Package ‘GeNetIt’

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Type Package

Title Spatial Graph-Theoretic Genetic Gravity Modelling

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Description Implementation of spatial graph-theoretic genetic gravity models. The model framework is applicable for other types of spatial flow questions. Includes functions for constructing spatial graphs, sampling and summarizing associated raster variables and building unconstrained and singly constrained gravity models.

Depends R (>= 3.6.0)

Imports exactextractr, methods, nlme, sp, spdep, raster, rgeos, sf

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URL `https://github.com/jeffreyevans/GeNetIt`

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RoxygenNote 7.1.0

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R topics documented:

`area.graph.statistics` *Statistics for edges (lines) based on a defined scale (area).*

Description

Samples rasters for each edge and calculates specified statistics for buffer distance

Usage

```
area.graph.statistics(...)
```

Arguments

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

Note

Please note that this function has been deprecated, please use graph.statistics with the buffer argument.

`build.node.data` *Build node data*

Description

Helper function to build the origin/destination node data structure.

Usage

```
build.node.data(x, group.ids, from.parms, to.parms = NULL)
```

Arguments

`x`	A data.frame containing node (site) data
`group.ids`	Character vector of unique identifier that can be used to join to graph
`from.parms`	Character vector of independent "from" variables
`to.parms`	Character vector of independent "to" variables. If NULL is the same as from.parms

Value

data.frame

Note

Unless a different set of parameters will be used as the destination (to) there is no need to define the argument "to.parms" and the "from.parm" will be used to define both set of parameters.

The resulting data.frame represents the origin (from) and destination (to) data structure for use in gravity model. This is node structure is also know in the gravity literature as producer (from) and attractor (to).

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

Examples

```
data(ralu.site)

# Build from/to site (node) level data structure
site.parms = c("AREA_m2", "PERI_m", "Depth_m", "TDS")
site <- build.node.data(ralu.site@data, group.ids = c("SiteName"),
                        from.parms = site.parms )
```

`compare.models` *Compare gravity models*

Description

Prints diagnostic statistics for comparing gravity models

Usage

```
compare.models(...)
```

Arguments

`...`	gravity model objects

Details

Results include model name, AIX, BIC, log likelihood, RMSE and number of parameters

Value

data.frame of competing model statistics

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

Examples

```
library(nlme)
  data(ralu.model)

x = c("DEPTH_F", "HLI_F", "CTI_F", "cti", "ffp")
( null <-  gravity(y = "DPS", x = c("DISTANCE"), d = "DISTANCE",
                 group = "FROM_SITE", data = ralu.model, method = "ML") )

( gm_h1 <- gravity(y = "DPS", x = x, d = "DISTANCE", group = "FROM_SITE",
                 data = ralu.model, ln = FALSE, method="ML") )
( gm_h2 <- gravity(y = "DPS", x = x[1:3], d = "DISTANCE", group = "FROM_SITE",
                data = ralu.model, ln = FALSE, method="ML") )
( gm_h3 <- gravity(y = "DPS", x = x[c(4:5)], d = "DISTANCE", group = "FROM_SITE",
                data = ralu.model, ln = FALSE, method="ML") )

compare.models(null, gm_h1, gm_h2, gm_h3)
```

`dmatrix.df` *Distance matrix to data.frame*

Description

Coerces distance matrix to a data.frame object

Usage

```
dmatrix.df(x, rm.diag = TRUE)
```

Arguments

`x`	Symmetrical distance matrix
`rm.diag`	(TRUE/FALSE) remove matrix diagonal, self values.

Value

data.frame object representing to and from values

Note

Function results in data.frame object with "X1" (FROM), "X2" (TO) and "distance" columns. The FROM column represents to origin ID, TO represents destination ID and distance is the associated matrix distance. These results can be joined back to the graph object using either the origin or destination ID's.

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

Examples

```
library(sp)
pts <- cbind( x=runif(15, 480933, 504250), y=runif(15, 4479433, 4535122))
  pts <- SpatialPointsDataFrame(pts,
           data.frame(ID=paste(”ob”,1:nrow(pts),sep=””)))

# Create distance matrix
dm <- spDists(pts, pts)
  colnames(dm) <- pts@data[,”ID”]
  rownames(dm) <- pts@data[,”ID”]

# Coerce to data.frame with TO and FROM ID's and associated distance
dm.df <- dmatrix.df(dm)
  head(dm.df)
```

`dps`

dps genetic distance matrix for Columbia spotted frog (Rana luteiventris)

Description

Subset of data used in Murphy et al., (2010)

Format

A 29 x 29 genetic distance matrix:

