y, x, plot=TRUE, span=0.80)
par(opar)
```

`logistic.regression` *Logistic and Auto-logistic regression*

Description

Performs a logistic (binomial) or auto-logistic (spatially lagged binomial) regression using maximum likelihood or penalized maximum likelihood estimation.

It should be noted that the auto-logistic model (Besag 1972) is intended for exploratory analysis of spatial effects. Auto-logistic are know to underestimate the effect of environmental variables and tend to be unreliable (Dormann 2007). Wij matrix options under style argument - B is the basic binary coding, W is row standardized (sums over all links to n), C is globally standardized (sums over all links to n), U is equal to C divided by the number of neighbors (sums over all links to unity) and S is variance-stabilizing. Spatially lagged y defined as: W(y)ij=sumj_(Wij yj)/ sumj_(Wij) where; Wij=1/Euclidean(i,j) If the object passed to the function is an sp class there is no need to call the data slot directly via "object@data", just pass the object name.

Usage

```
logistic.regression(
  ldata,
  y,
  x,
  penalty = TRUE,
  autologistic = FALSE,
  coords = NULL,
  bw = NULL,
  type = "inverse",
  style = "W",
  longlat = FALSE,
  ...
)
```

Arguments

`ldata`	data.frame object containing variables
`y`	Dependent variable (y) in ldata
`x`	Independent variable(s) (x) in ldata
`penalty`	Apply regression penalty (TRUE/FALSE)
`autologistic`	Add auto-logistic term (TRUE/FALSE)
`coords`	Geographic coordinates for auto-logistic model matrix or sp object.
`bw`	Distance bandwidth to calculate spatial lags (if empty neighbors result, need to increase bandwidth). If not provided it will be calculated automatically based on the minimum distance that includes at least one neighbor.
`type`	Neighbor weighting scheme (see autocov_dist)
`style`	Type of neighbor matrix (Wij), default is mean of neighbors
`longlat`	Are coordinates (coords) in geographic, lat/long (TRUE/FALSE)
`...`	Additional arguments passed to lrm

Value

A list class object with the following components:

- model - lrm model object (rms class)
- bandwidth - If AutoCov = TRUE returns the distance bandwidth used for the auto-covariance function
- diagTable - data.frame of regression diagnostics
- coefTable - data.frame of regression coefficients
- Residuals - data.frame of residuals and standardized residuals
- AutoCov - If an auto-logistic model, AutoCov represents lagged auto-covariance term

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Besag, J.E., (1972) Nearest-neighbour systems and the auto-logistic model for binary data. Journal of the Royal Statistical Society, Series B Methodological 34:75-83

Dormann, C.F., (2007) Assessing the validity of autologistic regression. Ecological Modelling 207:234-242

Le Cessie, S., Van Houwelingen, J.C., (1992) Ridge estimators in logistic regression. Applied Statistics 41:191-201

Shao, J., (1993) Linear model selection by cross-validation. JASA 88:486-494

See Also

`lrm`

`autocov_dist`

Examples

```
require(sp)
require(spdep)
require(rms)
data(meuse)
  coordinates(meuse) <- ~x+y
    meuse@data <- data.frame(DepVar=rbinom(dim(meuse)[1], 1, 0.5),
                             meuse@data)

#### Logistic model
lmodel <- logistic.regression(meuse, y='DepVar',
                  x=c('dist','cadmium','copper'))
  lmodel$model
    lmodel$diagTable
      lmodel$coefTable

#### Logistic model with factorial variable
lmodel <- logistic.regression(meuse, y='DepVar',
            x=c('dist','cadmium','copper', 'soil'))
  lmodel$model
    lmodel$diagTable
      lmodel$coefTable

### Auto-logistic model using 'autocov_dist' in 'spdep' package
lmodel <- logistic.regression(meuse, y='DepVar',
            x=c('dist','cadmium','copper'), autologistic=TRUE,
            coords=coordinates(meuse), bw=5000)
  lmodel$model
    lmodel$diagTable
      lmodel$coefTable
  est <- predict(lmodel$model, type='fitted.ind')

#### Add residuals, standardized residuals and estimated probabilities
VarNames <- rownames(lmodel$model$var)[-1]
  meuse@data$AutoCov <- lmodel$AutoCov
    meuse@data <- data.frame(meuse@data, Residual=lmodel$Residuals[,1],
                     StdResid=lmodel$Residuals[,2], Probs=predict(lmodel$model,
                     meuse@data[,VarNames],type='fitted') )

#### Plot fit and probabilities
resid(lmodel$model, "partial", pl="loess")
# plot residuals
resid(lmodel$model, "partial", pl=TRUE)

# global test of goodness of fit
resid(lmodel$model, "gof")

# Approx. leave-out linear predictors
lp1 <- resid(lmodel$model, "lp1")

# Approx leave-out-1 deviance
-2 * sum(meuse@data$DepVar * lp1 + log(1-plogis(lp1)))
```

```
# plot estimated probabilities at points
spplot(meuse, c('Probs'))
```

---

max_extent *Maximum extent of multiple rasters*

Description

returns a extent polygon representing maximum extent of input rasters

Usage

```
max_extent(x, ...)
```

Arguments

`x`	raster class object
`...`	additional raster class objects

Value

a SpatialPolygons sp class object

Note

Creates a maximum extent polygon of all specified rasters

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)

r1 <- raster(extent(61.87125, 76.64458, 23.90153, 37.27042))
r2 <- raster(extent(67.66625, 81.56847, 20.38458, 35.67347))
r3 <- raster(extent(72.64792,84.38125,5.91125,28.13347 ))

( e <- max_extent(r1, r2, r3) )
plot(e)
  plot(as(extent(r1),"SpatialPolygons"),col="red",add=TRUE)
  plot(as(extent(r2),"SpatialPolygons"),col="red",add=TRUE)
  plot(as(extent(r3),"SpatialPolygons"),col="red",add=TRUE)
```

`moments`	*moments*

Description

Calculate statistical moments of a distribution

Usage

```
moments(x, plot = FALSE)
```

Arguments

`x`	numeric vector
`plot`	plot of distribution (TRUE/FALSE)

Value

A vector with the following values:

- min Minimum
- 25th 25th percentile
- mean Arithmetic mean
- gmean Geometric mean
- hmean Harmonic mean
- median 50th percentile
- 7th5 75th percentile
- max Maximum
- stdv Standard deviation
- var Variance
- cv Coefficient of variation (percent)
- mad Median absolute deviation
- skew Skewness
- kurt Kurtosis
- nmodes Number of modes
- mode Mode (dominate)

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

Examples

```
x <- runif(1000,0,100)
( d <- moments(x, plot=TRUE) )
( mode.x <- moments(x, plot=FALSE)[16] )
```

---

morans.plot *Autocorrelation Plot*

Description

Autocorrelation plot (Anselin 1996), following Chen (2015), aka, Moran's-I plot (univariate or bivariate)

Usage

```
morans.plot(
  x,
  y = NULL,
  coords = NULL,
  type.ac = c("xy", "yx"),
  dist.function = "inv.power",
  scale.xy = TRUE,
  scale.morans = FALSE,
  ...
)
```

Arguments

`x`	Vector of x response variables
`y`	Vector of y response variables
`coords`	A matrix of coordinates corresponding to [x,y]
`type.ac`	Type of autocorrelation plot ("xy", "yx")
`dist.function`	("inv.power", "neg.exponent")
`scale.xy`	(TRUE/FALSE) scale the x,y vectors
`scale.morans`	(FALSE/TRUE) standardize the Moran's index to an expected [-1 to 1]?
`...`	Additional arguments passed to plot

Details

The argument "type" controls the plot for x influencing y (type="xy") or y influencing x (type="yx"). If y is not defined then the statistic is univariate and only the "xy" plot will be available. The linear relationship between x and its spatial lag (Wx) is indicative of the spatial autoregressive process, underlying the spatial dependence. The statistic can be autocorrelation (univariate or cross-correlation (bivariate). The quadrants are the zero intercept for random autocorrelation and the red line represents the trend in autocorrelation. The quadrants in the plot indicate the type of spatial association/interaction (Anselin 1996). For example the upper-left quadrant represents negative associations of low values surrounded by high and the lower-right quadrant represents negative associations of high values surrounded by low.

Value

A plot of the scaled variable against its spatially lagged values.

Note

if y is not specified the univariate statistic for x is returned. the coords argument is only used if k = NULL. Can also be an sp object with relevant x,y coordinate slot (ie., points or polygons). If w = NULL, the default method for deriving spatial weights matrix, options are: inverse power or negative exponent. If scale.xy = FALSE it is assumed that they are already scaled following Chen (2015).

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Chen., Y. (2015) A New Methodology of Spatial Cross-Correlation Analysis. PLoS One 10(5):e0126158. doi:10.1371/journal.pone.0126158

Anselin, L. (1996) The Moran scatterplot as an ESDA tool to assess local instability in spatial association. pp. 111-125 in M. M. Fischer, H. J. Scholten and D. Unwin (eds) Spatial analytical perspectives on GIS, London, Taylor and Francis

Anselin, L. (1995) Local indicators of spatial association, Geographical Analysis, 27:93-115

Examples

```
library(sp)
library(spdep)
 data(meuse)
  coordinates(meuse) <- ~x+y

# Autocorrelation (univariate)
  morans.plot(meuse$zinc, coords = coordinates(meuse))

# Cross-correlation of: x influencing y and y influencing x
opar <- par(no.readonly=TRUE)
  par(mfrow=c(1,2))
    morans.plot(x=meuse$zinc, y=meuse$copper, coords = coordinates(meuse),
                scale.morans = TRUE)
    morans.plot(x=meuse$zinc, y=meuse$copper, coords = coordinates(meuse),
                scale.morans = TRUE, type.ac="yx")
par(opar)
```

mwCorr *Dutilleul moving window bivariate raster correlation*

Description

A bivarate raster correlation using Dutilleul's modified t-test

Usage

```
mwCorr(...)
```

Arguments

`...`	Parameters to be passed to the modern version of the function

nni *Average Nearest Neighbor Index (NNI)*

Description

Calculates the NNI as a measure of clustering or dispersal

The nearest neighbor index is expressed as the ratio of the observed distance divided by the expected distance. The expected distance is the average distance between neighbors in a hypothetical random distribution. If the index is less than 1, the pattern exhibits clustering; if the index is greater than 1, the trend is toward dispersion or competition. The Nearest Neighbor Index is calculated as:

- Mean Nearest Neighbor Distance (observed) D(nn) = sum(min(Dij)/N)
- Mean Random Distance (expected) D(e) = 0.5 SQRT(A/N)
- Nearest Neighbor Index NNI = D(nn)/D(e) Where; D=neighbor distance, A=Area

Usage

```
nni(x, win = "hull")
```

Arguments

`x`	An sp point object
`win`	Type of window 'hull' or 'extent'

Value

list object containing NNI = nearest neighbor index, z.score = Z Score value, p = p value, expected.mean.distance = Expected mean distance, observed.mean.distance = Observed meand distance.

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Clark, P.J., and F.C. Evans (1954) Distance to nearest neighbour as a measure of spatial relationships in populations. Ecology 35:445-453

Cressie, N (1991) Statistics for spatial data. Wiley & Sons, New York.

Examples

```
require(sp)
data(meuse)
  coordinates(meuse) <- ~x+y
    nni(meuse)
```

`nth.values` *Nth values*

Description

Returns the Nth highest or lowest values in a vector

Usage

```
nth.values(x, N = 2, smallest = FALSE)
```

Arguments

`x`	Numeric vector
`N`	Number of (Nth) values returned
`smallest`	(FALSE/TRUE) Return the highest, else smallest values

Value

Numeric vector of Nth values

Note

This function returns n lowest or highest elements in a vector

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
nth.values(1:20, N=3, smallest = TRUE)
nth.values(1:20, N=3)
```

`o.ring` *Inhomogeneous O-ring*

Description

Calculates the inhomogeneous O-ring point pattern statistic (Wiegand & Maloney 2004)

The function K(r) is the expected number of points in a circle of radius r centered at an arbitrary point (which is not counted), divided by the intensity l of the pattern. The alternative pair correlation function g(r), which arises if the circles of Ripley's K-function are replaced by rings, gives the expected number of points at distance r from an arbitrary point, divided by the intensity of the pattern. Of special interest is to determine whether a pattern is random, clumped, or regular.

Using rings instead of circles has the advantage that one can isolate specific distance classes, whereas the cumulative K-function confounds effects at larger distances with effects at shorter distances. Note that the K-function and the O-ring statistic respond to slightly different biological questions. The accumulative K-function can detect aggregation or dispersion up to a given distance r and is therefore appropriate if the process in question (e.g., the negative effect of competition) may work only up to a certain distance, whereas the O-ring statistic can detect aggregation or dispersion at a given distance r. The O-ring statistic has the additional advantage that it is a probability density function (or a conditioned probability spectrum) with the interpretation of a neighborhood density, which is more intuitive than an accumulative measure.

Usage

```
o.ring(x, inhomogeneous = FALSE, ...)
```

Arguments

`x`	spatstat ppp object
`inhomogeneous`	(FALSE/TRUE) Run homogeneous (pcf) or inhomogeneous (pcfinhom)
`...`	additional arguments passed to pcf or pcfinhom

Value

plot of o-ring and data.frame with plot labels and descriptions

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Wiegand T., and K. A. Moloney (2004) Rings, circles and null-models for point pattern analysis in ecology. Oikos 104:209-229

Examples

```
library(spatstat.core)
data(lansing)
    x  <- spatstat.geom::unmark(split(lansing)$maple)
    o.ring(x)
```

`oli.asw` *Query AWS-OLI*

Description

Query of Amazon AWS OLI-Landsat 8 cloud service

Usage

```
oli.asw(path, row, dates, cloud.cover = 10, processing)
```

Arguments

`path`	landsat path
`row`	landsat row
`dates`	dates, single or start-stop range in YYYY-MM-DD format
`cloud.cover`	percent cloud cover
`processing`	processing level ("L1GT" or "L1T")

Value

data.frame object with:

- entityId - Granule ID
- L = Landsat
- X = Sensor
- SS = Satellite
- PPP = WRS path
- RRR = WRS row
- YYYYMMDD = Acquisition date
- yyyymmdd = Processing date
- CC = Collection number

- TX = Collection category
- acquisitionDate - POSIXct YYYY-MM-DD (eg., 2015-01-02)
- cloudCover -
- processingLevel - USGS processing level
- path - Landsat path
- row - Landsat row

Note

Amazons AWS cloud service is hosting OLI Landsat 8 data granules https://registry.opendata.aws/landsat-8 https://aws.amazon.com/blogs/aws/start-using-landsat-on-aws/

USGS Landsat collections: https://www.usgs.gov/core-science-systems/nli/landsat Pre-collection processing levels: "L1T", "L1GT", "L1G" Collection 1 processing levels: "L1TP", "L1GT", "L1GS" "L1T" and "L1TP" - Radiomertically calibrated and orthorectified (highest level processing) "L1GT" and "L1GT" - Radiomertically calibrated and systematic geometric corrections "L1G" and "L1GS" - Radiomertically calibrated with systematic ephemeris correction

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
## Not run:
# Query path 126, row 59, 2013-04-15 to 2017-03-09, <20% cloud cover
( p126r59.oli <- oli.asw(path=126, row=59, dates = c("2013-04-15", "2017-03-09"),
                          cloud.cover = 20) )

# Download images from query
 bands <- c("_B1.TIF", "_B2.TIF", "_B3.TIF", "_B4.TIF", "_B5.TIF",
            "_B6.TIF","_B7.TIF", "_B8.TIF", "_B9.TIF", "_B10.TIF",
         "_B11.TIF", "_BQA.TIF","_MTL.txt")
  for(i in 1:length(p126r59.oli$download_url)) {
    oli.url <- gsub("/index.html","",p126r59.oli$download_url[i])
 all.bands <- paste(oli.url, paste0(unlist(strsplit(oli.url, "/"))[8], bands), sep="/")
   for(j in all.bands) {
        try(utils::download.file(url=j, destfile=basename(j), mode = "wb"))
       }
  }

## End(Not run)
```

optimal.k *optimalK*

Description

Find optimal k of k-Medoid partitions using silhouette widths

Usage

```
optimal.k(x, nk = 10, plot = TRUE, cluster = TRUE, clara = FALSE, ...)
```

Arguments

`x`	Numeric dataframe, matrix or vector
`nk`	Number of clusters to test (2:nk)
`plot`	Plot cluster silhouettes(TRUE/FALSE)
`cluster`	Create cluster object with optimal k
`clara`	Use clara model for large data
`...`	Additional arguments passed to clara

Value

Object of class clust "pam" or "clara"

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

References

Theodoridis, S. & K. Koutroumbas(2006) Pattern Recognition 3rd ed.

See Also

`pam` for details on Partitioning Around Medoids (PAM)

`clara` for details on Clustering Large Applications (clara)

Examples

```
require(cluster)
  x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
             cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))

  clust <- optimal.k(x, 20, plot=TRUE, cluster=TRUE)
    plot(silhouette(clust), col = c('red', 'green'))
      plot(clust, which.plots=1, main='K-Medoid fit')
```

```
# Extract multivariate and univariate mediods (class centers)
  clust$medoids
    pam(x[,1], 1)$medoids

# join clusters to data
  x <- data.frame(x, k=clust$clustering)
```

---

optimized.sample.variance
Optimized sample variance

Description

Draws an optimal sample that minimizes or maximizes the sample variance

Usage

```
optimized.sample.variance(x, n, type = "maximized")
```

Arguments

x	A vector to draw a sample from
n	Number of samples to draw
type	Type of sample variance optimization c("maximized", "minimized")

Value

A data.frame with "idx" representing the index of the original vector and "y" is the value of the sampled data

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
  data(meuse)
  coordinates(meuse) <- ~x+y

n = 15
# Draw n samples that maximize the variance of y
( max.sv <- optimized.sample.variance(meuse$zinc, 15) )

# Draw n samples that minimize the variance of y
( min.sv <- optimized.sample.variance(meuse$zinc, 15,
             type="minimized") )
```

```
# Plot results
plot(meuse, pch=19, col="grey")
  plot(meuse[max.sv$idx,], col="red", add=TRUE, pch=19)
    plot(meuse[min.sv$idx,], col="blue", add=TRUE, pch=19)
   box()
    legend("topleft", legend=c("population","maximized variance",
           "minimized variance"), col=c("grey","red","blue"),
           pch=c(19,19,19))


# Raster example (not memory safe)
library(raster)
  r <- raster(system.file("external/test.grd", package="raster"))

# Calculate optimal sample variance and coerce to SpatialPointDataFrame
#   using xyFromCell
    ( min.sv <- optimized.sample.variance(getValues(r), n, type="minimized") )
     min.sv <- sp::SpatialPointsDataFrame(xyFromCell(r, min.sv[,"idx"],
                                         spatial=TRUE), data=min.sv)
    ( max.sv <- optimized.sample.variance(getValues(r), n) )
     max.sv <- sp::SpatialPointsDataFrame(xyFromCell(r, max.sv[,"idx"],
                                         spatial=TRUE), data=max.sv)

plot(r)
  plot(max.sv, col="blue", add=TRUE, pch=19)
  plot(min.sv, col="red", add=TRUE, pch=19)
  box()
legend("topleft", legend=c("maximized variance", "minimized variance"),
       col=c("red","blue"), pch=c(19,19))
```

`outliers` *Outliers*

Description

Identify outliers using modified Z-score

Usage

```
outliers(x, s = 1.4826)
```

Arguments

x	A numeric vector
s	Scaling factor for mad statistic

Value

value for the modified Z-score

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Iglewicz, B. & D.C. Hoaglin (1993) How to Detect and Handle Outliers, American Society for Quality Control, Milwaukee, WI.

Examples

```
# Create data with 3 outliers
   x <- seq(0.1, 5, length=100)
   x[98:100] <- c(100, 55, 250)

# Calculate Z score
    Z <- outliers(x)

# Show number of extreme outliers using Z-score
    length(Z[Z > 9.9])

# Remove extreme outliers
    x <- x[-which(Z > 9.9)]
```

---

overlap *Niche overlap (Warren's-I)*

Description

Similarity Statistic for Quantifying Niche Overlap using Warren's-I

The overlap function computes the I similarity statistic (Warren et al. 2008) of two overlapping niche estimates. Similarity is based on the Hellenger distance. It is assumed that the input data share the same extent and cellsize and all values are positive.

The I similarity statistic sums the pair-wise differences between two predictions to create a single value representing the similarity of the two distributions. The I similarity statistic ranges from a value of 0, where two distributions have no overlap, to 1 where two distributions are identical (Warren et al., 2008). The function is based on code from Jeremy VanDerWal

Usage

```
overlap(x, y)
```

Arguments

`x`	A matrix, rasterLayer or sp raster class object
`y`	A matrix, rasterLayer or sp raster class object with the same dimensions of x

Value

A value representing the I similarity statistic

Author(s)

Jeffrey Evans <jeffrey_evans@tnc.org> and Jeremy VanDerWal

References

Warren, D. L., R. E. Glor, M. Turelli, and D. Funk. (2008). Environmental Niche Equivalency versus Conservatism: Quantitative Approaches to Niche Evolution. Evolution 62:2868-2883.

Examples

```
# add degree of separation in two matrices
p1 <- abs(matrix(1:50,nr=50,nc=50) +
         runif(n = 2500, min = -1, max = 1))
p2 <- abs(matrix(1:50,nr=50,nc=50) +
         rnorm(n = 2500, mean = 1, sd = 1))

# High overlap/similarity
( I <- overlap(p1,p2) )
```

`parea.sample` *Percent area sample*

Description

Creates a point sample of polygons where n is based on percent area

Usage

```
parea.sample(
  x,
  pct = 0.1,
  join = FALSE,
  min.samp = 1,
  max.samp = NULL,
  sf = 4046.86,
  stype = "hexagonal",
  ...
)
```

Arguments

x	sp SpatialPolygonsDataFrame object
pct	Percent of area sampled
join	Join polygon attributed to point sample
min.samp	Minimum number of samples
max.samp	Maximum number of samples
sf	Scaling factor (default is meters to acres conversion factor)
stype	Sampling type ('random', 'regular', 'nonaligned', 'hexagonal')
...	Additional arguments passed to spsample

Value

A SpatialPointsDataFrame with polygon samples

Note

This function results in an adaptive sample based on the area of each polygon

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
require(sp)
sr1=Polygons(list(Polygon(cbind(c(180114, 180553, 181127, 181477, 181294,
  181007, 180409, 180162, 180114), c(332349, 332057, 332342, 333250, 333558,
  333676, 332618, 332413, 332349)))),'1')
sr2=Polygons(list(Polygon(cbind(c(180042, 180545, 180553, 180314, 179955,
  179142, 179437, 179524, 179979, 180042), c(332373, 332026, 331426, 330889,
  330683, 331133, 331623, 332152, 332357, 332373)))),'2')
sr=SpatialPolygons(list(sr1,sr2))
srdf=SpatialPolygonsDataFrame(sr, data.frame(row.names=c('1','2'), PIDS=1:2))

ars <- parea.sample(srdf, pct=0.20, stype='random')
  plot(srdf)
    plot(ars, pch=20, add=TRUE)
```

parse.bits *Parse bits*

Description

Returns specified bit value based on integer input

Data such as MODIS the QC band are stored in bits. This function returns the value(s) for specified bit. For example, the MODIS QC flag are bits 0-1 with the bit value 00 representing the "LST produced, good quality" flag. When exported from HDF the QC bands are often in an 8 bit integer range (0-255). With this function you can parse the values for each bit to assign the flag values.

Usage

```
parse.bits(x, bit, depth = 8, order = c("reverse", "none"))
```

Arguments

`x`	Integer value
`bit`	A single or vector of bits to return
`depth`	The depth (length) of the bit range, default is 8
`order`	c("reverse", "none") sort order for the bits

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```

 # Return value for bit 5 for integer value 100
 parse.bits(100, 5)

 # Return value(s) for bits 0 and 1 for integer value 100
 parse.bits(100, c(0,1))

 # Return value(s) for bits 0 and 1 for integer values 0-255
 for(i in 0:255) { print(parse.bits(i, c(0,1))) }

## Not run:
#### Applied Example using Harmonized Landsat Sentinel-2 QC

# Create dummy data and qc band
 library(raster)
 r <- raster(nrow=100, ncol=100)
   r[] <- round(runif(ncell(r), 0,1))
 qc <- raster(nrow=100, ncol=100)
   qc[] <- round(runif(ncell(qc), 64,234))
 # Calculate bit values from QC table
 ( qc_bits <- data.frame(int=0:255,
  cloud = unlist(lapply(0:255, FUN=parse.bits, bit=1)),
  shadow = unlist(lapply(0:255, FUN=parse.bits, bit=3)),
  acloud = unlist(lapply(0:255, FUN=parse.bits, bit=2)),
  cirrus = unlist(lapply(0:255, FUN=parse.bits, bit=0)),
  aerosol = unlist(lapply(0:255, FUN=parse.bits, bit=c(7,6)))) )

 # Query the results to create a vector of integer values indicating what to mask
 m <- sort(unique(qc_bits[c(which(qc_bits$cloud == 1),
                            which(qc_bits$shadow == 1)
     ),]$int))

 # Apply queried integer values to mask image with QA band
 qc[qc %in% m] <- NA
 r <- mask(r, qc)

## End(Not run)
```

`partial.cor` *Partial and Semi-partial correlation*

Description

Calculates a partial or semi-partial correlation with parametric and nonparametric options

Usage

```
partial.cor(
  x,
  y,
  z,
  method = c("partial", "semipartial"),
  statistic = c("kendall", "pearson", "spearman")
)
```

Arguments

`x`	A vector, data.frame or matrix with 3 columns
`y`	A vector same length as x
`z`	A vector same length as x
`method`	Type of correlation: "partial" or "semipartial"
`statistic`	Correlation statistic, options are: "kendall", "pearson", "spearman"

Details

Partial and semipartial correlations show the association between two variables when one or more peripheral variables are controlled to hold them constant.

Suppose we have three variables, X, Y, and Z. Partial correlation holds constant one variable when computing the relations two others. Suppose we want to know the correlation between X and Y holding Z constant for both X and Y. That would be the partial correlation between X and Y controlling for Z. Semipartial correlation holds Z constant for either X or Y, but not both, so if we wanted to control X for Z, we could compute the semipartial correlation between X and Y holding Z constant for X.

Value

data.frame containing:

- correlation correlation coefficient
- p.value p-value of correlation
- test.statistic test statistic
- n sample size
- Method indicating partial or semipartial correlation
- Statistic the correlation statistic used

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
air.flow = stackloss[,1]
water.temperature = stackloss[,2]
acid = stackloss[,3]

# Partial using Kendall (nonparametric) correlation
partial.cor(air.flow, water.temperature, acid)

scholar <- data.frame(
  HSGPA=c(3.0, 3.2, 2.8, 2.5, 3.2, 3.8, 3.9, 3.8, 3.5, 3.1),
 FGPA=c(2.8, 3.0, 2.8, 2.2, 3.3, 3.3, 3.5, 3.7, 3.4, 2.9),
  SATV =c(500, 550, 450, 400, 600, 650, 700, 550, 650, 550))

# Standard Pearson's correlations between HSGPA and FGPA
cor(scholar[,1], scholar[,2])

# Partial correlation using Pearson (parametric) between HSGPA
#   and FGPA, controlling for SATV
partial.cor(scholar, statistic="pearson")

# Semipartial using Pearson (parametric) correlation
partial.cor(x=scholar[,2], y=scholar[,1], z=scholar[,3],
            method="semipartial", statistic="pearson")
```

plot.effect.size *Plot effect size*

Description

Plot function for effect.size object

Usage

```
## S3 method for class 'effect.size'
plot(x, ...)
```

Arguments

x	A effect.size object
...	Additional arguments passed to plot

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

plot.loess.boot *Plot Loess Bootstrap*

Description

Plot function for loess.boot object

Usage

```
## S3 method for class 'loess.boot'
plot(x, ...)
```

Arguments

x	A loess.boot object
...	Additional arguments passed to plot

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Cleveland, WS, (1979) Robust Locally Weighted Regression and Smoothing Plots Journal of the American Statistical Association 74:829-836

Efron, B., and R. Tibshirani (1993) An Introduction to the Bootstrap Chapman and Hall, New York

Hardle, W., (1989) Applied Nonparametric Regression Cambridge University Press, NY.

Tibshirani, R. (1988) Variance stabilization and the bootstrap. Biometrika 75(3):433-44.

Examples

```
n=1000
x <- seq(0, 4, length.out=n)
y <- sin(2*x)+ 0.5*x + rnorm(n, sd=0.5)
sb <- loess.boot(x, y, nreps = 99, confidence = 0.90, span = 0.40)
plot(sb)
```

`point.in.poly` *Point and Polygon Intersect*

Description

Intersects point and polygon feature classes and adds polygon attributes to points

If duplicate argument is TRUE and more than one polygon intersection occurs, points will be duplicated (new row added) and all attributes joined. However, if duplicate is FALSE, with duplicate intersections, a new column for each unique intersecting polygon will be returned and the points will not be duplicated. For example, if a point intersect three polygons, three new columns will be added representing the polygons ID.

Usage

```
point.in.poly(x, y, sp = TRUE, duplicate = TRUE, ...)
```

Arguments

`x`	sp SpatialPointsDataFrame or SpatialPoints or sf point object
`y`	sp SpatialPolygonsDataFrame or sf polygon object
`sp`	(TRUE/FALSE) Return an sp class object, else returns sf class object
`duplicate`	(TRUE/FALSE) Return duplicated features with more than one polygon intersection
`...`	Additional arguments passed to sf::st_join

Value

A SpatialPointsDataFrame or sf

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 #### Simple one-to-one feature overlay.
 require(sp)
   data(meuse)
   coordinates(meuse) = ~x+y
   meuse@data$test.na <- NA

   sr1=Polygons(list(Polygon(cbind(c(180114, 180553, 181127, 181477, 181294,
     181007, 180409, 180162, 180114), c(332349, 332057, 332342, 333250, 333558,
     333676, 332618, 332413, 332349)))),'10')
   sr2=Polygons(list(Polygon(cbind(c(180042, 180545, 180553, 180314, 179955, 179142,
     179437, 179524, 179979, 180042), c(332373, 332026, 331426, 330889, 330683,
     331133, 331623, 332152, 332357, 332373)))),'20')
   sr3=Polygons(list(Polygon(cbind(c(179110, 179907, 180433, 180712, 180752, 180329,
     179875, 179668, 179572, 179269, 178879, 178600, 178544, 179046, 179110),
     c(331086, 330620, 330494, 330265, 330075, 330233, 330336, 330004,
     329783, 329665, 329720, 329933, 330478, 331062, 331086)))),'30')
   sr4=Polygons(list(Polygon(cbind(c(180304, 180403,179632,179420,180304),
     c(332791, 333204, 333635, 333058, 332791)))),'40')
   sr=SpatialPolygons(list(sr1,sr2,sr3,sr4))
   polys=SpatialPolygonsDataFrame(sr, data.frame(row.names=c('10','20','30','40'),
                                  PIDS=1:4, y=runif(4)))
   polys@data$pid <- polys@data$PIDS + 100

 plot(polys)
   plot(meuse, pch=19, add=TRUE)

 # Point in polygon overlay
 pts.poly <-  point.in.poly(meuse, polys)
   head(pts.poly@data)

 # Count points in each polygon
 tapply(pts.poly$cadmium, pts.poly$pid, FUN=length)

 #### Complex many-to-one feature overlay.
 require(sf)
 p <- sf::st_polygon(list(rbind(c(0,0), c(1,0), c(1,1), c(0,1), c(0,0))))
 polys <- sf::st_sf(sf::st_sfc(p, p + c(.8, .2), p + c(.2, .8)))
 pts <- sf::st_sf(sf::st_sample(polys, size=100))

 # Duplicates points for each new polygon, no attributes so returns IDs for features
 pts.poly.dup <-  point.in.poly(pts, polys)
   head(pts.poly.dup@data)

## Not run:
 # **** Should throw error due to lack of attributes ****
   pts.poly <- point.in.poly(pts, polys, duplicate = FALSE)
```

```
## End(Not run)

 # Coerce to sp class objects
 x <- as(pts, "Spatial")
   x <- SpatialPointsDataFrame(x, data.frame(IDS=1:nrow(x), pty=runif(nrow(x))))
 y <- as(polys, "Spatial")
   y <- SpatialPolygonsDataFrame(y, data.frame(IDS=1:nrow(y), py=runif(nrow(y))))

 # Returns point attributes with column for each unique polygon
 pts.poly <- point.in.poly(x, y, duplicate = FALSE)
   head(pts.poly@data)

 # Duplicates points for each new polygon, joins all attributes
 pts.poly.dup <-  point.in.poly(x, y)
   head(pts.poly.dup@data)

 # Count points in each polygon
 tapply(pts.poly.dup$IDS.x, pts.poly.dup$IDS.y, FUN=length)
```

`poly.regression` *Local Polynomial Regression*

Description

Calculates a Local Polynomial Regression for smoothing or imputation of missing data.

This is a wrapper function for loess that simplifies data smoothing and imputation of missing values. The function allows for smoothing a vector, based on an index (derived automatically) or covariates. If the impute option is TRUE NA values are imputed, otherwise the returned vector will still have NA's present. If impute and na.only are both TRUE the vector is returned, without being smoothed but with imputed NA values filled in. The loess weight function is defined using the tri-cube weight function w(x) = (1-|x|^3)^3 where; x is the distance of a data point from the point the curve being fitted.

Usage

```
poly.regression(
  y,
  x = NULL,
  s = 0.75,
  impute = FALSE,
  na.only = FALSE,
  ci = FALSE,
  ...
)
```

Arguments

`y`	Vector to smooth or impute NA values
`x`	Optional x covariate data (must match dimensions of y)
`s`	Smoothing parameter (larger equates to more smoothing)
`impute`	(FALSE/TRUE) Should NA values be inputed
`na.only`	(FALSE/TRUE) Should only NA values be change in y
`ci`	(FALSE/TRUE) Should confidence intervals be returned
`...`	Additional arguments passed to loess

Value

If ci = FALSE, a vector of smoothed values, otherwise a list object with:

- loess - A vector, same length of y, representing the smoothed or inputed data
- lower.ci - Lower confidence interval
- upper.ci - Upper confidence interval

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

See Also

`loess` for loess ... model options

Examples

```
x <- seq(-20, 20, 0.1)
y <- sin(x)/x + rnorm(length(x), sd=0.03)
p <- which(y == "NaN")
y <- y[-p]
r <- poly.regression(y, ci=TRUE, s=0.30)

plot(y,type="l", lwd=0.5, main="s = 0.10")
  y.polygon <- c((r$lower.ci)[1:length(y)], (r$upper.ci)[rev(1:length(y))])
  x.polygon <- c(1:length(y), rev(1:length(y)))
  polygon(x.polygon, y.polygon, col="#00009933", border=NA)
     lines(r$loess, lwd=1.5, col="red")

# Impute NA values, replacing only NA's
y.na <- y
y.na[c(100,200,300)] <- NA
p.y <- poly.regression(y.na, s=0.10, impute = TRUE, na.only = TRUE)
y - p.y

plot(p.y,type="l", lwd=1.5, col="blue", main="s = 0.10")
  lines(y, lwd=1.5, col="red")
```

`polygon_extract` *polygon raster extract*

Description

Fast method for extracting raster values to polygons

This method for raster extraction uses the raster cell indices and is quite a bit faster with polygon data than other methods. This is especially true with large raster stacks (eg., time-series). The cell indices are returned using `cellnumbers`. If ids argument is provided a column with values from the associate column are included otherwise "row_names" is returned which corresponds to the rownames in the source polygon object. Please note that if use.terra = TRUE it will coerce to a terra class if not already. With large data the coercion overhead may be worth it, providing speed gains. If the raster is a terra SpatRaster it will operate in its native class. The cells = TRUE argument will return the cell indices which could be used at a later time.

Usage