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

`flow` *Convert distance to flow*

Description

Converts distance to flow (1-d) with or without data standardization

Usage

```
flow(x, standardize = FALSE, rm.na = FALSE, diag.value = NA)
```

Arguments

`x`	A numeric vector or matrix object representing distances
`standardize`	(FALSE/TRUE) Row-standardize the data before calculating flow
`rm.na`	(TRUE/FALSE) Should NA's be removed, if FALSE (default) the will be retained in the results
`diag.value`	If x is a matrix, what diagonal matrix values should be used (default is NA)

Value

A vector or matrix representing flow values

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

Examples

```
#### On a distance vector
flow(runif(10,0,1))
flow(runif(10,0,500), standardize = TRUE)

# With NA's
d <- runif(10, 0,1)
  d[2] <- NA
flow(d)
flow(d, rm.na=TRUE)

#### On a distance matrix
dm <- as.matrix(dist(runif(5,0,1), diag = TRUE, upper = TRUE))
flow(dm)
```

`graph.statistics` *Point sample and statistics for edges (lines)*

Description

Samples rasters for each edge and calculates specified statistics

Usage

```
graph.statistics(x, r, stats = c("min", "mean", "max"), buffer = NULL)
```

Arguments

`x`	sp SpatialLinesDataFrame or sf LINE object
`r`	A rasterLayer, rasterStack or rasterBrick object
`stats`	Statistics to calculate. If vectorized, can pass a custom statistic function.
`buffer`	Buffer distance, radius in projection units. For statistics based on edge buffer distance

Value

data.frame object of statistics

Note

...

Examples

```
 library(sp)
 library(spdep)
 library(raster)
   data(rasters)
   data(ralu.site)

 xvars <- stack(rasters)

  dist.graph <- knn.graph(ralu.site, row.names = ralu.site$SiteName,
                          max.dist = 1500)
   str(dist.graph@data)

 skew <- function(x, na.rm = TRUE) {
           if (na.rm) x <- x[!is.na(x)]
           sum( (x - mean(x)) ^ 3) / ( length(x) * sd(x) ^ 3 )
  }

# Moments on continuous raster data
```

```
 system.time( {
  stats <- graph.statistics(dist.graph, r = xvars[[-6]],
               stats = c("min", "median", "max", "var", "skew"))
 } )

# Proportional function on nominal raster data
p <- function(x) { length(x[x < 52]) / length(x) }

  system.time( {
   nstats <- graph.statistics(dist.graph, r = xvars[[6]],
                stats = "p")
  } )

# Based on 500m buffer distance around line(s)
 system.time( {
  stats <- graph.statistics(dist.graph, r = xvars[[-6]],
               stats = c("min", "median", "max", "var", "skew"),
  buffer = 500)
 } )

 dist.graph@data <- data.frame(dist.graph@data, stats, nstats)
   str(dist.graph@data)
```

`gravity` *Gravity model*

Description

Implements Murphy et al., (2010) gravity model

Usage

```
gravity(y, x, d, group, data, ln = TRUE, constrained = TRUE, ...)
```

Arguments

`y`	Name of dependent variable
`x`	Character vector of independent variables
`d`	Name of column containing distance
`group`	Name of grouping column (from or to)
`data`	data.frame object containing model data
`ln`	Natural log transform data (TRUE/FALSE)
`constrained`	Specify constrained model, if FALSE a linear model (lm) is run (TRUE/FALSE)
`...`	Additional argument passed to nlme or lm

Details

The "group" factor defines the singly constrained direction (from or to) and the grouping structure for the origins. To specify a null (distance only or IBD) model just omit the x argument.

By default constrained models are fit by maximizing the restricted log-likelihood (REML), for maximum likelihood use the type="ML" argument which is passed to the lme function. If ln=TRUE the input data will be log transformed

Value

formula Model formula

gravity Gravity model

AIC AIC value for selected model

log.likelihood Restricted log-likelihood at convergence

x data.frame of independent variables

y Vector of dependent variable

groups Ordered factor vector of grouping variable

fit Model Fitted Values

Note

Depends: nlme, lattice

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

References

Murphy, M. A. & J.S. Evans. (in prep). GenNetIt: graph theoretical gravity modeling for landscape genetics