```
polygon_extract(
  r,
  p,
  ids = NULL,
  cells = FALSE,
  asList = TRUE,
  use.terra = FALSE
)
```

Arguments

`r`	RasterLayer, RasterStack, RasterBrick or SpatRaster object
`p`	sf polygon data
`ids`	A unique id field contained in p, will be assigned to output otherwise will return rownames
`cells`	FALSE | TRUE - Return cell index ids
`asList`	TRUE | FALSE - Output list object
`use.terra`	FALSE | TRUE - Use terra for extracting indices

Value

A list object containing a data.frame for each polygons raster values, as columns. Additional columns are "row_names" or which ever column is passed to the ids argument and "cells" if cells = TRUE. If asList = FALSE a data.frame will be returned

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sf)
library(raster)

nc <- sf::st_read(system.file("shape/nc.shp", package="sf"))
  nc <- sf::st_cast(nc, "POLYGON")

#### multi-band
i=100; j=100
r <- do.call(raster::stack, replicate(20,
          raster::raster(matrix(runif(i*j), i, j))))
      names(r) <- paste0("time", 1:nlayers(r))
    extent(r) <- extent(nc)
   proj4string(r) <- st_crs(nc)$proj4string

plot(r[[1]])
  plot(st_geometry(nc), add=TRUE)

( e <- polygon_extract(r, nc) )
( e <- polygon_extract(r, nc, ids="CNTY_ID") )

# Column means
lapply(e, function(x) apply(x[,2:ncol(x)], MARGIN=1, FUN=mean) )

#### Single band mean
( e <- polygon_extract(r[[1]], nc, ids="CNTY_ID") )
  unlist(lapply(e, function(x) mean(x[,2], na.rm=TRUE) ))


# Leveraging cell ids, pulls values, calculates
# new value, and assigns to source cell using
# index from cells = TRUE

e <- polygon_extract(r, nc, cells=TRUE)
e <- data.frame(
  cells=unlist(lapply(e, function(x) as.numeric(x[,22]))),
  means=unlist(lapply(e, function(x) apply(x[,2:22], MARGIN=1, FUN=mean)))
)

# copy raster and assign NA's
r2 <- r[[1]]
  r2[] <- rep(NA, ncell(r))

# assign using cell indices
r2[e$cells] <- e$means
  plot(r2)

# benchmark against raster extract
system.time({
  e <- polygon_extract(r, nc)
})
```

```
system.time({
  e <- raster::extract(r, nc)
})
```

`polyPerimeter` *Polygon perimeter*

Description

Calculates the perimeter length(s) for a polygon object

Usage

```
polyPerimeter(x)
```

Arguments

x	sp class SpatialPolygonsDataFrame object

Value

A vector of polygon perimeters

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
p1 <- Polygons(list(Polygon(cbind(c(2,4,4,1,2),c(2,3,5,4,2)))), "1")
p2 <- Polygons(list(Polygon(cbind(c(5,4,2,5),c(2,3,2,2)))), "2")
p3 <- Polygons(list(Polygon(cbind(c(4,4,5,10,4),c(5,3,2,5,5)))),"3")
polys <- SpatialPolygons(list(p1,p2,p3), 1:3)

polyPerimeter(polys)
```

pp.subsample *Point process random subsample*

Description

Generates random subsample based on density estimate of observations

The window type creates a convex hull by default or, optionally, uses the maximum extent (envelope). The resulting bandwidth can vary widely by method. the 'diggle' method is intended for bandwidth representing 2nd order spatial variation whereas the 'scott' method will represent 1st order trend. the 'geometry' approach will also represent 1st order trend. for large datasets, caution should be used with the 2nd order 'likelihood' approach, as it is slow and computationally expensive. finally, the 'stoyan' method will produce very strong 2nd order results. '

Usage

```
pp.subsample(
  x,
  n,
  window = "hull",
  sigma = "Scott",
  wts = NULL,
  gradient = 1,
  edge = FALSE
)
```

Arguments

`x`	An sp class SpatialPointsDataFrame or SpatialPoints object
`n`	Number of random samples to generate
`window`	Type of window (hull or extent)
`sigma`	Bandwidth selection method for KDE, default is 'Scott'. Options are 'Scott', 'Stoyan', 'Diggle', 'likelihood', and 'geometry'
`wts`	Optional vector of weights corresponding to point pattern
`gradient`	A scaling factor applied to the sigma parameter used to adjust the gradient decent of the density estimate. The default is 1, for no adjustment (downweight < 1 | upweight > 1)
`edge`	Apply Diggle edge correction (TRUE/FALSE)

Value

sp class SpatialPointsDataFrame containing random subsamples

Note

Available bandwidth selection methods are:

- Scott - (Scott 1992), Scott's Rule for Bandwidth Selection (1st order)
- Diggle - (Berman & Diggle 1989), Minimise the mean-square error via cross validation (2nd order)
- likelihood - (Loader 1999), Maximum likelihood cross validation (2nd order)
- geometry - Bandwidth is based on simple window geometry (1st order)
- Stoyan - (Stoyan & Stoyan 1995), Based on pair-correlation function (strong 2nd order)
- User defined - using a numeric value for sigma

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Berman, M. and Diggle, P. (1989) Estimating weighted integrals of the second-order intensity of a spatial point process. Journal of the Royal Statistical Society, series B 51, 81-92.

Fithian, W & T. Hastie (2013) Finite-sample equivalence in statistical models for presence-only data. Annals of Applied Statistics 7(4): 1917-1939

Hengl, T., H. Sierdsema, A. Radovic, and A. Dilo (2009) Spatial prediction of species distributions from occurrence-only records: combining point pattern analysis, ENFA and regression-kriging. Ecological Modelling, 220(24):3499-3511

Loader, C. (1999) Local Regression and Likelihood. Springer, New York.

Scott, D.W. (1992) Multivariate Density Estimation. Theory, Practice and Visualization. New York, Wiley.

Stoyan, D. and Stoyan, H. (1995) Fractals, random shapes and point fields: methods of geometrical statistics. John Wiley and Sons.

Warton, D.i., and L.C. Shepherd (2010) Poisson Point Process Models Solve the Pseudo-Absence Problem for Presence-only Data in Ecology. The Annals of Applied Statistics, 4(3):1383-1402

Examples

```
require(spatstat.core)
require(sp)
data(bei)
  trees <- as(bei, 'SpatialPoints')
    n=round(length(trees) * 0.10, digits=0)
      trees.wrs <- pp.subsample(trees, n=n, window='hull')
        plot(trees, pch=19, col='black')
          plot(trees.wrs, pch=19, col='red', add=TRUE)
            box()
             title('10% subsample')
          legend('bottomright', legend=c('Original sample', 'Subsample'),
                 col=c('black','red'),pch=c(19,19))
```

print.cross.cor *Print spatial cross correlation*

Description

print method for class "cross.cor"

Usage

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

Arguments

x	Object of class cross.cor
...	Ignored

print.effect.size *Print effect size*

Description

print method for class "effect.size"

Usage

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

Arguments

x	Object of class effect.size
...	Ignored

`print.loess.boot` *Print Loess bootstrap model*

Description

print method for class "loess.boot"

Usage

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

Arguments

`x`	Object of class loess.boot
`...`	Ignored

`proximity.index` *Proximity Index*

Description

Calculates proximity index for a set of polygons

Usage

```
proximity.index(x, y = NULL, min.dist = 0, max.dist = 1000, background = NULL)
```

Arguments

`x`	A polygon class sp or sf object
`y`	Optional column in data containing classes
`min.dist`	Minimum threshold distance
`max.dist`	Maximum neighbor distance
`background`	Optional value in y column indicating background value

Value

A vector equal to nrow(x) of proximity index values, if a background value is specified NA values will be returned in the position(s) of the specified class

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Gustafson, E.J., & G.R. Parker (1994) Using an Index of Habitat Patch Proximity for Landscape Design. Landscape and Urban Planning 29:117-130

Examples

```
library(sp)
library(rgeos)

# Create test polygons
data(meuse)
  coordinates(meuse) = ~x+y
  meuse_poly <- gBuffer(meuse, width = meuse$elev * 5, byid = TRUE)
    meuse_poly$LU <- sample(c("forest","nonforest"), nrow(meuse_poly),
                            replace=TRUE)

# All polygon proximity index 1000 radius
( pidx <-proximity.index(meuse_poly, min.dist = 1) )
  pidx[pidx > 100] <- 100

# Class-level proximity index 1000 radius
( pidx.class <- proximity.index(meuse_poly, y = "LU", min.dist = 1) )
  pidx.class[pidx.class > 100] <- 100

# plot index for all polygons
meuse_poly$pidx <- pidx
  spplot(meuse_poly, "pidx")

# plot index for class-level polygons
meuse_poly$cpidx <- pidx.class
  spplot(meuse_poly, "cpidx")

# plot index for just forest class
forest <- meuse_poly[meuse_poly$LU == "forest",]
  spplot(forest, "cpidx")
```

`pseudo.absence` *Pseudo-absence random samples*

Description

Generates pseudo-absence samples based on density estimate of known locations

Usage

```
pseudo.absence(
  x,
  n,
  window = "hull",
  Mask = NULL,
  s = NULL,
  sigma = "Scott",
  wts = NULL,
  KDE = FALSE,
  gradient = 1,
  p = NULL,
  edge = FALSE
)
```

Arguments

`x`	An sp class SpatialPointsDataFrame or SpatialPoints object
`n`	Number of random samples to generate
`window`	Type of window (hull OR extent), overridden if mask provided
`Mask`	Optional rasterLayer class mask raster. The resolution of the density estimate will match mask.
`s`	Optional resolution passed to window argument. Caution should be used due to long processing times associated with high resolution. In contrast, coarse resolution can exclude known points.
`sigma`	Bandwidth selection method for KDE, default is 'Scott'. Options are 'Scott', 'Stoyan', 'Diggle', 'likelihood', and 'geometry'
`wts`	Optional vector of weights corresponding to point pattern
`KDE`	save KDE raster (TRUE/FALSE)
`gradient`	A scaling factor applied to the sigma parameter used to adjust the gradient decent of the density estimate. The default is 1, for no adjustment (downweight < 1 | upweight > 1)
`p`	Minimum value for probability distribution (must be > 0)
`edge`	Apply Diggle edge correction (TRUE/FALSE)

Details

The window type creates a convex hull by default or, optionally, uses the maximum extent (envelope). If a mask is provided the kde will represent areas defined by the mask and defines the area that pseudo absence data will be generated.

Available bandwidth selection methods are:

- Scott (Scott 1992), Scott's Rule for Bandwidth Selection (1st order)
- Diggle (Berman & Diggle 1989), Minimize the mean-square error via cross validation (2nd order)
- likelihood (Loader 1999), Maximum likelihood cross validation (2nd order)
- geometry, Bandwidth is based on simple window geometry (1st order)
- Stoyan (Stoyan & Stoyan 1995), Based on pair-correlation function (strong 2nd order)

- User defined numeric distance bandwidth

Note; resulting bandwidth can vary widely by method. the 'diggle' method is intended for selecting bandwidth representing 2nd order spatial variation whereas the 'scott' method will represent 1st order trend. the 'geometry' approach will also represent 1st order trend. For large datasets, caution should be used with the 2nd order 'likelihood' approach, as it is slow and computationally expensive. finally, the 'stoyan' method will produce very strong 2nd order results.

Value

A list class object with the following components:

- sample SpatialPointsDataFrame containing random samples
- kde sp RasterLayer class of KDE estimates (IF KDE = TRUE)
- sigma Selected bandwidth of KDE

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Berman, M. and Diggle, P. (1989) Estimating weighted integrals of the second-order intensity of a spatial point process. Journal of the Royal Statistical Society, series B 51, 81-92.

Fithian, W & T. Hastie (2013) Finite-sample equivalence in statistical models for presence-only data. Annals of Applied Statistics 7(4): 1917-1939

Hengl, T., H. Sierdsema, A. Radovic, and A. Dilo (2009) Spatial prediction of species distributions from occurrence-only records: combining point pattern analysis, ENFA and regression-kriging. Ecological Modelling, 220(24):3499-3511

Loader, C. (1999) Local Regression and Likelihood. Springer, New York.

Scott, D.W. (1992) Multivariate Density Estimation. Theory, Practice and Visualization. New York, Wiley.

Stoyan, D. and Stoyan, H. (1995) Fractals, random shapes and point fields: methods of geometrical statistics. John Wiley and Sons.

Warton, D.i., and L.C. Shepherd (2010) Poisson Point Process Models Solve the Pseudo-Absence Problem for Presence-only Data in Ecology. The Annals of Applied Statistics, 4(3):1383-1402

Examples

```
library(raster)
library(sp)
data(meuse)
data(meuse.grid)
  coordinates(meuse) = ~x+y
  coordinates(meuse.grid) = ~x+y
  proj4string(meuse.grid) <- CRS("+init=epsg:28992")
  gridded(meuse.grid) = TRUE
  r <- raster(meuse.grid)
```

```
    # Using a raster mask
    pa <- pseudo.absence(meuse, n=100, window='hull', KDE=TRUE, Mask = r,
                         sigma='Diggle', s=50)
      col.br <- colorRampPalette(c('blue','yellow'))
        plot(pa$kde, col=col.br(10))
          plot(meuse, pch=20, cex=1, add=TRUE)
            plot(pa$sample, col='red', pch=20, cex=1, add=TRUE)
              legend('top', legend=c('Presence', 'Pseudo-absence'),
                     pch=c(20,20),col=c('black','red'))

  # With clustered data
  library(sp)
  library(spatstat.core)
  data(bei)
    trees <- as(bei, 'SpatialPoints')
      trees <- SpatialPointsDataFrame(coordinates(trees),
                          data.frame(ID=1:length(trees)))
        trees.abs <- pseudo.absence(trees, n=100, window='extent', KDE=TRUE)

  col.br <- colorRampPalette(c('blue','yellow'))
    plot(trees.abs$kde, col=col.br(10))
     plot(trees, pch=20, cex=0.50, add=TRUE)
        plot(trees.abs$sample, col='red', pch=20, cex=1, add=TRUE)
          legend('top', legend=c('Presence', 'Pseudo-absence'),
                 pch=c(20,20),col=c('black','red'))
```

---

pu *Biodiversity Planning Units*

Description

Subset of biodiversity planning units for Haiti ecoregional spatial reserve plan

Format

A sp SpatialPolygonsDataFrame with 5919 rows and 46 variables:

UNIT_ID Unique planning unit ID

DR_Dr_A Biodiversity target

DR_Dr_L Biodiversity target

Ht_Dr_A Biodiversity target

Ht_Dr_L Biodiversity target

DR_Ms_A Biodiversity target

DR_Ms_L Biodiversity target

Ht_Ms_L Biodiversity target

DR_LM_M	Biodiversity target
H_LM_M_L	Biodiversity target
H_LM_R_L	Biodiversity target
DR_LM_R_L	Biodiversity target
DR_Rn_L	Biodiversity target
DR_LM_R_S	Biodiversity target
DR_Rn_S	Biodiversity target
DR_Ms_S	Biodiversity target
Ht_Ms_A	Biodiversity target
DR_Ms_E	Biodiversity target
DR_Ms_I	Biodiversity target
DR_Rn_E	Biodiversity target
DR_Rn_I	Biodiversity target
H_LM_R_E	Biodiversity target
Ht_Ms_E	Biodiversity target
Ht_Rn_E	Biodiversity target
DR_Rn_A	Biodiversity target
Ht_Rn_A	Biodiversity target
Ht_Rn_I	Biodiversity target
Ht_Dr_E	Biodiversity target
Ht_Ms_S	Biodiversity target
Ht_Dr_S	Biodiversity target
Ht_Rn_L	Biodiversity target
Ht_Th_A	Biodiversity target
Ht_Th_L	Biodiversity target
Ht_Th_S	Biodiversity target
Ht_Dr_U	Biodiversity target
Ht_Dr_I	Biodiversity target
Ht_Ms_I	Biodiversity target
H_LM_M_A	Biodiversity target
H_LM_M_E	Biodiversity target
H_LM_R_A	Biodiversity target
H_LM_M_S	Biodiversity target
H_LM_R_I	Biodiversity target
H_LM_R_S	Biodiversity target
Ht_Rn_S	Biodiversity target
Ht_Ms_U	Biodiversity target
Ht_Rn_U	Biodiversity target

Source

https://www.conservationgateway.org

References

Evans, J.S., S.R. Schill, G.T. Raber (2015) A Systematic Framework for Spatial Conservation Planning and Ecological Priority Design in St. Lucia, Eastern Caribbean. Chapter 26 in Central American Biodiversity : Conservation, Ecology and a Sustainable Future. F. Huettman (eds). Springer, NY.

`quadrats` *Quadrats*

Description

Creates quadrat polygons for sampling or analysis

Usage

```
quadrats(x, s = 250, n = 100, r = NULL)
```

Arguments

`x`	A sp or sf polygon object defining extent
`s`	Radius defining single or range of sizes of quadrats
`n`	Number of quadrats
`r`	A rotation factor for random rotation, default is NULL

Value

an sp or sf polygon object with rotated polygon

Note

The radius (s) parameter can be a single value or a range of values, representing a randomization range of resulting quadrat sizes. The rotation (r) parameter can also be used to defined a fixed rotation or random range of quadrat rotations. You can specify each of these parameters using an explicit vector that will be sampled eg., seq(100,300,0.5)

Examples

```
library(sp)
library(raster)
library(rgeos)
data(meuse)
  coordinates(meuse) <- ~x+y
  e <- gConvexHull(meuse)

# Fixed size 250 and no rotation
s <- quadrats(e, s = 250, n = 50)
  spplot(s, "ID")

# Variable sizes 100-300 and rotation of 0-45 degrees
s <- quadrats(e, s = c(100,300), n = 50, r = c(0,45))
  spplot(s, "ID")

# Variable sizes 100-300 and no rotation
s <- quadrats(e, s = c(100,300), n = 50)
  spplot(s, "ID")
```

`random.raster` *Random raster*

Description

Create a random raster or raster stack using specified distribution

Usage

```
random.raster(
  r = NULL,
  n.row = 50,
  n.col = 50,
  n.layers = 1,
  x = seq(1, 10),
  min = 0,
  max = 1,
  mean = 0,
  sd = 1,
  p = 0.5,
  s = 1.5,
  distribution = c("random", "normal", "seq", "binomial", "gaussian")
)
```

Arguments

`r`	Optional existing raster defining nrow/ncol

`n.row`	Number of rows
`n.col`	Number of columns
`n.layers`	Number of layers in resulting raster stack
`x`	A vector of values to sample if distribution is "sample"
`min`	Minimum value of raster
`max`	Maximum value of raster
`mean`	Mean of centered distribution
`sd`	Standard deviation of centered distribution
`p`	p-value for binomial distribution
`s`	sigma value for Gaussian distribution
`distribution`	Available distributions, c("random", "normal", "seq", "binomial", "gaussian", "sample")

Details

Options for distributions are for random, normal, seq, binomial, gaussian and sample raster(s)

Value

RasterLayer or RasterStack object with random rasters

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)

# Using existing raster to create random binomial
r <- raster(system.file("external/rlogo.grd", package="raster"))
r <- random.raster(r, distribution="binomial")

# default; random, nrows=50, ncols=50, nlayers=1
rr <- random.raster(n.layer=5)

# specified; binomial, nrows=20, ncols=20, nlayers=5
rr <- random.raster(n.layer=5, n.col=20, n.row=20,
                    distribution="binomial")

# specified; gaussian, nrows=50, ncols=50, nlayers=1
rr <- random.raster(n.col=50, n.row=50, s=8,
                    distribution="gaussian")

# specified; sample, nrows=50, ncols=50, nlayers=1
rr <- random.raster(n.layer=1, x=c(2,6,10,15), distribution="sample" )
  freq(rr)
```

raster.change *Raster change between two nominal rasters*

Description

Compares two categorical rasters with a variety of statistical options

This function provides a various statistics for comparing two classified maps. Valid options are:

- kappa - Cohen's Kappa
- wkappa - Cohen's Weighted Kappa (not yet implemented)
- t.test - Two-tailed paired t-test
- cor - Persons Correlation
- entropy - Delta entropy
- cross-entropy - Cross-entropy loss function
- divergence - Kullback-Leibler divergence (relative entropy)

Kappa and t-test values < 0 are reported as 0. For a weighted kappa, a matrix must be provided that correspond to the pairwise weights for all values in both rasters. Delta entropy is derived by calculating Shannon's on each focal window then differencing them (e(x) - e(y))

Usage

```
raster.change(
  x,
  y,
  d = c(3, 3),
  stat = c("kappa", "wkappa", "t.test", "cor", "entropy", "cross-entropy",
    "divergence"),
  w = NULL,
  out.raster = NULL,
  mask = FALSE,
  force.memory = FALSE
)
```

Arguments

`x`	First raster for comparison, rasterLayer class object
`y`	Second raster for comparison, rasterLayer class object
`d`	Rectangular window size, must be odd but not necessarily square
`stat`	Statistic to use in comparison, please see details for options.
`w`	Weights if stat="kappa", must represent same classes as input rasters
`out.raster`	Optional output raster
`mask`	(FALSE/TRUE) mask output to original rasters
`force.memory`	(FALSE/TRUE) Force in memory processing, may fail with insufficient RAM

Value

A raster layer or stack object one of the following layers:

- kappa Kappa or Weighted Kappa statistic (if stat = "kappa")
- correlation Paired t.test statistic (if stat = "cor")
- entropy Delta entropy (if stat = "entropy")
- divergence Kullback-Leibler divergence (if stat = "divergence")
- cross.entropy Cross-entropy (if stat = "cross.entropy")
- t.test Paired t.test statistic (if stat = "t.test")
- p.value p-value of the paired t.test statistic (if stat = "t.test")

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Cohen, J. (1960). A coefficient of agreement for nominal scales. Educational and Psychological Measurement, 20:37-46

McHugh M.L. (2012) Interrater reliability: the kappa statistic. Biochemia medica, 22(3):276–282.

Kullback, S., R.A. Leibler (1951). On information and sufficiency. Annals of Mathematical Statistics. 22(1):79–86

Examples

```
 library(sp)
 library(raster)
 data(meuse.grid)
 r1 <- sp::SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
                                  data = meuse.grid)
r1 <- raster(r1)
  na.idx <- which(!is.na(r1[]))
  r1[na.idx] <- round(runif(length(na.idx), 1,5),0)
 r2 <- sp::SpatialPixelsDataFrame(points = meuse.grid[c("x", "y")],
                                  data = meuse.grid)
r2 <- raster(r2)
  r2[na.idx] <- round(runif(length(na.idx), 1,5),0)

s = 11
 ( r.kappa <- raster.change(r1, r2, d = s, mask = TRUE) )
 ( r.ttest <- raster.change(r1, r2, d = s, stat="t.test", mask = TRUE) )
 ( r.ent <- raster.change(r1, r2, d = s, stat="entropy", mask = TRUE) )
 ( r.cor <- raster.change(r1, r2, d = s, stat="cor", mask = TRUE) )
 ( r.ce <- raster.change(r1, r2, d = s, stat = "cross-entropy", mask = TRUE) )
 ( r.kl <- raster.change(r1, r2, d = s, stat = "divergence", mask = TRUE) )

 opar <- par(no.readonly=TRUE)
```

```
par(mfrow=c(3,2))
  plot(r.kappa, main="Kappa")
  plot(r.ttest[[1]], main="Paired t-test")
  plot(r.ent, main="Delta Entropy")
  plot(r.cor, main="Rank Correlation")
  plot(r.kl, main="Kullback-Leibler")
  plot(r.ce, main="cross-entropy")
par(opar)
```

raster.deviation *Raster local deviation from the global trend*

Description

Calculates the local deviation from the raster, a specified global statistic or a polynomial trend of the raster.

The deviation from the trend is derived as [y-hat - y] where; y-hat is the Nth-order polynomial. Whereas the deviation from a global statistic is [y - y-hat] where; y-hat is the local (focal) statistic. The global = TRUE argument allows one to evaluate the local deviation from the global statistic [stat(x) - y-hat] where; stat(x) is the global value of the specified statistic and y-hat is the specified focal statistic.

Usage

```
raster.deviation(x, type = "trend", s = 3, degree = 1, global = FALSE)
```

Arguments

`x`	raster object
`type`	The global statistic to represent the local deviation options are: "trend", "min", "max", "mean", "median"
`s`	Size of matrix (focal window), not used with type="trend"
`degree`	The polynomial degree if type is trend, options are 1 and 2.
`global`	Use single global value for deviation or cell-level values (FALSE/TRUE). Argument is ignored for type="trend"

Value

raster class object of the local deviation from the raster or specified global statistic

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Magee, Lonnie (1998). Nonlocal Behavior in Polynomial Regressions. The American Statistician. American Statistical Association. 52(1):20-22

Fan, J. (1996). Local Polynomial Modelling and Its Applications: From linear regression to nonlinear regression. Monographs on Statistics and Applied Probability. Chapman and Hall/CRC. ISBN 0-412-98321-4

Examples

```
  library(raster)
  data(elev)

# local deviation from first-order trend, global mean and raw value
r.dev.trend <- raster.deviation(elev, type="trend", degree=1)
r.dev.mean <- raster.deviation(elev, type="mean", s=5)
r.gdev.mean <- raster.deviation(elev, type="mean", s=5, global=TRUE)

opar <- par(no.readonly=TRUE)
par(mfrow=c(2,2))
  plot(elev, main="original")
  plot(r.dev.trend, main="dev from trend")
  plot(r.dev.mean, main="dev of mean from raw values")
  plot(r.gdev.mean, main="local dev from global mean")
par(opar)
```

`raster.downscale` *Raster Downscale*

Description

Downscales a raster to a higher resolution raster using a robust regression

Usage

```
raster.downscale(
  x,
  y,
  p = NULL,
  n = NULL,
  filename = FALSE,
  scatter = FALSE,
  ...
)
```

Arguments

`x`	Raster class object representing independent variable(s)
`y`	Raster class object representing dependent variable
`p`	Percent sample size
`n`	Fixed sample size
`filename`	Name of output raster
`scatter`	(FALSE/TRUE) Optional scatter plot
`...`	Additional arguments passed to predict

Value

A list object containing:

- downscale downscaled raster (omitted if filename is defined)
- model rlm model object
- MSE Mean Square Error
- AIC Akaike information criterion

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
## Not run:
 library(raster)
 elev <- raster::getData('alt', country='SWZ', mask=TRUE)
 tmax <- raster::getData('worldclim', var='tmax', res=10,
                         lon=8.25, lat=46.8)
 tmax <- crop(tmax[[1]], extent(elev))

 # Downscale temperature
 tmax.ds <- raster.downscale(elev, tmax, scatter=TRUE)
   opar <- par(no.readonly=TRUE)
     par(mfrow=c(2,2))
     plot(tmax, main="Temp max")
     plot(elev, main="elevation")
       plot(tmax.ds$downscale, main="Downscaled Temp max")
   par(opar)

## End(Not run)
```

`raster.entropy` *Raster Entropy*

Description

Calculates entropy on integer raster (i.e., 8 bit 0-255)

Entropy calculated as: H = -sum(Pi*ln(Pi)) where; Pi, Proportion of one value to total values Pi=n(p)/m and m, Number of unique values. Expected range: 0 to log(m) H=0 if window contains the same value in all cells. H increases with the number of different values in the window.

Maximum entropy is reached when all values are different, same as log(m) max.ent <- function(x) log(length(unique(x)))

Usage

```
raster.entropy(
  x,
  d = 5,
  categorical = FALSE,
  global = FALSE,
  filename = FALSE,
  ...
)
```

Arguments

`x`	Object of class raster (requires integer raster)
`d`	Size of matrix (window)
`categorical`	Is the data categorical or continuous (FALSE/TRUE)
`global`	Should the model use a global or local n to calculate entropy (FALSE/TRUE)
`filename`	Raster file written to disk
`...`	Optional arguments passed to writeRaster or dataType

Value

raster class object or specified format raster written to disk

References

Fuchs M., R. Hoffmann, F. Schwonke (2008) Change Detection with GRASS GIS - Comparison of images taken by different sensor.

Examples

```
require(raster)
  r <- raster(ncols=100, nrows=100)
    r[] <- round(runif(ncell(r), 1,8), digits=0)

rEnt <- raster.entropy(r, d=5, categorical = TRUE, global = TRUE)
  opar <- par(no.readonly=TRUE)
    par(mfcol=c(2,1))
      plot(r)
        plot(rEnt)
  par(opar)
```

---

raster.gaussian.smooth

Gaussian smoothing of raster

Description

Applies a Gaussian smoothing kernel to smooth raster.

Usage

```
raster.gaussian.smooth(x, sigma = 2, n = 5, type = mean, ...)
```

Arguments

`x`	raster object
`sigma`	standard deviation (sigma) of kernel (default is 2)
`n`	Size of the focal matrix, single value (default is 5 for 5x5 window)
`type`	The statistic to use in the smoothing operator (suggest mean or sd)
`...`	Additional arguments passed to raster::focal

Value

raster class object of the local distributional moment

Note

This is a simple wrapper for the focal function, returning local statistical moments

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
      library(raster)
      r <- raster(nrows=500, ncols=500, xmn=571823, xmx=616763,
                  ymn=4423540, ymx=4453690)
   proj4string(r) <- crs("+proj=utm +zone=12 +datum=NAD83 +units=m +no_defs")
      r[] <- runif(ncell(r), 1000, 2500)
      r <- focal(r, focalWeight(r, 150, "Gauss") )

    # Calculate Gaussian smoothing with sigma(s) = 1-4
    g1 <- raster.gaussian.smooth(r, sigma=1, nc=11)
    g2 <- raster.gaussian.smooth(r, sigma=2, nc=11)
    g3 <- raster.gaussian.smooth(r, sigma=3, nc=11)
    g4 <- raster.gaussian.smooth(r, sigma=4, nc=11)

   opar <- par(no.readonly=TRUE)
   par(mfrow=c(2,2))
     plot(g1, main="Gaussian smoothing sigma = 1")
     plot(g2, main="Gaussian smoothing sigma = 2")
     plot(g3, main="Gaussian smoothing sigma = 3")
     plot(g4, main="Gaussian smoothing sigma = 4")
   par(opar)
```

`raster.invert` *Invert raster*

Description

Inverts (flip) the values of a raster

Usage

```
raster.invert(x)
```

Arguments

x	raster object

Value

raster class object with inverted (flipped) raster values

Note

Inverts raster values using the formula: (((x - max(x)) * -1) + min(x)

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
    library(raster)
    r <- raster(nrows=500, ncols=500, xmn=571823, xmx=616763,
                ymn=4423540, ymx=4453690)
      r[] <- runif(ncell(r), 1, 100)
   r <- focal(r, focalWeight(r, 150, "Gauss") )
    r.inv <- raster.invert(r)

  opar <- par(no.readonly=TRUE)
      par(mfrow=c(1,2))
        plot(r, main="original raster")
        plot(r.inv, main="inverted raster")
  par(opar)
```

`raster.kendall` *Kendall tau trend with continuity correction for raster time-series*

Description

Calculates a nonparametric statistic for a monotonic trend based on the Kendall tau statistic and the Theil-Sen slope modification

Usage

```
raster.kendall(
  x,
  intercept = FALSE,
  p.value = FALSE,
  z.value = FALSE,
  confidence = FALSE,
  tau = FALSE,
  ...
)
```

Arguments

`x`	A rasterStack object with at least 5 layers
`intercept`	(FALSE/TRUE) return a raster with the pixel wise intercept values
`p.value`	(FALSE/TRUE) return a raster with the pixel wise p.values
`z.value`	(FALSE/TRUE) return a raster with the pixel wise z.values
`confidence`	(FALSE/TRUE) return a raster with the pixel wise 95 pct confidence levels
`tau`	(FALSE/TRUE) return a raster with the pixel wise tau correlation values
`...`	Additional arguments passed to the raster overlay function

Details

This function implements Kendall's nonparametric test for a monotonic trend using the Theil-Sen (Theil 1950; Sen 1968; Siegel 1982) method to estimate the slope and related confidence intervals.

Value

Depending on arguments, a raster layer or rasterBrick object containing:

- raster layer 1 slope for trend, always returned
- raster layer 2 intercept for trend if intercept TRUE
- raster layer 3 p value for trend fit if p.value TRUE
- raster layer 4 z value for trend fit if z.value TRUE
- raster layer 5 lower confidence level at 95 pct, if confidence TRUE
- raster layer 6 upper confidence level at 95 pct, if confidence TRUE
- raster layer 7 Kendall's tau two-sided test, reject null at 0, if tau TRUE

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Theil, H. (1950) A rank invariant method for linear and polynomial regression analysis. Nederl. Akad. Wetensch. Proc. Ser. A 53:386-392 (Part I), 53:521-525 (Part II), 53:1397-1412 (Part III).

Sen, P.K. (1968) Estimates of Regression Coefficient Based on Kendall's tau. Journal of the American Statistical Association. 63(324):1379-1389.

Siegel, A.F. (1982) Robust Regression Using Repeated Medians. Biometrika, 69(1):242-244

See Also

`kendallTrendTest` for model details

`overlay` for available ... arguments

Examples

```
 library(raster)
 r.logo <- stack(system.file("external/rlogo.grd", package="raster"),
                 system.file("external/rlogo.grd", package="raster"),
      system.file("external/rlogo.grd", package="raster"))

 # Calculate trend slope with p-value and confidence level(s)
 # ("slope","intercept", "p.value","z.value", "LCI","UCI","tau")
   k <- raster.kendall(r.logo, p.value=TRUE, z.value=TRUE,
                       intercept=TRUE, confidence=TRUE,
                       tau=TRUE)
     plot(k)
```

raster.mds *Raster multidimensional scaling (MDS)*

Description

Multidimensional scaling of raster values within an N x N focal window

An MDS focal function. If only one value provided for s, then a square matrix (window) will be used. If window.median = FALSE then the center value of the matrix is returned and not the median of the matrix

Usage

```
raster.mds(r, s = 5, window.median = FALSE, ...)
```

Arguments

`r`	Raster layer
`s`	Window size (may be a vector of 1 or 2) of n x n dimension.
`window.median`	(TRUE/FALSE) Return the median of the MDS matrix values.
`...`	Additional arguments passed to raster::focal

Value

A raster class object or raster written to disk

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Quinn, G.P., & M.J. Keough (2002) Experimental design and data analysis for biologists. Cambridge University Press. Ch. 18. Multidimensional scaling and cluster analysis.

Examples

```
 library(raster)
 r <- raster(system.file("external/rlogo.grd", package="raster"))
   r <- r / cellStats(r, "max")

 diss <- raster.mds(r)
 diss.med <- raster.mds(r, window.median = TRUE)

opar <- par(no.readonly=TRUE)
   par(mfrow=c(2,2))
   plot(r)
```

```
     title("R logo band-1")
   plot( focal(r, w = matrix(1, nrow=5, ncol=5), fun = var) )
     title("Variance")
     plot(diss)
       title("MDS")
     plot(diss.med)
       title("Median MDS")
par(opar)
```

raster.modified.ttest *Dutilleul moving window bivariate raster correlation*

Description

A bivarate raster correlation using Dutilleul's modified t-test

This function provides a bivariate moving window correlation using the modified t-test to account for spatial autocorrelation. Point based subsampling is provided for computation tractability. The hexagon sampling is recommended as it it good at capturing spatial process that includes nonstationarity and anistropy.

Usage