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

See Also

`groupedData` for how grouping works in constrained model

`lme` for constrained model ... options

`lm` for linear model ... options

Examples

```
library(nlme)
data(ralu.model)
str(ralu.model)

# Gravity model
```

```
x = c("DEPTH_F", "HLI_F", "CTI_F", "cti", "ffp")
( gm <- gravity(y = "DPS", x = x, d = "DISTANCE", group = "FROM_SITE",
                data = ralu.model, ln = FALSE) )

# Plot gravity results
 par(mfrow=c(2,3))
   for (i in 1:6) { plot(gm, type=i) }

# log likelihood of competing models
 x = c("DEPTH_F", "HLI_F", "CTI_F", "cti", "ffp")
 for(i in x[-1]) {
   x1 = c(x[1], x[-which(x %in% i)])
   ll <- gravity(y = "DPS", x = x1, d = "DISTANCE", group = "FROM_SITE",
                data = ralu.model, ln = FALSE)$log.likelihood
  cat("log likelihood for parameter set:", "(",x1,")", "=", ll, "\n")
 }

# Distance only (IBD) model
gravity(y = "DPS", d = "DISTANCE", group = "FROM_SITE",
        data = ralu.model, ln = FALSE)
```

`gravity.es` *Effect Size*

Description

Cohen’s D effect size for gravity models

Usage

```
gravity.es(x, actual.n = FALSE, alpha = 0.95)
```

Arguments

`x`	gravity model object
`actual.n`	(FALSE/TRUE) Use actual N or degrees of freedom in calculating Confidence Interval
`alpha`	confidence interval

Details

Calculate Cohen’s D statistic for each effect in a gravity model object

Value

data.frame of parameter effect size

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

Cohen, J. (1988) Statistical power for the behavioral sciences (2nd ed.). Hillsdale, NJ: Erlbaum

Examples

```
library(nlme)
  data(ralu.model)

x = c("DEPTH_F", "HLI_F", "CTI_F", "cti", "ffp")
gm_h1 <- gravity(y = "DPS", x = x, d = "DISTANCE", group = "FROM_SITE",
                data = ralu.model, ln = FALSE, method="ML")

gravity.es(gm_h1)
```

`knn.graph` *Saturated or K Nearest Neighbor Graph*

Description

Creates a kNN or saturated graph SpatialLinesDataFrame object

Usage

```
knn.graph(
  x,
  row.names = NULL,
  k = NULL,
  max.dist = NULL,
  sym = FALSE,
  long.lat = FALSE,
  drop.lower = FALSE
)
```

Arguments

`x`	sp SpatialPointsDataFrame object
`row.names`	Unique row.names assigned to results
`k`	K nearest neighbors, defaults to saturated (n(x) - 1)
`max.dist`	Maximum length of an edge (used for distance constraint)

`sym`	Create symmetrical graph (FALSE/TRUE)
`long.lat`	(FALSE/TRUE) Coordinates are longitude-latitude decimal degrees, in which case distances are measured in kilometers
`drop.lower`	(FALSE/TRUE) Drop lower triangle of matrix (duplicate edges)

Value

SpatialLinesDataFrame object with:

- i Name of column in x with FROM (origin) index
- j Name of column in x with TO (destination) index
- from_ID Name of column in x with FROM (origin) region ID
- to_ID Name of column in x with TO (destination) region ID
- length Length of each edge (line) in projection units or kilometers if long.lat = TRUE

Note

...

Author(s)

Jeffrey S. Evans jeffrey_evans@tnc.org and Melanie Murphy melanie.murphy@uwyo.edu

References

Murphy, M. A. & J.S. Evans. (in prep). "GenNetIt: gravity analysis in R for landscape genetics"

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

Examples

```
   library(sp)
   data(ralu.site)

 # Saturated spatial graph
 sat.graph <- knn.graph(ralu.site, row.names=ralu.site@data[,"SiteName"])
   head(sat.graph@data)

 # Distanced constrained spatial graph
 dist.graph <- knn.graph(ralu.site, row.names=ralu.site@data[,"SiteName"],
                         max.dist = 5000)

opar <- par(no.readonly=TRUE)
 par(mfrow=c(1,2))
plot(sat.graph, col="grey")
  points(ralu.site, col="red", pch=20, cex=1.5)
     box()
     title("Saturated graph")
plot(dist.graph, col="grey")
```

```
  points(ralu.site, col="red", pch=20, cex=1.5)
     box()
     title("Distance constrained graph")
par(opar)
```

`node.statistics` *raster statistics for nodes*

Description

returns raster value or statistics (based on specified radius) for node

Usage

```
node.statistics(x, r, buffer = NULL, stats = c("min", "median", "max"))
```

Arguments

`x`	sp class SpatialPointsDataFrame object
`r`	A rasterLayer, rasterStack or rasterBrick object
`buffer`	Buffer distance, radius in projection units
`stats`	Statistics to calculate. If vectorized, can pass a custom statistic function.