```
raster.modified.ttest(
  x,
  y,
  x.idx = 1,
  y.idx = 1,
  d = "AUTO",
  sub.sample = FALSE,
  type = "hexagon",
  p = 0.1,
  size = NULL
)
```

Arguments

x	x raster for correlation, SpatialPixelsDataFrame or SpatialGridDataFrame object
y	y raster for correlation, SpatialPixelsDataFrame or SpatialGridDataFrame object
x.idx	Index for the column in the x raster object
y.idx	Index for the column in the y raster object
d	Distance for finding neighbors
sub.sample	Should a sub-sampling approach be employed (TRUE/FALSE)
type	If sub.sample = TRUE, what type of sample (random or hexagon)
p	If sub.sample = TRUE, what proportion of population should be sampled
size	Fixed sample size

Value

A SpatialPixelsDataFrame or SpatialPointsDataFrame with the following attributes:

- corr Correlation
- Fstat The F-statistic calculated as [degrees of freedom * unscaled F-statistic]
- p.value p-value for the test
- moran.x Moran's-I for x
- moran.y Moran's-I for y

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Clifford, P., S. Richardson, D. Hemon (1989), Assessing the significance of the correlation between two spatial processes. Biometrics 45:123-134.

Dutilleul, P. (1993), Modifying the t test for assessing the correlation between two spatial processes. Biometrics 49:305-314.

See Also

modified.ttest for test details

Examples

```
## Not run:
library(gstat)
library(sp)

data(meuse)
data(meuse.grid)
coordinates(meuse) <- ~x + y
coordinates(meuse.grid) <- ~x + y

# GRID-1 log(copper):
v1 <- variogram(log(copper) ~ 1, meuse)
x1 <- fit.variogram(v1, vgm(1, "Sph", 800, 1))
G1 <- krige(zinc ~ 1, meuse, meuse.grid, x1, nmax = 30)
gridded(G1) <- TRUE
G1@data = as.data.frame(G1@data[,-2])

# GRID-2 log(elev):
v2 <- variogram(log(elev) ~ 1, meuse)
x2 <- fit.variogram(v2, vgm(.1, "Sph", 1000, .6))
G2 <- krige(elev ~ 1, meuse, meuse.grid, x2, nmax = 30)
gridded(G2) <- TRUE
G2@data <- as.data.frame(G2@data[,-2])
G2@data[,1] <- G2@data[,1]
```

```
corr <- raster.modifed.ttest(G1, G2)
  plot(raster::raster(corr,1))

corr.rand <- raster.modifed.ttest(G1, G2, sub.sample = TRUE, type = "random")
corr.hex <- raster.modifed.ttest(G1, G2, sub.sample = TRUE, d = 500, size = 1000)
  head(corr.hex@data)
    bubble(corr.hex, "corr")

## End(Not run)
```

`raster.moments` *Raster moments*

Description

Calculates focal statistical moments of a raster

Usage

```
raster.moments(x, type = "mean", s = 3, p = 0.75)
```

Arguments

`x`	raster object
`type`	The global statistic to represent the local deviation options are: "min", "min", "mean", "median", "var, "sd", "mad", "kurt", "skew", "quantile"
`s`	Size of matrix (focal window), can be single value or two values defining the [x,y] dimensions of the focal matrix
`p`	if type="quantile", the returned percentile.

Value

raster class object of the local distributional moment

Note

This is a simple wrapper for the focal function, returning local statistical moments

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
    library(raster)
    r <- raster(nrows=100, ncols=100, xmn=571823, xmx=616763,
                ymn=4423540, ymx=4453690)
    proj4string(r) <- crs("+proj=utm +zone=12 +datum=NAD83 +units=m +no_defs")
    r[] <- runif(ncell(r), 1000, 2500)
    r <- focal(r, focalWeight(r, 150, "Gauss") )

  # Calculate 10th percentile for 3x3 window
  r.p10 <- raster.moments(r, type="quantile", p=0.10)
```

`raster.transformation` *Statistical transformation for rasters*

Description

Transforms raster to a specified statistical transformation

Transformation option details:

- norm - (Normalization_ (0-1): if min(x) < 0 (x - min(x)) / (max(x) - min(x))
- rstd - (Row standardize) (0-1): if min(x) >= 0 x / max(x) This normalizes data
- `with negative distributions`
- std - (Standardize) (x - mean(x)) / sdv(x)
- stretch - (Stretch) ((x - min(x)) * max.stretch / (max(x) - min(x)) + min.stretch) This will stretch values to the specified minimum and maximum values (eg., 0-255 for 8-bit)
- nl - (Natural logarithms) if min(x) > 0 log(x)
- slog - (Signed log 10) (for skewed data): if min(x) >= 0 ifelse(abs(x) <= 1, 0, sign(x)*log10(abs(x)))
- sr - (Square-root) if min(x) >= 0 sqrt(x)

Usage

```
raster.transformation(x, trans = "norm", smin = 0, smax = 255)
```

Arguments

`x`	raster class object
`trans`	Transformation method: "norm", "rstd", "std", "stretch", "nl", "slog", "sr" (please see notes)
`smin`	Minimum value for stretch
`smax`	Maximum value for stretch

Value

raster class object of transformation

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

Examples

```
  library(raster)
  r <- raster(nrows=100, ncols=100, xmn=571823, xmx=616763,
              ymn=4423540, ymx=4453690)
    r[] <- runif(ncell(r), 1000, 2500)

 # Postive values so, can apply any transformation
for( i in c("norm", "rstd", "std", "stretch", "nl", "slog", "sr")) {
  print( raster.transformation(r, trans = i) )
   }

 # Negative values so, can't transform using "nl", "slog" or "sr"
r[] <- runif(ncell(r), -1, 1)
   for( i in c("norm", "rstd", "std", "stretch", "nl", "slog", "sr")) {
  try( print( raster.transformation(r, trans = i) ) )
   }
```

`raster.vol` *Raster Percent Volume*

Description

Calculates a percent volume on a raster or based on a systematic sample

Usage

```
raster.vol(x, p = 0.95, sample = FALSE, spct = 0.05)
```

Arguments

x	raster class object
p	percent raster-value volume
sample	base volume on systematic point sample (TRUE/FALSE)
spct	sample percent, if sample (TRUE)

Value

if sample (FALSE) binary raster object with 1 representing designated percent volume else, if sample (TRUE) n sp SpatialPointsDataFrame object with points that represent the percent volume of the sub-sample

Note

Since this model needs to operate on all of the raster values, it is not memory safe

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
require(raster)
  r <- raster(ncols=100, nrows=100)
    r[] <- runif(ncell(r), 0, 1)
    r <- focal(r, w=focalWeight(r, 6, "Gauss"))
    r[sample(1000, 1:ncell(r))] <- NA

  # full raster percent volume
  p30 <- raster.vol(r, p=0.30)
  p50 <- raster.vol(r, p=0.50)
  p80 <- raster.vol(r, p=0.80)

opar <- par(no.readonly=TRUE)
    par(mfrow=c(2,2))
    plot(r, col=cm.colors(10), main="original raster")
    plot(p30, breaks=c(0,0.1,1), col=c("cyan","red"), legend=FALSE,
      main="30% volume")
    plot(p50, breaks=c(0,0.1,1), col=c("cyan","red"), legend=FALSE,
      main="50% volume")
    plot(p80, breaks=c(0,0.1,1), col=c("cyan","red"), legend=FALSE,
      main="80% volume")
par(opar)
```

---

raster.Zscore *Modified z-score for a raster*

Description

Calculates the modified z-score for all cells in a raster

Usage

```
raster.Zscore(x, p.value = FALSE, file.name = NULL, ...)
```

Arguments

`x`	A raster class object
`p.value`	Return p-value rather than z-score raster (FALSE/TRUE)
`file.name`	Name of raster written to disk
`...`	Additional arguments passed to writeRaster

Value

raster class object or raster written to disk

Note

Since this functions needs to operate on all of the raster values, it is not memory safe

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)
r <- raster(nrows=824, ncols=767, xmn=2451905, xmx=3218905,
            ymn=-2744771, ymx=-1920771, resolution = 5000)
  r[] <- runif(ncell(r), 0, 1)

# Modified z-score
z <- raster.Zscore(r)

# P-value
p <- raster.Zscore(r, p.value = TRUE)
```

`rasterCorrelation` *Raster correlation*

Description

Performs a simple moving window correlation between two rasters

Usage

```
rasterCorrelation(x, y, s = 3, type = "pearson", file.name = NULL, ...)
```

Arguments

`x`	raster class object for x
`y`	raster class object for y
`s`	Scale of window. Can be a single value, two values for uneven window or a custom matrix. Must be odd number (eg., s=3, for 3x3 window or s=c(3,5) for 3 x 5 window)
`type`	Type of output, options are: "pearson", "spearman",
`file.name`	Name of output raster (optional)
`...`	Additional arguments passed to writeRaster

Value

raster class object or raster written to disk

Note

Depends: raster

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 library(raster)
 b <- brick(system.file("external/rlogo.grd", package="raster"))
 x <- b[[1]]
 y <- b[[3]]
 r.cor <- rasterCorrelation(x, y, s = 5, type = "spearman")
 plot(r.cor)
```

`rasterDistance` *Raster Distance*

Description

Calculates the Euclidean distance between a set of points and the cells in a raster. This is a drop-in replacement for the raster distanceFromPoints function using the RANN algorithm for calculating distance, resulting in a large improvement in processing speed.

Usage

```
rasterDistance(x, y, reference = NULL, scale = FALSE)
```

Arguments

`x`	rasterLayer, sp SpatialPoints or sf POINTS object
`y`	sp SpatialPoints or sf POINTS object
`reference`	A raster to use as a reference if x is points object
`scale`	(FALSE/TRUE) Perform a row standardization on results

Value

a distance raster of class rasterLayer

Note

This replicates the raster distanceFromPoints function but uses the Arya & Mount Approximate Near Neighbor (ANN) C++ library for calculating distances. Where this results in a notable increase in performance it is not memory safe, needing to read in the entire raster and does not use the GeographicLib (Karney, 2013) spheroid distance method for geographic data.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Arya S., Mount D. M., Netanyahu N. S., Silverman R. and Wu A. Y (1998), An optimal algorithm for approximate nearest neighbor searching, Journal of the ACM, 45, 891-923.

See Also

`distanceFromPoints`,`distance`

Examples

```
library(raster)
r <- raster(ncol=100,nrow=100)
  r[] <- sample(c(0,1), ncell(r), replace = TRUE)

majority <- function(x){
 m <- table(x)
 names(m)[which.max(m)][1]
}
r <- focal(r, matrix(1,11,11, byrow=TRUE), majority)

 pts <- rasterToPoints(r, spatial=TRUE)
   cls <- pts[pts$layer == "1",]
 d <- rasterDistance(pts, cls, reference = r, scale=TRUE)
   dev.new(height=8,width=11)
     plot(d)
       points(cls,pch=19,cex=0.5)
```

remove.holes *Remove polygon holes*

Description

Removes all holes (null geometry) in polygon sp class objects

Usage

```
remove.holes(x)
```

Arguments

x	SpatialPolygons or SpatialPolygonsDataFrame class object

Value

SpatialPolygonsDataFrame object with all holes removed

Note

A hole is considered a polygon within a polygon representing null geometry

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 library(sp)
 Sr1 = Polygon(cbind(c(2,4,4,1,2),c(2,3,5,4,2)))
 Sr2 = Polygon(cbind(c(5,4,2,5),c(2,3,2,2)))
 Sr3 = Polygon(cbind(c(4,4,5,10,4),c(5,3,2,5,5)))
 Sr4 = Polygon(cbind(c(5,6,6,5,5),c(4,4,3,3,4)), hole = TRUE)
 polys <- SpatialPolygons(list(Polygons(list(Sr1), "s1"),
                 Polygons(list(Sr2), "s2"),
                 Polygons(list(Sr3, Sr4), "s3/4")), 1:3)

opar <- par(no.readonly=TRUE)
   par(mfrow=c(1,2))
     plot(polys, col = 1:3, main="with hole")
     plot(remove.holes(polys), col = 1:3, main="with hole removed")
par(opar)
```

rm.ext *Remove extension*

Description

Removes file extension (and path) from string

Usage

```
rm.ext(x)
```

Arguments

x	A character vector representing a file with extension

Value

The file name with extension and file path stripped off

Examples

```
rm.ext("C:/path/file.txt")
```

rotate.polygon *Rotate polygon*

Description

rotates polygon by specified angle

Usage

```
rotate.polygon(
  p,
  angle = 45,
  sp = FALSE,
  anchor = c("center", "lower.left", "upper.right")
)
```

Arguments

p	A polygon object of sf or sp class
angle	Rotation angle in degrees
sp	(FALSE | TRUE) Output sp class object
anchor	Location to rotate polygon on options are "center", "lower.left" and "upper.right"

Value

an sp or sf polygon object with rotated polygon

Note

The anchor is the location that the rotation is anchored to. The center is the centroid where the lower.left and upper.right are based on the min or max of the coordinates respectively.

Examples

```
library(sp)
library(rgeos)

data(meuse)
  coordinates(meuse) <- ~x+y

e <- gConvexHull(meuse)
  e30 <- rotate.polygon(e, angle=30, sp=TRUE)

plot(e, main="rotated 30 degrees")
  plot(e30, add=TRUE)
```

`sa.trans` *Trigonometric transformation of a slope and aspect interaction*

Description

The Trigonometric Stage (1978) [slope * cos(aspect)] or [slope * sin(aspect)]

An a priori assumption of a maximum in the NW quadrant (45 azimuth) and a minimum in the SW quadrant can be replaced by an empirically determined location of the optimum without repeated calculations of the regression fit. In addition it is argued that expressions for the effects of aspect should always be considered as terms involving an interaction with slope (Stage, 1976)

For slopes from 0 bounded from -1 to 1. Greater than 100 out of the -1 to 1 range.

An alternative for slopes with values approaching infinity is to take the square root of slope/100 to reduce the range of values.By default this model test all values greater than 100 to 101

Usage

```
sa.trans(
  slope,
  aspect,
  type = "cos",
  slp.units = "degrees",
  asp.units = "degrees"
)
```

Arguments

`slope`	slope values in degrees, radians or percent
`aspect`	aspect values in degrees or radians
`type`	Type of transformation, options are: "cos", "sin"
`slp.units`	Units of slope values, options are: "degrees", "radians" or "percent"
`asp.units`	Units of aspect values, options are: "degrees" or "radians"

Value

A vector of the modeled value

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Stage, A. R. 1976. An Expression of the Effects of Aspect, Slope, and Habitat Type on Tree Growth. Forest Science 22(3):457-460.

Examples

```
sa.trans(slope = 48.146, aspect = 360.000)

library(raster)
data(elev)
sa <- raster::terrain(elev, opt=c("slope", "aspect"), unit="degrees")
scosa <- raster::overlay(sa[[1]], sa[[2]], fun = sa.trans)
```

`sample.annulus` *Sample annulus*

Description

Creates sample points based on annulus with defined inner and outer radius

Usage

```
sample.annulus(x, r1, r2, n = 10, ...)
```

Arguments

`x`	sp SpatialPoints or SpatialPointsDataFrame class object
`r1`	Numeric value defining inner radius of annulus (in projection units)
`r2`	Numeric value defining outer radius of annulus (in projection units)
`n`	Number of samples
`...`	Additional arguments passed to spsample

Value

sp SpatialPointsataFrame OBJECT

Note

Function can be used for distance based sampling. This is a sampling method that can be used to capture spatially lagged variation.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
library(rgeos)
data(meuse)
coordinates(meuse) <- ~x+y
proj4string(meuse) <- CRS("+init=epsg:28992")
xy <- meuse[2,]

rs100 <- sample.annulus(xy, r1=50, r2=100, n = 50, type = "random")
rs200 <- sample.annulus(xy, r1=100, r2=200, n = 50, type = "random")

plot(rs200, pch=20, col="red")
  points(rs100, pch=20, col="blue")
  points(xy, pch=20, cex=2, col="black")
  box()
  legend("topright", legend=c("50-100m", "100-200m", "source"),
         pch=c(20,20,20), col=c("blue","red","black"))
```

`sample.line` *Systematic or random point sample of line(s)*

Description

Creates a systematic or random point sample of an sp SpatialLinesDataFrame object based on distance spacing, fixed size or proportional size

The sdist argument will produce an evenly spaced sample, whereas n produces a fixed sized sample. The p (proportional) argument calculates the percent of the line-length. The LID column in the @data slot corresponds to the row.names of the SpatialLinesDataFrame object.

Usage

```
sample.line(
  x,
  d = 100,
  p = NULL,
  n = NULL,
  type = "regular",
  longlat = FALSE,
  min.samp = 1,
  ...
)
```

Arguments

`x`	sp class SpatialLinesDataFrame object
`d`	Sample distance. For regular sample.
`p`	Proportional sample size (length * p), expected value is 0-1. For regular or random.
`n`	Fixed sample size. For regular or random
`type`	Defines sample type. Options are "regular" or "random". A regular sample results in a systematic, evenly spaced sample.
`longlat`	TRUE/FALSE is data in geographic units, if TRUE distance is in kilometers
`min.samp`	Minimal number of sample points for a given line (default is 1 point)
`...`	Additional argument passed to spsample

Value

sp SpatialPointsDataFrame object.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 require(sp)
 sp.lines <- SpatialLines(list(Lines(list(Line(cbind(c(1,2,3),c(3,2,2)))),
              ID="2")))
 sp.lines <- SpatialLinesDataFrame( sp.lines, data.frame(ID=1:2,
                                    row.names=c(1,2)) )

opar <- par(no.readonly=TRUE)
par(mfrow=c(2,2))
 # Create systematic sample at 20 km spacing
 reg.sample <- sample.line(sp.lines, d = 20, type = "regular",
                           longlat = TRUE)
   plot(sp.lines)
     plot(reg.sample, pch = 20, add = TRUE)
  box()
  title("systematic d = 20")

 # Create fixed size (n = 20) systematic sample
 reg.sample <- sample.line(sp.lines, n = 20, type = "regular",
                           longlat = TRUE)
   plot(sp.lines)
     plot(reg.sample, pch = 20, add = TRUE)
     box()
  title("systematic n = 20")

 # Create fixed size (n = 20) random sample
 rand.sample <- sample.line(sp.lines, n = 20, type = "random",
                            longlat = TRUE)
   plot(sp.lines)
     plot(rand.sample, pch = 20, add = TRUE)
     box()
     title("rand n = 20")

 # Create proportional (p = 0.10) random sample
 rand.sample <- sample.line(sp.lines, p = 0.10, type = "random",
                            longlat = TRUE)
   plot(sp.lines)
     plot(rand.sample, pch = 20, add = TRUE)
     box()
  title("rand p = 0.10")
par(opar)
```

sample.poly *Sample Polygons*

Description

Creates an equal sample of n for each polygon in an sp Polygon class object

Usage

```
sample.poly(x, n = 10, type = "random", ...)
```

Arguments

x	sp class SpatialPolygons or SpatialPolygonsDataFrame object
n	Number of random samples
type	Type of sample with options for: "random", "regular", "stratified", "nonaligned", "hexagonal", "clustered", "Fibonacci". See "spsample" for details.
...	Additional arguments passed to spsample

Value

sp SpatialPointsDataFrame object

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
 library(raster)
 library(sp)
   p <- raster(nrow=10, ncol=10)
   p[] <- runif(ncell(p)) * 10
   p <- rasterToPolygons(p, fun=function(x){x > 9})
   s <- sample.poly(p, n = 5, type = "random")
     plot(p)
       plot(s, pch = 20, add = TRUE)
       box()
       title("Random sample (n=5) for each polygon")
```

`sampleTransect` *Sample transect*

Description

Creates random transects from points and generates sample points along each transect

Usage

```
sampleTransect(x, min.length, max.length, id = NULL, ...)
```

Arguments

`x`	A sp point object
`min.length`	Minimum length of transect(s)
`max.length`	Maximum length of transect(s)
`id`	A unique identification column in x
`...`	Additional arguments passed to sample.line

Note

Function create random direction and length transects and then creates a point sample along each transect. The characteristic of the sample points are defined by arguments passed to the sample.line function

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
data(meuse)
coordinates(meuse) <- ~x+y
proj4string(meuse) <- CRS("+init=epsg:28992")
meuse <- meuse[sample(1:nrow(meuse),10),]

transects <- sampleTransect(meuse, min.length=200,
                    max.length=500, min.samp = 3)
  plot(transects$transects)
    plot(transects$samples, pch=20, add=TRUE)
```

---

sar *Surface Area Ratio*

Description

Calculates the Berry (2002) Surface Area Ratio based on slope

Usage

```
sar(x, s = NULL, ...)
```

Arguments

`x`	raster object
`s`	cell resolution (default is NULL, not needed if projection is in planar units)
`...`	Additional arguments passed to raster::calc

Value

raster class object of Berry (2002) Surface Area Ratio

Note

SAR is calculated as: resolution^2 * cos((degrees(slope) * (pi / 180)))

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Berry, J.K. (2002). Use surface area for realistic calculations. Geoworld 15(9):20-1.

Examples

```
library(raster)
data(elev)
surface.ratio <- sar(elev, s=90)
plot(surface.ratio)
```

---

se.news   *spatialEco news*

Description

Displays release notes

Usage

```
se.news(...)
```

Arguments

`...`	not used

---

separability   *separability*

Description

Calculates variety of two-class sample separability metrics

Available statistics:

- M-Statistic (Kaufman & Remer 1994) - This is a measure of the difference of the distributional peaks. A large M-statistic indicates good separation between the two classes as within-class variance is minimized and between-class variance maximized (M <1 poor, M >1 good).
- Bhattacharyya distance (Bhattacharyya 1943; Harold 2003) - Measures the similarity of two discrete or continuous probability distributions.
- Jeffries-Matusita distance (Bruzzone et al., 2005; Swain et al., 1971) - The J-M distance is a function of separability that directly relates to the probability of how good a resultant classification will be. The J-M distance is asymptotic to v2, where values of v2 suggest complete separability
- Divergence and transformed Divergence (Du et al., 2004) - Maximum likelihood approach. Transformed divergence gives an exponentially decreasing weight to increasing distances between the classes.

Usage

```
separability(
  x,
  y,
  plot = FALSE,
  cols = c("red", "blue"),
  clabs = c("Class1", "Class2"),
  ...
)
```

Arguments

`x`	X vector
`y`	Y vector
`plot`	plot separability (TRUE/FALSE)
`cols`	colors for plot (must be equal to number of classes)
`clabs`	labels for two classes
`...`	additional arguments passes to plot

Value

A data.frame with the following separability metrics:

- B - Bhattacharryya distance statistic
- JM - Jeffries-Matusita distance statistic
- M - M-Statistic
- D - Divergence index
- TD - Transformed Divergence index

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Anderson, M. J., & Clements, A. (2000) Resolving environmental disputes: a statistical method for choosing among competing cluster models. Ecological Applications 10(5):1341-1355

Bhattacharyya, A. (1943) On a measure of divergence between two statistical populations defined by their probability distributions'. Bulletin of the Calcutta Mathematical Society 35:99-109

Bruzzone, L., F. Roli, S.B. Serpico (1995) An extension to multiclass cases of the Jefferys-Matusita distance. IEEE Transactions on Pattern Analysis and Machine Intelligence 33:1318-1321

Du, H., C.I. Chang, H. Ren, F.M. D'Amico, J. O. Jensen, J., (2004) New Hyperspectral Discrimination Measure for Spectral Characterization. Optical Engineering 43(8):1777-1786.

Kailath, T., (1967) The Divergence and Bhattacharyya measures in signal selection. IEEE Transactions on Communication Theory 15:52-60

Kaufman Y., and L. Remer (1994) Detection of forests using mid-IR reflectance: An application for aerosol studies. IEEE T. Geosci.Remote. 32(3):672-683.

Examples

```
norm1 <- dnorm(seq(-20,20,length=5000),mean=0,sd=1)
norm2 <- dnorm(seq(-20,20,length=5000),mean=0.2,sd=2)
  separability(norm1, norm2)

s1 <- c(1362,1411,1457,1735,1621,1621,1791,1863,1863,1838)
s2 <- c(1362,1411,1457,10030,1621,1621,1791,1863,1863,1838)
  separability(s1, s2, plot=TRUE)
```

`sg.smooth` *Savitzky-Golay smoothing filter*

Description

Smoothing of time-series data using Savitzky-Golay convolution smoothing

Usage

```
sg.smooth(x, f = 4, l = 51, d = 1, na.rm, ...)
```

Arguments

`x`	A vector to be smoothed
`f`	Filter type (default 4 for quartic, specify 2 for quadratic)
`l`	Convolution filter length, must be odd number (default 51). Defines degree of smoothing
`d`	First derivative (default 1)
`na.rm`	NA behavior
`...`	not used

Value

A vector of the smoothed data equal to length of x. Please note; NA values are retained

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

References

Savitzky, A., and Golay, M.J.E. (1964). Smoothing and Differentiation of Data by Simplified Least Squares Procedures. Analytical Chemistry. 36(8):1627-39

Examples

```
 y <- c(0.112220988, 0.055554941, 0.013333187, 0.055554941, 0.063332640, 0.014444285,
        0.015555384, 0.057777140, 0.059999339, 0.034444068, 0.058888242, 0.136665165,
        0.038888458, 0.096665606,0.141109571, 0.015555384, 0.012222088, 0.012222088,
        0.072221428, 0.052221648, 0.087776810,0.014444285, 0.033332966, 0.012222088,
        0.032221869, 0.059999339, 0.011110989, 0.011110989,0.042221759, 0.029999670,
        0.018888680, 0.098887801, 0.016666483, 0.031110767, 0.061110441,0.022221979,
        0.073332526, 0.012222088, 0.016666483, 0.012222088, 0.122220881, 0.134442955,
        0.094443403, 0.128887475, 0.045555055, 0.152220547, 0.071110331, 0.018888680,
        0.022221979, 0.029999670, 0.035555165, 0.014444285, 0.049999449, 0.074443623,
        0.068888135, 0.062221535, 0.032221869, 0.095554501, 0.143331751, 0.121109776,
        0.065554835, 0.074443623, 0.043332856, 0.017777583, 0.016666483, 0.036666263,
        0.152220547, 0.032221869, 0.009999890, 0.009999890, 0.021110879, 0.025555275,
        0.099998899, 0.015555384, 0.086665712, 0.008888791, 0.062221535, 0.044443958,
        0.081110224, 0.015555384, 0.089999005, 0.082221314, 0.056666043, 0.013333187,
        0.048888352, 0.075554721, 0.025555275, 0.056666043, 0.146665052, 0.118887581,
        0.125554174, 0.024444176, 0.124443069, 0.012222088, 0.126665279, 0.048888352,
        0.046666153, 0.141109571, 0.015555384, 0.114443190)

 plot(y, type="l", lty = 3, main="Savitzky-Golay with l = 51, 25, 10")
   lines(sg.smooth(y),col="red", lwd=2)
   lines(sg.smooth(y, l = 25),col="blue", lwd=2)
   lines(sg.smooth(y, l = 10),col="green", lwd=2)

#### function applied to a raster stack  and sp object
library(raster)

random.raster <- function(r=50, c=50, l=10, min=0, max=1){
  do.call(stack, replicate(l, raster(matrix(runif(r*c, min, max),r,c))))
}
r <- random.raster()

# raster stack example
( r.sg <- calc(r, sg.smooth) )

# sp SpatialPixelsDataFrame example
r.sp <- as(r, "SpatialPixelsDataFrame")
r.sp@data <- as.data.frame(t(apply(r.sp@data, MARGIN=1, FUN=sg.smooth)))
```

---

shannons *Shannon's Diversity (Entropy) Index*

Description

Calculates Shannon's Diversity Index and Shannon's Evenness Index

Usage

```
shannons(x, counts = TRUE, ens = FALSE, margin = "row")
```

Arguments

`x`	data.frame object containing counts or proportions
`counts`	Are data counts (TRUE) or relative proportions (FALSE)
`ens`	Calculate effective number of species (TRUE/FALSE)
`margin`	Calculate diversity for rows or columns. c("row", "col")

Value

data.frame with "H" (Shannon's diversity) and "evenness" (Shannon's evenness where H / max(sum(x))) and ESN

Note

The expected for H is 0-3+ where a value of 2 has been suggested as medium-high diversity, for evenness is 0-1 with 0 signifying no evenness and 1, complete evenness.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Shannon, C. E. and W. Weaver (1948) A mathematical theory of communication. The Bell System Technical Journal, 27:379-423.

Simpson, E. H. (1949) Measurement of diversity. Nature 163:688

Roth, D. S., I. Perfecto, and B. Rathcke (1994) The effects of management systems on ground-foraging ant diversity in Costa Rica. Ecological Applications 4(3):423-436.

Examples

```
# Using Costa Rican ant diversity data from Roth et al. (1994)
data(ants)

# Calculate diversity for each covertype ("col")
shannons(ants[,2:ncol(ants)], ens = TRUE, counts = FALSE, margin = "col")

# Calculate diversity for each species ("row")
ant.div <- shannons(ants[,2:ncol(ants)], ens = TRUE, counts = FALSE,
                    margin = "row")
  row.names(ant.div) <- ants[,1]
  ant.div
```

`shift` *shift*

Description

Shift a vector by specified positive or negative lag

Usage

```
shift(x, lag = 1, pad = NA)
```

Arguments

`x`	A vector
`lag`	Number of lagged offsets, default is 1
`pad`	Value to fill the lagged offset with, default is NA

Value

a vector, length equal to x, with offset length filled with pad values

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
x <- 1:10

shift(x, 1)     # shift positive (from beginning of vector) by 1
shift(x, -1)    # shift negative (from end of vector) by 1
shift(x, 5, 0)  # Shift by 5 and fill (pad) with 0
```

`similarity` *Ecological similarity*

Description

Uses row imputation to identify "k" ecological similar observations

Usage

```
similarity(
  x,
  k = 4,
  method = "mahalanobis",
  frequency = TRUE,
  scale = TRUE,
  ID = NULL
)
```

Arguments

`x`	data.frame containing ecological measures
`k`	Number of k nearest neighbors (kNN)
`method`	Method to compute multivariate distances c("mahalanobis", "raw", "euclidean", "ica")
`frequency`	Calculate frequency of each reference row (TRUE/FALSE)
`scale`	Scale multivariate distances to standard range (TRUE/FALSE)
`ID`	Unique ID vector to use as reference ID's (rownames). Must be unique and same length as number of rows in x

Value

data.frame with k similar targets and associated distances. If frequency = TRUE the freq column represents the number of times a row (ID) was selected as a neighbor.

Note

This function uses row-based imputation to identify k similar neighbors for each observation. Has been used to identify offsets based on ecological similarity.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Evans, J.S., S.R. Schill, G.T. Raber (2015) A Systematic Framework for Spatial Conservation Planning and Ecological Priority Design in St. Lucia, Eastern Caribbean. Chapter 26 in Central American Biodiversity : Conservation, Ecology and a Sustainable Future. F. Huettman (eds). Springer, NY.

Examples

```
library(sp)
data(pu)
kNN <- similarity(pu@data[2:ncol(pu)], k = 4, frequency = FALSE,
                  ID = pu@data$UNIT_ID)
```

```
kNN <- similarity(pu@data[2:ncol(pu)], k = 4, frequency = TRUE,
                  ID = pu@data$UNIT_ID)
p <- kNN$freq
clr <- c("#3288BD", "#99D594", "#E6F598", "#FEE08B",
         "#FC8D59", "#D53E4F")
p <- ifelse(p <= 0, clr[1],
       ifelse(p > 0 & p < 10, clr[2],
         ifelse(p >= 10 & p < 20, clr[3],
        ifelse(p >= 20 & p < 50, clr[4],
          ifelse(p >= 50 & p < 100, clr[5],
            ifelse(p >= 100, clr[6], NA))))))
plot(pu, col=p, border=NA)
  legend("topleft", legend=c("None","<10","10-20",
         "20-50","50-100",">100"),
         fill=clr, cex=0.6, bty="n")
  box()
```

smooth.time.series *Smooth Raster Time-series*

Description

Smooths pixel-level data in raster time-series and can impute missing (NA) values.

Usage

```
smooth.time.series(x, f = 0.8, smooth.data = FALSE, ...)
```

Arguments

x	A raster stack/brick or sp object with a @data slot
f	Smoothing parameter (see loess span argument)
smooth.data	(FALSE/TRUE) Smooth all of the data or just impute NA values
...	Additional arguments passed to raster calc (for writing results to disk)

Details

This function uses a LOESS regression to smooth the time-series (using the smooth.data = TRUE argument). If the data is smoothed, it will be replaced by a loess estimate of the time-series (estimated distribution at the pixel-level). The results can dramatically be effected by the choice of the smoothing parameter (f) so caution is warranted and the effect of this parameter tested. Alternately, with smooth.data = FALSE, the function can be used to impute missing pixel data (NA) in raster time-series (stacks/bricks).

Value

A raster stack or brick pr data.frame object with imputed NA values or smoothed data.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

See Also

`loess` for details on the loess regression

`calc` for details on additional (...) arguments

Examples

```
## Not run:
 random.raster <- function(r=50, c=50, l=10, min=0, max=1){
   do.call(stack, replicate(l, raster(matrix(runif(r*c, min, max),r,c))))
 }
 r <- random.raster()

 #### Smooth time-series using raster stack/brick
 r.smooth <- smooth.time.series(r, f = 0.6, smooth.data = TRUE)

 #### sp SpatialPixelsDataFrame example
 r <- as(r, "SpatialPixelsDataFrame")

 # extract pixel 100 for plotting
 y <- as.numeric(r@data[100,])

 # Smooth data
 r@data <- smooth.time.series(r, f = 0.6, smooth.data = TRUE)

 # plot results
 plot(y, type="l")
   lines(as.numeric(r@data[100,]), col="red")
     legend("bottomright", legend=c("original","smoothed"),
         lty=c(1,1), col=c("black","red"))

 # coerce back to raster stack object
 r <- stack(r)


## End(Not run)
```

`sobal` *Sobel-Feldman operator*

Description

An isotropic image gradient operator using a 3x3 window

The Sobel-Feldmanh operator is a discrete differentiation operator, deriving an approximation of the gradient of the intensity function. abrupt discontinuity in the gradient function represents edges, making this a common approach for edge detection. The Sobel-Feldman operator is based on convolving the image with a small, separable, and integer matrix in the horizontal and vertical directions. The operator uses two 3x3 kernels which are convolved with the original image to calculate approximations of the derivatives - one for horizontal changes, and one for vertical. Where x is defined here as increasing in the right-direction, and y as increasing in the down-direction. At each pixel in the raster, the resulting gradient can be combined to give the gradient intensity, using: SQRT(Gx^2 Gy^2). This can be expanded into the gradient direction using atan(Gx/Gy)

Usage

```
sobal(x, method = "intensity", ...)
```

Arguments

`x`	A raster class object
`method`	Type of operator ("intensity", "direction", "edge")
`...`	Additional arguments passed to raster::overlay or, if method="edge", raster::focal (if you want a file written to disk use filename = "" argument)

Value

A raster class object or raster written to disk

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Sobel, I., & G. Feldman, (1969) A 3x3 Isotropic Gradient Operator for Image Processing, presented at the Stanford Artificial Intelligence Project (SAIL).

Examples

```
library(raster)
r <- brick(system.file("external/rlogo.grd", package="raster"))
s.int <- sobal(r[[1]])
s.dir <- sobal(r[[1]], method = "direction")
s.edge <- sobal(r[[1]], method = "edge")

opar <- par(no.readonly=TRUE)
par(mfrow=c(2,2))
  plot(r[[1]])
  plot(s.int, main="intensity")
  plot(s.dir, main="direction")
  plot(s.edge, main="edge")
par(opar)
```

sp.kde *Spatial kernel density estimate*

Description

A weighted or unweighted Gaussian Kernel Density estimate for spatial data

Usage

```
sp.kde(
  x,
  y = NULL,
  bw = NULL,
  newdata = NULL,
  nr = NULL,
  nc = NULL,
  standardize = FALSE,
  scale.factor = NULL,
  mask = TRUE
)
```

Arguments

`x`	sp SpatialPointsDataFrame object
`y`	Optional values, associated with x coordinates, to be used as weights
`bw`	Distance bandwidth of Gaussian Kernel, must be units of projection
`newdata`	A Rasterlayer, any sp class object or c[xmin,xmax,ymin,ymax] vector to estimate the kde extent
`nr`	Number of rows used for creating grid. If not defined a value based on extent or existing raster will be used
`nc`	Number of columns used for creating grid. If not defined a value based on extent or existing raster will be used
`standardize`	Standardize results to 0-1 (FALSE/TRUE)
`scale.factor`	Optional numeric scaling factor for the KDE (eg., 10000), to account for small estimate values
`mask`	(TRUE/FALSE) mask resulting raster if newdata is provided

Value

Raster class object containing kernel density estimate

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
library(raster)
  data(meuse)
  coordinates(meuse) <- ~x+y

# Unweighted KDE (spatial locations only)
pt.kde <- sp.kde(x = meuse, bw = 1000, standardize = TRUE,
                 nr=104, nc=78, scale.factor = 10000 )

# Plot results
  plot(pt.kde, main="Unweighted kde")
    points(meuse, pch=20, col="red")

#### Using existing raster(s) to define grid ####

# Weighted KDE using cadmium and extent with row & col to define grid
e <- c(178605, 181390, 329714, 333611)
cadmium.kde <- sp.kde(x = meuse, y = meuse$cadmium, bw = 1000,
                      nr = 104, nc = 78, newdata = e,
   standardize = TRUE,
   scale.factor = 10000  )
plot(cadmium.kde)
  points(meuse, pch=19)

# Weighted KDE using cadmium and raster object to define grid
r <- raster::raster(raster::extent(c(178605, 181390, 329714, 333611)),
                    nrow=104, ncol=78)
  r[] <- rep(1,ncell(r))
cadmium.kde <- sp.kde(x = meuse, y = meuse$cadmium, bw = 1000,
                      newdata = r, standardize = TRUE,
   scale.factor = 10000  )
plot(cadmium.kde)
  points(meuse, pch=19)

# Weighted KDE using cadmium and SpatialPixelsDataFrame object to define grid
data(meuse.grid)
coordinates(meuse.grid) = ~x+y
proj4string(meuse.grid) <- CRS("+init=epsg:28992")
gridded(meuse.grid) = TRUE
cadmium.kde <- sp.kde(x = meuse, y = meuse$cadmium, bw = 1000,
                      newdata = meuse.grid, standardize = TRUE,
   scale.factor = 10000  )
plot(cadmium.kde)
  points(meuse, pch=19)
```

sp.na.omit *sp na.omit*

Description

Removes row or column NA's in sp object

Usage

```
sp.na.omit(x, col.name = NULL, margin = 1)
```

Arguments

`x`	Object of class SpatialPointsDataFrame OR SpatialPolygonsDataFrame
`col.name`	The name of a specific column to remove NA's from
`margin`	Margin (1,2) of data.frame 1 for rows or 2 for columns

Note

This function will remove all NA's in the object or NA's associated with a specific column.