Value

data.frame object of at-node raster values or statistics

Note

If no buffer is specified, at-node raster values are returned

Examples

```
library(sp)
library(spdep)
library(raster)
  data(rasters)
  data(ralu.site)

xvars <- stack(rasters)

skew <- function(x, na.rm = TRUE) {
          if (na.rm) x <- x[!is.na(x)]
          sum( (x - mean(x)) ^ 3) / ( length(x) * sd(x) ^ 3 )
}
```

```
# without buffer (values at point)
system.time( {
 stats <- node.statistics(ralu.site, r = xvars[[-6]],
             stats = c("min", "median", "max", "var", "skew"))
} )

# with 1000m buffer (values around points)
system.time( {
 stats <- node.statistics(ralu.site, r = xvars[[-6]], buffer = 1000,
             stats = c("min", "median", "max", "var", "skew"))
} )

dist.graph@data <- data.frame(dist.graph@data, stats, nstats)
  str(dist.graph@data)
```

`plot.gravity` *Plot gravity model*

Description

Diagnostic plots gravity model with 6 optional plots.

Usage

```
## S3 method for class 'gravity'
plot(x, type = 1, ...)
```

Arguments

`x`	Object of class gravity
`type`	Type of plot (default 1, model structure I)
`...`	Ignored

Value

defined plot

Note

Plot types available: 1 - Model structure I, 2 - Model structure II, 3 - Q-Q Normal - Origin random effects, 4 - Q-Q Normal - Residuals , 5 - Fitted values, 6 - Distribution of observed verses predicted

Depends: nlme, lattice

Author(s)

Jeffrey S. Evans <jeffrey_evans@tnc.org> and Melanie Murphy <melanie.murphy@uwyo.edu>

References

Murphy, M. A. & J.S. Evans. (in prep). "GenNetIt: gravity analysis in R for landscape genetics"

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

`predict.gravity` *Predict gravity model*

Description

predict method for class "gravity"

Usage

```
## S3 method for class 'gravity'
predict(object, newdata, ...)
```

Arguments

`object`	Object of class gravity
`newdata`	New data, matching model parameters, used for obtaining the predictions
`...`	Arguments passed to predict.lme or predict.lm

Value

Model predictions

`print.gravity` *Print gravity model*

Description

summary method for class "gravity"

Usage

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

Arguments

`x`	Object of class gravity
`...`	Ignored

`ralu.model` *Columbia spotted frog (Rana luteiventris) data for specifying gravity model. Note, the data.frame is already log transformed.*

Description

Subset of data used in Murphy et al., (2010)

Format

A data.frame with 190 rows (sites) and 19 columns (covariates):

ARMI_ID Unique ID

FROM_SITE Unique from site ID

TO_SITE Unique to site ID

FST FST genetic distance

DPS DPS genetic distance

DISTANCE Graph edge distance

DEPTH_F At site water depth

HLI_F Heat Load Index

CTI_F Wetness Index

DEPTH_T At site water depth

HLI_T Heat Load Index

CTI_T Wetness Index

hli Heat Load Index

cti Wetness Index

ffp Frost Free Period

err27 Roughness at 27x27 scale

rsp Relative Slope Position

ridge Percent Ridge Line

hab_ratio Ratio of suitable dispersal habitat

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

`ralu.site`	*Subset of site-level spatial point data for Columbia spotted frog (Rana luteiventris)*

Description

Subset of data used in Murphy et al., (2010)

Format

A SpatialPointsDataFrame with 31 obs. of 17 variables:

SiteName	Unique site name
Drainage	Source drainage
Basin	source basin
Substrate	Wetland substrate
NWI	USFWS NWI Wetland type
AREA_m2	Area of wetland
PERI_m	Perimeter of wetland
Depth_m	Depth of wetland
TDS	...
FISH	Fish present
ACB	...
AUC	...
AUCV	...
AUCC	...
AUF	...
AWOOD	...
AUFV	...

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

`rasters` *Subset of raster data for Columbia spotted frog (Rana luteiventris)*

Description

Subset of data used in Murphy et al., (2010)

Format

A raster RasterStack:

rows 426

columns 358

resoultion 30 meter

projection "+proj=utm +zone=11 +datum=NAD83 +units=m +no_defs +ellps=GRS80 +towgs84=0,0,0"

cti Compound Topographic Index ("wetness")

err27 Elevation Relief Ratio

ffp Frost Free Period

gsp Growing Season Precipitation

hil Heat Load Index

nlcd USGS Landcover

References

Murphy M.A., R. Dezzani, D.S. Pilliod & A.S. Storfer (2010) Landscape genetics of high mountain frog metapopulations. Molecular Ecology 19(17):3634-3649

`summary.gravity` *Summarizing Gravity Model Fits*

Description

Summary method for class "gravity".

Usage

```
## S3 method for class 'gravity'
summary(object, ...)
```

Arguments

`object`	Object of class gravity
`...`	Ignored

Note

Summary of lme or lm gravity model, AIC, log likelihood and Root Mean Square Error (RMSE) of observed verses predicted

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