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

Examples

```
library(sp)
data(meuse)
coordinates(meuse) <- ~x+y

# Display rows with NA
meuse@data[!complete.cases(meuse@data),]

# Remove all NA's in rows (and associated points)
meuse2 <- sp.na.omit(meuse)
  dim(meuse)
  dim(meuse2)

# Plot deleted points in red
plot(meuse, col='red', pch=20)
plot(meuse2, col='black', pch=20, add=TRUE)

# Remove NA's associated with specific column
meuse2 <- sp.na.omit(meuse, col.name = "om")
  head(meuse@data)
  head(meuse2@data)
```

spatial.select *Spatial Select*

Description

Performs a spatial select (feature subset) between a polygon(s) and other feature class

Performs a spatial select of features based on an overlay of a polygon (x), which can represent multiple features, and a polygon, point or line feature classes (y). User can specify a partial or complete intersection, using within argument, or within a distance, using distance argument, predicated on the query polygon. This function is similar to ArcGIS/Pro spatial select. Please note that for point to point neighbor selections use the knn function.

Usage

```
spatial.select(
  x,
  y = NULL,
  distance = NULL,
  predicate = c("intersect", "contains", "covers", "touches", "proximity",
    "contingency"),
  neighbors = c("queen", "rook")
)
```

Arguments

`x`	An sp or sf polygon(s) object that defines the spatial query
`y`	A sp or sf feature class that will be subset by the query of x
`distance`	A proximity distance of features to select (within distance)
`predicate`	Spatial predicate for intersection
`neighbors`	If predicate = "contingency" type of neighbors options are c("queen", "rook")

Value

An sp object representing a subset of y based on the spatial query of x or, if predicate = contingency a sparse matrix representing neighbor indexes

Note

Valid spatial predicates include: intersect, touches, covers, contains, proximity and contingency. See [DE-9IM topology model](https://en.wikipedia.org/wiki/DE-9IM) for detailed information on data predicates.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

See Also

`gIntersects` for details on intersect predicate

`gContains` for details on contain predicate

`gCovers` for details on covers predicate

`gTouches` for details on touches predicate

`gWithinDistance` for details on proximity predicate

`https://en.wikipedia.org/wiki/DE-9IM` for details on DE-9IM topology model

Examples

```
library(raster)
library(sp)

data(meuse)
  coordinates(meuse) <- ~x+y

spolys <- hexagons(meuse, res=100)
p <- raster(extent(spolys), res=800)
  p[] <- runif(ncell(p)) * 10
    p <- rasterToPolygons(p, fun=function(x){x > 6})

#### On polygons
sub.int <- spatial.select(p, spolys, predicate = "intersect")
sub.contains <- spatial.select(p, spolys, predicate = "contains")
sub.cov <- spatial.select(p, spolys, predicate = "covers")
sub.touches <- spatial.select(p, spolys, predicate = "touches")
sub.prox <- spatial.select(p, spolys, distance=100, predicate = "proximity")

opar <- par(no.readonly=TRUE)
par(mfrow=c(2,3))
  plot(spolys, main="all data")
    plot(p, add=TRUE)
  plot(sub.int, main="intersects")
    plot(p, add=TRUE)
  plot(sub.contains, main="contains")
    plot(p, add=TRUE)
  plot(sub.cov, main="covers")
    plot(p, add=TRUE)
  plot(sub.touches, main="touches")
    plot(p, add=TRUE)
  plot(sub.prox, main="Proximity 100m distance")
    plot(p, add=TRUE)
par(opar)

#### On points
#### note; touches is not relevant for points and intersect/contains/covers
####       yield the same results
sub.int <- spatial.select(p, meuse, predicate = "intersect")
sub.contains <- spatial.select(p, meuse, predicate = "contains")
sub.prox <- spatial.select(p, meuse, distance=200, predicate = "proximity")
```

```
opar <- par(no.readonly=TRUE)
par(mfrow=c(2,2))
  plot(meuse, main="all data", pch=20)
    plot(p, add=TRUE)
  plot(sub.int, main="intersects", pch=20)
    plot(p, add=TRUE)
  plot(sub.contains, main="contains", pch=20)
    plot(p, add=TRUE)
  plot(sub.prox, main="Proximity 200m distance", pch=20)
    plot(p, add=TRUE)
par(opar)

#### For rook or queen polygon contingency
spolys <- as(sf::st_make_grid(sf::st_sfc(sf::st_point(c(0,0)),
             sf::st_point(c(3,3))), n = c(3,3)), "Spatial")

spatial.select(spolys, predicate = "contingency")
spatial.select(spolys, predicate = "contingency", neighbors = "rook")
```

`spectral.separability` *spectral separability*

Description

Calculates spectral separability by class

Available statistics:

- Bhattacharyya distance (Bhattacharyya 1943; Harold 2003) measures the similarity of two discrete or continuous probability distributions.
- Jeffries-Matusita (default) distance (Bruzzone et al., 2005; Swain et al., 1971) is a scaled (0-2) version of Bhattacharyya. The J-M distance is asymptotic to 2, where 2 suggest complete separability.

Usage

```
spectral.separability(x, y, jeffries.matusita = TRUE)
```

Arguments

`x`	data.frame, matrix or vector of spectral values must, match classes defined in y
`y`	A vector or factor with grouping classes, must match row wise values in x
`jeffries.matusita`	(TRUE/FALSE) Return J-M distance (default) else Bhattacharyya

Value

A matrix of class-wise Jeffries-Matusita or Bhattacharyya distance separability values

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Bhattacharyya, A. (1943) On a measure of divergence between two statistical populations defined by their probability distributions'. Bulletin of the Calcutta Mathematical Society 35:99-109

Bruzzone, L., F. Roli, S.B. Serpico (1995) An extension to multiclass cases of the Jefferys-Matusita distance. IEEE Transactions on Pattern Analysis and Machine Intelligence 33:1318-1321

Kailath, T., (1967) The Divergence and Bhattacharyya measures in signal selection. IEEE Transactions on Communication Theory 15:52-60

Examples

```
#' # Create example data
require(MASS)
d <- 6                 # Number of bands
n.class <- 5           # Number of classes
n <- rep(1000, 5)
mu <- round(matrix(rnorm(d*n.class, 128, 1),
            ncol=n.class, byrow=TRUE), 0)

x <- matrix(double(), ncol=d, nrow=0)
  classes <- integer()
    for (i in 1:n.class) {
      f <- svd(matrix(rnorm(d^2), ncol=d))
      sigma <- t(f$v) %*% diag(rep(10, d)) %*% f$v
      x <- rbind(x, mvrnorm(n[i], mu[, i], sigma))
      classes <- c(classes, rep(i, n[i]))
    }
colnames(x) <- paste0("band", 1:6)
classes <- factor(classes, labels=c("water", "forest",
                  "shrub", "urban", "ag"))

# Separability for multi-band (multivariate) spectra
spectral.separability(x, classes)

# Separability for single-band (univariate) spectra
spectral.separability(x[,1], classes)
```

spherical.sd   *Spherical Variance or Standard Deviation of Surface*

Description

Derives the spherical standard deviation of a raster surface

Usage

```
spherical.sd(r, d, variance = FALSE, ...)
```

Arguments

`r`	Raster class object
`d`	Size of focal window or a matrix to use in focal function
`variance`	(FALSE|TRUE) Output spherical variance rather than standard deviation
`...`	Additional arguments passed to calc (can write raster to disk here)

Details

Surface variability using spherical variance/standard deviation. The variation can be assessed using the spherical standard deviation of the normal direction within a local neighborhood. This is found by expressing the normal directions on the surfaces cells in terms of their displacements in a Cartesian (x,y,z) coordinate system. Averaging the x-coordinates, y-coordinates, and z-coordinates separately gives a vector (xb, yb, zb) pointing in the direction of the average normal. This vector will be shorter when there is more variation of the normals and it will be longest–equal to unity–when there is no variation. Its squared length is (by the Pythagorean theorem) given by: R^2 = xb^2 + yb^2 + zb^2 where; x = cos(aspect) * sin(slope) and xb = nXn focal mean of x y = sin(aspect) * sin(slope) and yb = nXn focal mean of y z = cos(slope) and zb = nXn focal mean of z

The slope and aspect values are expected to be in radians. The value of (1 - R^2), which will lie between 0 and 1, is the spherical variance. and it's square root can be considered the spherical standard deviation.

Value

rasterLayer class object of the spherical standard deviation

Author(s)

Jeffrey S. Evans <jeffrey_evans<at>tnc.org>

See Also

`focal` for details on focal function

`calc` for details on ... arguments

Examples

```
library(raster)
data(elev)

ssd <- spherical.sd(elev, d=5)

slope <- terrain(elev, opt='slope')
aspect <- terrain(elev, opt='aspect')
```

```
hill <- hillShade(slope, aspect, 40, 270)
plot(hill, col=grey(0:100/100), legend=FALSE,
     main='terrain spherical standard deviation')
  plot(ssd, col=rainbow(25, alpha=0.35), add=TRUE)
```

srr *Surface Relief Ratio*

Description

Calculates the Pike (1971) Surface Relief Ratio

Usage

```
srr(x, s = 5, ...)
```

Arguments

x	raster object
s	Focal window size
...	Additional arguments passed to raster::calc

Value

raster class object of Pike's (1971) Surface Relief Ratio

Note

Describes rugosity in continuous raster surface within a specified window. The implementation of SRR can be shown as: (mean(x) - min(x)) / (max(x) - min(x))

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)
data(elev)
r.srr <- srr(elev, s=5)
  plot(r.srr, main="Surface Relief Ratio")
```

`stratified.random` *Stratified random sample*

Description

Creates a stratified random sample of an sp class object

Usage

```
stratified.random(x, strata, n = 10, reps = 1, replace = TRUE)
```

Arguments

`x`	sp class SpatialDataFrame object (point, polygon, line, pixel)
`strata`	Column in @data slot with stratification factor
`n`	Number of random samples
`reps`	Number of replicates per strata
`replace`	Sampling with replacement (TRUE|FALSE)

Value

sp SpatialDataFrame object (same as input feature) containing random samples

Note

If replace=FALSE features are removed from consideration in subsequent replicates. Conversely, if replace=TRUE, a feature can be selected multiple times across replicates. Not applicable if rep=1.

Depends: sp

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Hudak, A.T., N.L. Crookston, J.S. Evans, M.J. Falkowski, A.M.S. Smith, P. Gessler and P. Morgan. (2006) Regression modelling and mapping of coniferous forest basal area and tree density from discrete-return lidar and multispectral satellite data. Canadian Journal of Remote Sensing 32: 126-138.

Examples

```
require(sp)
  data(meuse)
    coordinates(meuse) <- ~x+y

# Create stratified variable using quartile breaks
x1 <- cut(meuse@data[,'cadmium'], summary(meuse@data[,'cadmium'])[-4],
          include.lowest=TRUE)
  levels(x1) <- seq(1,nlevels(x1),1)
x2 <- cut(meuse@data[,'lead'], summary(meuse@data[,'lead'])[-4],
          include.lowest=TRUE)
  levels(x2) <- seq(1,nlevels(x2),1)
meuse@data <- cbind(meuse@data, STRAT=paste(x1, x2, sep='.') )

# 2 replicates and replacement
ssample <- stratified.random(meuse, strata='STRAT', n=2, reps=2)

# 2 replicates and no replacement
ssample.nr <- stratified.random(meuse, strata='STRAT', n=2, reps=2,
                                replace=FALSE)

# n=1 and reps=10 for sequential numbering of samples
ssample.ct <- stratified.random(meuse, strata='STRAT', n=1, reps=10,
                                replace=TRUE)

# Counts for each full strata (note; 2 strata have only 1 observation)
tapply(meuse@data$STRAT, meuse@data$STRAT, length)

# Counts for each sampled strata, with replacement
tapply(ssample@data$STRAT, ssample@data$STRAT, length)

# Counts for each sampled strata, without replacement
tapply(ssample.nr@data$STRAT, ssample.nr@data$STRAT, length)

# Counts for each sampled strata, without replacement
tapply(ssample.ct@data$STRAT, ssample.ct@data$STRAT, length)

# Plot random samples colored by replacement
ssample@data$REP <- factor(ssample@data$REP)
  spplot(ssample, 'REP', col.regions=c('red','blue'))
```

`subsample.distance` *Distance-based subsampling*

Description

Draws a minimum, and optional maximum constrained, distance sub-sampling

Usage

```
subsample.distance(
  x,
  size,
  d,
  d.max = NULL,
  replacement = FALSE,
  latlong = FALSE,
  echo = FALSE
)
```

Arguments

`x`	A spatial polygons or points sp object
`size`	Subsample size
`d`	Minimum sampling distance
`d.max`	Maximum sampling distance
`replacement`	(FALSE/TRUE) Subsample with replacement
`latlong`	(FALSE/TRUE) Is the data in a geographic projection
`echo`	(FALSE/TRUE) Print min and max sample distances

Value

A subsampled spatial polygons or points sp object

Note

This function provides a distance constrained subsample of existing point or polygon data

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```


library(sp)
data(meuse)
  coordinates(meuse) <- ~ x+y

# Subsample with a 500m minimum sample spread
sub.meuse <- subsample.distance(meuse, size = 10, d = 500, echo = TRUE)
  plot(meuse, pch=19, main="min dist = 500")
    points(sub.meuse, pch=19, col="red")

# Check distances
dm <- spDists(sub.meuse)
```

```
  diag(dm) <- NA
cat("\n", "Min distance for subsample", min(dm, na.rm=TRUE), "\n")
cat("Max distance for subsample", max(dm, na.rm=TRUE), "\n")

  # Subsample with a 500m minimum and 3500m maximum sample spread
  sub.meuse <- subsample.distance(meuse, size = 10, d = 500, d.max = 3500)
    plot(meuse,pch=19, main="min dist = 500, max dist = 3500")
      points(sub.meuse, pch=19, col="red")

  # Check distances
  dm <- spDists(sub.meuse)
    diag(dm) <- NA
  cat("Min distance for subsample", min(dm, na.rm=TRUE), "\n")
  cat("Max distance for subsample", max(dm, na.rm=TRUE), "\n")
```

`summary.cross.cor` *Summary of spatial cross correlation*

Description

summary method for class "cross.cor"

Usage

```
## S3 method for class 'cross.cor'
summary(object, ...)
```

Arguments

`object`	Object of class cross.cor
`...`	Ignored

`summary.effect.size` *Summarizing effect size*

Description

Summary method for class "effect.size".

Usage

```
## S3 method for class 'effect.size'
summary(object, ...)
```

Arguments

`object`	Object of class effect.size
`...`	Ignored

`summary.loess.boot` *Summarizing Loess bootstrap models*

Description

Summary method for class "loess.boot".

Usage

```
## S3 method for class 'loess.boot'
summary(object, ...)
```

Arguments

`object`	Object of class loess.boot
`...`	Ignored

`swvi` *Senescence weighted Vegetation Index (swvi)*

Description

Modified Soil-adjusted Vegetation Index (MSAVI) or Modified Triangular Vegetation Index 2 (MTVI) weighted by the Normalized difference senescent vegetation index (NDSVI)

The intent of this index is to correct the MSAVI or MTVI index for bias associated with senescent vegetation. This is done by:

- deriving the NDSVI;
- applying a threshold to limit NDSVI to values associated with senescent vegetation;
- converting the index to inverted weights (-1*(NDSVI/sum(NDSVI)));
- applying weights to MSAVI or MTVI

The MSAVI formula follows the modification proposed by Qi et al. (1994), often referred to as MSAVI2. MSAVI index reduces soil noise and increases the dynamic range of the vegetation signal. The implemented modified version (MSAVI2) is based on an inductive method that does not use a constant L value, in separating soil effects, an highlights healthy vegetation. The MTVI(2) index follows Haboudane et al., (2004) and represents the area of a hypothetical triangle in spectral space that connects (1) green peak reflectance, (2) minimum chlorophyll absorption, and (3) the NIR shoulder. When chlorophyll absorption causes a decrease of red reflectance, and leaf tissue abundance causes an increase in NIR reflectance, the total area of the triangle increases. It is good for estimating green LAI, but its sensitivity to chlorophyll increases with an increase in canopy density. The modified version of the index accounts for the background signature of soils while preserving sensitivity to LAI and resistance to the influence of chlorophyll.

The Normalized difference senescent vegetation index (NDSVI) follows methods from Qi et a., (2000). The senescence is used to threshold the NDSVI. Values less then this value will be NA. The threshold argument is used to apply a threshold to MSAVI. The default is NULL but if specified all values (MSAVI <= threshold) will be NA. Applying a weight.factor can be used to change the influence of the weights on MSAVI.

Usage

```
swvi(
  red,
  nir,
  swir,
  green = NULL,
  mtvi = FALSE,
  senescence = 0,
  threshold = NULL,
  weight.factor = NULL,
  ...
)
```

Arguments

`red`	Red band (0.636 - 0.673mm), landsat 5&7 band 3, OLI (landsat 8) band 4
`nir`	Near infrared band (0.851 - 0.879mm) landsat 5&7 band 4, OLI (landsat 8) band 5
`swir`	short-wave infrared band 1 (1.566 - 1.651mm), landsat 5&7 band 5, OLI (landsat 8) band 6
`green`	Green band if MTVI = TRUE
`mtvi`	(FALSE | TRUE) Use Modified Triangular Vegetation Index 2 instead of MSAVI
`senescence`	The critical value, in NDSVI, representing senescent vegetation
`threshold`	Threshold value for defining NA based on < p
`weight.factor`	Apply partial weights (w * weight.factor) to the NDSVI weights
`...`	Additional arguments passed to raster calc function

Value

rasterLayer class object of the weighted MSAVI metric

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Haboudane, D., et al. (2004) Hyperspectral Vegetation Indices and Novel Algorithms for Predicting Green LAI of Crop Canopies: Modeling and Validation in the Context of Precision Agriculture. Remote Sensing of Environment 90:337-352.

Qi J., Chehbouni A., Huete A.R., Kerr Y.H., (1994). Modified Soil Adjusted Vegetation Index (MSAVI). Remote Sens Environ 48:119-126.

Qi J., Kerr Y., Chehbouni A., (1994). External factor consideration in vegetation index development. Proc. of Physical Measurements and Signatures in Remote Sensing, ISPRS, 723-730.

Qi, J., Marsett, R., Moran, M.S., Goodrich, D.C., Heilman, P., Kerr, Y.H., Dedieu, G., Chehbouni, A., Zhang, X.X. (2000). Spatial and temporal dynamics of vegetation

Examples

```
## Not run:
library(raster)
library(RStoolbox)

data(lsat)
lsat <- radCor(lsat, metaData = readMeta(system.file(
                 "external/landsat/LT52240631988227CUB02_MTL.txt",
                  package="RStoolbox")), method = "apref")

# Using Modified Soil-adjusted Vegetation Index (MSAVI)
( wmsavi <- swvi(red = lsat[[3]], nir = lsat[[4]], swir = lsat[[5]]) )
    plotRGB(lsat, r=6,g=5,b=2, scale=1, stretch="lin")
      plot(wmsavi, legend=FALSE, col=rev(terrain.colors(100, alpha=0.35)), add=TRUE )

# Using Modified Triangular Vegetation Index 2 (MTVI)
( wmtvi <- swvi(red = lsat[[3]], nir = lsat[[4]], swir = lsat[[5]],
                          green = lsat[[3]], mtvi = TRUE) )
  plotRGB(lsat, r=6,g=5,b=2, scale=1, stretch="lin")
    plot(wmtvi, legend=FALSE, col=rev(terrain.colors(100, alpha=0.35)), add=TRUE )

## End(Not run)
```

time_to_event *Time to event*

Description

Returns the time (sum to position) to a specified value

The time to event represents the sum of positions, in the vector, until the specified value is found ie., (0,0,1) would be 3 or, 2 with up.to=TRUE. The int argument allows for rounding a continuous variable. Since it may be difficult to fine an exact match to a floating point value rounding mitigates the problem. If you want a specific rounding value (eg., 1 decimal place) you can apply it to x first then pass it to the function.

Usage

```
time_to_event(x, y = 1, dir = c("LR", "RL"), int = FALSE, up.to = FALSE)
```

Arguments

`x`	A vector, representing time-series, to evaluate
`y`	Threshold value tor return position for
`dir`	Direction of evaluation c("LR", "RL")
`int`	FALSE | TRUE - Evaluate as integer (rounds to 0 decimal places)
`up.to`	FALSE | TRUE - Return value before event

Value

A vector value representing the time to event

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)

# Binomial instance
time_to_event(c(0,0,0,0,1,0,0,0,1,0))
time_to_event(c(0,0,0,0,1,0,0,0,1,0), up.to = TRUE)
time_to_event(c(0,0,0,0,1,0,0,0,1,0), dir="RL")

r <- do.call(raster::stack, replicate(20,raster::raster(matrix(sample(
             c(0,1), 1000, replace=TRUE), 100, 100))))
  ( t2e <- calc(r, fun=time_to_event) )

# Continuous threshold instance
( x <- runif(100, 0,7) )
time_to_event(x, y = 5, int=TRUE)

r <- do.call(raster::stack, replicate(20,raster::raster(matrix(
             runif(1000,0,7), 100, 100))))
  t2e <- function(x) { time_to_event(x, y=5, int=TRUE) }
  ( t2e <- calc(r, fun=time_to_event) )
```

topo.distance *Topographic distance*

Description

Calculates topographic corrected distance for a SpatialLinesDataFrame object

Usage

```
topo.distance(x, r, echo = FALSE)
```

Arguments

x	sp SpatialLinesDataFrame object
r	raster class elevation raster
echo	(FALSE/TRUE) print progress to screen

Value

Vector of corrected topographic distances same length as nrow(x)

Note

This function corrects straight-line (euclidean) distances for topographic-slope effect.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(sp)
library(raster)
library(GeNetIt)

# create example data
data(elev)
  r <- projectRaster(elev, res=c(1000,1000),
                     crs="+proj=aea +lat_1=29.5 +lat_2=42.5")
  e <- extent(616893.6,714697.3,5001027,5080542)
    elev <- crop(r,e)
      names(elev) <- "elev"
pts <- sampleRandom(elev, 10, sp=TRUE)
  pts$ID <- LETTERS[seq( from = 1, to = nrow(pts) )]

graph <- GeNetIt::knn.graph(pts, row.names=pts@data[,"ID"])
  proj4string(graph) <- proj4string(elev)
  head(graph@data)
```

```
plot(elev)
  plot(graph, cex=0.5, add=TRUE)
  plot(pts,pch=19,col="red",add=TRUE)

# Calculate topographical distance
( tdist <- topo.distance(graph, elev) )

# Increase in corrected distance
tdist - graph$length

# Percent increase in corrected distance
((tdist - graph$length) / graph$length) * 100
```

`tpi` *Topographic Position Index (tpi)*

Description

Calculates topographic position using mean deviations

Usage

```
tpi(x, scale = 3, win = "rectangle", normalize = FALSE, zero.correct = FALSE)
```

Arguments

`x`	A raster class object
`scale`	focal window size (n-cell x n-cell for rectangle or distance for circle)
`win`	Window type. Options are "rectangle" and "circle"
`normalize`	Apply deviation correction that normalizes to local surface roughness
`zero.correct`	Apply correction for zero values in matrix weights

Value

raster class object of tpi metric

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

De Reu, J., J. Bourgeois, M. Bats, A. Zwertvaegher, V. Gelorini, et al., (2014) Application of the topographic position index to heterogeneous landscapes. Geomorphology, 186:39-49.

Examples

```
 library(raster)
 data(elev)

# calculate tpi and plot
  tpi7 <- tpi(elev, scale=7)
  tpi025 <- tpi(elev, win = "circle", scale=0.025)
  tpi025.zc <- tpi(elev, win = "circle", scale=0.025,
                   zero.correct = TRUE)

opar <- par(no.readonly=TRUE)
    par(mfrow=c(2,2))
      plot(elev, main="original raster")
      plot(tpi7, main="tpi 7x7")
      plot(tpi025, main="tpi Circular window d=0.025")
   plot(tpi025, main="tpi Circular window d=0.025, zero correct")
par(opar)
```

`trasp` *Solar-radiation Aspect Index*

Description

Calculates the Roberts and Cooper (1989) Solar-radiation Aspect Index

Roberts and Cooper (1989) rotates (transforms) the circular aspect to assign a value of zero to land oriented in a north-northeast direction, (typically the coolest and wettest orientation), and a value of one on the hotter, dryer south-southwesterly slopes. The result is a continuous variable between 0 - 1. The metric is defined as: trasp = (1 - cos((pi/180)(a-30)) / 2 where; a = aspect in degrees

Usage

```
trasp(x, ...)
```

Arguments

`x`	raster object
`...`	Additional arguments passed to raster::calc

Value

raster class object of oberts and Cooper (1989) Solar-radiation Aspect Index

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Roberts. D.W., and Cooper, S.V. (1989). Concepts and techniques of vegetation mapping. In Land Classifications Based on Vegetation: Applications for Resource Management. USDA Forest Service GTR INT-257, Ogden, UT, pp 90-96

Examples

```
library(raster)
data(elev)
s <- trasp(elev)
  plot(s)
```

`trend.line` *trend.line*

Description

Calculated specified trend line of x,y

Usage

```
trend.line(x, y, type = "linear", plot = TRUE, ...)
```

Arguments

`x`	Vector of x
`y`	Vector of y
`type`	Trend line types are: 'linear', 'exponential', 'logarithmic', 'polynomial'
`plot`	plot results (TRUE/FALSE)
`...`	Additional arguments passed to plot

Value

A list class object with the following components:

- for type = 'linear' x is slope and y is intercept
- for type = 'exponential', 'logarithmic', or 'polynomial' x is original x variable and y is vector of fit regression line

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

Examples

```
x <- 1:10
y <- jitter(x^2)

opar <- par(no.readonly=TRUE)
  par(mfcol=c(2,2))
    trend.line(x,y,type='linear',plot=TRUE,pch=20,main='Linear')
    trend.line(x,y,type='exponential',plot=TRUE,pch=20,main='Exponential')
    trend.line(x,y,type='logarithmic',plot=TRUE,pch=20,main='Logarithmic')
    trend.line(x,y,type='polynomial',plot=TRUE,pch=20,main='Polynomial')
 par(opar)
```

`tri` *Terrain Ruggedness Index*

Description

Implementation of the Riley et al (1999) Terrain Ruggedness Index

The algebraic approximation is considerably faster. However, because inclusion of the center cell, the larger the scale the larger the divergence of the minimum value.

Recommended ranges for classifying Topographic Ruggedness Index:

- 0-80 - level terrain surface.
- 81-116 - nearly level surface.
- 117-161 - slightly rugged surface.
- 162-239 - intermediately rugged surface.
- 240-497 - moderately rugged surface.
- 498-958 - highly rugged surface.
- gt 959 - extremely rugged surface.

Usage

```
tri(r, s = 3, exact = TRUE, file.name = NULL, ...)
```

Arguments

`r`	RasterLayer class object
`s`	Scale of window. Must be odd number, can represent 2 dimensions (eg., s=c(3,5) would represent a 3 x 5 window)
`exact`	Calculate (TRUE/FALSE) the exact TRI or an algebraic approximation.
`file.name`	Name of output raster (optional)
`...`	Additional arguments passed to writeRaster

Value

raster class object or raster written to disk

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org

References

Riley, S.J., S.D. DeGloria and R. Elliot (1999) A terrain ruggedness index that quantifies topographic heterogeneity, Intermountain Journal of Sciences 5(1-4):23-27.

Examples

```
 library(raster)
 data(elev)
  ( tri.ext <- tri(elev) )
  ( tri.app <- tri(elev, exact = FALSE) )
  plot(stack(tri.ext, tri.app))
```

`vrm` *Vector Ruggedness Measure (VRM)*

Description

Implementation of the Sappington et al., (2007) vector ruggedness measure

Usage

```
vrm(x, s = 3, file.name = NULL, ...)
```

Arguments

`x`	Elevation raster class object
`s`	Scale of window. Must be odd number, can represent 2 dimensions (eg., s=c(3,5) would represent a 3 x 5 window)
`file.name`	Name of output raster (optional)
`...`	Additional arguments passed to writeRaster

Value

raster class object or raster written to disk

Note

This function measures terrain ruggedness by calculating the vector ruggedness measure

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Sappington, J.M., K.M. Longshore, D.B. Thomson (2007). Quantifying Landscape Ruggedness for Animal Habitat Analysis: A case Study Using Bighorn Sheep in the Mojave Desert. Journal of Wildlife Management. 71(5):1419-1426

Examples

```
 library(raster)
 data(elev)
   vrm3 <- vrm(elev)
   vrm5 <- vrm(elev, s=5)
   plot(stack(vrm3, vrm5))
```

`winsorize` *Winsorize transformation*

Description

Removes extreme outliers using a winsorization transformation

Winsorization is the transformation of a distribution by limiting extreme values to reduce the effect of spurious outliers. This is done by shrinking outlying observations to the border of the main part of the distribution.

Usage

```
winsorize(
  x,
  min.value = NULL,
  max.value = NULL,
  p = c(0.05, 0.95),
  na.rm = FALSE
)
```

Arguments

`x`	A numeric vector
`min.value`	A fixed lower bounds, all values lower than this will be replaced by this value. The default is set to the 5th-quantile of x.
`max.value`	A fixed upper bounds, all values higher than this will be replaced by this value. The default is set to the 95th-quantile of x.
`p`	A numeric vector of 2 representing the probabilities used in the quantile function.
`na.rm`	(FALSE/TRUE) should NAs be omitted?

Value

A transformed vector the same length as x, unless na.rm is TRUE, then x is length minus number of NA's

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

References

Dixon, W.J. (1960) Simplified Estimation from Censored Normal Samples. Annals of Mathematical Statistics. 31(2):385-391

Examples

```
set.seed(1234)
x <- rnorm(100)
x[1] <- x[1] * 10
winsorize(x)

plot(x, type="l", main="Winsorization transformation")
  lines(winsorize(x), col="red", lwd=2)
    legend("bottomright", legend=c("Original distribution","With outliers removed"),
        lty=c(1,1), col=c("black","red"))

# Behavior with NA value(s)
x[4] <- NA
winsorize(x)             # returns x with original NA's
winsorize(x, na.rm=TRUE) # removes NA's
```

wt.centroid *Weighted centroid*

Description

Creates centroid of [x,y] coordinates based on a weights field

Usage

```
wt.centroid(x, p, sp = TRUE)
```

Arguments

x	sp SpatialPointsDataFrame class object
p	Weights column in x@data slot
sp	Output sp SpatailPoints class object (TRUE | FALSE)

Value

A vector or an sp class SpatialPoints object of the weighted coordinate centroid

Note

The weighted centroid is calculated as: [Xw]=[X]*[p], [Yw]=[Y]*[p], [sXw]=SUM[Xw], [sYw]=SUM[Yw], [sP]=SUM[p] wX=[sXw]/[sP], wY=[sYw]/[sP] where; X=X COORDINATE(S), Y=Y COORDINATE(S), p=WEIGHT

Depends: sp

Examples

```
require(sp)
 data(meuse)
 coordinates(meuse) = ~x+y
 wt.copper <- wt.centroid(meuse, 'copper', sp=TRUE)
   wt.zinc <- wt.centroid(meuse, 'zinc', sp=TRUE)
     plot(meuse, pch=20, cex=0.75, main='Weighted centroid(s)')
       points(wt.copper, pch=19, col='red', cex=1.5)
         points(wt.zinc, pch=19, col='blue', cex=1.5)
        box()
legend('topleft', legend=c('all','copper', 'zinc'),
       pch=c(20,19,19),col=c('black','red','blue'))
```

zonal.stats *zonal.stats*

Description

Polygon zonal statistics of a raster

Usage

```
zonal.stats(x, y, stats = c("min", "mean", "max"))
```

Arguments

x	Polygon object of class SpatialPolygonsDataFrame
y	rasterLayer object of class raster
stats	Statistic or function

Value

data.frame, nrow(x) and ncol of function results

Note

This function calculates the zonal statistics between a polygon vector object and a raster. This provides the advantage of being able to accept any custom function, passed to the 'stats' argument. Please note that any custom function needs to have a 'na.rm' argument.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org>

Examples

```
library(raster)
library(sp)

# skewness function
skew <- function(x, na.rm = FALSE) {
   if (na.rm) x <- x[!is.na(x)]
   sum( (x - mean(x)) ^ 3) / ( length(x) * sd(x) ^ 3 )
  }

# percent x >= p function
pct <- function(x, p=0.30, na.rm = FALSE) {
  if ( length(x[x >= p]) < 1 )  return(0)
    if ( length(x[x >= p]) == length(x) ) return(1)
     else return( length(x[x >= p]) / length(x) )
}
```

```
# create some example data
p <- raster(nrow=10, ncol=10)
  p[] <- runif(ncell(p)) * 10
    p <- rasterToPolygons(p, fun=function(x){x > 9})
      r <- raster(nrow=100, ncol=100)
        r[] <- runif(ncell(r))
plot(r)
  plot(p, add=TRUE, lwd=4)

# run zonal statistics using skew and pct functions
z.skew <- zonal.stats(x = p, y = r, stats = "skew")
z.pct <- zonal.stats(x=p, y=r, stats = "pct")
  ( z <- data.frame(ID = as.numeric(as.character(row.names(p@data))),
                    SKEW=z.skew, PCT=z.pct) )
```

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